universität wien

DISSERTATION

Titel der Dissertation

Evolutionary Mechanics – From a Variational Principle to Applications

angestrebter akademischer Grad

Doktor/in der Naturwissenschaften (Dr. rer.nat.)

Verfasserin / Verfasser:	Mag. Peter Klimek
Matrikel-Nummer	0003615
Dissertationsgebiet (lt. Studienblatt):	A 091 411 Dr.-Studium der Naturwissenschaften Physik UniStG
Betreuerin / Betreuer:	O. Univ. Prof. DDr. Stefan Thurner

Wien am 17. November 2009

For Zita

Abstract

Evolution in its modern sense is the dynamical description of a system composed of a vast number of elements whose abundances change over time due to the accumulated interplay of interactions between them. This reasoning applies in a multitude of contexts, be it biological, ecological, economical or social, and gives rise to the observations that evolutionary systems are subject to continual variations under selective forces.

Traditional evolutionary approaches to study these systems can be divided into two classes. Their behavior can be modelled directly in the framework of differential equations, which makes it necessary to prestate each possible interaction. In this framework it is hard or even impossible to account for one of the main ingredients of evolutionary systems, the never-ending production of innovations. Secondly, more abstract and stylized models are studied relying to a large extend on *ad hoc* assumptions about the evolutionary processes at work. Thus they do not contribute to our understanding of how observed effects like punctuated equlibria and evolutionary phase transitions emerge from first principles.

In this work we propose a statistical physics model aimed at bringing together the 'best of both worlds'. We adopt a diversity framework which makes it possible to formalize the most general evolutionary interactions in a paradigmatic way. For these interactions (and also for a much larger class of dynamical systems) we develop a variational principle allowing us to employ the statistical mechanics machinery. The asymptotic diversity of such systems is worked out analytically in the mean field approximation, other key observables are quantitatively assessed. We succinctly incorporate specifying assumptions in our model and test its prediction against real world data in economic, biological and social settings.

Abstrakt

Evolution im modernen Sinn ist die dynamische Beschreibung eines Systems, welches aus einer sehr großen Anzahl von Elementen besteht, deren relative Häufigkeit sich durch das Zusammenspiel von Wechselwirkungen zwischen ihnen ändert. Dieses Verständnis kann in einer Vielfalt von Zusammenhängen angewendet werden, sei es biologisch, ökologisch, ökonomisch oder sozial, und führt zu den Beobachtungen dass diese Systeme ständig Variationen hervorbringen und selektiven Kräften unterliegen.

Untersuchungen von evolutionären Systemen kann man in zwei Klassen einteilen. Ihr Verhalten kann mit Hilfe von Differentialgleichungen direkt modelliert werden, dies erfordert es jedoch jede mögliche Wechselwirkung im vorhinein zu spezifizieren. Dadurch ist es schwer, wenn nicht unmöglich, eine der Haupteigenschaften von evolutionären Systemen zu beschreiben, die fortwährende Produktion von Innovationen. Zweitens kann man abstraktere und stilisiertere Modelle untersuchen, die dann zu einem großen Teil auf *ad hoc* Annahmen über die vorliegenden evolutionären Prozesse beruhen. Dadurch tragen sie nicht dazu bei unser Verständnis davon zu erweitern, wie beobachtete Effekte wie punktuierte Gleichgewichte und evolutionäre Phasenübergänge von grundlegende Prinzipien aus emergieren.

In dieser Arbeit schlagen wir ein Modell der statistischen Physik vor, welches darauf abzielt das 'Beste beider Welten' zu vereinigen. Wir verwenden eine Diversitätsbeschreibung die es ermöglicht die allgemeinste Form von evolutionären Wechselwirkungen paradigmatisch zu formulieren. Für diese Wechselwirkungen (und auch für eine wesentlich größere Klasse von dynamischen Systemen) entwickeln wir ein Variationsprinzip durch welches wir Ergebnisse und Methoden der Statistischen Mechanik benützen können. Die asymptotische Diversität solcher Systeme kann in einer Mean Field Näherung analytisch berechnet werden, andere wichtige Observable werden quantitativ ausgewertet. Wir bauen dann schrittweise spezifizierende Annahmen in unser Modell ein und testen seine Vorhersagen an gemessenen Daten aus ökonomischen, biologischen und sozialen Umfeldern.

Acknowledgments

I am greatly indebted to numerous people for giving me assistance, guidance or personal withstanding throughout the time which scientific results constitute this work.

First of all I thank my parents Eva and Manfred for their effort and dedication in opening up the possibility for me to pursue and complete my academic education. This thesis reflects their striving and endorsing to allow my brother and me to choose between options they never had.

I gratefully acknowledge the continual motivation, technical support and personal guidance I received from my supervisor Stefan Thurner. The thematic diversity of this work is also the result of him giving me the freedom to engage in and animate my own research ideas within his group. I hope I was able to pay this confidence back.

An infinite source of inspiration and competent advices to me was Rudolf Hanel. Without his intuitive insights large parts of this thesis would still cause me head-scratching – at least much more than they do now. I have to thank also all other colleagues of me for their support at the Complex Systems Research Group and for making my time here as enjoyable as one could hope for, I thank especially Dejan Stokic, Christoly Biely and Michael Szell.

Contents

Outline

This thesis compiles the published work of [1, 2, 3, 4, 5, 6] which contains the research efforts of my two and a half year stay at the Complex Systems Research Group in cooperation with Stefan Thurner, Rudolf Hanel and Renaud Lambiotte. We bring these research efforts here into a coherent picture which reflects how we understand and think of systems subject to evolution – a picture that sparked broad media interest. In particular we acknowledge the coverage by various BBC radios (World Service, Radio 5, Scotland), as well as OE1, and the numerous articles and editorials published for example in New Scientist, Nature News, Nature Physics, Sunday Times, Daily Telegraph, Moscow Times, Berliner Morgenpost, Standard, Wirtschaftblatt and Geo which helped in disseminating our ideas.

The structure of this work is as follows. After an informal historical introduction into evolutionary thinking in chapter 0 we turn to an extensive literature review and introduce the diversity framework in chapter 1. The general evolutionary interaction schemes are formulated in chapter 2. In chapter 3 we propose a variational principle for evolutionary systems, this part is not yet published, the manuscript is currently in preparation. In the latter chapters we discuss the orignal and published research results of [1, 2, 3, 4, 5, 6]. In chapter 4 we describe Schumpeterian economics as a quantifiable model of evolution [6]. We then discuss our model in a biological setting in chapter 5 based on [3]. We study the evolution of beliefs in chapter 6 as done in [1]. As a light-hearted but yet interesting application we bring our ideas to the field of governance in chapter 7 based on [4, 5]. We conclude with a summary in chapter 8.

0 Evolution of Evolution

Wherever then all the parts came about
just the way they would have been if they had come to be for an end,
such things survived, being organized spontaneously in a fitting way;
whereas those which grew otherwise perished and continue to perish.
Aristotle, 350 BC

It would not be a bold conjecture to claim that there is no school of thought which can not be traced back to the ancient Greeks. Let us make the case for evolutionary thought.

0.1 Pre-Darwin

One of the first documented evolutionary ideas is that life originated in deep sea and moved on to land later, as described by Anaximander (610-546 BC). It was Empedocles (490-430 BC) who was among the first to contemplate a non-supernatural origin for all living beings [7]. Aristotle (384-322 BC) devoted four volumes to natural history comprising research he conducted on and around the isle of Lesbos [8]. One of his remarkable results is the introduction of a hierarchical organization of living beings into his *scala naturae* ('Ladder of Life'), where immutable organisms are ranked according to the complexity of their structure, e.g. their ability to move. The field of evolution was therefore started already 2500 years before a certain Englishman's book would formulate biology's unifying central dogma.

Greek evolutionary ideas died out in Europe after the fall of the Roman Empire but were preserved and elaborated on in the Islamic world. During contact in the 12^{th}century Greek writings have been re-introduced in the West and triggered a vast number of Latin translations. Christian thinkers like Abelard and Aquinas combined Aristotle's views with the work of Plato. The latter earned himself a reputation as the 'anti-hero of evolution'. He claimed that all animal life forms in the real world are reflections of eternal ideas or essences; variations are due to imperfections of these reflections. This was combined with biblical *Genesis* and resulted in a *scala naturae* with God as the most complex being and Hell at the other end of the 'Ladder of Life' [9]. In between was a perfect chain of all known life forms with no empty links, all species could be represented by exactly one link. According to *Genesis* they remain forever fixed at their position and can never change. That is why it was sinful for humans to act like lower animals or equally seek a higher position, this would cut across the Christianized version of Plato's perfect universe.

The term 'evolution' made its first appearances in the Renaissance and Enlightenment of the $17^{\text{th}}$and 18^{th}century when the work by Rene Descartes fostered a mechanistic world view [10]. The emergence of physical sciences with the works of Galileo and Newton led scholars to think about natural history in terms of material processes. The dominating contemporary view held that evolution was a spiritual process. In fact, the term evolution was first used by Sir Matthew Hale by arguing against such non-spiritual mechanisms, claiming that it is absurd to think that the senseless collision of dead atoms bears the potential to lead to highly developed mammals [11]. Therefore, following Hale, these collisions must have the principles of the configuration of these life forms *in evolution* (from the Latin *evolutio*, 'to unroll like a scroll') which is absurd without divine interference. One of these absurdly theorizing thinkers was Erasmus Darwin, Charles Darwin's grandfather. He put forward that the great variety of living beings could have arisen from a few number of organisms, as described in his poem *Temple of Nature* [12];

First forms minute, unseen by spheric glass,
Move on the mud, or pierce the watery mass;
These, as successive generations bloom,
New powers acquire and larger limbs assume;
Whence countless groups of vegetation spring,
And breathing realms of fin and feet and wing.

Pre-Darwinian evolutionary theories of the 19$^{\text{th}}$century refused the idea of immutable species and advocated that some species share a common ancestor. Maybe the most notable example of such a theory is Lamarckian evolution (after Jean-Baptiste Lamarck), which proposes that simple life forms were generated spontaneously and, driven by an innate life force, complexify and adapt to their environment [13]. This was assumed to happen in a linear, ascending manner with man as the the pinnacle of evolution. This progressive transmutation of species became widely popular by the anonymously published book *Vestiges of the Natural History of Creation* by Robert Chambers [14] but suffered harsh critique from scholar circles, in part due to the lack of concrete materialistic processes guiding this complexification.

The belief that simple life forms could be generated spontaneously from inanimate matter was kept upright until the mid 19$^{\text{th}}$-century. This theory, which was first compiled from prior natural philosophers by Aristotle, was later subjected to empirical investigations. Most notably, Jan Baptist van Helmont (1580 1644) describes a recipe for mice (a piece of soiled cloth plus wheat for 21 days) and scorpions (basil, placed between two bricks and left in sunlight) [15]. Ultimately cell theory superseded spontaneous generation when Charles Cagniard de la Tour and Theodor Schwann observed cell division in yeast and Louis Pasteur conducted experiments which ruled out each other possible mechanism [16].

0.2 Darwin

Picture a young Englishman in the first half of the 19$^{\text{th}}$century [17]. His father wants him to study medicine – he finds the lectures dull and surgery distressing. He shares great interest in geology, where academic circles are currently deeply engaged in a controversial debate over the origin of minerals and rocks – neptunism (rocks formed from water) versus plutonism (from fire). He comes in touch with radical materialistic theories such as Lamarck's and rediscovers the work of his grandfather, but stays indifferent whether to accept such a line of reasoning.

His father, however, is deeply unsatisfied with him neglecting medical studies and sends him to Cambridge to become an Anglican parson. But first he prefers to spend his time riding, hunting and collecting beetles. The latter hobby brings him in touch with this time's leading biologists which saw scientific work as a religious discipline. He becomes deeply engaged in natural theology and works on the divine guidance of the adaptation of life forms.

Let us hold in here and point out that we are talking about a very diligent young Englishman. Later in his life, when he was facing the decision

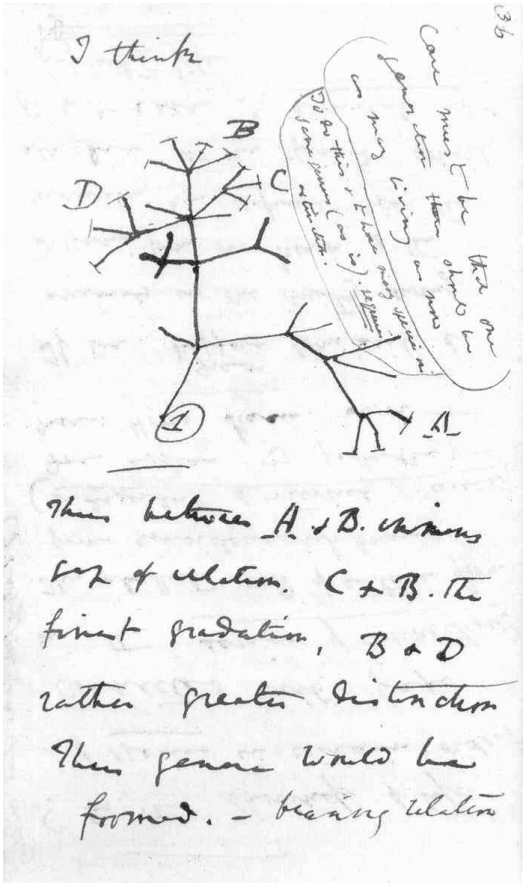

Figure 0.1: Excerpt from Charles Darwin's notebook (July 1837). Under the words 'I think' he pictured the first evolutionary tree.

Table 0.1: Transcription from one of Charles Darwin's notebooks where he contemplates whether to marry or not. He proofs the answer to be to marry.

This is the question

marry	not marry
• Children – if it Please God • Constant companion (& friend in old age) who will feel interested in one • object to be loved & played with • better than a dog anyhow • Home, & someone to take care of house • Charms of music & female chit - chat • These things good for one's health	• Freedom to go where one liked • choice of Society & little of it • Conversation of clever men at clubs • Not forced to visit relatives, & to bend in every trifle • anxiety of children • perhaps quarrelling • Loss of time • cannot read in the Evenings • fatness & idleness • anxiety and responsibility • less money for books • if many children forced to gain one's bread

Marry – Marry – Marry Q.E.D.

if to marry or not, he would assemble a list with pros and cons, see Tab. 0.1. After compiling these lists he weighs the argument that his wife might not like to live in London (which implies the sentence to degrade into an indolent, idle fool) against a life with only working, working, and nothing after all. This led Charles Darwin (1809-1882) finally to the proof that marrying is the better option. With this decision being reached, thinking didn't stop. 'It being proved necessary to Marry', he went on in his notebooks, 'When? Soon or Late'. We skip this discussion here, but these notes are conjectured to be written six months before his marriage with his cousin Emma Wedgwood.

Now it should be obvious that when such a diligent man faces the question of the creation of life, he would not be satisfied dwelling on books inside the university, instead he went on a voyage aboard the *H.M.S. Beagle* to chart the coastline of South America. With this trip around the world he could not only pursue his fondness of geological studies, he was searching for nothing less than the unique cradle of creation from which all life had spread around the globe.

Alone, what he found during this voyage did not correspond well with the thesis of a centre of creation. On the Galapagos islands he found tortoise shells to vary from island to island. Each island had each own race of mockingbirds. The fauna of Australia seemed so strange to him that

he was wandering if there was not a second creator at work. In South America he found fossils of a recently extinct animal resembling a giant armadillo but no evidence for a catastrophic event which might have triggered this extinction. One year after the return of the *Beagle* in 1836 he started two notebooks on the transmutation of species, one of which contained the first drawing of an evolutionary tree, see Fig.0.1. He played this close to the chest and continued to publish on geological issues, what has already brought him to the status of a scientific celebrity by then.

Secretly, he kept on working on his theory of transmutation. He seeked the advice of breeders concerning their experience with the variability of life. A pigeon breeder, for example, told Darwin that he could produce him any given feather within three years, but need six years to obtain head and beak. One key point in his theory, however, was still missing.

In 1838 he read 'for amusement' Thomas Robert Malthus '*An Essay On The Principle Of Population*' [18], one of this time's most influential books. In it the Anglican clergyman Malthus proposes the exponential growth model of populations, i.e. let $P(t)$ be the size of a population at time t, then starting with initial population P_0 and growth rate λ the population will grow according to $P(t) = P_0 \mathrm{e}^{\lambda t}$. Since the earth possesses only a limited capacity to sustain human life, he outlined the potential danger of population growth by predicting catastrophic consequences when the carrying capacity will finally be reached, as e.g. wars over resource. Shortly afterwards Pierre Francois Verhulst, after reading Malthus, worked out that in the presence of restricted resources the population will grow according to the logistic function $P(t) \propto (1 + e^{-t})^{-1}$ [19], thereby Malthus started the field of population ecology.

When Darwin read Malthus' treatise, he realized that he had now a strong formal tool at hands with which he could formulate his theories. As species breed beyond the available resources in wildlife, a struggle for existence will be the consequence which selects favorable variations of the descendants; he finally had a materialistic, non-spiritual mechanism at hands. He slowly began to understand its power by explaining the abundance of observations concerning the geographical distribution of species he made on his five year trip aboard the *Beagle*.

For twenty years he worked on the adaptation and variation of species without publishing a word of it, only discussing his idea with some close colleagues. Darwin was well aware of the harsh critiques other theories of transmutation, such as the *Vestiges* and Lamarckian evolution, were exposed to. When he received a manuscript by Alfred Russell Wallace containing the main ingredients of the very same theory he was working on for two decades, he quickly decided to go for a joint publication with Wallace. Thus his book *On the Origin of Species by Means of Natural Selection, or The Preservation of Favoured Races in the Struggle for Life* went in bookstores on 22 November, 1859 [20]. Thanks to the advocacy of some of his colleagues the theory of natural selection quickly diffused into scientific mainstream of the English speaking countries. It triggered a small epistemological revolution by providing the first cogent, non-spiritual and detailed mechanism able to account for a wealth of by then known facts about bio-geography. His notions were also quickly adopted in Germany with the work of August Weismann and Ernst Häckel, France, Southern Europe and Latin America followed later. By the end of the 19^{th}century transmutation of species was widely accepted, upon its driving force, whether it was natural selection or alternatives, less agreement was reached until the next quantum leap in the evolution of evolution was reached.

0.3 Post-Darwin

With the widespread acceptance of the transmutation of species the biology community split up into two factions. In one corner were the Mendelians, which advocated the discrete nature of variations fueled by the rediscovery of Gregor Mendel's laws of inheritance. In the other corner, the biometricians rejected discrete units of heredity and measured and subjected the gradual variations within a population to a statistical analysis. Both camps were reconciled with the groundbreaking work of Ronald A. Fisher around the 1920s, showing that natural selection

can change gene frequencies and the interplay of many genes can lead to continuous variations [21]. J.B.S. Haldane applied this theory to real-world examples [22] and Wright introduced the concept of an adaptive landscape on which a population moves around due to genetic drift and via variations eventually spreads out on to different adaptive peaks [23].

In subsequent decades the so-called modern evolutionary synthesis took place. The emphasis was more and more put on natural selection than on genetic drift. Field-biologists closely examined geological and local environmental factors and the actual genetic diversity of wildlife populations. Botany and paleobiology were also reformulated in a unified, evolutionary framework – the modern evolutionary synthesis, tyeing together many, if not all, biological disciplines. By 1950 natural selection acting on genetic variations was the only feasible and plausible mechanism of evolution.

The 1940s to 1960s saw the rise of molecular biology accompanied with the discovery of the DNA and the actual units of heredity – molecular evolution entered the picture. This gene-centered view reached its climax in the late 20^{th}century with works such as Richard Dawkins' *The Selfish Gene* [24] which relies on work on kin selection by W.D. Hamilton [25], John Maynard Smith [26] and George R. Price [27]. In the gene-centered view of evolution the molecular, i.e. genetic level has become the only level on which evolution takes place and each other description level of (organizations of) organism can be bootstrapped from it.

0.4 Evolution leaking out

From the very beginning the evolution of evolution (in the modern sense) was closely intertwined with sociological studies. In fact the underlying formal framework, Malthus' exponential growth model, stemmed from this research area. Especially the work on kin selection (i.e. how altruistic behavior of living beings can be understood through genetic factors) started the fields of sociobiology and evolutionary psychology. Evolution became a theoretical framework not only to study the origin of animals and humans, but also their behavior.

With the advent of more powerful hardware and software more and more complex evolutionary models could be studied and their predictions could be tested against ever growing amounts of data – the fields of systems biology and various Omics were started. Consequently the development of algorithms itself was subjected to evolution; algorithms get automatically modified and checked whether they perform certain tasks better. Taking this analogy even further, studies in artificial life try to mimick and understand biological evolution in terms of a huge computer simulation. Today, it transpires, technological development is nothing else than an instance of evolution.

The theory of evolution is currently thought of as not a theory in a strict scientific sense, but as a catalogue of observations, a phenomenology, regarding the development of systems composed of a large number of highly interdependent units. Whatever the actual realization of these units might look like – be it species, human individuals, MP3-players, algorithms or the idea of evolution – they come into existence through the interaction of other units and vanish after possibly contributing to the origin of yet another units. Whatever the actual characteristics of the interdepence might be – the units compete for natural or economic resources, computing time or the wealth of observation they are able to explain, get accordingly selected and thereby influence the selection of other units. The scope of these processes gets constantly enlargened. If we want to make headway in the understanding of evolution we have to be aware that we are dealing with the description of ubiquitious phenomena. We are describing a constantly shape-shifting flow of abstract entities, progressively producing and discarding innovations, undergoing gentle changes over time, accumulating them to seemingly erratic collective reorganizations.

0.5 Re-picturing evolution

The emerging understanding of the universality of evolutionary processes guiding the development of large, interconnected systems, the ever growing area of application of selection under competition for resources, makes it advantageous to re-cast evolution in more general terms, applicable to arbitrary fields of research. Let us call the basic units composing the system we aim to describe simply items – these items may be species, individuals, molecules, technological artefacts,... Note that these items, especially in biological applications, may but need not be identical to the units of inheritance.

There are three possible relationships between two randomly picked items: An item may benefit or suffer from the existence of another one or there may be no relation at all. Consider a parasite: it benefits from the existence of a host who in turn suffers from the parasite, as can be measured directly via the organisms' reproduction rate. Consider a chemical reaction $A_1 + A_2 \rightarrow B$, the chemical species B benefits from A_1 and A_2 as can be measured by its concentration $[B]$, whereas $[A_1]$ and $[A_2]$ decline. Or consider the semiconductor industry driving economic growth in the electronic market: both players benefit from each other. This can be directly assessed by its market value: in 2004 the semiconductor industry was a market of $ 213 billion and enabled the generation of approximately $ 1200 billion in electronic system businesses and $ 5000 billion in turn in services which amounts to 10% of world GDP [28]. However, for the vast majority of items there is no direct relationship: Lower Austria's asparagus production will be relatively unaffected by whether HD or Blu-Ray is chosen as standard for high definition video.

If item A benefits from the existence of item B we call B a *complement* for A henceforth. If B's existence is disadvantageous for A we call it a *substitute* for A [29]. Both, complements and substitutes, can be sets of items, rather than a single one. As a trivial example consider again the chemical reaction $A_1 + A_2 \rightarrow B$. The reaction will not take place if A_1 or A_2 is not available. This is to say, B is a substitute for the set $\{A_1, A_2\}$, but not for A_1 or A_2. This gives us a first hint at where one of the key difficulties lies in a general treatment of evolutionary systems. Items are manifestly *contextual*, i.e. the functional role of an item depends crucially on which items exist in its surrounding – its context. In the context of only A_1, for example, B has no relationship to A_1. If item A_2 comes into existence, B is enabled to serve as substitute for $\{A_1, A_2\}$. Thus the functional relationship between A_1 and B can only be determined in the context of A_2.

A reader who is familiar with chemical kinetics will not be surprised by this observation and maybe wonder why we adopt such an outlandish vocabulary for noting that the laws of mass action are non-linear. This vocabulary becomes handy when we turn to a less obvious question which, however, is one of the essential features of systems subject to evolution: How is a system driven by innovations?

Consider a large collection of existing items, for example Australian fauna and flora, chemicals in a pre-biotic pond or the set of all patents listed by the European Patent Office. Within this set of items, all complements and substitutes can be joined by lines. Now consider the set of all complements and substitutes which can possibly be produced from this already existing net within one step . We call this set the *adjacent possible* . If we introduce an item X from the adjacent possible into the existing net the contextual nature of the yet existing items comes into play. Item X can now serve as complement or substitute, as well as get complemented or substituted by any combination of existing items. Depending on if the beneficial influences outweigh the disadvantageous influences item X might survive or not – selection at work. If it gets selected it has ultimately changed the context of each other existing item and from this new context a yet new adjacent possible can be constructed. Even more, within this new context some of the existing items may lose their functionality and not be sustainable any more. Thus the introduction of some new items may provoke a cascade of creations but a cascade of destructions as well – a phenomenon referred to as Schumpeterian gales of destruction [30].

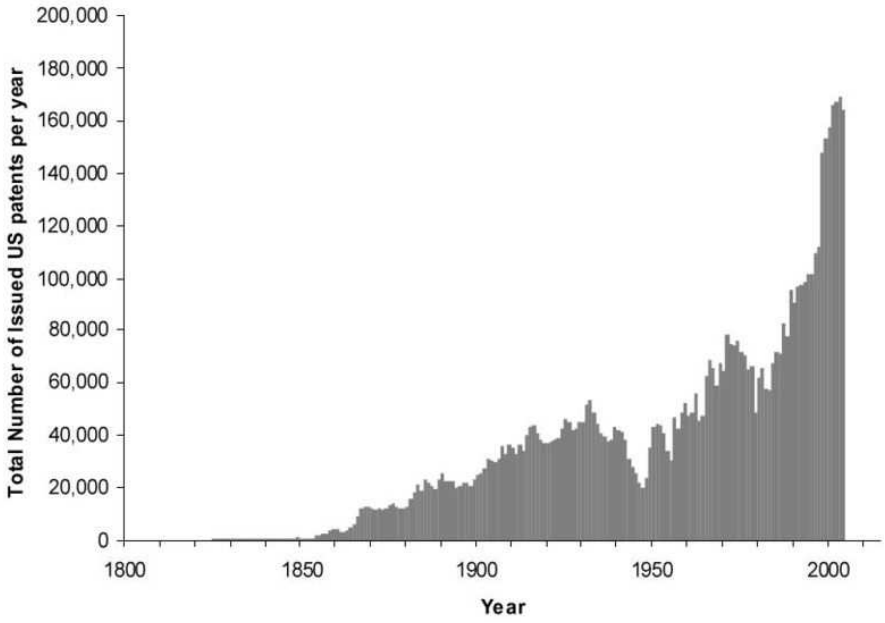

Figure 0.2: Number of all U.S. patents in the period 1800-2004.

In this manner a system may enter a never-ending chain of innovations and accompanying destructions which constantly alter the conditions under which newly produced and already existing items are to be assessed. On the other hand if the set of existing items is too small to allow an item from the adjacent possible to be a substitute or complement – or if the adjacent possible contains no items at all – the system will not produce any innovations. We call a system possessing the former characteristics *supracritical* and a system without the ability to produce innovations *subcritical*. As an example for a supracritical system consider the number of all patents listed in the U.S. Patent Office, see Fig.0.2, data from [31]. An exponential proliferation of technological innovations is clearly visible. Compare this observation to a list of innovated technologies within indigenous knowledge of an aboriginal people over the same timespan, this corresponds to a subcritical system.

To summarize these first crude sketches of a formal theory of evolutionary mechanics, we picture a system subject to evolution as a collection of items which can be replicated and/or recombined to produce new items – innovations. The introduction of this item can have a beneficial or suppressive influence on other, already existing items. We can quantify this influence by considering the differential change of all influences which get re-interpreted in the context of this new item, we thus obtain a fitness- or utility function from first principles. A rigorous formalization of these concepts and a detailed study of the dynamic of innovation-driven evolutionary systems is the goal and main result of this thesis.

1 Evolutionary dynamics unified

...it was Darwins chief contribution,
not only to Biology but to the whole of natural science,
to have brought to light a process by which contingencies a priori improbable,
are given, in the process of time, an increasing probability,
until it is their non-occurrence rather than their occurrence
which becomes highly improbable.
Sir Ronald Aylmer Fisher, 1890 - 1962

From its very beginning the theory of evolution was closely intertwined with mathematical models. One of the main influences for Darwin when he formulated his thoughts was Robert Malthus' exponential growth model of populations, as already mentioned in the introduction. The school of biometricians, founded by W.F.R Weldon soon realized that Darwinian evolution is a mathematical theory. It is a description of a dynamical system with kinetics driven by (natural) selection. The influence of selection can be pictured as a force. Just like a gas can be described through the accumulated collisional forces between all particles; just like our solar system can be modelled through the accumulated gravitational forces between its celestial bodies, the actions of selection, the advent and descent of entire ecosystems, can be understood through the combined and accumulated interactions between single species.

1.1 Axiomatic formulation of evolution

Assume that the abundance of an item i is measured by a variable x_i. We call the dynamic of a system composed of a large number of items *evolution* if each interaction present in the system can be understood as one of the following rules or a combination thereof [32, 34]:

- **Replication:** The abundance of items is variable and changes with a rate f_i called the Malthusian fitness of item i:
$$x_i \xrightarrow{f_i} 2x_i \quad . \tag{1.1}$$
At this point it is completely unspecified if item i is able to copy itself or not, or if it replicates via sexual reproduction. In fact, as we will see later, in the framework we develop here our findings are completely irrespective of this. This point will especially become crucial when we will turn to a discussion of the emergence of organizations.

- **Competition:** An interaction between two items i and j is called competition iff there exists a rate $p_{ij} > 0$ such that the abundance of only one of the two items proliferates, with the other one decreasing:
$$x_i + x_j \xrightarrow{p_{ij}} x_j \quad . \tag{1.2}$$
When we have a relation like this items i and j are competing with each other and item j dominates over i in this case. The rate p_{ij} can be thought of quantifying a flow of abundance from i to j.

- **Mutation:** Iff an item i and j are in a relation such that with a rate $q_{ij} > 0$ we find
$$x_i \xrightarrow{p_{ij}} x_j \quad , \tag{1.3}$$
we call this interaction mutation. In contrast to competition, item j is not required to be abundant before the mutation happens – it is generated.

Table 1.1: Five 'axioms' from which mathematical micro-evolutionary formulations are built.

replication	x_i	$\xrightarrow{f_i}$	$2x_i$	REP
competition	$x_i + x_j$	$\xrightarrow{p_{ij}}$	x_j	COMP
mutation	x_i	$\xrightarrow{q_{ij}}$	x_j	MUT
recombination	$x_j + x_l$	$\xrightarrow{\alpha_{ijl}}$	x_i	REC
development	$x_j + x_l$	$\xrightarrow{d_{ijl}}$	p_i	DEV

- **Recombination:** Item i is produced through a interaction called recombination iff there exists a $\alpha_{ijl} > 0$ such that

$$x_j + x_l \xrightarrow{\alpha_{ijl}} x_i \quad . \tag{1.4}$$

  In contrast to mutation, an item can be produced here only through the combination of more than one other item. Note that from a pure axiomatic point of view, we could start with a recombination process and by putting constraints on the right- and left-handside of Eq.1.4 recover the relations replication, competition and mutation. We will turn to a discussion of this later.

- **Development:** Suppose we are interested in the development of a certain trait or characteristic p_i which can be found in various items (a trait p_i could be e.g. haircolor across the world, the number of electrons a chemical species can donate or the number of red squares found in paintings in museums of modern arts). The trait p_i gets developed with a rate d_{ijl} according to

$$x_j + x_l \xrightarrow{d_{ijl}} p_i \quad . \tag{1.5}$$

We will refer to these five interactions as the 'axioms' of evolutionary systems, see Tab.1.1. They represent the highest level of detail under which such systems can be studied. For this reason we refer to a description based only on these axioms as 'micro-evolutionary dynamic'.

1.2 Micro-evolutionary dynamics

We will now lay out a generic framework for dynamical systems which are interacting through the above axioms. Therefore we will cast replication, competition, mutation, recombination and development succinctly into rate or differential equations. By doing so, we will rederive some basic equations of population genetics and game theory, thereby underpinning the claim of generality of these axioms.

Consider a population of a total number of N items which are abundant with concentrations n_i, $i = 1, \ldots, N$. Let us first assign to each item an unconstrained net growth $\gamma_i = \dot{n}_i$. From now on we will work with normalized concentrations and work with variables $x_i = n_i / \sum_{j=1}^{N} n_j$. Then the net growth becomes

$$\dot{x}_i = \gamma_i - x_i \sum_{j=1}^{N} \gamma_j \quad . \tag{1.6}$$

This is the generic form of a replicator equation. In this picture there is a compensation for excess production in the system. The abundances get constantly normalized such that for constant growth, $\gamma_i = \text{const}\ \forall i$, the system reaches a stationary state where the x_i are sorted according to their growth rate.

We will now incorporate axiom REP into Eq.1.6. Let us first imagine the most simple case of replication – items are able to copy itself. The growth rate is now frequency dependent,

$\gamma_i \to f_i x_i$ with f_i called the Malthusian fitness of item i. With this autocatalytic replication in equation 1.6 we obtain

$$\dot{x}_i = x_i \left(f_i - \sum_j f_j x_j \right) = x_i \left(f_i - \langle f \rangle \right) \quad , \tag{1.7}$$

which is referred to as the frequency dependent replicator equation [35], a microscopic description of axiom REP. Here the abundances get sorted and re-normalized until the mean value of the fitness becomes identical to the maximal fitness value within the population – only one item survives.

By axiom COMP the growth rate of items may not only depend on the actual frequency of the item itself, it may be subject to competitions with other items. Since any two out of the N given items can be in competition, we introduce a matrix $P = (p_{ij})$ with $i, j = 1, \ldots, N$ quantifying these interactions. P is usually called a payoff matrix with the picture in mind that when items i and j meet, i receives a payoff p_{ij} and j gets a payoff p_{ji} with respect to their ability to reproduce. Summing over all evolutionary payoffs of item i, its Malthusian fitness takes on the form $f_i = \sum_j p_{ij} x_j$. Substituting this into Eq.1.7 leads us to the game dynamical equation [36]

$$\dot{x}_i = x_i \left(\sum_j p_{ij} x_j - \sum_j x_j \sum_k x_k p_{jk} \right) \quad . \tag{1.8}$$

Proceeding in a similar vein, let us take axiom MUT into account by defining a mutation matrix $Q = (q_{ij})$, $i, j = 1, \ldots, N$, with q_{ij} as the rate under which item i proliferates due to mutations of item j. Summing over all possible mutations the growth rate for item i becomes $\dot{x}_i \propto \sum_j q_{ij} x_j \sum_k p_{jk} x_k$. In order to tighten the notation let us introduce the dilution flux Φ ensuring that at any given time $\sum_{i=1}^N \dot{x}_i = 0$. Thus the dilution flux is nothing else than the population average of the Malthusian fitness to which we compare the individual fitnesses of the items. With this notation we obtain a combination of axioms REP, COMP and MUT, the replicator-mutator equation [37]

$$\dot{x}_i = \sum_{j=1}^N q_{ij} x_j \sum_{k=1}^N p_{jk} x_k - x_i \Phi \quad . \tag{1.9}$$

Before we continue with casting our evolutionary axioms in terms of differential equations, let us discuss how Eq.1.9 is related to some well known population genetic and game-theoretic equations. Let us first rewrite the frequency dependent replicator equation into the generic form [38, 39]

$$\dot{x}_i = x_i (f_i(\mathbf{x}) - \Phi) \quad . \tag{1.10}$$

Here we allow the Malthusian fitness to be an arbitrary function of the abundances and have not yet incorporated mutations. However, in the vast majority of studies this functional dependence is assumed to be linear, just as we have done until now. The variable transformation

$$x_i = \frac{y_i}{1 + \sum_{i=1}^{N-1} y_i}, \quad i = 1, \ldots, N-1 \quad , \tag{1.11}$$

$$x_N = \frac{1}{1 + \sum_{i=1}^{N-1} y_i} \quad , \tag{1.12}$$

allows us to map the replicator equation Eq.1.10 onto the Lotka-Volterra equation for the $N-1$-dimensional case in variables $\dot{y}_i = \sum_{i=1}^{N-1} y_i f_i(\mathbf{y})$. On the other hand, by assuming that fitness

is constant and only taking mutations into account we rederive the quasi-species equation [40] as a special case of Eq.1.9,

$$\dot{x}_i = \sum_{j=1}^{N} q_{ij} x_j f_j - x_i \Phi \quad . \tag{1.13}$$

As long as we restrict ourself to constant or linear frequency-dependent replicators, i.e. restrict ourself to evolutionary systems described by only REP, COMP and MUT, the dynamic of the items is simply driven by two independent transfer matrices P and Q. At each instance individual fitness values are compared to the mean value, items with a fitness lower than average vanish. However, since fitness can also be frequency dependent, this may lead to a complex dynamical feedback which allows several items to co-exist – cooperation.

Let us recombine the frequency-dependent replicator equation Eq.1.10 with axiom MUT to obtain the replicator-mutator equation [37] for arbitrary fitness functions,

$$\dot{x}_i = \sum_{j=1}^{N} x_j f_j(\mathbf{x}) q_{ij} - x_i \Phi \quad . \tag{1.14}$$

We introduce now the simplest form of nonlinear frequency-dependent replicators, the recombinatory interaction of axiom REC. We can write this in compact form using the catalytic network equation [41]

$$\dot{x}_i = \sum_{j,k=1}^{N} \alpha_{ijk} x_j x_k - x_i \Phi \quad . \tag{1.15}$$

For the special case that the rate α_{ijk} factors according to $\alpha_{ijk} = q_{ij} p_{jk}$ Eq.1.15 becomes the replicator-mutator equation. The catalytic network equation encodes axioms REP, COMP, MUT and REC. Here we can observe that from a pure axiomatic point of view REC would suffice to derive REP, COMP and MUT. To this end we can split Eq.1.15 into a replication part $\mathcal{R}_i(\mathbf{x})$ and an interaction part $\mathcal{I}_i(\mathbf{x})$ in the following way:

$$\begin{aligned} \dot{x}_i &= \mathcal{R}_i(\mathbf{x}) + \mathcal{I}_i(\mathbf{x}) \quad , \\ \mathcal{R}_i(\mathbf{x}) &= x_i \left[\sum_j (\alpha_{iij} + \alpha_{iji}) x_j - \sum_{k,j} (\alpha_{kkj} + \alpha_{kjk}) x_j x_k \right] \quad , \\ \mathcal{I}_i(\mathbf{x}) &= \sum_{j,k \neq i} \alpha_{ijk} x_j x_k - x_i \sum_l \sum_{m,n \neq l} \alpha_{lmn} x_m x_n \quad . \end{aligned} \tag{1.16}$$

Equations 1.6 to 1.14 or alternatively evolutionary dynamics according to a subset of the above axioms can be derived from applying constraints to α acting on the individual terms in Eqs.1.16.

We can answer the question now how to formalize evolutionary systems in which items are not able to copy itself, i.e. we abandon axiom REP. Consider a set K of species with the property that for each item $i \in K$ there exists a pair $j, k \in K$ such that i gets produced by j and k via a recombination. The set K maintains itself without copying itself, we will call this property *self-maintaining*. Now consider a collection of disjoint self-maintaining sets $J, K, L, \ldots$. We allow interactions between these sets such that if two items of a productive pair reside in sets J and K, the item they produce is different from them but again contained in J or K. We can assign frequencies in terms of set variables by defining $x_K = \sum_{k \in K} x_{k \in K}$ as the relative frequency of set K. The frequency of item i within its own set is then given by $y_{i \in K} = x_{i \in K} / x_K$. Re-arranging the summation in Eq.1.15 according to this we get

$$\dot{x}_K = x_K \left(\sum_J C_{KJ} x_J - \langle C_{KJ} \rangle \right) \quad , \tag{1.17}$$

where we have introduced a growth coefficient C_{KJ} on this set level given by

$$C_{KJ} = \sum_{i\in K}\sum_{j\in J}\sum_{k\in K} \alpha_{i\in K, j\in J, k\in K} y_{i\in K} y_{j\in J} \quad . \tag{1.18}$$

Most remarkably, this is nothing else than a replicator equation as introduced in Eq.1.7 with the difference that the units on which this dynamic acts not individual, self-copying items are but self-maintaining sets of non-replicating items. Selection acts here on the level of conglomerate entities. Therefore we have encountered the first instance of organization – a collection of items (the self-maintaining sets) assumes a different functional relation than its mere constituents.

So far we considered evolutionary dynamics only on the population space. Now suppose we are interested in how this microscopic dynamic manifests on the dynamic of a phenotypic trait p_i (e.g. body mass, number of hairs or the IQ), i.e. we take axiom DEV into account and want to trace the development of a trait over an entire population. DEV is typically treated by assigning one value for the trait p_i to each species x_i. The population mean is then $E(p) = \sum_i p_i x_i$. It is now straightforward to compute $\dot{E}(p) = \sum_i p_i \dot{x}_i + \sum_i \dot{p}_i x_i$. The second term is $E(\dot{p})$ and describes a change in the trait itself, the first term describes the influence of the underlying population dynamics. We insert equation 1.15 for $\dot{x}_i$ to obtain

$$\begin{aligned} \dot{E}(p) &= \sum_{i,j,k} \alpha_{ijk} p_i x_j x_k - \sum_i p_i x_i \Phi \\ &= \sum_{i,j,k} \alpha_{ijk} p_j x_j x_k - E(p)\Phi + \sum_{i,j,k} \alpha_{ijk}(p_i - p_j) x_j x_k \quad . \end{aligned}$$

Remember that we defined the dilution flux as the mean fitness, i.e. $\Phi = E(f_i)$. By making use of the definition of the covariance $\mathrm{Cov}(X,Y) = E(X\cdot Y) - E(X)E(Y)$ we derive the Price equation [42]

$$\dot{E}(p) = \mathrm{Cov}(\Phi, p) + E(\dot{p}) + E(\phi\Delta_m p) \quad , \tag{1.19}$$

where we denote with $E(\phi\Delta_m p)$ the expected drift over time in the trait values due to mutations, $E(\phi\Delta_m p) = \sum_{i,j,k} \alpha_{ijk}(p_i - p_j) x_j x_k$. With axiom DEV we can thus re-derive the Price equation and describe how the application of evolutionary axioms REP, COMP, MUT and REC on an underlying level accumulates to a trajectory of a phenotypic trait which is spread out over an arbitrary number of items.

1.3 Macro-evolutionary dynamics

Studies of the above evolutionary equations have been often restricted to very special cases of interactions or very small system sizes. Typically one is interested in their fixed points, configurations of abundances which get restored after small disturbances. These states are called evolutionary stable states and are a dynamic property of the system. If one adopts a game-theoretic viewpoint one is usually interested in evolutionary stable strategies, a similar yet different concept. A strategy is evolutionary stable if – once adopted by each member of a population – it can not be invaded by any other strategy. For a discussion of these applications and further related concepts of equilibria see [39].

Our focus here lies somewhere else. We will be interested in systems composed of an arbitrary large number of items, which poses serious constraints on how we can build models. On a technical level the simulation of a macroscopic number of differential equations as given above can not be tackled using today's computing power, let alone the derivation of analytical solution. But more strikingly, we run into severe limitations on a conceptual level. One of the main characteristics of evolution is the continual production of innovations. The introduction of one item in Eq.1.15 would force us to introduce N^2 interaction terms. Besides the obvious impossibility to measure and therefore specify these interactions, each already existing interaction would have to

be re-assessed in the light of this innovation due to the contextual nature of evolutionary items. A systematic study of how innovations drive evolutionary systems is not feasible within this framework only. We will review some seminal and related work in the literature and examine how they deal with these difficulties. This way of proceeding is necessary since we leave the terrain on which research efforts of a multitude of groups over several decades can be put on a formal common ground. The models which we will examine now share in common that they aim at a description of complex collective behavior of evolutionary items which is not apparent from the study of a small number of them – macro-evolutionary dynamics. Finally we discuss how their levels of description are interrelated. We conclude this section by deducing a set of properties which we demand for a well-sound model of evolution.

1.3.1 Random catalytic reaction network

A common strategy to tackle the large-system problem is to assume that the interactions are to a large extend random, possibly under some constraints. This allows one to study generic properties of the underlying model without needing to specify the enormous number of possible relationships. We review here how this was done for Eq.1.15 in [41].

The problem amounts to specifying the α_{ijk}. Consider a system composed of N items. Remember that we can decompse Eq.1.15 into a replication and interaction term, see Eq.1.16. We introduce p here as the probability that a randomly chosen α_{ijk} is zero, i.e. there is no interaction rule for this triple of items. If there is an interaction, then with probability q it is a replication and with $(1-q)$ a recombination. With this parametrization we wish to be able to investigate the influence of replicator-mutator versus recombinatory dynamics. To this end define $\alpha_{ijk} \equiv a_{ij} t_{ij}^k$ with a_{ij} drawn randomly from a uniform distribution on (0,1) and

$$t_{ij}^k = \begin{cases} 1 & \text{with probability } \frac{1}{N-2}(1-p)(1-q) \text{ for } k \neq i,j \quad , \\ 0 & \text{with probability } \frac{1}{N}p \quad , \\ 1 & \text{with probability } \frac{1}{2}(1-p)q \text{ for } k = i \text{ or } j \quad . \end{cases} \tag{1.20}$$

A dynamical simulation of this system with $p = q = 0$ mostly leads to a final stable configuration within the concentration simplex given by $\sum x_i = 1$, sometimes the system reduces its dimension and reaches a set of items with no closed subsets. In these cases the entire surviving system becomes a single replicator.

To understand the behavior of this system at the stable point the authors investigated the dilution flux Φ of the system, which can be thought of as the productivity of the system. Via a mean field approach this can be estimated to be

$$\langle \Phi \rangle = \frac{1}{2}(1-p)(1+R) \quad . \tag{1.21}$$

Here the brackets denote an ensemble average (i.e. average over many realizations of α) and R is a correlation term given by the second moments of the concentrations. Thus the density of recombinatory interactions controls (almost linearly) the productivity of the system, whereas self-replicatory interactions introduce positive correlations. The final diversity in the system is always given by a self-maintaining subset of the items, which is often given by the entire network.

The authors also investigated very special topologies, such as coupled hypercycles. However, these structures are very unlikely to emerge randomly. In the generic case the system approaches a stable fixed point, seldomly showing oscillatory behavior within constant diversity. Therefore, these models are unable to explain or deal with innovations. This problem has subsequently be tackled by other authors.

1.3.2 Solé-Manrubia model

In the Solé-Manrubia model [43] species-species interactions are assumed to be linear, i.e. the interactions can be decomposed into REP, COMP and MUT. Therefore the authors introduce an explicit mechanism for creating innovations.

The interactions are recorded in an interaction matrix J whose elements J_{ij} give the strength of the coupling between two items. If $J_{ij} > 0$ the existence of item i contributes to the survival of item j, if $J_{ij} < 0$ item i has a suppressing influence on j. At initialization of the system each entry of J is nonzero and randomly drawn from the interval $(-1, 1)$. The abundance of item i is not described by a continuous concentration but by a binary variable $\sigma_i(t) \in \{0, 1\}$. Thus species i receives at time t a 'net support' $\sum_j J_{ji}\sigma_j(t)$. If this support drops below a certain threshold θ item i vanishes. Thus the resulting dynamical system, mimicking replicator-mutator dynamics, is given by

$$\sigma_i(t+1) = \Theta\left[\sum_{j=1}^{N} J_{ji}\sigma_j(t) - \theta\right] \quad , \tag{1.22}$$

where $\Theta(x)$ is the Heaviside step function being defined as $\Theta(x) = 1$ iff $x > 0$ and $\Theta(x) = 0$ otherwise. In addition the authors impose two mechanisms: Firstly, the system is driven by slow random mutations of the interaction matrix J. At each time step one connection for each species is chosen randomly and assigned a new value from the interval $(-1, 1)$ again at random. With this driving force the authors circumvent that the system reaches a stable point in which the global dynamic stops.

Secondly, innovations take place. After each iteration some items may vanish and are thought of as to leave 'empty niches' behind. These niches are immediately refilled by copies of a randomly chosen surviving species. Speciation is introduced by mutating the interaction matrix of these new item. Concrete, if item k is copied to replace item i the interactions are given by $J_{ij} = J_{kj} + \eta_{ij}$ and $J_{ji} = J_{jk} + \eta_{ji}$ with the η's drawn randomly from the interval $(-\epsilon, \epsilon)$.

The key feature of the Solé-Manrubia model is that it is able to produce 'mass extinctions'. For $\theta = 0$ and $\epsilon = 0.05$ the authors measured the probability $p(s)$ that at a given iteration s items become extinct to be $p(s) \propto s^{-\gamma}$ with $\gamma = 2.05 \pm 0.06$, i.e. the sizes of extinction events follow a power-law distribution. This finding is consistent with observations from fossil data. The model therefore reproduces a crucial property of evolutionary systems, the advent of mutations can have system-wide effects – or no effect at all. However, this property turns out to be parameter dependent. For $\theta \neq 0$ the extinction size distribution has an exponential cutoff. On a more conceptual level the model is not able to describe the influence of cooperating organizations of items, its interactions take only place on the individual-item-level. This has the effect that the driven dynamic and the innovation mechanism are *ad hoc* assumptions imposed on the system in order to allow the observation of the desired phenomena and does not enlargen our understanding on how such mechanisms may appear outside this simulation, emerging from single interactions given by our evolutionary axioms.

1.3.3 Jain-Krishna model

Insights into how non-trivial structures can emerge in evolutionary systems were provided by Jain and Krishna [44]. Their linear model describes the interactions between N items again by an interaction matrix J. At initialization an entry J_{ij} is nonzero with probability p. In this case it is either chosen randomly from the intervall $[-1, 1]$ if $i \neq j$ or from $[-1, 0]$ if $i = j$. Thus an interaction between two different species is equally likely to be positive as negative and the link from an item two itself can only be negative, i.e. items are not self-replicating. The items are described by concentrations x_i evolving in a replicator-mutator manner according to

$$\begin{aligned} \dot{x}_i &= f_i \quad \text{if } x_i = 0 \text{ or } f_i \geq 0 \quad , \\ &= 0 \quad \text{if } x_i = 0 \text{ and } f_i < 0 \quad , \end{aligned} \tag{1.23}$$

with the dynamic specified by

$$f_i = \sum_{j=1}^{N} J_{ij} x_j - x_i \sum_{k,j=1}^{N} J_{kj} x_j \quad . \tag{1.24}$$

In addition the authors assume a second evolution on a larger time-scale. Within one time-step of this simulation, Eqs.1.23 and 1.24 are iterated until the system approaches its attractor. In this attractor configuration the set of the items with the least frequencies, i.e. smallest values of x_i is determined. They are called the 'least-fit' items. One of them is randomly chosen and removed along with all its incoming and outgoing links. This item is replaced by a new item whose interactions are specified identical to the initial interaction matrix. This process is iterated many times.

The system behaves most interestingly for values of p below the percolation threshold. For the first couple of iterations the system remains in a state with a very low diversity. At some instance this changes radically and the whole system becomes populated. Observed over long time-spans, the diversity jumps erratically between states of full and very low diversity. This behavior can be understood through the emergence of autocatalytic sets. Starting from the initial network and subjecting it to mutation, at some point there may occur a configuration where, e.g., three items are suddenly arranged in a positive feedback cycle. Their relative abundances will proliferate and thus they will not be subject to a removal. As soon as a further item gets attached to it, this item will survive too. In this manner – all of a sudden – the entire system is turned into a single autocatalytic, self-maintaing set, the state of full diversity. Note that under the percolation threshold the occurrence of such a configuration goes exponentially to zero. Since the removal procedure continues to be at work, items from this set will constantly be removed. It may then happen that the removal of a given node leads to the breakdown of the catalytic set (the authors call such items 'keynode species') and the system is thrown back into a state of low diversity. Within this model the emergence of cooperation of items and their arrangement in highly non-random structure can be understood. However, these phenomenology still rests on some external assumptions in order to prevent the system from settling down into a fixed point.

1.3.4 NK model

Another approach to study large-scale evolutionary dynamics is to simulate a system with interactions given by the axioms directly rather than simulating the system of differential equations. A famous example for this strategy is the NK-model [45] and its relatives.

One simple version of an NK-model can be described as follows. The items representing basic units can be regarded as genes in this context. A genome is a sequence of N genes and each gene is a letter from an alphabet of size 2, i.e. a bit. Each gene has a functional dependence on K other genes within this genome. For each possible configuration of the K neighbors of each gene i we assign a different random fitness value w_i chosen from the interval $(0, 1)$ to i. This choice is quenched, i.e. at the beginning of the simulation we choose all possible fitness values under the above constraint, then they remain fixed throughout the evolution of the system. Thus if we encounter the same genome at two different instances of time it has the same fitness values. We can now assign a fitness value W to the entire genome, a possible choice for this is to take the average of the gene fitnesses,

$$W = \frac{1}{N} \sum_{j=1}^{N} w_j \quad . \tag{1.25}$$

The characteristics of this model are to a large extent independent on how we compose the genome's fitness from the individual fitnesses.

We can impose a metric on the space of all possible genomes by defining two genomes which vary in exactly one gene to have a distance of one. For a genome of length N this is a N-dimensional grid. We can assign the genome fitness W to each gridpoint as its function values. The resulting space is referred to as fitness landscape. In the following we assume that the only evolutionary forces are single-point mutations under which the genome moves on to an adjacent gridpoint on the fitness landscape if it possesses a higher value of W. How rugged this landscape is, depends on K. For the extreme cases, if $K = 0$ there will be almost surely a genome with a unique maximum in fitness. Since the contributions to W from each gene are totally independent the genome can smoothly travel to the global maximum. In the other case, $K = N - 1$, the fitnesses on adjacent gridpoints are totally uncorrelated with the fitness on the actual gridpoint of the genome, the landscape is extremely rugged. A global maximum will almost surely never by achieved, instead the genome will keep stuck in a local maximum. For choices of K in between we will find different degrees of 'ruggedness'.

With this being defined, we can turn to the most interesting cases of the NK-model. In this extensions we consider the co-evolution of multiple genomes. To this end we introduce S_i as the number of different genomes with which genome i interacts and C as the number of randomly chosen genes which have an effect on the fitness of species i. The resulting model is sometimes referred to as the $NKCS$-model.

In the course of a single mutation, a genome maximizes its fitness now taking account of the K genes in its own genome *and* of the CS_i genes which have an influence on it in the neighboring genomes – co-evolution. Genomes are placed in space, usually a regular lattice was chosen for this topology. In the one-dimensional case this implies $S_i = 2\ \forall i$, for two dimensions $S_i = 4\ \forall i$ and so on, one could study other more irregular topologies as well. In one case they were not allowed to move and the authors were interested in if the population finds a maximum in fitness in which the genomes rest and no further mutations take place. By varying K this behavior undergoes a phase transition. For low K each genome tries to reach its global fitness maximum. By doing so, it influences its neighbors and very likely 'pushes' them in a direction away from their maxima. In this regime co-evolutionary avalanches go on forever, the population is not able to reach a maximum. this kind of dynamic was called 'chaotic'. For very high K in contrast, each genome has a much shorter step length in its fitness landscape to reach a local maximum. Therefore the population is much easier able to find a state in which all genomes can rest in a local maximum. Co-evolutionary avalanches do not go on forever, the system is 'frozen'. Indeed, the $NKCS$-model has a critical value K_c under which it undergoes a continuous phase transition from the chaotic to the frozen regime.

In yet another variant of the $NKCS$-model genomes are allowed to move to adjacent lattice points. If they are already occupied competitive replacement takes place: the genome with higher fitness W survives. Additionally, genomes are also allowed to vary their K values. Two things are worth noticing about this model variant: If we count the number of species becoming extinct through replacement, their distribution over time is again a power-law. Further, by keeping track of the values of K that individuals obtain during their evolution, it turns out that they approach K_c over time. This poses some interesting questions. As Kauffman calls it, life organizes itself at the 'edge of chaos'. However, research is hindered in the direction of $NKCS$-model by their high complexity and the need to solely rely on computer simulations. This makes it increasingly harder to identify the relevant mechanisms for such findings and whether they are artefacts from a particular realization of this model or generic, universal features of a large class of such models.

1.3.5 Bak-Sneppen model

Instead of focussing on a concrete micro-evolutionary dynamical setting as laid out through variants of the catalytic network equation or extensively simulating systems like the $NKCS$-models, authors were also interested in the development of more stylized models of evolution.

The aim of the Bak-Sneppen model [46] is to single out the mechanism which generates the critical behavior in $NKCS$-models.

As starting point the authors took the observation that each item is placed on a fitness landscape, a possibly rugged function assigning to each item a chance of survival. A mutation has the effect of altering the position of an item on this landscape. In this picture they will be driven to adaptive peaks. Speciation is thought of as moving from one peak to an adjacent one through a series of – at first glance – malevolent mutations. The Bak-Sneppen model assumes that the time for such an speciation event can be modeled via the Arrhenius law of statistical physics. If B is a numerical value representing the relative height of the fitness barrier an item has to cross in order to reach an adjacent adaptive peak, the time t to get there will be given by

$$t = t_0 \mathrm{e}^{B/T} \quad , \tag{1.26}$$

where t_0 sets the time-scale and T depends on the mutation rate, a concept reminiscent of temperature. Now place many interdependent items on such a fitness landscape and ask for which item the next speciation event is most likely to be observed if B is large compared to T. This is the species i with the lowest barrier to mutation B_i, note that barriers are exponentially separated. The dynamics of the Bak-Sneppen model is defined in the following way: The item with lowest barrier to mutation B_i is picked and mutated. On this new adaptive peak it gets a randomly assigned new barrier to mutation $0 \leq B_i < 1$. Each item is coupled to K neighbors. Due to the new item introduced, the fitness barriers of these items will change too and we assign new random values $0 \leq B_i < 1$ to them again. This process is iterated.

The observable of interest in this model is the number of items which get a new B_i assigned after each speciation event. After a transient phase the typical value for the lowest barrier to mutation approaches a critical value $B_c \approx 2/3$. After approaching this regime each mutation triggers a co-evolutionary avalanche with power-law distributed sizes. Therefore this model displays self-organized criticality. Besides this and whether one accepts self-organized criticality as a driving mechanism of evolutionary systems, the explanation of many other key features lies clearly beyond the scope of this model.

1.3.6 λ-calculus

We have defined evolution as an ubiquituous framework to formally treat large systems of interconneceted items. The treatments of such systems we have encountered so far where mostly extensional in the sense that we pre-specified the entire set of dynamical rules and interactions and – due to the high complexity of the arisen models – investigated the resulting system by computer simulations. By doing so we have also encountered the ambiguity of how to specify this vast number of possible interactions and mostly resolve this issue by defining them as random. Another way to do this is to impose an inner structure on the evolutionary items out of which their interactions can be algorithmically constructed. This approach is inspired by chemistry, suppose you are given the number of protons, neutrons and electrons (inner structure) of two elements i and j (evolutionary items). With the knowledge of quantum mechanics it would (in principle) be possible to algorithmically work out if they react to form another chemical k, i.e. to calculate the value of α_{ijk}. The following model was constructed as a toy model for such systems, using λ-expressions as evolutionary items [32].

In this model the items are functions defined in the framework of the λ-calculus. The grammar of a λ-expression E is

$$E ::= x \mid \lambda x.E \mid (E)E \quad , \tag{1.27}$$

where x is a variable. The syntax is defined by two operations. The first, *abstraction* is written $\lambda x.E$ and means that E is a function of x. The procedure *application*, $(E)E$, is the application of a function to an argument. There is no syntactical distinction between function and argument. These operations inherit their meaning through *substitution*: $(\lambda x.A)B \rightarrow A\,[B/x]$ where the

latter indicates the substitution of all occurrences of x in A with B. The process of carrying out all possible substitutions is called *reduction* and yields, if existant, a unique expression called a *normal form*. All expressions are reduced to their normal form in this model, if there is none the expression is not allowed.

Now picture a reactor containing particles which are λ-expressions. Initially there are N randomly generated particles. At each instance two expressions A and B are picked and interact according to $A(B)$. If this expression has a normal form, say C, this particle is added to the reactor. In order to ensure constant size a randomly picked expression is subsequently removed from the reactor in this case. This procedure is iterated.

With this specification the model produces systems which are dominated by self-replicating or hypercyclically coupled λ-expressions, i.e. functions satisfying $(f)g = g \vee f \ \forall g$ or $f(f) = f$ constitute stable fixed points of the dynamic. More complex situations arise when we put firmer constraints on the kinds of λ-expressions we allow, especially when self-copying ones are forbidden. With this boundary condition the system encounters a nontrivial 'fixed-point' in the sense of a kinetic persistent behavior. A center of generators emerges from which the entire rest of the system can be spawned. These systems are self-maintaining and able to re-produce itself even under severe damage such as the random removal of elements – The system develops self-repairing organizations. In a next step the authors show that it is possible for two such organizations to coexist.

This model further clarifies the distinction between simple replicator dynamics (such as under copying-actions) and organizational development through catalytic interactions. Note that this behavior seems to be a generic property of constructive systems defined by formal languages, indeed other authors arrived at similar conclusions using different formal languages see e.g. [47].

1.3.7 Kauffman networks

Instead of measuring the effects items have on each other in terms of the relative changes in their abundances after interaction one may also model this influence explicitly. For example, if an item i vanishes once it encounters an item j, this can be coded in the following way: ascribe to each item i a state variable $\sigma_i(t)$ with $\sigma_i(t) = 0$ if the item is not existent at time t, and $\sigma_i(t) = 1$ if it is abundant. The above interaction can be expressed as $\sigma_i(t) \to \sigma_j(t+1)$, where '$\to$' stands for logical implication and 0 is interpreted as 'true', 1 as 'false'. Let us generalize this observation. Consider a collection of N items, each one being influenced by K other items (maybe including itself). Each possible interaction can be encoded as one of the 2^{2^K} Boolean logical functions mapping K bits to one bit. The time evolution in this system is given by

$$\sigma_i(t+1) = f_i(\sigma_{i_1}(t), \sigma_{i_2}(t), \ldots, \sigma_{i_K}(t)) \quad , \tag{1.28}$$

with the Boolean logical function $f_i : \{0,1\}^K \mapsto \{0,1\}$. If these functions are chosen randomly for each item from the set of all 2^{2^K} relations and the neighbors $\sigma_{i_1}(t)$, $\sigma_{i_2}(t), \ldots,$ $\sigma_{i_K}(t)$ are drawn randomly from the set of all items too, the resulting network is called a Random Boolean Network or Kauffman network [48]. Interestingly, the global behavior of this model is to a large extend independent of the actual choice of the f_i.

Usually one distinguishes the *quenched* from the *annealed* case. In quenched dynamics the rules f_i and neighbors for each node are chosen randomly in the beginning and then fixed, whereas in the annealed variant they are randomly drawn at each iteration. Since both versions will yield the same results qualitatively and in the $N \to \infty$ limit even exactly, we will drop this distinction here.

It is interesting to study the dynamics of this model in terms of stability. To this end consider two configurations of internal states $\mathcal{C}_j(t) = \{\sigma_i(t)\}_{i=1}^N$, with $j = 1, 2$ and their Hamming distance $d_t(\mathcal{C}_1(t), \mathcal{C}_2(t))$, i.e. the number of bits they differ in. When we start with two very similar configurations, $d_0 = m \ll N$, the question is if for large t this distance will stay small

compared to N or eventually span a macroscopic proportion of the system. It has been shown that the stability of Kauffman networks undergoes a phase transition at a critical connectivity $K_c = 2$. For $K < K_c$ the system is frozen, $\lim_{t\to\infty} \lim_{N\to\infty} d_t/N = 0$ whereas for $K > K_c$ the system is called 'chaotic', $\lim_{t\to\infty} \lim_{N\to\infty} d_t/N > 0$.

Originally this model was motivated as a model for genetic activity. The binary variables correspond to the respective gene being activated or not. Kauffman was interested in two things, the number of different limit cycles and their length. For both one can construe a biological metaphor, the number of different limit cycles for one genome can be thought of as the number of different cell types a stem cell can differentiate in, whereas their length corresponds to the duration of one cycle of such a cell type. In real world data both entities scale as $\sqrt{N}$ with the genome size N. Remarkably, this is the same scaling behavior that Kauffman networks possess when they are tuned to the critical point $K = K_c$. But again, the question remains open why nature should be exactly that fine-tuned.

1.3.8 Organization Theory

Chemical reactions are a prime example for recombinatory interactions. When it comes to the study of the dynamics of a large set of molecular species it is thus no surprise that theoretical chemistrists developed model to simulate such system efficiently. One approach to this problem which turned out to have a much broader scope of evolutionary phenomena than just chemistry is the theory of organizations [49].

Organization theory establishes firm topological characterizations of a collection of items. A set of items is *closed* if for all interactions all participating items are a member of the set (note that this is not the same definition of a closed set as usually adopted in topology). A set is *semi-self-maintaining* if every items 'used up' is also produced via interactions. A set that is closed and semi-self-maintaining is a *semi-organization*. If each item does not participate in any other interaction than those contained in the set and the internal production rate of the system is non-negative, the set is called *self-maintaining*. Finally, an *organization* is a closed and self-maintaining set.

The authors have been interested in the evolution of such an organization over time. Evolutionary items are binary strings and a well defined instruction table (allowing self-replication) was used giving a rule how to combine two strings s_1 and s_2 to form a third one $s_3 = A_{s_1}(s_2)$ with A being an automaton. The strings are initially placed in a reactor, each string having multiple copies summing up to N items in total. Two items meet at random and interact, additionally items are drained with a given rate – a catalytic flow system in a well stirred reactor.

The focus here lies on organizational evolution, rather than on the evolution of individual items. Thus the (concentration) state space is analyzed after N interactions in terms of the organizations it contains, which usually involves a high reduction in dimensionality. To this end generate the smallest closed set containing each item abundant at time t and find its biggest self-maintaining set S_t. Organizational evolution takes place in the space of all possible organizations. By introducing mutations (randomly negating 10 bits each time-step) the authors find three distinct behaviors. When $S_{t+1} \supset S_t$ the change is called upwards movement – the space of all accessible items has been enlargened . In contrast, if $S_{t+1} \subset S_t$ we find downwards movement meaning that the potential diversity of the system declined. Sometimes a combination of upwards and downwards movement can be found, labeled sidewards.

An interesting insight from this model is that movement in the space of organizations and change in actual diversity is mostly correlated (i.e. upwards movement leads to actual increase of items, downwards to decrease) but need not be the same. Sometimes upwards movement is accompanied by a loss of diversity. Relating the organizational level with the dynamical complexity of a system, this insight might bear the potential for interesting future research related to the emergence of complexity in systems subject to evolution.

1.3.9 Hanel-Thurner-Kauffman model

A fruitful approach to study properties of the catalytic network equation Eq.1.15 is to map it onto topological recurrence equations [50]. This allows to conduct large-scale investigations on recombinatory systems and even analytical calculations of some key quantities, at the expense of a higher abstraction level. A crucial insight here is to formally establish the existence of scale-invariant behavior of these system, i.e. behavior which is not size-dependent. This approach therefore allows to study systems of arbitrary dimensionality.

This model aims at explaining the dynamical origins of diversification in evolutionary system and its possible breakdown, i.e. crises. Suppose a model universe in which things get recombined to produce new things: chemicals react to form yet new compounds, technologies can be combined to create artefacts serving a new functionality, species influence the selection of other species and give rise to new mutant forms. Under which initial conditions will such a system bloom or starve? And if the system shows high diversity, under which conditions is this state sustainable?

We assume that an item i is described by its internal state $\sigma_i(t) \in \{0, 1\}$ at time t. The interaction topology is assumed to be completely random with respect to a homogeneous rule density. In the simplest case, each item has a mean number of r^+ tuples of items with a positive influence on it, i.e. for a system with N items we distribute r^+N nonzero entries randomly in the interaction table α.

Suppose there are initially on average $a_0 \equiv (1/N)\sum_{i=1}^{N} \sigma_i(0)$ items present. Whenever $\sigma_i(t) = 1$, $\sigma_j(t) = 1$ and $\alpha_{ijk} > 0$ item i and j can be recombined to produce item k, $\sigma_k(t + 1) = 1$. If there are only positive influences allowed, the final diversity of the system can be calculated by solving the recurrence relation

$$\begin{aligned} a_{t+1} &= a_t + \Delta a_t \quad , \\ \Delta a_{t+1} &= r^+(1 - a_{t+1})(a_{t+1}^2 - a_t^2) \quad . \end{aligned} \tag{1.29}$$

The asymptotic solution of these relations, $a_\infty(a_0, r^+)$, can be mapped on the Van der Waals equation of state, therefore this system possesses a creative phase transition of second order. Given a small number of initial elements the entire system becomes populated. In subsequent work the authors included destructive influences in very much the same manner and showed that in this phase of full diversity the introduction of a small number of defects which cascades through the network (i.e. if item i is turned off all items which are produced in no other way than through i are turned off too) can lead to a breakdown of the highly diverse state and the system is thrown back into a state of vanishing diversity – a destructive phase transition.

Negative influences can also be coded directly in α by defining a negative rule density along a parameter r^- analogous to r^+. Additionally, items decay with a pre-specified rate. This coupled dynamic may yield meta-bi-stability – systems are continually thrown from a phase of high diversity into one of low, reside there for an arbitrary number of iterations and are thrown back again, and so on. These results can also be extended to the case where an item is influenced not by two other elements (corresponding to α being an $N \times N \times N$ tensor) but by an arbitrary number, α is then an $N \times N \times \cdots \times N$ interaction tensor.

This is a minimal model which captures the main features of recombinatory dynamics and therefore establishes the analytic tractability of arbitrarily sized systems which are subject to evolution.

1.3.10 Model comparison

Each of the models we have investigated here presents a unique approach to study different facets of systems subject to evolution. As a common denominator they all make statements about the expected diversity of their realizations and its dynamic, as well as how the items are interdependent, i.e. if structure emerges. Furthermore their interactions are captured by the

evolutionary axioms to which external constraints have been added in varying degrees. We will now try to inter-relate them.

The straight-forward study of micro-evolutionary dynamics can be thought of as a special case of a model. Our system is then given by the directly observable abundances of items and the direct measurable rate coefficients of their interactions. If we would possess knowledge about all these variables, we could in principle simulate the system. This corresponds to a model with zero level of abstraction, the entities in our model are the directly measureable quantities. In turn this implies that there is a vast amount of variables to specify, we say this model has maximal specifity. Due to this high level of knowledge required to conduct experiments this approach is, of course, inapplicable to a huge number of systems where direct observation is limited (be it due to technical imperfections, funding money or more conceptual reasons). Even worse, each system would necessitate its own model. This can be overcome by trading specifity versus abstraction.

We will now attempt to rank the models according to their loss of specifity and their gain in abstraction. In doing so, the models gradually lose power to make quantitative predictions which can be tested against real world data but therefore give us insight into which ingredients constitute certain qualitative phenomena observable in evolutionary systems. Of course, this ranking will only be our subjective proposal and always lies in the eye of the beholder.

The model closest to micro-evolutionary dynamics are the random catalytic networks. Here we simulate the micro-evolutionary system directly under the assumption of random interactions. The Jain-Krishna model becomes less specific in focussing only on linear interactions which are again randomly, therefore it imposes an external selection mechanism. Such a mechanism is also present in the Solé-Manrubia model, we have additionally switched to binary internal states which brings us into position to make contact with spin-models known from the physics literature. In the Hanel-Thurner-Kauffman model interactions are binary random variables too, therefore the focus lies explicit on recombinatory interactions, no external selection mechanism is needed. The NK-model adds internal structure to evolutionary items on which the interactions are defined. As an abstraction to this, the Bak-Sneppen model sets out to reproduce the qualitative behavior of such an evolution on a fitness landscape with varying 'rugged'ness. Kauffman-networks study arbitrary logical connectives between items and gradually lose empirical underpinning of the interactions at work. In organization theory interactions are logical functions of bit-strings too, additionally a topological and set-theoretical structure is super-imposed and studied. We find the highest level of abstraction in the λ-calculus where evolutionary items become expressions of a universal computing language, i.e. a formalism in which every computable function can be expressed and evaluated. For a schematic illustration of the interrelation of models see Fig.1.1.

The task in modelling evolutionary systems is now clear. Starting with micro-evo-lutionary dynamics we will try to formulate a model by trading as much specifity as possible against the least amount of abstraction. To which extend this program is successful is indicated by the number of quantitative predictions which can be made on the basis of the model and tested against real data while constantly ensuring full compatibility with dynamics derived from our evolutionary axioms. To achieve this is the aim and purpose of this thesis. Referring to the sketch in Fig.1.1, we try to move along the arrow towards the point of a model with least amount of specifity and abstraction.

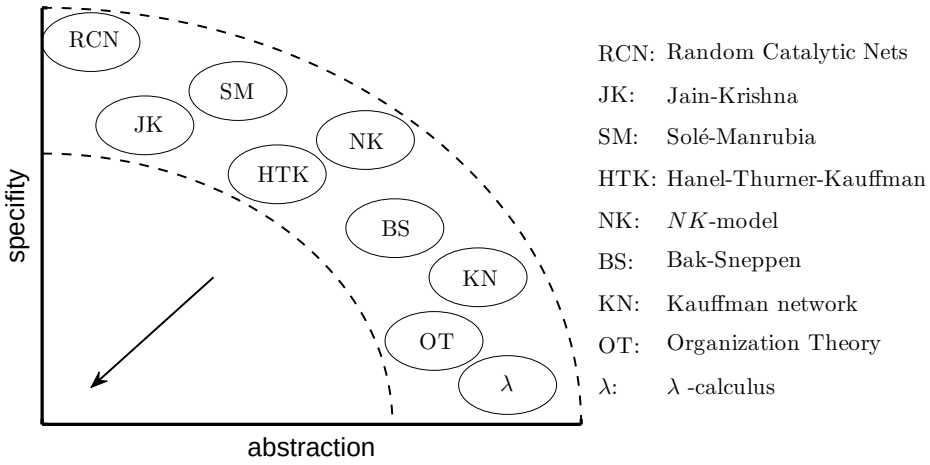

Figure 1.1: The inter-relation of the models discussed in this section is pictured symbolically along two dimensions, each corresponding to resources needed to make the model work. 'Specifity' indicates the amount of specific knowledge about the realization of the evolutionary system which is needed to formulate the model. 'Abstraction' corresponds to the grade of abstraction adopted in the model and therefore measures how stylized the model is compared to reality. The arrow points in the direction we aim for the remainder of this work.

2 Topology of Evolutionary Systems

Everything should be as simple as it is,
but not simpler.
Albert Einstein, 1879 - 1955

We seek the formulation of a model of evolution with minimal level of abstraction (i.e. with closest contact to the micro-evolutionary axioms given in Tab.1.1) and simultaneously the least degree of specifity, that is a minimal number of model parameters. We will go beyond the paradigmatic approach to model evolutionary systems as a linear network of interconnected items by focussing on the recombinatory part of the interactions. This is motivated by (i) our emphasis on the role of innovations, which means that certain recombinations of existing items introduce a new feature or quality in the system (the whole is more than the sum of its parts – metaphorically) and (ii) the observation that replication, mutation and competition are nothing else than special instances of recombinations.

2.1 Mapping Evolutionary Axioms to Power Set Topology

Traditional network theory assumes the elementary existing units to be identical to the elementary interacting units. An item i is here completely speciefied by its abundance and its interactions: the in- and outgoing links to other items. This is at variance with the contextual nature of evolutionary items: the functional role of an item i, its links, may depend on which other items are simultaneously abundant. Crudely speaking, hydrogen may be life saving to a human in combination with oxygen but death bringing in combination with chlorine. Yet all this three constituents can be produced independent, it is their combination that adds the life saving or death bringing quality. We have to develop a model where *functional elements are not individual items but collections of them.* Let us make this observation mathematically explicit.

Collect all N items of an evolutionary system into a set $\mathcal{N}$. This set contains items which may play a role in the system at any possible time and is possibly of infinite order. The *power set* $\mathcal{P}(\mathcal{N})$ of $\mathcal{N}$ is defined as the set of all subsets of $\mathcal{N}$. For example, if $\mathcal{N} = \{0, 1, 2\}$ then $\mathcal{P}(\mathcal{N}) = \{\{\ \}, \{0\}, \{1\}, \{2\}, \{0, 1\}, \{0, 2\}, \{1, 2\}, \{0, 1, 2\}\}$. So if $\mathcal{N}$ is of order N, $\mathcal{P}(\mathcal{N})$ is of order 2^N. Let $\mathbf{i}$ and $\mathbf{j}$ be two subsets of $\mathcal{N}$, i.e. two elements of $\mathcal{P}(\mathcal{N})$, $\mathbf{i}, \mathbf{j} \in \mathcal{P}(\mathcal{N})$. We subsumize the evolutionary axioms of replication, mutation, competition and recombination into the general interaction scheme

$$\mathbf{i} \xrightarrow{\alpha_{\mathbf{ij}}} \mathbf{j} \quad . \tag{2.1}$$

To see that this relation indeed encompasses the basic interactions we show how to rederive the axioms from relation 2.1.

- **replication:** Consider an item i described by abundance x_i. If $\mathbf{i} = \{i\}$ and $\mathbf{j} = \{i\}$ we recover axiom REP.

- **competition:** If the two subsets overlap we have the general structure of competition. Choose $\mathbf{i} = \{i, j\}$ and $\mathbf{j} = \{j\}$ to obtain COMP.

- **mutation:** This is the case that the subsets are of order 1 and do not overlap, MUT is given by $\mathbf{i} = \{i\}$ and $\mathbf{j} = \{j\}$.

- **recombination:** The prototype of a recombinatory interaction, REC, can be expressed as $\mathbf{i} = \{j, l\}$ and $\mathbf{j} = \{i\}$.

- **development:** We can investigate phenotypic traits via an assignment as given in DEV in exactly the same manner as before by keeping the definition $E(p) = \sum_i p_i x_i$ as above. In addition to that we can also assign traits to a selection of sets by assigning traits $p_{\mathbf{i}}$ to subsets $\mathbf{i}$.

We now aim for a topological description of a large system of items interacting through the general scheme of relation 2.1. To this end we will make use of the concept of a hypergraph – a generalization of the familiar graph concept.

From all possible 2^N subsets of N items not all of them have to be functional elements. Indeed, in a real system this holds for the vast majority of them. Assign to each member of the power set of $\mathcal{N}$ a 1 if a recombination of the elements this subset contains leads to a new item and 0 if not. That is, we collect all general interactions of the system and mark which subsets of items appear at the left-hand sides of the relations 2.1. They constitute a hypergraph H_{IN} given by the mapping

$$H_{IN} : \mathcal{P}(\mathcal{N}) \mapsto \{0, 1\} \quad . \tag{2.2}$$

Proceeding in a similar way we can collect all right-hand sides of the interactions in the system into a hypergraph H_{OUT} given by the map

$$H_{OUT} : \mathcal{P}(\mathcal{N}) \mapsto \{0, 1\} \quad . \tag{2.3}$$

The map $\alpha_{\mathbf{ij}}$ which we have introduced in relation 2.1 is then a homomorphism between H_{IN} and H_{OUT} – a linear map on the power set of $\mathcal{N}$

We will call the elements of $\mathcal{P}(\mathcal{N})$ which are mapped to a nonzero value by H_{IN} *in-sets* and the nonzeros of H_{OUT} will be called *out-sets* analogously. The in- and out-sets are hyperedges on the set of all items. As a generalizations to a normal graph, where edges can join only two vertices, a hyperedge can join an arbitrary number of them. If all hyperedges contain the same number of elements, i.e. have the same cardinality, the hypergraph is called *uniform*. The *degree* of an item i is the number of hyperedges it is contained in. A hypergraph is called *regular* if all vertices have the same degree. Subsequently we will study different hypergraph topologies by specifying the distributions of vertex degrees and hyperedge cardinalities.

The topology of an evolutionary system is completely specified by the collections of in-sets H_{IN}, out-sets H_{OUT} as well as the homomorphism α between them.

2.2 Setting Up the System's Dynamic

In the study of evolutionary systems one is mostly not interested in the exact abundance of a specific item, but only in if the system has the capability to sustain its existence, the diversity of the system is one of the main observable. Within this framework we can therefore switch from a continuous description of states, i.e. relative abundances x_i of item i, to binary internal states $\sigma_i(t) \in \{0, 1\}$. This can be pictured as introducing a threshold concentration $x_{i,c}$ for each i such that it is present, active or simply 'on' indicated by $\sigma_i(t) = 1$ if $x_i \geq x_{i,c}$. Otherwise it is not present, inactive or 'off', i.e. $\sigma_i(t) = 0$. The threshold has to be chosen for each item such that it assumes its functional role if it is abundant above this value and the interactions are negligible if they are below $x_{i,c}$. We define

$$\sigma_i(t) = \begin{cases} 0, & \text{if } x_i < x_{i,c} \\ 1, & \text{if } x_i \geq x_{i,c} \end{cases} \quad \text{at time } t. \tag{2.4}$$

However, interactions take place between *sets* of items. Therefore we also introduce a binary state for an in-set or out-set $\mathbf{i}$,

$$\sigma_{\mathbf{i}}(t) = \prod_{i \in \mathbf{i}} \sigma_i(t) \quad . \tag{2.5}$$

An arbitrary in- or out-set is 'on' iff all the items it contains are on. This definition mimicks the mass-action dependence in nonlinear evolutionary equations such as Eq.1.15. Note that here and henceforth italic indices denote individual items, whereas bold indices denote elements of the power set of all items.

In the most general and cumbersome case the entries of the map α can take arbitrary values – there is no *a priori* restriction to the reaction rates. Since our state variables are binary now, we can gain here descriptive clearance now too. For each entry of α we can again introduce critical threshold values $\alpha^+_{\mathbf{ij},c}$ and $\alpha^-_{\mathbf{ij},c}$. Let us define a map α^+ taking accont of positive interactions by

$$\alpha^+_{\mathbf{ij}} = \begin{cases} 0, & \text{if } \alpha_{\mathbf{ij}} < \alpha^+_{\mathbf{ij},c} \\ 1, & \text{if } \alpha_{\mathbf{ij}} \geq \alpha^+_{\mathbf{ij},c} \end{cases} \quad . \tag{2.6}$$

In the same spirit we handle negative interactions with a map α^- defined straightforwardly by

$$\alpha^-_{\mathbf{ij}} = \begin{cases} 0, & \text{if } \alpha_{\mathbf{ij}} > \alpha^-_{\mathbf{ij},c} \\ 1, & \text{if } \alpha_{\mathbf{ij}} \leq \alpha^-_{\mathbf{ij},c} \end{cases} \quad . \tag{2.7}$$

We have thus decomposed α into two separate maps α^+ and α^- which keep track of the functional relevant interactions. Note that they do not depend on time. If two or more items can be recombined or not is thought of depending on the laws of nature. For instance, if certain chemicals react or not depends on the inner structure of the involved molecules and their surrounding, chemical rules do not change dynamically. Two given biological species may compete e.g. for the same resources or not depending on their ecological context, but the possibility for them to compete stays unaltered. If it turns out to be useful or not to recombine two technologies also depends on which other technologies and constraints are currently available or present, but the mere possibility to recombine them is a constant property.

Adopting our proposed general evolutionary description language we can call two sets $\mathbf{i}$ and $\mathbf{j}$ linked through a nonzero entry in α^+ *complements*. The abundance of items in the in-set $\mathbf{i}$ makes the existence of the items in the out-set $\mathbf{j}$ favorable, the link is constructive. In case they are linked through α^- we can also refer to them as substitutes: the in-set $\mathbf{i}$'s abundance may be rendered anachronistic once out-set $\mathbf{j}$ manifests itself, the interaction is called destructive. These two processes of course depend on the entire surrounding of those items – whether the existence of an item turns out to be favorable or not can only be decided in the context of the entire network. We will devote a large part of this thesis to the study of exactly this interplay on a macroscopic scale.

Coming back to a more formal viewpoint, we have enlargened the space of all functional elements from the set of all items to its power set. With respect to this we have introduced interactions between those sets by the homomorphisms $\alpha^{\pm}$. We can reconcile their role now with a network point of view; α^+ and α^- are *adjacency matrices on the power set of all items*. But note that these dynamics only is linear if we look at only one iteration of the system. It is a nontrivial task to determine which active out-sets can be recombined to active in-sets. In our framework the problem of treating highly nonlinear systems has been shifted to exactly this point exactly.

For an illustration of the topology we have arrived at consider Fig.2.1. The circles correspond to items whose internal states are shown by different colors, gray if the item is active and white if inactive. We pick out an arbitrary item i whose internal state is on, $\sigma_i(t) = 1$. Item i is contained in two in-sets of cardinality two, in-sets $\mathbf{i}$ and $\mathbf{k}$. Since the other element in $\mathbf{i}$ is active

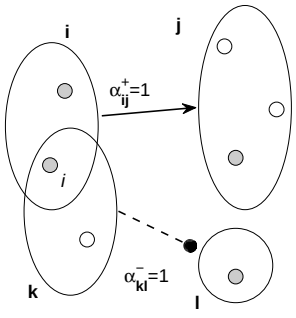

Figure 2.1: The circles show evolutionary items which are filled with gray color if their internal state is on and left white if they are off. We picked an item i and show one in-set **i** it is contained in having constructive influence on the out-set **j**. It also resides in in-set **k** with destructive influence on out-set **l**. Since **i** is on at the next time step all items in **j** are also on, whereas the item in **l** will not be de-activated through negative influence because in-set **k** is not active.

we have $\sigma_{\mathbf{i}}(t) = 1$ whereas $\sigma_{\mathbf{k}}(t) = 0$ since here the other item is inactive. The in-set **i** has a constructive influence on its complement, out-set **j** of cardinality three, as denoted by $\alpha^+_{\mathbf{ij}} = 1$. Since **i** is on we will have $\sigma_{\mathbf{j}}(t+1) = 1$ at the next time step, i.e. each item in **j** will be activated. Item i also resides in in-set **k** having destructive influence on its substitute out-set **l** of size one, indicated by $\alpha^-_{\mathbf{kl}} = 1$. But since the in-set **k** is not active out-set **l**, and the items it contains, will not be de-activated in the next time step.

2.3 Interaction Indication Functions

We conclude the topological prelude to the study of dynamics of evolutionary systems by introducing interaction indication functions. To determine whether a given item i will be active or not in the forthcoming timestep one needs to have knowledge of three things. In which out-sets is i contained? Which interaction are defined for these out-set through $\alpha^{\pm}$? And finally, which are the corresponding in-sets for these interactions? The idea is to construct an expression depending on the answers to these questions indicating whether an interaction takes place at time t or not.

Let us consider constructive influences. An in-set can give rise to such interactions if it is active. That is, in-set **i** can participate if $\sigma_{\mathbf{i}}(t) = 1$. It acts upon out-set **j** given by $\alpha^+_{\mathbf{ij}} = 1$. An interaction will only take place, if there is an item in **j** that is not active at time t, that is we have $\sigma_{\mathbf{j}}(t) = 0$. Thus saying that a constructive interaction between in-set **i** and out-set **j** happens at time t is equivalent to saying

$$\sigma_{\mathbf{i}}(t)\ \alpha^+_{\mathbf{ij}}\ (1 - \sigma_{\mathbf{j}}(t)) = 1 \quad . \tag{2.8}$$

We call the left-hand side of Eq.2.8 the *constructive interaction indication function*. Whenever this function yields one, a constructive interaction can take place and we will have $\sigma_{\mathbf{j}}(t+1) = 1$.

We proceed in a similar way for destructive influences. Again, an in-set **i** has to be on and there has to exist a destructive interaction with set **j** through $\alpha^-_{\mathbf{ij}} = 1$. But now the interaction will only take place if set **j** is already active at time t. Thus the occurrence of a destructive interaction is indicated by

$$\sigma_{\mathbf{i}}(t)\ \alpha^-_{\mathbf{ij}}\ \sigma_{\mathbf{j}}(t) = 1 \quad . \tag{2.9}$$

Whenever this relation holds, i.e. the *destructive* interaction indication function yields one, we will have $\sigma_{\mathbf{j}}(t+1) = 0$. Each item in set $\mathbf{j}$ gets deactivated in this iteration. Note that we could also deactivate out-set $\mathbf{j}$ by switching only one item in it to off. However, if we would impose this kind of dynamics we could equally well exclude the un-altered items from the out-set.

Let us reflect what these interaction indication functions exactly do. Quite remarkably, they map interactions to numbers. Each presently occurring interaction is assigned a unit of one. This observation is the key point to start our dynamical investigations.

3 Evolutionary Mechanics

The press, the machine, the railway, the telegraph
are premises whose thousand-year conclusion
no one has yet dared to draw.
Friedrich Nietzsche, 1844 - 1900

Evolutionary dynamics appears in a multitude of different contexts. Evolution basically describes how sets of elements, such as biological species, goods and services in an economy, groups of living beings, or chemical compounds, change over time. Examples are abundant in various areas. Chemical compounds react with other compounds to produce new chemicals. Integrated circuits performing specific computational tasks can be combined to create another circuit for a different computational task. Prey and predator may co-evolve by succinctly acquiring new traits and thereby develop into new species. In the following we will use *species* for elements in whatever context, chemicals, goods, biological species, etc. The removal or addition of a single species in an evolutionary system may have dramatic consequences. For example, in starfish removal experiments (e.g. Mukkaw Bay in Washington [51]) starfish are removed from an eco-system with the consequences that mussel populations explode and drive out most other species, while the urchin population destroys coral reefs. In 1904 English physicist John Ambrose Fleming accidentally manufactured the first vacuum tube which triggered a cascade of technological and economic co-evolutions and adaptations; in 2004 the semiconductor industry was a market of $ 213 billion and enabled the generation of approximately $ 1200 billion in electronic system businesses and $ 5000 billion in turn in services which amounts to 10% of world GDP [28]. Typically in evolutionary systems species are endogenously added or removed from a large system of mutually influencing species. Two species influence each other if the existence of one species has a positive or negative effect on the change of abundance of the other. The possibilities for interactions in evolutionary systems involve different natural, economic or social laws on a variety of time or length scales. The collective result of these ('microscopic') interactions between elements leads to ubiquitous well-known macro phenomena in evolutionary systems, such as punctuated equilibria, booms of diversification, breakdowns and crashes, or seemingly unpredictable responses to external perturbations. Maybe one of the most exciting questions in natural sciences today is to understand if evolutionary dynamics can be understood by a common underlying principle and – if yes – how such a principle might look like. Such a principle must be general enough to capture the multitude of different phenomena, and at the same time must be in a form which can be applied easily to specific problems.

3.1 Exorcising Darwin's Demon with a Variational Principle: Evolutionary Mechanics

In the present understanding of evolution the concept of *fitness* is of central importance. Usually the relative abundance of species (wrt other species) is described by replicator equations (first-order differential equations) and variants such as Lotka-Volterra equations [33, 35, 39]. Their mutual influence is quantified by a rate specifying how the abundance of one species changes upon contact with another. In biology this rate is called Malthusian fitness, in chemistry one refers to it as the reaction rate, in economics it is related to production functions. Similar proliferation rates could also be introduced for technological, financial or even historical contexts. In the following we subsume them all under the term *fitness*.

A distance between two species can be defined as the minimal number of evolutionary steps needed for one species to evolve into the other one (in biology this distance is often the number of single-point mutations two species differ in). In this way a metric is given on the space of all possible species. A *fitness landscape* assigns to each point in this space (that is to each species) its reproductive success or fitness. Evolution is sometimes pictured as an optimization problem where species evolve via adaptations toward peaks in this landscape. In this view evolutionary systems may approach a unique equilibrium once each species approaches its adaptive peak – with profound consequences. The idea of clearing markets and equilibrium economics is based on this line of reasoning and actually used for policy formulation.

The concept of fitness is limited however. To see this consider the following thought experiment. Suppose one -say a demon- would have exact knowledge about the abundance and fitness of each biological species in the universe. 'Knowing the fitness of a species' means knowledge of the functional dependence of its proliferation rate on the entire current environment (i.e. all other species). The omniscient hypothetical entity in possession of this knowledge could be called *Darwin's demon* for obvious reasons. The demon may be pictured as a super-biologist able to measure each species' abundance as well as the dependence of its proliferation rate on each other species in each habitat. That is, he knows the set of all existing species and can measure their associated fitness landscape to an arbitrary degree of exactness. What can the demon *predict* about the future course of evolutionary events, such as biodiversity in 100 million years or the time to the next mass extinction event? Surprisingly little, for the following reasons. A key characteristic of evolutionary systems is its potential to generate innovations, i.e. new species. In biological systems this can happen through mutations, in technological or economical ones through spontaneous ideas of an inventor, etc. Once a new species is created it becomes part of the very environment and thereby potentially changes the conditions for all already existing species and for those yet to arrive. To now assess the fitness of a new species one has to measure how it spreads in an environment it is now part of. The demon has information related to a different environment, one which only existed *before* arrival of the new species. Thus the demon may have an exact description of the *current* biosphere, but with the advent of each new species this description loses accuracy. Fitness thus always encodes *a posteriori* knowledge, and can not be used to make falsifiable predictions. The idea that evolution is guided by the principle 'survival of the fittest' is obviously tautological and translates into 'survival of whoever turned out to survive in hindsight'. To know how 'fit' a species will be somewhere in the future knowing how fit it was in the past is of no use. Instead *we have to understand how species and their fitness landscapes co-construct each other.*

To make headway in understanding the phenomenology of evolution, i.e. in identifying principles which guide evolutionary dynamics, a series of quantitative models have been suggested [45, 46, 43, 44, 54, 55, 49, 48, 53, 3, 52, 57]. Here explicit assumptions are made about how new species come into being, how they interact with each other and under which conditions or under which selective forces they vanish. Each of these models focuses on particular aspects of evolution. For example in Kauffman NK models [45] species are bit-strings with randomly assigned fitness values. Arthur [55] focuses on technological evolution with integrated circuits as species whose fitness is examined by how well they execute certain computational tasks. Jain and Krishna [44] consider ecological systems and elucidate the interplay between interaction topology and survival of species. In most of these models some *ad hoc* assumptions about the mechanisms are made. In the model by Jain and Krishna, for example, species are actively removed and added to the system, therefore innovations are externally enforced and not endogenously produced. Arthur compares the output of randomly assembled circuits to a prescribed list of desired computational tasks (such as bitwise addition). In the NK model only single-point mutations of bit-strings are allowed as evolutionary interactions. Although these assumptions are rectifiable in the specific contexts of their models, it is not at all clear whether conclusions derived on the basis of these assumptions are valid in different evolutionary contexts. Arthur's

model is not applicable if one cannot pre-specify a list of tasks or abilities that should evolve, Jain and Krishna's model does not apply to static interaction topologies such as closed chemical reaction networks, similarly one cannot devise NK models for e.g. economic settings, where dominant interactions are not given by single-point mutation of bit-strings. Thus the scope of all these models is limited.

To arrive at a general evolutionary description (without ad hoc specifications) one has to identify principles which are abstract enough to be applicable in each evolutionary context but which must be specific enough to make useful quantitative predictions. To meet these requirements, evolution can be pictured as a three-step production/destruction process. **Step 1:** New species come into being through recombination of already present species. That is, each species arises only under the condition that a given (and maybe not unique) set of other species or environmental factors exists. For example, to assemble an MP3-player all parts –including software– are needed. Sodium chloride can be produced by sodium hydroxide in solution with hydrochloric acid. Or with a healthy amount of oversimplification one can say that apes and steppe formation give rise to mankind. **Step 2:** The new species becomes part of the system and can now be combined with other, already existing species. One can legally download music for the MP3-player and listen to it, sodium chloride reacts with e.g. calcium carbonate in the Solvay process, mankind slashes forests and woodlands to create fields for agriculture. **Step 3:** As a consequence, through this recombination yet new species may come into being and other already existing ones may vanish or be destroyed. For example, MP3 currently drives CDs out of the market but can be combined with cell phones to give smartphones. Soda ash can be used to remove sulfur dioxide from flue gases in power stations which might help to reduce the current Holocene extinction event of biological species possibly influenced by the advent of mankind. In previous work models incorporating these types of production and destruction processes have been shown to reproduce a wide range of evolutionary phenomena, including booms of diversification [50], breakdowns of diversity [56] or punctuated equilibria [52]. Such processes further allow to understand stylized facts in time-series data on evolutionary systems, such as scale-free distributions of species lifetimes, the number of species per genus or the size of extinction events in fossil data [3], or GDP and business failures in economic markets [57].

In this work we propose a variational principle from which dynamics – identical to the dynamics of the production / destruction processes described above – can be derived. To this end we define the *evolutionary potential* of a species. This function measures in how many productions and destructions a species would (no longer) take part if it would enter (be removed from) the system. With this potential one obtains two formal representations of the system's dynamic. (i) The potential can be used to explicitly deduce a set of dynamical *update equations* of system diversity for production / destruction processes. (ii) Using this evolutionary potential and a measure for ongoing productions and destructions one can construct a *balance function*. The evolutionary process solving the dynamical update equations (i) always minimizes the balance function (ii). The balance function further allows asymptotic solutions for the system diversity (mean-field approximation). These analytic solutions are in good agreement with numerical simulations of the full model of productions and destructions. This is to a certain degree unexpected since the dynamics is dominated by strong and nonlinear interactions.

This description of evolutionary systems allows to understand how the set of abundant species and their fitness landscapes co-construct each other from first principles, as opposed to research strategies portrayed by Darwin's demon, where snapshots of regions of fitness landscapes are empirically explored. Accordingly the focus shifts from predicting 'microscopic' properties such as individual proliferation rates to estimating the occurrence of global, 'macroscopic' events.

This work is structured as follows. In section 3.2 we develop a general framework for evolutionary systems via a variational principle. We discuss deterministic and stochastic implementations and obtain asymptotic diversity solutions in a mean-field approximation. In section 3.3 we motivate and define the choice of evolutionary interactions as production and destruction rules as

in [57]. We treat the special cases of systems with only productive interactions in section 3.4 and the pure destructive case in section 3.5. Then we discuss the full model of productions *and* destructions in section 3.6. We discuss empirical relevance of this work in section 3.6.3 and turn to a conclude in 3.8.

3.2 General formulation of diversity dynamics

3.2.1 Dynamical systems

The abundance of species i is given by a binary state variable $\sigma_i(t) \in \{0,1\}$. If species i exists at time t, $\sigma_i(t) = 1$, otherwise $\sigma_i(t) = 0$. The system can be populated by N species (N arbitrarily large, even infinite). A particular configuration of the system is characterized by the N-dimensional vector in phase space $\vec{\sigma}(t) = (\sigma_i(t)) \in \Gamma = \{0,1\}^N$. The system's *diversity* $D(t)$ is given by $D(t) = \frac{1}{N}\sum_i \sigma_i(t)$.

At each time, species i may experience three scenarios, (i) annihilation $\sigma_i(t) = 1 \to \sigma_i(t+1) = 0$, (ii) nothing $\sigma_i(t) = \sigma_i(t+1)$ or (iii) creation $\sigma_i(t) = 0 \to \sigma_i(t+1) = 1$. Suppose that there exists a function $f_i(\vec{\sigma}(t)) : \{0,1\}^N \to \mathbb{R}$ indicating which of the transitions (i)-(iii) takes place. Specifically, let $f_i(\vec{\sigma}(t))$ indicate the following transitions

$$\begin{array}{lll} \text{(i)} & f_i(\vec{\sigma}(t)) < 0 & \Rightarrow \sigma_i(t+1) = 0 \\ \text{(ii)} & f_i(\vec{\sigma}(t)) = 0 & \Rightarrow \sigma_i(t+1) = \sigma_i(t) \\ \text{(iii)} & f_i(\vec{\sigma}(t)) > 0 & \Rightarrow \sigma_i(t+1) = 1 \end{array} \tag{3.1}$$

For (i) or (iii) a transition occurs if $\sigma_i(t) = 1$ or 0, respectively. That is, if $f_i(\vec{\sigma}(t)) \geq 0$ the system evolves according to

$$\sigma_i(t+1) = \sigma_i(t) + \Delta\sigma_i(t) \qquad \text{with} \qquad \Delta\sigma_i(t) = \operatorname{sgn}\left[(1-\sigma_i(t))f_i(\vec{\sigma}(t))\right]. \tag{3.2}$$

$\Delta\sigma_i(t)$ can only be non-zero if $\sigma_i(t) = 0$ *and* $f_i(\vec{\sigma}(t)) > 0$. Similarly, for $f_i(\vec{\sigma}(t)) \leq 0$ $\Delta\sigma_i(t) = \operatorname{sgn}\left[-\sigma_i(t)f_i(\vec{\sigma}(t))\right]$. Let us define the ramp function $R(x)$ by $R(x) \equiv x$ iff $x \geq 0$ and $R(x) \equiv 0$ iff $x < 0$. Using these definitions we can generically map the indicator function f_i from Eq.(3.1) onto the update equation

$$\begin{aligned} \sigma_i(t+1) &= \sigma_i(t) + \Delta\sigma_i(t) \quad , \\ \Delta\sigma_i(t) &= \operatorname{sgn}\left[\Big(1-\sigma_i(t)\Big)R\Big(f_i(\vec{\sigma}(t))\Big) - \sigma_i(t)R\Big(-f_i(\vec{\sigma}(t))\Big)\right] \quad . \end{aligned} \tag{3.3}$$

3.2.2 Variational principle for deterministic diversity dynamics

Consider a virtual displacement of $\sigma_i(t)$, $\sigma_i'(t) = \sigma_i(t) + \delta\sigma_i(t)$. Let us define [1] the *activity function* K_i as

$$K_i(\sigma_i'(t), \sigma_i(t)) \equiv \frac{\mu}{2}\left(\sigma_i'(t) - \sigma_i(t)\right)^2 \quad , \tag{3.4}$$

where we – for the moment – regard μ as a free parameter of the theory confined to the interval $\mu > 0$. We introduce the activity function as a tool to record the number of state changes in the system. Since $K_i \neq 0 \Leftrightarrow \sigma_i'(t) \neq \sigma_i(t)$ the sum $\sum_i K_i$ measures the total activity in the system and is by definition always positive semi-definite.

We define the *potential* V_i by

$$V_i(\sigma_i'(t), \vec{\sigma}(t)) \equiv \left|\Big(1-\sigma_i'(t)\Big)R\Big(f_i(\vec{\sigma}(t))\Big) - \sigma_i'(t)R\Big(-f_i(\vec{\sigma}(t))\Big)\right|, \tag{3.5}$$

[1] In analogy to kinetic energy.

Table 3.1: We exhaustively insert all possible values for $\sigma_i(t)$ and $\sigma_i'(t)$ in Eq.(3.3) and B_i for non-zero values of $f_i(\vec{\sigma}(t))$. For convenience we choose $|f_i(\vec{\sigma}(t))| = 1$ and confine the threshold to $0 < \mu < 2$. We underline the values of $\sigma_i'(t)$ for which B_i is a minimum, this underlined values always equal $\sigma_i(t+1)$.

$\sigma_i(t)$	$f_i(\vec{\sigma}(t))$	$\sigma_i'(t)$	K_i	V_i	B_i	$\sigma_i(t+1)$
0	-1	$\underline{0}$	0	0	0	0
0	-1	1	$\frac{\mu}{2}$	1	$1+\frac{\mu}{2}$	0
0	1	0	0	1	1	1
0	1	$\underline{1}$	$\frac{\mu}{2}$	0	$\frac{\mu}{2}$	1
1	-1	$\underline{0}$	$\frac{\mu}{2}$	0	$\frac{\mu}{2}$	0
1	-1	1	0	1	1	0
1	1	0	$\frac{\mu}{2}$	1	$1+\frac{\mu}{2}$	1
1	1	$\underline{1}$	0	0	0	1

which 'counts' the number of possible interactions for $\sigma_i'(t)$. Depending on $\sigma_i'(t)$ Eq.(3.5) will reduce to $V_i(\sigma_i'(t), \vec{\sigma}(t)) = |R(\pm f_i(\vec{\sigma}(t)))|$. A possible intuition behind Eq.(3.5) is that the function f_i acts as a 'field' on $\sigma_i(t)$ which is 'probed' by $\sigma_i'(t)$. From now on we will occasionally drop the σ-dependences in the balance functions for a clearer notation. The *balance function* B_i now reads $B_i \equiv K_i + V_i$.

K_i measures the *actual* activity in the system – it counts all state changes. Depending on these states, the potential V_i counts the *potential* activity in the newly obtained states. The function B_i therefore contains the full dynamical information of Eq.(3.3) which can now be expressed via a *variational principle*.

> *Given $\vec{\sigma}(t)$, the solution $\sigma_i(t+1)$ of Eq.(3.3) is identical to the value of $\sigma_i'(t)$ for which B_i assumes its minimum, i.e.*
>
> $$\sigma_i(t+1) = \underset{\sigma_i'(t)}{\operatorname{argmin}} \left[B_i\Big(\sigma_i'(t), \vec{\sigma}(t)\Big)\right] \quad , \tag{3.6}$$
>
> *with* $\underset{x}{\operatorname{argmin}}\,[f(x)]$ *denoting the value of x for which $f(x)$ takes its minimum.*

This is seen by exhaustive insertion. First, consider the case $f_i(\vec{\sigma}(t)) = 0$. From Eq.(3.3) $\Delta\sigma_i(t) = 0$ and $V_i = 0$ follows. The only possible term contributing to B_i is K_i and we have $K_i = 0$ if $\sigma_i'(t) = \sigma_i(t)$ and $K_i = \frac{\mu}{2} > 0$ otherwise. The balance function B_i takes its minimum, $B_i = 0$ at $\sigma_i'(t) = \sigma_i(t) = \sigma_i(t+1)$. Similar reasoning can be applied to the cases of a non-zero $f_i(\vec{\sigma}(t))$, see Tab.(3.2.2). This also clarifies the role of the parameter μ. One can think of it as an inertial threshold, the dynamics of Eq.(3.3) is only obeyed if the 'field' $f_i(\vec{\sigma}(t))$ describing a certain state-change exceeds the activity barrier set up by μ. There is always a choice for μ such that Eq.(3.3) holds.

3.2.3 Stochastic diversity dynamics

We define now a stochastic variant of diversity dynamics. In Eq.(3.3) a state transition $\sigma_i(t) \to \sigma_i(t+1)$ is *determined* by $\Delta\sigma_i(t) \in \{-1, 0, 1\}$. In contrast to this in the stochastic case studied now we will specify transition *probabilities* for this evolution.

From the variational principle Eq.(3.6) follows that Eq.(3.3) always minimizes the balance function B_i. In the stochastic variant we assume that the lower B_i the higher the probability

to find the system in the respective configuration $\sigma_i(t)$. In analogy to magnetic spin systems we define this probability as

$$p(\sigma_i(t)) \propto \mathrm{e}^{-\beta B_i(\vec{\sigma}(t))} \quad , \tag{3.7}$$

with the inverse temperture $\beta \equiv 1/T$ as a free parameter. To obtain transition probabilities we invoke the principle of detailed balance. Consider a transition $\sigma_i(t) \to \hat{\sigma}_i(t)$ with $\hat{\sigma}_i(t) \in \{\sigma_i(t), 1-\sigma_i(t)\}$, the principle of detailed balance states that $p(\sigma_i(t))p(\sigma_i(t) \to \hat{\sigma}_i(t)) = p(\hat{\sigma}_i(t))p(\hat{\sigma}_i(t) \to \sigma_i(t))$. With Eq.(3.7) this becomes

$$\frac{p(\sigma_i(t) \to \hat{\sigma}_i(t))}{p(\hat{\sigma}_i(t) \to \sigma_i(t))} = \frac{p(\hat{\sigma}_i(t))}{p(\sigma_i(t))} = \mathrm{e}^{-\beta(\hat{B}_i - B_i)} \quad , \tag{3.8}$$

with $\hat{B}_i \equiv B_i(\hat{\sigma}_i(t), \sigma(t)_{j\neq i})$. There are several ways to choose transition probabilites such that Eq.(3.8) is satisfied, we use here the Metropolis transition probabilities given by $p(\sigma_i(t) \to \hat{\sigma}_i(t)) = 1$ if $\hat{B}_i - B_i < 0$ and $p(\sigma_i(t) \to \hat{\sigma}_i(t)) = \exp[-\beta(\hat{B}_i - B_i)]$ otherwise. The stochastic case of diversity dynamics is fully specified by setting $\sigma_i(t+1) = \hat{\sigma}_i(t)$[2].

Whereas in the deterministic case the balance function B_i is minimized, in stochastic diversity dynamics we also have to account for 'disordering effects' due to non-zero temperature T as given in Eq.(3.7). We quantify this with Boltzmann-Gibbs entropy as a measure.

3.2.4 Mean-field approximation

Let us denote the expectation value of $\sigma_i(t)$ by $q_i(t) = \langle\sigma_i(t)\rangle$ and assume that the probability distribution factorizes, i.e. $p(\vec{\sigma}(t)) = \prod_i p_i(\sigma_i(t))$ with $p_i(\sigma_i(t)) = (1-q_i(t))\delta_{\sigma_i(t),0} + q_i(t)\delta_{\sigma_i(t),1}$. In this mean-field approximation the Boltzmann-Gibbs entropy s for item i is given by

$$\begin{aligned} s(\sigma_i(t)) &= -\langle \ln p_i(\sigma_i(t))\rangle \equiv s(q_i(t)) \quad , \\ s(q_i(t)) &= -\Big(1-q_i(t)\Big)\ln(1-q_i(t)) - q_i(t)\ln q_i(t) \quad . \end{aligned} \tag{3.9}$$

With this definition we obtain the 'free energy' functional $\phi(\sigma_i(t))$ for the system as

$$\phi(q_i(t)) = \langle B_i\rangle_{p(\vec{\sigma}(t))} - \frac{s(q_i(t))}{\beta} \quad . \tag{3.10}$$

The asymptotic state of item i, $q_i(t\to\infty) \equiv q_i$, is given by a minimum in free energy. The necessary condition for this, $\partial\phi(q_i)/\partial q_i = 0$, is $\frac{\partial\langle B_i\rangle}{\partial q_i} + \frac{1}{\beta}\ln\left(\frac{q_i}{1-q_i}\right) = 0$, and

$$q_i = \frac{1}{2}\left\{\tanh\left[-\frac{\beta}{2}\frac{\partial\langle B_i\rangle}{\partial q_i}\right] + 1\right\} \quad . \tag{3.11}$$

The self-consistent solution to Eq.(3.11) yields the asymptotic configuration.

3.3 General formulation of evolutionary interactions

Traditionally in the master equations framework[3] interactions are classified by transfer rates for abundances of species. The transfer rates measure how the change in abundance of a given species i is related to the abundance of other species $j_1, j_2, \ldots$. Depending on how i and $j_1, j_2, \ldots$ are chosen, one obtains different systems of differential equations which can be related to a specific form of evolutionary interactions. If species i with abundance x_i replicates with

[2] One can also define the dynamics 'backwards' through the transition probability $p(\hat{\sigma}_i(t) \to \sigma_i(t))$ which could be interpreted as inferring $\vec{\sigma}(t)$ from knowledge of $\vec{\sigma}(t+1)$.

[3] as is typical for traditional evolutionary biology.

rate f_i, the interaction is of type *replication* and is represented as $x_i \xrightarrow{f_i} 2x_i$, (replicator equation [35]). *Competition* is a mechanism where the replication rate of species i also depends on other species j through a transfer rate p_{ij}, $x_i + x_j \xrightarrow{p_{ij}} x_i$. This type of interactions is used in the game dynamical equation [36], which is a special case of the frequency dependent replicator equation [39, 38]. The mechanism *mutation* assigns a mutation or transfer rate q_{ij} between two species according to $x_i \xrightarrow{q_{ij}} x_j$, together with replication and competition we obtain the replicator-mutator equation [37], of which the quasispecies equation [40] is a special case. Replication can take place without replicators, species are then produced by *recombination* processes. In the case of three species i, j and k with a recombination rate α_{ijk}, this mechanism is $x_j + x_k \xrightarrow{\alpha_{ijk}} x_i$. The corresponding dynamical system is called *catalytic network equation* see e.g. [41]. It is formally possible to express replication, mutation and competition as special cases of the recombination mechanism [32, 34]. In this sense recombination mechanisms provide a unifying description of the other evolutionary interactions above – an observation we use as a starting point for our model.

In the general form of a recombination process an arbitrary number of species $j_1, j_2, \ldots, j_n$ influences a given species i. We distinguish two types of interactions of this form, (i) *constructive* interactions or productions where species i benefits from species $j_1, j_2, \ldots, j_n$ and (ii) *destructive* interactions or destructions where the j's are causing harm to i. In the master equation framework constructive interactions correspond to positive transfer rates, destructions to negative ones. We denote the set of species $j_1, j_2, \ldots, j_n = \mathbf{j}$. If the set of all species is $\mathcal{N}$, $\mathbf{j}$ is an element of the set of all subsets of $\mathcal{N}$, i.e. $\mathbf{j}$ is an element of the power set of $\mathcal{N}$, $\mathcal{P}(\mathcal{N})$. A recombination always maps an element from $\mathcal{P}(\mathcal{N})$ to an element from $\mathcal{N}$ via a transfer rate $\alpha_{i,\mathbf{j}}$, i.e. by a map $\alpha : \mathcal{P}(\mathcal{N}) \to \mathcal{N}$. From now on italic indices refer to elements of $\mathcal{N}$, e.g. $i \in \mathcal{N}$, while bold-face indices refer to elements of the power set, $\mathbf{j} \in \mathcal{P}(\mathcal{N})$. Transfer rates are represented by their sign. For convenience define binary state variables for sets of nodes, let $\sigma_{\mathbf{j}}(t) = \prod_{i \in \mathbf{j}} \sigma_i(t)$. The most general form of evolutionary interactions can then be written as

$$\sigma_{\mathbf{j}} \xrightarrow{\alpha_{i,\mathbf{j}}} \sigma_i \quad . \tag{3.12}$$

We summarize in Tab.(3.2) how the evolutionary interaction mechanisms of replication, competition, mutation and recombination are contained in Eq.(3.12) for special choices of $\mathbf{j}$. If there is a constructive interaction between $\mathbf{j}$ and i, i.e. $\mathbf{j}$ is a *constructive set*, we capture it in the *production rule table* $\alpha^+ : \mathcal{P}(\mathcal{N}) \to \mathcal{N}$ with $\alpha^+_{i,\mathbf{j}} = 1$, otherwise $\alpha^+_{i,\mathbf{j}} = 0$. Similarly, if the interaction in Eq.(3.12) is destructive, i.e. $\mathbf{j}$ is a *destructive set*, we record this in the *destruction rule table* $\alpha^- : \mathcal{P}(\mathcal{N}) \to \mathcal{N}$ with $\alpha^-_{i,\mathbf{j}} = 1$, otherwise $\alpha^-_{i,\mathbf{j}} = 0$. At some points in this work we will assume that the rule tables $\alpha^\pm$ are random tensors. In this case they are given by two parameters $n^\pm$ and $r^\pm$. n^+ is the cardinality of constructive sets, $|\mathbf{j}| = n^+$ in Eq.(3.12) and for random α^+ each species i has on average the same number r^+ of constructive sets, $\langle \sum_{\mathbf{j}} \alpha^+_{i,\mathbf{j}} \rangle_i = r^+$. Similarly α^- is given by n^- and r^-.

3.4 Constructive interactions

3.4.1 Constructive dynamical system

We first consider a system with constructive interactions only. We read Eq.(3.12) as 'from $\sigma_{\mathbf{j}}(t) = 1$ follows that $\sigma_i(t+1) = 1$'. In a chemical setting the chemical compounds contained in $\mathbf{j}$ react to give compound i, in an economic setting the goods $\mathbf{j}$ can be assembled to produce good i, see Fig.3.1(a). The constructive dynamical system characterized by Eq.(3.12) is given by

$$\Delta\sigma_i(t) = \operatorname{sgn}\left(\Big(1 - \sigma_i(t)\Big) \sum_{\mathbf{j} \in \mathcal{P}(\mathcal{N})} \alpha^+_{i,\mathbf{j}} \sigma_{\mathbf{j}}(t)\right) \quad , \tag{3.13}$$

Table 3.2: Summary of the traditional evolutionary interaction mechanisms: replication, competition, mutation and recombination. We indicate how the constructive/destructive set **j** has to be specified in Eq.(3.12) in order to recover the various mechanisms in our model.

mechanism				power set notation
replication	x_i	$\xrightarrow{f_i}$	$2x_i$	$\mathbf{j}=\{i\}$
competition	$x_i + x_j$	$\xrightarrow{p_{ij}}$	x_i	$\mathbf{j}=\{i,j\}$
mutation	x_j	$\xrightarrow{q_{ij}}$	x_i	$\mathbf{j}=\{j\}$
recombination	$x_j + x_k$	$\xrightarrow{\alpha_{ijk}}$	x_i	$\mathbf{j}=\{j,k\}$

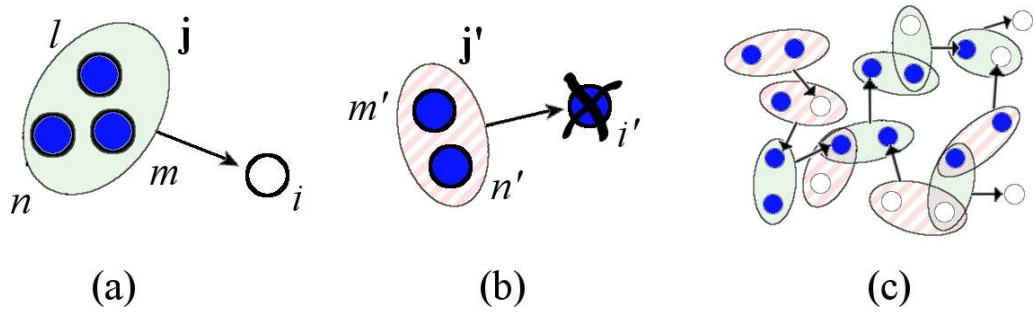

Figure 3.1: A graphical representation of constructive, destructive and combined interactions. (a) The constructive set **j** (green area) contains three species (circles) $\mathbf{j} = \{l, m, n\}$. They produce species i, i.e. $\alpha^+_{i,\mathbf{j}} = 1$. Since each of these species is active (indicated by the blue color of the circle) we have $\sigma_{\mathbf{j}}(t) = 1$ and $\sigma_i(t) = 0$, by Eq.(3.13) $\sigma_i(t+1) = 1$. (b) The destructive set **j'** (red striped area) of cardinality two is active since each of its contained items m', n' is active and interacting with item i' through $\alpha^-_{i',\mathbf{j}'} = 1$. Following Eq.(3.18), $\sigma_{i'}(t) = 1$ will be deactivated, $\sigma_{i'}(t+1) = 0$. (c) A pictorial description of a network with both constructive and destructive interactions at a point in time.

i.e. $f_i(\vec{\sigma}(t))$ from Eq.(3.1) becomes $f_i^+(\vec{\sigma}(t)) = \sum_{\mathbf{j}} \alpha^+_{i,\mathbf{j}} \sigma_{\mathbf{j}}(t)$.

3.4.2 Deterministic constructive diversity dynamics

In the limiting case of $T = 0$ i.e. $\beta \to \infty$ the system deterministically obeys the dynamics Eq. 3.13. The behavior of $D(t \to \infty)$ is well understood; this case is identical to the model studied in [50, 56] for random interaction topologies α^+ given by n^+, r^+ here. $D(\infty)$ was computed as a function of n^+, r^+ *and* $D(0)$. It was shown that this system has a phase transitions formally equivalent to the phase transition of a van der Waals Gas. There exists a critical diversity of initially species $D_c(0)$ above which the system is driven toward an almost fully populated state, see Fig.(3.2); below this threshold the dynamics freezes. All these findings are identical what we find here in the $T = 0$ case.

3.4.3 Stochastic constructive diversity dynamics

We next turn to non-zero temperature T. The crucial feature distinguishing deterministic and stochastic diversity dynamics is the *dependence on the initial conditions*. In the presence of stochastic perturbations the final diversity is not a function of the initial diversity $D(0)$. We

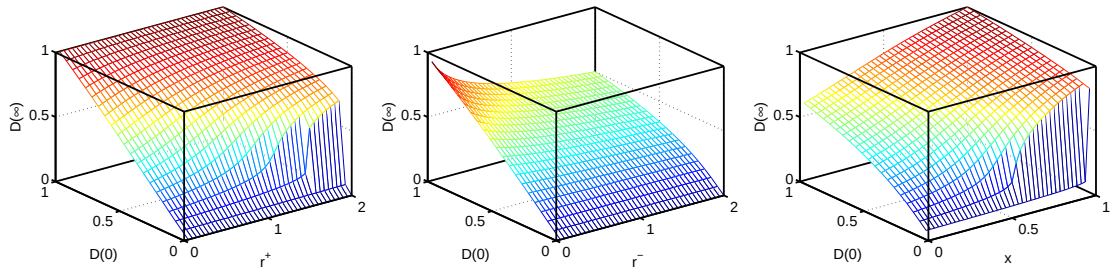

Figure 3.2: *Left:* Phase diagram of the constructive dynamics obtained via solution of the update equation. We see the creative phase transition in the $D(0)$-r^+ plane. Parameters where set to $\beta \to \infty, n^+ = 2$. *Middle:* Phase diagram of the destructive dynamics, with $n^- = 2$, $\beta \to \infty$. The higher r^-, the lower the final diversity. There is no destructive phase transition. *Right:* Phase diagram of the combination of constructive and destructive dynamic. We introduce a parameter x here to interpolate between both cases. We set $\beta \to \infty, n^\pm = 2$. The rule densities are then changed as $r^+ = 3x$ and $r^- = 1 - x$. We find a creative phase transition again.

employ a mean-field approach by assuming that the expectation value of a product equals the product of expectation values, $\langle g_1(\sigma) g_2(\sigma)\rangle = \langle g_1(\sigma)\rangle\langle g_2(\sigma)\rangle$. The expectation value of the constructive potential $\langle V_i^+\rangle_{p(\vec{\sigma}(t))}$ of species i is

$$\langle V_i^+\rangle_{p(\vec{\sigma}(t))} = \Big(1 - q_i(t)\Big) \sum_{\mathbf{j}\in\mathcal{P}(\mathcal{N})} \alpha^+_{i,\mathbf{j}} \prod_{j\in\mathbf{j}} q_j(t) \quad , \tag{3.14}$$

quantifying what *could* be produced given the actual configuration of the system[4].

As mentioned above, μ plays the role of a threshold. For $0 < \mu < 2$ a species gets activated by one constructive set, for $2 < \mu < 4$ at least two constructive sets are needed and etc. From now on we fix the threshold $\mu = 1$. The contribution to free energy is $K_i^+(t) = \frac{1}{2}(\Delta\sigma_i(t))^2$. We can estimate the expectation value $\langle K_i(t)\rangle_{p(\vec{\sigma}(t))}$ by making use of the dynamical relation Eq.(3.13), and get for the mean-field assumption

$$\langle K_i^+\rangle_{p(\vec{\sigma}(t))} = \frac{1}{2}\left(\Big(1 - q_i(t)\Big) \sum_{\mathbf{j}\in\mathcal{P}(\mathcal{N})} \alpha^+_{i,\mathbf{j}} \prod_{j\in\mathbf{j}} q_j(t)\right)^2 \quad . \tag{3.15}$$

Using this in Eq.(3.11) gives us the mean-field solution for arbitrary interaction topologies α^+. To compute it explicitly we assume random interaction topologies. The aim is to derive an expression for $\frac{\partial\langle B_i\rangle}{\partial q_i}$ in the limit $t \to \infty$. Note that $\frac{\partial\langle V_i\rangle}{\partial q_i} = -\sum_{\mathbf{j}\in\mathcal{P}(\mathcal{N})} \alpha^+_{i,\mathbf{j}} \prod_{j\in\mathbf{j}} q_j$. Due to the randomness in α^+ the same average 'field' is exerted on each species. With $q \equiv \langle q_i\rangle_i$ we get $\frac{\partial\langle V_i\rangle}{\partial q_i} = -r^+ q^{n^+}$. We apply the same reasoning to the distance-contribution $\langle K_i^+\rangle_{p(\sigma(t))}$. By first carrying out the derivation and then putting in the assumptions about α^+, we get

$$\frac{\partial\langle B_i\rangle}{\partial q_i} = -r^+ q^{n^+} - (1-q)(r^+ q^{n^+})^2 \quad , \tag{3.16}$$

and the self-consistent solution for the asymptotic abundance q,

$$q = \frac{1}{2}\left\{\tanh\left[\frac{\beta}{2}\left(r^+ q^{n^+} + (1-q)(r^+ q^{n^+})^2\right)\right] + 1\right\} \quad , \tag{3.17}$$

[4]Note that the structure of V_i^+ has a strong similarity to the potential of the paradigmatic Ising model. Our model diverges in the following ways: (i) interactions are defined not between nodes but between constructive sets and nodes and (ii) interactions are not symmetric, the action of $\mathbf{j}$ on i does not equal the action of i on $\mathbf{j}$.

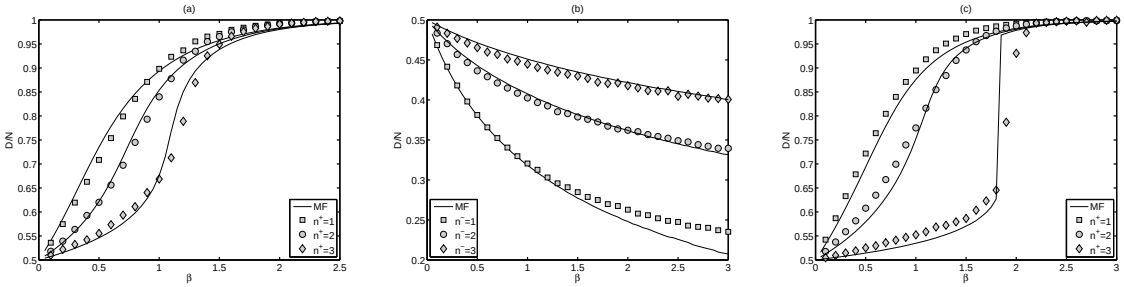

Figure 3.3: Diversity as a function of inverse temperature β for various dynamical systems obtained from a mean-field approach (lines) and Metropolis simulations (symbols). (a) Constructive dynamics with $r^+ = 2$. (b) Destructive dynamics with $r^- = 2$. (c) Combined dynamics with $r^+ = 3$, $r^- = 1$ and $n^- = 2$.

from which the diversity follows as $D(t \to \infty) = Nq$. We compare predictions of Eq.(3.17) with simulations results from a Metropolis algorithm. The later was implemented in the following way: We constructed a random α^+ and initialized the system with a random initial condition $\vec{\sigma}(0)$. After initialization the algorithm applies the following procedure to each species once within one timestep (random sequential update):

- Pick a species i randomly.
- Calculate $B_i = K_i + V_i$, according to Eqs.(3.4) and (3.5) with $\sigma_i'(t) = \sigma_i(t)$.
- Calculate $B_i = K_i + V_i$ with $\sigma_i'(t) = 1 - \sigma_i(t)$.
- Calculate $\Delta B = B_i\Big(\sigma_i'(t) = 1 - \sigma_i(t)\Big) - B_i\Big(\sigma_i'(t) = \sigma_i(t)\Big)$
- If $\Delta B < 0$ set $\sigma_i(t+1) = 1 - \sigma_i(t)$.
- If $\Delta B > 0$ set $\sigma_i(t+1) = 1 - \sigma_i(t)$ with probability $\mathrm{e}^{-\beta \Delta B}$.

We executed the algorithm for one realization of α^+ for 10^3 timesteps and averaged over this time-span after discarding transient behavior (typically about 50 iterations). We performed simulations for system sizes of $N = 10^2 - 10^4$ without noticing size effects on the results. However, the time-to-converge depends on N. We show the degree of agreement of simulations and Eq.(3.17) in Fig.3.3(a).

3.5 Destructive dynamics

3.5.1 Destructive dynamical systems

Assume now that only destructive interactions take place, e.g. two chemicals catalyzing the consumption of another chemical species, or biological species gaining (in symbiosis) an evolutionary advantage over another species. Eq.(3.12) is now read as 'from $\sigma_{\mathbf{j}}(t) = 1$ follows $\sigma_i(t+1) = 0$', see Fig.(3.1(b)). To formulate this as a dynamical system as in Eq.(3.3) set $f_i(\vec{\sigma}(t)) \to f_i^-(\vec{\sigma}(t)) = -\sum_{\mathbf{j}} \alpha_{i,\mathbf{j}}^- \sigma_{\mathbf{j}}(t)$ to get

$$\Delta\sigma_i(t) = \mathrm{sgn}\left(-\sigma_i(t) \sum_{\mathbf{j} \in \mathcal{P}(\mathcal{N})} \alpha_{i,\mathbf{j}}^- \sigma_{\mathbf{j}}(t)\right) \quad . \tag{3.18}$$

We discuss the deterministic ($T = 0$) and stochastic ($T > 0$) scenario.

3.5.2 Deterministic destructive diversity dynamics

In the deterministic case the asymptotic diversity $D(t \to \infty)$ is a function of the initial diversity. Let us discuss the case of a completely random destructive rule table α^-. By denoting $q(t) = D(t)/N$ we can derive an update equation for $q(t)$ following the same reasoning as in [50], $q(t+1) = q(t) - \Delta^- q(t)$ with $\Delta^- q(t) = r^- q(t)\Big(q^{n^-}(t) - q^{n^-}(t-1)\Big)$. In the limit of sparse rule densities r^- this leads to $q(t \to \infty) = q(0) - n^- r^- q^{n^-+1}$. In contrast to constructive dynamics, destructive dynamics do not exhibit a phase transition. With more species being destroyed the number of deactivated power nodes increases even faster, thus the process comes to a halt without reaching a strongly unpopulated state, see Fig.(3.2).

Stochastic destructive diversity dynamics

For a stochastic variant of the destructive dynamical system of Eq.(3.18) we repeat the analysis of the constructive case. We start with the corresponding destructive potential and distance terms,

$$\begin{aligned} \langle V_i^- \rangle_{p(\vec{\sigma}(t))} &= q_i(t) \sum_{\mathbf{j} \in \mathcal{P}(\mathcal{N})} \alpha^-_{i,\mathbf{j}} \prod_{j \in \mathbf{j}} q_j(t) \quad , \\ \langle K_i^- \rangle_{p(\vec{\sigma}(t))} &= \frac{1}{2} \left(q_i(t) \sum_{\mathbf{j} \in \mathcal{P}(\mathcal{N})} \alpha^-_{i,\mathbf{j}} \prod_{j \in \mathbf{j}} q_j(t) \right)^2 \quad . \end{aligned} \tag{3.19}$$

We proceed with the derivation of the destructive balance function B_i and get

$$\frac{\partial \langle B_i \rangle}{\partial q_i} = r^- q^{n^-} + q (r^- q^{n^-})^2 \quad , \tag{3.20}$$

and the self-consistent solution for the asymptotic abundance q,

$$q = \frac{1}{2} \left\{ \tanh \left[-\frac{\beta}{2} \left(r^- q^{n^-} + q (r^- q^{n^-})^2 \right) \right] + 1 \right\} \quad . \tag{3.21}$$

We compare this prediction to results of a Metropolis simulation in Fig.3.3(b). As is seen in the $n^- = 1$ case, the deviation between Eq.(3.21) and simulations increases with β. For higher n^- and r^- the same extent of deviation occurs for a higher value of β. The mean-field approximation starts to significantly differ from simulations once entropic effects become negligible and the system's evolution approaches the deterministic scenario, that is $\mathrm{e}^{-\beta \Delta B_i} \lesssim 1/N \ \forall i$ (on average less than one random state flip per iteration). To approximate $V_i^-(t) = \sigma_i(t) \sum_{\mathbf{j}} \alpha^-_{i,\mathbf{j}} \prod_{j \in \mathbf{j}} \sigma_j(t)$ at any time t we have to consider the species which have *not* been deactivated at $t-1$ – the system possesses memory. This is not captured in the mean-field approximation $\langle V_i^- \rangle = r^- q^{n^-}$ where we assume the populated species to be randomly distributed over N possible species at each time t. In the destructive case the mean-field approach thus works best whenever the random fluctuations are large enough to 'smear out' this memory effect, otherwise the system is better approximated by the deterministic description.

3.6 Combined dynamics

3.6.1 Combined dynamical systems

We now study the interplay of both constructive and destructive dynamics [52, 57]; the situation is sketched in Fig.(3.1(c)). Destructive interactions represent an implicit selection mechanism[57]. Each species may be targeted (influenced) by constructive *and* destructive interactions. Assume

that each interaction has equal influence. If the constructive forces outweigh the destructive ones the species prefers to be active and *vice versa*. For some systems other choices of weighting could be more appropriate (e.g. assuming that *one* destructive interaction outweighs any number of constructive ones – 'it is easier to destroy than to build'). It is straight-forward to incorporate alternative weighting schemes in the present framework.

To combine constructive and destructive interactions we add their indicator functions,

$$f_i(\vec{\sigma}(t)) = f_i^+(\vec{\sigma}(t)) + f_i^-(\vec{\sigma}(t)) = \sum_{\mathbf{j}} \alpha_{i,\mathbf{j}}^+ \sigma_{\mathbf{j}}(t) - \sum_{\mathbf{j}} \alpha_{i,\mathbf{j}}^- \sigma_{\mathbf{j}}(t) \quad , \tag{3.22}$$

and get for the dynamical equation

$$\Delta\sigma_i(t) = \mathrm{sgn}\left[\Big(1-\sigma_i(t)\Big)R(f_i(\vec{\sigma}(t))) - \sigma_i(t)R(-f_i(\vec{\sigma}(t)))\right] \quad . \tag{3.23}$$

The purely destructive or constructive dynamical systems are recovered by setting $\alpha^{\pm} = 0$.

3.6.2 Deterministic combined diversity dynamics

To obtain an estimate for the asymptotic diversity, we make again use of an update equation combining the finding for the constructive and destructive cases. If we denote $\Delta q^+(t)$ ($\Delta q^-(t)$) to be the average in-(de)crements in the constructive (destructive) scenario, we have to study the update equation $q(t+1) = q(t) + \Delta q^+(t) - \Delta q^-(t)$. This equation is solved making the same ansatz as in [50], yielding $q(t\to\infty) = q(0) - n^- r^- q^{n^-+1} + n^+ r^+ (1-q) q.^(n^+)$, see Fig.(3.2).

3.6.3 Stochastic combined diversity dynamics

Let us calculate $\langle B_i\rangle$ for the stochastic scenario. The expectation value of the distance-contribution, $\langle K_i\rangle_{p(\vec{\sigma}(t))}$, is more involved now. Constructive (destructive) dynamics take place under the condition that $f_i(\vec{\sigma}(t)) \geq 0 (\leq 0)$. Start with an expression for the probability that $f_i(\vec{\sigma}(t))$ is positive (negative) semidefinite, $p^{\pm}$. Consider random interaction topologies specified by $r^{\pm}, n^{\pm}$. Define $p(k, r^+)$ as the probability that there are exactly k active constructive interactions, that is $p(k, r^+) \equiv \binom{r^+}{k} q^{n^+ k}(1-q^{n^+})^{r^+-k}$. Analogously, $q(l, r^-)$ is the probability that exactly l out of r^- destructive interactions are active. Then

$$\begin{aligned} p^+ &= \sum_{k=1}^{r^+} p(k, r^+) \sum_{l=0}^{\min(k-1, r^-)} q(l, r^-) \quad , \\ p^- &= \sum_{l=1}^{r^-} q(l, r^-) \sum_{k=0}^{\min(l-1, r^+)} p(k, r^+) \quad . \end{aligned} \tag{3.24}$$

The average distance follows as

$$\langle K_i\rangle_{p(\sigma)} = \frac{1}{2}\Big((1-q_i)p^+ + q_i p^-\Big)^2 \quad , \tag{3.25}$$

and, abbreviating $f_i(\vec{\sigma}(t)) \equiv f_i$, the potential is

$$\langle V_i\rangle_{p(\sigma)} = \left|(1-q_i)\,R(f_i) - q_i R(-f_i)\right| \quad . \tag{3.26}$$

Taking the derivative with respect to q_i the mean-field result is

$$\frac{\partial\langle B_i\rangle}{\partial q_i} = -r^+ q^{n^+} + r^- q^{n^-} - \left[(1-q)p^+ + q p^-\right](p^+ - p^-) \quad , \tag{3.27}$$

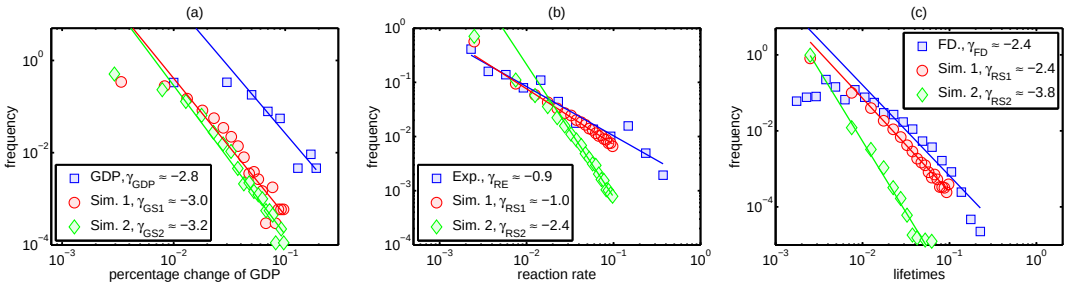

Figure 3.4: We compare the distribution of systemic observables of evolutionary systems with those of the combined stochastic model for two different parameter settings: *Simulation 1* with $\beta = 15$, $r^{\pm} = 5$, $n^{\pm} = 2$ and *Simulation 2* with $\beta = 15$, $r^{+} = 8$, $r^{-} = 12$, $n^{\pm} = 2$. Each distribution has been normalized (sum over all data points equals one). (a) The percent change of GDP of the UK since 1950 is compared to the model. (b) The reaction rate distribution in the model and in the metabolic network of *E. coli* is shown. (c) Species lifetime distributions as found in fossil data are well reproduced with the model.

with the self-consistent solution for the asymptotic abundance q

$$q = \frac{1}{2}\left\{\tanh\left[\frac{\beta}{2}\left(r^{+}q^{n^{+}} - r^{-}q^{n^{-}} + \left[(1-q)p^{+} + qp^{-}\right]\left(p^{+} - p^{-}\right)\right)\right] + 1\right\}. \tag{3.28}$$

Again we compare the MF prediction to results of a Metropolis simulation of the full model in Fig.3.3(c).

3.7 Discussion on Empirical Relevance

3.7.1 Economical setting

We interpret the model in different evolutionary contexts and compare its behavior to measured data. In an economic setting one can identify the number of active interactions as a measure for the productive output of an economy – for example the GDP [57]. An interaction is defined to be active iff $\sigma_i(t) = \sigma_{\mathbf{j}}(t) = \alpha^{\pm}_{i,\mathbf{j}} = 1$. We show in Fig.3.4(a) a comparison between the actual distribution of percent increments of the GDP of the UK and the number of active productions from the combined stochastic model for two different parameter settings. In one setting $\beta = 15$, $r^{\pm} = 5$, $n^{\pm} = 2$ is used, the other has a denser interaction topology, $\beta = 15$, $r^{+} = 8$, $r^{-} = 12$, $n^{\pm} = 2$. Both model and real-world GDP timeseries produce fat-tailed distributions, with power exponents in the range between -2 and -4. These features are also found in GDP timeseries of other countries and for a wide range of model parameters, see e.g. [57].

3.7.2 Chemical setting

Another possible interpretation of the combined stochastic system is a chemical reaction network. In this case chemical species $\mathbf{j} = \{j_1, j_2, \dots\}$ are producing or degrading chemical i. There are $N(r^{+} + r^{-})$ reactions. A reaction rate is defined as the frequency with which a certain reaction is active and a reaction is active if $\alpha^{\pm}_{i,\mathbf{j}} = 1$, $\sigma_i(t) = 1$ and $\sigma_{\mathbf{j}}(t) = 1$. This is compared to reaction rates in the metabolic network of *E. coli* [59] in Fig.3.4(b). Distributions of reaction rates in both cases, model and living organism, are fat-tailed. Least-squares fits to model power-laws yield exponents in the range of -1 to -3, depending on parameters. This compares well to the value of -1 found for *E. coli*.

3.7.3 Biological evolution setting

Translated into a macro-ecological setting, one can compare the distribution of lifetimes of species in the combined stochastic model (number of iterations a given species is unintermitted abundant) with the distribution of species lifetimes in fossil data [60] in Fig.(3.4(c)). Again one finds power-laws in the model with exponents between -2 and -4, which matches well with the paleontologic data, which suggest slopes between -2 and -3. Note that there is a strong dependence on the values used for the fit. We work with an intermediate choice in Fig.3.4(c).

3.8 Discussion

We propose a general framework to systematically study a large class of dynamical evolutionary systems defined on an arbitrate large number of species. The trajectory of existence of each species is governed by a function incorporating information of the surroundings – the existence of other species. We show how to express the resulting system dynamics via a variational principle. We discuss deterministic and stochastic variants. For the latter we derive a closed expression for the asymptotic diversity of evolutionary systems within a mean-field approximation. We discuss the quality of this approximation with respect to Metropolis simulations of the full model. Although the model explicitly introduces strong correlations between species' abundances the mean-field approximation for asymptotic diversities match the simulation data surprisingly well. The model can be seen as a generalization of several previous models, which are contained as special cases. The deterministic constructive case is identical to the random catalytic networks studied in [50]. In the model of Solé and Manrubia only linear interactions are allowed (i.e. $|j| = 1$ in Eq.(3.12)) and new species are created not by endogenous recombinations as here, but by an explicit mutation mechanism. As discussed in [57], $f_i(\vec{\sigma}(t))$ in our model plays the identical role as the randomly assigned fitness values in the Bak-Sneppen model [46]. To recover the NK-model [45], associate each species here with a random bit-string and allow interactions only between species who differ by single-point mutations.

We find that the model of constructive and destructive interactions reproduces stylized facts of man-made (economies) and natural evolutionary systems (metabolic networks, macro-ecology) across different orders of magnitude. We belief this adds empirical substance to our claim that we have identified a crucial and ubiquitous building block of evolutionary systems with recombinatory, non-linear interactions within a simple binary framework. The model systematically expands on the idea that the concept of fitness is an *a posteriori* concept. Fitness in the traditional sense can of course be reconstructed for every timestep in our model. It is nothing but the co-evolving network of rates of the actually active (productive) processes at a given time, see [57] for more details. It becomes clear that fitness can not be used as concept with much predictive value, even if a 'Darwinian Daemon' knowing all mutual influences at a given time would exist. The proposed model is 'Darwinian Daemon' free.

This work was supported in part by the Austrian Science Fund, FWF P19132.

4 Schumpeterian economic dynamics as a model of evolution

The essential point to grasp is that in dealing with capitalism we are dealing with an evolutionary process.
Joseph A. Schumpeter, 1883 - 1950

We will now develop the abstract model of evolution proposed in the former chapter into a minimum model for economic systems. Surprisingly, a qualitative description of this undertaking goes back to the economist J.A. Schumpeter. We have now a formal machinery at hands to understand his work *quantitatively*.

4.1 Introduction

The essence of the work of Joseph Schumpeter is to understand economic development and growth as an evolutionary process, out of equilibrium, driven by the appearance and disappearance of goods and services. Goods and services appear and disappear endogenously as a result of technological progress and innovation, which is driven by market participants (firms and consumers) maximizing their respective profit or utility functions. Trying to understand capitalist economy without these concepts is "... like Hamlet without the Danish prince" [61] [1].

Schumpeterian growth is based on the endogenous introduction of new goods, products, processes or services and is governed by the process of *creative destruction* [62, 61]. Creative destruction means that the appearance of a new good (through a successful innovation) can have devastating effects on seemingly well established goods, eventually driving them out of business. Examples include the collapse of horse carriage industry with the innovation of the combustion engine, or the disappearance of Polaroid cameras with the invention of the digital camera. The process of creative destruction is sometimes referred to as *gales of destruction*, pointing to the fact that economic consequences of innovation can be severe and massive. Excluding innovations leads to a stationary state which is described by Walrasian equilibrium [30]. Entrepreneurs, by transforming ideas into innovations, disturb this equilibrium and cause economic development. With this view Schumpeter aimed at a qualitative understanding of empirical economic facts such as business cycles, or fluctuations [62].

Surprisingly, current main stream economics, general equilibrium theory in particular, systematically focuses on situations where none of the above elements are present. By excluding evolutionary and dynamical aspects from economic models a mathematical treatment often becomes possible; this however comes at the price that many fundamental features of economics will as a consequence not be understood, see e.g. [64]. Most complex systems, and many aspects of economics in particular, can not be reduced to a few parameters - without throwing the prince out of *Hamlet*. Schumpeter himself criticized e.g. J.M. Keynes for proposing abstract models

[1] From [61] chapter 8: "The essential point to grasp is that in dealing with capitalism we are dealing with an evolutionary process [...] The fundamental impulse that sets and keeps the capitalist engine in motion comes from the new consumer goods, the new methods of production, or transportation, the new forms of industrial organization that capitalist enterprise creates [...] In the case of retail trade the competition that matters arises not from additional shops of the same type, but from the department store, the chain store, the mail-order house and the super market, which are bound to destroy those pyramids sooner or later. Now a theoretical construction which neglects this essential element of the case neglects all that is most typically capitalist about it; even if correct in logic as well as in fact, it is like Hamlet without the Danish prince."

Table 4.1: Moments of the percent-increment processes shown in Fig. 4.1 and model results for two choices of the model parameter p.

	mean	variance	skewness	kurtosis
GDP	0.58	1.04	0.26	6.30
business failures	6.23	939.68	2.58	17.49
patents	5.17	305.12	1.58	9.13
model (p=0.01)	0.70	138.90	0.43	3.77
model (p=0.0001)	0.21	40.11	0.81	9.63

on the basis of insubstantial evidence and for freezing all but a few variables. Of the remaining ones, one could then argue that one caused another in a simple fashion. For this the expression *Ricardian vice* was coined [63], for an overview see [65]. A dangerous consequence of this vice is that it suggests that valid policy conclusions could be derived. Note that what is today called Schumpeterian growth theory originated in the 1990s [66, 67, 68, 69, 70]. It relates output to labour, technology and population growth under various assumptions, and has little to do with the evolutionary aspects of Schumpeterian economics. Our following proposal of a dynamical, fully endogenous evolutionary model has nothing to do with these developments.

Schumpeter's contributions on economic development are phrased in non - mathematical terms – for a good reason: His ideas are non-equilibrium concepts based non-linear models of evolutionary processes, which are hard to (to some extent maybe impossible) capture in mathematical terms. Only in recent years there have been serious attempts to make evolution dynamics – including their endogenous destructive elements (see e.g. [54]) – a predictive and falsifiable theory, in the sense that quantitative models generate testable predictions on e.g. statistical features of evolutionary time series, such as the species diversity, species lifetimes, genera per species, etc. [45, 46, 43, 54, 71, 3, 52]. A large number of recent models are based on Kauffman networks, see e.g. [53] and references therein. Statistical features, often characterized by power-laws in corresponding distribution functions, can then be compared with e.g. fossil data. A particular experimental feature of evolutionary timeseries is the occurrence of so-called punctuated equilibria, which imply that the diversity of species is relative robust over large timescales, and only changes (often drastically) over very short timescales. This leads to non-Brownian processes showing clustered volatility. For pioneering work on punctuated equilibria see [72].

These features are also present in economic timeseries related to Schumpeterian dynamics. In Fig. 4.1 we show timeseries for GDP (as a proxy for economic productivity), the number of firm failures (as an example of destructive dynamics) and the number of patents issued in the US (for an estimate for the innovation potential). In all cases the percent increments of the timeseries show three characteristics: they show phases of relatively little activity followed by bursts of activity, they show clustered volatility, and they show non-Gaussian distributions, whose moments are summarized in Table 4.1.

The bottleneck of a formal understanding of Schumpeterian processes is the current understanding of evolutionary dynamics. The reason why progress is limited in this direction lies in the mathematical and conceptual difficulties in dealing with this type of dynamics. In particular the facts that the system is an open system (hard to find a 'constant' of motion, diversity, interactions, new possibilities constantly change). That the system does not reach an interesting or meaningful equilibrium is a direct consequence.

Some recent progress in a quantitative formulation of the dynamics of technological progress was made in [55], where certain products (logical circuits) are produced at random. Each of these products has a certain characteristic function (they compute something). According to their function these products get selected through an exogenous selection mechanism. Even though the model produces some realistic results in the spirit of Schumpeterian dynamics the

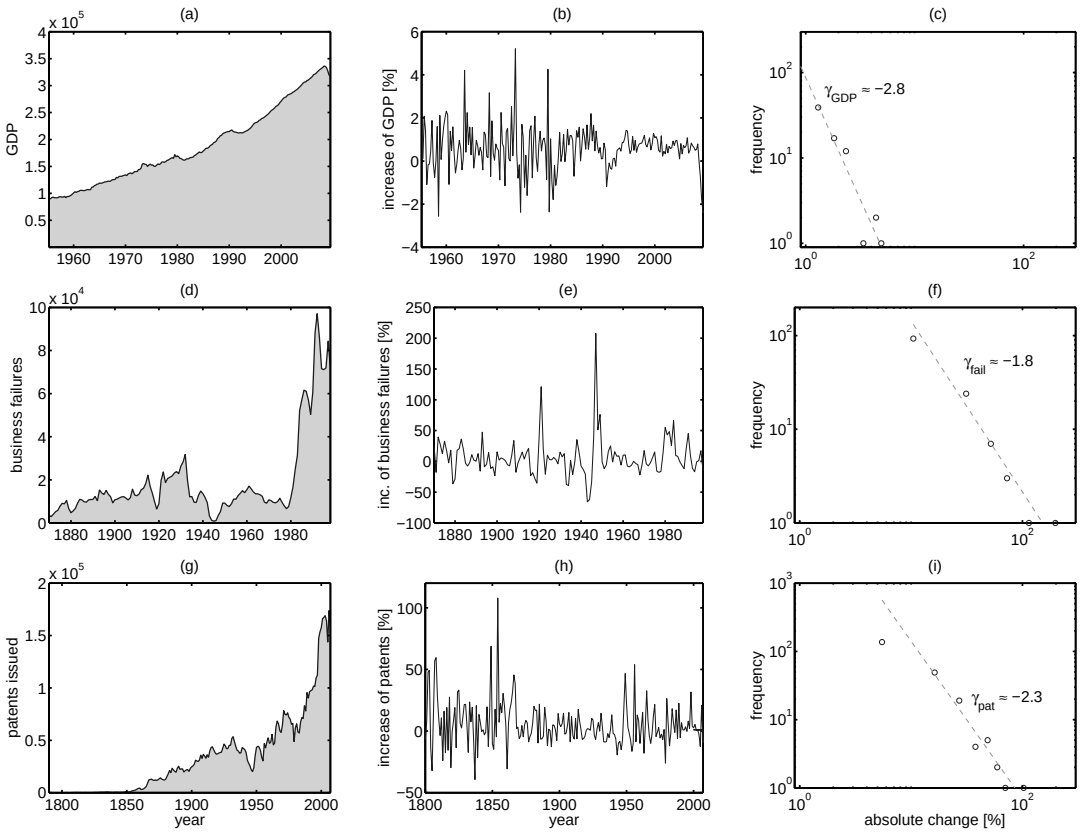

Figure 4.1: (a) GDP of the UK starting 1950 [73]. (b) Percent increase of GDP from (a). (c) Histogram for (b); a least squares fit to a power-law yields a slope of ≈ -2.8. (d)-(f) Number of business failures in the conterminous United States from 1870 onward, data from [31]. (e) Annual change in percent for (d), (f) histogram for (d); power-law exponent ≈ -1.8. (g) Total number of patents issued on inventions in the United States from 1790 to 2007, data from [31]. (h) Annual increase of patents in percent, starting 1800. (i) Histogram of absolute values of (h); power-law exponent ≈ -2.3.

necessity of exogenous utility or fitness functions for the selection process is unsatisfactory. By trying to get rid of such endogenous elements in describing evolutionary dynamics some purely endogenous models for creative and destructive processes have been proposed [50, 56]. These however miss a satisfactory combination of productive and destructive elements, which is attempted here.

In this paper we present a simple toy model that tries to capture the essence of Schumpeterian dynamics. It is (in principle) an open model, that endogenously produces new goods and services. These new elements in the system then 'interact' with each other (and with old existing goods) in the sense that these interactions can serve to aid the production of yet new goods and services. Which good can produce an other one is predetermined in an infinite hypothetical *production table* , which captures all possible (thinkable) combinations of goods that lead to the production of novel ones. Also the opposite is true, a good that gets produced can have an adverse effect on an existing good. Which good – given it gets produced – drives out which other good, is given by a predetermined *destruction table*.

This model builds on previous work developed in a biological context [52]. The aim of the present model is to provide a tool that allows to understand Schumpeterian dynamics, including its gales of destruction within a minimum framework. The model is able to provide an open, non-equilibrium concept and explains important dynamical facts of Schumpeterian dynamics. These include phases of boosts in economic development (measured in the diversity of available goods), phases of crashes, and phases of relative stability followed by turbulent restructuring of the entire economic 'world'. It is possible to interpret the successions of characteristic phases of construction, destruction and relative stability as 'business cycles'. We observe clustered volatility and power-laws in our model data. Within this model we are able to understand various phases of Schumpeterian dynamics as topological (emergent) properties of the dynamical production networks. Parts of the model are exactly solvable, for the full model however, we have to rely on a simple agent based computational realization.

4.2 Model

Schumpeterian economics is driven by the actions of 'entrepreneurs' who realize business ideas. The result of these actions are new goods and services which enter the economic scene – the market. Usually new goods and services are (re)combinations or substitutions of existing things. The Ipod is a combination of some electrical parts, Wikipedia is a combination of the internet and the concept of an encyclopedia. New goods and services can 'act on the world' in three ways: They can be used to produce other new things (as e.g. modular components), they can have a negative effect on existing things by suppressing their production or driving them out of the market (destruction), or they have no effect at all.

4.2.1 Goods

In our simple model all thinkable goods and services are components in a time-dependent N-dimensional vector $\vec{\sigma}(t)$. N can be very large, even infinite. For simplicity the components of this vector are binary. $\sigma_i(t) = 1$ means that good i is present (it exists) at time t, $\sigma_k(t) = 0$, means service k does not exist at t, either because it is not invented yet, or it got eliminated from the market. (In a more general continuous setting, the state vector $0 < \sigma_i(t) < 1$, could be the relative abundance of good i w.r.t. to the abundances of the other goods). New products come into being through combination of already existing products. An innovation – the production of a new good i – can only happen if all necessary components (e.g. parts) are simultaneously available (exist). If a combination of goods j and k is a method to produce i, both j and k must be available in the system. Technically $\sigma(t)$ can be seen as the *availability status*, if $\sigma_i(t) = (0)1$ product i is (not) accessible for production of future new goods, nor for the destruction of

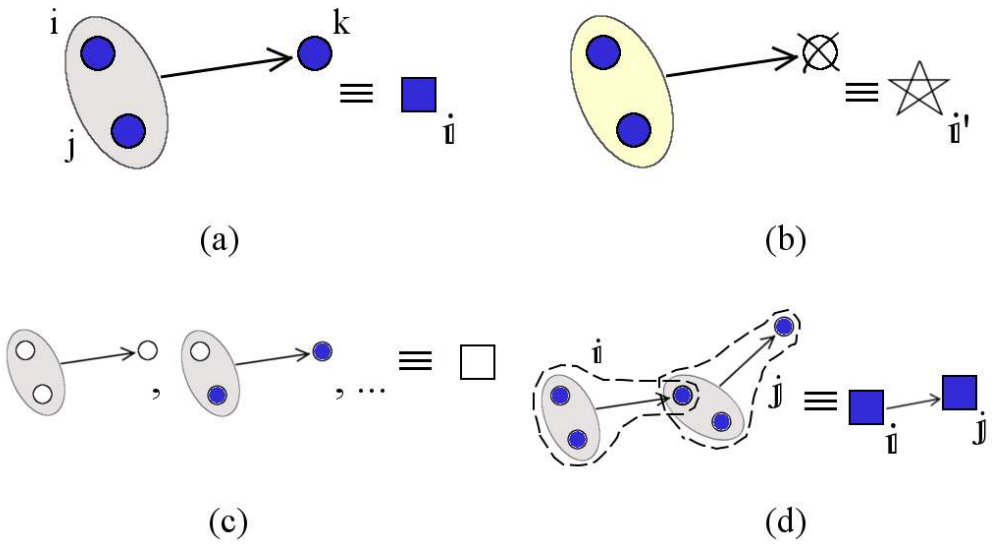

Figure 4.2: (a) Illustration of a production process. Products i and j reside in a productive set. There exists a production rule $\alpha^+_{ijk} = 1$. Thus product k becomes produced. This active production is depicted as a full square and indexed by **i**. (b) The same as (a) for a destruction process. Products i' and j' substitute k' via the destruction rule $\alpha^-_{i'j'k'} = 1$. (c) Examples of non-active productions (6 possible). Non-active productions are symbolized as open squares. (d) Definition of a link in the active production network: if a good produced by a production **i** is part of the productive set of an other active production **j**, production **j** gets a directed link from production **i**.

existing ones. The *product diversity* of the market is defined as $D(t) = \frac{1}{N}\sum_{i=1}^{N}\sigma_i(t)$.

4.2.2 Entrepreneurs/Production

Whether a product k can be produced from components i and j is encoded in a *production table*, α^+_{ijk}. If it is *possible* to produce good k from i and j (i.e. $\alpha^+_{ijk} > 0$), this is called a *production*. An entry in the production table is in principle a real number which quantifies the *rate* at which a good is produced. Here for simplicity an entry in α^+_{ijk} is assumed to be binary, 0 or 1. If goods i and j can produce k, $\alpha^+_{ijk} = 1$, goods i and j are called the *productive set* of k. If there is no production method associated with this combination, $\alpha^+_{ijk} = 0$. The production process is then given by

$$\sigma_k(t+1) = \alpha^+_{ijk}\sigma_i(t)\sigma_j(t) \quad , \tag{4.1}$$

regardless whether $\sigma_k(t) = 0$ or 1. If a production is *actually* producing k, (i.e. $\sigma_i(t) = \sigma_j(t) = \sigma_k(t) = \alpha^+_{ijk} = 1$), we call it an *active production*, see Fig. 4.2 (a).

The role of the entrepreneur is to discover that k can get produced as a combination of i and j, i.e. to discover and activate the production. In general, a particular good can be produced through more than one production method. In our (binary) notation the number of ways to produce good k is $N_k^{\text{prod}}(t) = \sum_{ij}\alpha^+_{ijk}\sigma_i(t)\sigma_j(t)$.

4.2.3 Competition/Destruction

If a new product can get produced and serves a purpose (or a need) which hitherto has been provided by another product, the new and the old products are now in competition. The good

that can be produced in a cheaper way or that is more robust etc., will sooner or later drive the other one from the market. This mechanism we incorporate in the model by allowing that a combination of two existing goods can lead to a destructive influence on another product. The combination of goods i' and j' produces a good l which then drives product k' out of the market. To keep it simple we say: the combination of i' and j' has a destructive influence on k'. We capture all possible destructive combinations in a *destruction rule table* $\alpha^-_{i'j'k'}$, see Fig. 4.2 (b). If $\alpha^-_{i'j'k'} = 1$, products i' and j' substitute product k'. We call $\{i', j'\}$ the *destructive set* for k'. Note that in this way we don't have to explicitly produce the competing good l. In the absence of a destruction process, $\alpha^-_{i'j'k'} = 0$. As before an *active destruction* is only happening if $\sigma_{i'}(t) = \sigma_{j'}(t) = \sigma_{k'}(t) = \alpha^-_{i'j'k'} = 1$. The elementary dynamical update for a destructive process reads (for a good which is present at time t, i.e. $\sigma_k(t) = 1$),

$$\sigma_k(t+1) = 1 - \alpha^-_{ijk}\sigma_i(t)\sigma_j(t) \tag{4.2}$$

In general , at any given time, a good k can be driven out of the market by more than one substitute – in our notation – by $N_k^{\rm destr}(t) = \sum_{ij} \alpha^-_{ijk}\sigma_i(t)\sigma_j(t)$ destructive pairs.

Imagine the N goods as circles assembled on a plane, see Fig. 4.3 (a). If they exist they are plotted as full blue circles, if they are not produced, they are white open circles. All existing goods have at least one productive set (pair of 2 existing (blue) circles); at time t there exist $N_i^{\rm prod}(t)$ such sets. Many circles will in the same way assemble to form destructive sets, the exact number for node i being $N_i^{\rm destr}(t)$. Now draw a circle around each productive and destructive set and connect each set with the good it is producing/destroying. The graph which is produced this way, Fig 4.3 (a) is the *economic web* [29] of products. In this web in general every good will be connected to several productive/destructive sets. To specify a dynamics we decide that if there exist more production processes associated with a particular good than there exist destructive processes associated with it, the good will be produced. If there are more destructive than productive sets associated with a good, it will not be produced, or it will get destroyed if it exists. If the number of productive and destructive sets for a good i are the same, the state of i will not be changed, i.e. $\sigma_i(t+1) = \sigma_i(t)$. More quantitatively this reads

$$\begin{aligned} N_i^{\rm prod}(t) > N_i^{\rm destr}(t) &\rightarrow \sigma_i(t+1) = 1 \\ N_i^{\rm prod}(t) < N_i^{\rm destr}(t) &\rightarrow \sigma_i(t+1) = 0 \\ N_i^{\rm prod}(t) = N_i^{\rm destr}(t) &\rightarrow \sigma_i(t+1) = \sigma_i(t). \end{aligned} \tag{4.3}$$

Note that a production or destruction is only active if both goods in its production / destruction set are currently available. Thus changes in the status of a product possibly induce changes in the status of active production / destruction network.

4.2.4 The active production network

It is essential to distinguish the production rules encoded in the tensors $\alpha^\pm$ and the *active production networks* $A(t)$. $\alpha^\pm$ is a collection of static rules of all potential ways to produce all thinkable goods. These rules exist regardless if goods exist or not. The production network $A(t)$ captures the set of actual active productions taking place at a given time t. It maps the state of the economy $\vec{\sigma}(t)$ (existing goods and services) with its rules α^+ onto the set of active productions. It can be derived in the following way. A *production* is defined as a pair (i, j) which produce a good k, and is nothing but a non-zero entry in α^+. There are Nr^+ productions in the economy, where r^+ is the (average) number of productions per good. Non-existing goods are open circles, the symbol used for a production is a square. A production is called an *active production* if the production set and the produced node all exist ($\sigma_i(t) = \sigma_j(t) = \sigma_k(t) = 1$). An active production is shown in Fig. 4.2 (a) symbolized as a filled square. In (c) we show

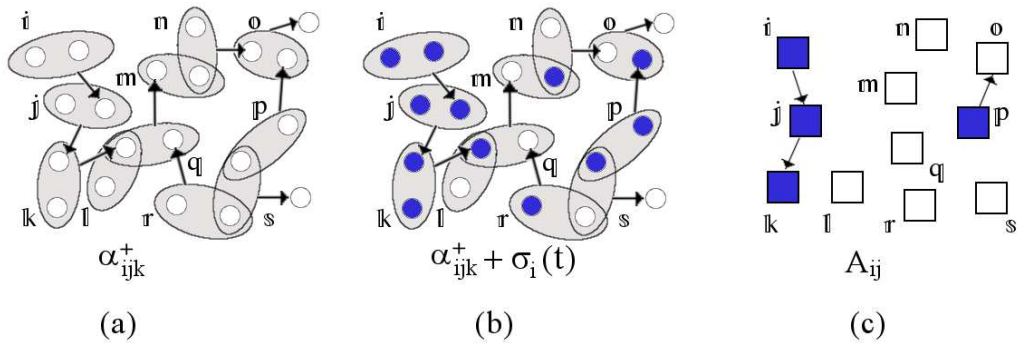

Figure 4.3: Comparison between static production rules α^+ (a) and active production networks $A(t)$ (c). Production rules are all possible combinations to produce all thinkable goods in an economy. They correspond to all non - zero entries in $\alpha^{\pm}$. In (b) the actual state of the system $\vec{\sigma}(t)$ (which goods exist) is superimposed on $\alpha^{\pm}$. Representing (b) not in terms of goods but in terms of productions we arrive at the active production network (c), using the definition for links in Fig. 4.2 (d).

some examples of non-active productions (open square). We label active productions by boldface indices, $\mathbf{i} \in \{1, \ldots Nr^+\}$. These constitute the nodes of the *active production network*. A directed link from active production node $\mathbf{i}$ to node $\mathbf{j}$ is defined if the *node* produced by production $\mathbf{i}$ is in the productive set of production $\mathbf{j}$, see 4.2 (d). It is then denoted as $A_{\mathbf{ij}} = 1$. This definition is illustrated in Fig. 4.2 (c). As an example of how to construct the active production network $A(t)$ from $\vec{\sigma}(t)$ and α^+, see Fig. 4.3. In Fig. 4.3 (a) we show a section of the static α^+, in (b) we superimpose the knowledge of which of these nodes actually exist at time t. In (c) all productions are shown as squares (active ones full, non-active ones empty). The links between the active productions constitute the active production network. In this way we map the production rule tensor α^+ onto a production (adjacency) matrix $A(t)$. It is defined on the space of all productions and links two nodes if one node is the product of an active production currently fed by another node. The active destruction network is obtained in the same way.

After having constructed the active production network, we then remove all unconnected nodes. To detect *dominant* links in this network, we introduce the following threshold: we remove all links from the active production network which exist less than a prespecified percentage of times h within a moving time-window of length T. So if $h = 95$ and $T = 100$, the network at time t, $A(t)$, only contains links which have existed more than 95 times within the timewindow $[t - T, t]$.

4.2.5 Spontaneous ideas and disasters

From time to time spontaneous ideas or inventions take place, without the need of the production network. Also from time to time goods disappear from the economy, say through some exogenous events. To model these we introduce a probability p with which a given existing good is spontaneously annihilated, or a non-existing good gets spontaneously invented. This is the only stochastic component of the model (besides the update sequence) and has an important effect as a driving force.

Clearly, we can relate the spontaneous innovation probability p to the temperature T of the system. More concrete, the stochastic driving with nonzero temperature is equivalent to the bounded rationality scenario we will discuss shortly.

Table 4.2: Summary of model parameters.

Variable		
$\sigma_i(t)$	state of good i. exists / does not exist	dynamic
$D(t)$	diversity at time t	dynamic
$A(t)$	active production network	dynamic
Parameter		
$\alpha^{\pm}$	productive/destructive interaction topology	fixed
$r^{\pm}$	rule densities	fixed
p	spontaneous-innovation parameter	fixed

4.2.6 A Schumpeterian algorithm

Consider you are at timestep t, the update to $t+1$ happens in the following three steps:

- pick a good i at random (random sequential update)
- sum all productive and destructive influences on i, i.e. compute $\Delta_i^{\pm}(t) \equiv \sum_{j,k=1}^{N} (\alpha_{ijk}^{+} - \alpha_{ijk}^{-})\ \sigma_j(t)\sigma_k(t)$. If $\Delta_i^{\pm}(t) > (<) 0$ set $\sigma_i(t+1) = 1(0)$. For $\Delta_i^{\pm}(t) = 0$ do not change, $\sigma_i(t+1) = \sigma_i(t)$
- with probability p switch the state of $\sigma_i(t+1)$, i.e. if $\sigma_i(t+1) = 1(0)$ set it to $\sigma_i(t+1) = 0(1)$
- continue until all goods have been updated once, then go to next timestep

As initial conditions ($t = 0$) we chose a fraction of randomly chosen initial goods, typically we set $D(0) \sim 0.05 - 0.2$.

In principle it is possible to empirically assess production or destruction networks in the real economy, however in practice this is unrealistic and would involve tremendous efforts. For a systemic understanding of Schumpeterian dynamics a detailed knowledge of these networks is maybe not necessary, and a number of statistical descriptions of these networks would suffice. The simplest implementation of a production/destruction network is to use random networks, i.e. to model $\alpha^{\pm}$ as a random tensors. These tensors can then be described by a single number r^{+} and r^{-} which are the constructive/destructive rule densities. With other words the probability that any given entry in α^{+} equals 1 is $P(\alpha_{ijk}^{+} = 1) = r^{+}\binom{N}{2}^{-1}$, or each product has on average $r^{\pm}$ incoming productive/destructive links from productive/destructive sets. Further, which goods form which productive sets is also randomly assigned, i.e. the probability that a given product belongs to a given productive/destructive set is $2r^{\pm}/N$ (for $r^{\pm} \ll N$).

Certainly real production networks carry structure and logic; the assumption that production networks are unstructured is unrealistic to some degree. For this reason we will look at scale-free versions of production/destruction topologies. Finally, note that $\alpha^{\pm}$ is fixed throughout the simulation.

4.3 Results

Implementing the system in a computer model we get a model dynamics as seen in Fig. 4.4, where we show the individual trajectories of 100 nodes. Time progresses from left to right. Each column shows the state of each of the goods $i = 1, \ldots, N$ at any given time. If good i exists at t, $\sigma_i(t) = 1$ is represented as a white cell, a black cell at position (i, t) indicates $\sigma_i(t) = 0$. It is immediately visible that there exist two distinct modes in the system's dynamics, a quasi stationary phase, where the set of existing products does practically not change over time, and a

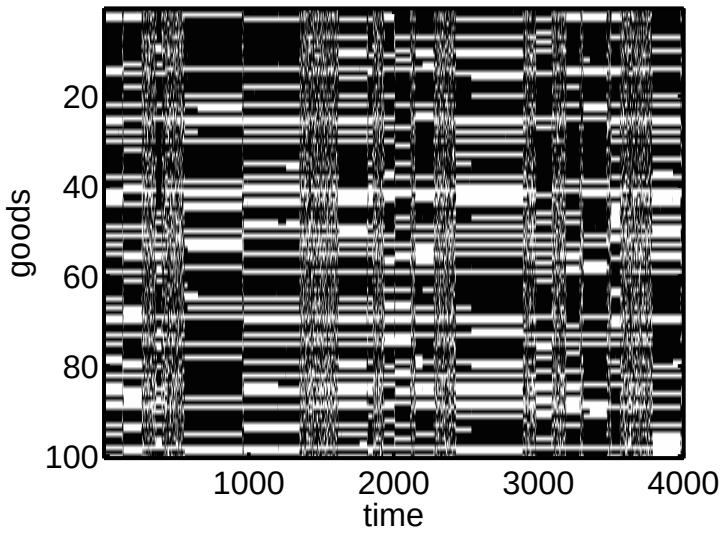

Figure 4.4: Individual trajectories of all goods for the parameter settings $r^+ = 10$, $r^- = 15$, $p = 2 \cdot 10^{-4}$, $N = 10^2$ and an initial diversity of 20 randomly chosen goods.

phase of massive restructuring. To extract the timeseries of diversity $D(t)$ we sum the number of all white cells within one column at time t and divide by N which is shown in Fig 4.5 (a). Again it is seen that the plateaus of constant product diversity (punctuated equilibria) are separated by restructuring periods, characterized by large fluctuations of the products that exist. Note that quasi stationary plateaus differ in value. Depending on parameter settings, stationary diversity levels may differ by up to 50%. These fluctuations are by no means Gaussian, as can be inferred from Fig. 4.5 (b), where the histogram of the percent-changes in the diversity timeseries, $R_t = (D(t) - D(t-1))/D(t-1)$, is shown. The skew in the distribution is absent when looking at the increment distribution of $D(t)$. For this parameter setting the dynamics of the system does not reach a static or frozen state, stationary phases and chaotic ones continue to follow each other. We have checked this up to 10^6 simulation timesteps.

For the number of active productions (a proxy for our model 'GDP') and destructions (model 'business failures') at every timestep we fitted the corresponding (percent increment) histograms to power-laws (not shown). The exponents are ≈ -2.6 for the productions and ≈ -2.8 for the destructions, respectively. While the exponent for productions coincides well with the one estimated from the GDP (Fig. 4.1 (c)), the destructive one is larger than for the business failures, Fig. 4.1 (f).

However, the dynamics changes with altering the 'innovative' rate p, see Fig. 4.6. In the situation where there is a rate of $p = 0.01$, (a)-(b), i.e. in a system of $N = 100$ there is about one spontaneous innovation or destruction per timestep, we observe extended restructuring processes, almost never leading to plateaus. For $p = 10^{-4}$ (one innovation/destruction every 100 timesteps) the situation is as described above, (c)-(d). When p gets too small ($p \ll N^{-1}$) the system is eventually not driven from a stationary state and freezes (e)-(f). In the next section we will discuss alternatives to the driving process, where innovation rates p get replaced by *product lifetimes* or alternative competition models. These alternatives also drive the system dynamically away from frozen states.

We have studied under which topological circumstances the generic dynamics is maintained for p in the range of $[10^3 - 10^5]$. If there are too many destructive influences w.r.t. constructive ones ($r^+ \ll r^-$) the system will evolve toward a state of low diversity in which innovations are mostly suppressed. If there are much more constructive than destructive interactions ($r^- \ll r^+$),

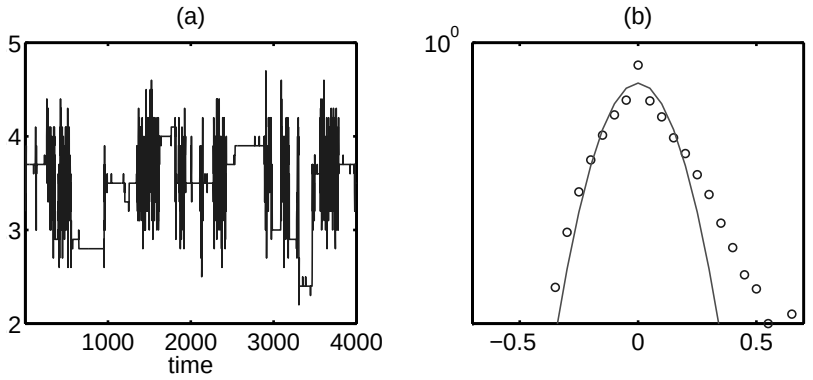

Figure 4.5: (a) Diversity $D(t)$ from the simulation in the previous figure which shows a punctuated pattern. The system jumps between phases of relatively few changes – the plateaus – and chaotic restructuring phases. The length of the chaotic phases is distributed as a power law which is identical with the fluctuation lifetime distributions shown in Fig. 4.9. (b) Histogram over the percent-increments of diversity. The line is a Gaussian distribution with the same mean and variance.

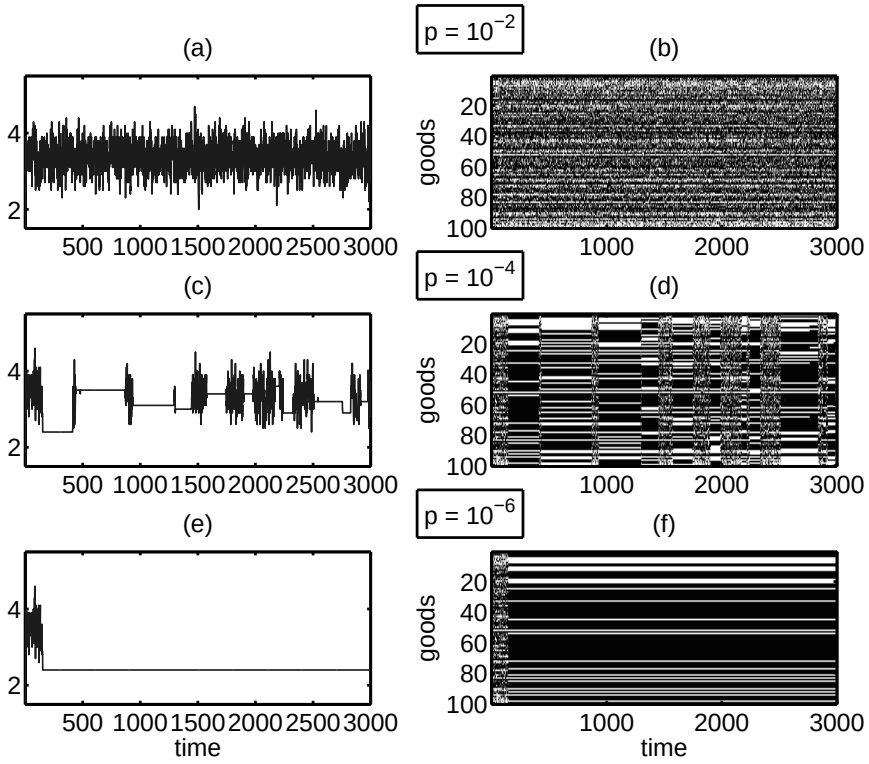

Figure 4.6: Timeseries of goods and system diversity as in the previous figures for various values of p. For high innovation rates the system never settles into plateaus, $p = 0.01$ (a)-(b), for intermediate levels $p = 10^{-4}$ plateaus form (c)-(d), and for low levels $p = 10^{-6}$ the system freezes, (e)-(f).

i.e. little competition, the system is expected to saturate in a highly diverse state. In between these two extremal cases we find sustained dynamics as described above. This regime is indeed very broad, and does not need a finetuning of r^+ and r^-.

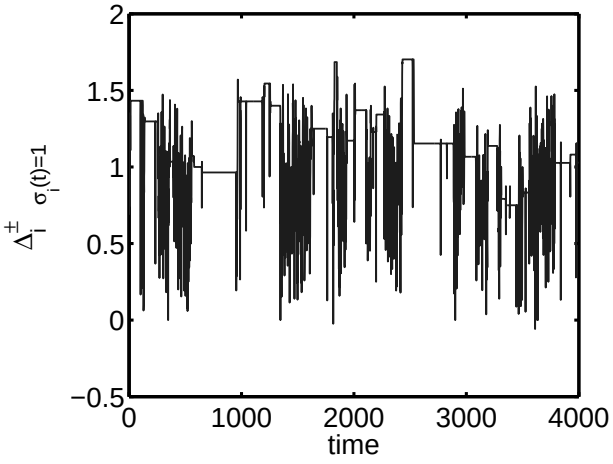

Figure 4.7: Difference between active production and destruction influences per node $\langle \Delta_i^{\pm} \rangle_{\sigma_i(t)=1}$, averaged over all active nodes for the same run displayed in Fig. 4.5.

Let us finally give an intuitive explanation of what drives the dynamics of the system. The dynamics can be interpreted as if products tend to populate locations in product-space which are locally characterized by high densities of productive rules and low densities of destructive influences. If the system remains in such a basin of attraction this results in diversity plateaus. Small perturbations can force the activated population of goods out of these basins. Products undergo a restructuring phase until an other basin of attraction is found. To quantify this Fig. 4.7 shows $\langle \Delta_i^{\pm} \rangle_{\sigma_i(t)=1}$, averaged over all active nodes, for the simulation with time series shown in Fig. 4.5). This quantity indicates the surplus of production over destruction rules. Stable phases in diversity (plateaus in diversity in Fig. 4.5) are always associated with higher values of $\langle \Delta_i^{\pm} \rangle_{\sigma_i(t)=1}$ than in the restructuring (chaotic) phases. Typical values in the stable phases lie between one and two, meaning that the average node can lose one productive pair and still be sustained. In the chaotic phases $\langle \Delta_i^{\pm} \rangle_{\sigma_i(t)=1}$ tends toward zero. Note here that once a node is deactivated it is not considered in the average anymore. This is the reason why $\langle \Delta_i^{\pm} \rangle_{\sigma_i(t)=1} \geq 0$.

4.4 Results on model variants

4.4.1 More realistic competition

We studied the influence of hierarchical suppression as a more realistic mechanism of competition. We start again with productive rules which are distributed randomly as above. Then for each node, we identified its productive set. If for example sets $\mathbf{i}, \mathbf{j}, \mathbf{k}$ all produce node l we randomly assign a hierarchy on these sets, say $\mathbf{j} \to \mathbf{i} \to \mathbf{k}$, meaning $\mathbf{j}$ dominates $\mathbf{i}$, and $\mathbf{i}$ dominates $\mathbf{k}$. This domination could mean for example $\mathbf{j}$ produces l cheaper than $\mathbf{i}$, and $\mathbf{k}$ is the most expensive way to assemble l. The intuition behind this approach is that if a more efficient way to produce node l is available, as here for example the production $\mathbf{i}$ for good l is cheaper than production $\mathbf{k}$, and $\mathbf{i}$ will supersede the old one ($\mathbf{k}$) and thus suppress its productive set. If we find an even better rule e.g. $\mathbf{j}$, this again suppresses the less efficient productions $\mathbf{i}$ and $\mathbf{k}$.

Technically, say the nonzero entries in α^+ producing l are $\alpha^+_{\mathbf{i},l} = \alpha^+_{\mathbf{j},l} = \alpha^+_{\mathbf{k},l} = 1$. We then impose the domination network for product l in the following way: Suppose $\mathbf{i} = \{i_1, i_2\}$ and $\mathbf{k} = \{k_1, k_2\}$ then we encode the hierarchical suppression in α^- by setting $\alpha^-_{\mathbf{i},k_1} = \alpha^-_{\mathbf{i},k_2} = 1$ and $\alpha^-_{\mathbf{j},k_1} = \alpha^-_{\mathbf{j},k_2} = \alpha^-_{\mathbf{j},i_1} = \alpha^-_{\mathbf{j},i_2} = 1$. We repeat this step for each node $l \in \{1, \ldots, N\}$. Except for this alternative construction of α^- the model stays completely the same as before. In Fig. 4.8 we show the dynamical features of this model variant. Note that the slope in the production

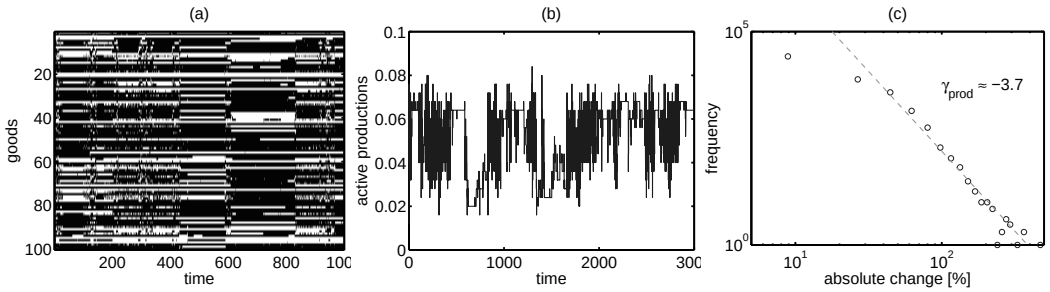

Figure 4.8: Trajectories (a), number of total active productions at time t (b), and (c) histogram of percent increments of (b), for the more realistic competition process described in 4.4.1. Parameters $r^+ = 2.5$, $r^- = 2$ and $p = 10^{-3}$.

increments is somewhat steeper than for the original model.

4.4.2 Topology of production and destruction networks

Results are surprisingly robust with respect to changes in production/destruction topology $\alpha^{\pm}$. We have studied the dynamics on a *scale-free* production/destruction networks. In particular we investigated three possibilities to introduce power-law degree distributions: (i) the number of productive/destructive sets per node ('in-degree') follows a power-law, (ii) the number occurrences of a given node in productive/destructive sets follows a power-law ('out-degree') or (iii) both in-degree' and 'out-degree' are distributed in a scale-free manner.

For all choices the dynamical pattern of stochastic transitions between static and chaotic phases is retained. The presence of hubs somewhat stabilizes the system, i.e. generally with increasing exponent in the topological power-laws, lifetimes of plateaus increase.

Note, that the size of the productive/destructive sets is not limited to two. Exactly the same qualitative dynamical features of the system are recovered for any values of productive/destructive set sizes, $n^{\pm}$, as long as $n^+ > 1$. For $n^{\pm} = 1$ the dynamics becomes linear and the system does not behave critical any more. In the same manner, the number of produced goods per productive set need not be restricted to one. One can think of one set producing/destroying more than one good. We have studies variations in set sizes of this kind and found no changes in the qualitative dynamical behavior.

4.4.3 Asymmetry in production and destruction

For some circumstances it might be a realistic assumption that destructive influences have a larger impact than productive ones, i.e. that it is easier to destroy something than to 'create' something. A simple way to study this is to enforce to set $\Delta_i^{\pm}(t)$ to a negative value, as soon as there is at least one active destructive interaction pointing to good i, e.g. $N_i^{\mathrm{destr}}(t) > 0 \rightarrow \Delta_i^{\pm}(t) = -1$. Note that this is similar to changing a majority rule to an unanimity rule [74]. The dynamical patterns we observe are robust concerning this variant. The same applies if we choose an 'intermediate' model variant where we introduce a threshold $m > 0$, below which $\Delta_i^{\pm}(t)$ is set to be negative, i.e. if $\Delta_i^{\pm}(t) < m \rightarrow \Delta_i^{\pm}(t+1) = -1$.

4.4.4 Modular structure of production/destruction networks

It may be reasonable to impose a modular structure on the production/destruction topology. We constructed modules with different and random topologies which differ from each other by different values of $r^{\pm}$. Several modules (up to ten) of different densities $r^{\pm}$ were then linked by a few connecting links. By increasing the density of these connections between the modules, the

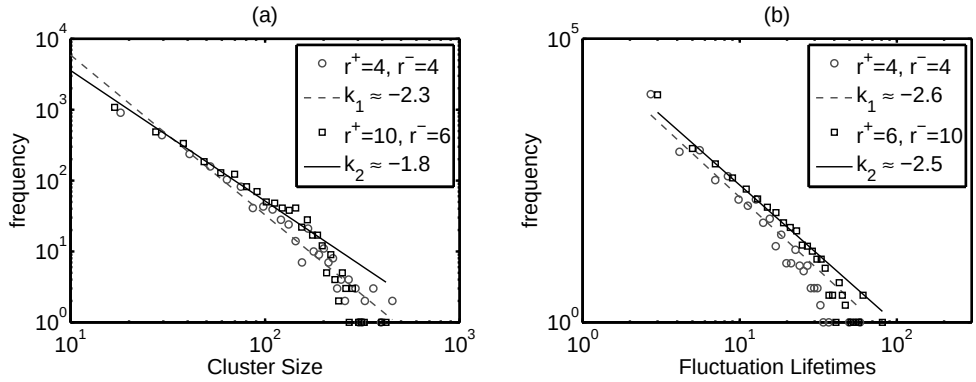

Figure 4.9: Cluster size distribution (a) and fluctuation lifetime distribution (b) of a system of size $N = 1000$ for different densities r^+ and r^-. The slopes for power-law fits for $r^+ = r^- = 4$ are $k_1 = -2.3$ for the sizes, and $k_1 = -2.6$ for fluctuation durations, while for $r^+ = 10$ and $r^- = 6$, we get $k_2 = -1.8$ for sizes, and $k_2 = -2.5$ for durations. Given that these parameter settings correspond to highly different scenarios, the similarity of power exponents indicates some degree of robustness.

system gradually undergoes a transition from a regime where each module behaves independently to a regime where the entire system's behavior becomes dominated by the most densely connected modules.

4.4.5 Finite lifetime of goods and services

It might be reasonable to consider that goods do not exist infinitely long, even in the case where no destructive set points at it. One might want to introduce a decay rate of goods, i.e. a good i decays with probability λ. For this model variant we find the same qualitative results as reported below. This decay rate can serve as a stochastic driving force, keeping the system from a frozen state. This means that even for $p = 0$, for finite λ the system does not freeze.

4.4.6 Bounded rationality

If a product *can* get produced it does not mean that it actually *will* get produced. To incorporate this possibility we say that if a good can get produced, it will actually get produced with a probability q. This means that that if a good should be produced or destroyed according to Eq. (4.3), this happens only with probability q. With probability $1 - q$ the opposite happens, i.e. if something should get produced – it will not, if something should be destroyed – it will continue to exist. This probability can either be seen as a spontaneous idea of an entrepreneur or as a lack of rationality. This variant is formally almost exactly the same as driving the system with the innovation parameter p; the scenarios only differ if the sign of $\Delta^{\pm}(t)$ changes exactly when the p or q event happens, which is rare.

We recover the exact model of the former chapter if we replace q by the 'Boltzmann factor' $\mathrm{e}^{-\beta\Delta B}$.

4.4.7 Variations in the update

The qualitative behavior of the model does not change if we employ a parallel update or a sequential update in a deterministic order. The only impact of these changes is that the system needs longer to find frozen states in parallel updating.

4.5 Understanding Schumpeterian dynamics

The high level of generality of the presented model of Schumpeterian dynamics allows several ways of understanding. We discuss two ways. First we show a correspondence to self-organized critical (SOC) sandpile models. Second, we understand Schumpeterian dynamics on the basis of the eigenvalues of the active production network.

4.5.1 Schumpeterian dynamics is a SOC sandpile

Schumpeterian dynamics in our implementation can be seen as a self-organized critical system. To see the direct similarities to a sandpile model [58] we proceed in the following way: set $p = 0$ and wait until the system reached a frozen state, which we define as one or less changes in $\vec{\sigma}$ occurring over five iterations [2]. We then flip one randomly chosen component σ_i. This perturbation may or may not trigger successive updates. In Fig. 4.9 (a) the cluster size (total number of goods that get updated as a consequence of this perturbation) distribution is shown . The observed power-laws reflect typical features of self-organized criticality: one spontaneous (irrational) event may trigger an avalanche of restructuring in the economy; the power-laws demonstrate that large events of macroscopic size are by no means rare events, but rather the rule than the exception. We show the distribution of 'fluctuation-lifetimes' in Fig. 4.9 (b), i.e. the number of iterations which the system needs to arrive at a frozen state. The distribution of 'lifetimes' also follows a power-law, which confirms the existence of self-organized criticality in our model in the sense of [58].

4.5.2 Eigenvalues, keystone productions

To understand Schumpeterian dynamics it seems natural to study the topology of the active production network. In particular the question arises of how topology is related to the outcome of the dynamical system. The simplest quantitative measure related to dynamics on networks is to compute the maximum real eigenvalue of the active production network $A(t)$. In Fig. 4.10 (a) we show a plot of the diversity vs. the maximum real eigenvalue of the adjacency associated to the active production adjacency network. The latter have been constructed as described in Section 4.2.4, however without using the filtering, i.e. $h = 1$ and $T = 1$. There is a correlation of about $\rho \sim 0.85$ the slope is ~ 16.

In Figs. 4.10 (b) and (c) we demonstrate that the dependence of the maximum eigenvalue is rather independent of the choice h and T, and thus justifies the approach, whenever h and T remain in reasonable limits. For the chaotic phases the maximal eigenvalue is mostly zero which indicates an directed acyclic graph. When a maximal eigenvalue of one is found this indicates one or more simple cycles [72]. On the plateaus we typically find values larger than one which is a sign of a larger number of interconnected cycles in A. In this sense the plateaus are characterized by a long-lasting high level of 'cooperation', whereas in the chaotic phase cooperation between cyclically driven production paths is absent. This is the topological manifestation of collective organization which the model produces.

The situation here is similar to what was found in a model of biological evolution by Jain and Krishna [44]. Unlike the dynamics of the active production/destruction network A, in their model, Jain and Krishna update their interaction matrix through a selection mechanism. They

[2] More precisely, we count the number of changes of states between two consecutive time steps, i.e. the quantity $\Delta\sigma(t) = \sum_i |\sigma_i(t+1) - \sigma_i(t)|$. If $\Delta\sigma(t)$ is not higher than one, within five iterations, i.e. $\Delta\sigma(t') \leq 1 \ \forall \ t' \in \{t, t+1, \ldots, t+5\}$, we call the state of the system quasi stationary. Now if the system is in such a state and gets perturbed, our definition ensures that we still remain in the same stationary state if this perturbation dies out within five iterations. On the other hand, if the perturbation triggers a cascade and spreads over the system, there will soon be more than one update between two iteration and the system escapes the stationary state.

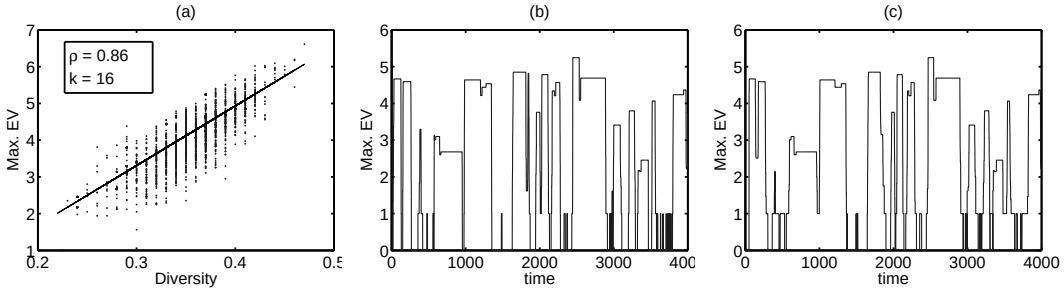

Figure 4.10: (a) At each time step we construct the active production network $A(t)$ for the run of Fig. 4.5, with $h = 1$ and $T = 1$. Its maximal eigenvalue is plotted vs. the system's diversity at that time t. Every point represents one timepoint. (b)-(c) Comparison of the maximum EV when computed with filtering, using $T = 20$, $h = 0.95$ (b) and $T = 50$, $h = 0.8$ (c) for the same run shown in Fig. 4.5.

were among the first [3] to relate the topology of the dynamical interaction matrix to the diversity of the system. In particular they could show that the highly populated phases in the system is always associated with autocatalytic cycles and keystone species, i.e. species building up these cycles. Drastic increase in diversity is associated to the spontaneous formation of such cycles, the decline of species diversity is triggered by breaking a cycle. Even though we do not have any explicit selection mechanism in the model the relation between topological structure of A and and the state of the dynamical system is the same as in [44]. To explicitly show the relation between eigenvalues, cycles and product diversity we show the trajectory of the maximum eigenvalue of A together with snapshots of active production networks along the trajectory in Fig. 4.11.

4.6 Discussion

We try to capture the essence of Schumpeterian economic dynamics in a simple dynamical model, where goods and services co-evolve with their 'activated' production networks. New goods and services are endogenously produced through re-combinations of existing goods. New goods entering the market may compete against already existing goods and as a result of this competition mechanism existing goods may be driven out from the market - often causing cascades of secondary defects (Schumpeterian gales of destruction).

The model leads to a generic dynamics characterized by phases of relative economic stability followed by phases of massive restructuring of markets – which can be interpreted as Schumpeterian business 'cycles'. Cascades of construction and destruction produce typical power-law distributions, both in cascade size and in times of restructuring periods. The associated power exponents are rather robust under the chosen parameters governing the density of productive/destructive rules. The model can be fully understood as a self-organized critical system.

Alternatively the diversity dynamics generated by the model can be understood along the same lines as the evolution model of Jain and Krishna [44]. As in [44] we are able to relate the diversity of the system to topological properties of the active production network. The maximum real eigenvalue of the active production networks correlates strongly with diversity. Further we were able to identify 'keystone' productions, which – when removed – dramatically reduce the maximum eigenvalue. To a certain extend it is also possible to relate the model to the Bak-Sneppen model [46], in the sense that the local quantity $\Delta_i^{\pm}$ can be thought of playing the role of the random fitness in the Bak-Sneppen model.

Model timeseries of product diversity and productivity reproduce several stylized facts of

[3] In [72] this has been already anticipated before.

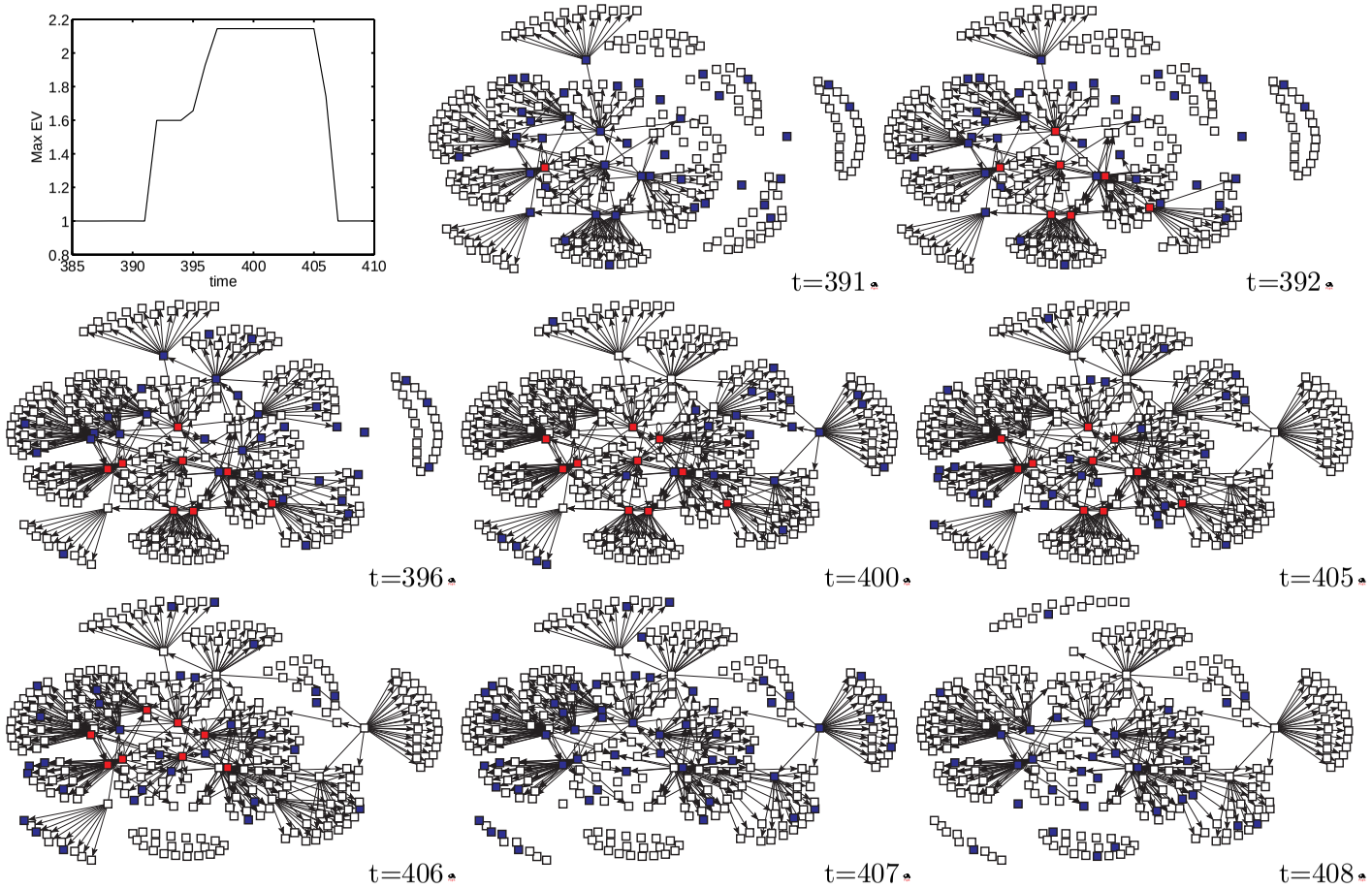

Figure 4.11: Onset and breakdown of cooperation. We show the trajectory of the maximum eigenvalue of A in (a) for $T = 50$ and $h = 0.8$. In the particular example the eigenvalue starts at around 1 builds up to a plateau at about 2.1 and then drops to about 1 again. The effective production networks along this trajectory are shown. At first the network contains simple cycles (maximal eigenvalue equals one). At each time step we show 'keystone' productions as red nodes. A keystone production is defined as a node which – if it was removed from $A(t)$ – would result in a reduction of the maximum eigenvalue of more than 10% (when compared to the maximum eigenvalue of A).Typically keystone nodes are components of cycles. Note, active destruction graphs can be constructed in the same way but will always be much sparser than active production networks.

economic timeseries on long timescales such as GDP or business failures, including non-Gaussian fat tailed distributions, volatility clustering etc. We have studied a series of more realistic model variants. Remarkably, the majority of the statistical results holds qualitatively also for these variants, and a certain degree of universality of the model is indicated. So far we have not analyzed universality issues in much detail.

5 Pruning the Tree of Life – Biological Evolution

As buds give rise by growth to fresh buds, and these,
if vigorous, branch out and overtop on all sides many a feebler branch,
so by generation I believe it has been with the great Tree of Life,
which fills with its dead and broken branches the crust of the earth,
and covers the surface with its ever-branching and beautiful ramifications.
Charles Darwin, 1809 - 1882

We will adopt the general framework of this thesis to incorporate a model of biological evolution. To this end we explicitly split the interaction topology into (linear) mutations and (non-linear) recombinatory interactions. Furthermore we will incorporate the destructive interactions by a more feasible, less random principle.

5.1 Introduction

Quantitative interest in evolutionary models originates from the fact that fossil data from different sources [75, 60] shows power law behaviour with typical exponents for three observables: (i) the distribution of sizes of extinction events, (ii) the lifetime of species and (iii) the number of species per genus, see e.g. [54] for an overview.

One of the first quantitative models of evolution was the NK model proposed by Kauffman [48], where species evolve and compete on a rugged fitness landscape. A species' fitness and therefore lifetime is given by its genome and the randomly associated fitnesses to the respective genes. In a similar vein Bak and Sneppen [46] refined Kauffman's ideas to a model exhibiting self-organized criticality. Here it is assumed that the fitness landscape possesses valleys and peaks and over time a species will mutate "across" a fitness barrier to an adjacent peak. In contrast to these models, where there is no explicit species-species interaction, Solé and Manrubia [43] constructed a model focusing on interspecies dependencies. They incorporate a connection matrix containing the mutual support between two species. If this support drops below a critical value the species will not be able to maintain its existence anymore, it will go extinct. In contrast to the NK and Bak-Sneppen model which are *per se* critical, the Solé-Manrubia model's criticality is parameter dependent. For a review see again [54].

Recently a more general and abstract framework to treat systems subject to evolution was developed out of the notion of catalytic sets on networks [50]. We will use this approach to model species proliferation in the evolutionary system. As the main novelty of the present work we study the feasibility of k-core percolation [76] as a selection mechanism. k-core percolation is a systematic, iterative procedure where a node in a network is removed from a network if it sustains less than a fixed number of k links to other nodes. We show that evolutionary systems which grow according to a catalytic set dynamics combined with a k-core selection mechanism, reproduce power law behaviour as observed in fossil data

For the three observables: size of extinction events, lifetime and number of species per genus. The model explicitly describes the origination of species and their interactions, the fitness landscape is co-evolving with the topology specified by these interactions.

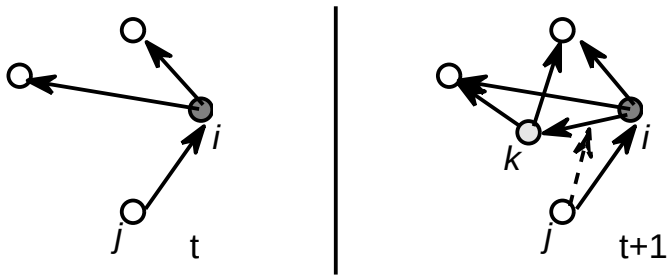

Figure 5.1: At time t (left panel) node i is chosen to mutate. It has one incoming link from j and two outgoing links. At time $t+1$ (right panel) node k came into existence through the mutation of i under the supportive influence of j. Here $m = 1$, i.e. k copies all outgoing links from i.

5.2 The Model

In the following species are represented as nodes in a network. We introduce two types of links between these nodes, the first type keeping the ancestral relations, the other type describing the interactions between species. These links are recorded in two separate adjacency matrices, as described below.

5.2.1 Growth

The system is initiated with a small number N_0 of species. These are assumed to be constantly present i.e. they are not subject to the selection mechanism. New species (nodes) are introduced as mutations of already existing ones. They will prove viable only if they receive some 'support' from other species. At each time step a species may be subject to a mutation which leads to a new node. The mutation is favored/suppressed through the influence of other already existing species. We identify the probability for the occurrence of a viable mutation with the effective growth rate λ of the system. In the absence of any selection mechanisms or extinctions the system diversity grows according to $N(t) = N_0 e^{\lambda t}$. To take into account ancestral relationships we introduce the *ancestral table* α, a three dimensional tensor with entries $\alpha_{ijk} \in \{0, 1\}$. Suppose that species i mutates and gives rise to a new species k and that species j provides support for the survival of k. In this case the ancestral adjacency matrix element $\alpha_{ijk} = 1$, otherwise $\alpha_{ijk} = 0$. Each species is associated to a genus. If species i is from genus g_i, its mutant k will most likely be assigned to the same genus g_i. However, with a small probability p^{gen} the mutation will be large enough that k constitutes a new genus $g_k \neq g_i$. The results will, as discussed later, only marginally depend on the actual choice of p^{gen}, we worked with a figure of $p^{gen} = 0.005$.

On top of this ancestral relationship, a new species will also interact with other species in its surrounding. The environment of a new species – its ecological context – will be strongly determined by the environment of its ancestors, i.e. the species the ancestors interact with. A given species k (descending from i) will thus be most likely to interact with more or less the same species as i. k receives a given fraction of interaction-links from i.

As a consequence of this growth rule with the particular copying mechanism, clusters of strongly interconnected, interacting species naturally emerge. In other words, species in a cluster are highly adapted to each other and form an environment to which can be referred to as an "ecological niche".

Interspecies dependencies are encoded in the interaction matrix I_{ij}. A general choice for the entries in I would be to introduce a probability that an entry is non-zero, i.e. there is an interaction between species i and j, and in this case let the values of I vary between -1 and $+1$, for inhibitive and stimulating influences. Evolutionary dynamics of this kind has been studied

[44] and it has been shown to lead to a proliferation of predominantly stimulating influences (positive entries). Thus, since here we are interested in a model for macro-evolution and not ecology, we assume only positive binary entries in I, i.e. $I_{ij} \in \{0, 1\}$ for no interaction, or stimulating influence, respectively.

For later use, the indegree of node i, κ_i^{in} is defined as the sum of the i-th line of the interaction matrix I, i.e. $\kappa_i^{in} = \sum_{\{x \in N(t)\}} I_{xi}$. Note that the number of species $N(t)$, and thus matrices α and I are here non-constant over time.

5.2.2 Growth dynamics

The model consists of a two-step process: a growth and diversification process, followed by a selection procedure. During one time step we apply the following procedure to each node in a random update:

- Pick a node i. With probability $1 - \lambda$ (same for all i) do nothing and pick another node, otherwise with probability λ do the following:
- Choose at random one of the nodes linking to i, say node j. Add a new node k to the network which is a mutation of either i or j. Set either $\alpha_{ijk} = 1$ or $\alpha_{jik} = 1$ with equal probability. This means that either i or j has mutated.
- Let us assume i mutated. Then the new species k receives an incoming link from i ($I_{ik} = 1$) and copies each outgoing link from i with a probability m, i.e. if i links to i' ($I_{ii'} = 1$), k links to i' with probability m. (If it links we set $I_{ki'} = 1$).
- With probability p^{gen} the new species k constitutes a new genus, otherwise k is associated with the same ancestor genus i.

Effectively, we employ a 'copying mechanism', where a node i gets copied (produces node k) together with the two types of links involved: In the case of the ancestral relationships either a link to i is established or, with same probability, one incoming link of i, namely from j, is copied. In the case of the species interactions each outgoing link from i is copied to k with probability m. See Fig. 5.1 for an illustration. A copying mechanism of this kind has been studied by Vázquez [77] and was applied in the context of protein interaction networks [78].

5.2.3 Selection as k-core pruning

By assuming that selection predominantly acts on species of low fitness, a quantitative measure for fitness is necessary. It was argued that a species' individual fitness should be related to the number of stable relationships that this species is able to maintain in its environment [79]. The higher this number, the more interactions ensure its survival. In this view one can directly identify the indegree of species i, κ_i^{in}, with its fitness; one can picture κ_i^{in} as the total 'support' i gets from its surroundings. In this view it is natural to implement the selection procedure in the following way:

Suppose there exists an exogenous stress level for all species, k^{stress} which fluctuates due to abiotic causes. It can be modelled as a random process drawn at each time step from a Poisson distribution $\Pr\left(k^{stress} = n\right) = \left(\theta^n \mathrm{e}^{-\theta}\right)/n!$. The mean θ of this distribution gives the average biotic stress in the system. Species with $\kappa_i^{in} < k^{stress}$ become removed from the network with all their links. As soon as these nodes are removed some of the surviving nodes will now have an indegree smaller than k^{stress} and become extinct too, and so on. In other words, at each time step only the k-core of the network survives, the network is pruned down to its k-core.

5.3 Theoretical estimates

We now estimate the distributions of three quantities which are observable in fossil data, extinction events, lifetime and species per genus. These are known to be compatible with power-law distributions, with exponents between 1.5 and 2 [54]. We analytically derive the exponents for extinction size γ_E, number of species per genus γ_S, and lifetimes γ_L, and discuss parameter (in)dependence of the results. We then compare them to simulations at the end of this section.

5.3.1 Size distribution of extinctions

We are interested in the number of species becoming extinct in each time step, i.e. the distribution of extinction sizes. It can be derived analytically by making some simplifying assumptions. A node i's indegree is given by $\kappa_i^{in} = \sum_{\{x \in N(t)\}} I_{xi}$. Since each node receives an incoming link from its ancestor, the minimal indegree in the network is one. Thus each species can survive if we prune the network with $k^{stress} \in \{0, 1\}$. The probability p_{surv} for the occurrence of a stress level k^{stress}, which does not lead to a single extinction event, is given by a Poisson process $p_{surv} = \sum_{n=0}^{1} \left(\theta^n \mathrm{e}^{-\theta}\right)/n! = \mathrm{e}^{-\theta}(1+\theta)$. With probability p_{surv} the diversity proliferates as $N(t+1) = N(t)(1+\lambda)$. We assume that the main contribution to extinction sizes stem from percolation with $k^{stress} = 2$, which is the case for reasonable choices of the parameters λ and θ. By reasonable choices we mean values for λ and θ where a nontrivial interplay between the growth and extinction dynamics can *de facto* be observed. Otherwise, keeping λ fixed and choosing θ too low the system would just grow exponentially, conversely for too high θ all species would vanish within a few iterations. We further make the simplifying assumption that if $k^{stress} > 1$ occurs, a constant fraction c of the entire population will go extinct. Thus from our assumptions follows the Ansatz that with probability $1 - p_{surv}$ the diversity behaves like $N(t+1) = N(t)(1-c)$.

Let us call the number of species becoming extinct at each time step $\Delta N^{\dagger}(t)$ and assume that $\Delta N^{\dagger}(t) = cN(t)$. Then we have $\Delta N^{\dagger}(t)/N_0 = \exp(\lambda t)$, or equivalently $t = (1/\lambda)\ln\left(\Delta N^{\dagger}(t)/N_0\right)$. Assume that an extinction event occurs at time $t+1$. The probability that the system has proliferated over the past T iterations is given by p_{surv}^T (T being an exponent), so the probability to find a specific extinction size ΔN^* is given by $\Pr\left(\Delta N^{\dagger}(t) = \Delta N^*\right) = p_{surv}^{(1/\lambda)\ln(\Delta N^*(t)/N_0)}$. Taking the natural logarithm on both sides and plugging in for p_{surv} we finally have $\ln\left(\Pr\left(\Delta N^{\dagger}(t) = \Delta N^*\right)\right) = \mathrm{const} + \left[(-\theta + \ln(1+\theta))/\lambda\right]\ln \Delta N^*$. Thus the distribution of extinction sizes follows a power-law with exponent γ_E depending on λ and θ:

$$\Pr\left(\Delta N^{\dagger}(t) = \Delta N^*\right) \propto (\Delta N^*)^{-\gamma_E}, \quad \gamma_E = \frac{\theta - \ln(1+\theta)}{\lambda} \quad . \tag{5.1}$$

A comparison between this prediction and simulation results from the full model (without assumptions) is shown in Fig. 5.2 for $\theta = 1$, revealing excellent agreement. Slopes from the simulation data were estimated using a maximum likelihood method [80], standard deviations are smaller than symbol size. This *a posteriori* justifies our simplifying assumption $\Delta N^{\dagger}(t) = cN(t)$. The difference to simulation data stems from the fact that also percolations with higher k occur albeit exponentially less likely.

5.3.2 Distribution of species per genus

Whereas the extinction-size distribution displays explicit parameter dependence on λ and θ, this will be shown to be not the case for the distributions of species per genus and lifetimes. Let us start with the indegree distribution of our growth model $p\left(\kappa_i^{in}\right)$ encoded in I, which is known to be scale-free [77]. Growing networks have scale-free degree distribution if they incorporate preferential attachment. How is preferential attachment present in the present model? Consider the avenue of a new species k due to a mutation of i under the supportive influence of j and a

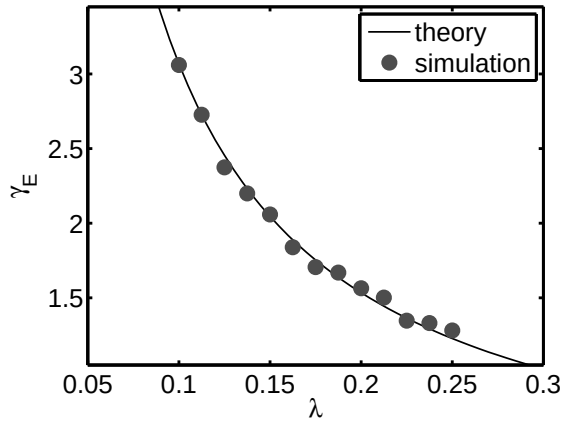

Figure 5.2: We compare the prediction from Eq. (5.1) (solid line) with simulation data (red circles) for $\theta = 1$.

randomly chosen, already existing node l. What is the probability that the indegree of l, κ_l^{in}, will increase by one? This can happen if l receives an incoming link from k because it already has an incoming link from i which happens with a probability proportional to the indegree of node l. This introduces preferential attachment and the resulting indegree distribution, as worked out in [77], follows a power law with

$$p\left(\kappa^{in}\right) \propto \kappa^{in^{-2}} \quad , \tag{5.2}$$

as long as the link-copying probability $m > 0.4\,(1)$ [77] , which we assume to hold.

Suppose our system size is N species. Denote the number of genera containing n_s species by $\bar{n}_g(n_s, N)$. It is then straight forward to derive the growth equation

$$\bar{n}_g(n_s, N+1) = \bar{n}_g(n_s, N) + \bar{n}_g(n_s - 1, N)w(n_s - 1) - \bar{n}_g(n_s, N)w(n_s) \quad , \tag{5.3}$$

where $w(n_s)$ is the probability for each genus of size n_s to increase its size by one. The dependence on p^{gen} is introduced in the boundary conditions given by $\bar{n}_g(n_s = 1, N+1)$. For each node associated to an already existing genus, the number of $p^{gen}/(1-p^{gen})$ nodes are added to this one per time step, so we get $\bar{n}_g(1, N+1) = \bar{n}_g(1, N) - w(1)\bar{n}_g(1, N) + p^{gen}/(1-p^{gen})$. We are interested in stationary solutions of Eq. 5.3, i.e. solutions which are independent of the actual system size N. For this let us define $n_g(n_s) \equiv N\bar{n}_g(n_s, N)$. The probability for a genus of size n_s to increase its size by one is obviously $w(n_s) = n_s/N$, this can be interpreted as the probability that a new node copies the genus information from a node of a genus of this respective size. Plugging all this into Eq. 5.3 we get the recursive relationship $n_g(n_s) = [(n_s-1)/(n_s+1)]\cdot n_g(n_s-1)$ from which one can readily conclude $n_g(n_s) = f(p^{gen})\cdot(n_s(n_s+1))^{-1}$ where $f(p^{gen})$ is a constant, thus we have $n_g(n_s) \propto n_s^{-2}$ to leading order.

An important feature of k-core percolation is that it preserves statistical invariants [81], that is, if the original network follows a scale-free degree distribution with a given exponent, its k-core has the same distribution up to the cut-off at k. The scale-free network architecture imposed by our growth and diversification rules will not be altered by extinction events. Thus the species per genus distribution of the model is

$$n_g\left(n_s\right) \propto n_s^{-2} \quad , \tag{5.4}$$

i.e. $\gamma_S = 2$, for the distribution of taxon sizes.

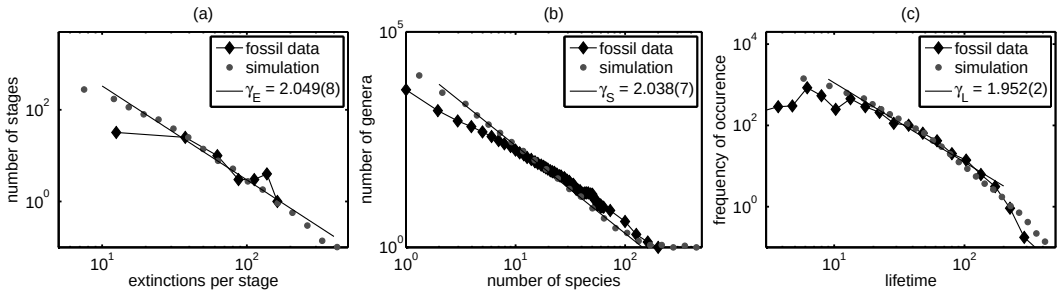

Figure 5.3: Comparison of fossil data [75, 60] (solid line with diamonds) with simulation data (red circles) for the three observables (a) extinction event size, (b) species per genus and (c) lifetimes. The straight line is the maximum likelihood estimate for the power-law exponent of the simulation data and indicates the range where the fit was applied.

5.3.3 Lifetime distribution

To estimate for the distribution of lifetimes of long living species, i.e. species which will not become extinct after the first few iterations, we ask for the lifetime τ_i of species i with an indegree κ_i^{in} drawn from $p\left(\kappa_i^{in}\right)$. The probability that the stress level will be higher than the node's indegree is $\Pr\left(k^{stress} > \kappa_i^{in}\right) = \sum_{k=\kappa_i^{in}+1}^{\infty} \left(\mathrm{e}^{-\theta}\theta^k\right)/k!$. The leading term in this sum is $k = \kappa_i^{in} + 1$. Consider that T iterations of the dynamics have taken place. We are asking for long lived species, i.e. that within $T \gg 1$ iterations there occurs no stress level higher than κ_i^{in}. Generally, the probability that within T trials with success probability $\Pr\left(k^{stress} > \kappa_i^{in}\right)$ zero successes are obtained is given by a binomial distribution. For large sample sizes T the binomial distribution approaches a Poisson distribution, independent of T. Accordingly, in our case the probability for zero successes (the occurrence of no stress level $k^{stress} > \kappa_i^{in}$) follows a Poisson distribution $\mathrm{e}^{-\Pr\left(k^{stress} > \kappa_i^{in}\right)}$. From this it can be concluded that the probability to encounter a species i with lifetime τ, i.e., $\Pr\left(\tau_i = \tau\right)$, can be estimated from the node's indegree only. One can identify a necessary criterion for the survival of a node, namely that it has an indegree κ_i^{in} which is not exceeded by the stress level k^{stress} for $T \gg 1$ iterations. So the probability to encounter a lifetime τ is given by the probability for the occurrence of a stress level higher than κ_i^{in},

$$\Pr\left(\tau_i = \tau\right) \propto p\left(\kappa_i^{in}\right) \mathrm{e}^{\Pr\left(k^{stress} > \kappa_i^{in}\right)} \quad . \tag{5.5}$$

The probability to find a node with lifetime τ is proportional to the probability of finding a node with a given indegree κ^{in}, truncated with the probability for the occurrence of specific stress levels. There exists a regime where $\Pr\left(\tau_i = \tau\right) \propto \Pr\left(\kappa_i^{in} = \kappa^{in}\right)$ holds and by virtue of Eq. (5.2) we find $\gamma_L = 2$, i.e.

$$\Pr\left(\tau_i = \tau\right) \propto \tau^{-2} \quad . \tag{5.6}$$

5.3.4 Simulations

We compare simulation results of the presented model to fossil data for extinctions and lifetime drawn from Sepkoski (1992), as well as species per genus after Willis (1922) in Fig. 5.3. The model was implemented in a MatLab program and executed until a statistics of $2 \cdot 10^4$ extinction events were accumulated. This corresponds to sample sizes of $10^5 - 10^6$ for individual lifetimes and numbers of species per genus, depending on the parameter settings. For $\lambda p_{surv} < c\left(1 - p_{surv}\right)$ the size of the network does not diverge over time and the samples can be obtained from a single run of the simulation. For $\lambda p_{surv} > c\left(1 - p_{surv}\right)$ the system tends to grow infinitely large; for practical purposes we aborted runs as soon as $N\left(t\right) > 10^4$ and iterated

Table 5.1: Exponents of the distributions of extinction sizes γ_E, species per genus γ_S, and lifetimes γ_L, as obtained from the fossil record and compared to the exponents of various well known evolution models. The value for γ_E from this model was obtained from simulations with $\lambda = 0.15, m = 1, \theta = 1$.

	γ_E	γ_S	γ_L
fossil data	2.0(2)	1.7(3)	1.5(1)
Kauffman, 1993	$\simeq$1	-	-
Bak and Sneppen, 1993	1 to 3/2	1	-
Solé and Manrubia, 1996	2.05(6)	-	2.05(6)
Newman, 2003	2.02(2)	1.03(5)	1.6(1)
present model	2.049(8)	2	2

until a satisfactory statistic was reached. For all three subplots the simulation data was fitted with a maximum likelihood estimation [80], the range of the fit is indicated by the range of the straight line. Subsequently the numerical results were binned logarithmically and, if necessary, shifted multiplicatively to enhance the clarity of the plots.

For the extinction events the resulting slope is parameter dependent, we used the setting $(\lambda = 0.15, m = 1, \theta = 1)$ to obtain agreement with the slope of $\gamma_E = 2.0\,(2)$ from the fossil data. Although not obvious from the sparse data shown here, the existence of a power-law in the extinction event sizes with this exponent in the Sepkoski database was reported by Raup [71] by comparing it to Monte-Carlo simulations of genus survivorships and by the sophisticated analysis of Newman and Palmer [54]. Both works favored a power-law over an exponential form. For the number of species per genus and lifetimes the distributions are independent of the parameter settings and given by the topology (which is a scale-free indegree distribution for values of $m > 0.4(1)$) of our network only, yielding $\gamma_S = 2, \gamma_L = 2$. We find a higher exponent in the species per genus distribution than in the database from [75], where $\gamma_S = 1.5(1)$. However, this exponent has to be taken with some care. We computed over all iterations, i.e. a long period of time, whereas Willis' data is taken from a snapshot. The latter favors long-living species which leads to a lower exponent than a measurement over long timespans. In addition, the mere existence of a power-law is intriguing. The exponent for the lifetime distribution can be estimated between 1.2 and 2.2 from the fossil data, depending on the range where the fit is applied. Our value of 2 compares to the intermediate value of 1.7(3) from the data. Our exponents are summarized and compared to several previous models in Table 5.1.

5.4 Discussion

We presented a model for evolution which reproduces statistical features observed in fossil data. An evolutionary system is modelled as a catalytic network with two superimposed network topologies, one incorporating species-species interactions, the other the phylogenetic tree structure. The fitness of species is given by the connectivity structure of the network, thus naturally a co-evolving fitness landscape arises. Fitness becomes nothing but a co-evolving topological entity, the more relationships a species is able to build and sustain, the fitter it becomes. Species interactions are introduced by a variant of preferential attachment known as 'copying mechanism' [77]. Without any further assumptions this mechanism leads to a natural emergence of "ecological niches", which in network terms relate to a high degree of clustering in the network.

In this model we have taken a gradualist viewpoint concerning speciation in assuming that the growth rate λ is constant. However, this choice was only made for reasons of simplicity. Benton and Pearson [82] propose that gradual speciations are more likely to occur in stable environments (as it is the case for e.g. marine plankton), whereas marine invertebrates and vertebrates are

more likely to show a punctuated pattern of speciation. The latter case could be naturally introduced in our model by assuming a functional dependence $\lambda \equiv \lambda(\theta)$, i.e. introducing a mechanism that couples the growth rate with the actual values of k^{stress}. Irrespective of this choice, the main characteristics of our model would not be altered. The number of species per genus and lifetimes only depends on topological features of the network which would not be affected by a varying growth rate. Our analysis for the extinction sizes would hold too, except that one has to set $\lambda = \lambda(\theta)$ in Eq. (5.2). The existence of the power law is independent of both the functional form of the growth rate and the stochastic stress level.

Our selection mechanism differs from the one studied by Solé and Manrubia [43] in that extinction avalanches spread over successive time steps in their model and that each species becoming extinct is immediately replaced by a randomly chosen one (therefore leading rather to a model for ecology where empty niches are re-filled), whereas in our model the selection mechanism acts on a 'snapshot' of the population and does not depend on which randomly chosen species replaces an extinct one. Our pruning procedure further differs from the selection mechanism adopted by Newman [54] in that each species has a randomly assigned fitness value (independent of interspecies relationships) and species below a given stress level become extinct, which is contrasted by mass extinctions of causally connected species in our model.

We suggested the use of k-core percolation as a mechanism to select species according to their fitness values. On a technical level this allows to understand the system by studying its k-core architecture. If the applicability of this mechanism to prune the 'tree of life' can be justified beyond the statistical features presented here, remains an open question.

6 Evolution of Beliefs: Opinion Formation

Society works not because we have consciously invented it,
but because it is an ancient product of our evolved predispositions.
It is literally in our nature.
Matt Ridley, *1958

We will now be concerned with the evolution of humans belief and how different opinions compete amongst each other.

6.1 Introduction

Many decisions of human beings are often strongly influenced by their social surroundings, e.g. the opinion of friends, colleagues or the neighborhood. Only a few types of decisions in few individuals emerge from absolute norms and firm convictions which are independent of the opinion of others. Much more common is the situation where some sort of social pressure leads individuals to conform to a group, and take decisions which minimize conflict within their nearest neighborhood. For example, if a large fraction of my friends votes for one party, this is likely to influence my opinion on whom to vote for; if I observe my peers realizing huge profits by investing in some stock this might have an influence on my portfolio as well; and if the fraction of physicist friends (coauthors) publishing papers on networks exceeds a certain threshold, I will have to reconsider and do the same; the social pressure would otherwise be just unbearable. Lately, the study of opinion formation within societies has become an issue of more quantitative research. In first attempts agents were considered as nodes on a lattice, and opinion dynamics was incorporated by the so-called voter model (VM) [83, 84] (only two neighbors influence each other at one timestep), the majority rule (MR) [85, 86, 87] (each member of a group adopts the state of the local majority), or the Axelrod model [88] (two neighbors influence themselves on possibly more than one topic with the objective to become more similar in their sets of opinions). In addition to this variety of interaction rules the underlying network topology was found to play a prominent role in the emergence of collective phenomena. Most observed structures of real-world networks belong to one of three classes: Erdös-Renyi (ER) [105], scale-free [89] or small-world networks [115]. This has been accounted for the VM [90, 91, 92] as well as for the MR on different topologies [94, 93]. For a review of further efforts in this directions see [95] and citations therein. Aiming at a coherent description of the co-evolution of topologies and opinions, network structure itself has been modeled as a dynamical process [96, 97, 98, 99, 100]. An alternative approach to model social interaction – which is *n*ot necessarily based on interpreting agents as some sort of Ising spins– was developed out of the notion of catalytic sets [50] (evolutionary approach), leading to an unanimity rule (UR) model [74] on arbitrary networks in an irreversible formulation.

There are basically two types of social influence [101, 102] which the model presented here should be able to capture. Conformity can arise as a consequence of informational influence. Here an individual assumes that others have more information on a given issue and is happy to accept the majority's opinion. On the other hand, with normative social influence, the mechanism of peer pressure can force an individual to publicly comply with the majority. Aside from the actual size of the majority subgroup, the question whether an agent is likely to conform or not depends also on other determinants [103], such as the social status or prestige of neighbors, the importance of the decision or the prepotency of the group's induced response. To take

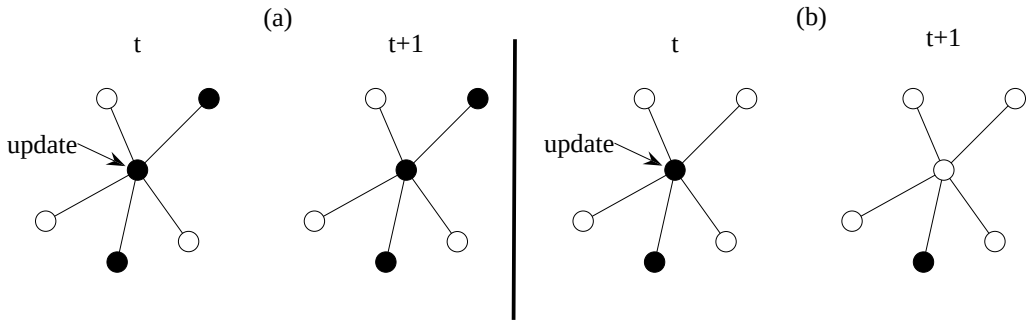

Figure 6.1: Update process for two different configurations of neighbors and an update threshold of $p_u = 0.8$. The node in the center gets updated. (a) Three out of five neighbors are in a different state, so the threshold is not exceeded and the node stays unchanged. (b) Four out of five neighbors are in a different state; $4/5 \geq 0.8$ thus the node adopts the state.

these dependencies into account, in the tradition of statistical physics we present a *r*eversible generalization to the UR and MR models introducing an arbitrary threshold governing updates ('laggard' parameter). The UR and MR are extremal cases of the model. In [104] the idea of a threshold was introduced in the context of global cascades in ER networks of 'early-adopters'. In contrast to this work, where updates were only allowed in one direction (irreversible), the following model is fully reversible in the sense that two opinions compete against each other in a fully symmetric way.

6.2 The Model

Each individual i is represented as a node in a network. The (binary) state of the node represents its opinion on some subject, yes/no, 0/1, Bush/Mother Theresa, etc. Linked nodes are in contact with each other, i.e. they 'see' or know each others opinion. The opinion formation process of node i is a three-step process (see Fig.6.1): Suppose i is initially in state '0'('1').

- Check the state of all nodes connected to i.
- If the fraction of state '1'('0')-nodes of i's neighbors exceeds a threshold p_u, i adopts opinion '1'('0').
- Otherwise i remains in state '0'('1').

As a substrate network we chose random graphs [105], i.e. N nodes are randomly linked with L links (self-interactions are forbidden), the average connectivity being $\bar{k} = L/N$. We do so to keep results most clear and exclude influences from complex network topologies. The update threshold p_u has to be higher than 0.5 in order to be meaningful in the above sense. The update is carried out asynchronously. In a network containing N nodes, at time t, there are A_t^0 nodes with opinion '0' and A_t^1 nodes with opinion '1'. The relative number of nodes are $a_t^{0/1} = A_t^{0/1}/N$. One time step is associated with applying the update procedure N times, i.e. each node gets updated once per timestep on average. As time goes to infinity, the relative population of nodes with opinion 0/1 will be denoted by $a_\infty^{0/1}$.

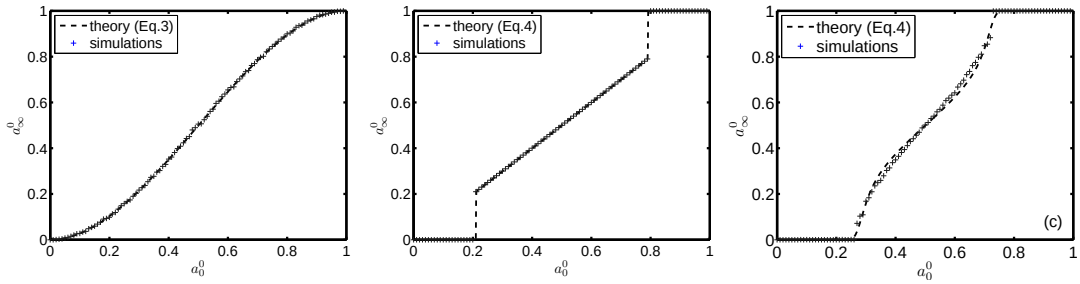

Figure 6.2: Asymptotic population sizes of the '0'-state fraction, a_∞^0, as a function of its initial size, a_0^0, for $N = 10^4$, $p_u = 0.8$. (a) $k = 2$ for all nodes (1D circle), (b) ER graph with $\bar{k} = 9000$ and (c) ER graph with $\bar{k} = 10$.

6.3 Analytical and Numerical Results

To derive a *master equation* for the evolution of this system we calculate opinion-transition probabilities via combinatorial considerations in an iterative fashion, motivated by [50]. A master equation for a_t^0 is found explicitly, the situation for a_t^1 is completely analogous. At $t = 0$, we have a fraction of a_0^0 nodes in state '0'. The probability that at time t one node belonging to a_t^0 will flip its opinion to '1' is denoted by $p_t^{0\to1}$. This probability is nothing but the sum over all combinations where more than a fraction of p_u of the neighbors are in state '1', weighted by the probabilities for the neighboring nodes to be either from a_t^0 or $a_t^1 = \left(1 - a_t^0\right)$,

$$p_t^{0\to1} = \sum_{i=\lceil \bar{k} p_u \rceil}^{\bar{k}} \binom{\bar{k}}{i} \left(1 - a_t^0\right)^i \left(a_t^0\right)^{\bar{k}-i} \quad , \tag{6.1}$$

where $\lceil . \rceil$ denotes the ceiling function, i.e. the nearest integer being greater or equal. The same consideration leads to an expression for the opposite transition $p_t^{1\to0}$, where 1 and 0 are exchanged in Eq.(6.1). The probability for a node to be switched from '0' to '1', $\Delta_0^{0\to1}$, is the product of the transition probability, $p_t^{0\to1}$, and the probability to be originally in the fraction a_0^0, i.e. $\Delta_0^{0\to1} = p_0^{0\to1} a_0^0$. The same reasoning gives $\Delta_0^{1\to0} = p_0^{1\to0}\left(1 - a_0^0\right)$ and provides the master equation for the first time step (i.e. updating each node once on average),

$$a_1^0 = a_0^0 + \Delta_0^{1\to0} - \Delta_0^{0\to1} \quad . \tag{6.2}$$

Let us now examine some special cases.

6.3.1 The low connectivity limit

Low connectivity. If $\bar{k}$ and the update threshold p_u are chosen such that $\lceil \bar{k} p_u \rceil = \bar{k}$ holds, the system arrives at a frozen state after one iteration. Here the update rule is effectively the unanimity rule in the sense that all linked nodes have to be in the same internal state to allow for an update. This can be either checked by direct inspection or by considering the following: Assume that after the first iteration no consensus has been reached which is equivalent to saying that we can find two neighboring nodes with different internal states, say agent i is in state 0, j holds state 1. To let agent i conform, each of his neighbors ought to be in state 1. But then i *could not* be in 0. Either the update to 1 would have already occurred or there is an agent k in i's neighborhood which also holds state 0 and will not conform because of his connectedness with i. The dynamics of the system freezes after the first iteration. Note that it is crucial that we carry out the updates random sequentially since for parallel updates the configuration would stay maximally random at any given time.

For the special case $k = 2$ (1D circle) the final population in state '0' is given by $a^0_\infty = a^0_1$. Inserting this in Eq.(6.2) yields

$$a^0_\infty = 3(a^0_0)^2 - 2(a^0_0)^3 \quad . \tag{6.3}$$

A comparison between the theoretical prediction of Eq.(6.3) and the simulation of this system (on a regular 1D circle network with $N = 10^4$) is seen in Fig.6.2(a).

6.3.2 Higher connectivities

For higher connectivities there are much more configurations allowing for potential updates, the evolution does not stop after one single iteration. Naively one would try to iterate Eq.(6.2), however since our dynamics are reversible this would not take into account specific histories of individual nodes. To estimate how likely a node can switch its state at $t = 1$ (e.g. an update $0 \to 1$) w.r.t. the initial populations (in this case a^0_0) we have to include the contributions from nodes changing their state at $t = 0$ and exclude the contributions from those which underwent the respective update at $t = 0$. We have, for example, $\Delta^{1\to0}_1 = \left(p^{1\to0}_1 - p^{1\to0}_0\right)\left(1 - a^0_0\right)$. For arbitrary times t this is straight forwardly seen to be $\Delta^{1\to0}_t = \left(p^{1\to0}_t - p^{1\to0}_{t-1}\right)\left(1 - a^0_0\right)$, and the master equation is given by the second order iteration $a^0_{t+1} = a^0_t + \Delta^{1\to0}_t - \Delta^{0\to1}_t$. Note that the p_t's depend on $a^0_{t-1}, a^0_{t-2}, \ldots a^0_0$ and therefore include the influence of nodes switching forth and back on the system's evolution from the initial populations. Inserting for a^0_t in a recursive way yields the master equation

$$a^0_{t+1} = a^0_0 + p^{1\to0}_t\left(1 - a^0_0\right) - p^{0\to1}_t a^0_0 \quad . \tag{6.4}$$

Again, theoretical predictions of Eq.(6.4) agree perfectly with numerical findings, see Fig.6.2 (b). Three regimes can be distinguished: two of them correspond to a network in full consensus. Between these there is a mixed phase where no consensus can be reached.

High connectivity limit.

For the fully connected network the asymptotic population sizes can easily be derived: if $a^0_0 > p_u$ or $a^0_0 < 1 - p_u$ consensus is reached. For $1 - p_u < a^0_0 < p_u$ the system is frustrated and no update will take place, giving rise to a diagram like Fig.6.2(b). Compared to Fig.6.2(a) a sharp transition between the consensus phases and the mixed phase has appeared. We now try to understand the origin of this transition.

Intermediate regime.

The transition between the smooth solution for the final populations as a function of a^0_0 and the sharp one for higher connectivities becomes discontinuous when the possibility for an individual node to get updated *in a later timestep* ceases to play a negligible role. In Eq.(6.4) we do not assume any kind of correlations between configurations at different time steps, i.e. the configurations are assumed to be maximally random w.r.t. the constraining population sizes. The fact that Eq.(6.4) coincides with the numerical results for high connectivities justifies the assumption for high $\bar{k}$. However, as explained above when we have an unanimity rule the correlation is so strong that no updates take place on subsequent iterations. It is intuitively clear that there exists a regime in between where the no-correlation hypothesis loses its validity and evolution does not freeze after one iteration.

For $p_u = 0.8$ the sharp transition arises for values of $\bar{k}$ around 10. Fig.6.2(c) shows simulation data for ER graphs with $N = 10^4$ nodes and $\bar{k} = 10$ with $p_u = 0.8$. Here we already find two regimes with consensus and an almost linear regime in-between. The curve obtained from numerical summations of Eq.(6.4) resembles the qualitative behavior of the simulations up to deviations due to the no-correlation assumption. The dynamics of the system is shown in the

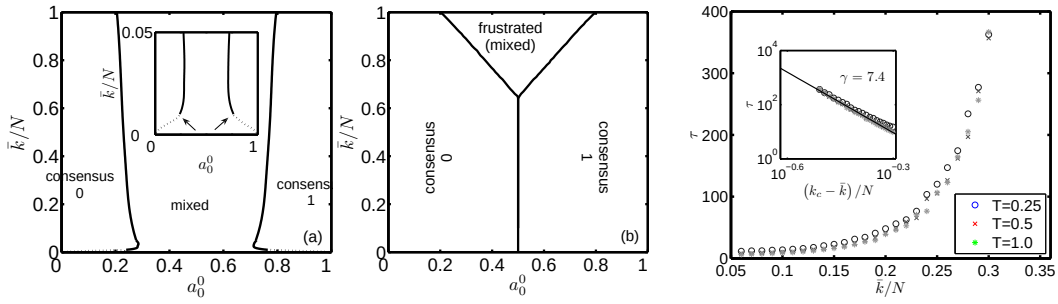

Figure 6.3: Phase diagram for a^0_∞ as a function of initial fraction size a^0_0 and connectedness, $\bar{k}/N$. Simulations where performed with ER graphs with $N = 10^3$ and $p_u = 0.8$. Two symmetrical regions of consensus and a mixed phase in between are observed. The dotted line indicates a smooth transition, the solid line a discontinuous one. *Inset:* Detail for small $\bar{k}$. Arrows mark the change from smooth to sharp transitions, positioned at $\bar{k}/N \sim 0.01$. (b) Phase diagram for $a^0_{\infty,\infty}$. Technically adjacency matrices with $N = 10^4$ were generated and checked by Monte-Carlo simulations whether they allow an update at fixed a^0_0 and $\bar{k}$. (c) Half-life time τ ($\bar{t}$ until half the population reached consensus) vs. relative number of neighbors for $T = 0.25, 0.5, 1$. *Inset:* Same in log-log scale. Scaling around the pole $k_c/N \sim 0.61$ with an exponent $\gamma \approx 7.4$ is suggested. 10^3 initial populations with $a^0_0 = 0.5$ and $N = 10^2$ were averaged.

phase diagram, Fig.6.3(a). It illustrates the size of the respective regimes and their dependence on the parameters a^0_0 and connectedness $\bar{k}/N$. The order parameter is a^0_∞. Along the dotted lines a smooth transition takes place, solid lines indicate discontinuous transitions from the consensus phase to the mixed phase. The change from smooth to sharp appears at $\bar{k}/N \approx 0.01$. For larger p_u the regions of consensus shrink toward the left and right margins of the figure.

6.4 Social Temperature

So far we assumed static networks. However, this is far from being realistic, as social ties fluctuate. We now check the robustness of the phase diagram when stochastically perturbing the underlying network structure, i.e. allowing links to randomly rewire with the rewirement process taking place on a larger time scale than the opinion update. Let us assume that the number of rewired links per rewirement-timestep is fixed to L', so that it becomes natural to define a *social temperature*, $T_{soc} = L'/L$. T_{soc} quantifies the individual's urge to reconsider a topic with new acquaintances, or equivalently, the fluctuation of ties in their social surrounding. Note that this process is substantially different from the (dis)assortative mixing scenarios in the literature [97].

The evolution of opinions in a network at $T_{soc} \neq 0$ is as follows: We fix a network and perform the same dynamics as for $T_{soc} = 0$, until the system has converged and no further updates occur. Then perturb the system by a rewirement step and randomly rewire L' links among the N nodes (N and L are kept constant over time), increase the time-unit for the rewirement steps by one and let the system relax into a (converged) opinion configuration. Iterate this procedure. Note that this process can be viewed as a dynamical map of the curves shown in Figs.6.2(a)-(c). With this view it becomes intuitively clear that consensus will be reached for a wider range of parameters, where the time to arrive there crucially depends on the value of $\bar{k}$.

To incorporate the temperature effect in the master equation we introduce the second timescale and denote the population in state '0' as $a^0_{t,\bar{t}}$. Here t is the time for the update process as before

and $\bar{t}$ is the time step on the temperature time scale, i.e. counts the number of rewirement steps. We use $a_0^0 \equiv a_{0,0}^0$. $a_{\infty,0}^0$ can be obtained from $a_{\infty,0}^0 = \lim_{t\to\infty}\left(a_{t,0}^0 + \Delta_{t,0}^{1\to 0} - \Delta_{t,0}^{0\to 1}\right)$ for high $\bar{k}$, and from Eq.(6.2) for low $\bar{k}$, when we only observe updates during the first iteration. This evolution is nothing but a dynamical map. The probabilities to find a configuration of neighbors allowing an update are no longer given only by $\Delta_{t,0}^{0\to 1}$ and $\Delta_{t,0}^{1\to 0}$, instead we have to count the ones constituted by a rewiring, which happens with probability T_{soc}. That is why we can consider this kind of evolution as a dynamical map of the former process, with $a_{\infty,0}^0$ as the initial population for the first rewirement step evolving to $a_{\infty,1}^0$, and so on. The transition probabilities are now given by $T_{soc}\Delta_{t,\bar{t}}^{1\to 0}$ and $T_{soc}\Delta_{t,\bar{t}}^{1\to 0}$, since only new configurations can give rise to an update. We thus assume the master equation for a system at $T \neq 0$ after the first rewiring to be

$$a_{\infty,\bar{t}+1}^0 = \lim_{t\to\infty}\left(a_{t,\bar{t}}^0 + T_{soc}\left(\Delta_{t,\bar{t}}^{1\to 0} - \Delta_{t,\bar{t}}^{0\to 1}\right)\right) \quad . \tag{6.5}$$

Furthermore, one expects the existence of a critical value k_c, below which the intermediate regime (mixed state) will disappear. This will occur whenever there is no chance that a configuration of neighbors can be found leading to an update. The value for k_c can be easily estimated: Say we have a node in state '1' and ask if an update to state '0' is possible under the given circumstances. For a given $\bar{k}$ this requires that there are at least $\lceil \bar{k}p_u \rceil$ neighbors in state '0' present in the set A_0^0. If $\bar{k}$ is above the critical value k_c it occurs that even if all nodes from A_0^0 were neighbors of the node in state '1', there are still too many other neighboring nodes (which are then necessarily in state '1') to exceed the update threshold. This means that we can not have updates if $\lceil \bar{k}p_u \rceil > A_0^0$, and we get $k_c = \frac{a_0^0 N}{p_u}$. For $p_u = 0.8$ and $a_0^0 = 0.5$, $k_c \approx 0.61N$.

We next consider the time-to-convergence in the system. To this end we measure the half-life time τ, of initial populations at $a_0^0 = 0.5$ for different connectivities $\bar{k}$, see Fig.6.3(c). The figure suggests that the observed scaling of τ could be of power-law type, with a pole at k_c/N, i.e. $\tau \propto \left(\frac{k_c - \bar{k}}{N}\right)^{-\gamma}$. The estimated critical exponent $\gamma \approx 7.4$ seems to be independent of temperature. Note, that the estimate is taken rather far from the pole at k_c, which suggests to interpret the actual numbers with some care.

The phase diagram for the $T_{soc} \neq 0$ system is shown in Fig.6.3(b). There are still three regimes, which are arranged in a different manner than before. Consensus is found for a much wider range of order parameters; the mixed phase is found for high connectivities, i.e. $\bar{k} > k_c$. The value of k_c at $a_0^0 = 0.5$, as found in Fig.6.3(b), is 0.63, slightly above the prediction of 0.61. This mismatch is because we used networks with inhomogeneous degree distributions (Poisson). Whether a network allows for an update or not is solely determined by the node with the lowest degree k, which explains why we can still observe updates when the average degree $\bar{k}$ is near to but already above k_c. Systems in the mixed phase are frustrated. k_c is linear in a_0^0 which we confirm by finding a straight line separating the frustrated from the consensus phase. For larger p_u the regions of consensus shrink. The solutions depicted in Fig.6.3(b) are independent of T_{soc}. Here we do not assume a (dis)assortative mixing scheme (linking preferences) and focus on stochastic perturbations instead. The explicit type of perturbation plays no role in this mechanism so we chose the simplest possible.

6.5 Conclusion

Summarizing we presented a model bridging the gap between existing MR and UR models. The conceptual novelty of this work is that we interpret opinion formation as a special case of the evolution of catalytic systems [50, 74]. This different perspective places opinion formation problems in a more general framework with respect to previous extensions and modifications of the 'Ising model' type in the literature, recently called the 'Ising paradigm' [106]. On a technical level this results in an algorithmically more feasible and straight-forward way to actually solve opinion formation models - for special cases even in closed form. In particular we studied opinion

dynamics on static random networks where agents adopt the opinion held by the majority of their direct neighbors only if the fraction of neighbors exceeds a pre-specified laggard-threshold, p_u. This system shows two phases, full consensus and a mixed phase where opinions coexist. We studied the corresponding phase diagram as a function of the initial opinion distribution and the connectivity of the underlying networks. As the laggard-parameter p_u increases the regions of full consensus shrink. Opinion formation models can be categorized by whether consensus is the only frozen state, as for the voter-model, MR, Sznajd-model, etc., [106], or models allowing for a continuum of stationary solutions, as bounded confidence, the UR, or the model presented here. The reported richness of stationary solutions arises from the interplay between the update threshold p_u and the random sequential update procedure *only*, and can not be attributed to network topology effects. For this reason we restricted this work to random networks. We introduced rewiring of the underlying network during the opinion formation process ('social temperature'). For $T_{soc} > 0$ the coexistence phase vanishes, the system can escape the frozen state $a_\infty^{0/1} \neq 1$, and global consensus is reached. In the case of 'usual' temperature (opinions of nodes switch randomly) [93], a different behavior is expected. For low temperature, the system also can escape the frozen state, however for higher values of T_{soc} the system undergoes a transition from an ordered to an unordered phase, where $a_\infty = 1/2$. In the formation of public opinion one can find two scenarios [107]: a trend toward consensus or a coexistence of different opinions. From our findings we can speculate that this difference could be related to our concept of social temperature. Even though laggards sometimes enjoy a bad reputation as being slow and backward-oriented, societies of laggards are shown to have remarkable levels of versatility as long as they are not forced to interact too much.

7 To How Many Politicians Should Government Be Left?

It seems like numerology to me. I understand the isn't-it-cool appeal of this sort of analysis, but I simply don't believe it. I think it's quackery.
Anonymous Referee

As a slightly more light-hearted conclusion of this work, we present an application of our ideas in the field of politics.

Finally something useful.

7.1 Introduction

Honorable statesmen, like Charles de Gaulle or Chester Bowles, arrived at the conclusion that 'politics is too important to be left to politicians'. The highest executive power in today's political landscape is mostly conferred upon committees called cabinets – the countries' governments – consisting of people having, according to Robert Louis Stevenson, the only profession for which no preparation is thought necessary. It is natural to ask to how many of them government can be left without furnishing a democratic collapse. The question to how many individuals government should be left to ensure democratic effectiveness was first tackled in a semi-humorous attempt by the British historian C. Northcote Parkinson [108]. His investigations lead to what is now known as the 'Coefficient of Inefficiency', conjecturing that a cabinet loses political grip, due to an inability of efficient decision-making, as soon as its membership passes a critical size of 19-22.

We show that Parkinson's conjectures about cabinet sizes and government efficiency hold empirically to remarkable levels of significance. By relating cabinet size to several governance indicators, assembled by the UNDP [109] (the Human Development Indicator), the CIA [110] and the World Bank [111], we confirm the hypothesis that the higher number of members in the highest executive committee, countries are more likely to be political less stable, less efficient and less developed. Note that we do *not* claim that there is any *causal* relationship (that is, remove a member and the government becomes more effective), but merely that the number of persons participating in decisions and thus the number of interests to be satisfied negatively *correlates* to the overall quality in a country's governance.

This case study in national governments serves as a motivation to extend the scope of this correlation to decision-making in groups in general. To this end we introduce a socio-physical dynamical model aimed to reproduce opinion formation processes in small groups. As the main result of this work we show the existence of a characteristic group size within such models which resembles the qualitative change of behaviour conjectured by Parkinson as the 'Coefficient of Inefficiency'.

7.2 Cabinet sizes and efficiency

We determine the actual number of members of the highest executive committee, the cabinet, for 197 self-governing countries and territories using data provided by the CIA [110]. For a complete

listing of them see Tab. 7.1 in the appendix. Cabinets vary between 5 and 54 members with a clearly visible peak between 13 and 20. All except three countries (Pakistan, Democratic Republic of Congo and Sri Lanka) are found in the range between 5 and 36. It is worth noting that all countries avoid cabinets with 8 members, a curious fact that was observed already some fifty years ago (Parkinson, 1957).

To determine whether cabinet size can serve as an indicator for efficient policy making we compare it with indicators reflecting complex issues of states which – to get advanced reasonably – need a certain consensus within the political leadership. One such indicator is the Human Development Indicator [109] (HDI) which assesses a country's achievement in different areas of human development. It is composed of the GDP, life expectancy at birth, the literacy and the gross enrolment ratio. A second indicator is assessed on behalf of the World Bank [111], measuring a country's governance along three dimensions: Political Stability (PS, indicating the likelihood that the government will be destabilised or overthrown), Voice & Accountability (VA, quantifying to which extent citizens can select their government) and Government Effectiveness (GE, measuring the quality of policy formulation and implementation). Note that none of these indicators includes any prior dependence on the cabinet size. Fig. 7.1 (c)-(f) show the average values for these 4 indicators versus cabinet size. Note that the value for these indicators falls below the global average (line) when cabinet size exceeds 20 (Parkinson's coefficient of inefficiency). Interestingly the frequency of cabinet-sizes peaks at this point and slightly below, see Fig. 7.1 (a),(b). This indicates that cabinets are most commonly constituted with memberships close to Parkinson's coefficient, but not above it and thus lends further support to the conjecture that a cabinet's functioning undergoes a remarkable change at this point. These observations strongly suggest a correlation between increasing cabinet size and a declining overall quality in governance and achievements for human development. To assert statistical significance of the data we compute the correlation coefficient of size and the 4 indicators, and the p-value for the null-hypothesis that size and indicator are not correlated. For the HDI, PS, VA, and GE we find correlation coefficients of $\rho = -0.88, -0.88, -0.82, -0.73$ and significance levels of $p = 4.8 \times 10^{-11}, 7.3 \times 10^{-12}, 2.9 \times 10^{-9}, 7.8 \times 10^{-7}$, respectively. Our results are thus significant against the null-hypothesis up to a p-value of $p \leq 10^{-6}$. Let us stress once more that this does not assert any causal relationship. The conclusion is that cabinet size can serve as an *indicator* for the overall quality of policy formulation and human development indices. To exclude the possibility that we observe this due to a trivial super-correlation with e.g. size of the countries, we compute the corresponding correlation coefficient and p-value for the area ($\rho = 0.24$, $p = 0.16$) and population ($\rho = 0.15$, $p = 0.40$), i.e. no significant correlations.

7.3 Opinion formation and group size

How can these facts be understood? Why should a cabinet size around 20 be special in the sense that it separates countries ranking above and below the global average of the studied indicators? The idea of this paper is to show in a simple model that in opinion formation processes there exists a critical number of individuals, above which it becomes exceedingly difficult to reach consensus in the group.

In general cabinets are subject to a law of growth. This has been elaborated in detail for British cabinets from the year 1257 up to the 20th century by Parkinson [108]. In a sense cabinets reflect the most important interest groups in a country. Besides core ministries (like finance, inner and outer affairs, etc.), which exist in nearly all countries, some interests strongly depend on the region's characteristics. OPEC countries, for example, sustain a ministerial post for petroleum; countries with mixed ethnicities sometimes have a minister for each of them. A secretary for land mining or aviation will more probably be found in Africa than in Europe, to name only a few examples. Also the political climate is represented, e.g. the number of parties taking part in the government. On the one hand there is always pressure from outside groups

Table 7.1: Number of members on the highest level of the executive committee as of 10/09/2007.

Size	Countries
5	Liechtenstein, Monaco
6	Macao, Nauru
7	Cook Islands, Micronesia, Netherlands Antilles, Switzerland, Tuvalu
9	Aruba, China, Palau, Seychelles
10	Andorra, Comoros, Dominica, Saint Kitts and Nevis, San Marino
11	Antigua and Barbuda, Belize, Cyprus, Marshall Islands, Timor-Leste
12	Bahamas, Bermuda, Grenada, Iceland, Kiribati, Paraguay, Saint Vincent and Grenadines
13	Argentina, Bangladesh, Brunei, Hong Kong, Japan, Luxembourg, Malta, Nepal, Nicaragua, St Lucia, Sao Tome & Principe, Samoa
14	Austria, Estonia, Guatemala, Kuwait, Lithuania, Quatar, Tonga, Uruguay, Vanatu
15	Barbados, Belgium, Cape Verde, Colombia, Croatia, El Salvador, France, Georgia, Hungary, Ireland, Rwanda
16	Albania, Botswana, Czech Rep., Fiji, Germany, Jamaica, Kyrgyzstan, Panama, Romania, Singapore, Slovakia, Swaziland
17	Gambia, Laos, Montenegro, Netherlands, Portugal, Spain, Tajikistan, United Kingdom, United States
18	Armenia, Bolivia, Central African Rep., Costa Rica, Djibouti, Greece, Haiti, Peru, Slovenia, Trinidad and Tobago
19	Bosnia and Herzegovina, Bulgaria, Denmark, Dominican Rep., Eritrea, Kazakhstan, Latvia, Lesotho, Libya, Macedonia, Mexico, Moldova, Mongolia, Norway, Suriname
20	Finland, Guinea, Guyana, Honduras, Liberia, Mauritius, Poland, Solomon Islands, Thailand
21	Bahrain, Chile, Guinea-Bissau, Iraq, Morocco, Nigeria, Philippines, Russia, Uzbekistan
22	Ethiopia, Korea (South), Lebanon, Malawi, Sweden, Vietnam
23	Burundi, Maldives, Saudi Arabia, Sierra Leone, Zambia
24	Benin, Israel, Mozambique, Namibia, Ukraine, United Arabian Emirates
25	Jordan, Mauritania, Serbia, Taiwan, Togo, Turkey, Uganda
26	Azerbaijan, Ecuador, Tanzania
27	Australia, Brazil, Italy, Kenya, Malaysia, New Zealand, Papua New Guinea, Syria, Tunisia, Turkmenistan
28	Afghanistan, Madagascar, Mali
29	Equatorial Guinea, South Africa, Venezuela
30	Burkina Faso, Cambodia, Congo (Rep. of), Egypt
31	Angola, Belarus, Chad, Ghana
32	Algeria, Canada, Cuba, Somalia
33	Iran, Sudan, Zimbabwe
34	Korea (North), Niger, Oman, Yemen
35	Burma (Myanmar), Cote d'Ivoire, Indonesia
36	Cameroon, Gabon, India, Senegal
38	Pakistan
40	Congo (Dem. Rep. of)
54	Sri Lanka

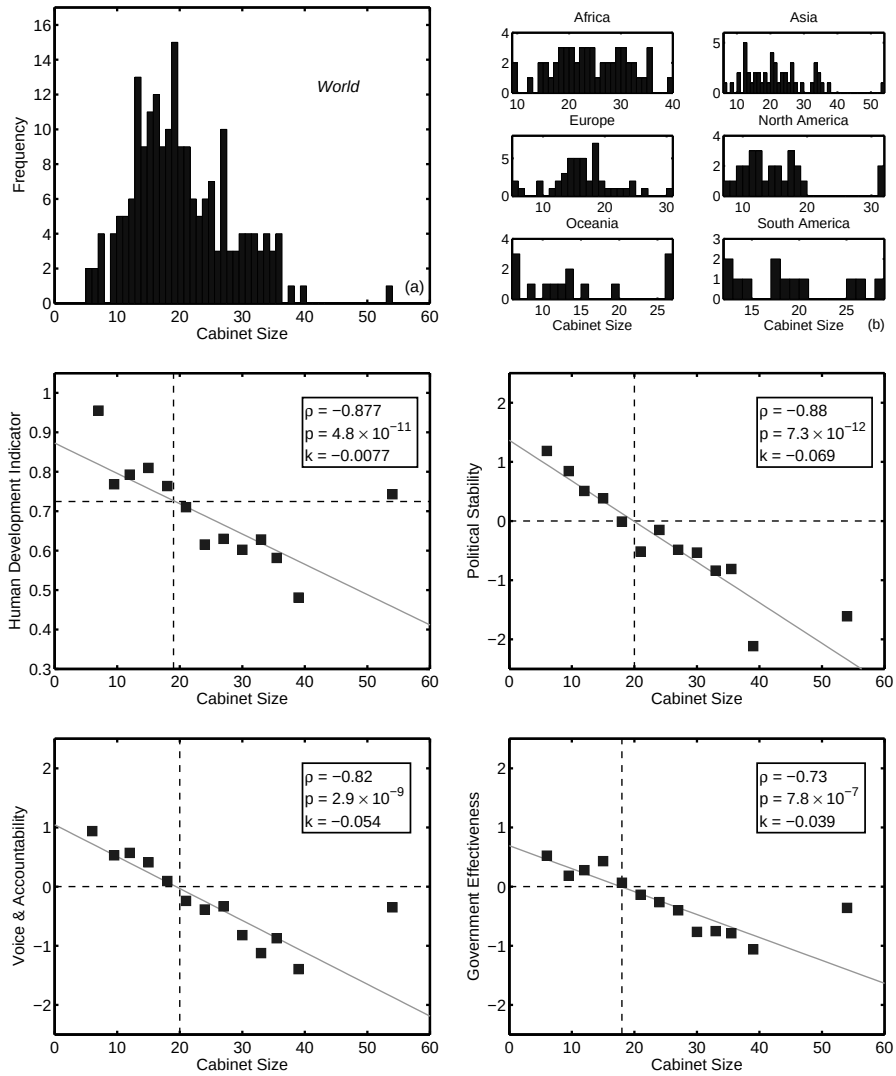

Figure 7.1: Histograms of (a) the world's cabinet sizes, (b) for each continent show that the cabinet sizes for Europe, America and Oceania follow the same pattern with the vast majority of countries lying below 20, whereas in Africa and Asia cabinets tend to grow beyond this point. There is no cabinet with eight members. Cabinet size is negatively correlated with (c) the Human Development Indicator, (d) Political Stability, (e) Voice & Accountability and (f) Government Effectiveness. For each indicator the line separating countries ranking above and below the global average lies around 20. The correlation is highly significant to a p-value of $p \leq 10^{-6}$.

seeking to be included and represented in decision-making processes, on the other hand it is obvious that the larger the decision-making body, the more difficult consensus is reached. It is one of the classical challenges of governance to find a balance between these two competing forces: wide representation and effective leadership.

It is a trivial observation that the higher the membership of the group, the higher the probability that the group may be divided into internal factions and will not reach consensus. However, it is not clear how the incremental change in this likelihood by enlarging a group of size N to $N+1$ depends on N. If one additional voting member would lead to a significant decrease in consensus finding, there should be resistance to enlargement, if an additional member does not further complicate the opinion formation process, there should be no reason to exclude him/her.

In case there exists a characteristic group size below which adding one member significantly decreases the ability to reach consensus, and above which this incremental decrease becomes smaller, it is reasonable to conjecture that this characteristic size is critical for the functioning of a decision-making group. In case of a cabinet, above this critical size there is less restriction to the admission of more representatives due to outside pressure, which in turn implies that a loss in efficiency is more likely. If a cabinet exceeds this point (coefficient of inefficiency) it gradually loses its ability to be an institution where decisions are reached and remains merely a nominal executive. In this case the effective executive power might not be in the hands of governments anymore.

Speaking in general terms, we study finite-size effects of the group size on the probability to obtain consensus in an opinion formation process. We will now describe our main results in showing that such a critical point does exist within a large class of simple opinion formation models.

7.4 A model for opinion formation in small-world groups

In recent years physics has repeatedly crossed disciplinary boundaries toward a quantitative understanding of social phenomena [112, 113, 106]. A topic of mayor interest is to uncover the relevant mechanisms driving collective decision-making processes, the study of opinion formation models [83]. The system is composed of interconnected agents, holding an internal state e.g. a binary opinion (like a spin in the Ising model), which interact by a given microscopic dynamical rule [85, 84, 88, 86, 91]. These local rules quantify the social influence individuals have upon each other. Depending on how these rules and inter-agent networks are specified, the system will evolve either toward a state given by maximal consensus [114], or alternatively the system may get stuck in a so-called 'frozen state' which is usually strongly determined by the initial conditions of the system [1]. In the latter model the group is composed of N individuals (nodes in a network), each one holding an internal state 0 or 1, for example a binary (yes/no) vote on a given topic. Two agents who have social or informational influence upon each other are connected by a link in the network. For the inter-agent network we chose a small-world network [115] where each node can potentially influence k other nodes in its local neighborhood and, with some probability L, also nodes in the more distant neighborhood. For example, imagine agents having the same party affiliation (local neighborhood) where they can influence each other in debates etc. With a certain probability (L) these agents might also talk to cabinet members of the opposite party, due to e.g. overlapping responsibilities, sympathy, etc. An impressive number of social networks was shown to be of the small-world type [116], for the remainder we consider this network as static over time. As a dynamical rule we implement a 'majority rule' with a predefined threshold [104, 1] $h \in (0.5, 1]$. Here one node adopts the state of the majority of its neighbours only if this majority exceeds the fraction of its neighbors hk, otherwise the node's internal state stays unchanged. The threshold h takes statistically account of various determinants whether an agent will conform to the majority's opinion. These determinants include the social status or prestige of the neighbors, the importance of the decision or the

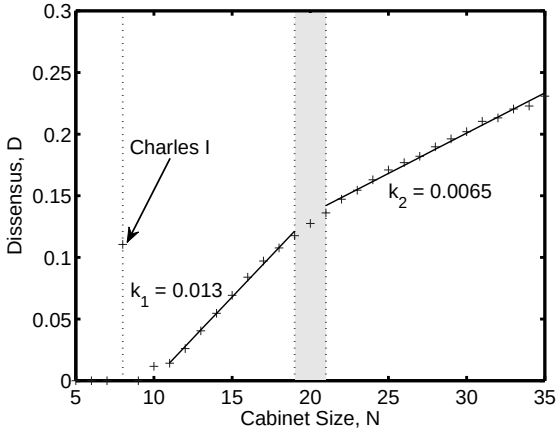

Figure 7.2: Simulation results for the dissensus parameter $D(N)$ versus cabinet size. For $N < 10$ consensus is always reached except in the 'Charles I' scenario for $N = 8$. As cabinet size increases dissensus becomes more likely. For $10 \leq N < 18$ each new member adds a dissensus-increment of $k_1 = 0.013$. The range between 19 and 21 (position of the conjectured coefficient of inefficiency) is shaded. Beyond this size the increment in dissensus by each new member is lowered to $k_2 = 0.0065$, which confirms the existence of a critical point. This point separates two scenarios where in the first an increase in size has a comparably large negative impact on efficiency, an effect that diminishes in the second scenario where the admission of a new member has a minor effect.

prepotency of the group's induced response [102, 103]. For $h > 0.5$ the pure majority rule is recovered [85]. We choose $L = 0.1$, $h = 0.6$ and $k = \min[N - 1, 8]$. Parameter dependence of our results is discussed in the appendix, however, most findings are robust.

The evolution of this model is given by a random sequential application of the dynamical rule. In one iteration the described update procedure is applied once to each node in a random order. After a sufficient number of iterations the system will reach a stationary state where no more updates take place. The question here is whether this state is consensus, i.e. all nodes are in the same internal state, or not. The initial condition is determined by the fraction of nodes in the two respective states, let us call the number of nodes initially in 0 A_i and the final population in this state A_f. For our purposes we want to determine the group's general ability to avoid dissensus. Therefore we define (as the order parameter) the 'dissensus' parameter,

$$D(N) = \left\langle \Theta\left(1 - \frac{\max(A_f, N - A_f)}{N}\right)\right\rangle_{A_i} \quad , \tag{7.1}$$

where $\Theta(x)$ is the Heaviside step function and $\langle\cdot\rangle_{A_i}$ denotes the average over all possible initial conditions. A_i is drawn with uniform probability from $(0, 1, \ldots N)$. According to this the opinions are randomly assigned to the individual nodes. $D(N)$ is the expectation value of a final state without consensus and measures the group's proneness to end up in dispute. It only depends on the group-size N. Dissensus vs. N is shown in Fig. 7.2 for fixed k. For groups of less than 10 members consensus can always be reached, with the notable exception of $N = 8$ (we refer to this case as 'Charles I'. Why? See explanation below). For $10 < N < 20$ increase of group size leads to increasing dissensus with a constant rate (slope) of $k_1 = 0.013$. This behaviour changes at $N \sim 20$, where increments become considerably smaller; a linear fit yields a slope of $k_2 = 0.0065$.

These findings are closely related to the changes the topology undergoes with different group-sizes. For $N < 10$ the network is fully connected - each member can directly influence each

other. The choice of the update threshold h assures that consensus can be reached in this range for each N (with the exception of $N = 8$). As the group grows there appear nodes which are not directly linked. Order phenomena emerge. A necessary prerequisite for dissensus is that there is a minority of at least five members (for the chosen h and k, since $5 > hk = 0.6$). When five adjacent nodes hold the same state none of them can be updated anymore (since each of them will have maximally four neighbours in a different state which is not enough to reach a majority). In case one state is dominating in a local neighbourhood this may establish a stable cluster of at least five nodes, depending on the actual update sequence. These sensitivities concerning the initial distribution of nodes interplaying with the random sequence of updates makes it impossible to solve the model analytically, but on the other hand give rise to the observed nontrivial behaviour. With the avenue of a new group member more possibilities are opened up to establish stable clusters of different opinions. This is nothing but the forming of internal coalitions. It is straight-forward to see what happens if group size passes the critical region between 19 and 21. At this point two nodes arise which do not have any neighbours in common. Beyond this size also four internal groupings can be established. In other words, the number of ways to reach a dissensus has significantly expanded. The admission of one more member will thus have a lesser impact than in the smaller group. This constitutes the existence of a critical size which arises at the point where independent conversations between nodes can take place in the network. For large group sizes, as the maximal distance between two nodes increases (their correlation decreases), it becomes almost inevitable that balanced initial distributions lead to internal coalitions. These results hold, in principle, for every model of the opinion formation process which allows the formation of stable clusters, i.e. introduces (realistic) spatial correlations. Here this feature is incorporated by highly clustered small-world structure in combination with the random sequential updates.

The time has arrived to mention the case of $N = 8$. As stated above this is the only feasible cabinet size which has been avoided by all countries now and fifty years ago. Without claiming any scientific relevance of this point, it is amusing that with our choice of $h = 0.6$ is is possible to reproduce exactly this effect. In this case each node has seven neighbours and the network is fully connected. When the initial distribution is given by $A_i = 4$ the majority seen by the members is $4/7 \approx 0.57 < h$, so the threshold is not exceeded. This accounts for one out of nine initial distributions and we find $D(8) = \frac{1}{9} = 0.\overline{1}$. In British history this number was chosen only *once* for a cabinet [108]. It might not come as a surprise that this occurred under the reign of Charles I, King of England, Scotland and Ireland, who became famous for being beheaded after advocating the Divine Right of Kings, levying taxes without the Parliament's consent and therefore triggering the First English Civil War [117].

7.5 Description of the datasets

7.5.1 Cabinet Size

The cabinet size for 197 self-governing countries and territories is extracted from a weekly updated database provided by the CIA [110], as of November 9, 2007. We are interested in the number of persons in the highest executive committee. This accounts for a country's cabinet where we counted the number of Minister or Secretaries including the Prime Minister (if he is a member of the cabinet, as it is mostly the case but not always, e.g. Switzerland) and his vice(s). We do not include members of cabinets who hold a redundant office (e.g. Minister-Assistants or Minister of States). Attention has to be paid to the fact that in many cases the same person holds more than one office in a cabinet, we always count the number of persons and not offices. The obtained values are listed in Tab. 7.1. The only country where data is available but not included in our considerations is Bhutan. Here all but three members of the cabinet withdrew their office due to a new law stating the illegality of political party affiliation for cabinet members. The current caretaker regime does not formulate new governmental policies and only maintains

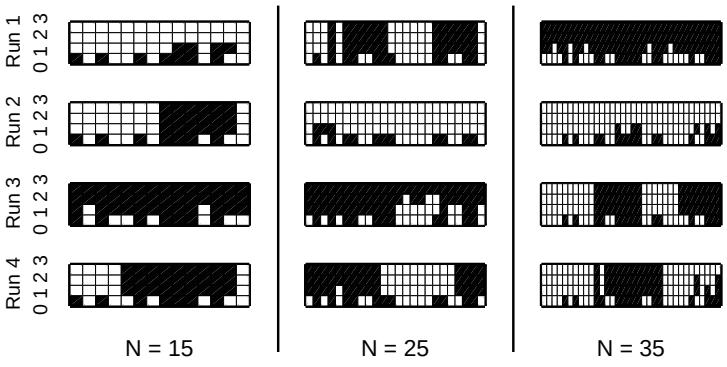

Figure 7.3: Evolution of the opinion formation process in groups of three different sizes ($N = 15, 25, 35$). Each individual is a box, whose opinion is either black or white. For each value of N we show 4 independent update-runs, all starting with the same initial configurations and the same network. In each run we show time steps 0,1,2,3, where time 0 corresponds to the initial configuration. Line 1 is obtained by the iterative application of the opinion formation protocol on the initial configuration in a random sequence of updates. The next lines (2,3) in are obtained in the same way. The particular sequence is seen to play a crucial role for the final state at time 3. Two different trajectories leading to consensus (all colors white or black at time 3) or dissensus (mixed colors) are shown for each size. It becomes apparent that once a cluster of five neighboring nodes with the same internal state has been established, this is stable over time. The question of con-or dissensus is thus equivalent to asking whether clusters with different states can appear (i.e. internal coalitions are built) which in turn crucially depends on the update sequence. Groups having passed the coefficient of inefficiency, as it is the case for $N = 25$ and $N = 35$, allow the formation of four clusters.

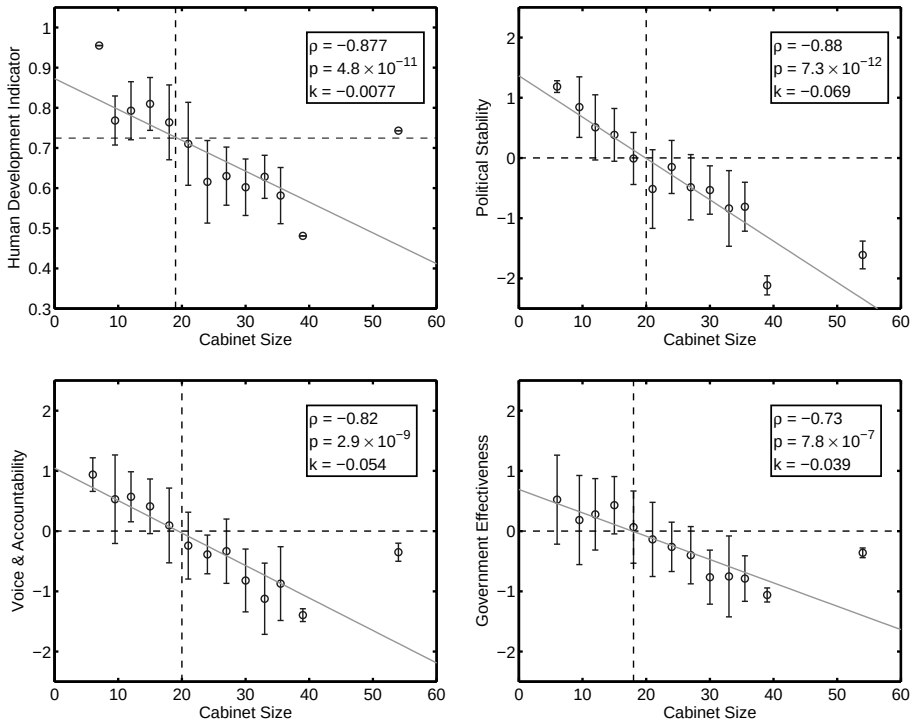

Figure 7.4: The diagrams for the cabinet size versus the Human Development Indicator and the three governance indicators Political Stability, Voice & Accountability and Government Effectiveness exhibit the same dependencies. For each indicator the correlation coefficient ρ, p-value and the slope k are listed. The confidence levels vary between $p \leq 10^{-6}$ and $p \leq 10^{-11}$. The error bars show the standard deviations stemming from the averaging (see text), when the data comes from only one country the literature's standard deviation is used (with the exception of the HDI, where no error margins are provided). The horizontal dashed lines show the global average, the positions of the vertical lines are given by the intersections between the linear fit and this average. For all indicators these cabinet sizes are found between 18 and 20.

day-to-day business.

7.5.2 Human Development Indicator

The Human Development Indicator (HDI) is published in the Human Development Report [109] on behalf of the United Nations Development Programme (UNDP) on an annual basis. It compares the achievements in human development of 173 countries along three dimensions. The indicator is equally weighted composed of the standard of living (measured by the gross domestic product), knowledge (as given by the adult literacy rate and gross enrolment ratio) and a long and healthy life (given by the life expectancy at birth). Each index is normalized on a scale between 0 and 1, the HDI is then the arithmetical mean of those three. Unfortunately, no standard deviations are available.

7.5.3 Governance Indicators

The World Bank publishes annually six dimensions of governance in the Worldwide Governance Indicator research project. We use current data [111] based on several hundred individual variables from 33 separate data sources by 30 different organisations. From this six aggregate

indicators are constructed. We consider in the present work three dimensions of governance.

Political Stability and Absence of Violence. This measures the perceptions of the likelihood that the government will be destabilised or overthrown by non-constitutional means. Aggregates for this indicator include the military coup risk, armed conflicts, social unrest, internal and external conflicts, government stability, political troubles, fractionalisation of the political spectrum, risk of political instability, etc.

Voice & Accountability. This measures to which extent people are able to participate in the selection of their government as well as basic human freedoms. Aggregates include political rights, freedom of the press, government censorship, military in politics, democratic accountability, institutional permanence, representativeness, hardening of the regime, transparency of government policies, etc.

Government Effectiveness. This measures the quality of public and civil services, the degree of independence from political pressures and the quality of policy formulation. Aggregates are government instability and ineffectiveness, institutional failure, e-government, quality of bureaucracy, public spending composition, satisfaction with public transport systems, policy consistency and forward planning, management of public debt, health services and education, trust in government, etc.

The governance indicators are measured in units following a normal distribution with zero mean and a standard deviation of one in each period, the vast majority of points lies between -2.5 and 2.5, standard deviations are provided.

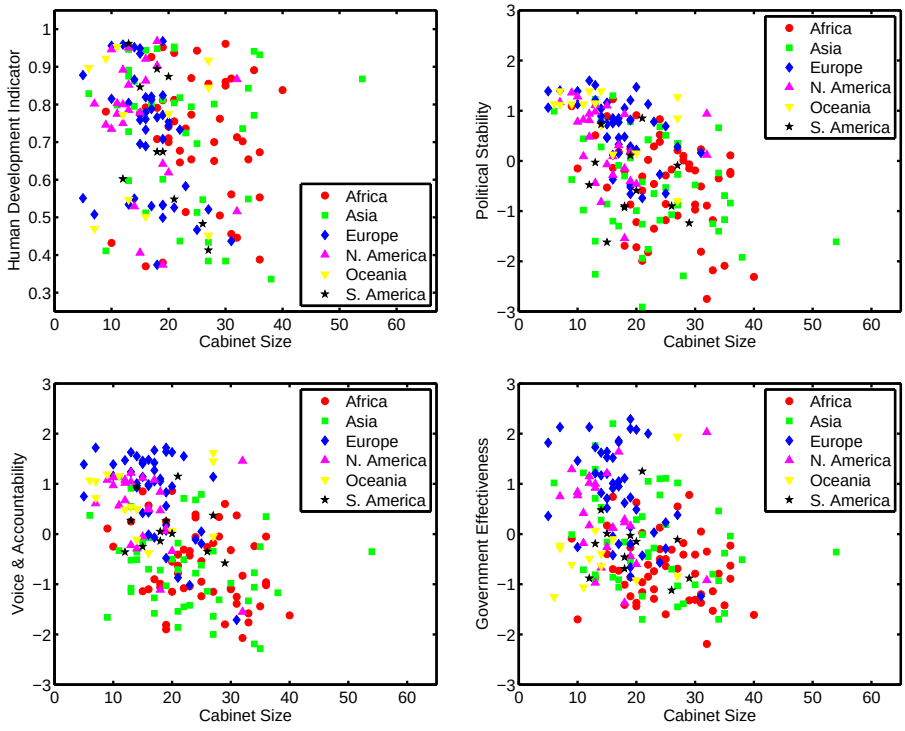

Figure 7.5: The regional correlations in both, the indicators and the cabinet size, can also be seen from the raw data. Each point represents one country with coordinates given by the cabinet size and the respective indicator. The colour corresponds to the continent where the capital is found to be. Countries from Europe, America and Oceania dominate the north-western regions of the diagrams, countries from Asia and Africa are more likely to be found in the south-eastern regions.

Fig. 7.4 shows the interdependency between cabinet size and these indicators. For each size the mean values and standard deviations of the indicators are computed (standard deviations from

the literature are used if only one country has the respective size, since this error is comparably small to the deviations from our averaging). From these values we computed the correlation coefficient ρ and the p-value. Subsequently we bin the cabinet sizes with an interval of three and compute the error bars by Gaussian error propagation.

Let us discuss the implications of these correlations in more detail. These governance indicators give us a tool to investigate a country's political climate in more concise directions than the Human Development Indicator. The indicator Political Stability can be interpreted as a measure for the influence of constitutional and non-constitutional forces on a destabilisation of the government and is therefore related to the number of interests and interest groups that have to be satisfied. This is also reflected in the composition of the cabinet, thus the negative correlation with the cabinet-size. A naive interpretation of our results makes the conclusion tempting that a dictatorship would be the most effective form of decision-making. The indicator Voice & Accountability, however, reveals that exactly the opposite holds. It quantifies to which extent citizens have elected their current leaders. A country with a low value here is thus more likely to be reigned by a sovereign leader or council which often confers executive, legislative and jurisdicative powers onto one hand. In this case the nominal executive council, the cabinet, is less influent and important than in countries where it is indeed the highest executive council. We find that this tends to increase the membership of the cabinet which can be understood through the minor importance and therefore exclusivity of it. Government Effectiveness gives us insight into the quality of policy formulation in the government and is thus directly related to a cabinet's ability to find consensus on an issue in question and advance it reasonably. Let us stress that the actual size of the cabinet is not included in the aggregates. Furthermore, this indicator also measures how efficient this policies are implemented from the government downward to the citizens.

In Fig. 7.5 we show the raw data for the indicators versus cabinet size. A colour code for the continents shows regional clustering of the points. Countries from Europe, America and Oceania are more likely to be found in the north-western region of the plots than countries from Asia and Africa.

7.6 Simulation details

The numerical results are obtained by counting the frequency of final configurations without consensus out of 10^5 realisations. In each run we first create a regular 1D ring where each node is connected to its k nearest neighbors. Each link is then deleted with probability L and new links are randomly created such that there are Nk links in total and each node has exactly k links again.

Influence of the model parameter. The number of neighbours k determines the position of the critical point. The driving mechanism is the allowance for internal coalitions, i.e. the formation of stable clusters. When the network is fully connected we either encounter consensus or a frozen system, depending on h. Our choice of $h = 0.6$ is primarily motivated by giving rise to a frozen state for a fully connected network with $N = 8$ and a balanced initial distribution, i.e. an equal number of nodes being initially in state 0 and 1. For other choices one may encounter different frozen states. For fixed model parameters and increasing group sizes there is always a point where stable clusters begin to emerge. It is this point where the increase in dissensus not stemming from an initially frozen state sets in. Note that for our choices in the case of $N = 10$ the main contributions in dissensus still com from frozen systems, here an evolution toward a dissensus state is highly unlikely. Finally the critical point, where an increase in group size leads to considerably smaller increments in the dissensus, can be found when four cluster can be formed for given h and k. With increasing L the topology becomes less regular and approaches a random graph for $L = 1$. In other words, the neighbourhoods of two neighbouring nodes are becoming more independent with increasing L and local correlations diminish. Consensus can

be easier reached for networks with higher L. Fig. 7.6 shows $D(N)$ for different parameter settings and confirms the above stated observations.

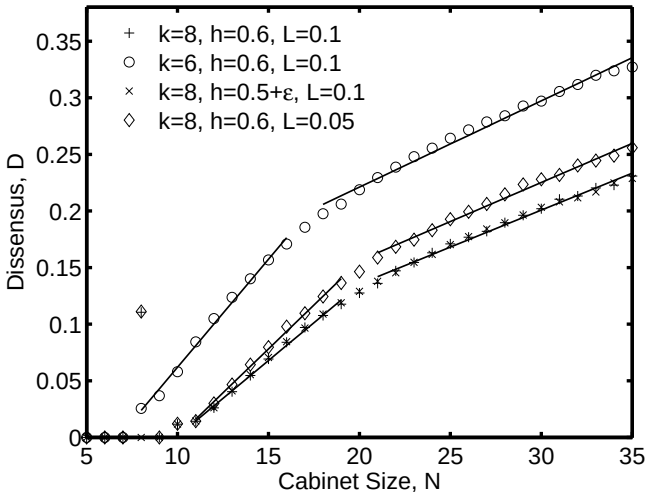

Figure 7.6: $D(N)$ for four different settings of the model parameters (k, h, L) are shown. As a reference we show $D(N)$ for $(8, 0.6, 0.1)$ again (pluses). Decreasing the connectivity of the group's network, parameter setting $(6, 0.6, 0.1)$, circles, shifts the position of the critical point and increases the tendency toward dissensus. Adjusting the threshold such that we recover the pure majority rule, $(8, 0.5 + \epsilon, 0.1)$, crosses, has no impact on $D(N)$ due to our choice of k, except that we do not find the 'Charles I' scenario in this case. Of course, for the same k, L and $h > 5/8 = 0.6125$ we would find an increase in dissensus. Lowering L and therefore increasing the spatial correlations in the network hardens the finding of consensus too, as can be seen from the settings $(8, 0.6, 0.05)$ (diamonds).

8 Summary

Evolutionary thinking is based on well-grounded observations of how systems composed of a large number of interconnected items behave on a collective level. New items come constantly into being, interact with already existing ones and get accordingly selected on the basis of how 'useful' or 'fit' they are in their environment. These interactions in turn possibly alter the boundary conditions of the entire system and therefore bring new innovations forth. In recent decades this line of reasoning transcended from the fields of biology and population ecology into social, economic and technological contexts.

We explained what traditional quantitative attempts to study such systems achieved – but also what they did not. A physicist is accustomed to treat dynamical systems by extracting the relevant variables, specifying initial and boundary conditions and then sitting down and calculate. Evolutionary systems defy this approach when it comes to the study of innovations. We argued that items are manifestly contextual in the sense that their functional role is first and foremost defined by their environment and may radically change with it. To talk slang, boundary conditions co-evolve. We learned that the 'fitness' or 'utility' of an item can be related to the adjacent possible which is the potential of all new substitutes or complements a new item might bring to a system. We quantified this concept with interaction indication functions and formulated a variational principle on this basis. Using this principle, we employed the statistical physics machinery to define a free energy for evolutionary systems allowing us to obtain asymptotic diversities via a simple minimization procedure.

We showed how based on the current understanding of constituent relations in evolutionary systems we can define a general interaction scheme. We suggest to go beyond the usual network approach and regard the topology of evolutionary systems to be defined as an adjacency matrix on the power set of all existing items. We studied versions of this model both analytically and empirically in economic, biological and social settings. We are able to reproduce a significant number of stylized facts found in real-world natural or man-made systems, spanning orders of magnitudes.

Finally we showed how our master equation approach to quantify the adjacent possible can be used in solving an opinion formation problem and applied this in the context of political decision-making as envisaged by Parkinson's Law as a semi-satiric reprise.

List of Figures

List of Tables

Bibliography

[1] Klimek P., Hanel R., Thurner S., Opinion Formation in Laggard Societies; *Europhysics Letters* **82**, 2, 28008 (2008).

[2] Hanel R., Klimek P., Thurner S., Studies in the Physics of Evolution: Creation, Formation, Destruction; *Proceedings of SPIE* **6802**, 80206 (2008).

[3] Klimek P., Thurner S., Hanel R., Pruning the Tree of Life: k-core Percolation as Selection Mechanism; *Journal of Theoretical Biology* **256**, 142-6 (2009).

[4] Klimek P., Hanel R., Thurner S., Parkinson's Law Quantified: Three Investigations on Bureaucratic Inefficiency; *Journal of Statistical Mechanics: Theory and Experiment* **P03008** (2009).

[5] Klimek P., Hanel R., Thurner S., To How Many Politicians Should Government Be Left?; *Physica A* **388**, 18, 3939-47 (2009).

[6] Thurner S., Klimek P., Hanel R., Schumpeterian economic dynamics as a quantifiable minimum model of evolution ; to appear in *New Journal of Physics* (2009).

[7] Campbell, G., *Empedocles.* Internet Encyclopedia of Philosophy. http://www.iep.utm.edu/e/empedocl.htm #H 4.

[8] Hardie, R.P., R. K. Gaye, *Physics by Aristotle.* http://classics.mit.edu/Aristotle/physics.2.ii.html.

[9] Lovejoy, A., *The Great Chain of Being: A Study of the History of an Idea* (Harvard University Press, Cambridge, 1936).

[10] Bowler, P. J., *Evolution: The History of an Idea* (University of California Press, Berkeley, 2003).

[11] Goodrum, M. R., Atomism, Atheism, and the Spontaneous Generation of Human Beings: The Debate over a Natural Origin of the First Humans in Seventeenth-Century Britain; *Journal of the History of Ideas* **63** 2, 207224 (2002).

[12] Darwin, E., *The Temple of Nature or The Origin of Society* (Jones & Company, London, 1825).

[13] Lamarck, J.-B., *Philosophie Zoologique ou Exposition des Considérations Relatives á l'Histoire Naturelle des Animaux* (Reprinted by University of Chicago Press, Chicago, 1984).

[14] Chambers, R., *Vestiges of the Natural History of Creation* (John Churchil, London, 1844).

[15] Ducheyne, S., *Joan Baptista Van Helmont and the Question of Experimental Modernism*; *Physis: Rivista Internazionale di Storia della Scienza* **43**, 305-332 (2005).

[16] Pasteur, L., Des Générations Spontanées; *Confrences Faite aux 'Soires Scientifiques de la Sorbonne'*, 257-265 (1993).

[17] Desmond, A, Moore, J., *Darwin* (Michael Joseph, Penguin Group, London, 1991).

[18] Malthus, T. R., *An Essay on the Principle of Population* (J. Johnson, in St. Paul's Churchyard, London , 1798).

[19] Verhulst, P. F., Notice Sur la Loi que la Population Poursuit dans son Accroissement; *Correspondance Mathmatique et Physique* **10**. 113121 (1838).

[20] Darwin, C., *On the Origin of Species by Means of Natural Selection, or the Preservation of Favoured Races in the Struggle for Life (1st ed.)* (John Murray, London, 1859).

[21] Fisher, R. A., *The Genetical Theory of Natural Selection* (Clarendon Press, Oxford, 1930).

[22] Haldane, J.B.S., *The Causes of Evolution* (Princeton University Press, New Jersey, 1990).

[23] Wright, S., *Evolution: Selected Papers* (University of Chicago Press, Chicago, 1986).

[24] Dawkins, R., *The Selfish Gene* (Oxford University Press, New York, 1976).

[25] Hamilton, W. D., The Genetical Evolution of Social Behavior; *Journal of Theoretical Biology* **7** (1), 152 (1964).

[26] Smith, J. M., Group Selection and Kin Selection; *Nature* **201** (4924), 11451147 (1964).

[27] Price, G.R., Fisher's Fundamental Theorem Made Clear; *Annals of Human Genetics* **36**, 129-140 (1972).

[28] Semiconductor Industry Association Factsheet, http://www.sia-online.org/cs/industry_resources/industry_fact_sheet.

[29] Kauffman, S. A., Thurner S., Hanel, R., The Evolving Web of Future Wealth; *Scientific American* (May 2008 online).

[30] Schumpeter, J. A., *Theorie der Wirtschaftlichen Entwicklung* (Duncker & Humblot, Leipzig, 1912).

[31] U.S. Bureau of the Census *Historical Statistics of the United States, Colonial Times to 1970, Bicentennial Edition, Part 1 & 2* (Washington, D.C., 1975); More recent data from http://factfinder.census.gov.

[32] Fontana, W., Wagner, G., Buss, L., Beyond Digital Naturalism; *Artificial Life* **1**, 211-227 (1994).

[33] Volterra, V., *Variations and fluctuations of the number of individuals in animal species living together.* In *Animal Ecology* (New York, McGrawHill, 1931).

[34] Page, K., Nowak, M., Unifying Evolutionary Dynamics; *Journal of Theoretical Biology* **219**, 93-98 (2002).

[35] Crow, J. F., Kimura, M., *An Introduction to Population Genetics* (Burgess Publishing Co., Minneapolis, MN, 1970).

[36] Schuster, P., Sigmund, K., Replicator Rynamics; *Journal of Theoretical Biology* **100**, 533-538 (1983).

[37] Hadeler, K. P., Stable Polymorphism due to Selection Depending on the Composition of a Population; *SIAM Journal of Applied Mathematics* **41**, 1-7 (1981).

[38] Taylor, P. J., Jonker, L., Evolutionary Stable Strategies and Game Dynamics; *Mathematical Biosciences* **40**, 145-156 (1978).

[39] Hofbauer, J., Sigmund, K., *Evolutionary Games and Population Dynamics* (Cambridge University Press, Cambridge, 1998).

[40] Eigen, M., McCaskill, J., Schuster, P., The Molecular Quasispecies; *Advances in Chemical Physics* **75**, 149-263 (1989).

[41] Stadler, P. F., Fontana, W., Miller, J. H., Random Catalytic Reaction Networks; *Physica D* **63**, 378-392 (1993).

[42] Price, G. R., Selection and Covariance; *Nature* **227**, 520-521 (1970).

[43] Solé, R. V., Manrubia, S. C., Extinction and Self-Organized Criticality in a Model of Large-Scale Evolution; *Physical Review E* **54**, R42-5 (1996).

[44] Jain, S., Krishna, S., Autocatalytic Sets and the Growth of Complexity in an Evolutionary Model; *Physical Review Letters* **81**, 5684 (1998); Large Extinctions in an Evolutionary Model: The Role of Innovation and Keystone Species; *Proceedings of the National Academy of Sciences* **99**, 2055 (2002).

[45] Kauffman, S. A., Metabolic Stability and Epigenesis in Randomly Constructed Genetic Nets; *Journal of Theoretical Biology* **22**, 437-67 (1969).

[46] Bak, P., Sneppen, K., Punctuated Equilibrium and Criticality in a Simple model of Evolution; *Physical Review Letters* **71**, 4083-4086 (1993).

[47] Goernerup, O., Crutchfield, J. P., Hierarchical Self-Organization in the Finitary Process Soup; *Artificial Life Journal* **14** 3 (2008), 245-254.

[48] Kauffman, S.A., *Origins of order: Self-organization and selection in evolution* (Oxford University Press, New York, 1993).

[49] Dittrich, P., Speroni di Fenizio, P., Chemical Organization Theory: Towards a Theory of Constructive Dynamical Systems; *Bulletin of Mathematical Biology* **69** (4), 1199-1231 (2007).

[50] Hanel R., Thurner S., Kauffman S. A., The Phase Transition of Random Catalytic Sets; *Physical Review E* **72**, 036117 (2005).

[51] Paine, R.T., A Note on Trophic Complexity and Community Stability; *The American Naturalist* **103** (929): 9193 (1969).

[52] Thurner, S., Hanel, R., Klimek, P., Physics of evolution: selection without fitness; to appear in *Physica A* (2009).

[53] Kadanoff L., Coppersmith S., Aldana M., Boolean Dynamics with Random Couplings; in *Perspectives and Problems in Nonlinear Science. A Celebratory Volume in Honor of Lawrence Sirovich*, Kaplan, E., Marsden, J. E., Sreenivasan, K. R., eds. (Springer Applied Mathematical Sciences Series 2002).

[54] Newman, M. E. G., Palmer, R. G., *Modeling Extinction* (Oxford University Press, New York, 2003).

[55] Arthur, B., The Evolution of Technology Within a Simple Computer Model: Research Articles; *Complexity* **11**, 23-31 (2006).

[56] Hanel R., Thurner S., Kauffman S. A., Towards a Physics of Evolution: Critical Diversity Dynamics at the Edges of Collapse and Bursts of Diversification; *Physical Review E* **76**, 036110 (2007).

[57] Thurner S., Klimek P., Hanel R., Schumpeterian Economic Dynamics as a Qquantifiable Minimum Model of Evolution; *Preprint* arXiv:0909.3482v1 [physics.soc-ph] (2009).

[58] Bak, P., Tang, C.,Wiesenfeld, K., Self-Organized Criticality: An Explanation of 1/f Noise; *Physical Review Letters* **59**, 381-84 (1987).

[59] Emmerling, M., et al., Metabolic Flux Responses to Pyruvate Kinase Knockout in *Escherichia coli*; *Journal of Bacteriology* **184**, 152-164 (2002).

[60] Sepkoski, J.J. Jr., A Compendium of Fossil Marine Animal Families, 2nd ed. *Milwaukee Public Museum Contributions in Biology and Geology* **83** (1992).

[61] Schumpeter, J. A., *Capitalism, Socialism and Democracy* (Harper, New York, 1947).

[62] Schumpeter, J. A., *Business Cycles* (McGraw-Hill, London, 1939).

[63] Schumpeter, J. A., *History of Economic Analysis* (Oxford University Press, New York, 1954).

[64] Geanakoplos, J., Farmer, J. D., The Virtues and Vices of Equilibrium and the Future of Financial Economics; *Preprint* q-fin/0803.2996v1 (2008).

[65] Kurz, H. D., *Ricardian Vice* (*International Encyclopedia of the Social Sciences*, 2nd Ed, Macmillan Reference, USA, 2008).

[66] Romer, P., Endogenous Technological Change; *Journal of Political Economics* **98** 5, 71-102 (1990).

[67] Segerstrom P., Anant T. C. A., Dinopoulos, E., A Schumpeterian Model of the Product Life Cycle; *American Economic Review* **80**, 1077-92 (1990)

[68] Grossman, G., Helpman E., Quality Ladders in the Theory of Growth; *Review of Economic Studies* **58**, 43-61 (1991).

[69] Aghion, P., Howitt, P., A Model of Growth through Creative Destruction; *Econometrica* **60**, 323-51 (1992).

[70] Romer, P., The Origins of Endogenous Growth; *Journal of Economic Perspectives* **8**, 3-22 (1994).

[71] Raup, D.M., A Kill Curve for Phanerozoic Marine Species; *Paleobiology* **18**, 80-88 (1991).

[72] Bagley, R. J., Farmer, J. D., Fontana W., Evolution of a Metabolism; in *Artificial Life II*, 141-158C.G. Langton et al. eds. (Addison-Wesley, 1991).

[73] http://www.statistics.gov.uk/StatBase/TSDdownload1.asp

[74] Lambiotte, R., Thurner, S., Hanel, R., Unanimity Rule on Networks; *Physical Review E* **76**, 046101 (2007).

[75] Willis, J.C., *Age and Area* (Cambridge University Press, Cambridge 1922).

[76] Goltsev, A.V., Dorogovtsev, S.N., Mendez, J.F.F., k-core (Bootstrap) Percolation on Complex Networks: Critical Phenomena and Nonlocal Effects; *Physical Review E* **73**, 056101 (2006).

[77] Vázquez, A., Growing Network with Local Rules: Preferential Attachment, Clustering Hierarchy, and Degree Correlations; *Physical Review E* **67**, 056104 (2003).

[78] Vázquez, A., Flammini, A., Maritan, A., Vespignani, A., Modeling of Protein Interaction Networks; *ComplexUs* **1**, 38 (2003).

[79] de Duve, C., The Onset of Selection; *Nature* **433**, 581-582 (2005).

[80] Clauset, A., Shalizi, C.R., Newman, M.E.J., Power-Law Distributions in Empirical Data; *Preprint* arXiv:0706.1062 [physics.data-an] (2007).

[81] Corominas-Murtra, B., Mendes, J.F.F., Solé, R.V., Nested subgraphs of complex networks; *Journal of Physics A: Mathematical and Theoretical* **41**, 385003 (2008).

[82] Benton, M.J. and Pearson, P.N., Speciation in the Fossil Record; *Trends in Ecology and Evolution* **16**, 405-411 (2001).

[83] Liggett, T.J., *Stochastic Interacting Systems* (Springer Verlag, New York, 1999).

[84] Ben-Naim, E., Frachebourg, L., Krapivsky, P.L., Coarsening and Persistence in the Voter Model; *Physical Review E* **53**, 3078 (1996).

[85] Galam, S., Majority Rule, Hierarchical Structures, and Democratic Totalitarianism: A Statistical Approach; *Journal of Mathematical Psychology* **30**, 426434 (1986).

[86] Krapivsky, P.L., Redner, S., Dynamics of Majority in Two-State Interacting Spins Systems; *Physical Review Letters* **90**, 238701 (2003).

[87] Mobilia, M., Redner, S., Majority versus Minority Dynamics: Phase Transition in an interacting two-state Spin System; *Physical Review E* **68**, 046106 (2003).

[88] Axelrod, R., The Dissemination of Culture, *Journal of Conflict Resolution* **41**, 203 (1997).

[89] Albert, R., Barabasi, A.-L., Statistical Mechanics of Complex Networks; *Reviews of Modorn Physics* **74**, 47 (2002).

[90] Sood, V., Redner, S., Voter Model on Heterogeneous Graphs *Physical Review Letters* **94**, 178701 (2005).

[91] Castellano, C., Loretto, V., Barrat, A., Cecconi, F., Parisi, D., Comparison of Voter and Glauber Ordering Dynamics on Networks; *Physical Review E* **71**, 066107 (2005).

[92] Castellano, C., Vilone, D., Vespignani, A., Incomplete Ordering of the Voter Model on Small-World Networks; *Europhys. Lett.* **63**, 153 (2006).

[93] Lambiotte, R., How Does Degree Heterogeneity Affect an Order-Disorder Transition; *Europhysics Letters* **78**, 68002 (2007).

[94] Lambiotte, R., Ausloos, M., Holyst, S.H., Majority Model on a Network with Communities; *Phys. Rev. E* **75**, 030101 (2007).

[95] Stauffer, D., Sociophysics Simulations; *Computing in Science and Engineering* **5**, 71 (2003); Sociophysics Simulations II: Opinion Dynamics; *AIP Conference Proceedings* **779**, 56-68 (2005).

[96] Biely, C., Dragosits, K., Thurner, S., Prisoner's Dilemma on Dynamic Networks Under Perfect Rationality; *Physica D* **228**, 40-48 (2007).

[97] Holme, P., Newman, M.E.J., Nonequilibrium phase transition in the coevolution of networks and opinions; *Physical Review E* **74**, 056108 (2006).

[98] Caldarelli, G., Capocci, A., Garlaschelli, D., Self-organized network evolution coupled to extremal dynamics; *Nature Physics* **3**, 813 - 817 (2007).

[99] Vazquez, F., Eguíluz, V.M., San Miguel, M., Generic Absorbing Transition in Coevolution Dynamic; *Physical Review Letters* **100**, 108702 (2008).

[100] Biely, C., Hanel, R., Thurner, S., Socio-Economical Dynamics as a Solvable Spin System on Co-evolving Networks; *European Physical Journal B* **67**, 285-290 (2009).

[101] Stangor, C., *Social Groups in Action and Interaction* (Psychology Press, New York, 2004).

[102] Asch, S.E., *Social Psychology* (Englewood Cliffs, Prentice Hall, New Jersey 1952).

[103] Kelman, H., Compliance, Identification, and Internalization. Three Processes of Attitude Change; *Journal of Conflict Resolution* **2**, 51-60 (1958).

[104] Watts, D.J., A Simple Model of Global Cascades on Random Networks; *Proceedings of the National Academy of Sciences* **99**, 5766-5771 (2002).

[105] Erdős, P., Rényi, A., On random graphs; *Publicationes Mathematicae Debrecen* **6**, 290 (1959).

[106] Castellano, C., Fortunato, S., Loreto, V., Statistical physics of social dynamics; *Reviews of Modern Physics* **81**, 591-646 (2009)

[107] http://www.gallup.com/poll/topics.aspx.

[108] Parkinson, C.N., *Parkinson's Law and Other Studies in Administration* (Buccaneer Books, Cutchogue, 1957).

[109] UNDP, *Human Development Report 2007/2008* (United Nations Development Programme, New York, 2007).

[110] CIA, *Chiefs of State and Cabinet Members of Foreign Governments* (Central Intelligence Agency, Washington D.C., 2007).

[111] Kaufmann, D., Kraay, A., Mastruzzi, M, 2007. Governance matters VI: Aggregate and individual governance indicators, 1996-2006. *Policy, Research Working Paper* WPS 4280.

[112] Helbing, D., *Quantitative Sociodynamics* (Kluwer, Dordrecht, 1995).

[113] Schweitzer, F., *Self-Organization of Complex Structures: From Individual to Collective Dynamics* (Gordon & Breach, Amsterdam, 1997).

[114] Lambiotte, R., Redner, S., Dynamics of Non-Conservative Voters; *Europhysics Letters* **82** 1, 18007 (2008).

[115] Watts, D.J., Strogatz, S.H., Collective Dynamics of 'Small-World' Networks; *Nature* **393**, 440 (1998).

[116] Watts, D.J., *Small Worlds* (Princeton University Press, Princeton, NJ, 1997).

[117] Carlton, C., *Charles I: The Personal Monarch* (Routledge, London, 1995).

Personal information

Surname(s) / First name(s)	**Klimek, Peter**
Address(es)	Complex Systems Research Group, Medical University of Vienna; Währinger Gürtel 18-20, A-1090, Vienna, Austria
Telephone(s)	++43 1 40400 2080 Mobile: ++43 660 55 36 522
Email(s)	peter.klimek@meduniwien.ac.at
Nationality(-ies)	Austria
Date of birth	17/08/1982

Education

Jul 2009	WE-Heraeus Summer School 'Steps in Evolution', Bremen, Germany.
Dec 2008	Santa Fe Institute Complex Systems Summer School in Bariloche, Argentina.
Oct 2007 - Dec 2009 [1]	**PhD** in natural sciences (physics), University of Vienna. Advisor: Stefan Thurner.
May 2007 - Dec 2009	**Research associate**, Complex Systems Research Group, MU Vienna.
Feb 2006 - Mar 2007	**Diploma student**, Institute for Quantum Optics and Quantum Information, Austrian Academy of Sciences. Advisor: Časlav Brukner.
Oct 2000 - Mar 2007	Master program in theoretical physics at the University of Vienna (honors).
Jun 2000	Higher education entrance qualification (honors).
Sep 1992 - Jun 2000	Realgymnasium Wenzgasse, GRg13 (Vienna), specialization in biology, chemistry and physics.

Talks

May 2009	CAMP0801, Rome, Italy. *Mean Field Solution of an Hyperspin Ising Model.*
Jul 2008	$\Sigma\Phi$2008, International Conference in Statistical Physics, Kolymbari, Greece. *Parkinson's Law quantified.*
Feb 2008	72^{th} annual session of the DPG, Berlin, Germany. *To how many politicians should government be left?*
Sep 2007	CCP2007, Brussels, Belgium. *Opinion formation in laggard societies.*
Jul 2007	University of Applied Arts, Vienna, Austria. *Nonlinearity, nondeterminism, self-referentiality and all that.*
Feb 2007	Seminar, Vienna, Austria. *Logical complementarity in quantum computation.*
Nov 2006	IQOQI Breakfast Talk, Vienna, Austria. *Computation: classical bounds and quantum violation.*

Publications

2009

P. Klimek, S. Thurner, R. Hanel, 'Evolutionary Mechanics via a Variational Principle', *in preparation*.

R. Hanel, P. Klimek, S. Thurner, 'Physics of Evolution: Selection without Fitness', to appear in *Physica A*.

S. Thurner, P. Klimek, R. Hanel, 'Schumpeterian economic dynamics as a quantifiable minimum model of evolution', to appear in *New Journ. Phys.*

T. Paterek, R. Prevedel, J. Kofler, P. Klimek, M. Aspelmeyer, A. Zeilinger, Č. Brukner, 'Logical independence and quantum randomness', to appear in *New Journ. Phys*.

P. Klimek, R. Hanel, S. Thurner, 'Parkinson's Law quantified: three essays on bureaucratic inefficiency', *J. Stat. Mech.* P03008.

[1] projected

P. Klimek, S. Thurner, R. Hanel, 'Pruning the tree of life: k-core percolation as selection mechanism', *J. Theor. Biol.* **256**, 142-6.

2008 P. Klimek, R. Hanel, S. Thurner. 'To how many politicians should government be left?', *Physica A* **388**, 18, 3939-3947.

R. Hanel, P. Klimek, S. Thurner, 'Studies in the physics of evolution: creation, formation, destruction', *Proc. of SPIE* **6802**, 680206.

P. Klimek, R. Lambiotte, S. Thurner, 'Opinion formation in laggard societies', *Europhysics Letters* **82**, 2, 28008.

Skills

languages	German (mother tongue), English (fluent), Latin.
programming languages	MatLab, Mathematica, C, FORTRAN.
software	MS Office, OpenOffice.org, LaTeX, Adobe Photoshop, Adobe Final Cut, Pajek, GIMP.

In the Media (Selection)

Interviews	BBC Radio World Service: The Forum. Live Interview (15.04.09).
	Berliner Morgenpost: Die Acht ist eine ausweglose Zahl (25.01.09).
	BBC Radio Scotland: Live Interview (19.01.09).
	BBC Radio 5: Live Interview (11.01.09).
	Austrian National Radio OE1: Dimensionen (20.06.08).
In Print	New Scientist: Explaining the curse of work (14.01.09).
	The Daily Telegraph: Eight people on committee leads to decision deadlock, scientists say (12.01.09).
	The Australian Times: Committees of 8 decidedly indecisive (12.01.09).
	The Sunday Times: Number's up for 'unlucky' eight (11.01.09).
	New Scientist: Editorial: Parkinson's Law is alive and well (07.01.09).
	GEO Magazin: Begrenzt regierfähig (Nr. 11/08).
	Wirtschaftsblatt: Wissenschafter zeigen: Bürokratie erzeugt Ineffizienz (04.09.08).
	Nature News: Battling bureaucracy with math (22.08.08).
	The Moscow Times: Austrians Suggest Small Is Better (23.05.08).
	Der Standard: Auf die Größe kommt es an (21.05.08).

Other Activities

Jul 2006 - Jul 2007	Production and moderation of the TV format 'community.talk' on OKTO.
Jun 2005 - Oct 2006	Assistant teacher in mathematics und physics.
	Lernfreunde Young Enterprises Media GmbH & Co OEG.
since Jan 2004	Co-founder and -operator of the Realgymnasium Wenzgasse alumni network.