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Towards a physics of evolution: Critical diversity dynamics at the edges of collapse and bursts of diversification

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Systems governed by standard mechanisms of biological or technological evolution are often described by catalytic evolution equations. We study the structure of these equations and find an analogy with classical thermodynamic systems. In particular we can demonstrate the existence of several distinct phases of evolutionary dynamics: a phase of fast growing diversity, one of stationary, finite diversity, and one of rapidly decaying diversity. While the first two phases have been subject to previous work, here we focus on the destructive aspects – in particular the phase diagram – of evolutionary dynamics. The main message is that within a critical region massive loss of diversity can be triggered by very small external fluctuations. We further propose a dynamical model of diversity which captures spontaneous creation and destruction processes fully respecting the phase diagrams of evolutionary systems. The emergent timeseries show rich diversity dynamics, including power laws with similar exponents as observed in actual economical data, e.g. firm bankruptcy data. We believe the present model presents a possibility to cast the famous qualitative picture of Schumpeterian economic evolution, into a quantifiable and testable framework.

I. INTRODUCTION

Maybe the most intuitive way to think of evolution dynamics is in the context of technological innovation. There, innovation is a three step process. First, new elements (goods, products, things) come into being through the process of (re)combination and substitution of already existing elements. Second, these new things then undergo a ‘valuation’ or selection process based on their ‘utility’ associated to them. This ‘utility’ strongly depends on the surroundings into which the new element was ‘born’. Surroundings are defined as the set of all other yet existing things. Third, if the new thing ‘survives’ (i.e. gets selected by its surroundings) it will itself form part of the surroundings, and will as such influence the valuation process for all new things entering the system in future timesteps. In this view of evolutionary processes, biological evolution is a special case of technological innovation, where recombination and substitution happens on the DNA scale through sexual reproduction and random inventions (mutations).

To formally capture the dynamics of an evolving system which is governed by a combination/substitution mechanism, imagine that the system is characterized by a d dimensional state vector x . Each component x_i quantifies the abundance of element i . The total maximum number of elements that can potentially ever exist in the system is bounded from above by d . (Note that it was shown in [1] that the limit $d \rightarrow \infty$ exists and is well de-

fined). Its dynamics is governed by the famous equation

$$\frac{\partial}{\partial t} x_i = \sum_{j,k} \alpha_{ijk} x_j x_k - x_i \sum_{j,k,l} \alpha_{ljk} x_j x_k \quad , \quad (1)$$

where the second term ensures normalization of x . x thus captures the *relative* abundances of existing elements. The tensor elements α_{ijk} serve as a ‘rule table’, telling which combination of two elements j and k can produce a third (new) element i . The element α_{ijk} is the rate at which element i can get produced, given the elements j and k are abundant at their respective concentrations x_j and x_k . Equation (1) has a long tradition; some of its special cases, depending on the particular choice of α , are the Lotka Volterra replicators see e.g. in [2], the hypercycle [3], or the Turing gas [4]. Equation (1) has been analyzed numerically [5, 6], however system sizes are extremely limited. In contrast to the amount of available qualitative and historical knowledge on evolution [7], surprisingly little effort has been undertaken to solve Eq. (1) explicitly.

To understand the dynamics of Eq. (1) analytically it was suggested in [1] to make three assumptions: (i) the focus is shifted from the actual concentration of elements x_i , to the system’s diversity. Diversity is defined as the number of existing elements. An element exists, if $x_i > 0$, and does not exist if $x_i = 0$. (ii) For simplicity, the rule table α is assumed to have binary entries, 0 and 1 only, (iii) the location of the non-zero entries is perfectly random. To characterize the number of these entries the number r is introduced, which is the rule table density or the density of *productive* pairs. The total number of productive pairs in the system (i.e. the number of non-zero entries in α) is consequently given by $r d$.

With these assumptions, the idea in [1] was to rewrite Eq. (1) into a dynamical map whose asymptotic limit

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could be found analytically. The only variable of the corresponding map is r . The initial condition, i.e., the initial size of present elements is assigned a_0 . The solution of the system is the asymptotical value ($t \rightarrow \infty$) of diversity, a_∞ . The amazing result of this solution, (as a function of r and the initial condition a_0) is that evolutionary systems of the type of Eq. (1) have a phase transition in the r - a_0 plane. In one of the two phases – after a few iterations – no more elements can be built up from existing ones and the total diversity converges to a finite number (sub-critical phase). The other phase is characterized that the advent of new elements creates so many more possibilities to create yet other elements that the system ends up producing all or almost all possible d elements. This we call the super-critical or ‘fully populated’ phase. Even though the existence of a phase transition was hypothesized some time ago in [8], it is surprising that the phase transition is mathematically of exactly the same type as a Van der Waals gas. (It is maybe noteworthy that the Fisher structure (linear form of Eq. (1)) does not have such a transition, for this a non-linear model is needed). Note that this model is a mathematically tractable variant of the so called bit-string model of biological evolution, introduced in [8].

The dynamics discussed so far assumes that a system is starting with some initial diversity a_0 , which increases over time, up to a final asymptotic level, a_∞ . However, also the opposite dynamics is possible. Imagine one existing element, say i , is removed from the system, a species is dying out, or a technical tool gets out of fashion or production. This removal can imply that other elements, which needed i as a production-input will also cease to exist, unless some other way exists to produce them (not involving i). Note, that all the necessary information is stored in α .

The first part of this paper studies the dynamics of evolutionary systems which exist in the highly populated phase, and where δ_0 elements get kicked out at the initial timestep. These defected elements may trigger others to default as well. We demonstrate the existence of a new phase transition in the δ_0 - r plane, meaning that for a fixed rule density r there exists a critical value of initial defects, above which the majority of elements will die out in a cascade of secondary defects.

However, this is only part of the story. In reality, the final diversity a_∞ will not be a constant, but will be subject to fluctuations. The relevant parameter will become the diversity (number of nonzero elements in x) over time, a_t . In particular, there are two types of fluctuations: elements will get created spontaneously at a given rate, and existing elements will go extinct at another rate. The second part of this work proposes a dynamical model of an evolutionary system incorporating these spontaneous processes, compatible with their inherent phase diagrams. The model is characterized by the rule density r , one creation and one destruction process, the latter ones modeled by simple Poisson processes. We study the resulting dynamics and find several character-

istics typical to critical systems such as destructive economical dynamics, e.g. described qualitatively by J. A. Schumpeter a long time ago [9]. An example from biology are the large extinctions of species over short timescales, see e.g. [10] and references therein.

II. THE CREATIVE PHASE TRANSITION

The dynamics of diversity (number of existing elements over time) has been analytically solved in [1]. To be self-consistent in this section we review the argument: It is first assumed that the system has a growing mode only (tensor elements α_{ijk} are zero or one but never negative). For this situation Eq. (1) was projected onto a dynamical map, whose asymptotic solutions can be found.

If the number of non-zero elements in $x(t)$ is denoted by a_t , it was shown in [1] that the non-linear, second order recurrence equations associated with Eq. (1) are given by

$$a_{t+1} = a_t + \Delta a_t \quad , \quad \Delta a_{t+1} = \frac{r}{d} \left(1 - \frac{a_{t+1}}{d}\right) (a_{t+1}^2 - a_t^2) \quad , \quad (2)$$

with the initial conditions a_0 being the initial number of present elements and $a_{-1} \equiv 0$, by convention. The question is to find the final diversity of the system, a_∞ . These equations are exactly solvable in the long-time limit. For this end define, $c_t \equiv \Delta a_{t+1} / \Delta a_t$, and look at the asymptotic behavior, $c \equiv \lim_{t \rightarrow \infty} c_t$. From Eq. (2) we get

$$c = 2r \left(1 - \frac{a_\infty}{d}\right) \frac{a_\infty}{d} \quad . \quad (3)$$

On the other hand we can estimate a_∞ asymptotically by

$$a_\infty = a_0 \sum_{t=0}^{\infty} c^t = \frac{a_0}{1-c} \quad . \quad (4)$$

Introducing Eq. (3) into Eq. (4) one gets a third order equation, whose solutions are the solution to the problem. Remarkably these solutions are mathematically identical to the description of real gases, i.e. Van der Waals gases. As real gases our system shows a phase transition phenomenon. The corresponding phase diagram, as a function of the model parameter r and the initial condition a_0 is shown in Fig. 1. Formally, the relation to the Van der Waals gas can be made more explicit by defining, $V \equiv a_\infty / d$ and $\tau \equiv a_0 / d$. Using this in Eqs. (3) and (4) gives $V - \tau = 2r(1 - V)V^2$. Renaming variables

$$P \equiv \frac{1}{V} + \frac{1}{2rV^3} \quad \text{and} \quad T \equiv \frac{\tau}{2rV^3} \quad (5)$$

leads to

$$\left(P - \frac{1}{V^2}\right)V = T \quad , \quad (6)$$

which is exactly a Van der Waals gas of point-particles with constant (negative) internal pressure.

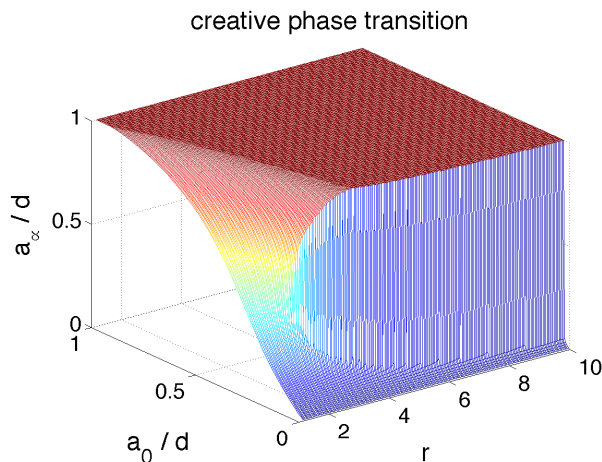


FIG. 1: Phase diagram of the creative dynamics over the r - a_0 space.

III. THE DESTRUCTIVE PHASE TRANSITION

In the dynamics studied so far diversity can only increase due to the positivity of the elements in α . It is important to note that in this setting the phase transition can not be crossed in the backward direction. This is because of two reasons. First, the system *forgets* its initial condition a_0 once it has reached the (almost) fully populated state. This means that after everything has been produced one can not lower the initial set size any more. In terms of the Van der Waals gas equation analogy we can *not* lower the 'temperature' and we can *not* cross the phase transition in the backward direction. Second, if r is a homogeneous characteristic of the system then it is also impossible to manipulate the 'pressure' of the system and we remain in the fully populated phase for ever.

The natural question thus arises what happens to the dynamics if one randomly kills a fraction of elements in the fully (or almost fully) populated phase. In the case that an element k gets produced by a single pair (i, j) and one of these – either i or j – gets killed, k can not be produced any longer. We call the random removal of i a *primary defect*, the result – here the stop of production of k – is a *secondary defect*, denoted by S^{def} . The question is whether there exist critical conditions of r and a primary defect density δ_0 , such that cascading defects will occur.

As before we approach this question iteratively, by asking how many secondary defects will be caused by an initial set of D_0 randomly removed elements in the fully populated phase. We define the primary defect density $\delta_0 \equiv D_0/d$. The possibility for a secondary defect happening to element k requires that all productive pairs, which can produce k , have to be destroyed, i.e. at least one element of the productive pair has to be eliminated (On average there are r production pairs for k). This requires some 'book-keeping' of the number of elements

that partially have lost some of their productive pairs due to defects. We introduce a book-keeping set G_n of sequences g_{nl} , $G_n = \{g_{n0}, g_{n1}, g_{n2}, g_{n3}, \dots\}$, where $d g_{nl}$ denotes the number of elements that have lost l ways to be produced (i.e. productive pairs), given that initially n elements have been eliminated.

To be entirely clear, let us introduce the first defect. This defect will on average affect $2r$ productive pairs in the system, i.e., there will be $2r$ elements that loose one way of being produced (Why? Since there are dr productive pairs there are $2dr$ indices referring to an element involved in denoting the pairs. Consequently there are $2r$ indices on average per element). We naturally assume $d \gg d\delta_0 \gg r > 1$, and disregard the vanishingly small probability that one element loses two or more of its productive pairs by one primary defect.

Before the first defect we have $G_0 = \{1, 0, 0, \dots\}$, meaning that there are d entities that have lost none of their producing pairs. The first defect will decrease this number $d \rightarrow d - 2r$, i.e., we get $2r$ elements that have lost one of their producing pairs. Consequently we find $G_1 = \{1 - p, p, 0, 0, \dots\}$, where p is defined as $p \equiv 2r/d$. Now, defecting the second element will affect another $2r$ elements through their producing pairs. This time we affect an element that has lost none of its producing pairs with probability $1 - p$, and with probability p we affect an element that already has lost one of its producing pairs. Iterating this idea of subsequent defects leads to the recurrence relations

$$\begin{aligned} g_{n+1,0} &= g_{n,0}(1-p) & \text{and} \\ g_{n+1,k} &= g_{n,k} + (g_{n,k-1} - g_{n,k})p \end{aligned} \quad (7)$$

It is easy to show that $g_{n,k}$ follows a binomial law, $g_{n,k} = \binom{n}{k} p^k (1-p)^{n-k}$. The number of secondary defects after n introduced defects, denoted by S_n^{def} , is just the number of all entities that have lost *all* of their (on average) r producing pairs and can be estimated by $d \sum_{k \geq r} g_{n,k}$. Defining

$$S_n^{\text{def}} = \sum_{k \geq r} g_{n,k} \quad , \quad (8)$$

one finds the update equation for S_n^{def} by inserting (7) into (8),

$$S_{n+1}^{\text{def}} = S_n^{\text{def}} + p g_{n,r-1} \quad . \quad (9)$$

Now, if $d\delta_0$ and $d\delta_1$ are the numbers of primary and secondary defects respectively, one has to identify

$$\delta_1 = S_{d\delta_0}^{\text{def}} \quad . \quad (10)$$

This is nothing but

$$\begin{aligned} \delta_1 &= p \sum_{n \geq r}^{d\delta_0} g_{n,r-1} \\ &= p \sum_{n \geq r}^{d\delta_0} \binom{n}{r-1} p^{r-1} (1-p)^{n-r+1} \quad . \end{aligned}$$

Since we assume $d \gg d\delta_0 \gg r > 1$, Stirling's approximation is reasonable, $\ln(n!) \sim n \ln(n) - n + \frac{1}{2} \ln(2\pi n)$, so that the binomial coefficient is approximated by, $\binom{n}{m} \sim \left(\frac{n}{m}\right)^m e^m (2\pi m)^{-1/2}$, where $(1 - m/n)^{n-m} \sim \exp(-m)$, for $n \gg m$. Further one can approximate $(1-p)^{n-r+1} \sim \exp(-np)$. Inserting these approximations into Eq. (11), and replacing the sum by an integral one gets

$$\delta_1 = \frac{p^r}{\sqrt{2\pi}} (r-1)^{\frac{1}{2}-r} e^{r-1} \int_r^{d\delta_0} dx x^{r-1} e^{-xp} \quad (11)$$

Since $p d\delta_0 = 2r\delta_0$, and by approximating $pr \sim 0$ (for the lower limit) we rewrite the integral

$$\int_r^{d\delta_0} dx x^{r-1} e^{-xp} \sim p^{-r} \int_0^{2r\delta_0} dy y^{r-1} e^{-y} \quad (12)$$

and we can finally compute

$$\delta_1 = \gamma(r) f(r, \delta_0) \delta_0^r \quad (13)$$

with

$$\begin{aligned} \gamma(r) &= \frac{1}{r} \frac{(2r)^r}{\sqrt{2\pi}} (r-1)^{\frac{1}{2}-r} e^{r-1} \\ f(r, \delta_0) &= \sum_{n=0}^{\infty} \frac{1}{n!} \frac{r}{r+n} (-2r\delta_0)^n \end{aligned} \quad (14)$$

Here f is obtained by expanding the exponential in the integral of Eq. (12) into a Taylor series.

What remains to be done is to iterate Eq. (13). There are two possible ways of doing so. In the first iteration scheme we think of collecting the primary and secondary defects together and assume that we would start with a new primary defect set of size $\delta'_0 = \delta_0 + \delta_1$. The tertiary defects therefore would be estimated by $\delta_2 = \delta'_1 - \delta_1$, where δ'_1 are the secondary defects associated with δ'_0 . This leads to the recursive scheme (A),

$$\Delta_n \equiv \sum_{k=1}^n \delta_k \quad , \quad \delta_{n+1} = \gamma(r) f(r, \Delta_n) \Delta_n^r - \Delta_n + \delta_1 \quad (A). \quad (15)$$

The second way to iterate Eq. (13) is to assume that we use the $d\delta_1$ secondary defects as primary defects on the smaller (rescaled) system $d(1-\delta_0)$ so that we look at a new primary defect-ratio $\delta'_0 = \delta_1/(1-\delta_0)$. The result δ'_1 then has to be rescaled inversely to give the tertiary defects in the original scale, i.e. $\delta_2 = (1-\delta_0)\delta'_1$. Iterating this idea leads to the recurrence relation (B),

$$\begin{aligned} \Delta_n &\equiv \sum_{k=1}^n \delta_k \quad , \\ \delta_{n+1} &= \gamma(r) (1 - \Delta_{n-1})^{1-r} f\left(r, \frac{\delta_n}{1 - \Delta_{n-1}}\right) \delta_n^r \quad (B), \end{aligned} \quad (16)$$

with $\Delta_0 \equiv 0$.

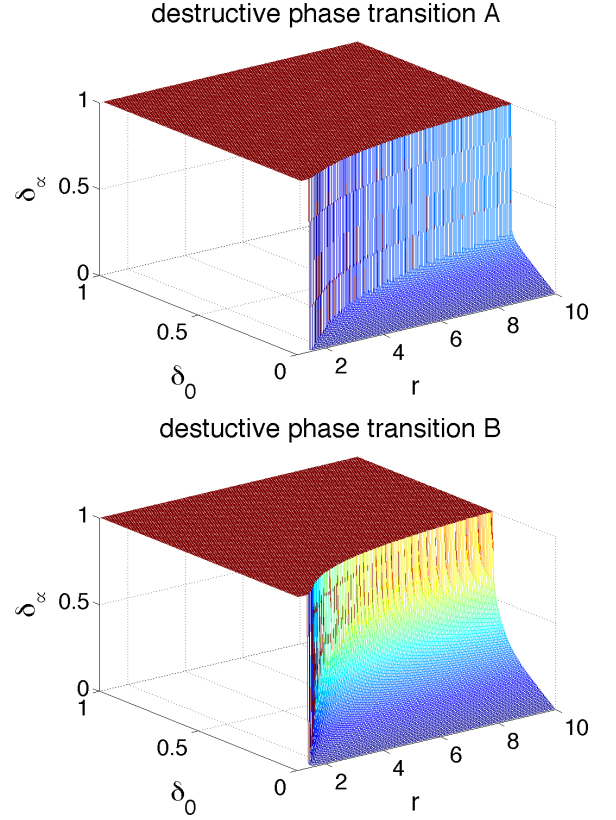


FIG. 2: Phase diagram for the defect dynamics for two ways of iterating Eq. (13) described in the text.

The result in terms of a phase diagram of the two possible iteration schemes (A) and (B) is given in Fig. 2 (a) and (b), respectively. The asymptotic defect size δ_∞ (for $t \rightarrow \infty$) is shown as a function of the parameters r and the initial defect density δ_0 . As before a clear phase transition is visible, meaning that at a fixed value of r there exists a critical number of initial defects at which the system will experience a catastrophic decline of diversity. Unfortunately, an analytical solution for the asymptotic iterations of Eq. (13) seems to be beyond the capabilities of the authors. It is interesting that for complete destruction of diversity (plateau in Fig. 2) not very large values of δ_0 are necessary.

IV. COMBINED DYNAMICS: CREATIVE GALES OF DECONSTRUCTION

Having established the existence of phase transitions in both the creative and destructive regimes, and are equipped with the update equations for the respective cases Eqs. (2) and (13), it is natural to couple these update equations and to study their combined dynamics. The relevant variable now becomes the diversity in the system as a function of time, a_t . However, the question how this should be done is neither trivial nor uniquely

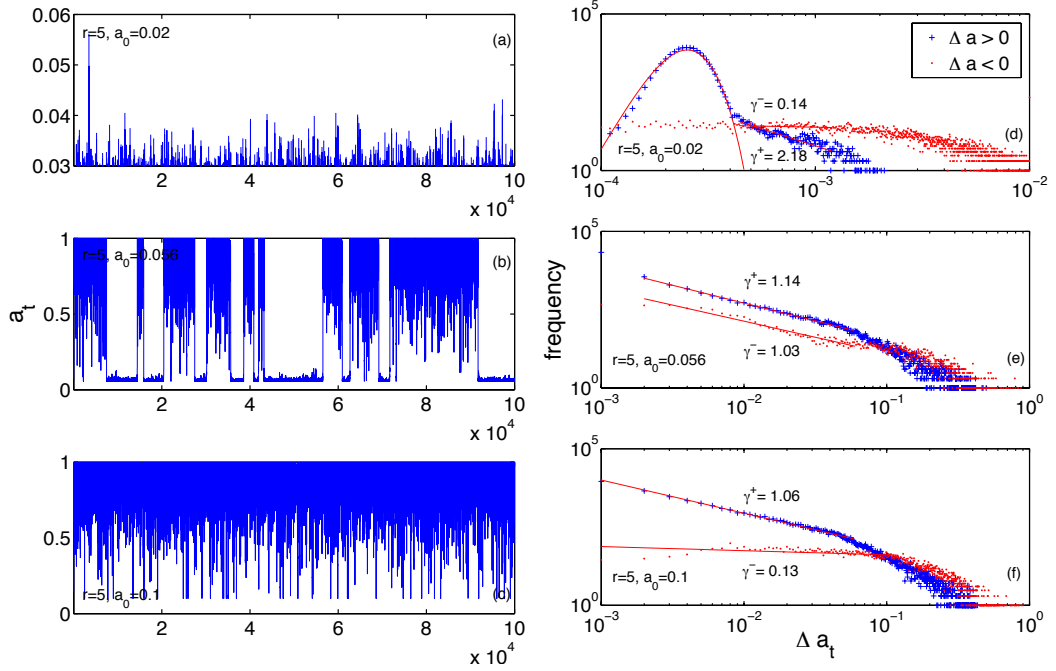


FIG. 3: Time series (left) and time increment distribution (right) of the coupled dynamics for a fixed $r = 5$ and fixed Poissonian rates η and χ^\pm . The variable varied is $a_0 = 0.02, 0.056$, and 0.1 . Straight lines are fits to power laws with the slopes given by γ^+ (+) and γ^- (dots), indicating whether $\Delta a > 0$ or < 0 . The Poissonian resembling the creative driving noise in is also seen as a solid line in (d).

determined.

One realistic scenario might be that at any point in time some goods/species/elements may come into being spontaneously and others go extinct at certain rates. First, for the introduction of new elements we introduce a stochastic rate, $\chi^+ > 0$ of a Poisson process, so that $(d - a_t)\chi_t^+$ new species may be expected in one time unit. Note, that there are $d - a_t$ 'un-populated' elements in the system. These randomly created elements are elements that did not get produced through (re)combination or substitution of existing ones, but are 'out of the blue' inventions. The natural time unit we are supplied with is one creative generation $a_t \rightarrow a_{t+1}$. The spontaneous creation may eventually increase the critical threshold and the system may transit into the highly diverse phase (think of this process to randomly alter a_0 in the creative update dynamics).

On the other hand there are spontaneous processes that destroy or remove species at a stochastic rate, $\chi^- > 0$ (Poisson process), such that about $a_t\chi_t^-$ new defects may be expected per time unit. It can not be assumed a priori that the iterative accumulation of secondary defects in the system, as described above, operates at the same time scale as the spontaneous or the deterministic creative processes.

For making an explicit choice we may assume that during one time unit there happen η_t generations of secondary defects, taking into account the relative ratio of innovative and secondary defect generations processed

per time unit. We assume that η_t can be modeled by a Poisson process whose rate, $\langle \eta_t \rangle = \eta$ becomes a parameter of the model. For the computations below we have chosen $\eta = 0.1$.

When we look at the way secondary defects evolve in generations we are left with a culminated number of secondary defects $\Delta_{\eta_t t}$ after η_t generations and a remainder $\delta_{\eta_t t}$, which would have to be added to $\Delta_{\eta_t t}$ in the next defect-generation, $\eta_t + 1$ but which – by assumption – is falling into the book-keeping of the next creative-generation time step $t + 1$. What we say is that during time step $t \rightarrow t + 1$, there are $\Delta^- a_t = d\Delta_{\eta_t, t}$ species removed from the system, where $\Delta_m t = \sum_{k=0}^{m-1} \delta_{k t}$ is the cumulated ratio of secondary defect ratios $\delta_{k t}$ of defect-generation k at time step t . The remaining defects of generation η_t have to be accounted for in the next time step together with the newly introduced spontaneous defects, so that $\delta_{0 t+1} = \frac{a_t}{d}\chi_t^- + \delta_{\eta_t, t}$. The update of defect generations now can be performed η_t times according to

$$\delta_{m+1 t} = (1 - \Delta_m t) \gamma_r f(r, \tilde{\delta}_m t) \tilde{\delta}_m^r t, \quad (17)$$

where we have considered the rescaling approach (B) to secondary defect generations. A similar equation can be derived for scheme (A). For convenience of notation we write for the rescaled defect ratios, $\tilde{\delta}_m t \equiv \frac{\delta_m t}{1 - \Delta_m t}$. If now, by coincidence, the remaining defects from the last time step and the spontaneously introduced defects are sufficiently many and there are enough defect-generations η_t processed in that time step, the culminating secondary

defects may lead to a break down of the system from the high to the low diversity regime.

All that is left is to insert this dynamics into the creative update equation. To do so we first note that without defects, Δa_t depends on both a_t and a_{t-1} . However, due to the occurring defects a_{t-1} will not remain what it was when t becomes updated to $t+1$, but will be decreased by the occurring defects in this time span. For this reason it is convenient to introduce a new variable b_t which takes the place of a_{t-1} in the coupled update process. More precisely, $b_{t+1} \equiv a_t - \Delta^- a_t$. For the growth condition to be well defined we require $a_t > b_t$, which is guaranteed by $a_{t+1} = b_{t+1} + \Delta^+ a_t$ where

$$\Delta^+ a_t \equiv \frac{r}{d} \left(1 - \frac{a_t}{d}\right) (a_t^2 - b_t^2) + (d - a_t) \chi_t^+ \quad , \quad (18)$$

is the number of deterministically (by the creative update law) and spontaneously introduced species in the creative-generation t . This sort of coupling allows to take a look at how diversity of systems may evolve over time, driven by the spontaneous creation and destruction processes χ^\pm , which may reflect exogenous influences, while on the other hand the average number of defect-generations η per creative generation t , and the average number of productive pairs per species r express endogenous properties of the system, i.e. whether the defects process slow or fast (η), and the average dependency (r) of the catalytic network.

We study the resulting timeseries for this dynamics for several values of r , a_0 , η , and χ^\pm . In Fig. 3, by fixing $r = 5$ and the Poisson rates η , and χ^\pm and by varying a_0 (as a lower bound) from 0.01 to 0.1, we cross the creative phase transition line from the sub-critical to the fully populated phase (super-critical) (a)-(c). When the system is prepared at the critical phase, at $a_0 = 0.056$ (b), we observe a flip-flop transition between the two phases. The flip-flop transitions happen over very short time intervals. In Fig. 3 (d)-(f) the corresponding increment distributions of $\Delta a_t \equiv a_t - a_{t-1}$ are shown. The distribution for positive Δa is power-law in all cases,

while a power behavior for the $\Delta a < 0$ is only observed in the critical phase. Power-law fits to the exponents yield $\gamma \sim 1$. Within the regions of the populated and the low-diversity phases the distribution for the $\Delta a < 0$ case is much flatter. The Poissonian driving in the creative dynamics in the sub-critical region is clearly seen for $a_0 = 0.02$ in Fig. 3 (d).

V. CONCLUSION

We have shown the existence of a new phase transition in systems capable of evolutionary dynamics. The main message is that given the system is in its highly diverse state, the removal of a relatively small fraction of elements can cause drastic declines in diversity. We then proposed a dynamical model to study timeseries of diversity in systems governed by the evolution equation (1) under the influence of external spontaneous creation and destruction processes. We emphasize that we strictly stick to the structure of Eq. (1) and do not discuss variants, such as the beautiful work of [11] where a linear version (resembling catalytic equations) was studied, however with an explicit 'selection' mechanism incorporated in a dynamic rule table, i.e. $\alpha(t)$.

We think that with the methodology presented in this paper it could – in principle – become possible to arrive at a quantitative formulation of economic dynamics which e.g. J.A. Schumpeter has heuristically and qualitatively described as 'creative gases of deconstruction'. As an example for destructive processes which can be quantified in real world situations one can think of bankruptcies of firms. In this context the existence of a power law with a very similar exponent – to those resulting from our model – has been described in [12]. Let us finally mention that the model presented here does of course not only relate to technological evolution but to any biological, social, or physical system governed by evolution equations of the type of Eq. (1).

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- [1] R. Hanel, S.A. Kauffman, S. Thurner, Phys. Rev. E **72**, 036117 (2005).
 - [2] M. Nowak, *Evolutionary dynamics: exploring the equations of life*, (Belknap Press, Mass., 2006).
 - [3] M. Eigen, P. Schuster, *The hypercycle*, (Springer Verlag, Berlin, 1979).
 - [4] W. Fontana, in *Artificial life II*, edited by C.G. Langton, C. Taylor, J.D. Farmer, S. Rasmussen (Addison Wesley, Redwood City, CA, 1992), pp. 159-210.
 - [5] J.D. Farmer, S.A. Kauffman, N.H. Packard, *Physica D* **22**, 50-67 (1986).
 - [6] P.F. Stadler, W. Fontana, J.H. Miller, *Physica D* **63**, 378 (1993).
 - [7] S.J. Gould, *The structure of evolutionary theory* (Harvard University Press, Cambridge Mass., 2002).
 - [8] S.A. Kauffman, *The origins of order*, (Oxford University Press, London, 1993).
 - [9] J.A. Schumpeter, *Theorie der wirtschaftlichen Entwicklung*, (Wien, 1911).
 - [10] M.E.J. Newman and R.G. Palmer, *Modeling extinction*, (Oxford University Press, New York, 2003).
 - [11] S. Jain and S. Krishna, *Phys. Rev. Lett.* **81**, 5684-5687 (1998); *Proc. Natl. Acad. Sci. USA* **99**, 2055-2060 (2002).
 - [12] Y. Fujiwara, *Physica A* **337**, 219-230 (2004).