Universal growth constraints of human systems

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Scale independence is a ubiquitous feature of complex systems which implies a highly skewed distribution of resources with no characteristic scale. Research has long focused on why systems as varied as protein networks, evolution and stock actions all feature scale independence. Assuming that they simply do, we focus here on describing exactly how this behaviour emerges. We show that growing towards scale independence implies strict constraints: the first is the well-known preferential attachment principle and the second is a new form of temporal scaling. These constraints pave a precise evolution path, such that even an instantaneous snapshot of a distribution is enough to reconstruct the past of the system and predict its future. We validate our approach on diverse spheres of human activities ranging from scientific and artistic productivity, to sexual relations and online traffic.

Human systems are often characterized by extreme inequalities. One may think of the distribution of wealth between individuals, the sizes of cities, or the frequencies of sexual activities to name a few. Interestingly, inequality often tends to manifest itself through a scale independent behaviour. In layman’s terms, these systems are said to be scale independent because of the absence of a characteristic scale. Taking the distribution of wealth as an example, the worldwide average income is meaningless because the variance is too wide. Neither the very poor nor the very wealthy can be reduced to average individuals; the former are too numerous while the latter are obscenely richer than the average.

Mathematically, this behaviour takes the form of a power-law distribution. That is, the number $N_k$ of individuals having a share $k$ (e.g. personal income or sexual partners) of the total resource $K$ (total wealth or sexual activities) roughly follows $N_k \propto k^{-\gamma}$. One of the first robust observation of scale independent systems concerns the distribution of occurrences per unique words in prose as illustrated in Fig. 1(left).

In this paper, we build upon two general premisses to describe the growth of scale independent systems. Firstly, we assume that the underlying distribution roughly follows $N_k \propto k^{-\gamma}$ such that a power law is an adequate approximation for all $k$ (with $\gamma > 1$ for normalization of the asymptotic state). Secondly, we follow the distribution of a resource or property that can only increase or stagnate, namely the total activities of an individual (both past and present).

We use diverse databases to validate our approach: scientific productivity of authors on the arXiv e-print archive (arXiv), one month of user activities on the Digg social news website (Digg), productivity of actors on the Internet Movie Database (IMDb), sexual relations in a Brazilian escort community (sexual) and the writings of William Shakespeare, Miguel de Cervantes Saavedra and Johann Wolfgang von Goethe.
FIG. 1: Scale independence, preferential attachment and delayed temporal scaling in prose samples. (left) Power-law distribution of word occurrences in the writings of authors in three different languages. Power law with scale factor $\gamma = 1.75$ is plotted to guide the eye. (middle) Preferential attachment in written text with a linear relation for comparison. The algorithm to obtain $G(k)$ is given in the Methods section. (right) Average birth function for samples of 1000 words, this procedure is based on the translational invariance of written texts and yields better statistics. Fit of Eq. (21) are overlayed using $b = 0$ and $\alpha = 0.22$, $\alpha = 0.25$ and $\alpha = 0.28$ for Goethe’s, Cervantes’ and Shakespeare’s writings respectively. This asymptotic scaling is related to what is generally known as Heaps’ law in linguistics[15], but is here given a much more general expression for all $t$.

I. CONSTRAINED GROWTH

Let us now consider the growth of a hypothetical system where each individual possesses a share $k_i(t)$ of the total resource $K(t)$ at time $t$. Because the system is constantly growing, both in terms of its total population $N(t)$ and of each individual’s share, time can be measured as the total number of events. These events can only take two forms: birth events which increase the total population $N(t + 1) = N(t) + 1$ by adding a new individual with $k_i(t) = 1$; and growth events which imply $k_i(t + 1) = k_i(t) + 1$ for a given individual $i$.

We then introduce two functions: a birth function $p(t)$ that follows the probability that the $t$-th event is a birth event, and a growth function $G(k)$ that describes the average chances (unnormalized probability) for an individual with current share $k$ of being involved in the next growth event. Assuming that individuals with the same share are indiscernible, the state of an average individual $i$ of share $k_i$ can be followed through a mean-field model:

$$k_i(t + 1) = \left[1 + \frac{1 - p(t + 1)}{\sum_j G(k_j(t))} G(k_i(t))\right]$$

Consequently, the probability that a growth event involves any individual of current share $k$ is given by $N_k(t)G(k)/\sum_k N_k(t)G(k')$ where $N_k(t)$ is the number of individuals with share $k$ at time $t$. This yields the following master equation (for $k \in \mathbb{N}$):

$$N_k(t + 1) = N_k(t) + p(t)\delta_{k,1} + [1 - p(t)] \frac{N_{k-1}(t)G(k - 1) - N_k(t)G(k)}{\sum_m N_m(t)G(m)}$$

with $N_0(t) = 0 \ \forall t$. For this model to be of any use, at least partial knowledge of $G(k)$ and $p(t)$ is required. Setting $G(k) = k$ and a constant $p(t)$ brings the model back to the classic preferential attachment process[3]. Our goal is to investigate the form and impact of the temporal dependency $p(t)$ and of the leeway given to $G(k)$.
A. The growth function

The behavior of the growth function \( G(k) \) can be constrained with the following logic\textsuperscript{[17]]. Our goal is to obtain \( G(k) \) solely on the basis of Eq. \((2)\). Instead of measuring \( G(k) \) directly by looking at what leaves the compartment \( N_k(t) \), we can equivalently look at what arrives in the compartments \( k' > k \) during the time step \( t \to t + 1 \). We write this as the difference between what is in \( k' > k \) at \( t + 1 \) [i.e. \( \sum_{i=k+1}^{\infty} N_i(t+1) \)] and what was in \( k' > k \) at time \( t \) [i.e. \( \sum_{i=k+1}^{\infty} N_i(t) \)]. We then rearrange Eq. \((2)\) and sum over all \( k' > k \):

\[
\sum_{i=k+1}^{\infty} [N_i(t+1) - N_i(t)] = \sum_{i=k+1}^{\infty} \left\{ p(t) \delta_{i,1} + [1 - p(t)] \frac{N_{i-1}(t)G(i-1) - N_i(t)G(i)}{\sum_m N_m(t)G(m)} \right\}
= [1 - p(t)] \frac{N_k(t)G(k)}{\sum_m N_m(t)G(m)}.
\]

This last expression can be interpreted as two measures of the activity in compartment \( N_k(t) \) between \( t \) and \( t + 1 \). The left side measures the mean number of arrivals in compartment \( N_k(t) \) with \( k' > k \); i.e. the mean number of individuals which left compartment \( N_i(t) \). The right side is explicitly the ratio of the activity involving the \( k \)-th compartment, \( N_k(t)G(k) \), to the total growth activity, \( \sum_m N_m(t)G(m) \), times the probability, \( 1 - p(t) \), that a growth event has occurred during the time step. From this equivalence, \( G(k) \) is readily obtained

\[
G(k) = \frac{\sum_m N_m(t)G(m)}{1 - p(t)} \frac{1}{N_k(t)} \sum_{i=k+1}^{\infty} [N_i(t+1) - N_i(t)] .
\]

For \( k \gg 1 \), we can replace the sum by an integral, and using our first hypothesis, i.e. \( N_k(t) = A(t)k^{-\gamma}N(t) \), where \( A(t) \) is a normalization factor, we find:

\[
G(k) \approx \frac{\sum_m N_m(t)G(m)}{1 - p(t)} \left[ \frac{A(t+1)N(t+1) - A(t)N(t)}{A(t)N(t)} \right] \frac{k}{\gamma - 1} .
\]

The temporal dependency of the first factor is of no concern, since \( G(k) \) only makes sense when comparing the relative values for different \( k \). Hence, for a given time \( t \), all factors independent of \( k \) can be removed to finally obtain:

\[
G(k) \propto k
\]

at least for values of \( k \) higher than an appropriate lower bound. The linear relation between the probability of growth of an individual and its present size, often called preferential attachment, is a recurrent hypothesis in scale-independent growth models\textsuperscript{[2],[18]}. See Fig. 1(middle) for examples.

B. The birth function

On the other hand, and as far as we know, the birth function \( p(t) \) is unheard of in the literature. Our definition is equivalent to the time derivative \( \dot{N}(t) \) of \( N(t) \). While at this point we have little information on the behavior of \( N(t) \), our choice of time (in number of events) implies that \( \dot{K}(t) = 1 \) such that

\[
p(t) = \dot{N}(t) = \dot{N}(t) = \frac{\dot{N}(t)}{\dot{K}(t)} = \frac{\dot{N}(t)}{\sum_{m=1}^{k_{\text{max}}(t)} m\dot{N}_m(t) + k_{\text{max}}(t)k_{\text{max}}(t)N_{k_{\text{max}}(t)}(t)} .
\]
where we assumed \( k_{\text{max}}(t) \gg 1 \) to apply Leibniz rule for differentiation.

Under our first premiss, \( N_k(t) = A(t)N(t)k^{-\gamma} \) where \( A(t) \) is the inverse of an incomplete Riemann zeta function, \( A(t) = \left( \sum_k N(t)k^{-\gamma} \right)^{-1} \), whose rate of change falls rapidly to 0. We write

\[
p(t) = \frac{\dot{N}(t)}{A(t)\dot{N}(t) + A(t)\dot{N}(t)k_{\text{max}}(t)k^{-\gamma}N(t) + \dot{N}(t)k_{\text{max}}(t)kn^{-1}}.
\]

(8)

At this point we must distinguish between two different cases.

**Case \( \gamma \in (1,2] \).** The sum over \( m^{-\gamma} \) can be evaluated as an integral\(^{19} \) for \( t \gg 1 \) such that \( k_{\text{max}}(t) \gg 1 \). This yields

\[
p(t) \approx \frac{\dot{N}(t)}{k_{\text{max}}^{2-\gamma}(t)\dot{N}(t) + k_{\text{max}}(t)k_{\text{max}}^{-\gamma}(t)N(t)}.
\]

(9)

The second term of the denominator is much smaller than the third as their ratio scales as \( k_{\text{max}}^{-1}(t) \). Keeping the terms scaling with the largest exponent [and assuming that \( A(t) \) has converged to a constant since \( k_{\text{max}}(t) \gg 1 \)], we write:

\[
p(t) \approx \frac{\dot{N}(t)}{k_{\text{max}}^{2-\gamma}(t)\dot{N}(t) + k_{\text{max}}(t)k_{\text{max}}^{-\gamma}(t)N(t)}.
\]

(10)

It is natural to consider the following temporal scaling Ansätze: \( N \sim c_1 t^{\beta_k} \) and \( k_{\text{max}}(t) \sim c_2 t^{\beta_k} \) (which will shortly be confirmed to be consistent with one another and with our model). It is then easily shown that the two terms of the denominator have the exact same behaviour, such that

\[
p(t) = \frac{c_1 \beta n^{-\beta_n-1}}{c_2^{2-\gamma} c_1 \beta n(t)^{2-\gamma} t^{\beta_k} + c_2^{2-\gamma} c_1 \beta n(t)^{2-\gamma} t^{\beta_k} + \beta_n^{-1}} = \left[ \frac{\beta_n}{\beta_n + \beta_k} \right] (c_2 t^{\beta_k})^{2-\gamma} \sim a_1 k_{\text{max}}^{-2}(t) .
\]

(11)

So, in the case \( \gamma \in (1,2) \), we find \( p(t) \propto k_{\text{max}}^{-2}(t) \). The limiting case \( \gamma = 2 \) is somewhat pathological and the decrease is logarithmic rather than algebraic.

**Case \( \gamma > 2 \).** The sum over \( m^{-\gamma} \) converges to a constant \( C \) for \( t \gg 1 \). We thus write

\[
p(t) \approx \frac{\dot{N}(t)}{A(t)\dot{N}(t) - CA(t)k_{\text{max}}(t)k^{-\gamma}N(t) + \dot{N}(t)k_{\text{max}}(t)k^{-\gamma}(t)N(t)}.
\]

(12)

Once again, the second term of the denominator is quickly smaller than the third which allows us to simplify to:

\[
p(t) \approx \frac{\dot{N}(t)}{CN(t) + k_{\text{max}}(t)k^{-\gamma}(t)N(t)}.
\]

(13)

Using the same Ansätze as before, we find that

\[
p(t) = \frac{c_1 \beta_n^{-\beta_n-1}}{Cc_1 \beta n(t)^{2-\gamma} t^{\beta_k} + c_2^{2-\gamma} c_1 \beta n(t)^{2-\gamma} t^{\beta_k} + \beta_n^{-1}} = \frac{\beta_n}{C \beta n + \beta_k (c_2 t^{\beta_k})^{2-\gamma}} = \frac{1}{C} \left[ \frac{1}{1 + \frac{\beta n}{c_2^{2-\gamma} t^{\beta_n} k_{\text{max}}(t)}} \right] \approx a_2 k_{\text{max}}^{-2}(t) + b_2
\]

where \( a_2 \) and \( b_2 \) are constants. For \( k_{\text{max}}(t) \gg 1 \), the leading term is then simply \( p(t) \sim b_2 \).
General case. We can write a general form including the two separate cases:

\[
p(t) \propto \begin{cases} 
  k_{\text{max}}(t) & \text{if } 1 < \gamma \leq 2 \\
  k_{\text{max}}(t) + \text{constant} & \text{if } \gamma \geq 2
\end{cases}
\] (15)

or directly

\[
p(t) = a_0 k_{\text{max}}(t)^{-\alpha} + b_0
\] (16)

with appropriate free parameters.

Self-consistent form of \(k_{\text{max}}(t)\). To evaluate \(k_{\text{max}}(t)\), we use Eq. (1) with the form \(G(k) = k\) to follow \(k_{\text{max}}(t)\) once this dynamics becomes effective

\[
k_{\text{max}}(t + 1) = \left[1 + \frac{1 - p(t + 1)}{t + \tau}\right] k_{\text{max}}(t),
\] (17)

where \(\tau = K(0)\) (initial conditions) such that \(\sum_k G(k) = t + \tau\). This expression fixes the derivative in the limit of large \(t\):

\[
\frac{d}{dt} k_{\text{max}}(t) = \frac{1 - p(t)}{t + \tau} k_{\text{max}}(t).
\] (18)

Since \(p(t)\) is limited to the range \([0, 1]\) we can write, without loss of generality, \(p(t) = f(t) + b\) where \(\lim_{t \to \infty} f(t) = 0\). This form yields the exact solution:

\[
k_{\text{max}}(t) = C_1 (t + \tau)^{1-b} \exp \left[ - \int_{t^*}^{t} \frac{f(t')}{t' + \tau} dt' \right]
\] (19)

where \(t^*\) is an appropriate lower bound such that Eq. (18) is applicable. As \(f(t)\) is bounded and decreases to zero, the exponential factor converges rapidly to one and we find the general solution for large \(t\):

\[
k_{\text{max}}(t) = C_1 (t + \tau)^{1-b}.
\] (20)

Basically, Eq. (18) implies a linear \((b = 0)\) or sub-linear \((b > 0)\) growth for \(k_{\text{max}}(t)\). Using Eq. (20) into Eq. (16), we obtain a consistent functional form for the birth function:

\[
p(t) \approx a (t + \tau)^{-\alpha} + b.
\] (21)

Note that the temporal scaling for \(p(t \gg 1)\) and \(k_{\text{max}}(t \gg 1)\) justifies a posteriori the two Ansätze used earlier.

Observations of this relation in empirical data are given in Fig. 1(right). Asymptotic integration of this complete models yields \(\gamma = (2 - b)/(1 - b)\) when \(\gamma > \frac{3}{2}\) and \(\alpha = 2 - \gamma\) with \(b = 0\) when \(1 < \gamma < 2\). These relations provide starting points for the application of our model.

II. RECONSTRUCTING THE PAST

The model based on Eq. (2) may be used to replicate the growth of empirical distributions. Our objective is in part to verify the presence of constraints on the birth, Eq. (21), and growth, Eq. (4), of individuals; but also to use these constraints to determine the past and future of different systems solely from a snapshot of their present distribution.

Our model consists of iterating Eq. (2) for all \(k\), with a given combination of \(p(t)\) and \(G(k)\), until time \(t\) reaches the size \(K\) of the system’s present state. Hereafter, we do not at any point show actual fits of the temporal data, but instead find the optimal combination of \(p(t)\) and \(G(k)\) that minimizes the error produced by Eq. (2) when modelling the present state of a given system.
FIG. 2: Parameter sweep. Quality of our ability to model the growth of the database of sexual activities with $G(k) = k$ and various $p(t)$. The quality measure is given by $1/\Delta$ (see Eq. 22) and its maximal values is indicated with a dotted line at $1/\Delta = 62.68$ corresponding to 1.6% of misassigned shares $k_i(t_f)$ at $\alpha = 0.53$, $\tau = 3600$ and $b = 0$. Note that these figures are projections of a 4 dimensional fitness landscape.

A. Algorithm

Before we describe our algorithm, let us consider the following analogy. We are given a semi-infinite vertical chain of buckets. In the bottom of each one we can drill a small hole of various width by setting a function $G(k)$ such that the $k$-th bucket has a hole of size $G(k)$. The first bucket, at the top of the chain, is placed under a dripping faucet whose flow is controlled in time by the function $p(t)$. Our goal is to adjust both the flow of the water $p(t)$ and the width of the holes $G(k)$ in order to reach a target quantity $\tilde{N}_k(t_f)$ of water for each bucket $k$ after a time $t_f$. Since the function $G(k)$ has an infinite number of degrees of freedom, this means that for any $p(t)$ we could find a $G(k)$ respecting (at least to a certain degree) the target distribution. Therefore, we must constrain $p(t)$ first, having a few degrees of freedom, and then optimize $G(k)$ accordingly.

We thus initially set $G(k) = k$, as previously determined, and we evaluate the quality of our model for the evolution of the system as obtained with different choice of $p(t)$. Initially assuming $G(k) = k$ does not reduce the range of reproducible scale exponents $\gamma$; all scale independent distributions can be modeled with appropriate $p(t)$. In the worst case scenario, $p(t)$ has four degrees of freedom, but we remove one with our knowledge of the final population (or total quantity of water) which sets $\langle p(t) \rangle = \sum_k \tilde{N}_k(t_f)/t_f$. We can further reduce the number of possible parameters through simple conditions; for instance $p(t) \in [0, 1]$. For each tested $p(t)$, we use the previously defined model (see Eq. (2)). The quality of a given model $\{\tilde{N}_k(t_f)\}$ on the final empirical state $\{N_k(t_f)\}$ is measured in terms of the number of individuals (or water drops) $\Delta$ that were assigned the wrong share (to the wrong bucket):

$$\Delta(p(t), G(k)) = \sum_k |\tilde{N}_k(t_f) - N_k(t_f)|/2 .$$

While a logarithmic error (i.e. $\propto \log |\tilde{N}_k(t_f) - \log N_k(t_f)|$) was also tested, but an absolute error proved to be more robust to the noisy tails of the distributions where the data falls to $N^{-1}$ while the model falls to zero. We then sweep through the possible combinations of parameter — $\alpha \in [0, 1]$, $\tau \in [0, \infty]$, $b \in [0, 1]$ and $a$ fixed with $\langle p(t) \rangle$ — to determine the function $p(t)$ that leads to the minimal possible error $\Delta$. See Fig. 2 for an example of this parameter sweep.

B. Results

While the systems studied in Fig. 3 vary in nature, age and distributions, our results seem to indicate that they follow qualitatively the same evolution. Indeed, our results confirm the presence
FIG. 3: Temporal scaling and preferential attachment in human systems. From left to right: birth function with temporal scaling of the form \((t + \tau)^{-\alpha}\); growth function with preferential attachment; scale independent distributions. (left) The orange curves represent birth functions leading to predictions within 25% of the minimal error between model and empirical data (present state only). The empirical black curves are presented solely for comparison as no temporal data is needed for our reconstruction of the past. Likewise, maximal-likelihood estimates of \(p(t)\), calculated with temporal data, are shown in blue to highlight the accuracy of our model. (middle and right) Growth function and present distribution; as all curves obtained with the different \(p(t)\) are similar, only the ones obtained with the absolute minimum are shown. The systems are, from top to bottom: distribution of papers per author in the arXiv \([N(t) = 386,267\text{ at } t = 1,206,570]\), votes per user on Digg \([N(t) = 139,409\text{ at } t = 3,018,197]\), movies per actor on IMDb \([N(t) = 1,707,525\text{ at } t = 6,288,201]\) and relations per individual in the sexual data \([N(t) = 16,730\text{ at } t = 101,264]\). The empirical growth functions are obtained with a simple algorithm described in the Methods section.

of both a delayed regime of temporal scaling and preferential attachment in all cases. Point estimates (maximum-likelihood estimation with temporal data) of the relevant parameters are given on Table 1 and are visually compared with our model (which again does not require temporal data) in Fig. 3 (left).

Because of the form \(p(t) = a(t + \tau)^{-\alpha} + b\), the complementary probability (i.e. the probability that the \(t\)-th event is a growth event) follows the same form with \(a' = -\alpha a\) and \(b' = 1 - b\). This fact is highlighted with the case of IMDb in Fig. 3, the oldest considered system. In fact, Eq. (16)
TABLE I: Point estimates of the delay and the exponent of the temporal scaling obtained with temporal data (maximum-likelihood estimation).

| system  | arXiv | Digg | IMDb | sexual |
|---------|-------|------|------|--------|
| \( \alpha \) | 0.58  | 0.95 | 0.46 | 0.60   |
| \( \tau \)  | 12066 | 60364| 62882 | 3038   |
| \( b \)    | 0.240 | 0.012| 0.976| 0.072  |

implies that \( p(t) \) is a decreasing function of time only as long as \( k_{\text{max}}(t) \) always increases. In the IMDb, death events (removal of certain individuals from the growth function) could be the cause of this effect, yet interestingly do not appear to affect the efficiency of our model. Furthermore, notice that IMDb is not only the sole system for which \( p(t) \) is an increasing function, but also the only system for which \( G(k) \) has an initially non-linear behaviour. With hindsight, this initial regime of the growth function probably corresponds to the so-called star system: actors with little experience are far less likely to be chosen for a role than experienced actors. The system then accelerates the introduction rate of new actors to preserve its scale independence. While this interpretation is speculative at best, the fact remains that these effects are observed in the temporal data and that our model is able to extract them solely from the present distribution.

In fact, with the exception of one much smaller system (sexual data), the quality of our reconstruction of the past is surprisingly good considering that it requires no temporal data whatsoever. For instance, the Digg user activity distribution led us to determine with very high precision that 25% of votes are due to new users 12 hours into the month, whereas this proportion falls below 2% by the end of the month.

Perhaps this is the crucial point: the results confirm that our model embodies intrinsic constraints of scale independence. These constraints appear to clearly define the possible paths that a system can follow. A snapshot of its present state is then sufficient to determine where it comes from and where it is heading. This naturally leads to a second question: can we use the reconstructed past of a system to predict its future?

III. PREDICTING THE FUTURE

To turn our model into a predictive tool is a simple matter. We first eliminate the statistical fluctuations present in the reconstructed growth function. These stem not from the form of the growth function itself but merely from the system’s finite size and the stochastic nature of the dynamics. Hence, these fluctuations must be eliminated by applying a linear fit to the asymptotic behaviour of the reconstructed \( G(k) \). A prediction can then be obtained by iterating Eq. (2) from a chosen present state to a desired future time.

We apply this predictive model to the largest databases, i.e. actor productivity in the IMDb and user activities on Digg. The results are shown in Fig. 4 (top). By using the activity distribution on Digg after only three days (again without any temporal data, only the current activity distribution per user), we can extrapolate the distribution over the period of a month. In contrast, assuming a constant birth rate (as in classical preferential attachment\(^\text{[3,5,6]}\)) would lead to a predicted final population of 475,000 users. Our model correctly compensates for repeated traffic and predicts a population of 115,000 users; closer to the correct value of 139,000 and missing only some sudden
FIG. 4: **Prediction of present state from a snapshot of a past distribution.** The model uses only the distribution at 30% (IMDb) and 10% (Digg) of the system’s history (in blue) to reconstruct the past (i.e. the birth and growth functions) and predict the future (in orange) of the database (in black). (top) Past, present (actual and predicted) distributions. (bottom) Relative change of each compartment $N_k$ measured as $\left[ N_k(t_f) - N_k(t_i) \right] / N_k(t_i)$; where $N_k(t_f)$ is either the actual distribution or a prediction. For comparison, a prediction using the classical preferential attachment model is shown in green.

bursts of new user influx. This observation embodies the strength of our model and the importance of a time dependent birth rate. Similar results are obtained for actor productivity on the IMDb. Quite remarkably, we reproduce the state of the system at year 2012 from its state at year 1974. Given that extrapolation is a delicate procedure, it seems not unlikely that these agreements are not coincidental. As a comparison, the classic preferential attachment model shown in Fig. 4 (bottom) is incapable of discerning whether the scaling exponent of a system is increasing or decreasing with time. As this classic model ignores the temporal dependency introduced here, this certainly highlights the importance of linking the temporal and structural features of complex systems.

**IV. CONCLUDING REMARKS**

It is important to keep in mind that our analysis is in no way restricted by the nature of the systems under study. Considering that scale independent systems are ubiquitous in science and everyday life, but that temporal data on their growth is seldom available, our framework provides a new investigation line to reconstruct their past and to forecast their future.

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19. In this regime, the sum diverges as $k_{\text{max}}(t) \to \infty$. The question is: how fast? The sum can be replaced by $\sum m^{1-\gamma} = \sum k^\gamma m^{1-\gamma} + \int_{k^*}^{k_{\text{max}}(t)} m^{1-\gamma} dm$ for an appropriate bound $k^*$. When the total sum diverges, the main contribution is obviously from the integral as the other term is finite. Hence, for $k_{\text{max}}(t) \gg 1$, the divergence occurs in $\int_{k^*}^{k_{\text{max}}(t)} m^{1-\gamma} dm \propto k_{\text{max}}^{2-\gamma}(t)$.

V. METHOD

A. Description of databases

**Prose samples.** Text files for the works of William Shakespeare, Miguel de Cervantes Saavedra and Johann Wolfgang von Goethe were downloaded from the Project Gutenberg at [www.gutenberg.org/]. Punctuation marks
and Project Gutenberg disclaimers were removed from the files manually.

While not a human system, but certainly a man-made one, these prose samples were used to get better statistics on the birth function. While human systems are unique and time dependent, written texts feature a translational invariance. This property allows us to gain better statistics of their growth by considering multiple samples of equal length as different realizations of the same process.

Time $t$ and resource $K(t)$ correspond to the total number of written words. Individuals correspond to unique words and their share $k_i(t)$ to their number of occurrences.

**Scientific authorships on the arXiv.** This database consists of a chronological list of all author names appearing on papers of the arXiv preprint archive (in order of publication date). It was compiled using the arXiv API to gain a full list of scientific publications available from http://arxiv.org/ as of April 2012.

Time $t$ and resource $K(t)$ correspond to the total number of paper authorships. Individuals correspond to authors and their share $k_i(t)$ to their number of publications.

**Digg user activities** Digg (http://digg.com/) is a social news website where registered users can vote on news or other types of articles that they deem interesting. This database is a list of all user votes on top stories (frontpage) over a period of one month in 2009.

Time $t$ and resource $K(t)$ correspond to the total number of votes. Individuals correspond to registered users and their share $k_i(t)$ is their respective number of votes.

**IMDb castings** The Internet Movie Database (http://www.imdb.com/) consists of an impressive amount of cross referenced lists (released films, cast and crew, etc.). These databases can be accessed or downloaded in various ways: see http://www.imdb.com/interfaces for details. From the list of actors featured on IMDb, which state all movies in which they have appeared, and the list of movie release dates, we built the chronological sequence of ‘castings’.

Time $t$ and resource $K(t)$ correspond to the total number of castings (a given actor playing in a given film). Individuals correspond to unique actors and their share $k_i(t)$ is the total number of films in which they have appeared.

**Sexual activities in a Brazilian community** This database was built from a public online forum for male clients who evaluate relations with female prostitutes. After preliminary results using the client and prostitute databases separately, we concluded that it was not necessary to distinguish between the two. The simplified database is thus a list of unique IDs corresponding to either a client or a prostitute, in chronological order of sexual relations (at time of online posting).

Time $t$ and resource $K(t)$ correspond to the total number of such IDs (two times the total number of relations). Individuals correspond to unique IDs (either client or prostitute) and their share $k_i(t)$ is their respective number of relations.

**TABLE II: Summary of database sizes and quantities.**

| Quantities      | prose | arXiv | Digg | IMDb | Sexual |
|-----------------|-------|-------|------|------|--------|
| Individuals     | unique words | authors | users | actors | clients/prostitutes |
| $N(t_f)$        | 502 on average | 386,267 | 139,409 | 1,707,565 | 16,730 |
| Resource        | written words | papers | votes | castings | sexual activities |
| $K(t_f) = t_f$  | cut at 1000 | 1,206,570 | 3,018,197 | 6,288,201 | 101,264 |
B. Measuring the birth function

**Prose samples** The translational (or temporal) invariance of written text implies that we can consider different samples of equal length from the same author as different realizations of the same experiment. The files were thus broken into samples of equal length and analysed separately. Each experiment can be reduced to a binary sequence of ones (when the word is a new word; i.e. a birth event) and zeros (when the word is an old one; a growth event). The birth function \( p(t) \) of a given author can then be obtained by simply averaging all binary sequences.

**Other systems** In other systems, since preliminary tests excluded the possibility of temporal invariance, another procedure must be used. The simplest one is to merely apply a running average on the binary sequence of birth and growth events. We used temporal windows of \( \Delta t \) equal to 1% of the total system size (final time \( t_f \)) for the two largest databases (Digg and IMDb) and between 0.5% and 1% of system size for the others. This method was shown to preserve the delayed temporal scaling on a random binary sequence whose elements were drawn from a known probability distribution following \( p(t) \).

C. Measuring the growth function

In this section, we detail the procedure used to obtain the growth function \( G(k) \) of a system from its temporal data, \( t \in [0,t_f] \). We use the following notation: we keep in memory every encountered individual \( i \), its number of apparitions (or current share) \( k_i(t) \), \( N_k(t) \) as the number of individuals with share \( k_i(t) = k \) and the total population \( N(t) \) after time \( t \). Starting from \( t = 1 \), we proceed as follows.

1. **Event.** If the \( t \)-th individual is new, add it to memory and note:
   \[
   N(t) = N(t-1) + 1 \\
   k_{N(t)}(t) = 1 \\
   N_1(t) = N_1(t-1) + 1
   \]
   and go to step 4. If the individual is already in memory, go to step 2.

2. **Chances.** We increment a function of chances
   \[
   C(k,t) = C(k,t-1) + N_k(t-1)/N(t-1) \quad \forall \; k
   \]
   and go to step 3.

3. **Success.** Noting \( i \) the individual involved in the current event, increment a function of successes
   \[
   S(k_i(t-1),t) = S(k_i(t-1),t-1) + 1 \\
   S(k,t) = S(k,t-1) \quad \forall \; k \neq k_i(t-1)
   \]
   and the following variables
   \[
   k_i(t) = k_i(t-1) + 1 \\
   N_{k_i(t-1)}(t) = N_{k_i(t-1)}(t-1) - 1 \\
   N_{k_{i+1}}(t) = N_{k_{i+1}}(t-1) + 1
   \]
   and go to step 4.

4. **Repeat.** If we have reached the end of the database, go to step 5. Otherwise, go to step 1.

5. **Calculation.** The growth function is finally given by:
   \[
   G(k) = S(k,t_f)/C(k,t_f) \quad \forall \; k.
   \]
D. Reconstructing the empirical growth function

Once the best possible $p(t)$ has been found, we adjust the growth function $G(k)$ by iterating the following algorithm:

1. **Initialization.** We fix $p(t)$ and we first consider $G(k) = k$.

2. **Growth.** We iterate the following equation from $t = 1$ with $N_k(1) = \delta_{k1}$ up to $t_f$:
   \[
   N_k(t + 1) = N_k(t) + p(t)\delta_{k1} + \frac{1 - p(t)}{\sum_{G(k)N_k(t)}} [G(k-1)N_{k-1}(t) - G(k)N_k(t)] .
   \]

3. **Correction.** For all $k$, we adjust $G(k)$:
   \[
   \tilde{G}(k) = G(k) \frac{N_k(t_f)/\sum_{i=k}^{\infty} N_i(t_f)}{N_k(t_f)/\sum_{i=1}^{\infty} N_i(t_f)}
   \]

4. **Iteration.** We set $G(k) = \tilde{G}(k)$ and return to step 2.

At step 3, the adjustment factor is simply the ratio of “the quantity of individuals/water that made it to share/bucket $k$ but did not go to $k + 1$”, as calculated in the model versus the target distribution. This algorithm is usually iterated 4 or 5 times to obtain a converged growth function.

E. Maximum-likelihood estimation

We search for a $p(t)$ that maximizes the logarithm of the likelihood $\mathcal{L}$ of a given binary sequence $\{y_i\}$ of birth ($y_i = 1$) and growth events ($y_i = 0$):

\[
\log \mathcal{L}(\tau, \alpha, b \mid \{y\}) = \sum_{i=1}^{t_f} y_i \log p(t) + (1 - y_i) \log (1 - p(t)) .
\]