

Innovation-exnovation dynamics on trees and trusses

Edward D. Lee * and Ernesto Ortega-Díaz 
Complexity Science Hub, Metternichgasse 8, Vienna, Austria

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Innovation and its complement exnovation describe the progression of realized possibilities from the past to the future, and the process depends on the structure of the underlying graph. For example, the phylogenetic tree represents the unique path of mutations to a single species. To a technology, paths are manifold, like a “truss.” We solve for the phase diagram of a model, where a population innovates while outrunning exnovation. The dynamics progress on random graphs that capture the degree of historical contingency. Higher connectivity speeds innovation but also increases the risk of system collapse. We show how dynamics and structural connectivity conspire to unleash innovative diversity or to drive it extinct.

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Living systems are constantly disrupted by the opposing forces of innovation and exnovation [1,2]. The processes grow and shrink the “space of the possible” (SOP) [3], the set of innovations often represented as technologies (e.g., patents [4]), mutations (e.g., genotypes, phenotypes [5]), or cultural practices (e.g., spelling norms [6,7]). How stable is such diversity to changes in relative rates of innovation-exnovation and SOP structure, for example, biodiversity under climate-induced extinction and ecosystem fragmentation?

The role of the competing forces is well recognized, but often unconsidered. Evolutionary processes, for example, are driven by mutation and selection on top of competitive dynamics. A classic example is Van Valen’s Red Queen, where competitors must constantly develop new strategies to keep up with the changing competitive landscape [8]. In society, we often think of the Schumpeterian rise and fall of industries as a crucial element of the free market in the process of creative destruction [9]. Innovations are successful novelties [5] that arise from combinatorial search and randomness in the process of discovery [10]. One insightful formulation of potential novelties is the Pólya urn [11,12], which has been extended to include variations such as social interactions that bias the search process [13]. Alternatively, innovation is formulated as the discovery of a percolating path [14]. On the other side is the process of exnovation, sometimes framed as a problem of extinction [15], of forgetting [6], or of obsolescence [11], but which has generally received less attention. Thus, these processes constitute two complementary sides of change: innovation refers to the process via which biological or social systems realize new and impactful possibilities, and exnovation how that set is truncated through obsolescence, desuetude, forgetting, and extinction. Yet, examples of

mathematical treatment relating them are few and in some cases, like combinatorial novelty, the role of exnovation in facilitating, unleashing, or inhibiting innovation is left out [16].

We propose a simple model to account for the race between innovation and exnovation. We model the SOP by formalizing it as a directed graph $\mathcal{G}(\mathcal{U}, E)$ with vertices, or sites, $u \in \mathcal{U}$ representing possibilities and edges E connecting innovations that lead from one to the other. The graph consists of K parallel branches distinguishing phylogenetic taxa or as separate lines of inquiry. The space is bounded by Kauffman’s “adjacent possible” (the set of all things one step away from what we know [3]) to the “adjacent obsolescent” (the set of all things one step away from exnovation [2]). A natural and important extension is to hypergraphs [17], but we do not consider these here. As a result, the space grows into the adjacent possible and shrinks away from the adjacent obsolescent in a kind of competition between the two fronts. A crucial element that we introduce is an explicit account of the SOP’s structure.

The classic representation of the SOP in biology is the phylogenetic tree of life, where every branching point indicates the emergence of a new species [18]. This means that a species is the result of following a unique path of mutations through evolutionary history. On the other hand, we might think of technological development as less constrained to a fixed order. Imagine the alternative history of motor transportation, where the electric vehicle first becomes dominant rather than the internal combustion engine, the world where quantum mechanics comes after general relativity, or Cixin Liu’s fictional, Trisolaran world where the intensive use of computers precedes the vacuum tube or transistor. In this simplified framing, biological history is physically contingent, or a tree-like SOP (in the classical sense [19]), whereas technological development is like a truss, where the next innovation can follow from any in the previous generation as we show in Fig. 1(a) [20]. To traverse the extremes, we take a single connectivity parameter γ that ranges from $\gamma = 0$ (tree-like) to $\gamma = 1$ (truss-like) and corresponds to the probability that any site from the previous generation leads into an adjacent branch in the following generation in addition to its own branch. Thus, the connectivity allows us to explore a range

*Contact author: edlee@csh.ac.at

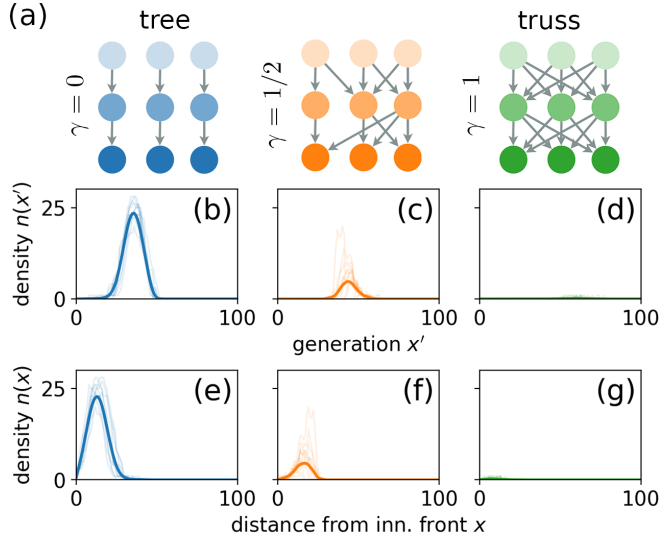


FIG. 1. (a) Space of the possible, as a directed graph $\mathcal{G}$, extending down into the adjacent possible and disappearing at the adjacent obsolescent at the top. Connectivity γ ranges from 0 (tree-like) to 1 (truss-like) for branch number $K = 3$. (b–d) Population density $n(x, t)$ for varying γ in automaton simulation in unpinned, free coordinate system, such that newer sites have larger x . Thick line is averaged over $K = 50$ branches and $R = 10^2$ replicas. Faint lines show a few individual replica branches. (e–g) Agent population in pinned coordinate system. Averaged over 10^2 replicas ($r_0 = 1/5$, $r_d = 0.98$, $v_o = 1/25$, $I = 2$).

of graph structures that titrate between a contingent and a path-independent SOP. In the following sections, we specify the model, discuss our mean-field formulation, solve the phase diagram, and provide some notes about our findings.

I. MODEL SPECIFICATION

Agents such as species or firms possess certain innovations, which we model as occupying sites in the SOP. As a general population dynamics intended to capture a wide range of scenarios, we consider several essential terms [2]: we include the total influx of new agents as a rate r_0 (e.g., reproduction or startup firms), agents leaving the system with rate r_d (e.g., death or bankruptcy), and mimetic innovation as rate r as replication toward the direction of innovation (e.g., mutation or spin-off firms). At the innovation front, agents cannot simply copy through mimetic innovation, but must also extract the site from the adjacent possible, the ease of which we capture with innovativeness factor I to modulate replication at the front. Finally, we specify the exnovation velocity v_o at which the adjacent obsolescent progresses and removes nodes, simultaneously excising the populating agents from system dynamics. All the rates can be scaled in terms of the replication rate r without changing the following equations, leaving us with four dynamical parameters. Taking this general framework as a minimal parameterization of the population dynamics, we explore what happens as the structure of the SOP changes.

The aforementioned elements correspond to the averaged population dynamics for $n(u, t)$, the number of agents occu-

pying site u at time t . After rescaling time by the replication rate $rt \rightarrow t$ and all other rates to be unitless, we obtain

$$\partial_t n(u, t) = \frac{r_0}{|\mathcal{G}(t)|} - r_d n(u, t) + \sum_{u' \in \partial_u^+} \frac{n(u', t)}{|\partial_u^-|}. \quad (1)$$

The SOP appears in Eq. (1) in terms of its size $|\mathcal{G}(t)|$, the number of sites between the adjacent possible and the adjacent obsolescent. The second term captures agent death. Additionally, we denote the set of sites downstream of site u as ∂_u^- , upstream as ∂_u^+ , and their number with absolute values such that the last term captures how agents replicate uniformly across downstream sites. Equation (1) captures agent population dynamics but not how the fronts move.

The innovation front is defined as the set of sites that are upstream of the adjacent possible, $u \in \partial_{-1}^+$. The innovation front consists of sites in the SOP, and the adjacent possible is the set of sites that are one step away from being innovated into the graph [3]. Discovery of the next innovation is not the same as mimetic replication, so the innovativeness accounts for how easily $I > 1$ (or laboriously $I < 1$) they are found. The graph grows with the summed discovery rate at each site on the innovation front (as if each agent were independently attempting to push into the adjacent possible) and the typical number of downstream nodes that enter the SOP, $\langle |\partial_0^-| \rangle$, or all together, $I \langle |\partial_0^-| \rangle \sum_{u' \in \partial_{-1}^+} n(u', t)$ [21]. As the complement, the adjacent obsolescent is the set of all points in the SOP that are one step away from exnovation. Falling behind the adjacent obsolescent excises the population from future dynamics, here captured as an abrupt loss in population, $n(u, t \geq t') = 0$ for all u behind the front, $u \in \partial_{\mathcal{O}}^+$, for all time beyond the time of exnovation t' . Taking the two fronts and considering the case when the system size is large, the rate of change in the size of the SOP is

$$\partial_t |\mathcal{G}(t)| = I \langle |\partial_0^-| \rangle \sum_{u \in \partial_{-1}^+} n(u, t) - v_o \langle |\partial_{\mathcal{O}}^-| \rangle \sum_{u \in \partial_{\mathcal{O}}^+} 1. \quad (2)$$

Equation (2) accounts for tension between a growing innovation front and elimination behind the exnovation front. In many systems, innovation and exnovation are coupled, but we take the simplifying assumption that they are parameterized by fixed rates and use those fixed rates as control parameters to study system behavior.

To verify the calculations that we develop, we construct an automaton simulation, allowing us to access the full stochasticity of the system behind the mean-field equations. In the limit that we take a small time interval $dt \ll 1$ to iterate the dynamics, we can specify the change in agent number per site that corresponds to Eq. (1) to be from a Poisson distribution. As for the graph structure, the dynamics summarized by Eq. (2) refer to the two different processes of innovation and exnovation. The former constitutes a thin line of sites that can move into the adjacent possible, where each site independently expands into the adjacent possible with rate proportional to the occupancy, mimetic replication rate, and innovativeness (note that in the limit $dt \ll 1$, only one site can expand at a time). The latter expands from any site already obsolescent with the fixed obsolescence rate. We use the numerical computation library JAX for random number generation and matrix multiplication to simulate the movement of

the fronts and agent reproduction and death on a random graph parameterized by connectivity γ . We incorporate an adaptive timescale that changes at each time step to ensure that the steps are sufficiently small to keep front velocities in the linear regime. Thus, we have a way of checking how the mean-field approximations describe a more complete instantiation of the dynamics.

II. MEAN-FIELD FORMULATION

Under weak coupling of the branches, we can find a rounded shape in the density function as in Figs. 1(b)–1(d) as the locations of the two fronts diffuse. The decay in the density toward the leading site of each branch reflects the tendency of the innovation front to deplete itself given that it tends to speed up when agents accumulate. The decay near the opposite end, the lagging site, represents the variability in the location of the exnovation front, behind which the density is zero. Most agents are typically found in between the two fronts for long-lived innovation trains, leading to a single-humped innovation train that drifts to the right.

The density relative to the innovation front, however, is of primary interest. We would like to incorporate this aspect into the mean-field equations. To track the innovation front, we pin each branch of the graph onto a unidimensional coordinate system such that the innovation front is fixed at $x = 0$, the adjacent possible at $x = -1$, and a “pseudogap” in the density describes $x \geq 0$. In this way, x corresponds directly to the age of the generation, where the newest nodes have the smallest value of x . Then, we assume branch symmetry to take an average over the densities on each of K respective branches. If the typical branch has time-dependent length $L(t)$, the exnovation front is located at $x = L(t) - 1$. This is consistent with a mean-field, continuous-time formulation for the population dynamics,

$$\partial_t n(x, t) = \frac{r_0}{L(t)} - r_d n(x, t) + n(x + 1, t) - \tilde{I} n(0, t) [n(x, t) - n(x - 1)], \quad (3)$$

$$\partial_t L = \tilde{I} n(0, t) - \tilde{v}_o. \quad (4)$$

Equation (3) accounts for per site growth, death, replication, and in the last term drift in the coordinate system due to the movement of the innovation front. Equation (4) describes the rate at which the distance between the innovation and exnovation fronts changes (in the large- L limit). Both equations implicitly incorporate aspects of structural connectivity as represented by modified exnovation velocity $\tilde{v}_o$ and modified innovativeness $\tilde{I}$.

The modified terms represent faster front velocities because (i) there are multiple paths through which to advance and (ii) because fronts may be superseded when adjoining, further advanced branches feed into a given branch. Consider the fully connected limit $\gamma = 1$, where the corrected velocity for either exnovation or innovation must be $\tilde{v}_o = v_o[1 + \gamma(K - 1)]$ as all front sites (on each branch) move together. This argument does not generalize to $\gamma < 1$ because the fronts are not synchronized.

Take the front that is furthest ahead to be at $y = 0$; i.e., no other branch is further ahead. The fraction of leading fronts

at y is $p(y)$. There are two scenarios for a branch with front at $y \geq 0$: (i) it moves with probability $v_o dt$ or (ii) it does not with probability $1 - v_o dt$ in short time $dt \ll 1$.

Case (i): The front moves by one lattice site, and it expands out to a fraction γ of its neighbors. The effective velocity at which the front on a single branch moves is then $v_o[K^{-1} + \gamma(1 - K^{-1})]$. There are $Kq(y)$, for cumulative distribution $q(y) \equiv \sum_{y'=0}^y p(y')$, exnovation fronts in any layer y (the cumulative term accounts for the assumption that any exnovated site can propagate downstream). Now, we average over all the layers $v_o \sum_{y=0}^{\infty} p(y)[1 + \gamma(K - 1)q(y)] = v_o[1 + \bar{q}\gamma(K - 1)]$, taking $\bar{q} = \sum_y p(y)q(y)$. The innovation front is different because every site can only be innovated once, and so the leading site on a given branch is the only one that can advance into the adjacent possible. As a result, the velocity is $n(0)I[1 + \bar{p}\gamma(K - 1)]$ for $\bar{p} \equiv \sum_{y=0}^{\infty} p(y)^2$ and the averaged, stationary innovation front density is $n(0)$.

Case (ii): The front does not move, but it effectively jumps ahead to $y' - 1$ if an adjacent branch at $y' < y$ feeds in ahead of it. For the exnovation front, each layer ahead of it has $q(y')K$ fronts that individually move with rate v_o and feed into the branch at layer y with probability γ , or $v_o\gamma K \Delta y_1$ and $\Delta y_1 \equiv \sum_{y'=1}^{\infty} p(y) \sum_{y' < y} q(y')(y - y' + 1)$. The argument is the same for the innovation, except that each layer ahead $y' < y$ has $p(y')K$ fronts to obtain $\Delta y_2 \equiv \sum_{y'=1}^{\infty} p(y) \sum_{y' < y} p(y')(y - y' + 1)$.

To complete the calculation, we need $p(y)$. In the limit $\gamma \rightarrow 1$, where fronts are thinly distributed around the leading front, they escape promotion to the front only rarely. This picture suggests as an approximation the Poisson distribution $p(y) = e^{-\lambda} \lambda^{-y} / y!$ (here, we are considering either many random replicas or $K \gg 1$). The mean λ is the mean distance $\bar{y}$. Note that this form for the probability distribution has the correct limits $\lim_{\gamma \rightarrow 0} p(y) = \delta(y)$ and a uniform distribution when $\gamma \rightarrow 1$. Considering leading sites that move between $y = 0$ and $y = 1$, we obtain a self-consistency condition under steady state $\gamma = e^{-\lambda} / (1 + \lambda)$ or an implicit solution for λ in terms of γ .

All together, the corrected front velocities when $K \gg 1$ are given by

$$\begin{aligned} \tilde{v}_o &\equiv v_o[1 + \bar{q}\gamma K + \gamma K \Delta y_1], \\ \tilde{I} &\equiv I[1 + \bar{p}\gamma K + \gamma K \Delta y_2]. \end{aligned} \quad (5)$$

The first two terms in each line of Eq. (5) account for self-promotion of a site and the second term promotion from branches that are further ahead (note that this approximation ignores the fronts that are behind others on the same branch, if temporarily). Equation (5) obeys the expected limits: $\lim_{\gamma \rightarrow 0} \tilde{v}_o = v_o$ and $\lim_{\gamma \rightarrow 1} \tilde{v}_o = v_o(1 + \gamma K)$ as well as $\lim_{\gamma \rightarrow 0} \tilde{I} = I$ and $\lim_{\gamma \rightarrow 1} \tilde{I} = I(1 + \gamma K)$, or the cases when the branches are fully independent or perfectly synchronized. We show how the calculated front velocities compare with the automaton simulation in Fig. 2. Along with the modified velocities, Eqs. (3) and (4) describe the averaged dynamics given distance x to the innovation front and over the ensemble of random graphs that are characterized by γ . For both fronts, redundant paths to children nodes increase velocity over independent branches, distinguishing the truss from the tree.

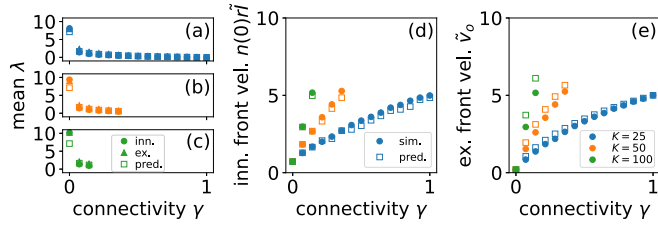


FIG. 2. (a–c) Predicted average distance to the leading front λ against automaton simulation for innovation and exnovation fronts given branch numbers $K = 25$, $K = 50$, and $K = 10^2$, respectively. For sufficiently large K and γ , the system collapses and no value is given. Comparison of front velocities for (d) innovation and (e) exnovation fronts. Averaged over $R = 25$ replicas, $r_0 = 1/5$, $r_d = 0.98$, $v_o = 1/25$, and $I = 2$.

III. PHASE DIAGRAM AND COMPARTMENT MODEL

Naïvely, we expect three types of solutions [2]: *runaway*, where the innovation front outpaces exnovation; *collapse*, when the exnovation front catches up with innovation; and *balanced*, where innovation and exnovation velocities match. From *in silico* experiments, we observe more exotic behaviors such as multiple fixed points, depending on initial conditions. We also observe a separation of timescales, where the total density settles rapidly at a fixed value but the system size $L(t)$ relaxes much more slowly. We also find that the trivial fixed point $L = 0$ can have a large stochastic basin of attraction. To characterize the observations, we propose an analytic approximation to Eqs. (3) and (4).

The fronts constitute key elements of the model, and they constitute “interfaces” that are coupled through the flow of agents in the “bulk” in between. This is the compartment model. The bulk has length $L^*(t) = L(t) - 2$, accounting for the two fronts, and number of agents $N^*(t) = N(t) - n(0, t) - n(L - 1, t)$, discounting the front densities. To couple the bulk with the fronts, we make the approximation that the density inside the bulk can be treated homogeneously or that $n(x, t) = N^*(t)/L^*(t)$ for $1 \leq x \leq L - 2$. This approximation obtains a closed set of four equations that can be solved at stationarity to obtain the order parameters $N_{\pm} = (B \pm \sqrt{C})/2A$ and $L_{\pm} = (B' \pm \sqrt{C'})/2A'$, denoting two solutions for either sign of the radical, but the negative solution only holds for $r_d < 1$. Additionally, we find a quadratic solution for n_{L-1} and $n_0 = \tilde{v}_o/\tilde{I}$. We do not enumerate the terms in A , B , C and their prime counterparts here. Nonphysical (negative or complex) solutions reveal when the system displays infinite growth or collapse, and we solve for these lines to draw the phase diagram in Fig. 3.

Collapse implies the disappearance of the bulk, or $L \leq 2$. From the bulk-interface approximation, we find the boundary to the collapsed region or the blue region in Fig. 3(a). The solid blue line delineates this regime as where the exnovation velocity exceeds innovation’s. In panels (b) and (c) corresponding to $r_d > 1$ and $r_d < 1$, respectively, we show again the boundary of the collapsed regime as we vary structural parameters. The collapsed regime emerges for sufficiently large branching number and connectivity—this signals the role of branch-spanning connections in facilitating system collapse.

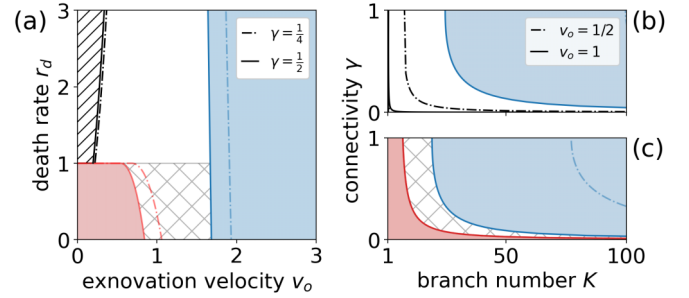


FIG. 3. (a) Dynamical phase diagram by death rate r_d and exnovation velocity v_o (other parameters $r_0 = 125$, $I = 2$, $K = 12$). (b), (c) Structural phase diagram by connectivity γ and branch number K ($r_0 = 25$, $I = 2$, $r_d = 5/2$ for the top panel and $r_0 = 50/3$, $I = 2$, $r_d = 5/3$ for the bottom panel). Lines distinguish values of connectivity γ or exnovation velocity v_o . Red regions are runaway, blue collapsed, white steady state, single-line hatched low-density, and cross-hatched bistable phases from the compartment model.

Divergence is when either $N \rightarrow \infty$, which implies that $L \rightarrow \infty$, or just $L \rightarrow \infty$ regardless of N . Thus, we can search for where L diverges. At those lines, L crosses over to negative or imaginary solutions, so we solve for where $\Im[L] \geq 0$. In the dynamical phase diagram as in Fig. 3(a), the physical solution delineates the regime of complex L . This alone, however, is insufficient because L becomes negative but remains real on a line that cuts through the runaway region in the bottom left of Fig. 3(a). The crossover to negative values is at $r_d = 1$ and for all values v_o smaller than the value at which the transition to complex solutions peaks, $v_o = v_o^*$, and bends down and away from $r_d = 1$. These two conditions together delineate the red, runaway regime.

To the right of the runaway region, we find a bistable regime indicated by the cross-hatched region in Fig. 3(a). Here, both solutions $N_{\pm}$ and $L_{\pm}$ are viable, but the $+$ solutions are stable and the $-$ solutions unstable.

In the remaining region, we find a single stable and finite solution in the white regions of Fig. 3. In the diagonal hashed region, we find a stable low-density phase, where the density drops below unity, $\mathbb{R}[N - L] < 0$. This “Byzantine” phase displays high but slowly changing diversity (resulting from slow exnovation). Considering the structural phase space, connectivity has little effect on density for small K , showing insensitivity to interdependence. Finally, appreciable densities occupy relatively small volumes of the stable phase, limited to a thin sliver bordering runaway for $r_d < 1$. This is especially notable as K becomes large, where collapse dominates. Stability is in this sense unusual in large systems, and thriving population dynamics are limited to a small region of parameter space, where relatively independent lineages survive better than interconnected ones. Since many living systems display wide and persistent diversity [2] under resource constraints, lower-dimensional SOPs might play a role in system resilience.

IV. DISCUSSION

We present a simplified population dynamics of agents coupled to a moving SOP that distinguishes divergent (hierarchical) and convergent (truss-like) paths of development to mimic biology-like vs technology-like systems [22,23]. The

phase boundaries change with the number of branches and the connectivity between them; thus, we identify how agent dynamics and structure of the SOP conspire to either enhance or hamper the race between innovation and exnovation.

A particular question on which the model touches is how few systems remain constant in structure over time. The “tree of life” is rife with cross-cutting connections as organisms exchange DNA or RNA [24,25]. Species experience population bottlenecks or separate as ecosystems divide as with the disappearance of the Bering Strait or as demonstrated by Darwin’s finches. Economies may decouple, scientific fields split, or new interdisciplinary centers arise. Perhaps counterintuitive to the notion that crossing bridges helps to develop new ideas, we find that increasing connectivity between adjacent branches also risks system stability, even if it increases the innovation rate. This trade-off between system survival and speedy innovation suggests a type of evolutionary or cultural speed limit [26] that takes into account the underlying graph structure. As a second observation, we find that the regions of parameter space that would entail competition with more than one agent per innovation constitute a relatively small fraction of the space, centered around SOPs with fewer branches and weaker connectivity. This is perhaps relevant to the emergence of modularity in adaptive, resource-constrained systems [28].

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DATA AVAILABILITY

The code for the project is available [29].

APPENDIX A: NOTE ON AUTOMATON SIMULATION

To verify the calculations that we develop, we construct a highly parallelized, graphical processing unit accelerated, and scalable automaton simulation, allowing us to access the full stochasticity of the system behind the mean-field equations. We use the numerical computation library JAX for random number generation and matrix multiplication to simulate the movement of the fronts and agent reproduction and death on a random graph. We incorporate an adaptive timescale that changes at each time step to ensure that the steps are sufficiently small to keep front velocities in the linear regime. Agent dynamics are Poisson distributed and are not sensitive to corrections from the linear approximation. Thus, we have a way of checking how the mean-field approximations describe a more complete instantiation of the dynamics.

To check the stability of the mean-field solutions under stochastic dynamics, we simulate them with the automaton. We initialize random replicas with conditions as given by the

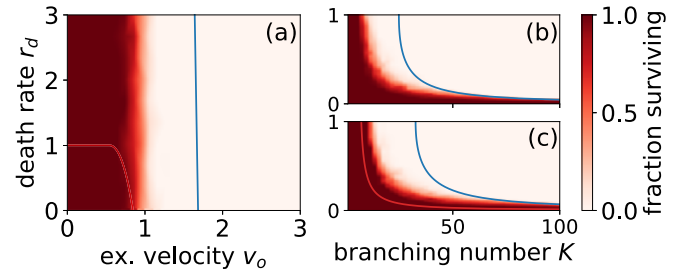


FIG. 4. Fraction of surviving branches calculated over $R = 50$ replicas at time $t = 20$, given steady-state initial conditions from stable compartment model solutions corresponding to N_- and L_- (except at runaway zones, where initial conditions are capped at $N \leq 10^4$ and $L \leq 10^2$). Red and blue contours delineate runaway and collapsed regions from Fig. 3. (a) Dynamical phase diagram. (b) Structural phase diagram for $r_d > 1$. (c) Structural phase diagram for $r_d < 1$. Parameters from Fig. 3.

compartment model at steady state, taking uniform density in the bulk $n(x, t = 0) = N_+^*/L_+^*$ and the steady-state interface values, and evaluate the fraction of surviving branches per replica at time $t = 20$ across the phase diagrams as shown in Fig. 4—since collapse is a fixed point, the fraction cannot increase with time. As expected, empty branches are more likely as we approach the boundaries of the collapsed phase in blue, where small system size makes it more likely that random fluctuations leave the system in the collapsed configuration. The compartment model formulation captures the general contours of the automaton simulation, although the trivial attractor is larger than as indicated by the approximation. This reflects the error from our approximation of $\tilde{v}_o$ in Fig. 4(a) and the large K approximation in panels (b) and (c). For large K in the structure space [panels (b) and (c)], the transition from collapse to runaway is compressed into a small and diminishing range of γ as we increase K . Since γ is symmetric with respect to the number of incoming upstream edges and outgoing downstream edges, the compression indicates the importance of outgoing edges to the dynamics, which determines how quickly density drops at the innovation front.

APPENDIX B: NOTE ON COMPARTMENT MODEL

The fronts constitute key elements of the model, and they constitute “interfaces” that are coupled through the flow of agents in the “bulk” in between. This is the compartment model as described in the main text. This approximation obtains a closed set of four equations,

$$\begin{aligned} \partial_t N &= r_0 - r_d N + N - n_0 - \tilde{v}_o n_{L-1}, \\ \partial_t L &= \tilde{I} n(0) - \tilde{v}_o, \\ \partial_t n_0 &= r_0/L - r_d n_0 \\ &\quad + (N - n_0 - n_{L-1})/(L - 2) - \tilde{I} n_0^2, \\ \partial_t n_{L-1} &= r_0/L - r_d n_{L-1} - \tilde{v}_o [n_{L-1} \\ &\quad - (N - n_0 - n_{L-1})/(L - 2)]. \end{aligned} \quad (\text{B1})$$

Equation (B1) can be solved at stationarity to obtain the order parameters $N_{\pm}$ and $L_{\pm}$.

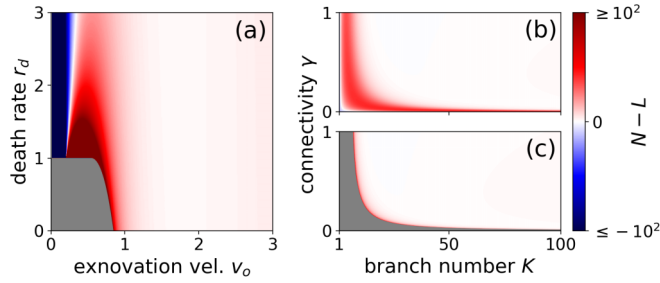


FIG. 5. Comparison of total agent number and lattice length, $N_+ - L_+$, with parameters from Figs. 3(a), 3(b), and 3(c), respectively. Runaway region in gray.

Collapse implies the disappearance of the bulk, or $L \leq 2$. From the bulk-interface approximation, we get as the condition delineating the collapsed regime, $r_d = (-b + \sqrt{b^2 - 4ac})/2a$, with $a = 2\tilde{v}_o(1 + \tilde{v}_o)$, $b = 4\tilde{v}_o^3 - \tilde{I}r_0(1 + \tilde{v}_o)$, and $c = 2\tilde{v}_o^3(\tilde{v}_o - 1) - \tilde{I}r_0(1 + \tilde{v}_o^2)$, having disposed of the three other nonphysical solutions.

Divergence, in contrast, is when either $N \rightarrow \infty$, which implies that $L \rightarrow \infty$, or just $L \rightarrow \infty$ regardless of N . Thus, we can search for where L diverges. At those lines, L crosses over to negative or imaginary solutions, so we solve for where $\Im[L] \geq 0$. In the dynamical phase diagram as in Fig. 3(a), the physical solution (out of four) delineating the regime of complex L is

$$r_d = \frac{1}{4\tilde{v}_o} \left\{ \tilde{I}r_0 + 3\tilde{v}_o - \tilde{v}_o^2 - \left[(\tilde{I}r_0 + 3\tilde{v}_o - \tilde{v}_o^2)^2 + 8\tilde{v}_o(\tilde{v}_o^2 + \tilde{v}_o^3 - 2\sqrt{\tilde{I}\tilde{v}_or_0(1 + \tilde{v}_o^2)}) \right]^{1/2} \right\}. \quad (\text{B2})$$

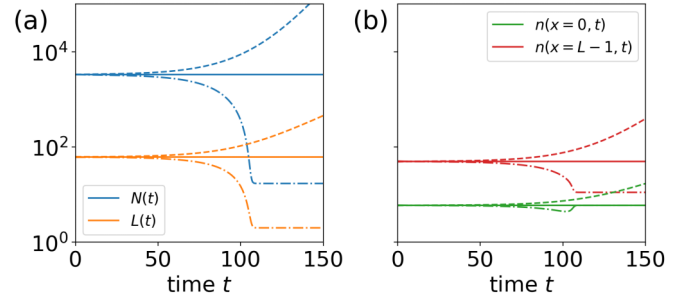


FIG. 6. Bifurcating trajectories on initial conditions by (a) population $N(t)$ in blue and length $L(t)$ in orange and (b) number at innovation front $n(0, t)$ in green and exnovation front $n(L-1, t)$ in red. Each line represents a different initial condition perturbed from the unstable solution N_- and L_- , where for dashed line $L(0) = L_- + 1$, solid line $L(0) = L_-$, and dot-dashed line $L(0) = L_- - 1$. The latter converges to the stable solution N_+ and L_+ .

In Fig. 5, we show the density $N - L$ according to the compartment model for comparison with Fig. 3. As with the dynamical phase diagram, we see that the stable regime shows a low-density phase for $v_o > 1$ and $r_d < 1$. The region of substantial density is confined to around the runaway region. For comparison, the structural phase diagrams in panels (b) and (c) show again that the regions of appreciable density are concentrated around the bottom and left-hand sides of the diagrams.

To the right of the runaway region, we find a bistable regime indicated by the cross-hatched region in Fig. 3(a). Here, both solutions $N_{\pm}$ and $L_{\pm}$ are viable (in particular, N_- and L_- satisfy the steady-state conditions only in this regime), but the $+$ solutions are stable and the $-$ solutions unstable. Fluctuations around the unstable solution lead to divergence or to the stable solution. We show example trajectories of this outcome in Fig. 6.

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