A stochastic process of scientific discovery.

Consider an infinite population of scientists conducting a sequence of idealized experiments \( \xi(t) := (M_P(t), \theta, D(t), S, K^{(t)}) \), indexed by time \( t = 1, 2, \ldots \) where \( M_P(t) \) belongs to a set of probability structures \( \mathcal{M} = \{M_1, M_2, \ldots, M_L\} \) known to all scientists. Further, assume that there are \( A \) distinct scientist types in the population, each with a well-defined research strategy \( R \in \mathcal{R} = \{R_0, R_1, \ldots, R_A\} \) of proposing a model in their experiment. These strategies depend on the type of scientist and a global model \( M_{G(t)} \in \mathcal{M}, K(t) \), which represents the consensus of the scientist population at time \( t \). The population of scientists aims to find the true model \( M_T \in \mathcal{M} \). A scientist selected to conduct an experiment at time \( t \), uses her background knowledge \( K(t) \) to propose a new candidate model \( M_P(t) \).

Specifically, we define \( K(t) \) as a probability distribution \( P(M_P| R(t)), M_G(t) \), where \( \{M_P, M_{G(t)}\} \in \mathcal{M}^2 \), and \( R(t) \in \mathcal{R} \).

The initial conditions of our stochastic process include the true model \( M_T \), true parameter values \( \theta_T \) of \( M_T \), an initial global model \( M_{G(0)} \), a method for model selection \( S \), and the sample size of the data \( n \). At each time step, an idealized experiment \( \xi(t) \) is performed and new data \( D(t) \) of size \( n \) is generated independent of everything else from distribution \( M_T(\theta_T) \). Each experiment is performed by a scientist randomly selected from \( A \) types in the population using the categorical distribution with probabilities \( (p_1, p_2, \ldots, p_A) \). The selected scientist proposes a model \( M_P(t) \) with probability \( P(M_P| R(t), M_G(t)) \) conditional on a research strategy fully specified by her type and the current global model. Given the data \( D(t) \), model scores under the proposed model and the current global model are calculated as \( S(M_P(t)) \) and \( S(M_G(t)) \), respectively. The model with favorable score (i.e., smaller for both AIC and SC) is set as the new global model \( M_{G(t+1)} \). This mechanism represents how scientific consensus is updated in light of new evidence.

A defining property of our stochastic process with no replication is that \( K^{(t)} \) depends only on quantities at time \( t \). If \( R_a \in \mathcal{R} \) depends only on \( M_{G(t)} \) for all \( a \), the transition from \( M_{G(t)} \) to \( M_{G(t+1)} \) admits the Markov property and the stochastic process representing the scientific process is a Markov chain with transition probabilities given by

\[
\mathbb{P}(M_{G(t+1)} = M_{\ell}| M_{G(t)} = M_i) = \sum_{\alpha=1}^{A} \mathbb{P}(S(M_{\ell}) < S(M_i)) \mathbb{P}(M_{\ell}| R_a, M_i) \mathbb{P}(R_a).
\]

(1)

On the right hand side of Eq. (1), the last term is the probability of selecting a scientist with research strategy \( R_a \) independent of all else, the middle term is the
probability of proposing the model $M_t$ given the current global model $M_G$ and the scientist type $a$ with research strategy $R_o$ selected. The probability $\mathbb{P}(S(M_t) < S(M_i))$ depends on $M_T$ via $D(t)$ generated and it is obtained by $\int_{\Theta} \int_{D(t)} \mathbb{P}(S(M_t) < S(M_i)| D) \mathbb{P}(D|\theta) \mathbb{P}(\theta) dD d\theta$, where $\mathbb{P}(\theta)$ is the probability of parameter, $\mathbb{P}(D|\theta)$ is the likelihood of the data, and $\mathbb{P}(S(M_t) < S(M_i)| D)$ is the probability that the proposed model $M_t$ has a more favorable score than $M_i$ conditional on data. We have $\mathbb{P}(S(M_t) = S(M_i)) = 1$ when $\ell = i$ and the model selection method $S$ is a continuous variable so that $\mathbb{P}(S(M_t) \leq S(M_i)) = \mathbb{P}(S(M_t) < S(M_i))$ and by convention we set $\mathbb{P}(S(M_t) < S(M_i)) = 1$. Further, $\mathbb{P}(M_t|R_a, M_i) > 0$ for all $a, i, \ell$ so that transition probabilities are nonzero for all models and scientist types. This second condition guarantees that our Markov chain is ergodic, which implies that it has a unique stationary distribution—its limiting distribution for visiting a model.

When there are no replication experiments in the system, $K(t)$ is defined as $\mathbb{P}(M_P|R(t), M_G(t))$ which states that conditional on $R(t)$ and $M_G(t)$, the probability of proposing a model is independent of the past time steps. Let $R_o \in \mathcal{R}$ be the replicator strategy. Given the proposed and global models at time $t − 1$, the replicator strategy at time $t$, $R_o(t)$, is to perform an experiment at time $t$, using the exact same proposed and global models as those at time $t−1$, but with new data $D(t)$ generated under $M_T(\theta_T)$. Since $R_o \in \mathcal{R}$ depends on $M_G(t−1)$, the transition from $M_G(t)$ to $M_G(t+1)$ does not admit the Markov property anymore and the stochastic process representing the scientific process is a higher order Markov chain. The transition probabilities of the Markov chain at time $t$ can be expressed by conditioning on whether a scientist chosen at a given time is a replicator:

$$
\begin{align*}
\mathbb{P}(R(t) \neq R_o) &\mathbb{P}(M_G^{t+1} | M_G^{t}) + \\
\mathbb{P}(R(t) = R_o) [\mathbb{P}(R(t−1) \neq R_o) \mathbb{P}(M_G^{t+1} | M_G^{t}, M_G^{t−1})] + \cdots + \\
\mathbb{P}(R(t−1) = R_o) &[\mathbb{P}(R^{t−1} \neq R_o) \mathbb{P}(M_G^{t+1} | M_G^{t}, M_G^{t−1}, \ldots, M_G^{(0)})] \cdots].
\end{align*}
$$

In Eq. (2), the first term in the sum is the joint probability of choosing a scientist who is not a replicator at time $t$ and the transition probability from global model at time $t$ to global model at time $t + 1$. Since the scientists are chosen independently of all else, the joint probability is written as the product of choosing a scientist who is not a replicator at time $t$, given by $\mathbb{P}(R(t) \neq R_o)$, and the probability of transition to the global model at time $t + 1$ is given by Eq. (1). The second term in the sum is the joint probability of choosing a scientist who is a replicator at time $t$ and the transition probabilities to a model. We write the second term as the product of $\mathbb{P}(R(t) = R_o)$ and the transition probabilities when a replicator is chosen. If the scientist at time $t$ is a replicator, she replicates the experiment at time
step $t - 1$, which might be a replication experiment itself. Therefore, the transition probabilities to a model within the first brackets is a sum of two probabilities. The first term is the joint probability of choosing a scientist who is not a replicator and the transition probability in that case, and the second term is the probability of choosing a replicator given by $P(R^{(t-1)} = R_a)$ at time step $t - 1$, and the transition probability in that case. This is a recursive equation, in the sense that the transition probabilities at time $t$ depend on the transition probabilities at time $t - 1$. An implication is that the transition probabilities at time $t$ are path dependent. Therefore, when a replicator scientist is included in the population, we have a higher order Markov chain, whose long term dynamics are feasible to obtain with a forward simulation method.

For the process with replicator, we lift the assumption $P(M_i | R_{a}, M_i) > 0$ for all $a, i, \ell$ that we imposed in the process without a replicator. This assumption increases the connectivity of the transition probability matrix, which makes calculations in the long-term behavior of the Markov chain straightforward. Due to our new process not admitting the Markov property, these calculations are irrelevant in the analysis of the process with a replicator. Therefore, we drop the assumption of transitioning from a model to any other model to be nonzero. Removing this assumption allows us to define scientist types that visit only the subset of all models consistent with a specific research strategy. This property of the process renders the effects of each research strategy on the process outcomes well-pronounced.