Measuring frequency-dependent selection in culture

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Cultural traits such as words\textsuperscript{1}, names\textsuperscript{2}, decorative styles\textsuperscript{3}, and technical standards\textsuperscript{4} often assume arbitrary values and are thought to evolve neutrally\textsuperscript{2,3,5–7}. But neutral evolution cannot explain\textsuperscript{3} why some traits come and go in cycles of popularity\textsuperscript{6} while others become entrenched\textsuperscript{4,10}. Here we study frequency-dependent selection—where a trait’s tendency to be copied depends on its current frequency regardless of the trait value itself. We develop a maximum-likelihood method to infer the precise form of frequency-dependent selection from time series of trait abundance, and we apply the method to data on baby names and pet dog breeds over the last century. We find that the most common names tend to decline by 2%-6% per year on average; whereas rare names—1 in 10,000 births—tend to increase by 1%-3% per year. This specific form of negative frequency dependence explains patterns of diversity\textsuperscript{11} and replicates across the United States, France, Norway and the Netherlands, despite cultural, linguistic and demographic variation. We infer a fixed fitness offset between male and female names that implies different rates of innovation. We also find a strong selective advantage for biblical names in every frequency class, which explains their predominance among the most common names. In purebred dog registrations we infer a form of negative frequency dependence that is consistent with a preference for novelty, in which each year’s newest breeds outgrow the previous by about 1%/year, which also recapitulates boom-bust cycles in dog fanciers\textsuperscript{9}. Finally, we define the concept of effective frequency-dependent selection, which enables a meaningful interpretation of inferred frequency dependence even for complex mechanisms of evolution. Our analysis generalizes neutral evolution to incorporate pressures of conformity and anti-conformity as fundamental forces in social evolution, and our inference procedure provides a quantitative account of how these forces operate within and across cultures.

Humans adopt millions of different first names, hundreds of different dog breeds, and virtually one word for baseball—even though names\textsuperscript{2}, dog breeds\textsuperscript{9}, and words\textsuperscript{12} are all chosen from arbitrary alternatives. Why do skirt lengths continuously fluctuate\textsuperscript{13} while media formats\textsuperscript{14} enjoy long periods of stasis? What’s in a name, if a rose by any other name would smell as sweet?

Here we advance frequency-dependent selection to unify different domains of evolution. We develop a method to quantify the form of frequency dependence, which has been difficult to observe in biological data. Socially relevant traits in humans evolve by cultural transmission, through mechanisms of imitation, learning, and innovation\textsuperscript{15,16}. Nonetheless, models of biological evolution that describe the dynamics of types in reproducing populations\textsuperscript{17} can be used to describe the dynamics of social traits inherited by cultural transmission\textsuperscript{7,18–20}. The neutral model of evolution\textsuperscript{5} attributes changes in a population’s composition to the accumulated effects of indiscriminate random copying, which already recapitulates empirical aspects of names\textsuperscript{2} and words\textsuperscript{12}. Here we generalize the neutral model by introducing selection—adjusting the propensity to copy different traits—in the case when selection depends solely on a type’s frequency in the population. This frequency-dependent selection remains blind to any distinguishing features of the types themselves and so constitutes an exchangeable model of evolution\textsuperscript{23} which is mathematically tractable despite high dimensionality. This generalization of neutrality is analogous to density-dependent extensions\textsuperscript{22} of neutral biodiversity theory in ecology\textsuperscript{25}, and it corresponds to coordination and anti-coordination games in evolutionary game theory\textsuperscript{26}. By incorporating selection, the model encompasses a spectrum of behavior from rapid diversification\textsuperscript{22} to intractable entrenchment of a single type\textsuperscript{11,29}. The model is an effective base case for social evolution, because it captures the selective pressures that are common to all types.

Biologists seldom have the opportunity to measure precisely how selection depends on frequency in the wild. Despite this lacuna, frequency-dependent selection has been long-studied\textsuperscript{29–30} and commonly invoked in explanations of genetic diversity\textsuperscript{31}, immune escape\textsuperscript{32},
altruistic behavior, sex ratios, mating preferences, reproductive timing, and speciation.

Cultural traits in humans, by contrast, “fossilize” ubiquitously, often leaving complete records of the abundance of alternative types over time. Cultural data therefore provide a rich source of empirical patterns that we can use to infer specific forms of frequency dependence in cultural evolution, and to provide a proof of concept for studying how social behavior governs selection on genetic and morphological traits in biology.

Evolutionary model and parameter inference

We model evolution as a Wright-Fisher process, where the growth rate $e^s(p)$ associated with a trait depends on the trait’s current frequency $p$ in the population, via a frequency-dependent selection coefficient $s(p)$. The functional form of frequency-dependent selection, $s(p)$, is assumed common to all traits, so that $s(p)$ completely specifies the competitive environment of the exchangeable model (Fig. 1a). The case $s(p) \equiv 0$ recovers neutral evolution, whereas $s(p)$ linearly increasing or linearly decreasing with $p$ recover textbook formulations of positive and negative frequency-dependent selection. Mutations (innovations) occur at rate $\mu$ per generation and always produce novel types.

We infer the form of frequency-dependent selection $\hat{s}(p)$ and the mutation rate $\hat{\mu}$ from time series of trait frequencies, by maximum likelihood (S1.1). We parameterize frequency dependence by assuming $s(p)$ is a piecewise-constant function (Fig. S1), which associates a selection coefficient $s_i$ with each frequency range (bin) $i$ with $p \in [l_i, u_i]$. This parameterization approximates a vast space of possible frequency-dependent growth laws. Maximizing likelihood gives equations for the selection parameters $\hat{s}_i$ that are separable from the mutation rate $\hat{\mu}$ and independent of population size, but inseparable from each other so that no analytic solution for the $\hat{s}_i$ exists. Instead, we iteratively approximate the maximum likelihood $\hat{s}_i$ to arbitrary precision by optimizing a convex surrogate minorant function (S1.10; code released publicly). And so we obtain a nonparametric approximation of $s(p)$; more data allows either finer frequency resolution at a given level of precision, or more precise estimates of selection at a given resolution of frequency bins.

We compute confidence intervals on parameters by two methods—one derived analytically from Fisher information and one derived empirically from an Efron bootstrap adapted for time series data (S1.6). We display only the more conservative, bootstrap confidence intervals, because these are both wider and less sensitive to model misspecification. We furthermore control for biases due to censorship of rare types (S1.7) and due to sampling error (S1.8) respectively by deriving analytic upper- and lower-bound imputations of missing data and inferring $\hat{s}(p)$ from a synthetic time series of samples from the static distribution of observed frequencies. Both biases primarily affect low frequencies. We also empirically estimate bias due to discrete time interval data (S2.1, Fig. 1b, Netherlands).

Frequency-dependent selection in baby names

Naming is a natural case study for frequency-dependent selection in cultural evolution. Whereas Galton, Lotka, and Fisher studied inheritance of family names as a model of extinction by stochastic drift, we study first names. First names rarely have observable lines of inheritance, and yet contemporary research has implicated drift as well as a diverse host of psychological and social forces in the dynamics of first names. This rich catalog includes novelty bias, immigration and assimilation, class imitation and aversion, trend momentum, phonological affects, and cultural broadcasts.

We examined frequency dependence in the dynamics of first names in the United States (US) using the Social Security Administration baby name database, which includes first name, birth year, and assigned sex of nearly all Social Security Card recipients born in the United States. We inferred the frequency-dependent growth curve $\hat{s}(p)$ (Fig. 1) from a time series beginning at the administration’s inception in 1935, using the 245 million individuals whose names occur in at least 1 in 10,000 births (Fig. 1b). By omitting names yet more rare, as well as any frequency bins with fewer than 5 names, we remove noise and bias that would otherwise arise from sampling or censorship in the US dataset.
Figure 1: Frequency-dependent selection on first names. Fitness is frequency-dependent (a) when the growth rate of a trait depends on the trait’s frequency $p$ in the population. Traits with log-fitness $s(p)$ above the mean selection coefficient $\bar{s}$ tend to increase in abundance, while those below the mean fitness tend to decrease. We infer frequency-dependent selection from time series of names given at birth (e: U.S. Social Security Administration database, 5% sample). A name’s fitness depends on its current frequency (b) in the United States, the Netherlands, France, and Norway, while any particular name (e.g. Sarah, François, Bjørn) may occupy different frequency bins and growth rates from year to year. Uncensored anonymized counts from the Netherlands allow us to probe any affects arising from temporal discretization, as well as study frequencies lower than the annual birth cohort size, by aggregating data into either 1-year or 5-year time intervals. All four countries show similar patterns of negative frequency-dependence (c), with an intercept at zero growth rate for names at frequencies between 8 and 32 births per 10,000 (vertical grey lines). Selection favoring names more rare than this intercept, and disfavoring names more common, corresponds to different slopes in the distribution of name frequencies (d), which features cusps near the points of zero growth. In all panels shaded boxes indicate frequency bin boundaries and bootstrap 95% confidence intervals (S1.6). Bins with fewer than 5 names or bias possibly exceeding 0.8%/year are omitted.

According to our maximum-likelihood inference, when a name is rare, at frequency near 1 in 10,000 births, it has an intrinsic growth rate of 1.4%/year whereas the most common names, above 1 in 100 births, decline at -1.6%/year (Fig. 1b). Between these two extremes, the growth rate of a name declines linearly with its log-frequency ($r^2=0.98$). The frequency of any particular name varies over time (such as “Sarah”, Fig. 1b), so the same name can be favored by selection at some times and disfavored at others.

Our inference of frequency-dependent selection on names, $\hat{s}(p)$, easily rejects neutrality, $s(p) \equiv 0$, with a $p$-value <0.0001, in contrast to prior studies that could not reject neutrality from the stationary distribution of name frequencies

Negative frequency dependence reflects what it means to be a name: a name’s value derives predominantly from its uniqueness. For example, parents are known to abandon names that are becoming too popular. In aggregate, this and many other psychological and social factors repress a name when it is common and promote it when rare.

Cross-cultural patterns of name dynamics and diversity

France, the Netherlands, and Norway also publish comprehensive time series of first names (Table S2), and we infer similar patterns of frequency-dependent selection despite the different names, naming conventions, languages, cultures, demographics, and population sizes across these countries (Fig. 1c-e, S2.1). The curve $\hat{s}(p)$ intersects zero growth at a frequency that is consistent across countries—between 8 and 32 in 10,000 births (Fig. 1c)—to within a factor of four (Fig. 1d), despite a nearly 70-fold difference in population sizes (Table S2). This means that different cultures have similar sensitivities to what specific frequencies make a name desirable or undesirable.
Figure 2: Growth laws for female, male, biblical, and non-biblical names in the United States. Frequency-dependent fitness differs between the subpopulations of names given to females and males (a) and between biblical and non-biblical names (b), with higher fitness among male and biblical names. The inferred frequency-dependent fitness for the entire population (black) is the weighted average fitness of its subpopulations. Lower growth rates for female names across all frequencies is consistent with dilution caused by higher rates of innovation among female names. Biblical names, by contrast, preclude innovation and they avoid dilution through higher intrinsic fitness, as evidenced by their inferred frequency-dependent growth law (b) and the enrichment of biblical names among top names (c).

The frequency where selection transitions from favoring to disfavoring names is further reflected in the stationary distribution of name frequencies—the diversity of names. Plotting the fraction of names that exceed a given frequency on log-log axes (Fig. 1d) reveals two distinct regimes punctuated by a cusp near the frequency of zero growth, across all four countries. The diversity of favored, rare names shows a clear power-law slope, whereas a steep cutoff occurs among the common, disfavored names. Prior studies have reported either a power law with a single slope or predicted two regimes, whereas here we confirm two distinct regimes that furthermore correspond to our inference of whether names are favored or disfavored by selection. Our inference uses time series data and a dynamical model, yet it explains general features of the frequency distribution of names averaged over time.

Gendered and biblical names: growth laws within subpopulations

Names given to males or females represent subpopulations that may differ in their growth rates and forms of frequency-dependence. By stipulation, however, our exchangeable model treats all types in the population uniformly. A modest extension to the model allows us to infer a frequency-dependent growth curve within a subpopulation of types. We simultaneously infer a single, time-independent “wildtype” fitness for the remainder of the population, which calibrates the zero point of growth rate. Separate inferences for mutually-exclusive subpopulations produce frequency-dependent growth laws for each subpopulation that are consistent with the growth law measured for the whole population as the weighted average of subpopulations. This protocol accurately reconstructs the form of frequency-dependent selection in subpopulations, even when subpopulations have radically different growth laws (Fig. S2).

Separating male and female persons in the US dataset—treating for example “Frances,M” and “Frances,F” as distinct names in different subpopulations—we find an appreciable difference in growth rates (~0.66%/year, Fig 2a). This fitness difference between male and female names is roughly constant across the full range of name frequencies (Pearson $\rho=0.40$, $p=0.33$). Of course the total number of male names cannot increase relative to female names over time because the ratio of female to male persons is constrained to roughly 1:1. And so the constant difference in growth rates between male and female names must be compensated by different rates of innovation: the lower growth rates of extant female names must be balanced by a greater influx and higher turnover of novel female names. The rate of innovation (mutation) affects what selection value corresponds to zero net growth (Eq. S19).
in S1.2) and hence displaces $s(p)$ uniformly across frequencies, as observed in Fig 2a.

There are 1.63 female names per male name in the dataset, compared to 0.98 female persons per male person. A range of mechanisms have been proposed to explain the greater diversity of female names, including a more diverse standing repertoire for recombination and spelling variation44,45, greater sensitivity to fads48, and gender-specific tastes in etymology and phonology52. Our result suggests that different innovation processes, rather than different dynamics, explain the elevated diversity of female names.

Biblical and non-biblical names also represent distinct subpopulations of names, and there are striking patterns in their overall frequencies over time45,53. Whereas some studies attribute the dynamics of biblical names to variation in religiosity per se53, associated for example with Catholicism54, others conclude that biblical names are subject to the same social pressures as the population of names as a whole45.

We infer that biblical names also experience negative frequency-dependent selection, and yet they enjoy substantially greater fitness than non-biblical names, across all frequencies (Fig. 2b). Since selection favors biblical names regardless of their frequency, we should expect to find enrichment for biblical names among the top names. Indeed we observe this enrichment: biblical names account for nearly 40% of names in the highest frequency bin compared to only 2% of names in the lowest frequency bin (Fig. 2). Enrichment also explains the reduced fitness advantage of biblical names relative to the whole population at higher frequencies (Fig. 2b), simply because the whole population includes those high fitness biblical names.

By extension, any idiosyncratic advantages—including biblical meaning or phonology51—are especially likely to predominate among names at the highest frequencies. And so, because our exchangeable model ignores idiosyncratic selective benefits, inferred selection among the top names represents a combination of the frequency-dependent disadvantage to any common name and frequency-independent advantage associated with those particular names.

**Frequency-dependent selection and novelty bias in dog breed preference**

Preferences—from movie genres to fashion trends—are among the earliest case studies of cultural evolution18. In particular, breed preferences among purebred dog collectors follow trends in popular culture55,56, even to the exclusion of the health or behavioral attributes of the dogs themselves9. And so the breed preference of a collector can be studied as a cultural trait9,55,56.

We infer the form of frequency-dependent selection $\hat{s}(p)$ in dog breed preferences (Fig. 3a) from a complete annual time series of purebred dog registrations with the American Kennel Club (AKC) from 1926 to 200557 encompassing over 50 million dogs (Fig. 3b, S2.2). We find strong negative frequency dependence—that rare breeds have higher growth rates on average than common ones (Fig. 3a)—indicating that the diversity of breeds is maintained by selection rather than drift and innovation alone56.

Yet selection on frequency per se cannot explain boom-bust cycles. The predictable pattern of rise and fall in breed preferences (Fig. 3c) implies that a type has different fitnesses for the same frequency at different times, which is incompatible with fitness determined by frequency alone. More generally, dynamics of cultural traits including names often feature boom-bust cycles58,59 and trend momentum60 that have been attributed to a preference for novelty11 or rapid abandonment of recent fads48.

Rather, we illustrate that frequency dependence and boom-bust cycles can both arise as joint consequences of an underlying mechanism of novelty bias. We simulate selection for novelty—a fundamentally non-exchangeable process—using a Wright-Fisher model in which each novel type enters the population at rate $\mu$ per capita per generation, and it has a yet greater fitness $\Delta s$ than the previous type (Fig. 3d). We then infer frequency-dependent selection $\hat{s}(p)$ from the simulation output and we choose parameters so that the inference from the output matches the inference from the AKC data. The resulting novelty bias simulations produce boom-bust cycles (Fig 3c) with timescale and amplitude similar to those in the AKC data (Fig 3b). Adjusting the parameters $\mu$ and $\Delta s$ while fixing the population size $N$ and drift rate $1/N_e$ to match the AKC data, we find good agreement between the two inferences (Fig. 3a) whenever $N\mu\Delta s$—the average increase in selective benefit per year
Figure 3: Frequency dependence in dog breeds We infer negative frequency-dependent growth (a, blue) in a time series (b) of purebred dog registrations in the American Kennel Club (AKC), comprising 153 distinct breeds over 80 years. The rarest breed registrations increase on average by 16%/year while the commonest slowly decline. Popular dog breeds are subject to fads: several breeds, such as Greyhound (a-b, purple) and Rottweiler (a-b, orange), cover the entire frequency range. Simulations of a novelty bias model display similar boom-bust cycles (c) and match the frequency dependence inferred from the AKC data (a, green) with parameters $N\mu\Delta s=0.01$, representing an annual rate of selective improvement of 1%/year. Note that mean frequency-dependent selection $\hat{s}(p)$ inferred by maximum likelihood from 500 replicate simulations of the novelty bias model (a, green) overlaps with the true average frequency-dependent selection $\bar{s}$ of the novelty bias model (a, brown). Novelty bias parameters (a,c): $\mu=0.00004, \Delta s=0.00021, N=1,435,737, N_e=50,000$.

Effective frequency-dependence

The dynamics of human culture or biological evolution are far too complex to be circumscribed by a single mathematical formulation. Indeed, in all the cases we investigate, we do not propose that selection is determined by frequency alone, as it is in the exchangeable model. Nonetheless, many complex mechanisms of evolution, such as novelty bias, associate selection with frequency well enough that biologists often conflate them with frequency-dependent selection.

We tease apart this conflation by introducing the concept of effective frequency-dependent selection. We define effective frequency-dependent selection—much like effective population size—as the form of frequency-dependent selection that best matches the idealised (exchangeable) population dynamics to the true (complex, non-exchangeable) population dynamics. For example, the novelty bias model induces a characteristic effective frequency dependence (Fig 3a) even though the model is not itself exchangeable.

In a case of mathematical serendipity, our inference procedure measures effective frequency dependence for any evolutionary process. Specifically, frequency dependent selection...
\( \hat{s}(p) \) inferred by maximum likelihood under the exchangeable model converges to the true, average selection pressure \( \bar{s}_i \) on types within a given frequency range \( p \in (l_i, u_i) \) (Fig. 3, S1.3). This correspondence holds for any underlying selection mechanism, exchangeable or otherwise, because the maximum-likelihood selection coefficients (Eq. S13) equal the observed average selection within frequency ranges. This result is serendipitous because typically there is little to be gleaned from parameters inferred under a misspecified model. But in our case, inferred frequency dependence is meaningful regardless.

Furthermore, effective frequency dependence is “unreasonably effective” in describing models far beyond its scope. For example, we fit parameters of the novelty bias model by matching only exchangeable properties of the empirical data—effective frequency dependence—and yet the chosen parameters also recapitulate the characteristically non-exchangeable boom-bust cycles. And so, effective frequency dependence retains sufficient information to discriminate amongst the vast space of all complex evolutionary processes.

Discussion

Frequency-dependent selection offers an exchangeable lens on complex population dynamics, by ignoring differences between types. The diversity of social and psychological forces that drive cultural evolution has stimulated an equally diverse collection of models, often developed in isolation. This rich library brings specificity and realism, while the exchangeable lens provides a common currency for comparison and calibration across domains of culture.

Although here we study culture, what we highlight is an important universal aspect of population dynamics. As genetic and phenotypic time series in biology are increasingly available, inferring frequency dependence in biological contexts can elucidate intraspecific social and interspecific ecological processes underlying evolutionary change. Pursuing this program within the framework of exchangeable models will enable a broad consilience across domains of evolutionary theory, from biology to culture.

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Supplementary Information

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S1 Inference

S1.1 Likelihood maximization

We describe how to infer the form of frequency dependence in an exchangeable-allele Wright-Fisher model, from time-series data containing the counts of alternative types over a sequence of generations. We assume that the fitness of any type at a frequency $p$ follows some function $w(p)$, where the fitness $w$ is related to the corresponding selection coefficient $s$ via $w = e^s$. The Wright-Fisher process allows us to write the transition probabilities for exchangeable alleles of fitness $w(p)$ explicitly. Our goal is to infer the fitness function $w(p)$ from the time series of observed transitions.

If we let $X_{i,t}$ be a vector random variable of the count of each type $i$ at time $t$ and let the index $i \in 1, ..., k$ run over existing types (temporarily disregarding mutation), the Wright-Fisher process evolves as the stochastic process

$$X_{t+1} | X_t \sim \text{Multinom}(N_{t+1}, [\pi_1, \pi_2, ..., \pi_k]), \quad \pi_i = \frac{w(X_{i,t}/N_t)X_{i,t}}{\sum_{i=1}^k w(X_{i,t}/N_t)X_{i,t}}.$$  \hspace{1cm} (S1)

That is, $X_{t+1}$ given $X_t$ is a multinomial sample of $N_{t+1}$ total individuals, each having the probability $\pi_i$ to be of type $i$. We note that $\pi_i$ here depends on $X_t$ only, since $N_t$ is the total population of types 1, ..., $k$ at time $t$, $N_t = \sum_{i=1}^k X_{i,t}$. The fitness $w(p)$ is proportional to the expected per-capita reproductive output of a type currently at frequency $p$ in the population prior to enforcing any carrying capacity. That is, $w(p)$ is proportional to the intrinsic growth rate and is hence a relative fitness, relative to an arbitrary (unknown) standard: the multinomial probabilities in Eq. (S1) are unchanged if we multiply the fitness function $w(p)$ by a constant or, equivalently, add a constant to the selection coefficients $s(p)$.

This exchangeable Wright-Fisher process thus specifies the probability of observed counts $x_0, ..., x_T$ over $T$ successive transitions between generations as the product of conditional probabilities

$$\Pr(X_T = x_T | X_{T-1} = x_{T-1}) \Pr(X_{T-1} = x_{T-1} | X_{T-2} = x_{T-2}) \cdots \Pr(X_1 = x_1 | X_0 = x_0).$$
Each conditional probability follows the multinomial distribution function, $f(x, \pi)$

$$\Pr(X_t = x_t | X_{t-1} = x_{t-1}) = f(x_t, \pi(x_{t-1})) = \frac{n_t!}{x_1,t! \cdots x_k,t!} \pi_1(x_{t-1})^{x_1,t} \cdots \pi_k(x_{t-1})^{x_k,t},$$

(S2)

where $n_t = \sum_{i=1}^{k} x_{i,t}$ is the total population size in generation $t$. We write $\pi(x_{t-1})$ to emphasize that $\pi_i$ depends on counts $x$ (Eq. S1). Viewed as a function of the observed counts $x$, $f$ is the distribution function, whereas as a function of parameters, $f$ is the likelihood function. Thus, given a realization of the process $x_t$, the likelihood is $\prod_{t=1}^{T} f(x_t, \pi(x_{t-1}))$. When $w(p) = w(p|\theta)$ can be parameterized by a vector of smoothly-varying parameters $\theta$, we can infer the parameters using the method of maximum likelihood, up to an arbitrary constant factor.

Finding the optimal parameter set, in particular when $w(p|\theta)$ may have many parameters, may be challenging. When the log-likelihood is concave, good optimization algorithms are available. The likelihood of a sample path is the product of the conditional likelihoods, and therefore the sample path log likelihood has the same concavity the conditional likelihood.

Taking the log of Eq. (S2) gives the log likelihood function

$$\mathcal{L}(x|\theta) = \ln n_t! - \sum_{i=1}^{k} \ln x_{i,t}! + \sum_{i=1}^{k} x_{i,t} \ln \pi_i(x_{t-1}, \theta),$$  

(S3)

where we now write $\pi_i(x_{t-1}, \theta)$ to emphasize that by Eq. S1 $\pi_i$ depends on both $x$ and on the parameters $\theta$ that determine the function $w(p)$. To compute the derivative of the log likelihood, we first write Eq. S3 in terms of $w$ and bundle terms that are not a function of the parameters into a constant $c$. As conditional likelihoods always involve a transition from one step to the next, we use a prime (‘) to denote the succeeding timestep, so that $x_i$ and $x_{i-1}$ are written $x'_i$ and $x_i$ respectively, and likewise $n' = n_t = \sum_{i=1}^{k} x'_i$ and $n = n_{t-1} = \sum_{i=1}^{k} x_i$:

$$\mathcal{L}(x'|\theta) = \ln n'! - \sum_{i=1}^{k} \ln x'_i! + \sum_{i=1}^{k} x'_i \ln \frac{w(x_i/n, \theta)}{\sum_j w(x_j/n, \theta)}
= c + \sum_{i=1}^{k} x'_i \ln \frac{w(x_i/n, \theta)}{\sum_j w(x_j/n, \theta)}
= c + \sum_{i=1}^{k} x'_i \ln w(x_i/n, \theta) - n' \ln \left( \sum_j w(x_j/n, \theta) \right),$$

(S4)

Setting the derivative of the log likelihood with respect to $\theta$ to zero gives local extrema of the likelihood. The derivative is

$$\frac{d}{d\theta} \left( \sum_i x'_i \ln w(x_i/n, \theta) - n' \ln \left( \sum_i w(x_i/n, \theta) \right) \right)
= \sum_i x'_i \frac{d}{d\theta} \frac{w(x_i/n, \theta)}{w(x'_i/n, \theta)} - n' \frac{\sum_i x'_i \frac{d}{d\theta} w(x_i/n, \theta)}{\sum_i w(x_i/n, \theta)}$$

and hence extrema exist when

$$\sum_i x'_i \frac{d}{d\theta} \frac{w(x_i/n, \theta)}{w(x'_i/n, \theta)} = n' \frac{\sum_i x'_i \frac{d}{d\theta} w(x_i/n, \theta)}{\sum_i w(x_i/n, \theta)}.$$

(S5)

We parameterize $w(p)$ by assuming that $w$ is a piecewise-constant function of $p$, where the parameters $\theta = \{s_d\}$, $d = 1, \ldots, D$ are constant selection coefficients $\{s_d\}$ associated with
Figure S1: We let \( w(p) \) be a piecewise constant function with discontinuities at \( b_d \), and selection coefficient \( s_d \) within each bin \( d \). We let \( B(p) \) indicate the index \( d \) such that \( p \in (l_d, u_d) = (b_d-1, b_d] \).

a set of frequency intervals \( \{ (l_d, u_d] \} \) that are mutually-exclusive and exhaustive over the domain \((0, 1] \) of \( w(p) \) (Fig. S1). Any given parameterization specifies \( D \) frequency bins with \( D-1 \) boundaries in \((0, 1) \) labeled \( b_1, ..., b_{D-1} \), so that

\[
w(p|s) = e^{s B(p)} = \begin{cases} 
  e^{s_1} & p \in (0, b_1] \\
  e^{s_2} & p \in (b_1, b_2] \\
  \vdots & \vdots \\
  e^{s_D} & p \in (b_{D-1}, 1] 
\end{cases}
\]  

(S6)

For notational simplicity we let \( b_D = 1 \) and \( b_0 = 0 \) so that \( (b_0, b_D] \) is the full domain of \( w(p) \), and we use \( B(p) \) to indicate the index \( d \) such that \( p \in (l_d, u_d) = (b_d-1, b_d] \). We thereby infer the most likely fitness of types within each \( s_d \) frequency interval.

This \( w(p) \) is a discrete frequency-dependent fitness function which is a good approximation to continuous functions given a sufficient number of bins. The bin boundaries themselves are an arbitrary choice and cannot be inferred using maximum likelihood. Using finer frequency intervals gives successively better approximations until too little data is available within each interval to get sufficiently precise parameter estimates. This piecewise constant approximation to the true relationship is analogous to image reconstruction: the resolution limit on frequency bins is analogous to the trade-off between spatial precision and noise in images.

What remains is to specialize the maximum-likelihood condition (Eq. S5) to our parameterization of \( w(p) \) (Eq. S6), to introduce mutation, and to solve for the maximum likelihood parameters given an observed time series.

We deal first with mutation. The frequency 0 is not in the domain of \( w(p) \). Types that are present in the current generation but were absent—i.e. at frequency 0—in the previous generation must have arrived through some process such as innovation or immigration. The infinite-alleles Wright-Fisher process introduces new mutants stochastically at a constant rate \( \mu \) per individual per generation. Each mutant is assumed to be of a completely new type and given a new type identity so as to begin at initial frequency \( 1/N \) where \( N \) is the total population size. In data, however, types not seen in the preceding generation may appear at any frequency. We call the total count of all such novel individuals appearing in a given generation \( m_t \). We identify these novel individuals with mutants in the infinite-alleles Wright-Fisher process, and we show how to produce a maximum-likelihood estimate \( \hat{\mu} \) of \( \mu \).

We call these types “mutants”, but this is only a shorthand: we interpret \( \mu \) to be the rate of individuals with novel type appearing at whatever initial frequency by whatever process (mutation, innovation, immigration, proliferation within the data collection interval, etc.), assumed to be independent of the current composition of the population. It is tempting in the context of this study to identify \( \hat{\mu} \) with an estimate of some rate of cultural innovation, but our \( \mu \) conflates many processes generating new types in a population—including simply recalling names from a bygone era.

We modify the conditional likelihood expression to accommodate mutation, incorporating \( m_t \) observed new mutants and the parameter \( \mu \). Again focusing on the transition from generation \( t-1 \) to \( t \), we use the prime notation (\( \prime \)) to denote the later generation, but in
so doing we take on a change in semantics: absent mutation, we denoted total population size at time \( t \) as \( n_t = n' = \sum_{i=1}^{k} x_i' \), where indices 1, ..., \( k \) enumerate the types present at time \( t - 1 \). When mutations occur, however, \( n_t \) cannot simultaneously represent both the total population size at time \( t \) and also the sum of preexisting types, because the latter may exceed the former. We choose to let \( n_t \) denote the total population size of all individuals, mutant or otherwise, and retain the definition \( n' = \sum_{i=1}^{k} x_i' \), so that \( n' \) counts those individuals at time \( t \) that arose from types present in the previous generation. We define \( m' = m_t \), and hence \( n_t = n' + m' \) is the total population size of all individuals at time \( t \), including both preexisting types and new mutants. The new multinomial conditional log likelihood for this transition between generations, analogous to Eq. S3, is given by

\[
L(x'|s, \mu, x) = \ln(n' + m')! - \ln m'! - \sum_{i=1}^{k} \ln x_i'! + m' \ln \mu + \sum_{i=1}^{k} x_i' \ln \left( \frac{(1 - \mu) x_i w(x_i/n)}{\sum_{j=1}^{k} x_j w(x_j/n)} \right) \tag{S7}
\]

The equivalence to Eq. S3 can be seen by imagining some \( x_0' = m' \) and a corresponding \( \pi_0 = \mu \), rewriting the sums from \( i = 0 \) to \( k \), and multiplying the \( \pi_{i \neq 0} \) by \( (1 - \mu) \) to retain unity in the sum of probabilities. After rearranging terms and simplifying,

\[
L(x'|s, \mu, x) = \ln(n' + m')! - \ln m'! - \sum_{i=1}^{k} \ln x_i'! + m' \ln \mu + \sum_{i=1}^{k} x_i' \ln(x_i w(x_i/n|\theta)) \tag{S8}
\]

Considering only terms involving \( s \), this log likelihood is equal to Eq. S4. The additional terms involving \( m' \) and \( \mu \) do not affect derivatives with respect to the parameters \( s \), and hence Eq. S3 applies with respect to those regardless of the presence or absence of mutation. The full set of parameters \( \theta \) however includes the selection coefficients for each frequency bin as well as the mutation rate, which we write \( \theta = (\mu, s_1, s_2, \ldots, s_D) \).

We maximize the likelihood by setting the derivatives with respect to all parameters equal to zero. This results in a system of equations. The equation for \( \mu \) does not involve any other parameters and thus \( \mu \) can be estimated separately.

\[
\frac{\partial}{\partial \mu} L = \frac{m'}{\mu} - \frac{n'}{1 - \mu} = 0, \tag{S9}
\]

This implies that the maximum-likelihood estimate \( \hat{\mu} = m'/(n' + m') \) is simply the observed fraction of mutants. Over the time series then, \( \frac{\partial}{\partial m} \sum_{t=1}^{T} L_t = 0 \) implies

\[
\hat{\mu} = \frac{\sum_{t=1}^{T} m_t}{\sum_{t=1}^{T} n_t}, \tag{S10}
\]

The best estimate of mutation rate per individual per generation is simply the observed fraction of mutants over the entire time series.

The condition for the maximum-likelihood parameter \( \{\hat{s}_d\} \), then, is only the set of equations \( \frac{\partial}{\partial s_d} L = 0 \) for all \( d \in \{1, ..., D\} \). Thankfully, the derivatives \( dw/d\theta \) that appear in Eq. S5 are simply:

\[
\frac{\partial}{\partial s_d} w(p) = \begin{cases} e^{s_d} & B(p) = d \\ 0 & \text{otherwise} \end{cases} \tag{S11}
\]

Hence we can rewrite Eq. S5 using Eq. S6 with \( w(x_i/n|\theta) = e^{s_d(x_i/n)} \), and include terms \( e^{s_d} \) for \( \frac{\partial}{\partial s_d} w(x_i/n|\theta) \) whenever \( x_i/n \) is in bin \( d \). The factors \( (\frac{\partial}{\partial s_d} w(x_i/n))/w(x_i/n) \) in the left side of Eq. S5 are 1 when \( B(x_i/n) = d \) and 0 otherwise: They serve only to indicate for what \( i \) to count \( x_i' \) in the sum. Writing the maximum likelihood equations then mostly involves
maximum-likelihood parameters (Eq. S12) is linear in \( e_n \) followed by

Alternatively stated: if each increment of the data were replaced by the same increment

estimates of total population size: The variance in frequency increments are ignored. This indicates that

counts to frequencies. Thus, the inference depends on the frequencies of types, but not the
texts. Second, the derivatives of likelihood do not depend on

useful since the mechanisms of mutation are often unknown or ill-defined in cultural con-
temporary and effective population sizes (by whatever means) are also inde-
pendent. Thus, changing timescales or population sizes (while suitably transforming units)
has no effect on the inference of \( s_d \) in the diffusion limit assuming time intervals are short.
Alternatively stated: if each increment of the data were replaced by the same increment
followed by \( n \) generations of neutral Wright-Fisher evolution, the expected value of the
estimators of \( s_d \) are unchanged.

For a single transition between subsequent generations, the system of equations for the
maximum-likelihood parameters (Eq. S12) is linear in \( e_s, \ldots, e_D \). Nonetheless, the system
of equations for the full time series (Eq. S13) is difficult to solve, numerically or otherwise,
primarily because all \( s_j \) appear in multiple different denominators on the right hand side,
which makes the equation for each \( s_j \) non-linearly dependent on all other \( s_j \) in the general
case.

To the system of equations (Eq. S13) we use an MM or “Minorize and Maximize” algo-
rithmic strategy [12]. The strategy is to replace the likelihood \( \mathcal{L}(s) \) of the parameter vector \( s \)
with a family of surrogate minorant functions \( g(s|x^{(i)}) \) where \( x^{(i)} \) is the \( i \)th iterate designed
to approximate the maximum likelihood estimate \( \hat{s} \) as \( i \) becomes large. The minorant needs
two properties: \( g(s|x^{(i)}) = \mathcal{L}(s^{(i)}) \) and \( g(s|x^{(i)}) \leq \mathcal{L}(s) \). The minorant is guaranteed to
be at most \( \mathcal{L} \) everywhere and to match \( \mathcal{L} \) and its derivatives with respect to \( s_d \) at the point
\( s^{(i)} \). The consequence is that either \( s^{(i)} \) is the optimum of \( \mathcal{L} \), in which case the derivatives of
\( g \) and \( \mathcal{L} \) at \( s^{(i)} \) are zero, or else, providing that \( g \) and \( \mathcal{L} \) are smooth, the derivative of \( g \) is non-zero and the optimum of \( g \) lies somewhere between \( g(s^{(i)}|s^{(i)}) \) and the optimum of \( \mathcal{L} \). If we chose a \( g \) that is itself easy to optimize, we can monotonically approach the optimum of
\( \mathcal{L} \) by finding the optimum \( s \) for each minorant \( g(s|x^{(i)}) \) and choosing each successive optimum to be \( s^{(i+1)} \). Each iteration finds a parameter set \( s^{(i)} \) that closes the gap between
\( \mathcal{L}(s^{(i)}) \) and the true optimum of \( \mathcal{L}(\hat{s}) \).

The strategy requires an appropriate minorant. Many minorants are possible, such as a
quadratic approximation [8]. Examining the likelihood function Eq. S4 we notice that the
very last term,

\[ -n' \ln \left( \sum x_i w(x_i/n) \right) = -n' \ln \left( \sum x_i e^{s_{B(x_i/n)}} \right) \]
involves a sum inside the log, which gives rise to the troublesome denominator. This term is a convex function of \( w(p|s) \) and hence it is minorized by its linear-order Taylor expansion in \( w \) around \( w(p|s^{(i)}) \):

\[
- n' \ln \left( \sum_j x_j e^{s_j^{(i)} B(x_j/n)} \right) - n' \sum_{d=1}^D \left( e^{s_d} - e^{s_d^{(i)}} \right) \frac{\partial}{\partial e^{s_d}} \left[ \ln \left( \sum_{j=1}^k x_j e^{s_j B(x_j/n)} \right) \right]_{s=s^{(i)}}
\]

(S14)

Substituting this linear minorant for the convex term in Eq. (S4) produces a surrogate like-

\[
\text{produces the next iterate:}
\]

\[
g(s|s^{(i)}) = c + \sum_{d=1}^D \left[ \sum_{j:B(x_j/n)=d} x_j' s_d - n' e^{s_d} \frac{\sum_{j:B(x_j/n)=d} x_j}{\sum_{j=1}^k x_j e^{s_j B(x_j/n)}} \right]
\]

(S15)

The optimum \( s \), obtained by setting derivatives with respect to \( s_d \) to zero, is then given by the system of equations analogous to Eq. (S12):

\[
\sum_{j:B(x_j/n)=d} x_j' = n' e^{s_d} \left( \frac{\sum_{j:B(x_j/n)=d} x_j}{\sum_{j=1}^k x_j e^{s_j B(x_j/n)}} \right), \quad d \in \{1, ..., D\}.
\]

(S16)

Likewise, because a sum of conditional log likelihoods is minorized by a sum of their respective minorants, Eq. (S13) has its analog, for \( d \in \{1, ..., D\} \),

\[
\sum_{t=1}^T \left( \sum_{j:B(x_j,t-1/n_t-1)=d} x_j,t \right) = e^{s_d} \sum_{t=1}^T \left[ (n_t - m_t) \left( \frac{\sum_{j:B(x_j,t-1/n_t-1)=d} x_j,t-1}{\sum_{j=1}^k x_j,t-1 e^{s_j B(x_j,t-1/n_t-1)}} \right) \right].
\]

(S17)

In fact, the only difference between the systems Eqs. (S13) and (S17) is that the \( s_j \) in the denominator of the right side have been replaced by \( s_j^{(i)} \). This difference is crucial, however, as the solution for \( \{s_d\} \) in the system of equations Eq. (S17) is now trivial to solve, which produces the next iterate:

\[
s_d^{(i+1)} = \ln \left[ \sum_{t=1}^T \left( \sum_{j:B(x_j,t-1/n_t-1)=d} x_j,t \right) \right] - \ln \left[ \sum_{t=1}^T \left[ (n_t - m_t) \left( \frac{\sum_{j:B(x_j,t-1/n_t-1)=d} x_j,t-1}{\sum_{j=1}^k x_j,t-1 e^{s_j B(x_j,t-1/n_t-1)}} \right) \right) \right].
\]

(S18)

Here the right side of the equation involves only the previous iterate \( s^{(i)} \).

We initialize our MM algorithm by setting \( s_d^{(0)} = 0 \) for \( d \in \{1, ..., D\} \) and we iterate until no further change in \( s^{(i)} \) is achieved between iterations. That is, the derivative of the minorant at \( s^{(i)} \) has reached approximately zero. At this point, the minorant and \( L \) are both maximized.

As noted previously, the likelihood of the data are unchanged by adding a constant to the selection coefficient \( s_d \) in each frequency bin \( d \). We enforce the condition \( \sum_{d=1}^D s_d = 0 \) to achieve a unique maximum likelihood parameter set. We enforce the constraint by adding the appropriate constant at each iteration. (Absent any enforcement of the constraint, the MM iterates settle on an arbitrary value of \( \tilde{s} \) that indeed satisfies Eq. (S13) but the particular value \( \tilde{s} \) depends on the initial condition \( s^{(0)} \).)

### S1.2 Replacement fitness

In Figure 1 and elsewhere, we compute the replacement fitness, \( \tilde{w} \). The replacement fitness is a property of a time series, and it is the fitness, which, if a type with that (constant,
frequency-independent) fitness were introduced at the beginning of the time series, its expected frequency at the end of the time series would equal its initial frequency.

The population average fitness over time for generations \( t \in \{1, ..., T\} \) and counts \( x_{i,t} \) of types \( i \in \{1, ..., k_t\} \) at generation \( t \) is then

\[
\bar{s} = \left( \frac{1}{T} \right) \sum_{t=1}^{T} \log \left( \mu + \sum_{i=1}^{k_t} \frac{x_{i,t}}{n_t} e^{s_B(x_{i,t}/n_t)} \right).
\] (S19)

### S1.3 Average frequency-dependent selection

The average frequency-dependent selection can be computed from a realization of an evolutionary process when the fitness \( w_{i,t} \) of each type \( i \) is known, as in a simulation. Choosing frequency ranges as in Fig. [S1] the mean absolute fitness of types within a range \( d \) is their expected per capita total reproductive output over time,

\[
\bar{w}_d = \frac{\sum_t \sum_{i:B(x_i/n)=d} w_{i,t} x_{i,t}}{\sum_t \sum_{i:B(x_i/n)=d} x_{i,t}}
\] (S20)

The average selection within bin \( d \), \( \bar{s}_d \) is simply its log. In order to set the zero point of selection relative to the replacement fitness, we also subtract the replacement fitness, hence,

\[
\bar{s}_d = \ln \bar{w}_d - \bar{s}
\] (S21)

### S1.4 Wildtype fitness

Sometimes we do not know exact counts of every type in the population or we want to consider frequency-dependent fitness only within a subpopulation such as biblical or non-biblical names. In these cases we make use of a wildtype subpopulation with associated average fitness \( s_w \), and treat all types residing in that subpopulation (if they are known) as residing in their own bin regardless of their frequency. When counts are censored, for example, we do not know exact counts for some types, but we may still know or estimate the total number of censored individuals. Since the sum of types in a given bin in Eqs. [S13] is the same whether these types are labeled individually or all belong to an aggregate type, we rewrite Eqs. [S13] in terms of aggregate sums of wildtype individuals \( w_t \) and \( w'_{t} \) as follows for frequency range \( d \),

\[
\sum_{t=1}^{T} \left( \sum_{i:B(x_i,t-1/n_{t-1})=d} x_{i,t} \right) = \sum_{t=1}^{T} \left( n_t - m_t \right) \left( \frac{\sum_{i:B(x_i,t-1/n_{t-1})=d} e^{s_d x_{i,t-1}}}{w_{t-1} e^{s_w} + \sum_{j=1}^{k} e^{s_B(x_j,t-1/n_{t-1}) x_{j,t-1}}} \right)
\] (S22)

taken simultaneously with the following equation for the wildtype fitness \( s_w \),

\[
\sum_{t=1}^{T} (w'_{t-1}) = \sum_{t=1}^{T} \left( n_t - m_t \right) \left( \frac{e^{s_w} w_{t-1}}{w_{t-1} e^{s_w} + \sum_{j=1}^{k} e^{s_B(x_j,t-1/n_{t-1}) x_{j,t-1}}} \right).
\] (S23)

The wildtype aggregation \( w_{t-1} \) is the total number of wildtype individuals at generation \( t-1 \), and \( w'_{t-1} \) is the total number of generation-\( t \) progeny of wildtype individuals in generation \( t-1 \). One might expect \( w'_{t-1} \) to equal \( w_t \), yet the two accountings may differ. As an example suppose we let the wildtype represent types at frequency below \( f \); if a type transitions from below \( f \) at generation \( t-1 \) to above \( f \) at generation \( t \), it contributes to \( w_{t-1} \) and \( w'_{t-1} \) but not to \( w_t \). The aggregates support an exact analogy between the wildtype counts \( w_t \), wildtype progeny \( w'_{t} \) and wildtype fitness \( s_w \) and the counts, \( \sum_{i:B(x_i,t-1/n_{t-1})=d} x_{i,t-1} \), progeny \( \sum_{i:B(x_i,t-1/n_{t-1})=d} x_{i,t} \), and fitness \( s_d \) of frequency-range \( d \). Thus the wildtype aggregate acts as a frequency-independent bin, and we estimate its fitness in the same way.
Figure S2: **Inferring subpopulation frequency-dependent fitness from simulation.** We recover subpopulation frequency-dependent fitness from a simulated population composed of two subpopulations: a minority type (one third of mutants) with quadratic frequency-dependent fitness \( w(p) = 1 - 0.01(\log_{10} p + 4)(\log_{10} p + 2) \), and a majority type (two thirds of mutants) with linear frequency-dependent fitness \( w(p) = 1.012 - 0.006(\log_{10} p + 4) \). Both forms have a zero-growth intercept at \( 10^{-2} \). We simulate a Wright-Fisher process with fixed population size 20,000 and mutation rate 0.0003 for 50,000 generations after 20,000 generations of burn-in from a monomorphic initial population. Confidence bands are analytic 95% confidence intervals derived from Fisher information [S1.6].

### S1.5 Subpopulations

Wildtype aggregations [S1.4] also allow measurement of frequency-dependent selection among subpopulations. By treating all individuals who are not part of the focal subpopulation as part of the wildtype aggregation, those individuals do not contribute to inferred frequency-dependent selection, but do contribute to replacement fitness. Hence separate estimates for multiple mutually-exclusive subpopulations will be calibrated against the same replacement fitness as demonstrated in Fig S2.

### S1.6 Confidence intervals

We use two confidence intervals (CIs) in this study: a CI derived from the model and a CI based on a bootstrap. The model CI is an accurate theoretical prediction of the variance on the estimator subject to the assumption that the data is generated by the model. The bootstrap CI is 2.5% to 97.5% quantiles of a non-parametric bootstrap that generates an empirical distribution of the estimator by resampling the underlying data. A bootstrap
CI makes no assumption that the data are generated from the assumed model, but does assume that a resampling scheme is available that generates equally probable samples, such as multinomially resampling the observed dataset. Either of these assumptions may fail in practice. Corroboration between the two CIs, as we observe, supports the accuracy of the model and the underlying assumptions. When the CIs disagree, the bootstrap CI is more conservative, as it accounts for some failures of the model to describe the data.

For the large samples used to infer dog breeds and baby names, we use model confidence intervals on parameter inferences computed using the observed Fisher information, a measure of the curvature of the likelihood function at its maximum. With an identifiable parameter in the limit of many independent observations, the log-likelihood surface is approximately parabolic near its maximum. The observed information is the matrix of second partial derivatives of the likelihood function (Hessian matrix), evaluated at the most likely parameters, and its inverse is the variance-covariance matrix of the estimators \( \{ \hat{s}_d \} \). We compute 95% confidence intervals on each parameter as \( 1.96 \sigma_{\hat{s}_d} \), where \( \sigma_{\hat{s}_d} \) is simply the square root of the diagonal elements in the observed information matrix. As noted above, we enforce the relationship \( \sum_{d=1}^{D} \hat{s}_d = 0 \) among the inferred selection coefficients. And so, in practice, the Hessian has dimensions \( (D - 1) \times (D - 1) \), corresponding to \( s_1, \ldots, s_{D-1} \). We compute the corresponding variance in the estimator \( \hat{s}_D \) using the relationship \( \text{var}(\hat{s}_D) = \sum_{d=1}^{D-1} \text{var}(\hat{s}_d) + 2 \sum_{0 < e < d < D} \text{covar}(\hat{s}_e, \hat{s}_d) \).

We verified the accuracy of our parametric confidence intervals by simulation, using a parametric bootstrap. In particular, we simulated the model using US inferred parameters to generate samples equal in size to our data, and we verified that the 95% confidence intervals derived from observed Fisher information include the true parameters of the simulations 95% of the time after 1,000 trials, within binomial error.

We compute bootstrap CIs by resampling transitions within the time series. Bootstraps that accommodate the dependence relationships that may be present in time series is an open-ended topic, because generally there is no resampling scheme that logically guarantees resampled data to be equiprobable under the true generating process, in contrast to the bootstrap argument for independent samples. Nonetheless, in our case, the likelihood calculation sums over observations and expectations of change from one timestep to the next, and it is these transitions that are assumed to be independent across time periods and approximately independent between types. Unaccounted dependence between observations enters by either failures of the Markovian assumption in the true generating process, or by effects of competition between types induced by finite population size. We resample in a way that approximates independence and roughly preserves population size so that resampled transitions have similar frequencies to the originals.

We resample a given timestep by choosing at each timestep transitions \( x_i \to x'_i \) from that timestep in the data uniformly with replacement. We determine the number of transitions to include at each timestep by iteratively including another transition sample with probability \( \max(1, p - c/e - c) \) where \( c \) is population size of the types included thus far, \( p \) is the observed population size in the original data, and \( e \) is the expected population size increase by including one more transition sample. This guarantees that the expected resampled population size is equal to the observed population size, but allows statistical variation in population size from generation to generation. This resampling scheme is equivalent to a multinomial resampling of independent observations which accounts for robustness of the estimator to sampling noise, but also preserves the frequency interpretation of the original count data. The frequency associated with a given count is allowed to vary around its expectation in the bootstrap, and thus the bootstrap also represents robustness of the estimator to the inclusion or omission of observations due to sampling of the data, since such sampling omissions would cause the frequencies in observed data to fluctuate. The bootstrap CIs are conservative estimates of the true 95% CI.
S1.7 Accounting for Censorship

We might naively assume that time series are complete and uncensored. In the case of baby names however, most datasets censor annual counts below a certain threshold. In the United States (US), for example, the Social Security Administration censors, each year, any name that occurred fewer than five times. To be conservative with respect to biases due to censorship, we do not calculate or report selection coefficients for frequencies so small that they would correspond to censored counts or counts less than one for any generation in a time series. This frequency is

\[ f_{\text{min},t} = \max_{x} f_{\text{min},t} \]

where \( f_{\text{min},t} \) is the minimum frequency that would still be rounded to an uncensored count at generation \( t \), that is \( f_{\text{min},t} = c - 0.5/n_t \) where \( c \) is the minimum uncensored count (e.g. \( c = 5 \) for US or \( c = 1 \) if there is no censorship).

We do not ascribe counts at frequency below \( f_{\text{min}} \) to any frequency range, ascribing them instead to the wildtype aggregation (See S1.4). We count types at frequency below \( f_{\text{min}} \) among the wildtype—that is the sum \( w_{t-1} \) includes all counts \( x_{i,t-1} \) of types \( i \) existing in the data at generation \( t - 1 \) such that \( x_{i,t-1}/n_{t-1} < f_{\text{min}} \). Likewise \( w'_{t-1} \) includes both progeny of those wildtype individuals as well as the total count \( m_t \)—the sum of all types that did not appear in the data in generation \( t - 1 \)—which may be either mutant/immigrant types or progeny of unobserved types. Censorship therefore conflates true “mutants” with progeny of types at too low frequency to observe. This entails a new interpretation of mutation: rather than consider types appearing for the first time in the dataset as mutants arising from count zero, we simply consider them as types arising from some frequency too low to be observed in the data. Thus the wildtype fitness \( s_w \) accounts for the relative competitiveness (growth rate) of mutants, migrants or innovations as well as the progeny of types of unknown frequency or frequency below \( f_{\text{min}} \). Hence no mutation term enters the replacement fitness calculation (Eq. S19) because the affect of mutation on replacement fitness is subsumed into the contribution of the average fitness \( s_w \) of wildtype individuals.

Censorship also biases inferred selection coefficients for frequency ranges above \( f_{\text{min}} \), because transitions from a recordable frequency \( x > f_{\text{min}} \) to a lower frequency may not be representable in the data or may be censored, whereas transitions from \( x \) to a higher frequency are always recorded. The consequence for the associated selection coefficient depends on our interpretation of types that disappear from observation. If we “pessimistically” interpret the disappearance of a type from the data as a transition from frequency \( x \) to frequency 0, this negatively biases the associated selection coefficient by substituting zero for its true frequency, which could be anywhere between zero and the minimum observable frequency. This pessimistic interpretation provides a lower bound on the inferred selection coefficient associated with frequency \( x \). The corresponding “optimistic” interpretation or upper bound imputes the disappearance of a type as a transition to the minimum uncensored count—guaranteed to be greater than the maximum unobservable frequency.

We combine these upper and lower bound interpretations for individual transitions to produce “optimistic” and “pessimistic” interpretations of the full frequency-dependent selection curve by interpreting all partially observed transitions either optimistically or pessimistically. These interpretations are not strict upper or lower bounds on the selection coefficients per se, because transitions do not affect selection coefficients superpositively: an upper-bound interpretation of a transition from frequency \( x \) may lower the selection coefficient for frequency \( y \neq x \). However, because the dependence between inferences at different frequencies is typically weak, we treat the optimistic and pessimistic interpretations as approximate upper and lower bounds on all selection coefficients.

To compute the optimistic and pessimistic interpretations of the censored counts, we adjust Eq. [S13] to account for types at frequency below \( f_{\text{min}} \) as wildtype and to impute pessimistic and optimistic type counts. We use the following expression, which differs from Eq. S13 in that \( m_t \) is subsumed into \( w'_t \), \( n_t \) has been replaced with \( \hat{n}_t \), and some \( x_{i,t} \) have
been replaced with \( \hat{x}_{i,t} \) as described below:

\[
\sum_{t=1}^{T} \left( \sum_{i:B(x_{i,t-1}/n_{t-1})=d} \hat{x}_{i,t} \right) = \sum_{t=1}^{T} \left[ \hat{n}_{t} \left( \frac{\sum_{i:B(x_{i,t-1}/n_{t-1})=d} e^{s_{w}x_{i,t-1}}}{w_{t-1}e^{s_{w}} + e^{s_{w}}x_{i,t-1}} \right) \right]
\]

taken simultaneously with the following equation for the wildtype fitness \( s_{w} \),

\[
\sum_{t=1}^{T} (w_{t-1}) = \sum_{t=1}^{T} \left[ \hat{n}_{t} \left( \frac{e^{s_{w}w_{t-1}}}{w_{t-1}e^{s_{w}} + e^{s_{w}}x_{i,t-1}} \right) \right].
\]

The hatted quantities differ from what they replace as follows. The \( \hat{n}_{t} \) denotes the imputed total population size including individuals that are censored from the data, either by including known aggregate censored counts, independent measurements of total population size, or by imputing the full, uncensored population size. The \( \hat{w}_{t-1} \) is the imputed count that depends whether we compute the optimistic or pessimistic imputation. Under the pessimistic imputation, \( \hat{x}_{i,t} = x_{i,t} = 0 \). Under the optimistic imputation, \( \hat{x}_{i,t} = c \) where \( c \) is the minimum uncensored count possible in the dataset at that generation. It must be the case for all \( t \) that

\[
w'_{t-1} + \sum_{d=1}^{k_{t}} \sum_{i:B(x_{i,t-1}/n_{t-1})=d} \hat{x}_{i,t} = \hat{n}_{t},
\]

where \( k_{t} \) is the number of types present in data at time \( t \). We use this equation to define \( w'_{t-1} \) in terms of \( \hat{n}_{t} \) and the \( \hat{x}_{i,t} \). It follows that

\[
w'_{t-1} > \sum_{i: \hat{x}_{i,t}/\hat{n}_{t} < f_{min}} \hat{x}_{i,t}
\]

for types \( i \) occurring in the data. The range of the sum, the types \( i : \hat{x}_{i,t}/\hat{n}_{t} < f_{min} \), is the exact complement of types assigned to any frequency bin among types present in the data at generation \( t \). Furthermore,

\[
w_{t-1} = \sum_{j=1}^{k_{t-1}} x_{j,t-1} = \hat{n}_{t-1},
\]

and hence we use this as a definition of \( w_{t-1} \) in terms of \( \hat{n}_{t-1} \) and types that appear in the data at frequencies greater than \( f_{min} \). Hence \( w_{t-1} \) count both types that appear in the data at frequencies below \( f_{min} \) and types that do not appear in the dataset at all.

The two interpretations of the missing data give high and low estimates for selection coefficients on rare types. However, the fitness ascribed to rare types affects replacement fitness to some extent, so the optimistic estimate for rare types often leads to slightly lower estimates for common types through increasing the replacement fitness. In practice we use the spread between the estimates across the plotted region as a measurement of potential bias due to censorship and conflation of mutants with offspring of low-frequency types.

### S1.8 Sampling biases

The real process of naming and the Wright-Fisher process involve similar sampling noise, but a subtle discrepancy in the noise structure can causes bias in estimates, particularly at low frequencies. In the Wright-Fisher process, sampling noise (variance in frequencies from generation to generation) is exactly the multinomial variance due to sampling with replacement from the types present in the previous generation. The real process however samples names not strictly from the previous generation, but from some larger, unobserved population of names in an evolving cultural milieu. The discrepancy sometimes causes measurable bias in estimated selection coefficients, particularly frequencies corresponding to
low absolute counts. For example, the underlying Wright-Fisher process assumes exact lineal continuity from generation to generation, such as would be the case with last names or genes attributable to a particular parent. First names, rather, are copied from many sources, including bygone generations. Hence, some sequences that occur in the data are impossible under the Wright-Fisher process, such as when a name apparently goes extinct then reappears. Aside from being of statistical interest, this very discrepancy has interesting philosophical and scientific implications which we discuss at the end of this section.

We control for this bias by constructing time series of samples in which the only change from generation to generation is sampling noise, then we infer frequency-dependent selection from the time series of samples. First, we construct a fixed, time-independent metapopulation composed of all counts of all types summed over the duration of the dataset. Then we construct an artificial time series based on repeated samples with replacement from the metapopulation, matching population size to the data each generation. The average frequency of every type at every generation in the time series of samples is just its frequency in the metapopulation, and therefore no type changes frequency over time on average. Hence, in principle, there can be no selection and no frequency dependent growth. We then infer frequency-dependent selection in this time series of samples and take the magnitude of departure from neutrality to estimate the magnitude of potential bias. We typically find substantial bias at low frequencies where binomial sampling noise predominates.

Inferred frequency dependence in the time series of samples is possible because of apparent growth or decline from generation to generation due to fluctuations in sampled counts: If a type happens to be sampled below its frequency in the metapopulation, it appears to grow on average in the next generation, and the opposite occurs if it is sampled above its true frequency. Typically, these generation-to-generation fluctuations cancel over time and the inference converges to zero selection. However, in certain circumstances cancellation does not occur. For example, when a type appears to go extinct and then reappears, its decrease to extinction registers as negative selection and whereas its subsequent increases in registers as mutation or immigration rather than positive selection, causing drastic bias towards negative selection. A qualitatively similar phenomenon occurs if any type fluctuates below or above a bin boundary from generation to generation. The likelihood of these occurrences diminishes as sampling variance decreases with higher counts.

The net effect of sampling bias depends on the total population size, the bin boundaries, and the distribution of type frequencies. We do not attempt to predict the bias analytically. Instead we simply infer frequency dependence in the resampled time series to determine at what frequencies this bias exists. Experimentally, the bias typically only exists at frequencies corresponding to low counts, with the exact frequencies affected varying by dataset (Fig S3).

Finally, differences between cultural and genetic evolution spurred debate about how far a cultural Darwinian metaphor can be carried. Chief among the differences are starkly contrasting mechanisms of inheritance. Extinctions of species and genes are permanent, whereas languages with no speakers have been resurrected, leading to complications in interpreting “extinction” of cultural traits. Whereas family names and lineages may go extinct, a first name, word or language may persist in a cultural repertoire long after its last recorded instance in any dataset. The sampling bias we observe in names is instructive in exactly to what degree these differences are relevant to population-level change. On the one hand, the data manifestly violates the Wright-Fisher process because even a complete birth cohort of names is still a sample from a larger cultural repertoire, and absence of a name from one birth cohort does not imply absence in a subsequent cohort. On the other hand, the differences are negligible above a certain frequency and the dynamics of name frequencies can be meaningfully treated as a Wright-Fisher diffusion. The differences confuse measurements of mutation and extinction, but in measuring frequency-dependent selection, the discrepancies between cultural and genetic models only matter near the boundary at 0 frequency, where even alternative population-genetic models often behave differently.

S12
Table S1: Name dataset summary. For each name dataset used, the years, total number
of individuals, inferred variance-effective population sizes $\hat{N}_e$ and $\hat{N}_{e,s=0}$ assuming $s(p) = 0$ computed from model residuals, the level or type of censorship, the maximum sampling bias within in plotted range (in %/year), and the maximum censorship bias within the plotted range (in %/year).

S1.9 Inferring $N_e$

Our primary concern thus far has been estimating fitness as a function of frequency, which determines the mean change (advection) in the diffusion equation. The diffusion term is also of interest. In the diffusion limit of the Wright-Fisher process, the diffusion term is $(1/2) \partial^2/\partial x^2(x(1-x)/N)\phi(x,t)$, where $N$ is the number of allele copies in the Wright-Fisher process and $\phi(x,t)$ is the probability density at frequency $x$ at time $t$. The coefficient $x(1-x)/N$ describes that variance in gene frequency accrues at a rate of one binomial sampling per generation, and has the units of a transport coefficient: frequency $^2$/time. The parameter $N$ represents the variance effective population size, and it equals the census population size (or its geometric mean if it fluctuates) when one round of random sampling (a single multinomial draw) occurs at each time interval, $g$, i.e., one generation. For short time intervals, variance accrues linearly in time in the diffusion equation, and so if sampling is conducted at a different interval $g'$, $N'$ will be rescaled proportionately such that $g/g' = N'/N$. Thus, at sampling interval $g$ and census population size $N$, if the inferred effective population size $N_e$ differs from $N$, then there is an effective generation time $g_e = gN/N_e$ which is the time for the diffusion to accrue the same variance as one Wright-Fisher generation—one multinomial sample of the full census population.

We infer $N_e$ by rescaling frequency increments in order to produce homoscedastic updates under the inferred model parameters. If $r_i$ are the residuals of the data, $r_i = x_i - e_i$, where $x_i$ are the data and $e_i$ are the expectations under the model, then the rescaled increments are

$$Y_i = \frac{r_i}{\sqrt{x_i(1-x_i)}}.$$ (S24)

The rescaled increments $Y_i$ have variance $1/N_e$ per generation, so $N_e = 1/S$ where $S$ is the sample variance of the $Y_i$.

We estimate the effective population size $N_e$ and a generation time for baby names in each country in Table S2, where the generation time represents the characteristic timescale on which complete mixing of names occurs.

S2 Data Handling and Error Estimation

S2.1 Names

For United States baby names, we obtained public data from the United States Social Security Administration database of first names (https://www.ssa.gov/OACT/babynames/) 1880-2018. We omitted nine high frequency names that clearly resulted from coding errors around 1985 such as “Christop,M” and “Infant,F”. We omitted data up to and including 1935 as non-representative of a complete population of individuals. Births in the database that occur prior to 1935 represent cards issued to children and adults, as opposed to the post-1935 practice of issuing cards at birth. Hence the data prior to 1935 are incomplete
and contain unrealistically small birth cohorts. We consider as distinct names any spelling variants or the identical spelling in persons of different sex. The dataset indicates birth sex as a suffix on the name (either “M” or “F”). We conducted the inference considering each annual birth cohort to be a generation of the Wright-Fisher process, and infer parameters for \( s(p) \) composed of logarithmically increasing frequency ranges (bins) starting from 0.0001-0.0002 with bin boundaries increasing by powers of two (0.0001, 0.0002, 0.0004, etc.) following Hahn and Bentley\(^2\). We additionally infer but do not report fitness parameters for names more rare than 0.0001 whose frequency may or may not be known as described below.

The US data censors counts below 5. Hence, computing an accurate mutation rate is impossible and some fraction of individuals are missing (censored) from the dataset. To account for unobserved individuals, we conduct the inference using a frequency-independent wildtype fitness for censored, mutant and low-frequency types \( S_{1.4} \). We guess the fraction of missing individuals in the time series by imputing a \( \text{CENSORED} \) type which always counts 5% of the sum of the uncensored population each year. We derived the number 5% from the French dataset, in which aggregate counts of censored individuals are listed explicitly and the fraction of counts below 5 is known to be 4.5%. In the US dataset the true count of names at frequency below \( f_{\text{min}} \) (censored and uncensored) far exceed the sum of those names that appear uncensored in the data below \( f_{\text{min}} \). As described in S1.7, we pool the \( \text{CENSORED} \) type together with uncensored counts less than the maximum censored frequency \( f_{\text{min}}=2.1\times10^{-6} \) into the wildtype subpopulation. The inferred wildtype fitness explicitly conflates immigrant types, mutant types, and progeny of types with censored counts into an average growth rate of all unaccounted types. This wildtype fitness is necessary to compute the replacement fitness or zero point of growth but otherwise has no affect on reported results. The error in replacement fitness due to censorship and conflation of mutants with progeny of unobserved types is measured in the spread between optimistic and pessimistic selection coefficients at high frequencies and reported below.

We controlled for sampling bias by constructing time series of samples from the time-independent distribution of name frequencies as described in S1.8. The inference from this synthetic time series (Fig. S3) measures the magnitude of possible bias due to sampling unaccounted in the Wright-Fisher process.

At frequencies greater than 0.0001 in the US inference, censorship bias affects plotted frequencies by at most 0.06%/year and sampling bias by at most 0.08%/year although frequencies less than 0.0001 were affected by both censorship bias (S1.7) and sampling bias (S1.8, Fig. S3). Hence, we do not report inferred fitnesses for names below frequency 0.0001.

We further acquired baby name data from France 1900-2018 (Insee Fichier des prénoms\(^7\), retrieved July 3, 2020) and Norway 1880-2019 (Statistics Norway Names STATBANK\(^7\), retrieved Aug 18, 2020). Additionally we received complete, uncensored counts from a name corpus\(^23\) of the Netherlands 1946-2015 anonymized by Gerrit Bloothooft of Meertens Instituut and communicated by email. In France data, we ignored inexhaustive data prior to 1946 as indicated in the file metadata. France censors names that do not occur at least 20 times since 1946 and names that occur less than 3 times in any given year, but lists the totals of censored counts in years XXXX and types _PRENOMS_RARES_. We incorporated the censored counts into a wildtype aggregation with counts below \( f_{\text{min}}=3.4\times10^{-6} \), as with the US inference (S1.7), distributing the counts of unknown year uniformly across the dataset. In Norway data, we ignored records prior to 1946 because many contained missing values. Counts less than 4 are censored in Norway, so we again assumed 5% of the data to be censored in each year and incorporated the imputed censored counts into the wildtype aggregate of types below \( f_{\text{min}}=7.8\times10^{-5} \).

We excluded from plots any bins with less than 5 types or censorship or sampling bias exceeding 0.8%. Censorship bias in France and Norway was minimal except in the rarest frequencies in Norway, but sampling bias was substantial in both Norway and the Netherlands due to their small sizes. Hence, we first excluded any frequency bins for which the sampling bias control exceeded 0.8%/year (Fig. S3) with the exception of the highest-frequency bin in Norway. In the remaining (plotted) bins in all countries, censorship bias (as measured by
Figure S3: **Sampling bias controls by country.** Inference from synthetic time series composed of generations sampled with replacement from a static metapopulation of name frequencies derived from the data. Inference with 20 bins (a) at all frequencies shows bias at low frequencies in the US and France. The red box indicates the plot range of Fig 1. Panel (b) shows the control inference for the same bins and plot range as Fig 1. Red Xs indicate bins removed from the results for exceeding the error threshold (b, grey lines). We ignore the anomalous control in the highest bin in Norway: It is an artifact that occurs because the highest-frequency name in the metapopulation (Anne) is only slightly less than the bin boundary and occasionally passes into the highest bin only to return, registering low fitness.

With the exception of Norway, the sampling bias control for displayed bins was at most 0.4%/year. Norway was most affected by sampling error due to its small size. We kept the highest bin in Norway despite its control exceeding 0.8%/year because the control is anomalous: The most frequent name in Norway, “Anne”, has a frequency 0.0127 over all time, just under the highest frequency bin boundary of 0.0128. This name is the only name to occupy the highest bin in the time series of samples, entering the bin 7 times always to return the following timestep, registering negative growth. In the data by contrast, 17 names populate the highest frequency bin for sustained time periods, so we do not believe this bin is truly substantially affected by sampling bias. The root mean square RMS bias in Norway with the exception of the highest bin was 0.5%/year whereas for all other plotted bins combined the RMS bias was 0.14%/year. Finally, we observe from Fig. S3 that sampling bias does not substantially affect the fitness of common types and by extension the replacement fitness.

Lastly, there is error associated with sampling at finite time intervals. We conduct inference using the Wright-Fisher process, but in reality birth is a continuous process. The Wright-Fisher process corresponds to an underlying diffusion process only in the limit that generation times are short. We estimate the error introduced by using finite time intervals using the uncensored data from the Netherlands (Fig 1, Netherlands). When aggregating uncensored Netherlands counts at 1 and 2 year intervals, \( \hat{s}(\rho) \) curves differ by at most 0.6%/year (RMS error: 0.4) due to a combination of bias and pseudoreplication noise. Netherlands 1y and 5y inferences differ by at most 1.3%/year (RMS: 0.81, Fig 1), indicating the bias diminishes with finer sampling intervals. The bias introduced by 1-yearly sampling is therefore less than 0.6%/year in Netherlands data, which we take to be representative of all name datasets.
Figure S4: **AKC data handling and sampling bias.** In the inference from AKC data depicted in Fig. 3 (blue here), we ignored transitions to or from zero, removed outliers, removed data from the year of introduction of dog breeds, and severed time series at apparent discontinuities (S2.2). Here we show the inference from the raw data (red) as well as the inference from a time series of samples (black). The sampling bias inference does not exceed 23% proportional error on the magnitude of the inferred selection coefficient (blue curve) or 2.3%/year absolute magnitude, and remains well within the statistical error in each bin.

**S2.2 American Kennel Club**

We obtained from a public depository an annual time-series of breed registrations from the American Kennel Club (AKC), which includes a total of 53,697,706 dogs of 153 different breeds registered between the years 1926 and 2005. After checking data quality and removing outliers associated with known or imputed errors in breed classification, we inferred frequency-dependent selection using the procedure described in Section S1.1. We also measured sampling bias as described in Section S1.8. In the lowest two bins, sampling bias was appreciable but still less than statistical error, whereas sampling bias was otherwise negligible. The net effect on the inference of sampling bias and data handling including removing outliers, separating time series and ignoring transitions to or from zero is depicted in Fig. S4.

We used counts of dog breeds as they appear in the original data with the exception of counts 0, which we omitted from the inference procedure because of pervasive non-distinction between 0 and missing data in the original dataset. That is, when \( x_i = 0 \) or \( x'_i = 0 \), we simply omit \( x_i \) and \( x'_i \) from any sums in equations such as Eq. S18. Thus \( n_t \) is always zero (we do not infer mutation rate), \( n_t = n' = \sum_{i=1}^{k_{t-1}} x'_i \) where \( i \) ranges over the \( k_{t-1} \) types which were present (nonzero) at timestep \( t-1 \), and the sums over types in Eq. S18 involve only the \( k \) types which are present at \( t \), ignoring the subpopulation of types for which there is no data. We divided the frequency range into 10 bins, choosing bin boundaries by quantiles so that each bin incorporated a roughly equal share of transitions \( x_i \rightarrow x'_i \) (range: 848-894).

We excluded rows in the dataset (nominally, breeds) containing breed subtypes that are summed in other rows, e.g. the rows “Dachshund-XX” and “Dachshund-XX (long-haired)” are summed in “Dachshund”, and so we retain only “Dachshund”. We retained “Dachshund”, “English Toy Spaniel (All)”, “Fox Terrier”, “Manchester Terrier”, “Poodle” and “Spaniel (All Cockers)” while excluding all of their subtype rows.

We also removed artifactual discontinuities from the time series. The evolutionary models we fit have approximately continuous frequency trajectories, whereas the AKC data contains sharp discontinuities arising from reclassification of breeds or changing interpretation of registration data over time. Hence we omitted certain counts from the data or broke...
some time series into two separate time series (e.g. Greyhounds-pre1935 and Greyhound-1935onward). We detected anomalous discontinuities by fitting the frequency-dependent model to the raw data and examining residuals. We produced a p-value for each residual transition in frequency as its quantile in the Binomial distribution given its expected frequency and the current population size. The most improbable transition (Chinese Shar-Pei 1992→1993: 90,081→19,465, Bonferroni-corrected \( p<10^{-55} \)) occurred immediately after the Shar-Pei’s year of introduction in the dataset, suggesting that the count during the year of introduction differs in kind from subsequent counts. In fact, 84 breeds were introduced over the course of the time series, and 40 out of these 84 have unlikely transitions \( (p<0.1) \) immediately following their year of introduction (compared to 654 out of 8810 in the full data, indicating otherwise slightly conservative p-values). We conclude that counts are unreliable in the year a breed is first introduced into the dataset, and so we ignore all 84 such counts. Removing initial points from a time series does not bias the inference under the frequency dependent model.

We detected five other likely artifactual discontinuities by ranking transitions according to the magnitude of proportional change. We removed the count for Poodle in 1939 (effectively removing two transitions) because Poodle is a sum of breed subtypes and the “Poodle (miniature)” subtype was undefined in 1939. We also split the time series for Manchester Terrier at 1945/1946 (where it nominally experienced a transition 880→61), Curly-Coated Retriever at 1932/1933 (82→1), and Greyhound at 1934/1935 (12→1624). Manchester Terrier is a sum over two sub-types, and the end of the “Manchester Terrier (Toy)” time series in 1945 causes the discontinuity. We have no evidence that the abrupt transitions for Greyhound and Curly-Coated Retriever correspond to errors in the data beyond the fact that they are the two highest proportional changes in the entire dataset, and they are much larger than changes known to be artifacts of errors such as breed reclassification.

S3 Novelty bias model fits

We compared the form of frequency dependent selection inferred from the AKC time series to simulations of an evolutionary process that favors novel types—a novelty bias model. The novelty bias model is an infinite-alleles Wright-Fisher process in a population of \( N \) individuals with on average \( N\mu \) new types introduced per generation. We use four parameters: the constant census population size \( N_c \), the constant effective population size \( N_e \), the selection benefit to each novel type \( \Delta s \), and the per capita per generation mutation rate \( \mu \). We number each new type sequentially, giving type number 1 fitness 1 (selection coefficient \( s = 0 \)) and type number \( n \) selection coefficient \( s = n\Delta s \). Thus after long times, both the average selection coefficient in the population (mean fitness) and the selection coefficient of the fittest type increase at rate \( N\mu\Delta s \) per generation on average. Hence the relative fitness of the fittest type to the rest of the population is also constant on average after long times. We allow the strength of genetic drift to vary independently of census population size \( N \) by simulating \( g \) timesteps of neutral evolution between each round of mutation and selection, producing an effective population size \( N_e = N/g \). Hence one generation of simulation is composed of one Wright-Fisher timestep incorporating mutation and selection and \( g−1 \) timesteps of neutral Wright-Fisher evolution.

Notably, types in the novelty bias model are not exchangeable, as in our model of pure frequency dependent selection, but nevertheless the novelty bias model induces an effective frequency dependent growth rate—namely the average growth rate of types that fall in a given frequency range.

We fitted parameters of the novelty bias model to the AKC data by conducting grid searches across a range of \( \mu \) (10\(^{-7}\) to 0.005) and \( \Delta s \) (10\(^{-7}\) to 0.5) on a roughly log evenly spaced grids (Fig. S5). We recorded the average selection coefficient in simulations \( s_{ave} \) for types that fall in each frequency bin used in the AKC inference—that is, we measured the equilibrium effective frequency dependence in the novelty bias model. We searched for parameter sets that minimize the squared difference in the effective frequency dependence measured in the simulations versus the frequency dependence inferred from the AKC data,
Figure S5: Novelty bias approximation to AKC depending on parameters. Inferred frequency-dependent selection (a) and type diversity (b) match the AKC data for certain values for the parameters $\Delta s$, $\mu$ of the novelty bias model. The black dot indicates the chosen parameters in Fig. 3. Mean squared errors in selection coefficient (a) and proportional number of types ($\log(n_{\text{sim}}/n_{\text{AKC}})^2$) (b) are computed by averaging across bins and up to 12 replicate simulations.

by summing over frequency bins $(s_{\text{ave}} - \hat{s}_{\text{AKC}})^2$. We also looked for agreement in overall diversity of types by tracking the squared difference in the log average number of types in each frequency range in the simulation versus in the AKC data. Parameter sets that agreed in diversity were clustered in a narrow band of mutation rates; whereas parameter sets that agreed in effective frequency dependence were clustered in a narrow diagonal band with $\mu \Delta s \approx \text{const.}$ At all values of $N$ and $N_e$ investigated, these two bands had an identifiable intersection that produced good matches in both frequency dependence and diversity, indicating that $\mu$ and $\Delta s$ are identifiable given $N$ and $N_e$. Near the least-squares minimum, the measured shape of effective frequency dependence from simulations was similar for different values of $\Delta s$ holding other parameters constant, so we easily matched the range of selection coefficients between the simulation and AKC data (dominated by the growth rate of the rarest frequency bin) by binary search on $\Delta s$.

We took $N$ to equal the maximum census population size in the AKC dataset in order to cover the same range of frequencies, namely $N=1,435,737$. Increasing $N$ beyond this value and refitting $\mu$ and $\Delta s$ as above revealed optimal parameter sets that lie on a line of constant $N\mu\Delta s$. These results concord with the intuition that the average rate of fitness increase due to the appearance of novel types is what primarily determines the strength of the effective frequency dependence. Varying $N_e$ showed that the particular value of $N\mu\Delta s$ that coincided with the best fits was roughly proportional to $N_e$, indicating that $N_e$ and $N\mu\Delta s$ are not separately identifiable based on diversity and effective frequency dependence alone.
Conversely, determining $N_e$ produced an absolute estimate of $N\mu\Delta s=1.2\%$ without knowledge of $N$. Values of $N_e$ close to 10,000 and 50,000 produced stochastic fluctuations in novelty bias simulations that visually match those in the AKC time series, and $N_e \approx 50,000$ gave the best results for intermediate frequencies (Fig 3b vs c). The AKC dataset itself displays different levels of stochasticity over time, as its census population size varies over a factor of 30 from 46,788 in 1931 to 1,435,737 in 1992. To achieve this realistic $N_e$, we simulated with $N=1,435,737$ and $g = 30$ giving an $N_e = 47,857.9$. Given these values of $N$ and $N_e$, and following the fitting procedure described above, we chose $\mu = 0.00004$ (to match the diversity of existing types observed in the AKC time series) and we chose $\Delta s = 0.00021$ (to match the maximum $s$ in any frequency bin in the AKC inference). Since values of $N_e$ ranging from 15,000 to 150,000 are all plausible, and this range of $N_e$ far exceeds the error in finding best fits of $\mu$ and $\Delta s$ given $N_e$, we estimated $N\mu\Delta s=0.012$ up to roughly a factor of three in either direction.