

Why do species get a thin slice of π ? Revisiting Lewontin's Paradox of Variation

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Abstract

Under neutral theory, the level of polymorphism in an equilibrium population is expected to increase. Neutral theory predicts that genetic diversity increases with population size. However, yet observed levels of diversity across metazoans vary only two orders of magnitude, while census population sizes (N_c) are expected to while population sizes vary over several. This unexpectedly narrow range of diversity is a longstanding enigma in evolutionary genetics known as Lewontin's Paradox of Variation (1974). Since Lewontin's observation, it has been argued that While some have suggested selection constrains diversity across species, yet tests of this hypothesis seem to fall short of explaining the orders of magnitude reduction in diversity observed in nature. In this work. Here, I revisit Lewontin's Paradox and to assess whether current models of linked selection are likely to constrain capable of reducing diversity to this extent. To quantify the discrepancy between pairwise diversity and census population sizes across species, I combine genetic data previously published estimates of pairwise diversity from 172 metazoan taxa with estimates of census sizes from geographic occurrence data and population densities estimated from body mass. Next, I fit the relationship between previously published estimates of genomic diversity and these approximate census sizes to quantify Lewontin's Paradox. While previous across-taxa population genetic studies have avoided accounting for phylogenetic non-independence, I use phylogenetic comparative methods to investigate the diversity-census size relationship, estimate phylogenetic signal, and explore how diversity changes along the phylogeny. I consider whether the reduction in diversity predicted by models of recurrent hitchhiking and background selection could explain the observed pattern of diversity across species. Since the impact of linked selection is mediated by recombination map length, I also investigate how map lengths vary with census sizes. I find species with large census sizes have shorter map lengths, leading these species to . Using phylogenetic comparative methods, I show this relationship is significant accounting for phylogeny, but with high phylogenetic signal and evidence that some lineages experience shifts in the evolutionary rate of diversity deep in the past. Additionally, I find a negative relationship between recombination map length and census size, suggesting abundant species have less recombination and experience greater reductions in diversity due to linked selection. Even after using high estimates of the strength of sweeps and background selection, I find linked selection likely cannot explain the shortfall between predicted and observed diversity levels across metazoan species. Furthermore, the predicted diversity under linked selection does not fit the observed diversity-census size relationship, implying that processes other than background selection and recurrent hitchhiking must be limiting diversity. However, I show

41 [that even using strong selection parameter estimates, models of linked selection are unlikely to](#)
42 [explain the observed relationship between diversity and census sizes across species.](#)

43 A longstanding mystery in evolutionary genetics is that the observed levels of genetic variation
44 across sexual species are confined to an unexpectedly narrow range. Under neutral theory, the
45 average number of nucleotide differences between lineages (pairwise diversity, π) is determined by
46 the balance of new mutations and their loss by genetic drift (Kimura and Crow 1964; Malécot 1948;
47 Wright 1931). In particular, the expected diversity at neutral sites in a panmictic population of
48 N_c diploids is expected to be $\pi \approx 4N_c\mu$, where μ is ~~per-the~~ [per basepair per](#) generation mutation
49 rate. Given that metazoan germline mutation rates only differ 10-fold (10^{-8} – 10^{-9} , Kondrashov
50 and Kondrashov 2010; Lynch 2010), and census sizes vary over several orders of magnitude, one
51 would expected under neutral theory that heterozygosity should also vary over several orders of
52 magnitude. However, early allozyme surveys revealed that heterozygosity levels across a wide range
53 of species varied just an order of magnitude (Lewontin 1974, p. 208); this ~~anomaly~~ is known as
54 Lewontin’s “Paradox of Variation”. With modern sequencing-based estimates of π across taxa
55 ranging over only three orders of magnitude (0.01–10%, Leffler et al. 2012), Lewontin’s paradox
56 has persisted unresolved through the genomics era.

57 From the beginning, explanations for Lewontin’s Paradox have been framed in terms of the
58 neutralist–selectionist controversy (Gillespie 1991, 2001; Kimura 1984; Lewontin 1974). The neu-
59 tralist view is that beneficial alleles are sufficiently rare and deleterious alleles removed sufficiently
60 quickly, that levels of genetic diversity are shaped predominantly by genetic drift and mutation
61 (Kimura 1984). Specifically, *non-selective* processes decouple the effective population size implied
62 by observed levels of diversity $\hat{\pi}$, $\tilde{N}_e = \hat{\pi}/4\mu$, from the census size, N_c . By contrast, the selectionist
63 view is that the direct and indirect effects of linked selection suppress diversity levels across taxa,
64 specifically because the impact of linked selection is greater in large populations. Undoubtedly,
65 these opposing views represent a false dichotomy, as population genomic studies have uncovered
66 [both](#) complex demographic histories that impact diversity within a species (e.g. Palkopoulou et al.
67 2015; Zhao et al. 2013) ~~;-as-well-as-and~~ [evidence](#) that selection depresses genome-wide diversity
68 (e.g. Aguade et al. 1989; Begun and Aquadro 1992; Elyashiv et al. 2016; McVicker et al. 2009).

69 Possible Explanations of Lewontin’s Paradox

70 A resolution of Lewontin’s Paradox would involve a mechanistic description and quantification of
71 the evolutionary processes that prevent diversity from scaling with census sizes across species. This
72 would necessarily connect to the broader literature on the empirical relationship between diversity
73 and population size (Frankham 1996; Leroy et al. 2021; Nei and Graur 1984; Soulé 1976), and
74 the ecological and life history correlates of genetic diversity (Nevo 1978; Nevo et al. 1984; Powell
75 1975). Three categories of processes stand out as potentially capable of decoupling census sizes from
76 diversity: non-equilibrium demography, variance and skew in reproductive success, and selective
77 processes.

78 It has long been appreciated that effective population sizes are typically less than census popu-
79 lation sizes, tracing back to early debates between R.A. Fisher and Sewall Wright (Fisher and Ford
80 1947; Wright 1948). Possible causes of this divergence between effective and census population sizes
81 include demographic history (e.g. population bottlenecks), extinction and recolonization dynamics,
82 or the breeding structure of populations (e.g. the variance in reproductive success and population
83 substructure). Early explanations for Lewontin’s Paradox suggested bottlenecks during the last

84 glacial maximum severely reduced population sizes (Kimura 1984; Nei and Graur 1984; Ohta and
85 Kimura 1973), and emphasized that large populations recover to equilibrium diversity levels more
86 slowly (Nei and Graur 1984, Kimura 1984 p. 203-204). Another explanation is that cosmopolitan
87 species repeatedly endure extinction and recolonization events, which reduces effective population
88 size (Maruyama and Kimura 1980; Slatkin 1977).

89 While chance demographic events like bottlenecks and recent expansions have long-term impacts
90 on diversity (since mutation-drift equilibrium is reached on the order of size of the population),
91 characteristics of the breeding structure such as high variance (V_w) or skew in reproductive success
92 ~~also continuously~~ suppress diversity below the levels predicted by the census size (Wright 1938).
93 ~~In species like~~ For example, in many marine animals, females are highly fecund, and dispersing
94 larvae face extremely low survivorship, leading to high variance in reproductive success (Hauser
95 and Carvalho 2008; Hedgecock and Pudovkin 2011; Waples et al. 2018, 2013). Such “sweepstakes”
96 reproductive systems can lead to remarkably small ratios of effective population size to census
97 population size (e.g. N_e/N_c can range from 10^{-6} – 10^{-2}), since $N_e/N \approx 1/V_w$ (Hedgecock 1994; Nun-
98 ney 1993, 1996; Wright 1938), and require multiple-merger coalescent processes to describe their
99 genealogies (Eldon and Wakeley 2006). Overall, these reproductive systems diminish the diversity
100 in many species, but seem unlikely to explain Lewontin’s Paradox broadly across metazoans.

101 Alternatively, selective processes, and in particular the indirect effects of selection on linked
102 neutral variation, could explain the observed narrow range of diversity. The earliest mathematical
103 model of hitchhiking was proffered as a ~~solution to~~ explanation of Lewontin’s Paradox (Maynard
104 Smith and Haigh 1974). Since, empirical observations have demonstrated that linked selection
105 shapes patterns of genome-wide diversity, as evidenced by the correlation between recombination
106 and diversity in a variety of species (Aguade et al. 1989; Begun and Aquadro 1992; Cai et al. 2009;
107 Cutter and Payseur 2003; Stephan and Langley 1998). Theoretic work to explain this pattern
108 has considered diversity under a steady influx of new beneficial mutations (recurrent hitchhiking;
109 Stephan 1995; Stephan et al. 1992), and purifying selection against new deleterious mutations
110 (background selection, BGS; Charlesworth et al. 1993; Hudson and Kaplan 1995; Hudson and Ka-
111 plan 1994; Nordborg et al. 1996). Indeed, empirical work indicates background selection diminishes
112 diversity around genic regions in a variety of species (Charlesworth 1996; Hernandez et al. 2011;
113 McVicker et al. 2009), and now efforts have shifted towards teasing apart the effects of positive
114 and negative selection on genomic diversity (Elyashiv et al. 2016).

115 An important class of theoretic selection models pertaining to Lewontin’s Paradox are recurrent
116 hitchhiking models that decouple diversity from the census population size. These models predict
117 diversity when strongly selected beneficial mutations regularly enter and sweep through the popula-
118 tion, trapping lineages and forcing them to coalesce (Gillespie 2000; Kaplan et al. 1989). In general,
119 decoupling occurs under these hitchhiking models when the rate of coalescence due to selection is
120 much greater than the rate of neutral coalescence. ~~—Other selection models cannot alone decouple~~
121 ~~diversity from population size, ceteris paribus~~ (e.g. Coop and Ralph 2012, equation 22). Under other
122 linked selection models, the resulting effective population size is proportional to population size, and
123 thus these models cannot decouple diversity, all else equal. For example, ~~the reduction in diversity~~
124 ~~predicted under models of~~ background selection and polygenic fitness variation ~~is a proportion~~
125 ~~reduction in~~ predict diversity is proportional to population size, mediated by the total recombina-
126 tion map length and the deleterious mutation rate or fitness variation (Charlesworth et al. 1993;
127 Nicolaisen and Desai 2012; Nordborg et al. 1996; Robertson 1961; Santiago and Caballero 1995,
128 1998).

Recent Approaches Towards Solving Lewontin's Paradox

Recently, Corbett-Detig et al. (2015) used population genomic data to estimate the reduction in diversity due to background selection and hitchhiking across 40 species, and showed the impact of selection increases with two proxies of census population size, species range and with body size. ~~These authors~~ They argued this is evidence that selection could explain Lewontin's Paradox; however, in a re-analysis, Coop (2016) demonstrated that the observed scale of these reductions is insufficient to explain the orders-of-magnitude shortfall between observed and expected levels of diversity across species. Other recent work has found that certain life history characteristics related to parental investment, such as propagule size, are good predictors diversity in animals (Chen et al. 2017; Romiguier et al. 2014). Nevertheless, while these diversity correlates are important clues, they do not propose a mechanism by which these traits act to constrain diversity within a few orders of magnitude.

Here, I revisit Lewontin's Paradox by integrating a variety of data sets and assessing the predicted reductions in diversity under different selection models. Prior surveys of genetic diversity either lacked census population size estimates, used allozyme-based measures of heterozygosity, or included fewer species. To address these shortcomings, I first estimate census sizes by combining predictions of population density based on body size with ranges estimated from geographic occurrence data. Using these estimates, I quantify the relationship between census size and previously-published genomic diversity estimates across 172 metazoan taxa within nine phyla, ~~which provides~~ to provide a sense of the scale of the divergence between π and N_c that leads to Lewontin's Paradox.

Past work looking at the relationship between π and N_c has ~~largely ignored~~ been unable to fully account for phylogenetic non-independence across taxa (Felsenstein 1985). To address this shortcoming, I ~~account for phylogenetic non-independence across taxa using a synthetic time-calibrated phylogeny and phylogenetic~~ use phylogenetic comparative methods (PCMs) with a synthetic time-calibrated phylogeny to account for shared phylogenetic history. Moreover, ~~Lynch (2011) has argued that it is disputed whether considering phylogenetic non-independence is necessary in population genetics,~~ since coalescent times are much less than divergence times ~~, considering phylogenetic non-independence is unnecessary for traits like effective population size~~ (Lynch 2011; Whitney and Garland 2010). Using PCMs, I ~~test this conjecture by estimating~~ address this by estimating the degree of phylogenetic signal in the diversity census size relationship, and investigating how these traits evolve along the phylogeny.

Finally, I explore whether the predicted reductions of diversity under background selection and recurrent hitchhiking are sufficiently strong ~~enough~~ to resolve Lewontin's Paradox. These predicted reductions in diversity across species are ~~generously estimated using selection strength~~ estimated using strong selection parameters from *Drosophila melanogaster*, a species known to be strongly affected by linked selection. Given the effects of linked selection are mediated by recombination map length, I investigate how recombination map lengths vary with census population size using data from a previously-published survey (Stapley et al. 2017). I find map lengths are typically shorter in large-census-size species, increasing the effects of linked selection in these species, which might further decouple diversity from census size. Still, I find the combined impact of these selection models with available parameter estimates falls short in explaining Lewontin's Paradox, and discuss future avenues through which the Paradox of Variation could be fully resolved.

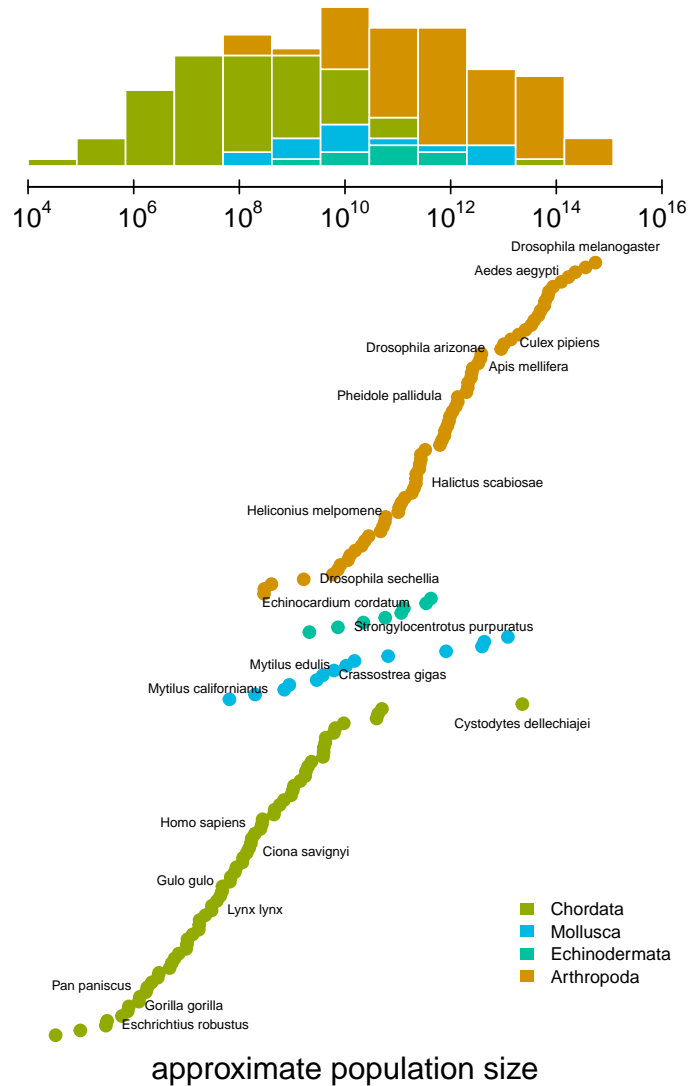


Figure 1: The distribution of approximate census population sizes estimated by this study. Some phyla containing few species were excluded for clarity.

171 Results

172 Estimates of Census Population Size

173 A major impediment in quantifying Lewontin's Paradox has been estimating census population
 174 sizes across many taxa, especially for extremely abundant, cosmopolitan species that define the up-
 175 per limit of ranges. Previous work has surveyed the literature for census size estimates (Frankham
 176 1996; Nei and Graur 1984; Soulé 1976), or used range and body size, body size, or qualitative
 177 categories as proxies for census size (Corbett-Detig et al. 2015; Leffler et al. 2012). To quan-
 178 tify the relationship between genomic estimates of diversity and census population sizes, I first
 179 approximate census population sizes for 172 metazoan taxa (Figure 1). My approach predicts pop-

180 ulation densities from body sizes using a previously-observed linear relationship that holds across
181 metazoans (Supplementary Figure S11; Damuth 1981, 1987). Then, from geographic occurrence
182 data, I estimate range sizes. Finally, I estimate population size as the product of these predicted
183 densities and range estimates (see Methods: *Macroecological Estimates of Population Size*). Note
184 that the relationship between population density and body size is driven by energy budgets, and
185 thus reflects macroecological equilibria (Damuth 1987); ~~consequently.~~ Consequently, population
186 sizes are underestimated for taxa like humans and their domesticated species ~~are underestimated.~~,
187 and overestimated for species with anthropogenically reduced densities or fragmented ranges. For
188 example, the population size of *Lynx lynx* is likely around 50,000 (IUCN 2020) which is around
189 two orders of magnitude smaller than my estimate. Additionally, the range size estimates do not
190 consider whether an area has unsuitable habitat, and thus may be overestimated for species with
191 particular niches or patchy habitats. While these methods to estimate census size are crude and
192 approximate, they can be efficiently calculated for numerous taxa and are sufficient to estimate the
193 scale of Lewontin’s Paradox (see Supplementary Information *Population Size Validation* for more
194 on validation based on biomass and other approaches).

195 Quantifying Lewontin’s Paradox

196 To determine which ecological or evolutionary processes could decouple diversity from census popu-
197 lation size, we first need to quantify this relationship across a wide variety of taxa. Previous work has
198 found there is a significant relationship between heterozygosity and the logarithm of population size
199 or range size, but these studies relied on heterozygosity measured from allozyme data (Frankham
200 1996; Leffler et al. 2012; Nei and Graur 1984; Soulé 1976). Here, I confirm these findings using
201 pairwise diversity estimates from genomic sequence data and the estimated census sizes (Figure 2).
202 The pairwise diversity estimates are from three sources: Leffler et al. (2012), Corbett-Detig et al.
203 (2015), and Romiguier et al. (2014), and are predominantly from either synonymous or non-coding
204 DNA (see Methods: *Diversity and Map Length Data*). Overall, an ordinary least squares (OLS)
205 relationship on a log-log scale fits the data well (Figure 2). The OLS slope estimate is significant
206 and implies ~~an increase in diversity of 0.09~~ a 13% percent increase in differences per basepair for
207 every order of magnitude census size grows (95% confidence interval ~~[0.08, 0.12]~~ [12%, 14%], adjusted
208 $R^2 = 0.26$; see also the OLS fit per-phyla, Supplementary Figure S5).

209 Notably, this relationship has few outliers and is relatively homoscedastic. This is in part
210 because of the log-log scale, in contrast to previous work (Nei and Graur 1984; Soulé 1976); see
211 Supplementary Figure S4 for a version on a log-linear scale. However, it is noteworthy that few taxa
212 have diversity estimates below $10^{-3.5}$ differences per basepair. Those that do, lynx (*Lynx Lynx*),
213 wolverine (*Gulo gulo*), and Massasauga rattlesnake (*Sistrurus catenatus*) face habitat fragmentation
214 and declining population sizes. These three species are all in the IUCN Red List, but are listed as
215 least concern (though their presence in the Red List indicates they are of conservation interest).
216 ~~I also investigated the relationship between species’~~ In Supplementary Information Section *Diver-*
217 sity and IUCN Red List Status, I explore more about the relationships between IUCN Red List
218 categories (an ordinal scale of how threatened a species is) and both diversity status, diversity, and
219 population size, finding that species categorized as more threatened have both smaller population
220 sizes and reduced diversity, compared to non-threatened species (Figure ??) consistent with past
221 work. A linear model of diversity regressed on population size has lower AIC when the IUCN
222 Red List categories are included, and the estimates of the effect of IUCN status are all negative on
223 diversity, though not all are significant in part because some categories have three or fewer species

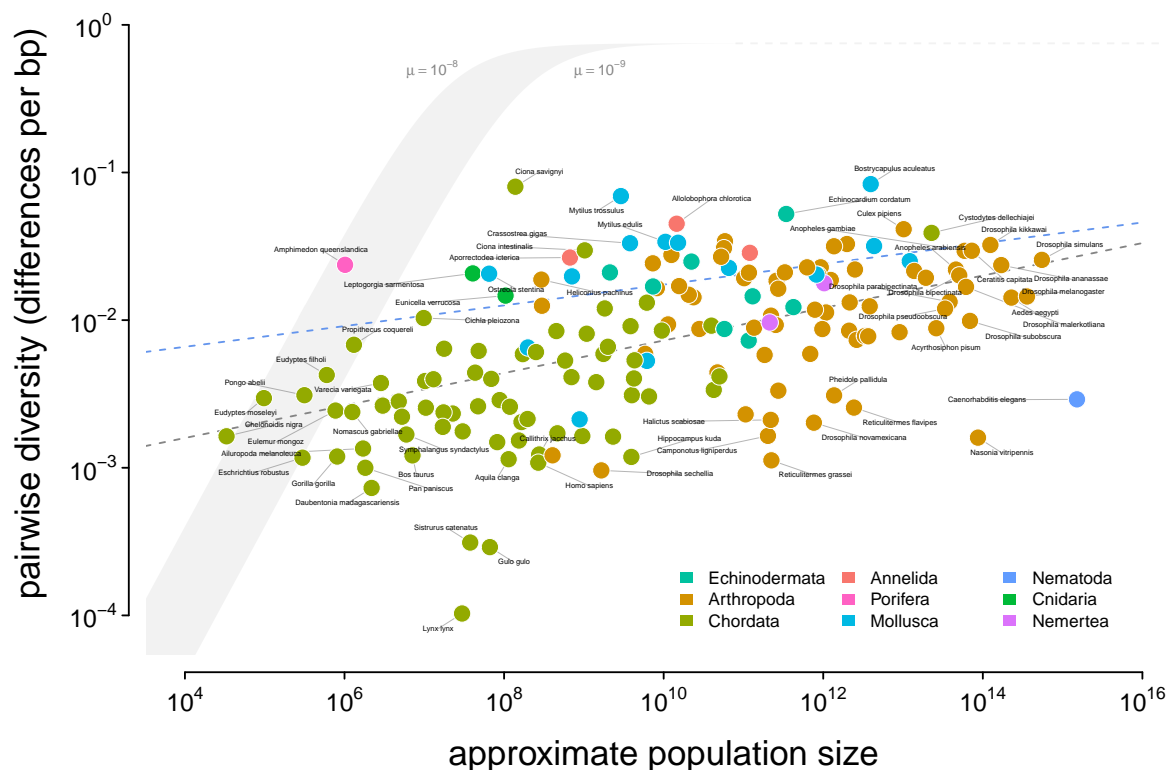


Figure 2: An illustration of Lewontin’s Paradox of Variation. Pairwise diversity (data from Leffler et al. 2012, Corbett-Detig et al. 2015, and Romiguier et al. 2014), which varies around three orders of magnitude, shows a weak relationship with approximate population size, which varies over 12 orders of magnitude. The shaded curve shows the range of expected neutral diversity if N_e were to equal N_c under the four-alleles model, $\log_{10}(\pi) = \log_{10}(\theta) - \log_{10}(1 + 4\theta/3)$ where $\theta = 4N_c\mu$, for two mutation rates, $\mu = 10^{-8}$ and $\mu = 10^{-9}$, and the light gray dashed line represents the maximum pairwise diversity under the four alleles model. The dark gray dashed line is the OLS regression fit, and the blue dashed line is the regression fit using a phylogenetic mixed-effects model. Points are colored by phylum. The species *Equus ferus przewalskii* ($N_c \approx 10^3$ and $\pi = 3.6 \times 10^{-3}$) was an outlier and excluded from this figure for visual clarity.

224 ~~(Supplementary Table S3).~~

225 ~~A version of Figure 2 with points colored by their IUCN Red List conservation status. Margin~~
 226 ~~boxplots show the diversity and population size ranges (thin lines) and interquartile ranges (thick~~
 227 ~~lines) for each category. NA/DD indicates no IUCN Red List entry, or Red List status Data~~
 228 ~~Deficient; LC is Least Concern, NT is Near Threatened, VU is Vulnerable, EN is Endangered, and~~
 229 ~~CR is Critically Endangered.~~

230 Phylogenetic Non-Independence and the Population Size Diversity Relationship

231 ~~In quantifying Lewontin’s Paradox, I have additionally fit some simple trait evolution models that~~
 232 ~~account for phylogenetic non-independence. One limitation of using ordinary least squares is that~~
 233 ~~shared phylogenetic history can create correlation structure in the residuals, which violates an~~
 234 ~~assumption of the regression model (Felsenstein 1985; Revell 2010). To address this shortcoming, I~~

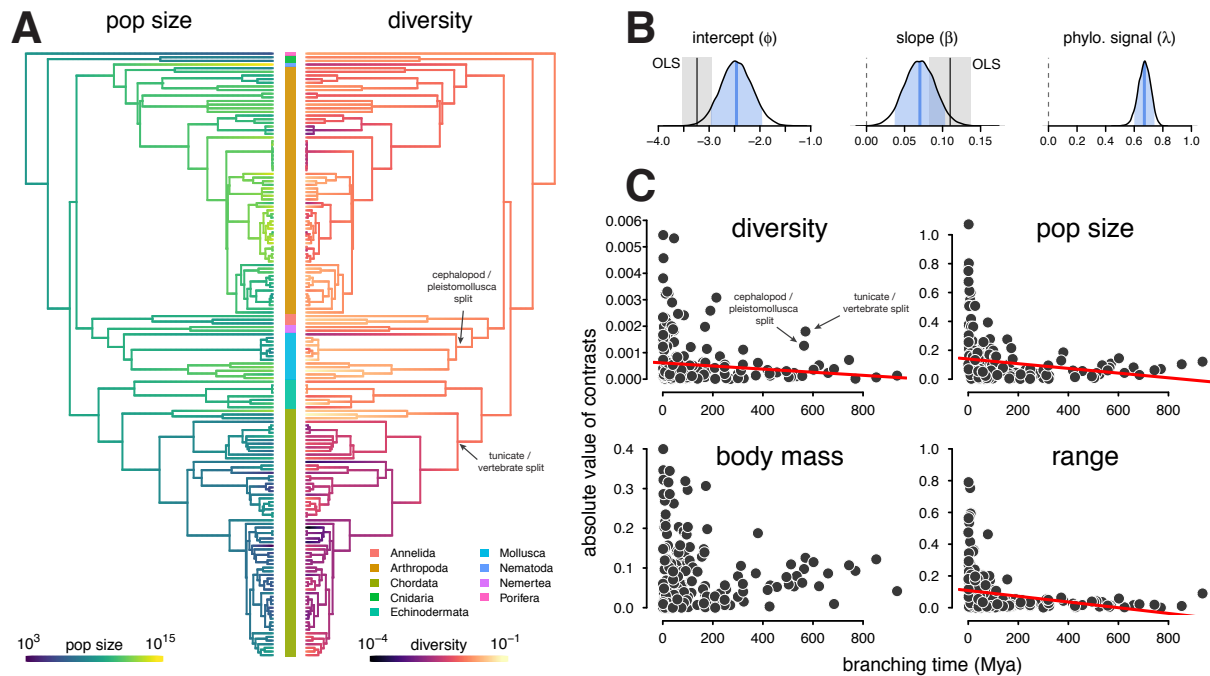


Figure 3: (A) The ancestral continuous trait estimates for the population size and diversity (differences per bp, log scaled) across the phylogeny of 166 taxa. The phyla of the tips are indicated by the color bar in the center. (B) The posterior distributions of the intercept, slope, and phylogenetic signal (λ , Vilmereuil and Nakagawa 2014) of the phylogenetic mixed-effects model of diversity and population size (log scaled). Also shown are the 90% credible interval (light blue shading), posterior mean (blue line), OLS estimate (gray solid line), and bootstrap OLS confidence intervals (light gray shading). (C) The node-height tests of diversity, population size, and the two components of the population size estimates, body mass, and range (all traits on log scale before contrast was calculated). Each point shows the standardized phylogenetic independent contrast and branching time for a pair of lineages. Red lines are robust regression estimates (and are only shown for statistically significant relationships at the $\alpha = 0.05$ level). Note that some outlier pairs with very high phylogenetic independent contrasts were excluded (in all cases, these outliers were in the genus *Drosophila*).

235 [fit this relationship using a phylogenetic mixed-effects model](#), investigated whether there is a signal
 236 of phylogenetic non-independence, estimated the continuous trait values on the phylogeny, and
 237 ~~assessed~~ [explored](#) how diversity and population size evolve. Prior population genetic comparative
 238 studies have lacked time-calibrated phylogenies and assumed unit branch lengths (Whitney and
 239 Garland 2010), a shortcoming that has drawn criticism (Lynch 2011). Here, I use a synthetic
 240 time-calibrated phylogeny created from the DateLife project (O’Meara et al. 2020) to account for
 241 shared phylogenetic history (see Methods: *Phylogenetic Comparative Methods*).

242 Using a phylogenetic mixed-effects model (Hadfield and Nakagawa 2010; Lynch 1991; Ville-
 243 mereuil and Nakagawa 2014) implemented in Stan (Carpenter et al. 2017; Stan Development Team
 244 2020), I estimated the linear relationship between diversity and population size (on a log-log scale)
 245 accounting for phylogeny, for the 166 taxa ~~with non-missing~~ [without missing](#) data and present in
 246 the synthetic chronogram. As with the ~~non-phylogenetic linear~~ regression, this relationship was
 247 positive and significant (95% credible interval [0.04, 0.11](#), [0.03, 0.11](#)), though somewhat attenuated

248 compared to the OLS estimates (Figure 23B). Since the population size estimates are based on
249 range and body mass, they are essentially a composite trait; fitting phylogenetic mixed-effects
250 models separately on body mass and range indicates these have significant negative and positive ef-
251 fects, respectively (Supplementary Figure S6; [see also Supplementary Figure S1 for the relationship](#)
252 [between diversity and the range categories of Leffler et al. 2012](#)).

253 With the phylogenetic mixed-effects model, I also estimated the variance of the phylogenetic
254 effect (σ_p^2) and the residual variance (σ_r^2), which can be used to estimate a measure of the phyloge-
255 netic signal, $\lambda = \sigma_p^2 / (\sigma_p^2 + \sigma_r^2)$ (Lynch 1991; Villemereuil and Nakagawa 2014; see Freckleton et al. 2002
256 for a comparison to Pagel’s λ). If the relationship between diversity and population size was free of
257 shared phylogenetic history, $\lambda = 0$ and all the variance could be explained by evolution on the tips;
258 this is analogous to Lynch’s conjecture that coalescent times should be free of phylogenetic signal
259 (2011). In the relationship between population size and diversity, the posterior mean of $\lambda = 0.67$
260 (90% credible interval [\[0.59, 0.75\]](#)[\[0.58, 0.75\]](#)) indicates that the majority of the variance perhaps
261 might be due to shared phylogenetic history (Figure 3B).

262 ~~A closer~~ [This high degree of phylogenetic signal suggests Gillespie’s \(1991\) concern that the](#)
263 [\$\pi\$ - \$N_c\$ relationship was driven by chordate-arthropod differences may be valid.](#) A visual inspection
264 of the estimated ancestral continuous values for diversity and population size on the phylogeny
265 indicates the high phylogenetic signal seems to be driven in part by chordates having low diversity
266 and small population sizes compared to non-chordates (Figure 3A). This ~~suggests Gillespie’s (1991)~~
267 ~~earlier critique that the π - N_c relationship was driven by chordate-arthropod differences may be~~
268 ~~valid.~~ ~~This~~ problem resembles Felsenstein’s worst-case scenario (Felsenstein 1985; Uyeda et al.
269 2018), where a singular event on a lineage separating two clades generates a spurious association
270 between two traits. ~~To further~~

271 [To](#) investigate whether clade-level differences dominated the relationship between diversity and
272 population size, I fit phylogenetic mixed-effects models to phyla-level subsets of the data for clades
273 with sufficient sample sizes (see Methods: *Phylogenetic Comparative Methods*). This analysis shows
274 a significant positive relationship between diversity and population size in arthropods, and positive
275 weak relationships in molluscs and chordates (Supplementary Figure S15). Each of the 90% credible
276 intervals for slope overlap, indicating the relationship between π and N_c is similar across these
277 clades.

278 ~~One limitation of the phylogenetic mixed-effects models employed here is that they assume traits~~
279 ~~evolve under constant rate Brownian motion.~~ ~~To test this assumption, I performed~~ [Additionally,](#)
280 [I have explored the rate of trait change through time using](#) node-height tests (Freckleton and
281 Harvey 2006). Node-height tests regress the absolute values of the standardized contrasts between
282 lineages against the branching time (since present) of these lineages. Under Brownian Motion
283 (BM), standardized contrasts are estimates of the rate of character evolution (Felsenstein 1985);
284 if a trait evolves under constant rate BM, this relationship should be flat. For both diversity and
285 population size, node-height tests indicate a significant increase in the rate of evolution towards the
286 present (robust regression p-values ~~0.028 and 0.00070~~ [0.023 and 0.00018](#), respectively; Figure 3C).
287 Considering the constituents of the population size estimate, range and body mass, separately, [the](#)
288 [rate of evolution of](#) range but not body mass shows a significant increase (p-value ~~1.9×10^{-7}~~) [in](#)
289 [rate](#) ~~1.03×10^{-7}~~ towards the present.

290 Interestingly, the diversity node-height test reveals two rate shifts at deeper splits (Figure 3C,
291 top left) around 570 Mya. These nodes represent the branches between tunicates and vertebrates in
292 chordates, and cephalopods and pleistomollusca (bivalves and gastropods) in molluscs. While the

293 cephalopod-pleistomollusca split outlier may be an artifact of having a single cephalopod (*Sepia*
294 *officinalis*) in the phylogeny, the tunicate-vertebrate split outlier is driven by the low diversity of
295 vertebrates and the previously-documented exceptionally high diversity of tunicates (sea squirts;
296 Nydam and Harrison 2010; Small et al. 2007). This deep node representing a rate shift in diversity
297 could reflect a change in either effective population size or mutation rate, and there is some evidence
298 of both in this genus *Ciona* (Small et al. 2007; Tsagkogeorga et al. 2012). Neither of these deep
299 rate shifts in diversity is mirrored in the population size node-height test (Figure 3C, top right).
300 Rather, it appears a trait impacting diversity but not census size (e.g. mutation rate or offspring
301 distributions) has experienced a shift on the lineage separating tunicates and vertebrates. At nearly
302 600 Mya, these deep nodes illustrate ~~a counterexample to Lynch's claim~~ that expected coalescent
303 times ~~do not can~~ share phylogenetic history ~~because they are less than divergence times, due to~~
304 ~~phylogenetic inertia in some combination of population size, reproductive system, and mutation~~
305 ~~rates.~~

306 Finally, an important caveat is the increase in rate towards the tips could be caused by mea-
307 surement noise, ~~or possibly uncertainty or bias in the divergence time estimates deep in the tree.~~
308 Inspecting the lineage pairs that lead to this increase in rate towards the tips indicates these rep-
309 resent plausible rate shifts, e.g. between cosmopolitan and endemic sister species like *Drosophila*
310 *simulans* and *Drosophila sechellia*; however, ruling out measurement noise entirely as an explanation
311 would involve considering the uncertainty of diversity and population size estimates.

312 **Assessing the Impact of Linked Selection on Diversity Across Taxa**

313 The above analyses reemphasize the drastic shortfall of diversity levels as compared to census
314 sizes. Linked selection has been proposed as the mechanism that acts to reduce diversity levels
315 from what we would expect given census sizes (Corbett-Detig et al. 2015; Gillespie 2000; Maynard
316 Smith and Haigh 1974). Here, I test this hypothesis by estimating the scale of diversity reductions
317 expected under background selection and recurrent hitchhiking, and compare these to the observed
318 relationship between π and N_e .

319 I quantify the effect of linked selection on diversity as the ratio of observed diversity (π) to the
320 estimated diversity in the absence of linked selection (π_0), $R = \pi/\pi_0$. ~~Here, π_0 would reflect only~~
321 ~~demographic history and non-heritable variation in reproductive success.~~ There are two difficulties
322 in evaluating whether linked selection could resolve Lewontin's Paradox. The first difficulty is
323 that π_0 is unobserved. Previous work has estimated π_0 using methods that exploit the spatial
324 heterogeneity in recombination and functional density across the genome to fit linked selection
325 models that incorporate both hitchhiking and background selection (Corbett-Detig et al. 2015;
326 Elyashiv et al. 2016). The second difficulty is understanding ~~of~~ how R varies across taxa, since we
327 lack estimates of critical model parameters for most species. Still, I can address a key question: if
328 diversity levels were determined by census sizes ($\pi_0 = 4N_e\mu$), are the combined effects of background
329 selection and recurrent hitchhiking sufficient to reduce diversity to observed levels? Furthermore,
330 does the relationship between census size and predicted diversity under linked selection across
331 species, $\pi_{BGS+HH} = R\pi_0$, match the observed relationship in Figure 2?

332 Since we lack estimates of key linked selection parameters across species, I ~~generously~~ param-
333 eterize the hitchhiking and BGS models using estimates from *Drosophila melanogaster*, a species
334 known to be strongly affected by linked selection (Sella et al. 2009). Under a generalized model of
335 hitchhiking and background selection (Coop and Ralph 2012; Elyashiv et al. 2016) and assuming
336 $N_e = N_c$, expected diversity is

$$\pi_{\text{BGS+HH}} \approx \frac{\theta}{1/B(U,L) + 2N_c S(\gamma, L, J)} \quad (1)$$

337 where $\theta = 4N_c\mu$, $B(U, L)$ is the effect of background selection, and $S(\gamma, L, J)$ is the rate of coa-
 338 luescence caused by sweeps (c.f. Elyashiv et al. 2016, equation 1, Coop and Ralph 2012 equation
 339 20). Under background selection models with recombination, the reduction is $B(U, L) = \exp(-U/L)$
 340 where U is the per diploid genome per generation deleterious mutation rate, and L is the recom-
 341 bination map length (Hudson and Kaplan 1995; Hudson and Kaplan 1994; Nordborg et al. 1996).
 342 This BGS model is similar to models of effective population size under polygenic fitness variation,
 343 and can account for other modes of linked selection (Robertson 1961; Santiago and Caballero 1995,
 344 1998, see Appendix Section A2). The coalescent rate due to sweeps is $S(\gamma, L, J) = \gamma/LJ$, where γ is
 345 the number of adaptive substitutions per generation, and J is the probability a lineage is trapped
 346 by sweeps as they occur across the genome (c.f. $J_{2,2}$ in equation 15 of Coop and Ralph 2012).

347 Parameterizing the model this way, I then set the key parameters that determine the impact
 348 of recurrent hitchhiking and background selection (γ , J , and U) to high values estimated from
 349 *Drosophila melanogaster* by Elyashiv et al. (2016). My estimate of [the adaptive substitutions](#)
 350 [per generation \(\$\gamma_{\text{Dmel}}\$ \)](#) based Elyashiv et al. implies [a rate of sweeps per basepair of \$\nu_{\text{BP,Dmel}} \approx\$](#)
 351 2.34×10^{-11} , which is close to other estimates from *D. melanogaster* (see Supplementary Figure
 352 S14A). The rate of deleterious mutations per diploid genome, per generation is parameterized
 353 using the estimate from Elyashiv et al., $U_{\text{Dmel}} = 1.6$, which is a bit greater than previous estimates
 354 based on Bateman-Mukai approaches (Charlesworth 1987; Mukai 1988; Mukai 1985). Finally, the
 355 probability that a lineage is trapped in a sweep, J_{Dmel} , is calculated from the estimated genome-wide
 356 average coalescent rate due to sweeps from Elyashiv et al. (see Supplementary Figure S14B and
 357 Methods: *Predicted Reductions in Diversity* for more details on parameter estimates). Using these
 358 *Drosophila* parameters, I then explore how the predicted range of diversity levels under background
 359 selection and recurrent hitchhiking varies across species with recombination map length (L) and
 360 census population size (N_c).

361 Previous work has found that the impact of linked selection increases with N_c (Corbett-Detig
 362 et al. 2015; see also Supplementary Figure S13A), and it is often thought that this is driven by
 363 higher rates of adaptive substitutions in larger populations (Ohta 1992), despite equivocal evidence
 364 (Galtier 2016). However, there is another mechanism by which species with larger population
 365 sizes might experience a greater impact of linked selection: recombinational map length, L , is
 366 known to correlate with body mass (Burt and Bell 1987) and thus varies inversely with population
 367 size. As this is a critical parameter that determines the genome-wide impact of both hitchhiking
 368 and background selection, I examine the relationship between recombination map length (L) and
 369 census population size (N_c) across taxa, using available estimates of map lengths across species
 370 (Corbett-Detig et al. 2015; Stapley et al. 2017). I find a significant non-linear relationship using
 371 phylogenetic mixed-effects models (Figure 4A; see Methods: *Phylogenetic Comparative Methods*).
 372 There is also a correlation between map length and genome size (Supplementary Figure S8) and
 373 genome size and population size (Supplementary Figure S7). [These findings are consistent with both](#)
 374 [the hypothesis that non-adaptive processes increase genome size in small- \$N_c\$ species](#) (Lynch and
 375 Conery 2003) [which in turn could increase map lengths, as well as the hypothesis that map lengths](#)
 376 [are adaptively longer to more efficiently select against deleterious alleles](#) (Roze 2021). Overall, the
 377 negative relationship between map length and census size indicates linked selection is expected to
 378 be stronger in short map length, high- N_c species.

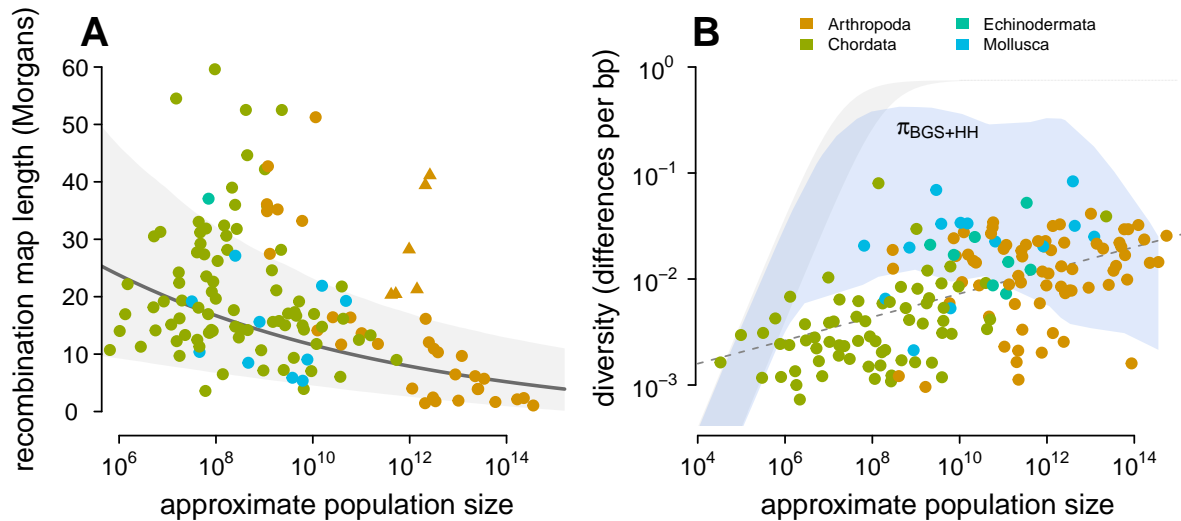


Figure 4: (A) The observed relationship between recombination map length (L) and census size (N_c) across ~~131–136~~ species with complete data and known phylogeny. Triangle points indicate ~~six~~ social taxa excluded from the model fitting since these have adaptively higher recombination map lengths (Wilfert et al. 2007). The dark gray line is the estimated relationship under a phylogenetic mixed-effects model, and the gray interval is the 95% posterior average. (B) Points indicate the observed π – N_c relationship across taxa shown in Figure 2, and the blue ribbon is the range of predicted diversity were $N_e = N_c$ for $\mu = 10^{-8}$ – 10^{-9} , and after accounting for the expected reduction in diversity due to background selection and recurrent hitchhiking under *Drosophila melanogaster* parameters. In both plots, point color indicates phylum.

379 Then, I predict the expected diversity (π_{BGS+HH}) under background selection and hitchhik-
 380 ing, were $N_e = N_c$, and assuming all species had the rate of sweeps and strength of BGS as
 381 *D. melanogaster*. Since neutral mutation rates μ are unknown and vary across species, I calcu-
 382 late the range of predicted π_{BGS+HH} estimates for $\mu = 10^{-8}$ – 10^{-9} (using the four-alleles model,
 383 Tajima 1996), and compare this to the observed relationship between π and N_c in Figure 4B.
 384 Under these parameters, linked selection begins to appreciably depress diversity around $N_c \approx 10^9$,
 385 since $S \approx 10^{-8}$ – 10^{-9} and linked selection dominates drift when $S > 1/2N$. Overall, this reveals
 386 two problems for the hypothesis that linked selection could solve Lewontin’s Paradox. First, low
 387 to mid- N_c species (census sizes between ~~10^6 – 10^4~~ ~~10^{14} – 10^{10}~~) have sufficiently long map lengths that
 388 their diversity levels are only moderately reduced by linked selection, leading to a wide gap be-
 389 tween predicted and observed diversity levels. For this not to be the case, the parameters that
 390 determine the strength of background selection and recurrent hitchhiking would need to be *higher*
 391 among these species than in *Drosophila melanogaster*. This would require that the rate of adap-
 392 tive mutations or the deleterious mutation rate be orders of magnitude higher for species within
 393 this range than in *Drosophila*, which is incompatible with the rate of adaptive substitutions across
 394 species (Galtier 2016) and mutation rates (Lynch 2010). Furthermore, linked selection has been
 395 quantified in humans, which fall in this census size range, and has been found to be relatively
 396 weak (Boyko et al. 2008; Cai et al. 2009; Hellmann et al. 2008; Hernandez et al. 2011; McVicker
 397 et al. 2009). Second, while hitchhiking and BGS can reduce predicted diversity levels for high- N_c
 398 species (~~$N_c > 10^{14}$~~ ~~$N_c > 10^{10}$~~) to observed levels, this would imply available estimates of π_0 are
 399 underestimated by several orders of magnitude in *Drosophila* (Supplementary Figure S13B). The

400 high reductions in π predicted here (compared to those of Elyashiv et al. 2016) are a result of using
401 N_c , rather than $N_c = \pi_0/4\mu$ in the denominator of Equation (1), which leads to a very high rate of
402 sweeps in the population. I do not consider selective interference, though the saturation of adaptive
403 substitutions per Morgan would only act to limit the reduction in diversity (Weissman and Barton
404 2012), and thus these results are conservative. Overall, while linked selection could decouple di-
405 versity from census size for high- N_c species, recurrent hitchhiking and background selection seem
406 unlikely to explain the observed patterns of diversity across species under our understanding of the
407 range of parameter estimates.

408 Discussion

409 Nearly fifty years after Lewontin’s description of the Paradox of Variation, how evolutionary, life
410 history, and ecological processes interact to constrain diversity across taxa to a narrow range re-
411 mains a mystery. ~~Since Wright (1931; 1938), population geneticists have appreciated that various~~
412 ~~demographic processes shrink effective population sizes compared to census sizes, yet it has remained~~
413 ~~unclear whether these neutral processes alone can explain~~ I revisit Lewontin’s Paradox ~~and across taxa~~
414 ~~diversity patterns. Alternatively, selective processes that act more strongly in larger populations~~
415 ~~could account for the observed narrow range of diversity. A critical first step to discerning the~~
416 ~~processes that act to transform census sizes to diversity levels across species is characterizing the~~
417 ~~observed π - N_c relationship.~~

418 ~~Here, for 172 taxa, I estimated the relationship~~ by first characterizing the relationship between
419 genomic estimates of pairwise diversity and approximate census population size across 172 metazoan
420 species. Previous surveys have used allozyme-based estimates, fewer taxa, or qualitative measures
421 of population size. My estimates of census population sizes are quite approximate, since they use
422 body size to predict density. An improved estimate might consider vagility (as Soulé 1976 did),
423 though this is harder to do systematically across many taxa. Future work might also use other
424 ecological information, such as total biomass ~~and estimated numbers of species within phyla,~~ or
425 species distribution modeling to improve census size estimates (Bar-On et al. 2018; Mora et al.
426 2011). Still, it seems more accurate estimates would be unlikely to change the qualitative findings
427 here, which resemble those of early surveys (Nei and Graur 1984; Soulé 1976).

428 One limitation of the dataset in this study is that diversity estimates are collated from a variety
429 of sources rather than estimated with a single bioinformatic pipeline. This leads to technical noise
430 across diversity estimates; perhaps the relationship between π and N_c found here could be tighter
431 with a standardized bioinformatic pipeline. In addition to this technical variation, there might
432 be systematic bioinformatic sources of bias in diversity estimates. For example high-diversity
433 sequences may fail to align to the reference genome and end up unaccounted for, leading to a
434 downward bias. Alternatively, high-diversity sequences might map to the reference genome, but
435 adjacent mis-matching SNPs might be mistaken for a short insertion or deletion. While these issues
436 might adversely affect the estimates in high-diversity species, it is unlikely they will qualitatively
437 change the observed π - N_c relationship.

438 Macroevolution and Across-Taxa Population Genomics

439 Lewontin’s Paradox arises from a comparison of diversity across species, yet ~~surprisingly, previous~~
440 ~~work on this problem has not considered the impact of phylogenetic non-independence.~~ I have

441 ~~addressed this limitation, showing that diversity does have a significant positive relationship with~~
442 ~~census size, after accounting for shared phylogenetic history among taxa it has been disputed~~
443 ~~whether such comparisons require phylogenetic comparative methods. Extending previous work~~
444 ~~that has accounted for phylogeny in particular clades (Leffler et al. 2012), or using taxonomical-level~~
445 ~~averages (Romiguier et al. 2014), I show that the positive relationship between diversity and census~~
446 ~~size is significant using a mixed-effects model with a time-calibrated phylogeny. Additionally, I~~
447 ~~find a high degree of phylogenetic signal, evidence of deep shifts in the rate of evolution of genetic~~
448 ~~diversity, and that arthropods and chordates form clusters, showing previous concern. Overall, this~~
449 ~~suggests that previous concerns about phylogenetic non-independence was warranted. Finally, this~~
450 ~~high degree of phylogenetic signal, as well as evidence of shifts in the rate of evolution of genetic~~
451 ~~diversity on deep timescales in molluscs and chordates, seem to contradict Lynch's in comparative~~
452 ~~population genetic studies were warranted (Gillespie 1991; Whitney and Garland 2010). Notably,~~
453 ~~Lynch (2011) claim that since~~ has argued that PCMs for pairwise diversity are unnecessary, since
454 ~~mutation rate evolution is fast and thus free of phylogenetic inertia, sampling variance should~~
455 ~~exceed the variance due to phylogenetic shared history, and coalescent times are much less than~~
456 ~~divergence times, they are not affected by shared phylogenetic history. Since my findings suggest~~
457 ~~PCMs are necessary in some cases, it is worthwhile to address these points.~~

458 ~~One can reconcile my findings with Lynch's claim by considering what evolutionary, ecological,~~
459 ~~life history, and demographic causal factors determine coalescent rates across species, and how these~~
460 ~~factors evolve across deep timescales. Lynch's conjecture that coalescent times~~ First, Lynch has
461 ~~correctly pointed out that while coalescent times are much less than divergence times and should be~~
462 ~~free of phylogenetic signal may be true shared history, the factors that determine coalescent times~~
463 ~~(e.g. mutation rates and effective population size) may not be (2011). In other words, coalescent~~
464 ~~times are free from phylogenetic shared history were we to condition on these causal factors that~~
465 ~~could be affected by shared phylogenetic history. In contrast, my My estimates of phylogenetic~~
466 ~~signal in diversity, by contrast, are not conditioned on these factors. Importantly, even "correcting~~
467 ~~for" phylogeny implicitly favors certain causal interpretations over others (Uyeda et al. 2018; West-~~
468 ~~oby et al. 1995). Future work could try to untangle what causal factors determine coalescent times~~
469 ~~across species, as well as how these factors evolve across macroevolutionary timescales. Second, it~~
470 ~~is a misconception that a fast rate of trait evolution necessarily reduces phylogenetic signal (Revell~~
471 ~~et al. 2008), and that if either or both variables in a regression are free of phylogenetic signal,~~
472 ~~PCMs are unnecessary (Revell 2010; Uyeda et al. 2018). The evidence of high phylogenetic signal~~
473 ~~found in this study suggests PCMs are needed, in part to avoid spurious results from phylogenetic~~
474 ~~pseudoreplication.~~

475 ~~Furthermore~~ Finally, beyond just accounting for phylogenetic non-independence, macroevolution
476 and phylogenetic comparative methods are a promising way to approach across-species population
477 genomic questions. For example, one could imagine that diversification processes could contribute
478 to Lewontin's Paradox. If large- N_c species were to have a rate of speciation that is greater than the
479 rate at which mutation and drift reach equilibrium (which is indeed slower for large N_c species), this
480 could act to decouple diversity from census population size. That is to say, even if the rate of random
481 demographic bottlenecks were constant across taxa, lineage-specific diversification processes could
482 lead certain clades to be systematically further from demographic equilibrium, and thus have lower
483 diversity than expected for their census population size.

484 Spatial and Demographic Processes

485 One limitation of this study is the inability to quantify the impact of spatial population genetic pro-
486 cesses on the relationship between diversity and census population sizes across taxa. The genomic
487 diversity estimates collated in this study unfortunately lack details about the sampling process
488 and spatial data, which can have a profound impact on population genomic summary statistics
489 (Battey et al. 2020). These issues could systematically bias species-wide diversity estimates; for
490 example, if diversity estimates from a cosmopolitan species were primarily from a single subpop-
491 ulation, diversity would be an underestimate relative to the entire population. However, biased
492 spatial sampling alone seems incapable of explaining the π - N_c divergence in high- N_c taxa. In the
493 extreme scenario in which only one subpopulation was sampled, F_{ST} would need to be close to
494 one for population subdivision alone to sufficiently reduce the total population heterozygosity to
495 explain the orders-of-magnitude shortfall between predicted and observed diversity levels. This is
496 because the equation for F_{ST} can be rearranged such that $H_S = (1 - F_{ST})H_T$, where H_S and H_T
497 are the subpopulation and total population heterozygosities; if $H_T = 4N_c\mu$, then only $F_{ST} \approx 1$ can
498 reduce H_S several orders of magnitude. Yet, across-taxa surveys indicate that F_{ST} is almost never
499 this high within species (Roux et al. 2016). Still, future work could quantify the extent to which
500 spatial processes contribute to Lewontin’s Paradox. For example, high- N_c taxa usually experience
501 range expansions, likely with repeated founder effects and local extinction/recolonization dynamics
502 that doubtlessly depress diversity. In particular, with the appropriate data, one could estimate the
503 empirical relationship between dispersal distance, range size, and coalescent effective population
504 size across taxa.

505 In this study, I have focused entirely on assessing the role of linked selection, rather than
506 demography, in reducing diversity across taxa. In contrast to demographic models, models of
507 linked selection have comparatively fewer parameters and more readily permit rough estimates
508 of diversity reductions across taxa. Still, a full resolution of Lewontin’s Paradox would require
509 understanding how the demographic processes across taxa with incredibly heterogeneous ecologies
510 and life histories transform N_c into N_e . With population genomic data becoming available for more
511 species, this could involve systematically inferring the demographic histories of tens of species and
512 looking for correlations in the frequency and size of bottlenecks with N_c across species.

513 How could selection still explain Lewontin’s Paradox?

514 In this study, my goal was not to accurately estimate the levels in diversity across species, but
515 rather to give linked selection the best possible chance to solve Lewontin’s Paradox. Still, I find
516 that even after parameterizing hitchhiking and background selection with strong selection param-
517 eter estimates from *Drosophila melanogaster*, the predicted patterns of diversity under linked se-
518 lection poorly fit observed patterns of diversity across species. ~~While~~ This result extends the
519 analysis by Coop (2016) showing that levels of π_0 estimated by Corbett-Detig et al. (2015) are not
520 decoupled from genome-wide average π , as would occur if linked selection were to explain Lewontin’s
521 Paradox. Here, my analysis goes a step further and suggests that models of recurrent hitchhiking
522 and background selection are not capable of explaining the observed relationship between π and
523 census size, in part because mid- N_c species have sufficiently long recombination map lengths to
524 diminish the effects of even strong selection. This finding supports the idea the levels of diversity
525 across species are primarily determined by past demographic fluctuations. Overall, while this sug-
526 gests these two common modes of linked selection seem unlikely to explain across-taxa patterns of

527 diversity, there are three major potential limitations of my approach that need further evaluation.

528 First, I approximate the reduction in diversity using homogeneous background selection and
529 recurrent hitchhiking models (Coop and Ralph 2012; Hudson and Kaplan 1995; Kaplan et al. 1989),
530 when in reality, there is genome-wide heterogeneity in functional density, recombination rates, and
531 the adaptive substitutions across species. Each of these factors mediate how strongly linked selection
532 impacts diversity across the genome. Despite these model simplifications, the predicted reduction
533 in diversity in *Drosophila melanogaster* is 85% (when using N_e , not N_c), which is reasonably close
534 to the estimated 77% from the more realistic model of Elyashiv et al. that accounts for the actual
535 position of substitutions, annotation features, and recombination rate heterogeneity (though it
536 should be noted that these both use the same parameter estimates). Furthermore, even though
537 my model fails to capture the heterogeneity of functionality density and recombination rate in
538 real genomes, it is still extraordinary conservative, ~~giving linked selection the best possible chance~~
539 ~~to decouple~~ likely overestimating the effects of linked selection to see if it could be capable of
540 decoupling diversity from census size and explain Lewontin’s Paradox. This is in part because
541 the strong selection parameter estimates from *Drosophila melanogaster* used, but also because I
542 assume that the effective population size is equal to the census size. Even then, this decoupling
543 only occurs in very high-census-size species, and implies that the diversity in the absence of linked
544 selection, π_0 , is currently underestimated by several orders of magnitude. Moreover, the study of
545 Corbett-Detig et al. (2015) did consider recombination rate and functional density heterogeneity in
546 estimating the reduction due to linked selection across species, yet their predicted reductions are
547 orders of magnitude weaker than those considered here by assuming that $N_e = N_c$ (Supplementary
548 Figure S13B). Overall, even with more realistic models of linked selection, current models of linked
549 selection seem fundamentally unable to fit the diversity-census-size relationship.

550 Second, my model here only considers hard sweeps, and ignores the contribution of soft sweeps
551 (e.g. from standing variation or recurrent mutations; Hermisson and Pennings 2005; Pennings
552 and Hermisson 2006), partial sweeps (e.g those that do not reach fixation), and the interaction
553 of sweeps and spatial processes. While future work exploring these alternative types of sweeps
554 is needed, the predicted reductions in diversity found here under the simplified sweep model are
555 likely relatively robust to these other modes of sweeps for a few reasons. First, the shape of
556 the diversity-recombination curve is equivalent under models of partial sweeps and hard sweeps,
557 though these imply different rates of sweeps (Coop and Ralph 2012). Second, in the limit where
558 most fitness variation is due to weak soft sweeps from standing variation scattered across the
559 genome (i.e. due to polygenic fitness variation), levels of diversity are well approximated by quan-
560 titative genetic linked selection models (~~QGLS Robertson 1961; Santiago and Caballero 1995, 1998~~
561 ~~)~~(Robertson 1961; Santiago and Caballero 1995, 1998). The reduction in diversity under these mod-
562 els is nearly identical to that under background selection models, in part because deleterious alleles
563 at mutation-selection balance constitute a considerable component of fitness variation (see Ap-
564 pendix Section A2; Charlesworth 2015; Charlesworth and Hughes 2000). Third, the parameters
565 from Elyashiv et al. (2016) are robust to many types of sweeps that result in substitution (e.g.
566 see p. 19 of their Supplementary Online Materials). Finally, I also disregarded the interaction of
567 sweeps and spatial processes. For populations spread over wide ranges, limited dispersal slows the
568 spread of sweeps, allowing for new beneficial alleles to arise, spread, and compete against other
569 segregating beneficial variants (Ralph and Coop 2010; Ralph and Coop 2015). Through limited
570 dispersal should act to “soften sweeps” and not impact my findings for the reasons described above,
571 future work could investigate how these processes impact diversity in ways not captured by hard

572 sweep models.

573 Third, other selective processes, such as fluctuating selection or hard selective events, could
574 reduce diversity in ways not captured by the background selection and hitchhiking model. Since
575 frequency-independent fluctuating selection generally reduces diversity under most conditions (No-
576 vak and Barton 2017), this could lead seasonality and other sources of temporal heterogeneity to
577 reduce diversity in large- N_c species with short generation times more than longer-lived species with
578 smaller population sizes. Future work could consider the impact of fluctuating selection on diver-
579 sity under simple models (Barton 2000) if estimates of key parameters governing the rate of such
580 fluctuations were known across taxa. Additionally, another mode of selection that could severely
581 reduce diversity across taxa, yet remains unaccounted for in this study, is periodic hard selective
582 events. These selective events could occur regularly in a species' history yet be indistinguishable
583 from demographic bottlenecks ~~from~~ with just population genomic data.

584 Measures of Effective Population Size, Timescales, and Lewontin's Paradox

585 Lewontin's Paradox ~~shows~~ describes the extent to which the effective population sizes implied by
586 diversity, \tilde{N}_e , diverge from census population sizes. However, there are a variety other effective
587 population size estimates calculable from different data and summary statistics (Caballero 1994;
588 Caballero 2020; Galtier and Rousselle 2020; Wang et al. 2016). These include estimators based on
589 the site frequency spectrum, observed decay in linkage disequilibrium, or temporal estimators that
590 use the variance in allele frequency change. These alternate estimators capture summaries of the
591 effective population size on shorter timescales than coalescent-based estimators (Wang 2005), and
592 thus could be used to tease ~~out~~ apart processes that impact the N_e - N_c relationship in the more
593 recent past.

594 Temporal N_e estimators already play an important role in understanding another summary of
595 the N_e - N_c relationship: the ratio N_e/N_c , which is an important quantity in conservation genetics
596 (Frankham 1995; Mace and Lande 1991) and in understanding evolution in highly-~~fecund~~ highly
597 fecund marine species. Surveys of the short-term N_e/N_c relationship across taxa indicate mean N_e/N_c
598 is on order of ≈ 0.1 (Frankham 1995; Palstra and Fraser 2012; Palstra and Ruzzante 2008), though
599 the uncertainty in these estimates is high, and some species with sweepstakes reproduction systems
600 like Pacific Oyster (*Crassostrea gigas*) can have $N_e/N_c \approx 10^{-6}$. Estimates of the N_e/N_c ratio are
601 an important, ~~and yet~~ under appreciated piece of solving Lewontin's Paradox. For example, if N_e
602 is estimated from the allele frequency change across a single generation (i.e. Waples 1989), N_e/N_c
603 constrains the variance in reproductive success (Nunney 1993, 1996; Wright 1938). This implies that
604 apart from species with sweepstakes reproductive systems, the variance in reproductive success
605 each generation (whether heritable or non-heritable) is likely insufficient to significantly contribute
606 to constraining \tilde{N}_e for most taxa. Still, further work is needed to characterize (1) how N_e/N_c varies
607 with N_c across taxa (though see Palstra and Fraser 2012, Figure 2), and (2) the variance of N_e/N_c
608 over longer time spans (i.e. how periodic sweepstakes reproductive events act to constrain N_e).
609 Overall, characterizing how N_e/N_c varies across taxa and correlates with ecology and life history
610 traits could provide clues into the mechanisms that leads propagule size and survivorship curves to
611 be predictive of diversity levels across taxa (Barry et al. 2020; Hallatschek 2018; Romiguier et al.
612 2014).

613 Finally, short-term temporal N_e estimators may play an important role in resolving Lewontin's
614 Paradox. These estimators, along with short-term estimates of the impact of linked selection
615 (Buffalo and Coop 2019, 2020), can inform us how much diversity is depressed across shorter

616 timescales, free from the rare strong selective events or severe bottlenecks that impact pairwise
617 diversity. It could be that in any one generation, selection contributes more to the variance of allele
618 frequency changes than drift, yet across-taxa patterns in diversity are better explained processes
619 acting sporadically on longer timescales, such as colonization, founder effects, and bottlenecks.
620 Thus, the pairwise diversity may not give us the best picture of the generation to generation
621 evolutionary processes acting in a population to change allele frequencies. Furthermore, certain
622 observed adaptations are inexplicable given implied long-term coalescent effective population sizes,
623 and are only possible if short-term effective population sizes are orders of magnitude larger (Barton
624 2010; Karasov et al. 2010).

625 Conclusions

626 In *Building a Science of Population Biology* (2004), Lewontin laments the difficulty of uniting pop-
627 ulation genetics and population ecology into a cohesive discipline of population biology. Lewontin's
628 Paradox of Variation remains a critical unsolved problem at the nexus of these two different dis-
629 ciplines: across species, we fail to understand the processes that connect a central parameter of
630 population ecology, census size, to a central parameter of population genetics, effective population
631 size. Given that selection seems to fall short in explaining Lewontin's Paradox, a full resolution will
632 require a mechanistic understanding the ecological, life history, and macroevolutionary processes
633 that connect N_c to N_e across taxa. While I have focused exclusively on metazoan taxa since their
634 population densities are more readily approximated from body mass, a full resolution must also
635 include plant species (with the added difficulties of variation in selfing rates, different dispersal
636 strategies, pollination, etc.).

637 Looking at Lewontin's Paradox through an macroecological and macroevolutionary lens begets
638 interesting questions outside of the [traditional](#) realm of population genetics. Here, I have found that
639 diversity and N_c have a surprisingly consistent relationship without many outliers, despite the wildly
640 disparate ecologies, life histories, and evolutionary histories of the taxa included. Furthermore, taxa
641 with very large census sizes have surprisingly low diversity. Is this explained by macroevolutionary
642 processes, such as different rates of speciation for large- N_c taxa? Or, are the levels of diversity
643 we observe today an artifact of our timing relative to the last glacial maximum, or the last major
644 extinction? Did large- N_c prehistoric animal populations living in other geological eras have higher
645 levels of diversity than our present taxa? Or, does ecological competition occur on shorter timescales
646 such that strong population size contractions transpire and depress diversity, even if a species is
647 undisturbed by climatic shifts or mass extinctions? Overall, patterns of diversity across taxa are
648 determined by many overlaid evolutionary and ecological processes occurring on vastly different
649 timescales. Lewontin's Paradox of Variation may persist unresolved for some time because the
650 ~~solution~~-[explanation](#) requires synthesis and model building at the intersection of all these disciplines.

651 Methods

652 Diversity and Map Length Data

653 The data used in this study are collated from a variety of previously published surveys. Of the
654 172 taxa with diversity estimates, 14 are from Corbett-Detig et al. (2015), 96 are from Leffler
655 et al. (2012), and 62 are from Romiguier et al. (2014). The Corbett-Detig et al. data is estimated
656 from four-fold degenerate sites, the Romiguier et al. data is synonymous sites, and the Leffler

657 et al. data is estimated predominantly from silent, intronic, and non-coding sites. All types of
658 diversity estimates from Leffler et al. (2012) were included to maximize the taxa in the study, since
659 the variability of diversity across functional categories is much less than the diversity across taxa.
660 Multiple diversity estimates per taxa were averaged. The total recombination map length data
661 were from both Stapley et al. (2017; ~~30-127~~ taxa), and Corbett-Detig et al. (2015; ~~11-9~~ taxa).
662 Both studies used sex-averaged recombination maps estimated with cross-based approaches; in
663 some cases errors in the original data were found, documented, and corrected. These studies also
664 included genome size estimates used to create Supplementary Figures S7 and S8.

665 Macroecological Estimates of Population Size

666 A rough approximation for total population size (census size) is $N_c = DR$, where D is the population
667 density in individuals per km^2 and R is the range size in km^2 . Since population density estimates
668 are not available for many taxa included in this study, I used the macroecological abundance-body
669 size relationship to predict population density from body size. Since body length measurements
670 are more readily available than body mass, I collated body length data from various sources (see
671 https://github.com/vsbuffalo/paradox_variation/); body lengths were averaged across sexes
672 for sexually dimorphic species, and if only a range of lengths was available, the midpoint was used.

673 Then, I re-estimated the relationship between body mass and population density using the data
674 in the appendix table of Damuth (1987), which includes 696 taxa with body mass and population
675 density measurements across mammals, fish, reptiles, amphibians, aquatic invertebrates, and ter-
676 restrial arthropods. Though the abundance-body size relationship can be noisy at small spatial
677 or phylogenetic scales (Chapter 5, Gaston and Blackburn 2008), across deeply diverged taxa such
678 as those included in this study and Damuth (1987), the relationship is linear and homoscedastic
679 (see Supplementary Figure S11). Using Stan (Stan Development Team 2020), I jointly estimated
680 the relationship between body mass from body length using the Romiguier et al. (2014) taxa, and
681 used this relationship to predict body mass for the taxa in this study. These body masses were
682 then used to predict population density simultaneously, using the Damuth (1981) relationship. The
683 code of this routine (`pred_popsizemissing_centered.stan`) is available in the GitHub repository
684 (https://github.com/vsbuffalo/paradox_variation/).

685 To estimate range, I first downloaded occurrence records from Global Biodiversity Informa-
686 tion Facility (*GBIF Occurrence Download* 2020) using the `rgbif` R package (Chamberlain and
687 Boettiger 2017; Chamberlain et al. 2014). Using the occurrence locations, I inferred whether a
688 species was marine or terrestrial, based on whether the majority of their recorded occurrences over-
689 lapped a continent using `rnaturalearth` and the `sf` packages (Pebesma 2018; South 2017). For
690 each taxon, I estimated its range by finding the minimum α -shape containing these occurrences.
691 The α parameters were set more permissive for marine species since occurrence data for marine
692 taxa were sparser. Then, I intersected the inferred ranges for terrestrial taxa with continental
693 polygons, so their ranges did not overrun landmasses (and likewise with marine taxa and oceans).
694 I inspected diagnostic plots for each taxa for quality control (all of these plots are available in
695 `paradox_variation` GitHub repository), and in some cases, I manually adjusted the α parameter
696 or manually corrected the range based on known range maps (these changes are documented in
697 the code `data/species_ranges.r` and `data/species_range_fixes.r`). The range of *C. elegans*
698 was conservatively approximated as the area of the Western US and Western Europe based on
699 the map in Frézal and Félix (2015). *Drosophila* species ranges are from the *Drosophila* Speciation
700 Patterns website, (Yukilevich 2017; Yukilevich 2012). To further validate these range estimates,

701 I have compared these to the qualitative range descriptions Leffler et al. (2012) (Supplementary
702 Figure S10) and compared my α -shape method to a subset of taxa with range estimates from IUCN
703 Red List (Chamberlain 2020; IUCN 2020; Supplementary Figure S9). Each census population size
704 is then estimated as the product of range and density.

705 Phylogenetic Comparative Methods

706 Of the full dataset of 172 taxa with diversity and population size estimates, a synthetic calibrated
707 phylogeny was created for 166 species that appear in phylogenies in DateLife project (O’Meara et al.
708 2020; Sanchez-Reyes and O’Meara 2019). This calibrated synthetic phylogeny was then subset for
709 the analyses based on what species had non-missing-complete trait data. The diversity-population
710 size relationship assessed by a linear phylogenetic mixed-effects model implemented in Stan (Stan
711 Development Team 2020), according to the methods described in (Villemereuil and Nakagawa 2014,
712 see `stan/phylo_mm_regression.stan` in the GitHub repository). This same Stan model was used
713 to estimate the same relationship between arthropod, chordate, and mollusc subsets of the data,
714 though a reduced model was used for the chordate subset due to identifiability issues leading to
715 poor MCMC convergence (Supplementary Figure S15).

716 The relationship between recombination map length and the logarithm of population size is non-
717 linear and heteroscedastic, and was fit using a lognormal phylogenetic mixed-effects model on the
718 130 species with complete data. Since social insects have longer recombination map lengths (Wilfert
719 et al. 2007), social taxa were excluded when fitting this model. All R_{hat} (Vehtari et al. 2019) values
720 were below 1.01 and the effective number of samples was over 1,000, consistent with good mixing;
721 details about the model are available in the GitHub repository (`phylo_mm_lognormal.stan`).
722 Continuous trait maps (Figure 3A and Supplementary Material-Information Figure S17) were cre-
723 ated using `phytools` (Revell 2012). Node-height tests were implemented based on the methods
724 in `Geiger` (Harmon et al. 2008; Pennell et al. 2014), and use robust regression to fit a linear
725 relationship between phylogenetic independent contrasts and branching times.

726 Predicted Reductions in Diversity

727 The predicted reductions in diversity due to linked selection are approximated using selection and
728 deleterious mutation parameters from *Drosophila melanogaster*, and the recombination map length
729 estimates from Stapley et al. (2017) and Corbett-Detig et al. (2015). The mathematical details of
730 the simplified sweep model are explained in the Appendix Section A1. I use estimates of the number
731 of substitutions, m , in genic regions between *D. melanogaster* and *D. simulans* from Hu et al. (2013).
732 Following Elyashiv et al. (2016), only substitutions in UTRs and exons are included, since they
733 found no evidence of sweeps in introns. Then, I average over annotation classes to estimate the
734 mean proportion of substitutions that are beneficial, $\alpha_{\text{Dmel}} = 0.42$, which are consistent with the
735 estimates of Elyashiv et al. and estimates from MacDonald–Kreitman test approaches (see Eyre-
736 Walker 2006, Table 1). Then, I use divergence time estimates between *D. melanogaster* and *D.*
737 *simulans* of 4.2×10^6 and estimate of ten generations per year (Obbard et al. 2012), calculating
738 there are $\gamma_{\text{Dmel}} = \alpha m / 2T = 2.26 \times 10^{-3}$ substitutions per generation. Given the length of the
739 *Drosophila* autosomes, G , this implies that the rate of beneficial substitutions per basepair, per
740 generation is $\nu_{BP, Dmel} = \gamma_{\text{Dmel}} / G = 2.34 \times 10^{-11}$. Finally, I estimate J_{Dmel} from the estimate of
741 genome-wide average rate of sweeps from Elyashiv et al. (Supplementary Table S6) and assuming
742 *Drosophila* $N_e = 10^6$. These *Drosophila melanogaster* hitchhiking parameter estimates are close to

743 other previously-published estimates (Supplementary Figure S14). Finally, I use $U_{\text{Dmel}} = 1.6$, from
744 Elyashiv et al. (2016). With these parameter estimates from *D. melanogaster*, the recombination
745 map lengths across species, and Equation (1), I estimate $\pi_{\text{BGS+HH}}$ (assuming $N_c = N_c$) across
746 all species. This leads to a range of predicted diversity ranges across species corresponding to
747 $\mu = 10^{-8}$ – 10^{-9} ; to visualize these, I take a convex hull of all diversity ranges and smooth this with
748 R’s `smooth.spline` function.

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761 Appendix

762 A1 Simplified Sweep Effects Model

763 I use a simplified model of the effects of recurrent hitchhiking and background selection (BGS)
764 occurring uniformly along a genome. Expected diversity is given by

$$\mathbb{E}(\pi) = \frac{\theta}{\theta + 1/B + 2NS} \quad (\text{A2})$$

$$\approx \frac{\theta}{1/B + 2NS} \quad (\text{A3})$$

765 (cf. equation 1 Elyashiv et al. 2016, and equation 20 of Coop and Ralph 2012). The BGS component
766 is given by Hudson and Kaplan (1995),

$$B(U, L) = N_e \exp\left(-\frac{U}{L}\right) \quad (\text{A4})$$

767 and the hitchhiking component is

$$S = \frac{\nu_{\text{BP}}}{r_{\text{BP}}} J \quad (\text{A5})$$

768 (cf. Coop and Ralph 2012 equation 20) where J is the probability that two lineages coalesce down
 769 to one, given sweeps occur uniformly along the genome. Under this homogeneous sweep model, J
 770 is

$$J = \int_0^L q_f(r)^2 dr \quad (\text{A6})$$

771 where $q_f(r)$ is the approximate probability that a lineage is trapped by a sweep to frequency f
 772 when it is r recombination fraction away from this sweep (cf. Coop and Ralph 2012 equation 15).

773 Since I use *Drosophila melanogaster* parameter estimates from Elyashiv et al. (2016), I now
 774 reconcile their model's S term with the simple model above. They estimate S in *Drosophila*
 775 *melanogaster* using a composite likelihood model that considers hitchhiking and background selec-
 776 tion simultaneously, using substitutions and stratifying by annotation. For a neutral position at
 777 site x , the coalescent rate due to sweeps is given by Elyashiv et al.'s equation 3,

$$S(x) = \frac{1}{T} \sum_{i_S} \alpha(i_S) \sum_{y \in a(i_S)} \int \exp(-r(x, y)\tau(s, N))g(s|i_S)ds \quad (\text{A7})$$

778 where T is the number of generations that substitutions accrue, $i_S = 1, \dots, I_S$ is the annotation
 779 class (e.g. exons, introns, UTRs), $\alpha(i_S)$ is the fraction of substitutions in annotation class i_S that
 780 are beneficial, $a(i_S)$ is the set of all substitutions in annotation class i_S , $\tau(s, N)$ is the fixation time
 781 of a site with additive effect s , and $g(s|i_S)$ is the distribution of selection coefficients for annotation
 782 class i_S .

783 Note, that we can recover the model of Coop and Ralph (2012) from this expression. Suppose
 784 there is only one annotation class, and α fraction of substitutions are beneficial, and one selection
 785 coefficient \bar{s} , (i.e. $g(s) = \delta_0(s - \bar{s})$), then

$$S(x) = \frac{\alpha}{T} \sum_{y \in a} \exp(-r(x, y)\tau(\bar{s}, N)). \quad (\text{A8})$$

786 Let the number of substitutions be $m := |a|$, and imagine their positions are uniformly dis-
 787 tributed on a segment of length G basepairs with the focal site is the middle at position $x = 0$.
 788 Then, each substitution y is a random distance $l_y \sim U(-G/2, G/2)$ away from the focal site. As-
 789 suming the recombination rate is a constant r_{BP} per basepair, and approximating the sum with an
 790 integral, we have,

$$S = \frac{\alpha}{T} \sum_{i=1}^m \mathbb{E}_{l_i} (\exp(-r_{\text{BP}}l_i\tau(\bar{s}, N))) \quad (\text{A9})$$

$$= \frac{\alpha}{TG} \sum_{i=1}^m \int_0^G \exp(-r_{\text{BP}}\ell\tau(\bar{s}, N))d\ell \quad (\text{A10})$$

$$= \frac{\alpha m}{TG} \int_0^G \exp(-r_{\text{BP}}\ell\tau(\bar{s}, N))d\ell \quad (\text{A11})$$

791 Using u -substitution with $r = \ell r_{\text{BP}}$ this simplifies to

$$S = \frac{\alpha m}{T G r_{\text{BP}}} \int_0^L \exp(-r\tau(\bar{s}, N)) dr \quad (\text{A12})$$

792 where $L = G r_{\text{BP}}$.

793 To simplify this notation, note that the rate of adaptive substitutions per basepair per generation
794 is $\nu_{\text{BP}} = \alpha m / GT$, so

$$S = \frac{\nu_{\text{BP}}}{r_{\text{BP}}} \int_0^L \exp(-r\tau(\bar{s}, N)) dr \quad (\text{A13})$$

795 This is analogous to the second term of Coop and Ralph (2012) equation 17, with $k = i = 2$
796 and $x = 1$ (e.g. conditioning on a sweep to fixation). Note that there appears to be a factor of
797 two error in Elyashiv et al. (2016) compared to Coop and Ralph (2012); here I include the factor
798 of two. Then,

$$S = \frac{\nu_{\text{BP}}}{r_{\text{BP}}} \underbrace{\int_0^L \exp(-2r\tau(\bar{s}, N)) dr}_J \quad (\text{A14})$$

799 where the integral is equal to J (c.f. $J_{2,2}$ of equation 15 in Coop and Ralph 2012) since a simple
800 model of $q_f(r) = f \exp(-2r\tau(s, N))$ and if we condition on fixation, $f = 1$. This expression is useful
801 to generalize across species, since we know N and L . Additionally, we have estimates of α and
802 m/T in *Drosophila* and other species. In Elyashiv et al, they consider the number of substitutions
803 per generation in genic regions only; it should be noted that the number of coding basepairs varies
804 little across species. For convenience, I define $\gamma = \alpha m / T$ as the number of adaptive substitutions
805 per generation per entire genome, such that $S(\gamma, L, J) = \gamma / L J$ used in the main text. Using the
806 estimates of $m \approx 4.5 \times 10^5$, $\alpha \approx 0.42$, and $T \approx 8.4 \times 10^7$ from the Supplementary Material of
807 Elyashiv et al., I arrive at $\gamma \approx 0.00226$ adaptive substitutions per generation, per genome. For
808 a ≈ 100 megabase genome, this translates to a $\nu_{\text{BP}} \approx 2.34 \times 10^{-11}$, which is close to previous
809 estimates (Supplementary Figure S14). For J , I use an empirical estimate calculated from the
810 genome-wide average of the rate of coalescent events due to sweeps, from Supplementary Table
811 S6 of Elyashiv et al. ($r_s = 2NS \approx 0.92$). This implies $J \approx 4.46 \times 10^{-4}$. Alternatively, I have
812 tried using the estimated distribution of selection coefficients from Elyashiv et al., but this led to
813 a weaker estimate of J , since the adaptive substitutions considered tend to cluster around genic
814 regions. Note that these *Drosophila* sweep parameters I have used are close to previous estimates
815 (Supplementary Figures S14 A and B).

816 A2 Background Selection and Polygenic Fitness Models

817 Throughout the main text, I use recurrent hitchhiking and background selection models to estimate
818 the reduction in diversity due to linked selection. Another class of linked selection models, which
819 I refer to as quantitative genetic linked selection models (QGLS; Robertson 1961; Santiago and

820 Caballero 1995, 1998), can also depress genome-wide diversity. Furthermore, these models may
821 depress diversity at neutral sites unlinked to the regions containing fitness variation. While I did
822 not explicitly incorporate these models into my estimates of the diversity reductions, their effect
823 is implicit in background selection models because they are analytically nearly identical. Here, I
824 briefly sketch out the connection between BGS and QGLS models.

825 Under the Santiago and Caballero (1998) model, the effective population size is $N_e^{\text{SC98}} =$
826 $N \exp(-C^2/(1-Z)L)$, where C^2 is the standardized heritable fitness variation, $1 - Z$ is the decay
827 of genetic variance through time, and L is the recombination map length. This model can ac-
828 commodate a variety of modes of selection such as selection on an infinitesimal trait (Santiago and
829 Caballero 1995, p. 1016), and the flux of either weakly advantageous or deleterious alleles (Santiago
830 and Caballero 1998, p. 2109). If the source of fitness variation is entirely the input of new deleteri-
831 ous mutations with heterozygous effect sh at rate U per diploid genome per generation, then under
832 mutation-selection balance, the equilibrium relative variance in reproductive success $C^2 = Ush$
833 (Crow and Kimura 1970; Caballero 2020, p. 167), and $Z = 1 - sh - 1/2N_c$ (Santiago and Caballero
834 1998). Thus, if $1/2N_c \ll sh \ll 1$, then $C^2/(1-Z) \approx U$ and $N_e^{\text{SC98}} \approx N \exp(-U/L)$, which is the
835 BGS model used in the main text and is a result of many background selection models with similar
836 assumptions (Hudson and Kaplan 1994 eqn. 15; Hudson and Kaplan 1995 eqn. 9; Nordborg et al.
837 1996 eqn. 4; Barton 1995 eqn. 22b). Intuitively, the similarity of these models reflects the fact that
838 a substantial proportion of heritable fitness variation is caused by the continual flux of deleterious
839 alleles across the genome under mutation-selection balance (Charlesworth 2015; Charlesworth and
840 Hughes 2000).

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Supplementary ~~Table and Figures~~ Information

S1 Population Size Validation

I validated the approximate census sizes I have estimated here using a few approaches. First, to check broad consistency, I compared the implied biomass from my estimates of body mass and census size per species with estimates of the total carbon biomass on earth by phylum (Bar-On et al. 2018). For species i with wet body mass m_i and census size N_i , the implied biomass is $m_i N_i$. For all species in a phylum S , this total sample biomass is $b_S = \sum_{i \in S} m_i N_i$. I then compare this wet biomass to the carbon biomasses by phylum by Bar-On et al. (2018). Across animal species, the ratio of dry to wet body mass, and carbon body mass dry body mass varies little. In their study, Bar-On et al. assume wet body mass has a 70% water content, and 50% of dry body mass is carbon mass, leading to a wet body mass to carbon mass factor of $1-0.7/0.5 = 0.15$. I use this factor to convert the total wet biomass to carbon biomass per phylum.

phylum	total species (T)	Bar-On et al.				Present study			
		biomass (B)	prop. biomass	biomass (b)	prop. biomass	num. species (n)	factor overrepresented	prop. total species ($f = n/T$)	factor (b/B)
Arthropoda	1.26×10^6	1.20	0.4635	2.80×10^{-4}	0.0102	68	0.02	5.41×10^{-5}	4.31
Chordata	5.41×10^4	0.87	0.3357	2.67×10^{-2}	0.9715	68	2.89	1.26×10^{-3}	24.40
Annelida	1.70×10^4	0.20	0.0772	1.23×10^{-5}	0.0004	3	0.01	1.76×10^{-4}	0.35
Mollusca	9.54×10^4	0.20	0.0772	4.56×10^{-4}	0.0166	13	0.21	1.36×10^{-4}	16.70
Cnidaria	1.60×10^4	0.10	0.0386	3.07×10^{-5}	0.0011	2	0.03	1.25×10^{-4}	2.45
Nematoda	2.50×10^4	0.02	0.0077	4.03×10^{-6}	0.0001	1	0.02	4.00×10^{-5}	5.03

Table S1: How the total carbon biomass estimates by phylum from Bar-On et al. (2018) compare to the implied biomass estimates from this study. All biomass estimates are carbon biomass, and the proportions are of total biomass with respect to the study. The proportion of biomass in this study compared to the Bar-On et al. estimates Bar-On et al. (2018) indicates chordates are overrepresented and arthropods are underrepresented in the present study; the factor that each phylum is overrepresented is given in the eighth column. Total species by phylum estimates are from Chapman et al. (2009), Nicol (1969), Reaka-Kudla et al. (1996), and Zhang (2013). The ratio column is the ratio of total biomass implied by the N_c estimates of each species in a phylum to the actual biomass of that phylum.

First, I compared the relative carbon biomass in this study to the relative carbon biomass on earth per phylum. This shows that this study's sample over represents chordate biomass (by a factor of ~ 3), and under represents in arthropod biomass (by a factor of 0.02) relative to the proportion of carbon biomass of these phyla on earth (see column eight of Supplementary Table S1). Second, to check whether the carbon biomass per phylum in the sample was broadly consistent with the total on earth by phylum (B_S for phylum S), I calculated the expected sample biomass if species were sampled randomly from the total species in a phylum, ($B_S \times n_S/T_S$, where n_S is the total number of species in the sample in phylum S , T_S is the total number of species in phylum S on earth). The fraction of total species on earth included in the sample in this study is depicted in Supplementary Figure S2.

Next, I look at the ratio of sample biomass per phylum, b_S to this expected biomass per phylum (Supplementary Table S1). The consistency is quite close for this rough approach and the non-random sample of taxa included in this study. The carbon biomass estimates for chordates implied by the census size estimates are ~ 24 -fold higher than expected, but is well within reasonable expectations given that the chordate sample includes many larger-bodied domesticated species (and is a biased sample in other ways). Similarly, the implied arthropod carbon biomass is quite close to what one would expect. Overall, these values indicate that the census size estimates here do not

1197 lead to implied biomasses per phylum that are outside the range of plausibility.

1198 Additionally, note that the body mass based estimates of density for *Drosophila* are similar to
1199 previously used estimates in surveys of census size and diversity. Nei and Graur (1984) suggested
1200 a maximum of 5 *Drosophila* per m², including regions of the range that are not inhabitable. Across
1201 *Drosophila*, the body mass based estimates suggest 10^{6.7} – 10^{7.6} individuals per km², or 4.5 – 36.3
1202 individuals per m², which are consistent with this previous estimate. Nei and Graur’s estimates of
1203 *Drosophila pseudoobscura*’s census size are four orders of magnitude smaller than mine, but their
1204 approach uses a speculated ratio of population sizes of different *Drosophila* species rather than
1205 range sizes (Nei and Graur 1984, p. 81).

1206 As another consistency check, I looked at the rank order of mammals by biomass. Whale
1207 species have the first and third highest biomass with 11.4 and 3.9 megatons of carbon biomass
1208 (for *Balaenoptera bonaerensis* and *Eschrichtius robustus*, respectively). While this seems high,
1209 a recent study shows that across whale species, pre-whaling carbon biomass was at the tens of
1210 megatons level (Pershing et al. 2010, Table 1 and Figure 1). Given that my census size estimates
1211 represent populations at a macroecological equilibrium, they would not reflect reduced density due
1212 to whaling or other anthropogenic causes. Humans had the second largest biomass, followed by
1213 wolf species (*Canis lupus* and *C. latrans*); as with whales, the population sizes for wolf species
1214 represent pre-anthropogenic densities and are overestimates compared to current population sizes,
1215 as expected.

1216 Finally, there are other estimates of approximate population sizes for some species that I
1217 compared my estimates to. The United Nation’s FAOSTAT database estimates the total number
1218 of horses (*Equus caballus*) on earth as ~60 million; the estimate in this study is close to 40 million.
1219 For other domesticated species like chicken (*Gallus gallus*), estimates range from 25 million to 19.6
1220 billion (FAOSTAT statistics database 2021; Robinson et al. 2014); the present study’s estimate lies
1221 in the middle at ~175 million. Again, this is a known limitation of this method, as the range is
1222 estimated from occurrence data and does not consider species’ niches. This present study’s estimate
1223 of the number of king penguins (*Aptenodytes patagonicus*) is about 3 million; the population size
1224 was recently estimated as 2.23 million pairs (Shirihai 2008).

1225 **S2 Sensitivity Analysis**

1226 **S3 Diversity and IUCN Red List Status**

1227 I also investigated the relationship between species’ IUCN Red List categories (an ordinal scale of
1228 how threatened a species is) and both diversity and population size, finding that species categorized
1229 as more threatened have both smaller population sizes and reduced diversity, compared to non-threatened
1230 species (Supplementary Figure S3) consistent with past work (Spielman et al. 2004). A linear model
1231 of diversity regressed on population size has lower AIC when the IUCN Red List categories are
1232 included, and the estimates of the effect of IUCN status are all negative on diversity, though not all
1233 are significant in part because some categories have three or fewer species (Supplementary Table
1234 S3).

	mean	2.5 %	97.5 %
β_0	-2.70 - 2.80	-3.00 - 3.20	-2.40 - 2.50
β_{LC}	-0.37 - 0.39	-0.55 - 0.57	-0.19 - 0.21
β_{NT}	-0.19 - 0.22	-0.80 - 0.83	0.41 - 0.39
β_{VU}	-0.31 - 0.34	-0.81 - 0.84	0.19 - 0.16
β_{EN}	-0.39 - 0.40	-0.71 - 0.73	-0.06 - 0.07
β_{CR}	-0.03	-0.65	0.59
β_{N_c}	0.06 - 0.08	0.04 - 0.05	0.09 - 0.11

Table S2: The regression estimates of full IUCN Red List population size model for diversity, $\log_{10}(\pi) = \beta_0 + \beta_{LC}LC + \beta_{NT}NT + \beta_{VU}VU + \beta_{EN}EN + \beta_{CR}CR + \beta_{N_c} \log_{10}(N_c)$; $df = 165$. Using AIC to compare this full model to a reduced model of $\log_{10}(\pi) = \beta_0 + \beta_{N_c} \log_{10}(N_c)$, ~~$AIC_{full} = 203.99$~~ $AIC_{full} = 204.9$, ~~$AIC_{reduced} = 212.46$~~ $AIC_{reduced} = 216.4$.

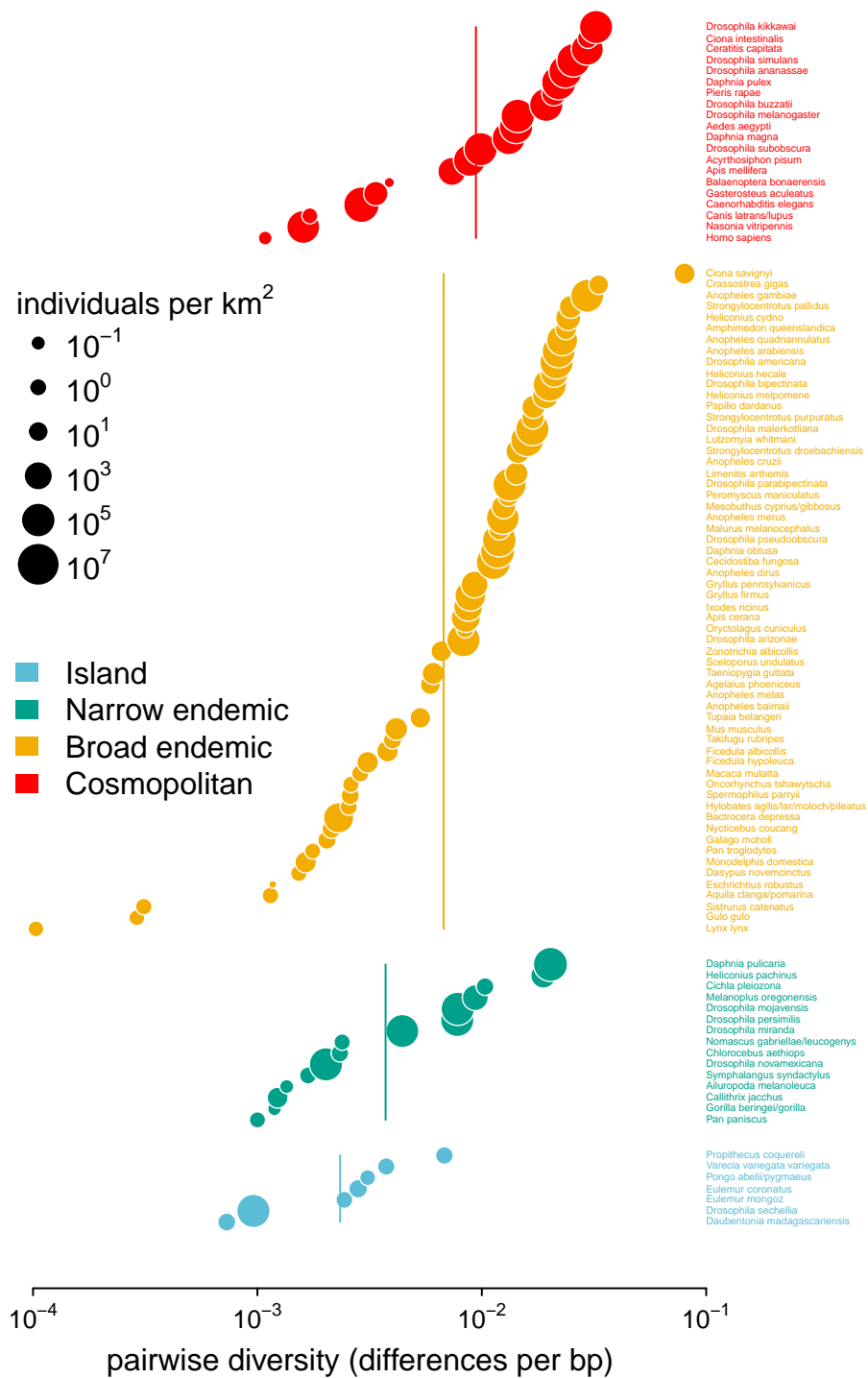


Figure S1: Pairwise diversity grouped by the range categories from Leffler et al. (2012), with point size indicating the predicted population density. The vertical lines are the range category group means.

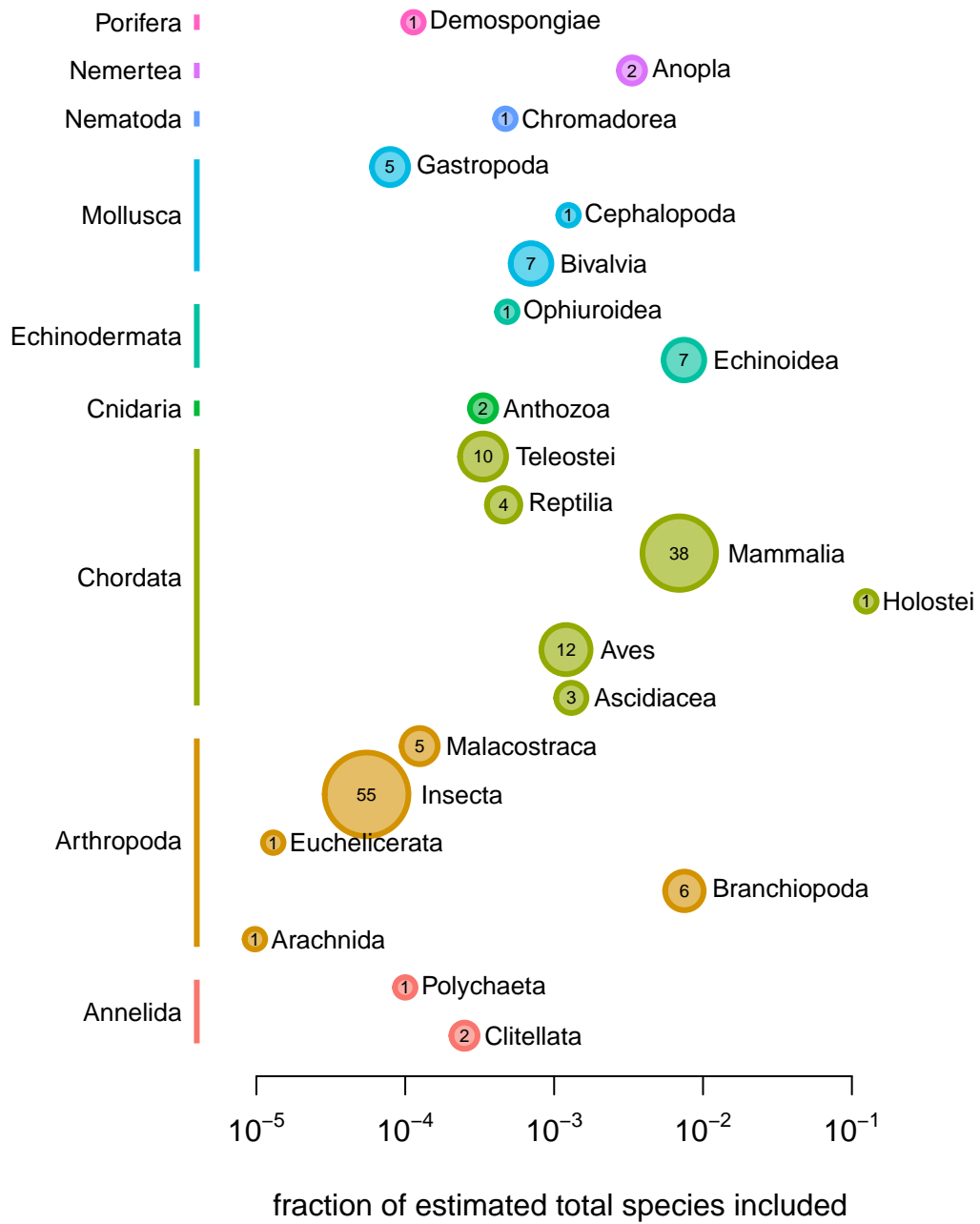


Figure S2: The fraction of total species on earth included in this study's sample, per class. The color of the points represents phylum, and the size of the point represents the absolute number of species by class.

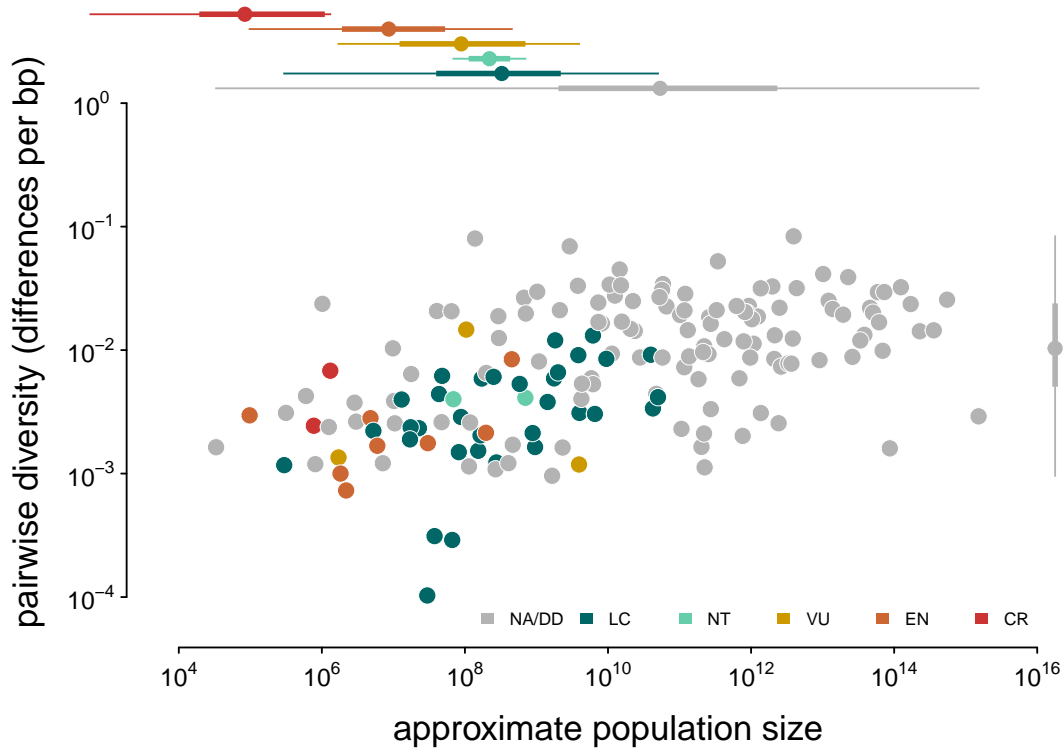


Figure S3: A version of Figure 2 with points colored by their IUCN Red List conservation status. Margin boxplots show the diversity and population size ranges (thin lines) and interquartile ranges (thick lines) for each category. NA/DD indicates no IUCN Red List entry, or Red List status Data Deficient; LC is Least Concern, NT is Near Threatened, VU is Vulnerable, EN is Endangered, and CR is Critically Endangered.

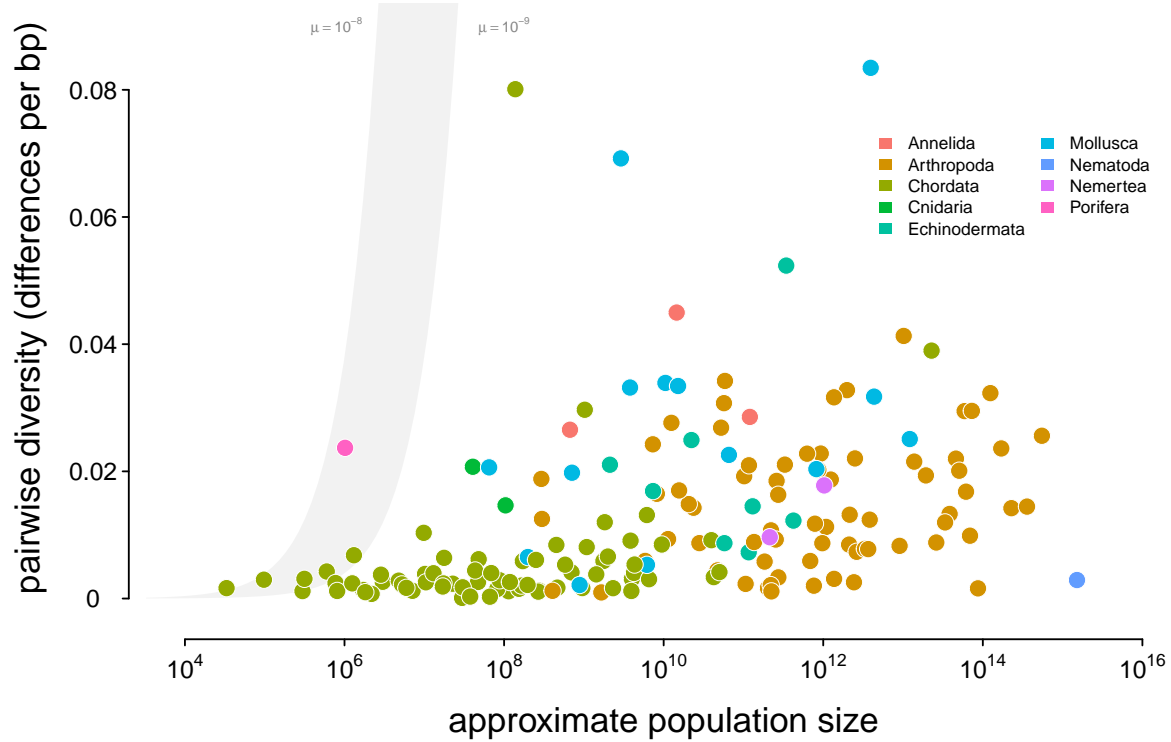


Figure S4: A version of Figure 2 with diversity on a linear, rather than log, scale. Points are colored by phylum, and the shaded region is the predicted neutral level of diversity assuming $N_e = N_c$ with mutation range ranging between $10^{-10} \leq \mu \leq 10^{-8}$.

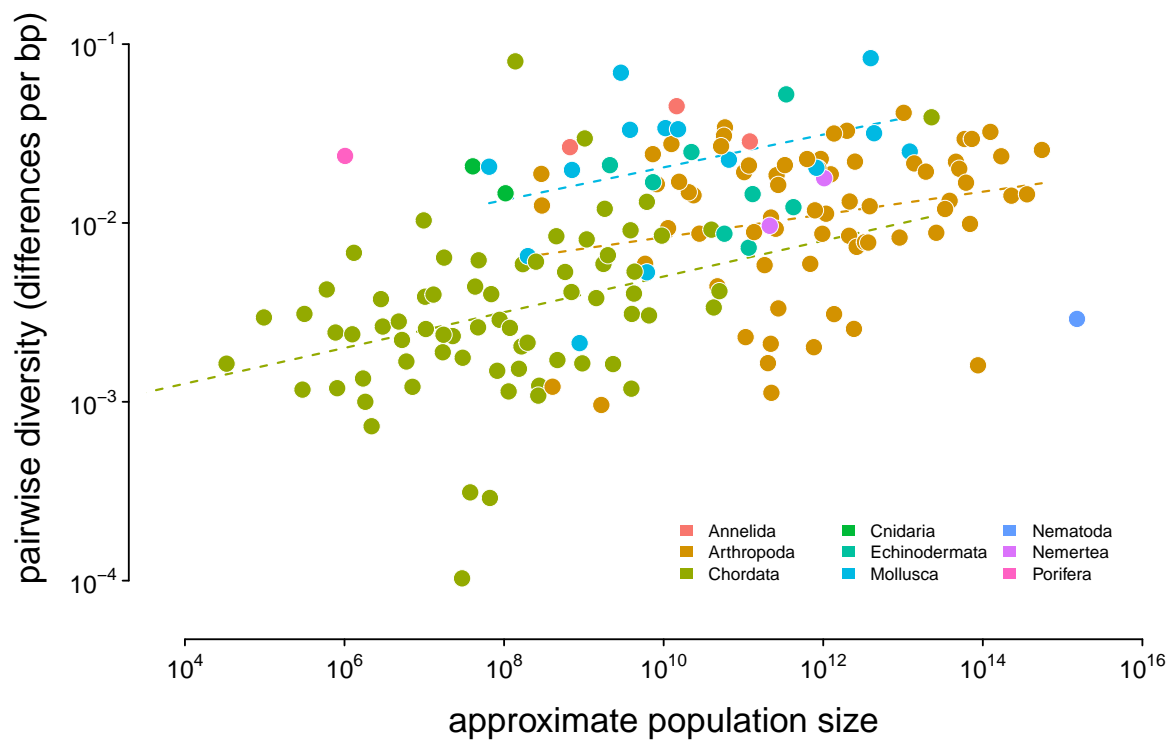


Figure S5: Diversity and approximate population size for 172 taxa, colored by phylum; the dashed lines indicate the non-phylogenetic OLS estimates of the relationship between population size and diversity grouped by phyla.

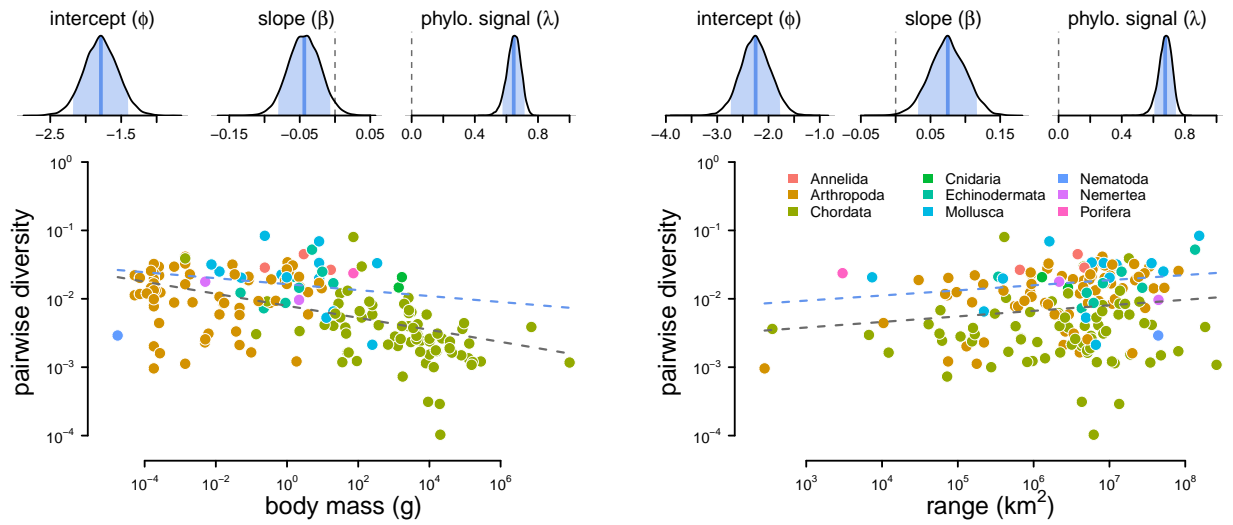


Figure S6: The relationship between diversity (differences per basepair) and body mass (left) and range (right) across 172 species. The top row are posterior distributions of parameters estimated using the phylogenetic mixed-effects model using 166 taxa in the synthetic phylogeny for the intercept, slope, and phylogenetic signal from the mixed-effects model. The bottom row contain each species as a point, colored by phyla. The gray dashed line is the non-phylogenetic standard regression estimate, and the blue dashed line is the relationship fit by the phylogenetic mixed-effects model.

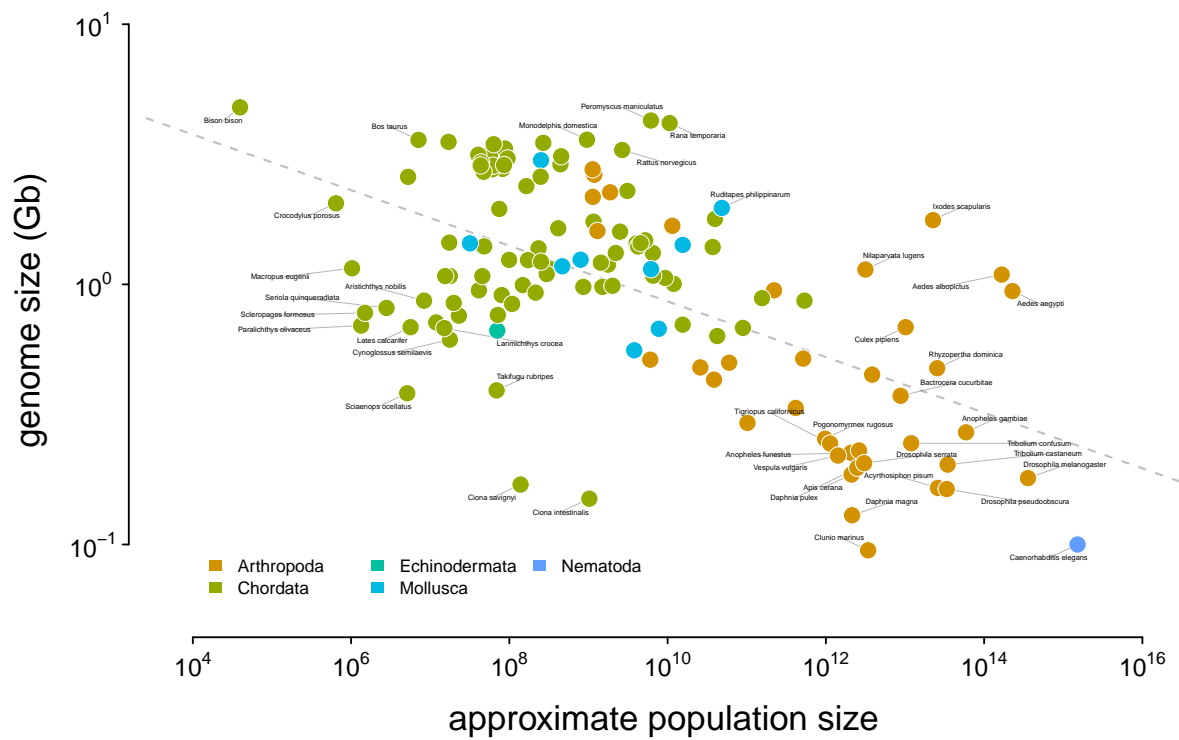


Figure S7: The relationship between genome size and approximate census population size. The dashed gray line indicates the OLS fit. Tiger salamander (*Ambystoma tigrinum*) was excluded because of its exceptionally large genome size (30Gbp).

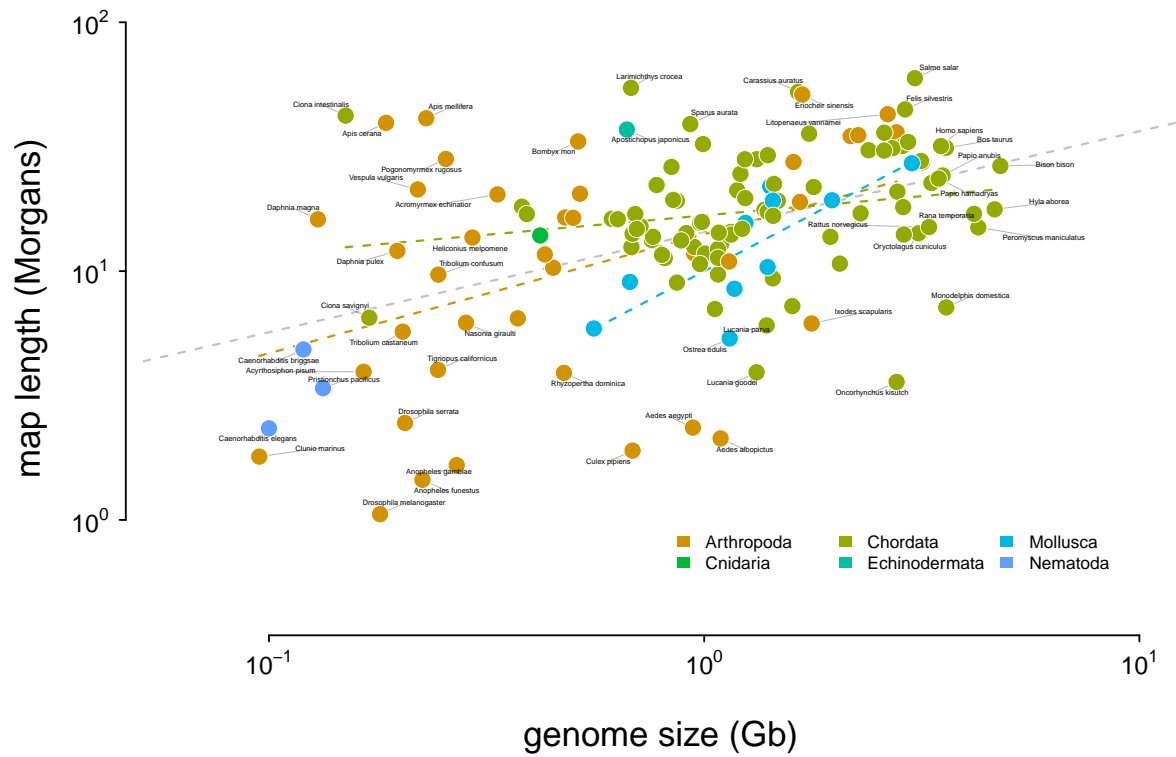


Figure S8: The relationship between genome size and recombination map length. The dashed gray line indicates the OLS fit for all taxa, and the dashed colored dashed lines indicate the linear relationship fit by phyla. Tiger salamander (*Ambystoma tigrinum*) was excluded because of its exceptionally large genome size (30Gbp).

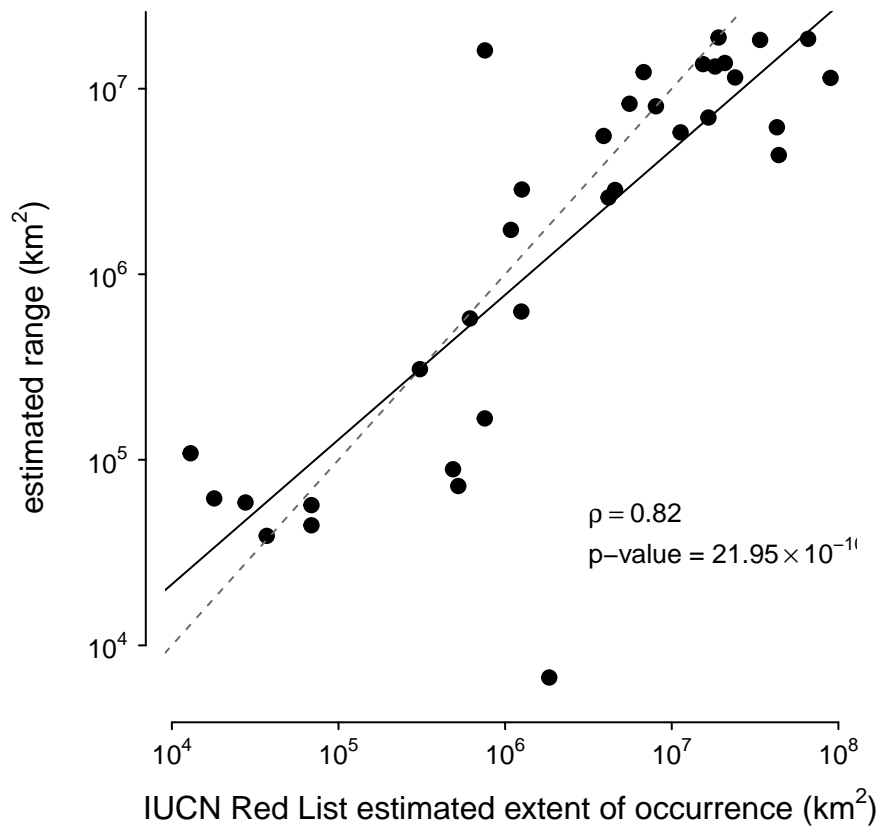


Figure S9: The correspondence between the ranges estimated with the alpha hull method applied to GBIF data used in this paper and IUCN Red List’s Extent of Occurrence for the subset of species in both datasets. Note that the IUCN Red List contains predominantly endangered species, which leads to ascertainment bias; still, the high correlation between the estimated ranges shows the alpha hull method works well.

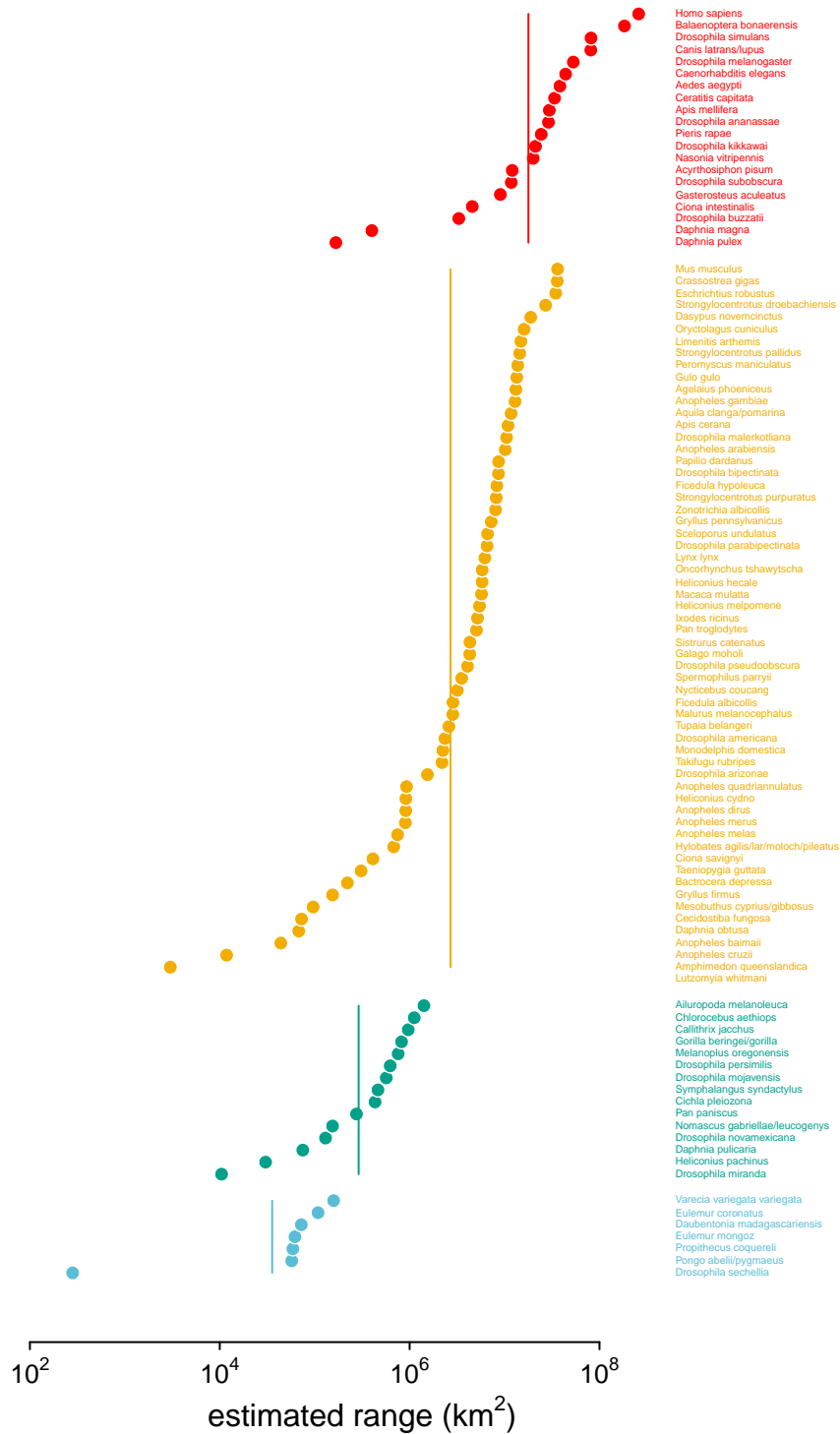


Figure S10: The estimated ranges using GBIF occurrence data, ordered within and colored by the original range category labels assigned in Leffler et al. (2012).

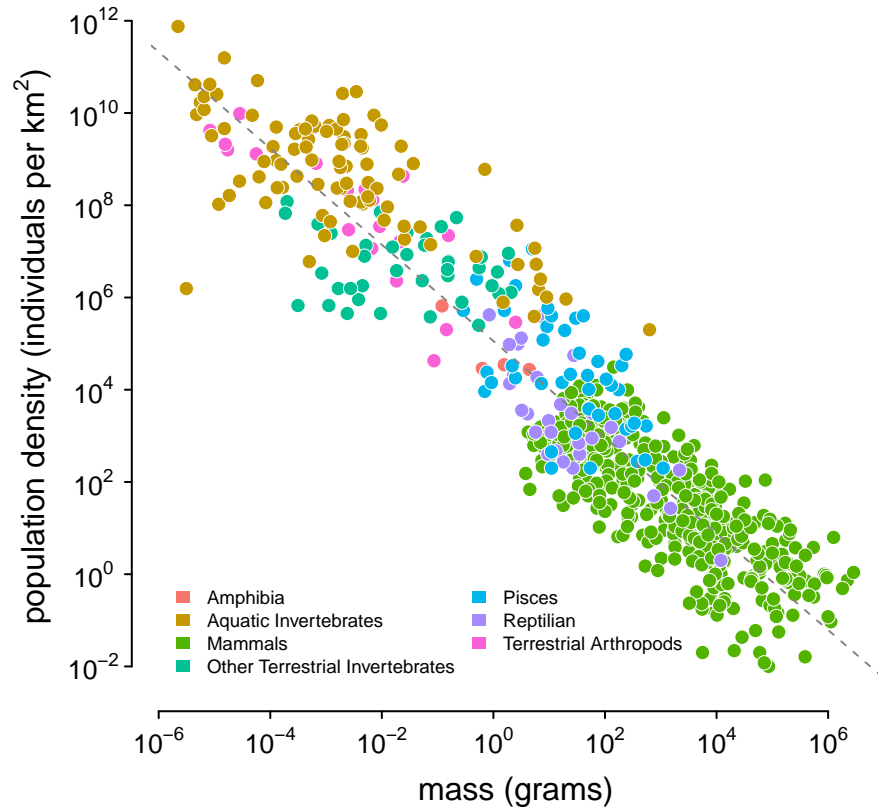


Figure S11: The appendix table of Damuth (1987); the color indicates Damuth’s original group labels. The dashed line was estimated using a lognormal regression model in Stan. References to each measurement are available in Damuth (1987).

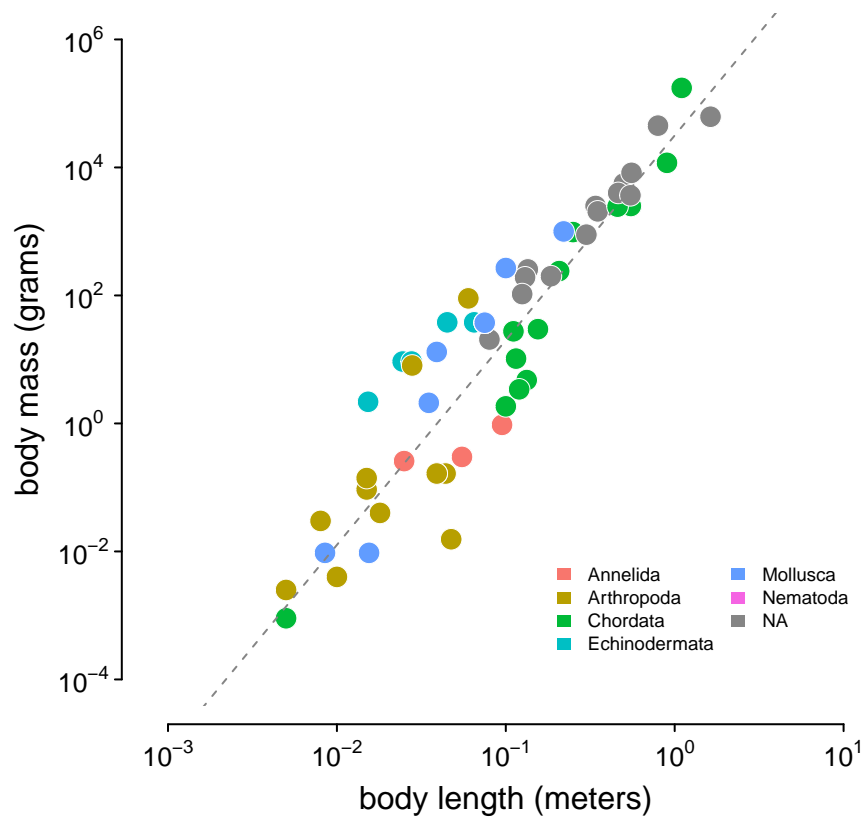


Figure S12: The relationship between body length (meters) and body mass (grams) in the Romiguier et al. (2014) data set, used to infer body masses for taxa. The gray dashed line is the line of best fit inferred using Stan.

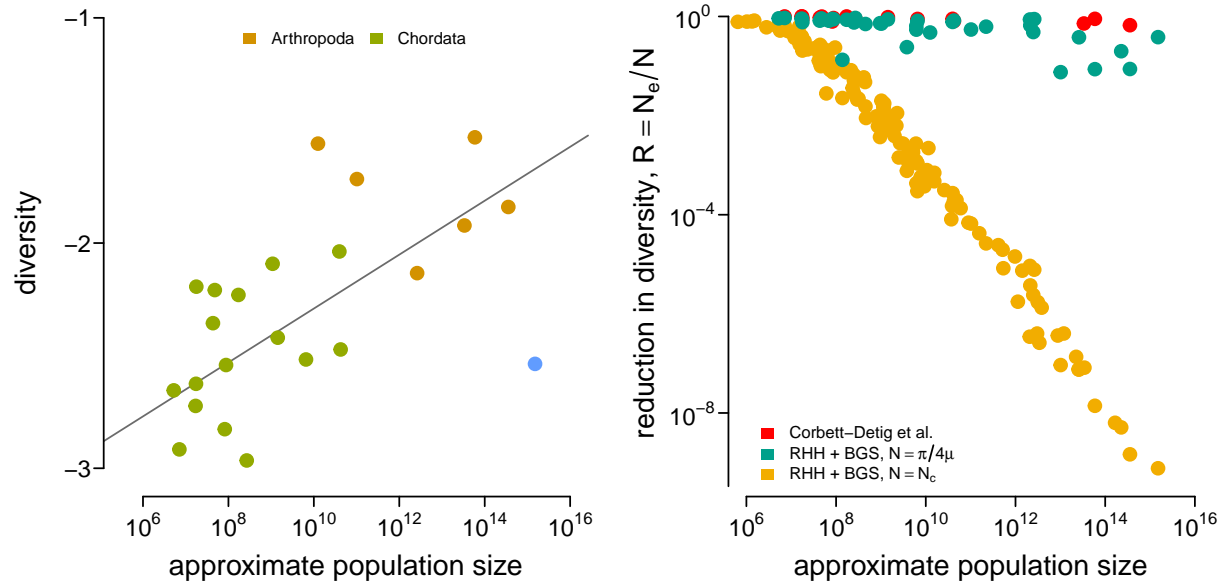


Figure S13: (A) The diversity data from Corbett-Detig et al. (2015) and the census population size estimated here for metazoan taxa. (B) The reductions in diversity, $R = N_e/N$, plotted against census size across species. The red points are the reductions estimated by Corbett-Detig et al. (2015). This confirms Corbett-Detig et al.'s (2015) finding that the impact of selection ($I = 1 - R$) increases with census population size (though, in the original paper size body size and range were used as separate proxy variables for census population size). The green and red points are the predicted reduction in diversity under the recurrent hitchhiking (RHH) and background selection (BGS) model using the *Drosophila melanogaster* parameters as described in the main text. The reduction in the diversity due to sweeps, from Equation (1), is determined by the term $2NS$. Green points treat N as the implied effective population size from diversity $\tilde{N}_e = \hat{\pi}/4\mu$, assuming $\mu = 10^{-9}$. Yellow points treat N as the census size, $N = N_c$. Overall, using the census size, e.g. $2N_cS$, leads to reductions in diversity that far exceed the empirical estimates of Corbett-Detig et al. and reasonable model-based predictions from \tilde{N}_e .

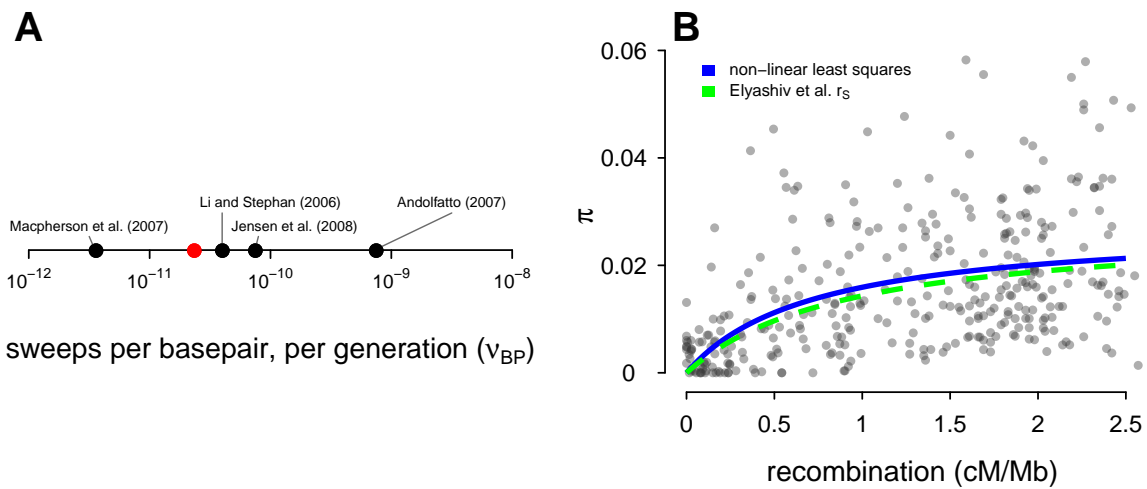


Figure S14: (A) The estimate of the number of sweeps per basepair, per genome (ν_{BP}) from Table 2 of Elyashiv et al. (2016) (the studies included are Andolfatto 2007; Li and Stephan 2006; Macpherson et al. 2007 and Jensen et al. 2008); the red point is my estimate used in this paper. (B) Points are the data from Shapiro et al. (2007). The blue line is the non-linear least squares fit to the data, and the green dashed line is the sweep model parameterized by the genome-wide average sweep coalescent rate $2NS \approx 0.92$ from the classic sweep and background selection model of Elyashiv et al. (2016) (r_s in Supplementary Table S6).

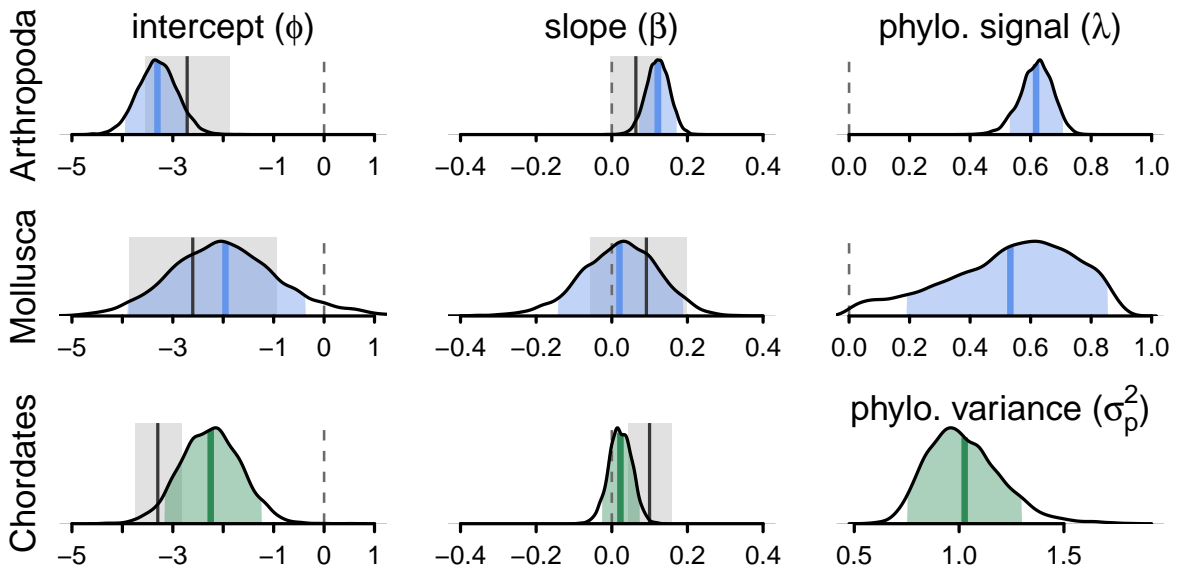


Figure S15: The posterior distributions for the parameters of the phylogenetic mixed-effects model of diversity and population size (this is analogous to Figure 3B) fit separately on chordates ($n = 68$), molluscs ($n = 13$), and arthropods ($n = 68$). The phylogenetic mixed-effects model for chordates indicated the best-fitting model had no residual variance ($\sigma_r^2 = 0$), so an alternate model without this variance component was used to ensure proper convergence; this model is shown in green. The light blue (green) shaded regions are the 90% credible intervals, the blue (green) lines the posterior averages, the gray shaded regions the OLS bootstrap 95% confidence intervals, and the gray lines the OLS estimate. Note that unlike Figure 3, the OLS estimate uses all taxa, not just those present in the phylogeny, since splitting the data by phyla reduces sample sizes (OLS with just the subset of taxa in the phylogeny is not significant for either chordates and arthropods). The vertical dashed gray line indicates zero.

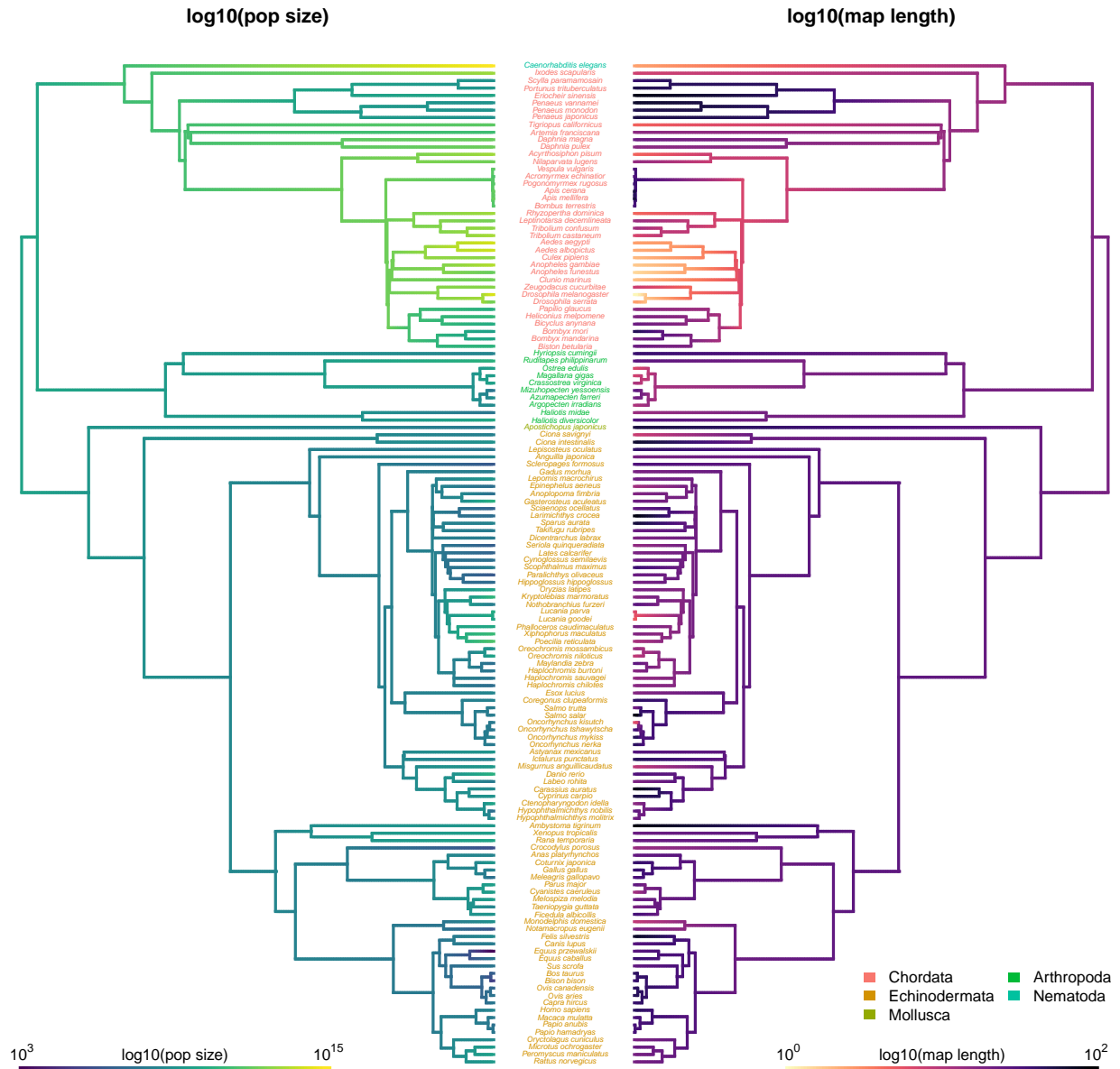


Figure S17