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1 **Studying speciation and extinction dynamics from phylogenies: addressing**
2 **identifiability issues**

3

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5

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13

14 **Keywords** Speciation, extinction, diversification, phylogenies, parameter identifiability,
15 model congruency

16

17 **Abstract**

18 A lot of what we know about past speciation and extinction dynamics is based on statistically
19 fitting birth-death processes to phylogenies of extant species. Despite their wide use, the
20 reliability of these tools is regularly questioned. It was recently demonstrated that vast
21 'congruent' sets of alternative diversification histories cannot be distinguished (i.e. are not
22 identifiable) using extant phylogenies alone, reanimating the debate about the limits of
23 phylogenetic diversification analysis. Here, we summarize what we know about the
24 identifiability of the birth-death process and how identifiability issues can be addressed. We

25 conclude that extant phylogenies, when combined with appropriate prior hypotheses and
26 regularization techniques, can still tell us a lot about past diversification dynamics.

27

28 **Glossary**

29 **Asymptotic (or theoretical) unidentifiability:** situation when there are distinct combinations
30 of the model parameters that cannot be told apart even in the limit of an infinite number of
31 observations

32 **Bias-variance trade-off:** trade-off between systematic model error due to limited flexibility
33 (bias) and uncertainty of the parameter estimates (variance)

34 **Extinction:** disappearance of a species, corresponding to the death of its last individual

35 **Homogeneous birth-death (BD) process:** birth-death process where speciation and
36 extinction rates are identical across lineages at any time. Rates may vary in time, but not
37 across lineages

38 **Identifiability:** when fitting statistical models, identifiability means that any two
39 combinations of parameter values can be distinguished

40 **Likelihood:** function of the parameters of a given model that measures the probability of the
41 observations given the model and its parameter values

42 **Model misspecification:** situation when the distribution of data implied by the model (under
43 best possible parameterization) differs from the distribution of data under the true generating
44 process

45 **Net diversification rate:** speciation rate minus extinction rate

46 **Practical unidentifiability:** situation when there are distinct combinations of the model
47 parameters that cannot be told apart from the limited number of observations available in
48 practice

49 **Reconstructed phylogeny:** estimated phylogenetic tree for present-day species (missing
50 lineages that have gone extinct and are thus unsampled)

51 **Regularization:** set of statistical techniques that consist in adding a regularization term (or
52 penalty) to the optimization function (typically the likelihood) to solve an ill-posed problem
53 or avoid overfitting

54 **Speciation:** process by which two populations of the same ancestral species give rise to two
55 distinct descendant species

56 **Extinction fraction:** extinction rate divided by speciation rate

57

58 **Molecular phylogenies and diversification dynamics**

59 The diversity of life on Earth has arisen from a succession of **speciation** and **extinction**
60 events (see Glossary). The rates at which ancestral species give rise to new daughter species
61 (the speciation rate, λ) or go extinct (the extinction rate, μ) reflect underlying ecological and
62 evolutionary processes, and shape species richness over geological timescales. Understanding
63 how these rates have changed through time has long been of interest to evolutionary biologists
64 [1–8]. While the first estimates of speciation and extinction rates were derived from the fossil
65 record, researchers now also widely use dated phylogenies of present-day species (so-called
66 ‘**reconstructed (or extant) phylogenies**’, thereafter referred to as ‘phylogenies’ for
67 simplicity) to study past speciation and extinction dynamics [9–12].

68

69 Nee *et al.* [13] showed, using the **homogeneous birth-death (BD) process**, that despite
70 extinct species being absent from a phylogeny, extinctions leave a distinctive signal in the
71 timing of branching patterns, known as the ‘pull of the present’. Under the assumption of
72 homogeneous and constant speciation and extinction rates, it is therefore possible to estimate
73 these rates from phylogenies. A wide range of more complex models grounded on the

74 homogeneous BD process have now been developed, and used to test hypotheses about past
75 diversification dynamics [14–22].

76

77 Increasing flexibility of the models brings new issues, however, such as parameters that may
78 not be **identifiable**. Here, we discuss the identifiability of speciation and extinction rates in a
79 variety of homogeneous BD models, and clarify the theoretical limits that non identifiability
80 imposes on phylogenetic diversification analysis. We conclude that although speciation and
81 extinction histories are statistically unidentifiable if the underlying functions are completely
82 unconstrained [23], this does not imply that phylogenies can't reveal speciation and extinction
83 dynamics [23,24]. We hold that in most practical scenarios, *a priori* hypotheses, biological
84 knowledge or statistical **regularization** can make the problem identifiable.

85

86 **Identifiability of speciation and extinction rates**

87

88 To clarify the issue of identifiability, it is useful to make a distinction between asymptotic (or
89 fundamental) and practical unidentifiability. **Asymptotic unidentifiability** corresponds to the
90 case when distinct parameter combinations cannot be told apart, even in the limit of an
91 infinite number of observations; **practical unidentifiability** corresponds to the case when
92 parameters cannot be told apart from the limited number of observations available in practice.

93

94 *Asymptotic identifiability of the homogeneous BD model*

95

96 Nee *et al.* [13] showed that the homogeneous constant rate BD model with complete sampling
97 (i.e. all present-day species are represented in the phylogeny) is asymptotically identifiable.

98 Incomplete sampling can be accounted for by assuming that each extant species is sampled

99 with the same probability ρ ($\rho < 1$), but already in this simple extension of the model, if ρ is
100 a parameter to be estimated, λ , μ and ρ are not asymptotically identifiable [25]. To solve this
101 identifiability problem, the fraction of present-day species represented in the phylogeny is
102 often included as prior information on ρ , which renders λ and μ asymptotically identifiable.
103

104 Extending the work of Nee, Stadler [16] showed that the « episodic » birth-death model
105 (EBD, also called birth-death-shift, BDS), where diversification rates are piecewise constant
106 (i.e. constant on successive time intervals, or epochs) is asymptotically identifiable. More
107 recently, Legried & Terhorst [26] confirmed this result and showed that it holds even if the
108 epochs are not fixed. However, the BDS model with mass extinction events, i.e. including the
109 possibility that sudden (simultaneous) extinction events can occur at the end of each epoch
110 (equivalent to sampling each species with an epoch-specific probability ρ), is not identifiable
111 [16].
112

113 In the case when $\lambda(t)$ (or $\mu(t)$) are smooth functions of time and are not constrained to follow
114 specific functional forms such as the exponential or any other biologically-motivated
115 function, Louca & Pennell [23] showed that there is an infinity of ‘congruent’ functions that
116 yield the same **likelihood**, meaning that this process is not asymptotically identifiable (Box
117 1).
118

119 *Practical identifiability of the homogeneous BD model*

120

121 When applying birth-death models to real data, a further issue arises: the size of phylogenies
122 is typically not huge. Finite data sizes impose limits to the identifiability of any given model,
123 as the confidence in the parameter estimates decreases with decreasing sample sizes. This is

124 well illustrated by estimates of the extinction rate and the extinction fraction ($\frac{\mu}{\lambda}$), which
125 typically have wide confidence intervals even for asymptotically identifiable models (see e.g.
126 Table S9 in [16]), such that accurate estimates often require sample sizes that are not achieved
127 in practice. Speciation rates, on the other hand, can be estimated with good accuracy on
128 phylogenies of moderate size for the constant-rate BD model [27], as well as for the BDS
129 model if the number of epochs is kept small [16]. Similarly, in BD models with rates that are
130 constrained to follow a specific and simple functional dependency (such as the exponential) to
131 time [14,15] or the environment [28], parameters determining the time- or environment-
132 dependency of the extinction rate have wide confidence intervals, while those associated with
133 the speciation rate can be estimated with good accuracy [15,28]. However, by the usual
134 arguments about degrees of freedom, the functional complexity that can be supported by a
135 typically-sized phylogeny of a few hundred tips is probably in the order of a few
136 parameters. Thus, practical identifiability alone dictates that we must put constraints on the
137 flexibility of the models used to infer diversification dynamics.

138

139 **Dealing with practical *versus* asymptotic identifiability issues**

140

141 Asymptotic and practical identifiability issues are common in science, and a large set of
142 ideas has emerged to address such problems. Practical identifiability issues are commonly
143 understood as manifestations of the **bias-variance trade-off**, which states that model
144 complexity must be adjusted to the data size to minimize the total error (bias + variance) of
145 the inference (Box 2). This can be achieved by a variety of statistical model selection or
146 regularization techniques (Box 2). For example, the practical identifiability of the
147 asymptotically identifiable BDS model (without mass extinctions) can be improved by
148 introducing temporally-autocorrelated rates drawn from a Bayesian prior, rendering parameter

149 estimates with time divided in hundreds of epochs identifiable on relatively small phylogenies
150 (200 tips) [29].

151

152 Addressing asymptotic identifiability issues, such as the non-identifiability of the BD model
153 with unconstrained λ and μ highlighted by Louca & Pennell [23], is a different problem, as
154 the error of our inference does not decrease with increasing data size. Yet there are
155 approaches for dealing with asymptotic identifiability as well, that we detail below.

156

157 **Reparametrization**

158

159 A solution to asymptotic identifiability issues is to reparameterize the model with identifiable
160 quantities. For example, in the BD model with incomplete sampling and free ρ (which needs
161 to be considered when total diversity is unknown, which is the case of most microbial and
162 insect groups), the net diversification rate $\lambda - \mu$ and $\lambda\rho$ are identifiable. The drawback of this
163 approach, however, is that the reparameterized quantities are often scientifically less
164 interesting. For example, Louca & Pennell (2020) [23] suggest estimating the pulled
165 speciation and diversification rates λ_p and r_p instead of $\lambda(t)$ and $\mu(t)$ (Box 1), but these
166 pulled rates are difficult to interpret biologically (see [30] for an attempt), which considerably
167 limits their practical utility.

168

169 **Independent data sources**

170

171 Another approach to dealing with asymptotic identifiability issues is to add additional,
172 independent data sources. Considerable progress has been made in recent years to use both
173 phylogenetic and fossil data, which is achieved by adding fossil sampling processes to the BD

174 process [31–38]. In the most elaborate versions of these “fossilized” Birth-Death (FBD)
175 models, two distinct sampling processes are considered: one with rate ψ for fossils with
176 character (or molecular) data, which are included in the tree, and one for simple fossil
177 occurrences without character data. The former process is asymptotically identifiable when λ ,
178 μ , and ψ are constant [34], unless samples are removed upon sampling [34,39]. The latter,
179 however, is irrelevant in the case of modeling diversification dynamics, as extinctions and
180 fossilizations are independent processes. As long as samples are not removed upon sampling,
181 the process remains identifiable even if the sampling probability at present ρ is unknown (a
182 case when the process is not identifiable from extant species alone), which illustrates that
183 fossils can alleviate identifiability issues [34].

184

185 Despite these encouraging results, more work is needed to determine if and under which
186 circumstances the FBD process is identifiable when λ , μ , and ψ vary as piecewise constant or
187 continuous functions of time, to assemble empirical datasets on which to apply FBD models
188 for diversification analyses (the FBD has so far mainly been applied to improve divergence
189 times rather than diversification rate estimates, but see e.g. [35,40]), to improve their
190 computational efficiency (current implementations limit the applicability of the model to
191 small datasets), as well as to assess whether the inclusion of fossils provide realistic estimates
192 of extinction rates [41] (see Outstanding questions).

193

194 **Constraints from *a priori* hypotheses**

195

196 Identifiability issues are more likely to arise the more flexible our models are. Flexibility is
197 put to the extreme by Louca & Pennell [23], who set the task to be able to identify any
198 possible functional forms $\lambda(t)$, $\mu(t)$ from extant phylogenies. A hypothesis-driven research

199 framework limits this complexity by comparing only a small number of alternative *a priori*
200 ideas about the underlying process [42]. Such *a priori* hypotheses will usually constrain the
201 functional forms of λ and μ and thus render the corresponding BD models identifiable.

202

203 The foundational study of Nee *et al.* [43] followed such a hypothesis-driven philosophy. After
204 demonstrating that their bird phylogeny was incompatible with a constant-rate diversification
205 model and grounded in Simpson's evolutionary theory of adaptive radiations [44], they
206 hypothesized that rates of cladogenesis might be affected by niche-filling processes. Finding
207 that a diversity-dependent model indeed fitted their data better, they concluded that diversity-
208 dependent cladogenesis was a more plausible scenario to explain the diversification of birds.

209

210 This hypothesis-driven approach has inspired more than 30 years of research in phylogenetic
211 diversification analyses [10]. Exponential time-dependencies have been used, for example, to
212 mimic early burst patterns expected from adaptive radiation theory [44], or as an
213 approximation to diversity-dependent cladogenesis [45] (see Box 3 for an illustration with the
214 Madagascan vangas, Vangidae). In the context of environment-dependent models, functional
215 hypotheses have often been derived from foundational theories of biodiversity, such as the
216 metabolic theory of biodiversity [18] and MacArthur & Wilson's theory of island
217 biogeography [20]. Phenomenological models, such as simple linear time- or environmental-
218 dependencies, have also been used, but typically either as null models [45] or as the simplest
219 way to model the effect of an explanatory environmental variable on evolutionary rates [18].
220 The primary goal of this research has been to fit, test and compare diversification scenarios
221 that were defined *a priori* to reflect different evolutionary hypotheses. Louca & Pennell's
222 congruent models do not correspond *a priori* to any evolutionary hypotheses, and would

223 never be considered in a hypothesis-driven model selection procedure in the first place [42]
224 (Box 3).

225

226 A drawback of hypothesis-driven research is that the biological conclusions we draw are
227 contingent on the *a priori* hypotheses we formulate. In particular, our hypotheses typically do
228 not correspond completely to the process underlying the empirical data (“the truth”). Still, it is
229 usually assumed that if a given hypothesis is statistically supported within a well-chosen set
230 of alternatives, it is likely that this hypothesis is the closest to the truth. Whether this is the
231 case for BD models, considering the existence of a large number of congruent models,
232 remains an open question to be explored in more details (see The future of phylogenetic-based
233 diversification research and Outstanding questions).

234

235 **Constraints on complexity and statistical regularization techniques**

236

237 Even in the absence of additional data or *a priori* hypotheses, there are certain philosophical,
238 statistical or information-theoretic principles that may allow us to prefer some congruent
239 solutions over others.

240

241 For example, a widely accepted scientific method of deciding between alternative
242 explanations is the principle of parsimony (or Occam’s razor, Box 2). If we follow this
243 traditional thinking in science, when several explanations with different degrees of
244 complexity are asymptotically unidentifiable, we should prefer the simplest, which is most
245 probably true, all other things equal. A possible solution to the identifiability issue highlighted
246 by Louca & Pennell [23] consists then in selecting the simplest diversification scenario in a
247 congruence class. This preference for simplicity is distinct from the problem of optimizing

248 complexity to avoid overfitting in the case of finite data, and applies to the case of infinite
249 data as well. Quantifying and penalizing complexity can be challenging, but it is a classical
250 problem that can be addressed with a variety of statistical regularization techniques (Box 2).

251
252 Penalizing complexity is just one example of a more general class of regularization
253 techniques that add additional constraints to solve an ill-posed (for example asymptotically
254 unidentifiable) problem [46]. Constraints can also come from prior biological knowledge,
255 information theory or model selection principles, added in the statistical inference in the form
256 of shrinkage estimators [47], or as priors in the case of Bayesian inference (Box 2). For
257 example, as shown by May *et al.* [19], using Bayesian priors that represent the prior belief
258 that on average 10% of species survive a mass-extinction event in the BDS model with mass
259 extinction events (an asymptotically unidentifiable model) allows distinguishing rate shifts
260 from mass extinction events. This example provides a clear counter-example to the
261 conclusion of Louca & Pennell that regularization cannot solve asymptotic identifiability
262 issues ([39], S2.2). Another well-known example in phylogenetics is the dating of divergence
263 times: substitution rates and time are unidentifiable with only sequence data from extant
264 species, but Bayesian priors on divergence times (e.g. informed by fossils) combined with
265 relaxed clock models solve this issue (see, e.g. Fig. 1 in [48]).

266

267 **The future of phylogenetic-based diversification research**

268

269 The asymptotic non-identifiability of the homogeneous BD process led Louca & Pennell [23]
270 to conclude that phylogenetic-based diversification research should switch from a focus on
271 speciation and extinction rates to a focus on the identifiable pulled rates. Yet, scientists
272 interested in testing specific evolutionary hypotheses would have a hard time formulating

273 their hypotheses in terms of these quantities, which do not correspond to a particular
274 biological mechanism. Moreover, estimating these rates from limited-size phylogenies is still
275 a challenging task (SI Text S2 & S3).

276

277 Instead of abandoning the goal of developing models with explicit hypotheses on speciation
278 and extinction rates, we argue to put more efforts in using all available data (including fossil
279 data), and testing how robust the inference from these models really is in practice, when using
280 either a hypothesis-driven research approach, or appropriate statistical regularization
281 techniques (Fig. 1). In this area, two key questions remain: how robust are biological
282 conclusions in practice, when we use a hypothesis-driven research framework, given the
283 existence of congruence classes? And can parsimony considerations or other regularizing
284 techniques successfully shrink solutions in the congruence class towards the truth? The
285 answer to these questions depends on the nature of congruence classes, for example on
286 whether congruence classes typically contain a wide range of disjunct models that all
287 correspond to reasonable biological hypotheses, or that have similar parsimony/regularization
288 properties, which remains to be explored by future research.

289

290 We can think of several ways to explore these questions, such as: i) Studying the geometric
291 properties of congruence classes mathematically, as L&P have started to do but without
292 definitive conclusions (their S.1.8). This would help make the regularization choices most
293 likely to render the models identifiable. ii) Simulating phylogenies under general eco-
294 evolutionary models [49–51] and checking whether the application of a hypothesis-driven
295 framework (with well-chosen *a priori* hypotheses) selects the hypothesis that best captures a
296 given simulated scenario; in comparison to the simulation analyses that are already usually
297 performed to evaluate the power and type I error rates of newly-developed methods, in which

298 simulations correspond exactly to one of the fitted models, this requires using less idealized
299 simulation models representing the eco-evolutionary processes that shape diversification
300 dynamics. iii) Pursuing current efforts to develop regularized models, as detailed in the
301 following paragraph, and use eco-evolutionary simulations (as in ii) to check whether these
302 models provide estimates of speciation and extinction rates that approach simulated rates.

303

304 Moreover, in real applications, practical identifiability is often as much a problem as
305 asymptotic identifiability. Given that regularization can solve practical as well as asymptotic
306 identifiability issues, developing suitable and biologically motivated regularization
307 approaches that act directly on speciation and extinction rates seems more promising to us.
308 Such approaches have already started to be developed (e.g. [19,29]), and including further
309 general ideas from statistics and machine learning, for example the fused lasso [52] or
310 generalized additive models (GAMs, [53,54]) could lead to further advances (Box 2).

311

312 The problems as well as their solutions discussed here are likely not limited to homogeneous
313 BD models. In recent years, models with diversification rates that vary across lineages have
314 been developed to understand why some groups of organisms are richer than others and to
315 avoid biased inferences linked to **model misspecification** [15,55–59]. Unlike for the
316 homogeneous BD model, for which all topologies are equally likely and therefore only
317 branching times are informative, both branching times and topology are informative in the
318 case of heterogeneous BD models. Despite this additional source of information, it is very
319 likely that models with heterogeneous rates are asymptotically unidentifiable in the absence of
320 any constraint. Working with biologically interpretable speciation and extinction rates has
321 helped regularizing this problem, for example by favoring rare rate shifts with large effects
322 corresponding to the invasion of new ecological space [55–57] or by favoring frequent shifts

323 with small effects corresponding to heritable rates, formalized by regularization in the form of
324 autocorrelated Bayesian priors [59,60].

325

326 **Concluding Remarks**

327

328 Identifiability issues naturally arise in approaches that try to infer the potentially unlimited
329 complexity of historical processes from limited contemporary data, and inference of past
330 diversification history from phylogenies of present-day species is no exception. These
331 identifiability issues are one of the reasons why scientists adhere to hypothesis-driven
332 research, use parsimony or regularization principles, or integrate multiple data types.
333 Phylogenetic-based diversification analyses have already adopted these methods in the past,
334 and need to pursue this effort to provide increasingly robust tools for understanding past
335 diversification histories from the data that is available today (see Outstanding Questions).

336

337 **Box 1: Model congruency and pulled diversification rates**

338 Louca & Pennell [23] consider the homogeneous (i.e. lineage-independent) stochastic birth-
339 death process of cladogenesis with rates of speciation (birth, λ) and extinction (death, μ) that
340 can change arbitrarily over time t . They show that for any given derivable (and therefore
341 continuous) time-dependent speciation function $\lambda > 0$ and extinction function $\mu \geq 0$, there
342 exists an infinite set of alternative functions $\lambda^* > 0$ and $\mu^* \geq 0$ such that the probability
343 distribution of extant trees under the corresponding birth-death processes M and M^* is
344 identical. Consequently, M or M^* yield identical likelihood values for any given empirical
345 tree, which implies that $\lambda(t)$ and $\mu(t)$ are not uniquely identifiable unless further constraints
346 are imposed on their functional form.

347 Louca & Pennell then re-parameterize the problem to have only identifiable quantities, which
348 they call the pulled rates. The pulled speciation rate is given by:

$$349 \lambda_p = \lambda(1 - \phi)$$

350 where ϕ is a function of time that denotes the probability that a lineage alive at time t has no
351 descendant in the phylogeny, and which analytical expression is given, for example, by Eq.2
352 in [15]. The pulled diversification rate is given by:

$$353 r_p = \lambda - \mu + \frac{1}{\lambda} \frac{d\lambda}{dt}$$

354 Congruent models are found by solving Eq. 2 in [23]:

$$355 \frac{d\lambda^*}{dt} = \lambda^*(r_p - \lambda^* + \mu^*)$$

356 Given any μ^* , we can compute λ^* using the solution to this equation, provided in Louca &
357 Pennell [23]'s SI (Eq. 39 & 40, $\eta_0 = \rho\lambda(0)$, $\mu_0 = \mu(0)$):

358

$$359 \lambda^*(t) = \frac{\eta_0 e^{\Lambda(t)}}{\rho + \eta_0 \int_0^t e^{\Lambda(s)} ds}$$

360 with

$$361 \Lambda(t) = \int_0^t [r_p(s) + \mu^*(s)] ds.$$

362 Alternatively, given any λ^* , we can compute μ^* as:

$$363 \mu^* = \frac{1}{\lambda^*} \frac{d\lambda^*}{dt} + \lambda^* - r_p$$

364

365 **Box 2 - Reasons and approaches to select simple models**

366 Deciding between alternative hypotheses through a preference for simplicity is ubiquitous in
367 statistics and the sciences. Mathematically, this is expressed by viewing the evidence in favor
368 of a respective hypothesis (or model, denoted by M) as a combination of:

$$369 \textit{Evidence} = \textit{Likelihood}(M) - \textit{Penalty} * \textit{Complexity}(M)$$

370 where the penalty term controls the “strength” of the preference for simplicity.

371 In statistics, the traditional motivation to favor simplicity is based on the bias-variance
372 trade-off, which posits that increasing model complexity reduces the systematic misfit (bias),
373 but at the cost of increasing variance (uncertainty) of the parameter estimates. One can prove
374 that, with limited data, inducing a bias towards simpler models decreases total estimation
375 error (bias + variance), even if the true underlying model is more complex. The complexity
376 penalty is selected to optimize the total error. This logic underlies most frequentist
377 regularization and model selection approaches.

378 There is a second argument for constraining model complexity, which is independent
379 of the data size and the bias-variance trade-off. This argument, known as the law of
380 parsimony or Occam's razor, relies on an *a priori* assumption that natural processes tend to be
381 simple and smooth. The principle of parsimony is not a mathematically provable law, but it
382 underlies centuries of thinking and experience from physics to machine learning, and from
383 philosophy as well (see [61] for a discussion).

384 When implementing preferences for simplicity, it typically makes no difference if they
385 originate from bias-variance or parsimony principles. The main difference is that in the
386 former the penalty is chosen from the data, such that more complex models are preferred as
387 the data size increases, whereas in the later the penalty is chosen independent of the data,
388 based on prior beliefs. How to best define complexity is a question of constant debate and
389 development in statistics: we may for example decide that a model is simple if it is
390 interpretable, if it involves less parameters, if it prevents fast variations, or yet other criteria.
391 Various statistical regularization techniques implementing these criteria exist. For example,
392 information-theoretical measures (e.g. the AIC or BIC, [42,62]) add a direct penalty for the
393 number of parameters, shrinkage estimators such as lasso or ridge or their corresponding
394 Bayesian priors add a penalty on the deviation of model parameters from zero [52] and

395 statistical smoothers [63] penalize the roughness of the fitted model (as in generalized
396 additive models GAMs, see [53,54]).

397

398 **Box 3: Diversification of the Madagascan vangas**

399 We illustrate hypothesis-driven research by performing an analysis of the diversification of
400 the Madagascan vangas (Vangidae) using the logic that would be applied in the field [64], but
401 simplified for illustrative purposes. We hypothesize that diversification followed an ‘Early
402 Burst’ pattern [65], with fast speciation at the origin of the group and subsequent slowdown,
403 rather than constant-rate diversification. The Early Burst pattern, related to the idea of
404 adaptive radiations [44], is modeled by an exponential decay of the speciation rates through
405 time, used as an approximation of diversity-dependence. We also consider the hypothesis that
406 a substantial number of extinction events occurred during the diversification of this group.
407 Among the four corresponding models, the model with an exponentially declining speciation
408 rate $\lambda(t) = \lambda_0 e^{\alpha t}$ (time t is measured from the present to the past), with speciation rate at
409 present $\lambda_0 = 0.018$, rate of decline $\alpha = 0.1$ and no extinction $\mu(t) = 0$, noted M, is best
410 supported by the data (see SI Table S1). We conclude that the hypothesis of Early Burst
411 diversification with negligible extinctions is the most likely of the four hypotheses we
412 considered.

413 In order to better grasp the nature of congruent models, we explore models congruent
414 to our best model M (see SI Text S1). First, we choose the extinction function to be a constant
415 $\mu_1^*(t) = \mu_0$ and compute $\lambda_1^*(t)$. Second, we choose the speciation function to be a constant
416 $\lambda_2^*(t) = \lambda_0$ and compute $\mu_2^*(t)$. We find (SI Text S1; Fig. I; here we take $\rho = 1$ as the tree
417 of the Madagascan vangas is complete [64]):

$$418 \lambda_1^*(t) = \frac{\lambda_0 e^{-\frac{\lambda_0}{\alpha} t} e^{(\alpha + \mu_0)t} e^{\frac{\lambda_0}{\alpha} e^{\alpha t}}}{1 + \lambda_0 e^{-\frac{\lambda_0}{\alpha} t} \int_0^t e^{(\alpha + \mu_0)s} e^{\frac{\lambda_0}{\alpha} e^{\alpha s}} ds}$$

419 and

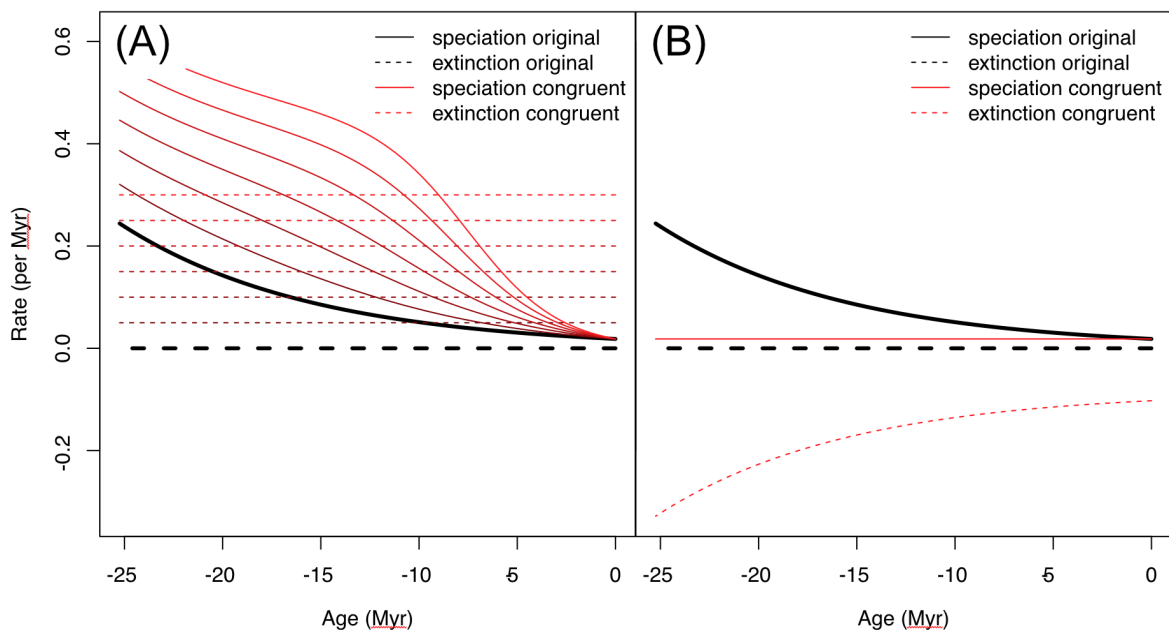
420

$$\mu_2^*(t) = \lambda_0 - \alpha - \lambda_0 e^{\alpha t}$$

421

422 The biological interpretation of these models and of their parameters is not obvious. The
423 equation for μ_2^* looks more interpretable at first, but it expresses the temporal change and the
424 extinction rate at present through the same parameter α , which means that a positive
425 extinction rate at present ($\alpha < 0$) will force extinction rates to decline over time. Here M_2^*
426 infers negative extinction rates, and is therefore not plausible (Fig. I). M_1^* infers a decline in
427 speciation rate from the origin of the group to the present for extinction rates μ_0 ranging from
428 at least 0.05 to 0.3, consistent with our previous results (Fig. I). While rate estimates do vary
429 substantially, the general temporal trend is preserved.

430

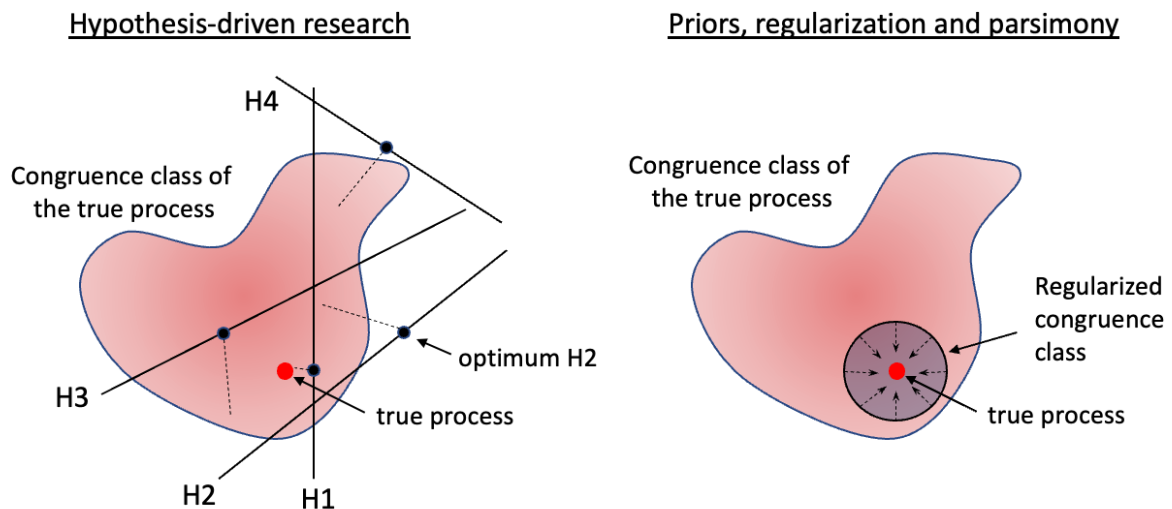


431

432 **Fig I. Diversification of the Madagascan vangas as inferred from congruent models.**

433 The black curves represent the dynamics of speciation (solid line) and extinction (dashed line)
434 corresponding to our best-fit model M (exponential decline in speciation rate, non-significant
435 extinctions). The colored curves illustrate the rate dynamics of congruent models that were

436 obtained by (A) fixing increasing values of a constant extinction rate (M_1^*) and (B) fixing the
 437 speciation rate to λ_0 (M_2^*). In the case of constant extinction (A), we can choose any value for
 438 μ_0 and find $\lambda_1^*(t)$ (so there is an infinity of congruent models), while in the case of constant
 439 speciation (B), λ_0 needs to be taken equal to the λ_0 of model M , as two congruent models
 440 necessarily have the same speciation rate at present if ρ is fixed [23] (so there is only one
 441 congruent model). Note that M_1^* infers a speciation rate decline regardless of the assumed
 442 extinction rate and that M_2^* infers biologically implausible negative extinction rates. See also
 443 Online Supplemental Information Figure S1 & S2.
 444



445
 446 **Fig. 1. Conceptual figure illustrating how constraints imposed by prior hypotheses and**
 447 **regularization may help to approach the true process.** Following Fig. 3 in [23], the pink
 448 area represents the congruence class of the true process (red circle). A: When considering a
 449 small number of biologically motivated hypotheses (H1 to H4), the models will usually be
 450 identifiable, meaning that the optimum solution under a given hypothesis is unique (one black
 451 circle per hypothesis), and we will select the hypothesis that comes closest to the congruence
 452 class (here, H1, dashed lines convey the distance to the congruence class). This hypothesis,
 453 which is the one with highest likelihood, is traditionally assumed to be the closest to the true
 454 process. B: Parsimony and regularization assumptions constrain the congruence class (grey
 455 circle). From the experience in other fields, we would expect the congruence class to be
 456 constrained towards the true process. These two expectations are likely to be met if

457 biologically and statistically (i.e. with respect to parsimony and regularity properties)
458 reasonable models within the congruence class cluster around the true process. Whether this
459 assumption holds in reality is a question for future research.

460

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466

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