



The missing link in biogeographic reconstruction: Accounting for lineage extinction rewrites history

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5

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32

33 ABSTRACT

34 Aim

35 In the most widely used family of methods for ancestral range estimation (ARE), dispersal, speciation,
36 and extirpation events are estimated from information on extant lineages. However, this approach fails
37 to consider the geographic distribution of extinct species and their position on the phylogenetic tree,
38 an omission that could compromise reconstruction. Here we present a method that models the
39 geographic distribution of extinct species and we quantify the potential inaccuracy in ancestral range
40 estimation when extinction rates are above zero.

41 Location

42 Global applications, with an example from the Americas

43 Taxon

44 All taxa, with an example from hummingbirds (*Amazilia*)

45 Methods

46 Methods capable of explicitly modelling extinct branches along with their reconstructed geographic
47 information (GeoSSE) have been overlooked in ARE analysis, perhaps due to the inherent complexity
48 of implementation. We develop a user-friendly platform, which we term LEMAD (Lineage Extinction
49 Model of Ancestral Distribution) that generalizes the likelihood described in GeoSSE for any number
50 of areas and under several sets of geographic assumptions. We compare LEMAD and extinction-free
51 approaches using extensive simulations under different macroevolutionary scenarios. We apply our
52 method to revisit the historical biogeography of *Amazilia* hummingbirds.

53 Results

54 We find that accounting for the lineages removed from a tree by extinction improves reconstructions
55 of ancestral distributions, especially when rates of vicariant speciation are higher than rates of *in situ*
56 speciation, and when rates of extinction and range evolution are high. Rates of *in situ* and vicariant
57 speciation are accurately estimated by LEMAD in all scenarios. North America as the most likely
58 region for the common ancestor of hummingbirds.

59 Main conclusions

60 Methods that neglect lineage extinction are less likely to accurately reconstruct true biogeographic
61 histories of extant clades. Our findings on an empirical dataset reconcile the Eurasian origin of
62 *Amazilia* with biogeographic reconstructions when lineage extinction is considered.

63

64

65 Key words: ancestral distribution, BioGeoBEARS, centre of origin, diversification events, extinction
66 rates, hummingbird evolution, in-situ speciation, vicariance.

67

68

70 Identifying the geographic centre-of-origin for diverse clades has long been of interest in
71 biogeography. This endeavour is made difficult because the presence or absence of a species at a
72 given location varies over time and, over longer time scales, species continuously appear and
73 disappear from the Earth (Barraclough & Vogler, 2000; Jablonski & Sepkoski, 1996; Losos & Glor,
74 2003). The distribution of clades is the result of shifts in the distribution of constituent species via
75 range shifts and speciation and extinction, but, in many cases, these processes may leave little fossil or
76 other tangible evidence of their history, meaning that inferences of centres-of-origin must be inferred
77 from data on extant species and extant ranges. A foundational field in modern biogeographic research
78 has been the reconstruction of the geographic distributions of ancestral lineages, in order to relate
79 biogeographic processes to extrinsic events (e.g., geological shifts, onset of ice ages) while
80 increasingly taking intrinsic, evolutionary processes into account.

81 For Ancestral Range Estimation (ARE), the two popular methods (DIVA, Dispersal
82 Vicariance Analysis; Ronquist, 1997 and DEC Dispersal-Extinction-Colonization model; Ree &
83 Smith, 2008) use the term “extinction” to refer to extirpation (i.e., local extinction), while true lineage
84 extinction is ignored. These approaches (hereafter Extinction Free approaches; EF) consider the
85 following events: dispersal, extirpation and speciation, and are therefore appropriate when all lineages
86 and speciation events are represented in the phylogeny, i.e., no branches are missing due to extinction.
87 However, the vast majority of available phylogenetic trees are reconstructions where extinction has
88 removed many branches, such that a pair of extant species that appear as sister species (or clades) in a
89 reconstructed tree might not be true sisters due to missing nodes. Using the geographic distributions
90 of the apparent pair of sister clades to infer whether in-situ speciation or vicariance occurred at the
91 node where they diverged (the putative common ancestor) may be unreliable because any extinct,
92 intermediary lineages are not only absent from the tree but any information on their geographic
93 distribution is also missing. Thus, attempting to infer in-situ speciation and vicariance events across a
94 phylogenetic reconstruction without accounting for extinct lineages could compromise the ancestral
95 range estimation (Fig. 1). Although the problem of extinct lineages in macroevolution and
96 biogeography has been pointed out by Sanmartín and Meseguer (2016) and more specifically for
97 ancestral range estimation by Crisp et al. (2011), the consequences of ignoring extinct lineages for
98 ARE are still unknown and unquantified.

99 One way forward is to model the potential past existence of lineages at any point of a tree
100 branch, which extinction subsequently removed, and to account for all the possible geographic
101 distributions of those extinct lineages. This is achieved in ClaSSE (Cladogenetic State change
102 Speciation and Extinction) and GeoSSE (Geographic State Speciation and Extinction) models
103 (Goldberg et al., 2011; Goldberg & Igić, 2012) where speciation, lineage extinction, dispersal and
104 extirpation events are part of the biogeographic dynamics. These models have been used for
105 describing how biodiversity accumulates over time in a dynamic context, and in particular, to explore
106 spatial differences in diversification rates (e.g., Ding et al., 2020; Meseguer et al., 2020). However,
107 their potential for estimating ancestral distributions has been almost overlooked (but see Lancaster &
108 Kay, 2013, Caetano et al. 2018). This is surprising, because the spatial distribution of ancestors is
109 estimated during -SSE likelihood calculation. Matzke (2014) and Ree & Sanmartín (2018)
110 acknowledged the utility of -SSE models but found that existing implementations were not easy to
111 use, especially with more than two regions. Here, we use extensive simulations to quantify the impact
112 of including lineage extinction in ancestral range estimation by comparing the outcome of EF
113 approaches to that of our new -SSE implementation, which we have also made available as a user-
114 friendly R package. We simulated biogeographic scenarios that differed in the relative rates of in-situ

115 and vicariant speciation along with different rates of lineage extinction to document variation in
116 performance of both approaches. Finally, we apply our approach to estimate the biogeographic history
117 of *Amazilia* hummingbirds. Evolutionary studies using DIVA and DEC have supported South
118 America as the most likely location of the first speciation event in hummingbirds (McGuire et al.,
119 2014), however the fossil record points to Eurasia as the source region of the hummingbird lineage
120 (Louchart et al., 2008; Mayr, 2004). This leaves a time gap of several million years and a geographic
121 gap of thousands of kilometres. Our approach shows that this spatiotemporal gap is explained when
122 lineage extinction is no longer neglected.

123

124 METHODS

125 *Extinction Free models: differences between DIVA and DEC*

126 Extinction Free methods (EF) require that the distribution of a clade be divided into regions
127 (letters are used for convention) so that the geographic distribution of a given species is coded by its
128 presence in those regions, and occupancy of multiple regions is indicated by the combination of
129 corresponding letters. A time-calibrated tree that includes all extant species is also needed (our
130 approach requires the same data, see below). Matzke (2013) upgraded DIVA (Ronquist, 1997) from
131 parsimony to likelihood in his BioGeoBEARS R package while maintaining its properties, whereas
132 DEC is a model originally developed in a likelihood framework (these methods differ in some
133 assumptions, see below). In such models, speciation is typically modelled as *in-situ* speciation
134 (occurring within a region, increasing local diversity) or vicariance (geographically mediated
135 divergence resulting in allopatry, i.e., complementary ranges). Here, we use the notation $DIVA_{events}$
136 and DEC_{events} to refer to the two sets of biogeographic assumptions and leave DIVA and DEC to refer
137 to the models of ancestral range estimation implemented in BioGeoBEARS. $DIVA_{events}$ assumes that
138 widespread species can split their ranges (vicariance) in any combination regardless of the number of
139 areas where daughter lineages inhabit (e.g., a species presents in region A, B, C and D can split in
140 AB-CD or A-BCD; widespread vicariance *sensu* Matzke, 2013) while DEC_{events} assumes that one of
141 the daughter lineages will be present at a single region (e.g., ABCD species splits in A-BCD or B-
142 ACD; narrow vicariance). For *in-situ* speciation and in contrast with $DIVA_{events}$, DEC_{events} allows
143 widespread lineages to speciation by having one population (i.e., one of the regions where it is
144 present) diverging from the rest and coexisting with the parental lineage: for instance, ABCD species
145 produces one daughter lineage which is present at ABCD and the other daughter which is restricted to
146 region A (*in-situ* subset hereafter; sympatry subset *sensu* Matzke, 2013).

147

148 *Lineage Extinction Model of Ancestral Distribution (LEMAD)*

149 We use the area/trait-dependent diversification framework (State-dependent Speciation and
150 Extinction, -SSE models; Maddison et al., 2007; Goldberg et al., 2011; Herrera-Alsina et al., 2019) to
151 model past changes in species' geographic distributions. We generalize the computation of the
152 likelihood described in GeoSSE (Goldberg et al., 2011) for any number of areas and under several
153 sets of geographic assumptions that facilitate its use in ancestral range estimation (ARE). Notice that
154 GeoSSE and ClaSSE (Goldberg & Igić, 2012) models have the same system of equations. During the
155 R package building process, we calculated the likelihood under GeoSSE (from diversitree package)
156 and LEMAD for a dataset (model parameters, tree and geographic distribution of species in two areas)
157 to confirm that the likelihoods are identical (Fitzjohn, 2012). Unlike EF methods, the -SSE framework
158 considers that, at any point along a tree branch, a lineage could have been present but went extinct,

159 with or without first producing (also extinct) descendants. To this end, the algorithm uses two coupled
160 differential equations (Appendix S1), where one accounts for the probability of a lineage being at a
161 given region (or set of regions), and the other reflects the probability of a lineage going extinct for the
162 same region (or set of regions). These equations are numerically integrated to obtain a likelihood
163 value for the data given the model with its parameters (dispersal/contraction, *in-situ* and vicariant
164 speciation). Different parameter combinations are tested to find the best combination (likelihood
165 optimization). With the parameters that maximize the likelihood, we compute the change in
166 probability for a lineage to be at each distribution from the present (tree tips) to the past (root) and
167 extract those probabilities at the nodes. Ancestral range probabilities were estimated by taking the
168 partial likelihoods from the downpass and rescaling them so that they summed to 1 at each node
169 (Nguyen, 2011). In summary, the model simultaneously considers the probabilities of dispersal,
170 extirpation and speciation (via *in-situ* or vicariance) for extant and extinct lineages. The likelihood of
171 the model is optimized, and the rates of geographic change, *in-situ* speciation and vicariance are
172 estimated. Lineage extinction can be estimated or fixed to a specific rate by the user. In short, Lineage
173 Extinction Model of Ancestral Distribution (LEMAD) computes the likelihood of the current
174 distribution of species (given the parameters of the model) where lineage extinction is a fundamental
175 part of the calculation. The R package lemad is available at <https://github.com/leonelhalsina/lemad>.

176 *General Assumptions in LEMAD*

177 Although the LEMAD model can account for differences in diversification rates across
178 regions (like in GeoSSE/ClaSSE original application), in LEMAD the rates of speciation and
179 extinction are constant across regions. This is achieved by assigning the same rate of speciation and
180 extinction to each area or combination of areas during the parameter setup. This simplification is
181 necessary to reduce the otherwise immense complexity of parameter space when the analysis is
182 performed for many regions; note that this assumption is the same in DIVA and DEC models. In
183 LEMAD we assume that shifts in the geographic distribution of species are the product of expansion
184 and contraction. For example, a species present in region A cannot instantaneously change to region
185 B. It has first to expand to region B (to be present in AB) followed by an extirpation event in A. These
186 assumptions are the same as in EF methods. Lineage extinction can be modelled in two ways:
187 extinction by extirpation and instantaneous extinction. In the former case, a lineage can undergo
188 extirpation events in different regions of its distribution (range contraction) and eventually go extinct
189 when it is extirpated from its last remaining region. This is similar to the idea of the empty range (\emptyset)
190 in Ree and Smith (2008). In the case of instantaneous extinction, a species can go extinct regardless of
191 the number of regions where it is present. Although extinction by extirpation is appropriate when
192 regions are small and each of them represents a single population (the extinction of a species takes
193 place once the last population disappears), the scale at which ARE is normally conducted renders this
194 type of extinction inappropriate (Polly & Sarwar, 2014). Furthermore, by using instantaneous
195 extinction we account for those events that involve a sudden decline in total population size that are
196 not related to standard dynamics of region colonization/extirpation, so we can measure the
197 contribution of each process independently. We therefore used instantaneous extinction in LEMAD,
198 but extinction by extirpation could also be enabled. Our model assumes that lineages, including
199 extinct lineages and ancestors, can be present in multiple regions, even if extant species are not. For
200 instance, with three regions (A, B, and C), LEMAD calculates the probability of the ancestors being
201 present in A, B, C, AB, AC, BC, or ABC (all possible combinations). By allowing this, we do not
202 constrain the model to only consider region-endemic lineages, which could lead to underestimation of
203 the importance of widespread historical lineages in shaping more narrow modern distributions.
204 However, the model is flexible enough to set any restriction in the number of permitted regions per

205 ancestral species. Note that LEMAD can handle any number of regions, however computation time
206 will exponentially increase with the number of regions. For instance, a phylogenetic tree with 66
207 species and 3 areas (yielding 7 possible ancestral areas) can take around 10 minutes of computing
208 time. With 4 areas (and 15 possible ancestral distributions) the calculation can take around 75
209 minutes. With 6 areas (and 63 possible states) the computing time can be as long as 100 hours.

210 LEMAD enables two different sets of biogeographic assumptions (i.e., LEMAD_{diva_events} and
211 LEMAD_{dec_events}; we refer to both models under the term LEMAD) that match DIVA_{events} and
212 DEC_{events}. As they are different parameterizations of the same model, the comparison of their
213 likelihoods is valid and straightforward.

214 *Accuracy Assessment*

215 In order to compare the accuracy of LEMAD and EF approaches under different extents of
216 extinction, we modelled a number of scenarios in which we: (i) simulated the evolutionary history of a
217 clade along with the geographic evolution of its species, (ii) fit both models and (iii) compared their
218 ancestral range estimations.

219 *Simulation procedure*

220 The simulation started with one lineage in a random region (A, B and C), or combination of
221 regions (AB, AC, BC, or ABC); lineages undergo the following events: dispersal, extirpation,
222 speciation, and extinction. The simulation runs in continuous time where the waiting time between
223 events is drawn from an exponential distribution (Gillespie algorithm; Doob, 1945; Gillespie, 1977).
224 The duration of the simulation is chosen to ensure a final clade size of 150 species given the
225 speciation rates (scenarios with high extinction were allowed to run longer, see below).

226 We kept track of the geographic distribution of lineages over time and of ancestor-descendant
227 relationships and used this as a record to build a phylogenetic tree of the clade. As a result, the
228 simulation produces a phylogenetic tree (without extinct branches, similar to standard reconstructed
229 trees) and the geographic distribution of extant species. Notice that species (ancestors and extant
230 lineages) could be in any of the seven states of the system (A, B, C, AB, AC, BC, or ABC).

231 *Model fitting*

232 We simulated two datasets that differed in modes of vicariance and in-situ speciation, following the
233 assumptions in DIVA_{events} and DEC_{events}. For the simulations under DIVA_{events}, we fitted DIVA (from
234 BioGeoBEARS) and LEMAD_{diva_events}. Similarly, the simulations under DEC_{events} were fit with DEC
235 (from BioGeoBEARS) and LEMAD_{dec_events}. Next, we extracted the most likely ancestral distribution
236 estimated by LEMAD and EF for every node in the phylogenetic reconstruction and compared to the
237 record of ancestors directly from simulated datasets. This is, for a given ancestor/node, we took the
238 distribution with the highest probability and compared to the distribution that was logged during the
239 simulation. We defined a node successfully inferred when both distributions matched completely (if A
240 is the simulated truth, only A would be a successful reconstruction. Neither AB nor ABC would be
241 correct). We counted the number of nodes that were successfully recovered by both models in two
242 sections of time during the history of the clade: recent and ancient time windows. We repeated the
243 simulation-inference procedure under 18 different parameter combinations: rates of in-situ speciation
244 = 0.02, 0.03, 0.04 and vicariance = 0.02, 0.03, 0.04 to combine into 3 scenarios with overall
245 speciation of 0.06; extinction = 0, 0.003, 0.03; dispersal/extirpation = 0.06, 0.6 (30 runs for each
246 combination). To measure the accuracy in parameter estimation, we used the rates (geographic
247 change, in-situ speciation and vicariance) that are estimated during the analysis and compared them to

248 the simulation generating rates. Lineage extinction was not estimated but was fixed to the generating
249 rate as we were interested in the performance of the other (more informative) parameters.

250 We were also interested in measuring whether phylogenetic reconstructions and geographic
251 data are informative about the modes of in-situ and vicariant speciation, which constitute the main
252 difference between $DIVA_{events}$ and DEC_{events} . Specifically, we measured the power of LEMAD to
253 detect different sets of biogeographic assumptions. To this end, we simulated datasets under
254 $DIVA_{events}$ and fitted $LEMAD_{diva_{events}}$ and $LEMAD_{dec_{events}}$ models and compared their likelihoods. It
255 is expected that $LEMAD_{diva_{events}}$ model should have higher likelihood than $LEMAD_{dec_{events}}$ because
256 the generating model was indeed, a $DIVA_{events}$ process. We counted the number of simulated datasets
257 where this was the case. We also conducted the complementary analysis: we simulated datasets under
258 DEC_{events} to fit and compare $LEMAD_{diva_{events}}$ and $LEMAD_{dec_{events}}$ models (30 runs for each case).

259 *An Empirical Example*

260 The geographic origin of the American avian family Trochilidae (Hummingbirds) is still
261 debated (McGuire et al., 2014). Previous ARE analyses have supported South America as the most
262 likely area where the common ancestor of hummingbirds lived (22 million years ago; McGuire et al.,
263 2007, 2014). Interestingly, the fossil record points to Eurasia as the source (Louchart et al., 2008;
264 Mayr, 2004) from which the first hummingbird lineage spread via the Bering Strait 34–28; therefore,
265 early diverging hummingbird lineages are expected to be found in North America. However, this is
266 not the case, which leaves a time gap of several million years. To determine whether LEMAD could
267 provide insights on this, we reconstructed the geographic distribution of a widespread and
268 representative hummingbird clade (*Amazilia sensu lato* and closely related species) using both
269 LEMAD and EF models. The phylogenetic tree was taken from McGuire et al. (2014) in combination
270 with geographic information from Ornelas et al. (2014). Extant species and extinct lineages could be
271 present in three regions: A) South America, B) Mesoamerica and C) North America (West from the
272 Isthmus of Tehuantepec) or a combination of them. We did not include Eurasia as a possible region as
273 1) no living species are present, and 2) the artificial inclusion of a Eurasian branch into the
274 phylogenetic reconstruction would bias the analysis and model the distribution of recent ancestors in
275 Eurasia which disagrees with the fossil record. As no information exists on how *in-situ* and vicariant
276 speciation occur in *Amazilia* (see first paragraph of Methods), we could not assume either $DIVA_{events}$
277 or DEC_{events} so we ran $LEMAD_{dec_{events}}$ and $LEMAD_{diva_{events}}$ and compared the fit using AIC weights.
278 Additionally, the models were combined with three different assumptions for rates of lineage
279 extinction: one in which extinction is the same as the estimate for speciation rate (using a standard
280 birth-death model: 0.15), one in which extinction is 10 times less frequent than speciation (0.015) and
281 one in which extinction is 10 times more frequent (1.5). Notice that by fixing extinction to a certain
282 rate, the rates of *in-situ* and vicariant speciation will adjust accordingly during the likelihood
283 optimization. Phylogenetic reconstructions often do not include all species in a group (due to a lack of
284 DNA samples for instance); LEMAD features functionality where the number of missing extant
285 species is taken into account during the calculation (the so-called sampling fraction in diversification
286 models; (Fitzjohn et al., 2009). We included this completeness information for the *Amazilia* dataset.

287

288 RESULTS

289 *Increase in accuracy by modelling extinct branches*

290 Our simulations indicate that the reconstruction of the biogeographic history of a clade is
291 notably improved when the set of branches that potentially existed and went extinct is incorporated

292 into the analysis. The extent of the improvement depends on the relative rates of *in-situ* and vicariance
293 speciation, extinction and dispersal/extirpation (range evolution). For instance, LEMAD is more
294 accurate than extinction free approaches (EF) when vicariance is higher than *in-situ* speciation and
295 there are high rates of range evolution. We find no parameter combination where EF outperforms
296 LEMAD.

297 Although we find that low rates of range evolution led to few differences between EF and
298 LEMAD, data simulated under the biogeographic assumptions of DEC_{events} shows that ancient nodes
299 are better estimated by LEMAD when lineage extinction is higher than zero. Under DIVA_{events} and
300 low rates of range evolution, neither ancient nor recent nodes are better estimated with LEMAD (Figs.
301 2 and 3).

302 The scenarios with high rates of range evolution show increased accuracy in ancestral range
303 estimation (ARE) when using LEMAD than when using EF. Under DIVA_{events}, the improvement is
304 limited to recent nodes but also ancient ones when rates of vicariance are higher than in-situ
305 speciation. Datasets with DEC_{events} show that LEMAD outperforms EF in recent nodes in all
306 scenarios; ancient nodes are also better estimated except when *in-situ* speciation is dominant.

307 Even though the differences between LEMAD and EF are more important as extinction rate
308 increases, simulations with zero extinction also suggest a better performance of LEMAD over EF
309 approaches in most cases. However, recent ancestors are correctly recovered by both approaches at
310 similar numbers when simulations featured low rates of range evolution. Finally, we find that the
311 LEMAD estimates for dispersal/extirpation, *in-situ* and vicariant speciation are accurate across all
312 parameter combinations and, importantly, the model can correctly detect statistical differences in their
313 relative contributions (Figs. S1 – S3). In summary we recommend using LEMAD when rates of
314 vicariant speciation are equal or higher than rates of in-situ speciation, and when range expansion and
315 contraction are highly dynamic (Table 1).

316

317 *Ability to distinguish the signal of DIVA_{events} and DEC_{events}*

318 For the simulations where *in-situ* subset was not assumed (DIVA_{events}; see methods), we fitted
319 LEMAD model in two versions: LEMAD_{diva_events} and LEMAD_{dec_events}. We find that in 86% of the
320 simulated datasets, LEMAD_{diva_events} has the highest statistical support and for the remaining 14% of
321 the simulations, LEMAD_{dec_events} was wrongly selected as the best model. It is important to note that in
322 the datasets where LEMAD chose the right [generating] model (i.e., DIVA_{events}) the average
323 difference in AIC weights is 0.43. In contrast, in simulations where the wrong model was selected, the
324 difference was minimal (mean of AIC weights = 0.02). When DEC_{events} was the generating model
325 (i.e., *in-situ* subset, see methods), LEMAD_{dec_events} is correctly selected 76% of the times over
326 LEMAD_{diva_events}. A potential explanation on why LEMAD failed to select the correct model in some
327 datasets is that in a three-area system like the one we are simulating, events of widespread vicariance
328 are not possible which makes DIVA_{events} and DEC_{events} less different from one another. Therefore, this
329 analysis mainly explored the traces of the *in-situ* subset assumption left in phylogenetic trees.

330 *Reconstruction of *Amazilia* biogeography*

331 We find higher likelihood for LEMAD models with DIVA_{events} than for LEMAD with
332 DEC_{events} (difference in AIC weights = 0.95) which suggests that widespread species speciate by
333 vicariance and not by in-situ speciation. Within LEMAD_{diva_events} we find models with smaller
334 extinction rate more likely, however, this result is not surprising as the estimated rate of extinction

335 from a birth-death model was close to zero (Table 2). Instead of comparing across extinction rates and
336 choosing the DIVA_{events} model with the best AIC, we explore the parameter estimates and the
337 reconstructed ancestral distributions for each model. Regardless of the assumed extinction rate, all
338 reconstructions point to North America as the most likely region for the common ancestor of
339 hummingbirds (Fig. 4). In such a scenario, our simulation analysis finds that LEMAD is 50-100%
340 more effective than EF approaches in inferring the clade's common ancestor.

341

342 DISCUSSION

343 We showed that ancestral range estimation can benefit from the -SSE framework by
344 modelling lineage extinction, and that methods that neglect lineage extinction are less likely to
345 accurately reconstruct true biogeographic histories of extant clades in a wide variety of scenarios. The
346 parametrization of the model allows competing hypotheses for centres-of-origin and *in-situ* versus
347 vicariant speciation to be distinguished. With it, we found that North America is the most likely place
348 of origin of *Amazilia* hummingbirds, which resolves a previous spatiotemporal disconnect between
349 the hypothesized source region and the origin of first species divergence.

350 Empirical studies in island biogeography provide insights on how vicariance/*in-situ* rates
351 contribute to biodiversity patterns. Speciation after dispersal largely contributes to building species
352 richness in small-sized islands and is responsible for the uniqueness of their assemblages (Losos &
353 Schluter, 2000; Stuart et al., 2012). Archipelagos with small islands are expected to have high rates of
354 vicariance and therefore LEMAD might be more appropriate for ancestral range estimation (ARE)
355 than EF approaches. Nonetheless *in-situ* speciation becomes more frequent than vicariance as the size
356 of the island increases which amounts to higher chances of geographic isolation and diversity of
357 habitats (Kisel & Timothy, 2010); in fact, islands over a threshold size show evidence of rapid
358 diversification (Algar & Losos, 2011; Losos & Schluter, 2000). Because the large geographic scale at
359 which ARE is normally conducted (continents or large-sized islands), *in-situ* speciation can be as
360 frequent as vicariance. In this scenario and when DEC_{events} are assumed, the improvement provided by
361 LEMAD is expected in recent and basal nodes. With DIVA_{events}, recent nodes are better estimated
362 than EF methods whereas basal nodes show a non-significant improvement.

363 Similar to EF models, LEMAD assumes constant rates (extinction, vicariance and *in-situ*
364 speciation), which might not match empirical datasets in some cases. For instance, McGuire et al.
365 (2014) reports an important variation in richness across hummingbird subclades. This can be due to
366 differential speciation (or extinction) rates among lineages (e.g., via diversity-dependent
367 diversification; Etienne and Haegeman, 2012). McGuire et al. (2014) found that the difference in
368 speciation rate between two subclades can be as large as 15-fold according to BAMM analysis.
369 Heterogeneity in diversification rates which is independent from trait states or geographic
370 distributions, is likely to be ubiquitous across taxonomic groups besides hummingbirds and it is
371 necessary to develop an ARE method that can handle this complexity. We argue that this should be
372 the next methodological step forward. If the variation in speciation rates across lineages is
373 consistently a result of regional differences (i.e., lineages inhabiting a given area experience higher
374 rates than in other regions), GeoSSE and GeoHiSSE (Caetano et al., 2018) are the proper tools to use.
375 However, if more than three regions (or trait states) are to be analysed, SecSSE (Herrera-Alsina et al.,
376 2019) can be used and with the right setup, it allows for character changes at cladogenetic events and
377 not just along the branches extends (like in ClaSSE model; for an example with habitat preference see
378 Aduse-Poku et al., 2022). Any tool that would consider variable speciation rates across lineages
379 should also incorporate variation in rates of expansion as the chances of vicariant events intrinsically

380 depend on lineage dispersal (i.e., only multi-region lineages can undergo vicariance). Furthermore,
381 opportunities for dispersal across regions can vary over time and assuming a single rate of range
382 expansion/contraction might not be realistic in some cases (e.g., Buerki et al., 2011). Unlike DEC, the
383 current implementation of LEMAD cannot handle this variation but the framework could be adapted
384 include it.

385 In previous studies, selecting DEC over DIVA was mostly based on the superior statistical
386 properties (likelihood based) of DEC when compared to the parsimony method used in DIVA. After
387 BioGeoBEARS was made available, researchers could confidently fit both methods to datasets and
388 compare likelihoods, but surprisingly analysis is generally conducted with DEC, rather than DIVA,
389 without justification. We recommend fitting both $LEMAD_{dec_events}$ and $LEMAD_{diva_events}$ to data and
390 comparing likelihoods, instead of discarding either biogeographic model a priori. Our simulations
391 show that LEMAD is capable of telling the two models apart, even though DEC_{events} are slightly less
392 likely to be correctly detected than $DIVA_{events}$. We find that not only the relative contributions of *in-*
393 *situ* and vicariant speciation, lineage extinction and range evolution directly influence the precision of
394 the ancestral reconstruction, but the set of biogeographic assumptions is also of paramount
395 importance. For instance, unlike $DIVA_{events}$, DEC_{events} attribute some speciation events as *in-situ*
396 subset instead of vicariance followed by dispersal (Ree et al., 2005). This is reflected in the estimates
397 for both processes in our analysis: even if the contributions of *in-situ* and vicariant speciation are the
398 same, we found high variability in vicariance estimates (higher than *in-situ* events) when DEC_{events}
399 underlies simulations. Similarly, when using $DIVA_{events}$, the estimates for *in-situ* speciation are likely
400 to be more variable than those for vicariance. In both cases, high rates of lineage extinction increase
401 the variability of rate estimates.

402 High rates of dispersal/extirpation have two main consequences on these biogeographic
403 analyses. First, the impact of ignoring extinct branches in accurate ARE is higher than in the presence
404 of low rates of range evolution. LEMAD is more likely to correctly track the change in geographic
405 distribution of ancestors along the branches of a phylogenetic tree than EF methods, even with zero
406 extinction. This could be due to how the likelihood at the root is handled by both approaches. In
407 LEMAD, the probabilities of all the areas are multiplied by speciation rates whereas EF approaches
408 do not consider speciation (Ree & Smith, 2008). This multiplication at the root (also called
409 “conditioning on extinction” because we are looking at a tree Nee et al., 1994) is used in all SSE
410 diversification models. This may be responsible for its overall higher precision, which is magnified in
411 systems with many range shifts. Second, with elevated rates of dispersal/extinction, the uncertainty
412 around speciation estimates is high. This is likely to occur because dispersal taking place right after
413 *in-situ* speciation (something expected with high rate of dispersal) looks similar to a vicariance event.
414 In a similar way, an extirpation event following vicariance could be mistaken for *in-situ* speciation.
415 Importantly, although the estimates show important variation, the model can correctly detect
416 statistical differences between rates of *in-situ* and vicariant speciation.

417 LEMAD allows for the evaluation of contrasting models that make explicit assumptions
418 regarding the rates of evolutionary events. Nonetheless, more meaningful hypotheses can be
419 contrasted with fossils or other extinction estimates, which in turn would render a more accurate
420 reconstruction of ancestral distributions (Mao et al., 2012). Alternatively, LEMAD can be modified to
421 include extinct tree branches along with their last known distribution (Zhang et al., 2022; for an
422 example of body size and extinct branches in a SSE implementation see Porto, 2022). The
423 incorporation of known distributions of ancestors (i.e., constraining an internal node to have a certain
424 distribution; see Meseguer et al., 2015) in LEMAD would be treated in a similar manner as the total
425 likelihood is computed at the tree root, when giving different weights to the various regions. This

426 feature, however, is not implemented yet. Dispersal could also be fixed to a specific rate, however,
427 empirical evidence for rates of dispersal is challenging to collect. Unsurprisingly, the large
428 geographical scale in ARE implies that regions are likely to be different from one another in both
429 biotic and abiotic factors. Lineage dispersal in this context does not only entail the mobility to new
430 localities but the successful arrival and further adaptation to potentially new conditions. It is likely
431 that dispersal estimates from mark-release-recapture techniques (e.g., Hill et al., 1996), or other field-
432 based measures would not be appropriate for ARE. One promising concept for testing with LEMAD
433 is the taxon cycle, which posits that phases of range expansion and contraction occur along with
434 habitat shifts (Ricklefs & Bermingham, 2002). The duration of these phases might offer a sensible
435 starting point for developing hypotheses on rates of dispersal/extirpation. Finally, LEMAD enables
436 the comparison of different assumptions on the distribution of the very first common ancestor to the
437 entire clade, i.e., the location of the centre-of-origin.

438 The biogeographic history for *Amazilia* hummingbirds reconstructed by LEMAD model
439 showed clear differences with its EF counterpart. LEMAD found North America as the most likely
440 region for the common ancestor of hummingbirds (Fig. 4). This finding contrasts with previous
441 studies where South America was found as the ancestral distribution. McGuire et al. (2014) proposed
442 a northern arrival of hummingbirds to America with further expansion into South America
443 immediately followed by extinction events that wiped out all hummingbird species from North
444 America (recolonization of North America came at a later stage). However, their EF analysis could
445 not prove this hypothesis. By considering extinction explicitly, our LEMAD analysis provides the
446 missing piece of this puzzle, reconciling the South American distribution of the common ancestor of
447 extant hummingbird species when ignoring extinction with North American distribution of the
448 ancestor when extinction is considered.

449

450 CONCLUSION

451 Lineage extinction seems less tangible than lineage formation; yet, we have shown that
452 incorporating it into biogeographic models is crucial for a better reconstruction of ancestral areas.
453 When using extinction-free methods, taxonomic groups can be inferred to have different centres of
454 origin, however, this could be the result of dissimilar extinction rates across clades rather than actual
455 differences in biogeographic histories. As a corollary, many taxa might have originated at the same
456 place, we think that there are broad patterns which are yet to be discovered.

457 DATA AVAILABILITY STATEMENT

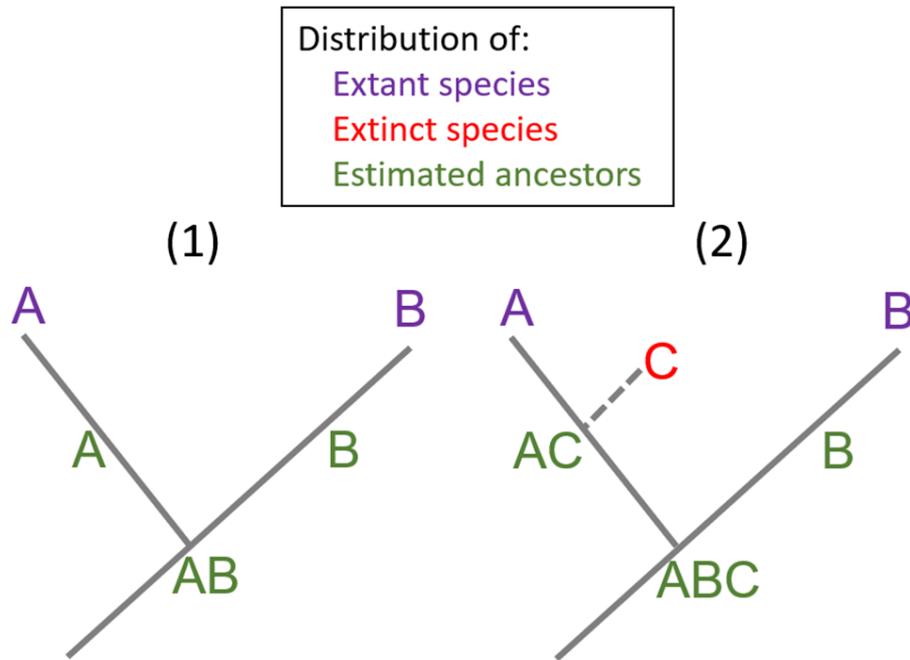
458 The R package *lemad* is available at <https://github.com/leonelhalsina/lemad>. And our code to
459 reproduce simulations will be available in a public repository.

460

461 FIGURE

462

463 Figure 1. The reconstruction of the ancestral distribution for a two-species clade inhabiting a region
464 with subregions A, B and C. We show the main difference between 1) Extinction Free (EF) method
465 and 2) Lineage Extinction Model of Ancestral Distribution (LEMAD). In contrast to EF, LEMAD
466 considers the missing lineages due to extinction and their geographic distribution in the analysis.

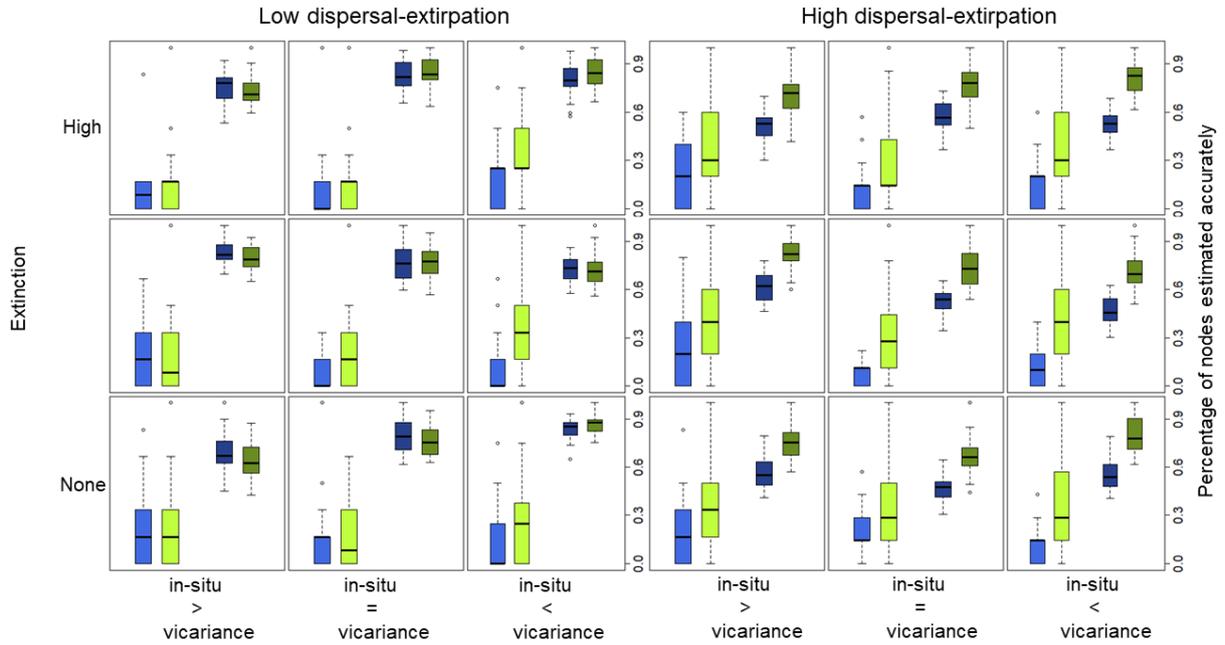


467

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469

470 Figure 2. Accuracy in Ancestral Range Estimation under DEC (in blue) and LEMAD (in green)
 471 models at recent (from half simulated time to present; dark shades) and ancient nodes (light shades).
 472 Eighteen scenarios were simulated with different rates of lineage extinction, range evolution
 473 (dispersal/extirpation) and relative contributions of *in-situ* speciation and vicariance. For each panel,
 474 the y-axis shows the standardized number of ancestors whose distribution was correctly estimated by
 475 the models.

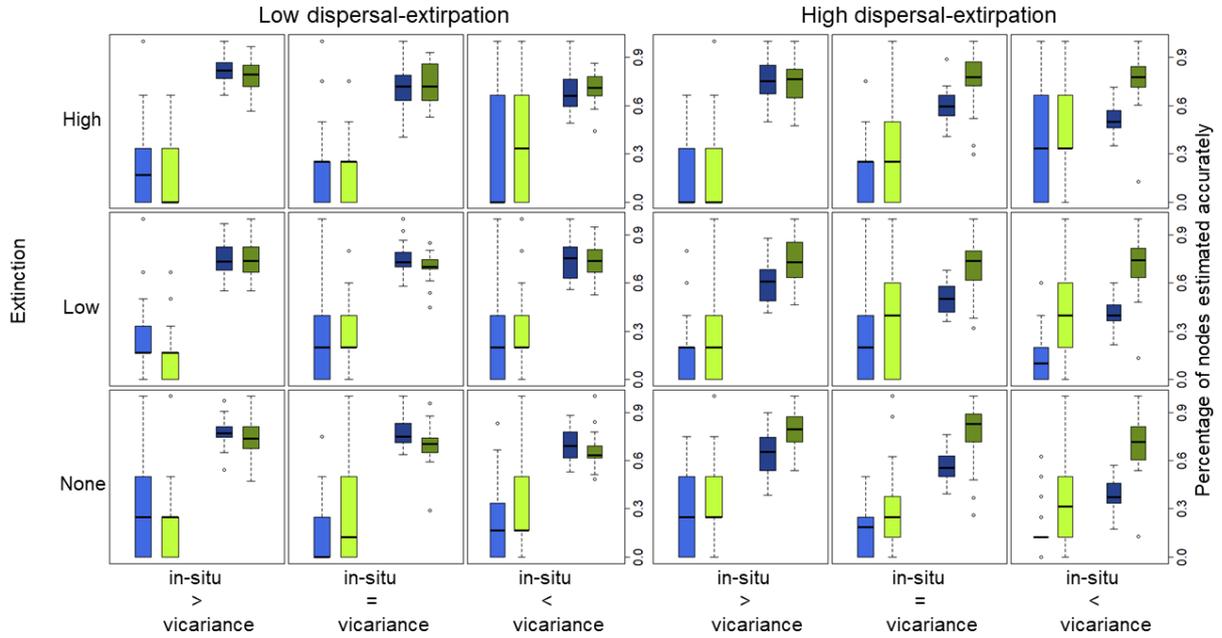


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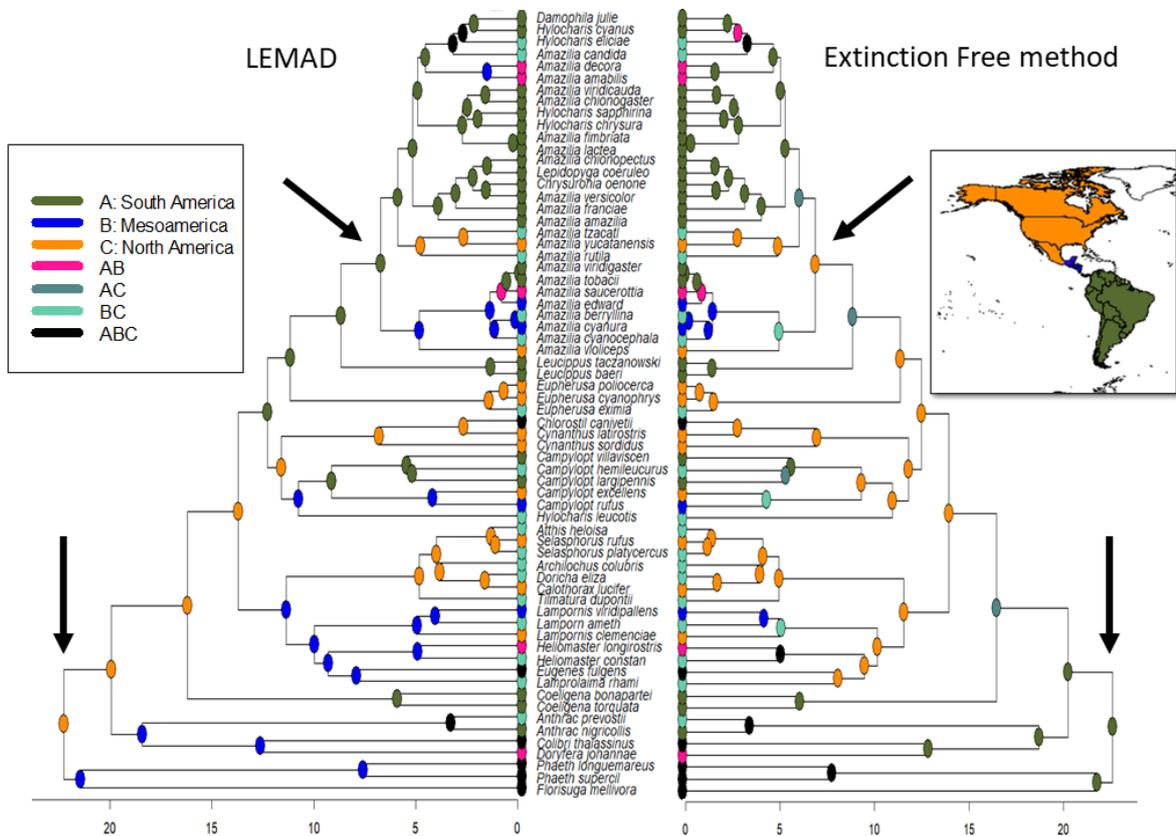
479 Figure 3. Accuracy in Ancestral Range Estimation under DIVA (in blue) and LEMAD (in green)
 480 models at recent (from half simulated time to present; dark shades) and ancient nodes (light shades).
 481 Eighteen scenarios were simulated with different rates of lineage extinction, range evolution and
 482 relative contributions of *in-situ* speciation and vicariance. For each panel, the y-axis shows the
 483 standardized number of ancestors whose distribution was correctly estimated by the models.



484

485

486 Figure 4. Estimated geographic distribution of “Amazilia” hummingbirds’ ancestors under two
 487 different approaches of state reconstruction. Extant and ancestral species (and extinct species in the
 488 case of LEMAD) could be present in A) South America, B) Mesoamerica and C) North America
 489 (West from Tehuantepec) or a combination of them. Coloured circles show the most-likely
 490 distribution. Arrows show some discrepancies between LEMAD and its Extinction Free method
 491 counterpart on the ancestral range estimation of the entire hummingbird clade and “Amazilia” group.



492

493 Table 1. Recommended scenarios to use LEMAD. Necessary condition is indicated with *

	Range evolution rate	Main speciation mode	Lineage extinction
When reconstructing nodes:			
Ancient	Any	Vicariance; Equal contribution of both modes	Intermediate, High
Recent	High*	Any	Any

494

495 Table 2. Summary of LEMAD models fitted to “Amazilia” hummingbird dataset under different
496 assumptions on rates of extinction and modes of in-situ and vicariant speciation.

Biogeographic model	Assumed extinction	Log likelihood	Free parameters	AIC weights
DIVA _{events}	0.015	-289.49	3	0.81
DIVA _{events}	0.15	-291.10	3	0.16
DEC _{events}	0.015	-293.08	3	0.02
DEC _{events}	0.15	-295.54	3	<0.01
DIVA _{events}	1.5	-333.82	3	<0.01
DEC _{events}	1.5	-347.36	3	<0.01

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629

630 BIOSKETCH

631 Leonel Herrera-Alsina focuses on how species diversity is spread across space and time. Rates of
632 diversification and species coexistence are regulated by the distribution of standing diversity and
633 geographic constraints which vary over time. To understand the interaction of these factors, he
634 develops dynamic models of diversification which provide theoretical predictions or are applied to
635 empirical datasets.

636 Editor: Erin Saupe