1   **Title**: The development of scientific consensus: analyzing conflict and concordance among

2   Avian phylogenies

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10   **Abstract**

11   Recent developments in phylogenetic methods and data acquisition have allowed for the

12   construction of large and comprehensive phylogenetic relationships. Published phylogenies

13   represent an enormous resource that not only facilitate the resolution of questions related to

14   comparative biology, but also provide a resource on which to gauge the development of

15   consensus across the tree of life. From the Open Tree of Life, we gathered 290 avian phylogenies

16   representing all major groups that have been published over the last few decades and analyzed

17   how concordance and conflict develop among these trees through time. Nine large scale

18   backbone trees (including a new synthetic tree from this study) were used for the consensus

19   assessment. We found that conflicts were over-represented both along the backbone (higher-level

20   neoavian relationships) and within the oscine Passeriformes. Importantly, although we have

21   made major strides in our knowledge of major clades, recent published comprehensive trees, as

22   well as trees of individual clades, continue to contribute significantly to the resolution of clades

23   in the avian phylogeny. These findings are somewhat unexpected, given that birds constitute a

24   relatively well-studied and small clade of the tree of life (i.e., Aves). Therefore, our analysis

25   highlights that much work is still needed before we can confidently resolve the less well studied

26   areas of the tree of life.

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28   **Key words:** phylogenetic conflicts, Aves, consensus development, supertrees

29

30   **Introduction**

31   Large and comprehensive phylogenies (i.e., including hundreds of taxa and based on genome-

32   scale datasets) have become more common as inference methods and sequencing techniques

33   capable of constructing enormous datasets have been developed (e.g., Smith and Donoghue 2008;

34   Rabosky et al. 2013; Zanne et al. 2014; Prum et al., 2015; Simion et al., 2017). These

35   phylogenies have, in many cases, given fresh views to macroevolution and transformed our

36   ability to address diverse sets of comparative biological questions from diversification,

37   morphological evolution, and rate heterogeneity (Brockington et al., 2015; Lin et al., 2016;

38   Scholl and Wiens, 2016). Comprehensive phylogenies that include all or nearly all taxa

39   constructed from supertree techniques also provide a means of determining where data collection

40   efforts should be focused (Davis and Page, 2014; Jetz et al., 2012; Hinchliff et al., 2015). While

41   these trees may facilitate interesting biological inquiries, they also provide a resource by which

42   we can better understand the development of consensus in the community through data

43   acquisition and comparison (e.g., Davis and Page, 2014). There have been efforts to better

44   understand the development of conflict and concordance among trees, with examination having

45   been conducted primarily with molecular data (e.g., Hinchliff and Smith 2014; Smith and

46   Stamatakis 2013; Smith et al. 2015). Nevertheless, phylogenetic resources, including TreeBASE

47   (Sanderson et al., 1994) and more recently the Open Tree of Life (Hinchliff et al., 2015;

48   McTavish et al., 2015), are now available to better analyze how inferred relationships across the

49   tree of life have changed through time.

50   The Open Tree of Life project has provided the community with several important

51   resources. The Open Tree Taxonomy (hereafter OTT; Rees and Cranston, 2017), unlike many

52   others available, attempts to include only phylogenetically appropriate taxa (e.g., without

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53   *incertae sedis*). It is also more comprehensive than other more commonly used taxonomies (e.g.,

54   NCBI) as it includes taxa regardless of whether they have molecular data associated. The Open

55   Tree of Life also constructs and serves a draft tree of all described species (Hinchliff et al., 2015),

56   the source data of which consists of published source trees identified, uploaded, and edited by

57   the community. This resource, while continually improving, provides significant opportunities to

58   address broad evolutionary questions that previously would have been impossible. Finally, the

59   project also, openly, provides the database of published phylogenies that have been curated by

60   the community (McTavish et al., 2015). Importantly, the taxa included in each phylogeny have

61   been mapped to a common taxonomy (i.e., OTT), which allows for comparisons to be performed

62   across datasets without an additional tedious and error prone step of name reconciliation. Instead,

63   this reconciliation has already been performed by those who uploaded the tree, often researchers

64   with close knowledge of the focal organisms.

65   Here, by utilizing the tree database from the Open Tree of Life, we assess the

66   concordance and conflict among the growing number avian phylogenies that have been

67   published during the last few decades. Methods that are used in this study can also be applied to

68   other living groups on Earth based on the Open Tree of Life resources. As the most diverse

69   extant tetrapod lineage with ~10,800 recognized extant species (Gill and Donsker, 2016) [and

70   potentially more than twice as many cryptic lineages; Barrowclough et al. (2016)], birds have

71   experienced a rapid radiation at deep clades where extremely short internodes exist (Hackett et

72   al., 2008; McCormack et al., 2013; Burleigh et al., 2015; Suh, 2016; Reddy et al., 2017).

73   Although substantial progress has been made on reconstruction of the Aves phylogeny,

74   discovering successive divergence of three monophyletic groups [i.e., Palaeognathae (the

75   tinamous and flightless ratites), Galloanserae (game birds and waterfowl), and Neoaves (all other

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76 living birds), Groth and Barrowclough, 1999; Cracraft et al., 2004], resolving the avian

77 phylogeny (especially within Neoaves) has continued to prove a difficult task of the evolutionary

78 biology community since the pioneering efforts of Sibley and Ahlquist (1990).

79   Explicitly assessing progress in avian phylogenetic inference has recently come to the

80 forefront of the community. By constructing a consensus tree based on six genome-scale

81 phylogenies from five independent studies (i.e., Hackett et al., 2008; McCormack et al., 2013;

82 Jarvis et al., 2014; Suh et al., 2015; Prum et al., 2015), Suh (2016) assessed the reproducibility of

83 various avian phylogenetic hypotheses. Due to the overwhelming conflict among the source trees

84 used (i.e., no higher-level clade could be supported by at least two out of the six trees), Suh

85 (2016) suggested that the very onset of the neoavian radiation produced an irresolvable nine-

86 taxon hard polytomy. Reddy et al. (2017) constructed a nearly identical summary consensus tree

87 to Suh (2016) using a smaller sample of three major hypotheses (i.e., Jarvis et al., 2014; Prum et

88 al., 2015; Reddy et al., 2017), but are more optimistic that more realistic biological-modelling

89 and, importantly, careful selection of data type, will enable further progress. We note that none

90 of the trees considered by Suh (2016) or Reddy et al. (2017) had reasonable sampling of

91 Passeriformes (songbirds; roughly 60% of extant avian species), so potential conflict could not

92 be ascertained within that clade. To date, these and other studies have mainly focused on

93 identifying causes of conflict, attributing tree differences to various factors including incomplete

94 lineage sorting (ILS; Jarvis et al., 2014; Suh et al., 2015), differences in data type (Jarvis et al.,

95 2014; Reddy et al., 2017), and insufficiency of taxon sampling (Prum et al., 2015). However,

96 while these issues of inference are important to keep in mind for future research, little effort has

97 been made to summarize the development and growth of consensus through time when

98 considering the corpus of published phylogenetic hypotheses.

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99   In this study, eight large-scale avian trees [i.e., Sibley and Ahlquist, 1990 (DNA-DNA

100   hybridization); Livezey and Zusi, 2007 (morphology); Hackett et al., 2008 (nuclear DNA); Jetz

101   et al., 2012 (GenBank mining); Davis and Page, 2014 (supertree); Jarvis, et al., 2014 (genomes);

102   Hinchliff et al., 2015 (synthetic tree); Prum et al., 2015 (phylogenomic)] published in different

103   time intervals are used as valuable backbones to assess trends of consensus and conflict.

104   Additionally, after filtering 290 source trees from the Open Tree of Life, we constructed a new

105   comprehensive synthetic bird tree based on certain tree choice criteria (by taxon group, sampling

106   scale, and year of publication) and use it for assessment as the largest avian tree to date. This

107   synthetic tree also serves as a resource for other researchers, and as a point from which we can

108   compare future comprehensive avian phylogenies.

109

110   **Methods**

111   *Source trees*

112   Avian phylogenetic hypotheses that have been published in the last few decades were

113   curated through the Open Tree of Life online curator (https://tree.opentreeoflife.org/curator),

114   following the protocol of Hinchliff et al. (2015). In general, published trees (as newick, NEXUS,

115   or NeXML format) were obtained by appealing to authors, or imported from TreeBASE

116   (Sanderson et al. 1994) and Dryad. We attempted to incorporate the source trees from the Davis

117   and Page (2014) supertree study. However, trees from this resource were found to be some form

118   of consensus (e.g., between parsimony and maximum likelihood) hypothesis and/or included

119   unsampled taxa (both extinct and extant) from the Davis and Page (2014) taxonomy. In sum,

120   these trees reflected neither a specific hypothesis nor the extent of sampling of the original

121   publication, and so were not included here. The full species-level tree (i.e., the "Tapestry" tree)

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122   of Sibley and Ahlquist (1990) has, to our knowledge, never been available in electronic format.

123   As part of this study, JWB constructed the tree with branch lengths from Figs. 357-368,371-385

124   of Sibley and Ahlquist (1990); this tree is now freely available from the Open Tree of Life

125   curator (study: ot_427). The taxon labels for each source tree sampled here were mapped to the

126   Open Tree of Life taxonomy (i.e., OTT) and trees were rooted with outgroup based on the

127   original study.

128   In total, 290 avian phylogenetic hypotheses were gathered from the existing resources in

129   the Open Tree of Life. They are all available in the git-based phylesystem repository (McTavish

130   et al., 2015; https://github.com/OpenTreeOfLife/phylesystem). The distribution of trees sampled

131   through time (Figure 1) reflects data availability rather than research effort, as historically

132   phylogenetic hypotheses have not been archived in machine-readable formats (Stoltzfus et al.,

133   2012; Drew et al., 2013). Among the sampled trees, seven historically trees were used as

134   backbones for later concordance and conflict analyses: Sibley and Ahlquist (1990), Livezey and

135   Zusi (2007), Hackett et al. (2008), Jetz et al. (2012), Davis and Page (2014), Jarvis et al. (2014),

136   and Prum et al. (2015). It is noteworthy that the Jetz et al. (2012) tree we used is the one with

137   genetic data only (6,670 tips) and constraint on Hackett et al. (2008) backbone. In addition to the

138   seven trees above, the Open Tree of Life synthesis tree version 7 (hereafter Opentree7, updated

139   in Sep 2016; Hinchliff et al., 2015) was also included as one of the backbone resources.

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141   *Construction of a new synthetic tree of Aves*

142   In addition to the individual phylogenetic trees that we collected from the Open Tree of

143   Life, we also assembled a novel synthetic avian tree using the "propinquity" pipeline from

144   Redelings and Holder (2017). This supertree method takes as input a taxonomy tree (i.e., OTT)

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145   and a set of ranked source trees. Of the 290 avian trees collected above, 183 were selected as

146   reflecting community consensus about phylogenetic hypotheses. In general, the method will

147   construct a supertree that displays the largest number of input tree edges and minimize the

148   amount of information that does not come from input trees. Moreover, by ranking input trees by

149   certain criteria, a group can be recovered from higher-ranked trees when conflicts exhibit in the

150   source trees. Because synthesis relies upon supertree construction, we excluded both superseded

151   trees (i.e., trees that have been proven to be incorrect by subsequent studies) and previous

152   supertrees. After grouping the bird resource trees into separate focal clades (e.g., by order), we

153   ranked the 183 bird trees based on mixed criteria, such as date of publication, extent of taxon and

154   character sampling, and degree of taxonomic overlap. The set of trees used for the construction

155   of the new synthesis are listed in Supplementary Information. As to conflicting clades, JWB and

156   NW performed the tree ranking order to make sure confident groupings were put in higher ranks.

157   The taxonomic tree with all taxa, derived from OTT, was then used to maximize leaf set for

158   comparison. After dividing the full data set into sub-problems based on uncontested taxa (that is,

159   taxa from OTT that are not conflicted by any source tree), propinquity constructs a summary tree

160   for each subproblem and grafts all summary trees into a single supertree. This result was then

161   grafted with taxonomy-only taxa to produce a complete synthetic tree. See Redelings and Holder

162   (2017) for more details.

163

164   *Conflict and concordance analyses*

165   In total, nine major phylogenies (eight published and one new synthetic tree as described

166   above) were used to conduct conflict and concordance analyses. To compare these trees with the

167   290 source trees, we added the comprehensive OTT set of taxa to each tree by using the same

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168   synthesis approach (see above) but with only the taxonomy and the one phylogeny in question.

169   Adding the full OTT set of taxa to the focal trees ensures an overlap of tip sets with each of the

170   290 source trees. The result was a comprehensive tree with only resolution of the single tree and

171   the taxonomy (i.e., the synthesis procedure preserves all the inferred relationships of the original

172   publication). Conflict and concordance analyses were conducted using the corresponding tools

173   utilized by the Open Tree of Life web service (available from

174   https://github.com/OpenTreeOfLife/reference-taxonomy). Python scripts to perform the analyses

175   are available in the bitbucket repository (https://bitbucket.org/blackrim/opentree_birds). For

176   these analyses, concordant and conflicting edges were identified as in Smith et al. (2013; 2015)

177   and Redelings and Holder (2017). More explicitly, because all sources trees are rooted, a source

178   tree edge j defines a rooted bipartition $S(j) = S_{in} \mid S_{out}$, where S_{in} and S_{out} represent the tip sets of

179   the ingroup and outgroup, respectively. For a given edge in tree A, concordance/conflict with

180   source tree B thus involves the overlap of tip sets. We define concordance between A and B ('A

181   *displays B*' in Redelings and Holder (2017)) when $B_{in} \subset A_{in}$ and $B_{out} \subset A_{out}$ (that is, ingroup tip

182   sets overlap, and outgroup tip sets overlap). [We note that Redelings and Holder (2017) use $\subseteq$

183   rather than $\subset$ because they deal with the more general case where individual trees may have

184   incomplete tip sets. Because we synthesize OTT with each source tree (above), we ensure that

185   each tree has a complete tip set]. On the other hand, edges in trees A and B are identified as

186   conflicting if none of the following are empty: $A_{in} \cap B_{in}$, $A_{in} \cap B_{out}$, or $B_{in} \cap A_{out}$ (that is, there is

187   reciprocal overlap in the ingroup and outgroup across trees; we note that Redelings and Holder

188   (2017) have a typo in this definition). We computed edge-specific values of concordance and

189   conflict for each of the nine major trees against all 290 source trees. All analyses were conducted

190   on the focal trees with comprehensive taxa added. Finally, we summarized the results on the

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191   eight original published tree topologies (i.e., removing the comprehensive taxa that were not

192   included in the original analysis) and the new synthetic tree.

193

194   **Results and Discussion**

195   *The synthetic tree of Aves*

196   The synthetic tree constructed in the current study contains 13,579 tips and 10,795

197   internal nodes, leaving 2,782 nodes (13,577-10,795, assuming a fully binary tree) to be resolved

198   by future studies. We note that this tip count is higher than the ~10,800 species recognized by

199   Gill and Donsker (2016). OTT is a synthetic taxonomy comprised of numerous source

200   taxonomies that sometimes disagree on the taxonomic status (e.g., species vs. subspecies) or

201   name of a taxon. As a result, there are duplicated taxa in OTT, although this is not expected to

202   influence our results. Comparatively, Opentree7 had more tips (13,756; due to a different version

203   of OTT) but far fewer internal nodes (7,157). Although the changes in taxonomy since

204   Opentree7 have caused the loss of tips in our synthetic tree (probably due to improvements in

205   name reconciliation in OTT), our new synthetic tree resolved ~ 3,500 more nodes than

206   Opentree7 through inclusion of more source trees (183 vs. 77). The higher-level inter-ordinal

207   relationships shown by the synthetic tree follow mostly that of Prum et al. (2015), which

208   possessed the highest source tree rank regarding the backbone topology. Other studies focusing

209   on individual clades (i.e., order- or family-specific) help to resolve lower level relationships

210   towards the tips. Thus, our new synthetic tree provides a better resource for researchers to

211   conduct evolutionary analyses on birds, and it also serves as a point on which we can measure

212   future improvements in our knowledge of the evolution of this group. However, the new

213   synthetic tree lacks branch lengths due to the difficulty of incorporating branch length

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214   information into the synthesis supertree procedure given that the input trees vary in branch length

215   presence, data type (i.e., DNA vs. morphology), branch length measurement (i.e., number of

216   changes vs. time), and scale. While branch lengths and divergence times are not the focus of this

217   study, future studies should examine new ways to incorporate divergence times to increase the

218   utility of this resource.

219

220   *The distribution of phylogenetic conflict*

221   One major aim of this study is to examine the distribution of concordance and conflict

222   across nine major bird phylogenies. Except for that from Sibley and Ahlquist (1990), all the

223   historically important backbone trees we considered were constructed since 2007. Each tree, at

224   the time of publication, represented major improvements in data collection and analysis, and

225   therefore also on the hypotheses about avian evolutionary history. The most recent trees agree on

226   many relationships despite being built using different methods [i.e., one tree is based on

227   morphological data (Livezey and Zusi, 2007), four are built with different scales of molecular

228   data (Hackett et al., 2008; Jetz et al., 2012; Jarvis et al., 2014; Prum et al., 2015), while the rest

229   were based on supertree methods (Davis and Page, 2014; Opentree7; our synthetic tree)]. Given

230   that Sibley and Ahlquist (1990) and Prum et al. (2015) represent the earliest and most recent

231   comprehensive hypotheses, respectively, results from these trees and the new synthesis tree are

232   discussed in more detail for comparison.

233   There are more conflicting edges (warmer colours, Figure 2) for higher-level

234   relationships (i.e., the backbone from Neognathae to Passeriformes) on the Sibley and Ahlquist

235   (1990) tree. This is to be expected given that many phylogenies have been published since 1990

236   that have contradicted the Sibley and Ahlquist (1990) "tapestry" hypothesis (see also discussion

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237   in Harshman, 1994). For instance, the rooting of this tree, with Galloanserae sister to

238   Paleognathae, has been refuted by all subsequent studies. The new synthetic tree has several

239   higher relationships (i.e., toward the base of Neoaves) that have higher conflict than that of Prum

240   et al. (2015), but this is likely due to the comprehensive nature of the tree. This pattern is largely

241   consistent with the neoavian polytomies posited by Suh (2016) and Reddy et al. (2017), although

242   these studies only considered a small number of phylogenomic studies for comparison. Many of

243   the conflicts among deepest neoavian relationships are also shared by Jetz et al. (2012), which

244   contributes many of the edges to the synthetic tree due to the extensive taxonomic sampling

245   (Figure 3). However, the Prum et al. (2015) tree (Figure 2) has comparatively fewer conflicting

246   edges toward the base of Neoaves. This may simply be due to significantly lower taxon sampling

247   (i.e., fewer sampled lineages means a smaller potential number of conflicts).

248   A more general pattern of conflict across the focal trees involved the Passeriformes

249   (songbirds). In fact, although the monophyly of Passeriformes is largely supported, the

250   relationships that diverge soon after crown Passeriformes (i.e., within the oscines) are highly

251   contested among the source trees. Sibley and Ahlquist (1990) have the highest conflict among

252   edges surrounding the Passeriformes clade, with six having 29-37 conflicting trees and 13-30

253   supporting trees. Similar patterns with strong conflict surrounding the edges of Passeriformes

254   were exhibited on the other focal trees. Prum et al. (2015) showed strong conflict at the base of

255   Passeriformes, with exceptionally high conflict leading to oscine songbirds. The synthetic tree

256   showed fewer conflicts at the base of Passeriformes, implying that many of the source trees that

257   contributed to the synthetic tree construction contradict the oscines relationships in Prum et al.

258   (2015), possibly due to the limited taxonomic sampling in the latter. We note that strong

259   phylogenetic conflict within Passeriformes was not evident in the studies of Suh (2016) and

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260   Reddy et al. (2017), as they only considered trees focused on inter-ordinal relationships.

261   Although conflict and concordance within Passeriformes has not previously been explicitly

262   evaluated, individual assessments of phylogenetic uncertainty have hinted that this may involve a

263   number of problematic relationships. For example, Burleigh et al. (2015) report that for clades

264   with < 50% bootstrap support, almost half of the families (195/399) and two thirds of the genera

265   (32/47) were within the oscine songbird clade. Given that Passeriformes represents ~60% of

266   extant avian species, these results together suggest that there is much work to be done in avian

267   phylogenetics than resolving the neoavian backbone.

268

269   *The resolution of the Aves phylogeny through time*

270   The trees on which we conduct conflict and support analyses represent either major

271   contributions or comprehensive analyses of the Aves clade. One central question regarding these

272   trees is how does our knowledge about clades change over time. For example, did recent

273   genomic studies such as Prum et al. (2015) contribute many unique clades to the literature, or

274   were these resolutions simply recapitulating results that had been published previously?

275   Although we are limited by the database of 223 available trees, we can begin to address these

276   questions. When compared to earlier studies, Sibley and Ahlquist (1990) contributes almost all

277   new relationships for bird phylogeny except for three edges (published before 1990) that involve

278   relationships of flycatchers, *Phrygilus*, and *Junco* (Figure 4). It is likely that more edges on

279   Sibley and Ahlquist (1990) had already been published in the older literature. However, we do

280   not have access to many of those trees because they are not available in electronic format. By

281   comparison, the Prum et al. (2015) study provides an updated view of the deep relationships of

282   birds (Figure 4). There are a range of dates (i.e., previous published hypotheses) supporting

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283   edges of the Prum et al. (2015) tree. While 143 edges had been reported in previous publications,

284   including many in Sibley and Ahlquist (1990), 47 edges were new to the Prum et al. (2015) tree.

285   This highlights that important contributions are still being made by large-scale genomic and

286   molecular studies.

287   The new synthetic tree reported here provides another interesting contrast. Although

288   comprehensive trees have been published before, including Jetz et al. (2012) and Davis and Page

289   (2014), our synthetic tree allows us to address whether new studies are contributing significant

290   new knowledge besides these comprehensive trees. The largest contributing study to the edges of

291   the synthetic tree is Jetz et al. (2012) with 4,820 (Figure 3). However, 1,890 edges were

292   contributed after 2012, and 223 were added from studies published after 2015. This underscores

293   the importance of not only large genomic studies, but also of trees of individual clades to the

294   knowledge of bird phylogeny.

295   Large phylogenies like those analyzed and created as part of this study have many

296   potential uses. They have been and continue to be used in large scale studies of biodiversity (e.g.,

297   Jetz et al., 2012; Cooney et al., 2017). As mentioned above, methods need to be developed to

298   apply dates to the synthetic trees and supertrees that are produced as part of comprehensive

299   analyses (Davis and Page, 2014; Hinchliff et al., 2015; Redelings and Holder, 2017). The

300   development of methods for applying divergence times will dramatically improve the utility of

301   comprehensive trees for further comparative studies. In addition to the larger comprehensive

302   trees, the Open Tree of Life tree repository (McTavish et al. 2015), with phylogenetic hypotheses

303   mapped to a common taxonomy, becomes increasingly useful as it continues to grow. As

304   demonstrated here, these trees can be used to gauge how our understanding changes, whether

305   new studies are contributing new edges, and localize the major sources of conflict. Furthermore,

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306   the relationships can serve to construct meaningful prior expectations for the resolution of clades

307   across the tree of life (e.g., as topological priors in a Bayesian reconstruction). It is noteworthy

308   that all these analyses depend on the availability of electronic tree files that are crucially

309   important for any publication that posits phylogenetic hypotheses, but archiving such resources

310   has not been common historically (Stoltzfus et al., 2012; Drew et al., 2013). As we continue to

311   improve our view of the tree of life, it will be instructive to examine how consensus builds across

312   major clades.

313

314   **Conclusion**

315   A fundamental goal for the field of evolutionary biology and systematics is the resolution

316   and construction of a complete tree of life. The resources for constructing comprehensive trees

317   (e.g., phylogenetic trees, molecular and morphological data sets, and comprehensive taxonomies)

318   are becoming available and are now of the quality that we can not only begin to construct

319   complete trees, but also refine and identify where more work is needed. Here, we demonstrate

320   that, while we have made major strides in our knowledge of some clades, new studies continue to

321   contribute new edges that resolve previously ambiguous relationships. We make this observation

322   on Aves, a relatively well-studied and small clade of the tree of life. Other parts of the tree of life

323   that are likely to have a lower density of phylogenetic information in the form of published

324   phylogenies or molecular data still need significant more work before they may be

325   comprehensively resolved.

326

327   **Acknowledgements**

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334   **Data availability**

335   All the software and data used for this study are freely available in repositories online. For the

336   source trees and software used in the analyses, please see

337   https://bitbucket.org/blackrim/opentree_birds.

338

339   **Author contributions**

340   JWB and NW gathered the input source trees and constructed the synthetic trees. JWB, NW, and

341   SAS wrote the manuscript and conducted the analyses.

342

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465   **Figure legends**
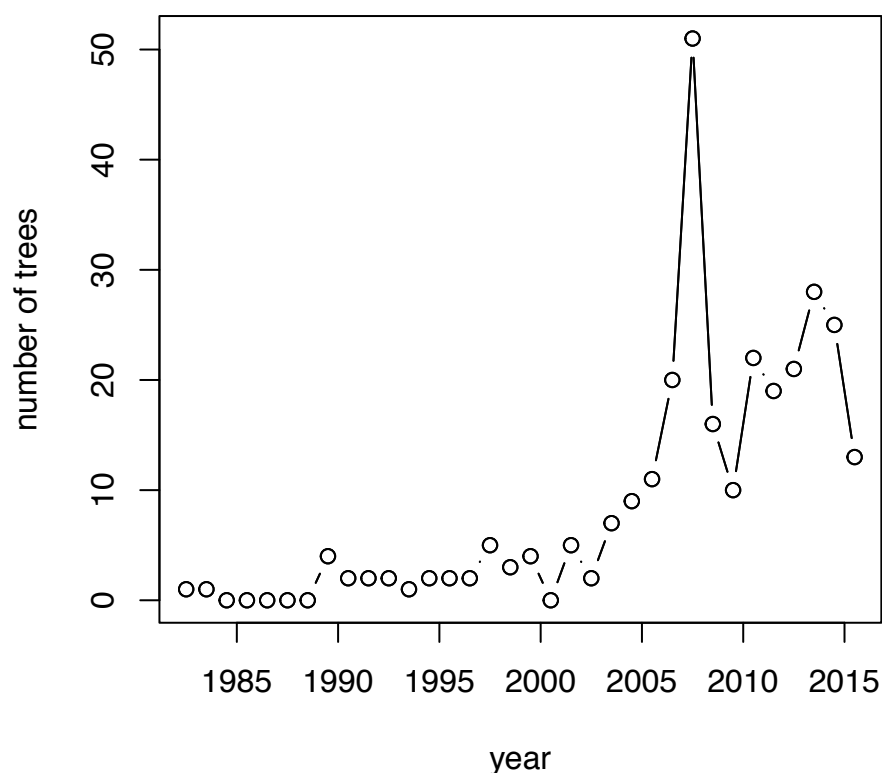

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467   **Figure 1** The number of published avian trees per year available in the Open Tree of Life tree
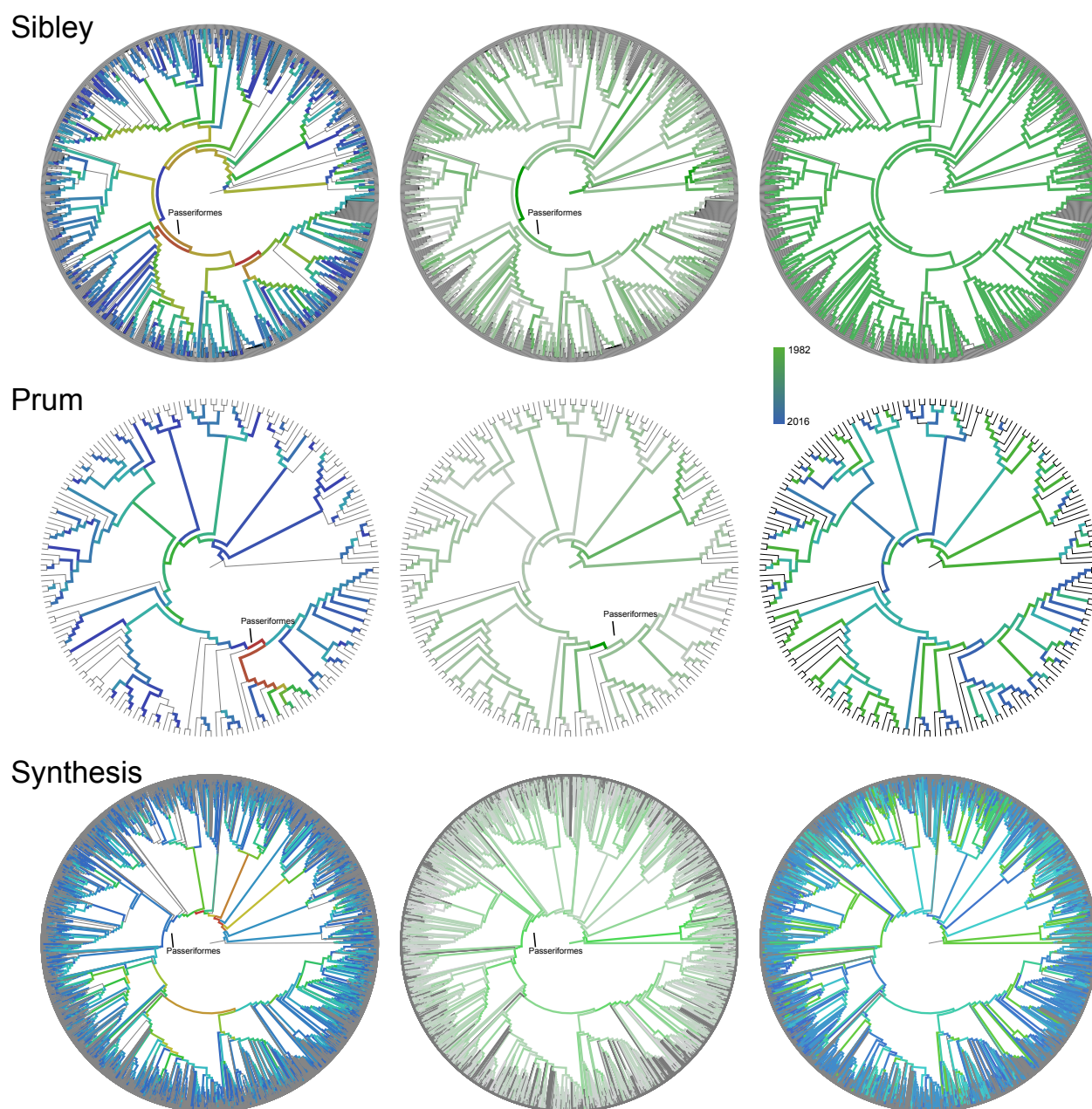
468   repository.

Figure 2 Conflicting (left, warmer colour represents more conflict), concordance (center, darker green represents more concordance), and chronological contribution (right) analyses based on three backbone trees. Conflict and concordance are measured as the number of source tree edges that conflict/support a given focal tree edge. Chronological contribution is measured as the first year in which the focal edge appeared in a published tree.
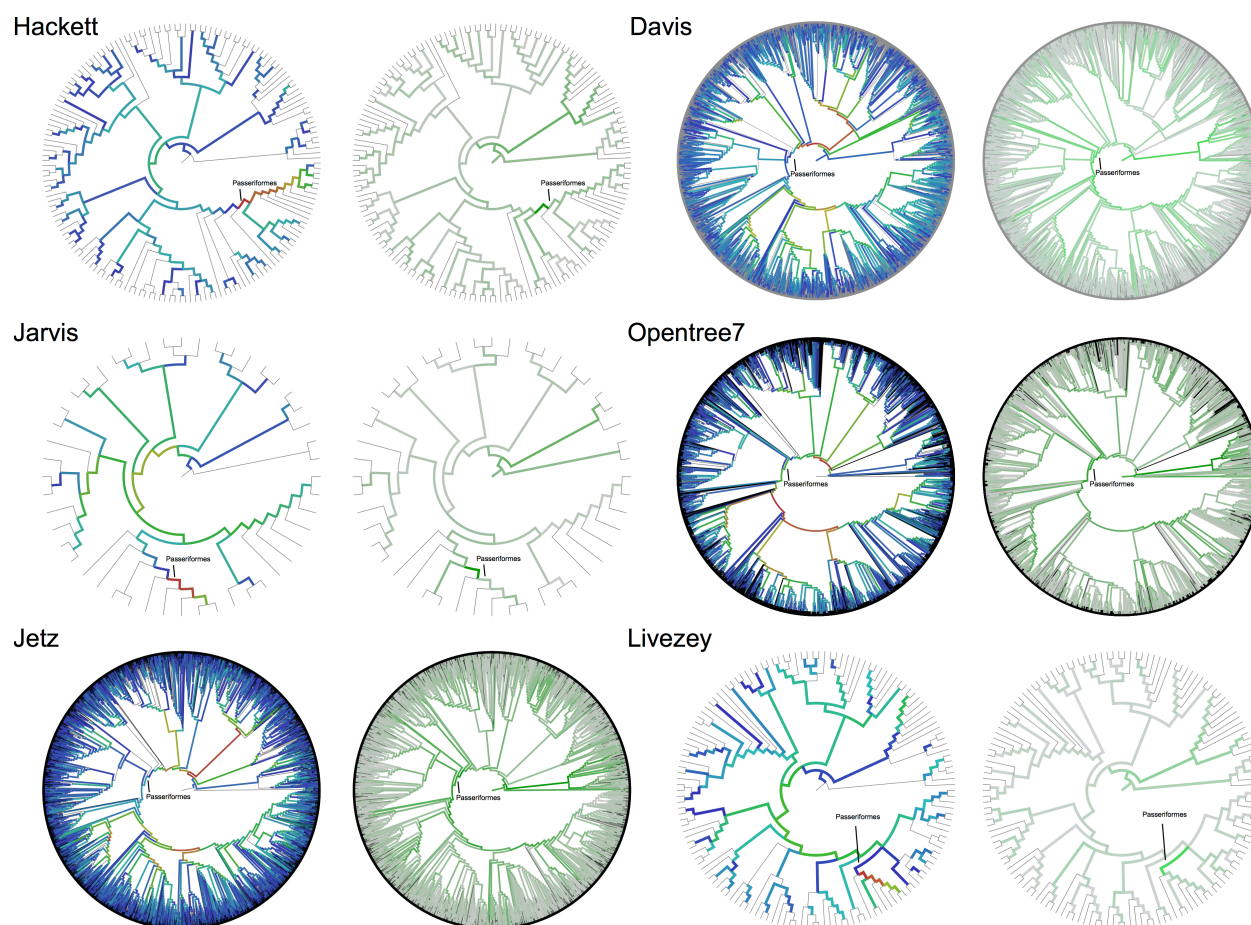
Figure 3 Distributions of conflict and concordance across the six-remaining major avian phylogenetic hypotheses. See Figure 2 for description of colours.
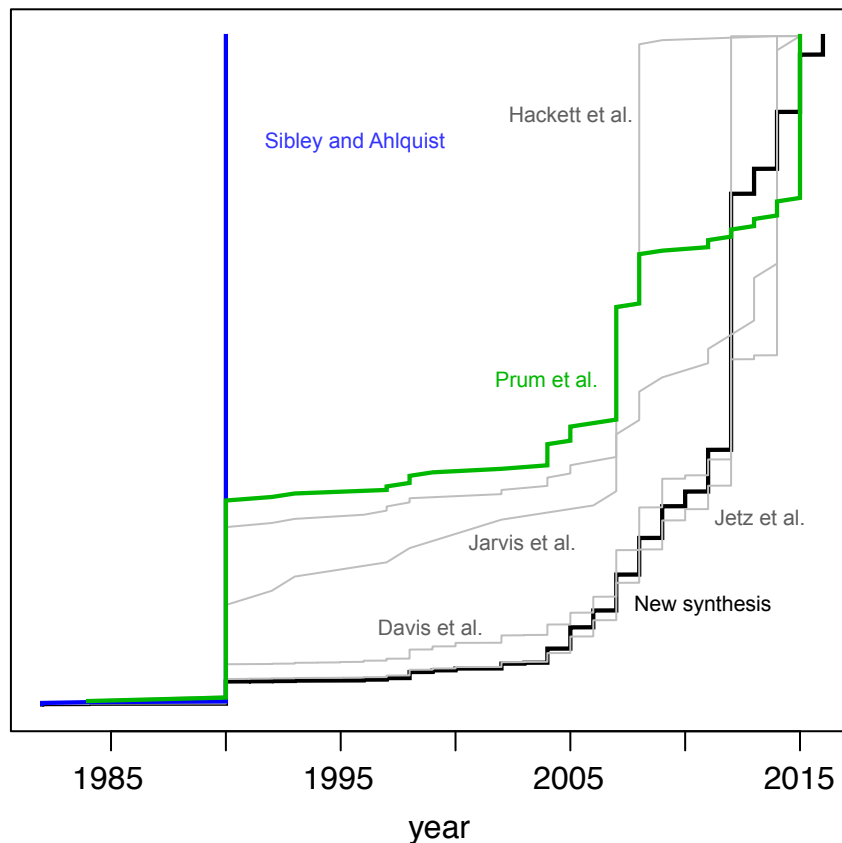
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Figure 4 The contribution of source tree support to each of the major avian phylogeny. The x

axis represents the source study year that first supports a clade in a focal tree, and y axis is the

proportional accumulation of clades on each tree.

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