**Supplementary information – Phylogenetic estimates of diversification rate are affected by molecular rate variation**

**Supplementary methods:**

Literature survey of diversification rate studies

**Supplementary Tables**

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**Figure S2.** Uncertainty in estimated node ages compared across three examples of BEAST analyses from the simulated alignments.

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**Figure S4.** ROC curve analysis of simulations under each of three sources of phylogenies (true, reconstructed with NPRS, and reconstructed with BEAST) and each of the three macroevolutionary methods (gamma, LASER, and TESS).

**Figure S5.** Posterior probability densities of extinction estimated by TESS for example evolutionary cases where the software TESS and LASER behave differently.

**Supplementary methods**

**Literature survey of diversification rate studies**

In order to ensure that the results of our simulation study are relevant to common practice in macroevolutionary studies, we used a literature survey to identify the most commonly used methods and the characteristics of typical datasets. We reviewed the literature of studies that estimated diversification rates or diversification dynamics from molecular phylogeneties. To access the relevant literature, we performed a search in the freely available scholarly literature database Google Scholar. We used the search term *phylogeny “diversification rates”* and extracted data from the first 100 articles published within a ten-year period (2005-2015) that used molecular phylogenies to make estimates of diversification rates or diversification rate dynamics. Studies that did not use empirically derived data – such as simulation studies or theoretical advances - were not considered.

From each article, we recorded data about the phylogenetic dataset and inference method and about the method used to estimate diversification rates dynamics. We recorded the number of sampled tips, the number of loci used for phylogeny inference, the length of the DNA alignment, the method used for branch length inference, and the number of calibrations used, the method for estimating diversification rate dynamics and the estimates of net diversification rates if available (Table S1).

*Characteristics of molecular data sets*

The mean publication date of the studies sampled was the second quarter of 2009. Twelve studies did not provide information about the number of loci used, either because the data was not produced in that study or because they used multiple phylogenies sampled from the literature. In the remaining 88 studies, the number of loci ranged from 1 to 83, and had median 4 (Table S2). Twenty-one studies did not provide information about the number of sequence base pairs in the alignment. The total alignment length summed across loci in the remaining 79 studies ranged from 511 nucleotides to 4.5 million, with median of 3773 alignment sites (Table S2). Eleven studies did not mention the number of tips sampled in phylogenies. These were studies that included several phylogenies sampled from the literature (Table S1). The number of tips sampled in the remaining 89 studies ranged from 21 to 55470, with a median of 133 tips (Table S2).

*Methods for phylogenetic inference*

Fifty-two studies used non-parametric rate smoothing (NPRS) as implemented in the software package r8s (Sanderson, 2003), while 38 studies used the uncorrelated lognormal distribution of rates as implemented in BEAST (Drummond & Rambaut, 2007), and six used the model of rate autocorrelation implemented in the package MULTIDIVTIME (Yang, 2007; Supplementary information Figure S1). Eighteen studies used multiple phylogenies derived from the literature, or designed methods that were suited to their dataset (e.g. molecular rate estimates using local clocks, or no molecular rate estimates at all). At least 9 studies used multiple methods for inferring branch lengths. Twelve studies did not mention the number of calibrations used, either because the study inferred changes in diversification rates from topology without inferring branch lengths from molecular data, or because phylogenetic data was taken from several other studies. The number of calibrations used in the remaining 88 studies ranged from 0 (for studies that used relative times) to 98, with a median of 2 calibrations (Table S2).

*Methods to estimate diversification rate dynamics*

Fifty-five studies used more than one method to estimate diversification rates or diversification rate dynamics. Thirty-two studies used the gamma statistic (Pybus & Harvey, 2000) to infer changes in diversification rates through time, while 26 studies used the model-testing method from the software package LASER (Rabosky, 2006). Twenty-three studies estimated net diversification rates using the methods by Magallón and Sanderson (2001), which uses a given rate of extinction. Other methods included: the topology-based method in the software SymmeTree (Chan & Moore, 2005), which uses the branching pattern to identify nodes that undergo a significant change in speciation rates; the likelihood-based methods MEDUSA (Alfaro *et al.*, 2009), which uses the model-testing as in LASER to identify nodes that undergo a change in diversification rates, and TreePar (Stadler, 2011), which uses a diversification model-selection approach similar to that of LASER. The latter three methods were used in 13, 12 and 4 studies, respectively (Figure S2). Nearly half of the studies sampled (46) used methods that were only used in less than five of the sample of studies. Less than half of the studies sampled (40) estimated net diversification rates. Thirteen studies used relative time to test if there were changes in diversification rates through time.

Fifty-three studies provided estimates of rates of speciation and/or extinction. Some of these studies estimated a single net diversification rate across the whole tree while others provided estimates of diversification rates through time. All but two studies included confidence intervals for the estimates. We report the mid point between the maximum and minimum estimate in each study. The reported estimates of net diversification rates ranged from 0.018 to 3.8 species per million years, and had median of 0.14 species per million years (Table S2).

***Summary***

We assumed that the sample of 100 studies provides a representative picture of the use of phylogenetic estimates of diversification rate in the 10 years period over which they were sampled. Median values provide a better summary than arithmetic means for the information recorded, because the data does not follow a normal distribution. Accordingly, we find that a representative data set has around 130 tips represented by 4 loci with a total of 3800 base pairs. Two methods of phylogenetic inference have been used with particularly high frequency compared to others: non-parametric rate smoothing using likelihood and the Bayesian implementation of uncorrelated log-normally distributed rates. The diversity of methods used for macroevolutionary inference using phylogenies makes it difficult to identify a typical approach. Nevertheless, according to the sampled studies, the two most common methods in macroevolutionary studies were the gamma statistic (Pybus & Harvey, 2000) and model-testing as implemented in the software LASER (Rabosky, 2006). The median reported value of diversification rate is approximately 0.14 species per million years.

**Table S1.** List of studies of diversification rates using phylogenetics included in the literature survey. The information taken from each study included the following. Sequence length: combined number of alignment sites used in the study, including all the loci used for phylogenetic analysis. Loci: Number of genetic loci (genes or other loci) used for phylogenetic analysis. Tree size: Number of taxa included in the phylogenetic analysis. Method: Software package or source of method used for inference of evolutionary timescales. Specifically, studies using r8s (Sanderson, 2003) and MULTIDIVTIME (Thorne & Kishino, 2002) used a method assuming rates of molecular evolution that were heritable or similar across neighbouring branches; studies using BEAST (Drummond & Rambaut, 2007) used an uncorrelated clock model with rates of molecular evolution across branches assumed to fall on a lognormal distribution; studies using PAUP 4.0 (Swofford, 1998) used a method assuming a constant rate of molecular evolution across branches; the study using RAxML (Stamatakis, 2014) used the branching pattern to estimate shifts in rates of diversification. Calibrations: The number of nodes in the phylogeny with external information about the timing of an evolutionary event. Diversification rate method: Names of software packages with particular methods or the names of methods used for estimating rates of diversification or changes in diversification rates through time or across lineages. Diversification rate estimate: Value or range of values of net diversification rates estimated (rate of speciation minus rate extinction). Studies for which the column Net Diversification Rates is YES estimated overall speciation minus extinction, whereas studies with a NO estimated speciation minus extinction for different lineages or for different points in time. Relative times: Studies that did not include external information about the timing of an evolutionary event, such that timescale estimates can only be interpreted as the times of events relative to each other, are marked with a YES in this column. A dash (-) indicates instances where information was not available from a publication.

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Reference | Sequence length | Loci | Tree size | Method | Calibra-tions | Diversification rate method | Diversificat-ion rate estimate | Relative times | Net diversification rates |
| Stadler, T. (2011). Mammalian phylogeny reveals recent diversification rate shifts. Proceedings of the National Academy of Sciences, 108(15), 6187-6192. | - | - | - | Mammal supertree from (Bininda-Emonds *et al.*, 2007) | - | TreePar package allowing speciation and extinction rates to vary through time (Stadler, 2013). | 0.05-1.6 | NO | YES |
| Ricklefs, R. E. (2006). Global variation in the diversification rate of passerine birds. Ecology, 87(10), 2468-2478. | - | - | 90 trees with 1 to 413 species | Clade ages from Sibley & Ahlquist, (1990); and (Barker *et al.*, 2004) | - | Net speciation minus extinction (Magallón & Sanderson, 2001) | 0.05-4.2 | NO | YES |
| Meredith, R. W., et al. (2011). Impacts of the Cretaceous Terrestrial Revolution and KPg extinction on mammal diversification. Science, 334(6055), 521-524. | 35603 | 26 | 164 | MCMCTREE (Yang, 2007), autocorrelated and gamma-distributed independent rates models. | 82 | Gamma statistic (Pybus & Harvey, 2000), LASER (Rabosky, 2006); TreePar (Stadler, 2013) | 0.2-1.6 | NO | YES |
| Hunt, T., et al. (2007). A comprehensive phylogeny of beetles reveals the evolutionary origins of a superradiation. Science, 318(5858), 1913-1916. | 1903 | 3 | 1880 | r8s (Sanderson, 2003) | 8 | Log(N)/t, which is a maximum likelihood estimate for net diversification rates with no extinction (Stanley, 1979) | 0.048-0.068 | NO | YES |
| Kozak, K. H., et al. (2006). Rapid lineage accumulation in a non-adaptive radiation: phylogenetic analysis of diversification rates in eastern North American woodland salamanders (Plethodontidae: Plethodon). Proceedings of the Royal Society B: Biological Sciences, 273(1586), 539-546. | 1100 | 2 | 44 | r8s (Sanderson, 2003) | 1 | Gamma statistic (Pybus & Harvey, 2000); DIVERSI (Paradis, 1998; using models for the probability of survival of species) | 0.16-0.8 | NO | NO |
| Hughes, C. & Eastwood, R. (2006). Island radiation on a continental scale: exceptional rates of plant diversification after uplift of the Andes. Proceedings of the National Academy of Sciences, 103(27), 10334-10339. | 1900 | 2 | 89 | r8s (Sanderson, 2003) | 1 | Log(N)/t (Stanley, 1979) | 2.49-3.72 | NO | YES |
| Bininda-Emonds, O. R., et al. (2007). The delayed rise of present-day mammals. Nature, 446(7135), 507-512. | - | - | 4510 | Supertree; dates of divergence established with local clocks and rate-smoothing | 30 | Gamma statistic (Pybus & Harvey, 2000); diversification rates within age ranges (Bininda-Emonds *et al.*, 2007) | 0.01-1.45 | NO | NO |
| Roelants, K., et al. (2007). Global patterns of diversification in the history of modern amphibians. Proceedings of the National Academy of Sciences, 104(3), 887-892. | 3750 | 5 | 171 | MULTIDIVTIME (Thorne & Kishino, 2002) and r8s (Sanderson, 2003) | 22 | Net speciation minus extinction (Magallón & Sanderson, 2001); gamma statistic (Pybus & Harvey, 2000) | 0.0154-0.0217 | NO | YES |
| Rabosky, D. L., et al. (2007). Exceptional among-lineage variation in diversification rates during the radiation of Australia's most diverse vertebrate clade. Proceedings of the Royal Society B: Biological Sciences, 274(1628), 2915-2923. | 3012 | 7 | 81 | r8s (Sanderson, 2003) | 1 | Net speciation minus extinction (Magallón & Sanderson, 2001) | 0.005-0.218 | NO | YES |
| Ramirez, S. R., et al. (2010). Phylogeny, diversification patterns and historical biogeography of euglossine orchid bees (Hymenoptera: Apidae). Biological Journal of the Linnean Society, 100(3), 552-572. | 4438 | 4 | 126 | r8s (Sanderson, 2003) | 5 | Survival analysis and relative cladogenesis test (Nee, May, & Harvey, 1994; GEIGER, Harmon, Weir, Brock, Glor, & Challenger, 2008) | - | NO | NO |
| Moyle, R. G., et al. (2009). Explosive Pleistocene diversification and hemispheric expansion of a “great speciator”. Proceedings of the National Academy of Sciences, 106(6), 1863-1868. | - | 3 | 65 | r8s (Sanderson, 2003) | 1 | Gamma statistic (Pybus & Harvey, 2000); log(N)/t (Stanley, 1979) | 1.95-2.63 | NO | YES |
| Beilstein, M. A., et al. (2010). Dated molecular phylogenies indicate a Miocene origin for Arabidopsis thaliana. Proceedings of the National Academy of Sciences, 107(43), 18724-18728. | 3798 | 2 | 177 | r8s (Sanderson, 2003) and BEAST (Drummond & Rambaut, 2007) | 6 | LASER (Rabosky, 2006) | 0.003-0.106 | NO | YES |
| Kazancıoğlu, E., et al. (2009). Influence of sexual selection and feeding functional morphology on diversification rate of parrotfishes (Scaridae). Proceedings of the Royal Society B: Biological Sciences, rspb20090876. | - | 5 | 276 | r8s (Sanderson, 2003) and BEAST (Drummond & Rambaut, 2007) | 4 | Net speciation minus extinction (Magallón & Sanderson, 2001); LASER (Rabosky, 2006); SymmeTree (Chan & Moore, 2005) | 0.06-0.267 | NO | YES |
| Rabosky, D. L. (2006). Likelihood methods for detecting temporal shifts in diversification rates. Evolution, 60(6), 1152-1164. | 1800 | 1 | 69 | r8s (Sanderson, 2003) | 1 | LASER (Rabosky, 2006) | 0.039-0.196 | NO | NO |
| Couvreur, T. L., et al. (2010). Molecular phylogenetics, temporal diversification, and principles of evolution in the mustard family (Brassicaceae). Molecular Biology and Evolution, 27(1), 55-71. | 10521 | 8 | 187 | BEAST (Drummond & Rambaut, 2007) | 1 | Gamma statistic; LASER (Rabosky, 2006); Net speciation minus extinction (Magallón & Sanderson, 2001) | 0.156-0.223 | NO | YES |
| Rabosky, D. L., & Lovette, I. J. (2008). Density-dependent diversification in North American wood warblers. Proceedings of the Royal Society B: Biological Sciences, 275(1649), 2363-2371. | 9557 | 7 | 25 | BEAST (Drummond & Rambaut, 2007) | 0 | Gamma statistic (Pybus & Harvey, 2000); LASER (Rabosky, 2006) | - | YES | NO |
| Smith, S. A., et al. (2011). Understanding angiosperm diversification using small and large phylogenetic trees. American Journal of Botany, 98(3), 404-414. | - | 6 | 55473 | RAxML (Stamatakis, 2014), no timetree | 0 | SymmeTree (Chan & Moore, 2005) | - | NO | NO |
| Eckert, A. J., & Hall, B. D. (2006). Phylogeny, historical biogeography, and patterns of diversification for *Pinus* (Pinaceae): Phylogenetic tests of fossil-based hypotheses. Molecular Phylogenetics and Evolution, 40(1), 166-182. | 1121 | 4 | 83 | r8s (Sanderson, 2003) | 10 | Gamma statistic (Pybus & Harvey, 2000); phylogenetic imbalance | - | NO | NO |
| Kozak, K. H., et al. (2005). Phylogenetic analysis of ecomorphological divergence, community structure, and diversification rates in dusky salamanders (Plethodontidae: Desmognathus). Evolution, 59(9), 2000-2016. | - | 6 | 113 | r8s (Sanderson, 2003) | 0 | Survival models (DIVERSI; Paradis, 1998) | - | YES | NO |
| Moreau, C. S., & Bell, C. D. (2013). Testing the museum versus cradle tropical biological diversity hypothesis: phylogeny, diversification, and ancestral biogeographic range evolution of the ants. Evolution, 67(8), 2240-2257. | 3324 | 5 | 311 | BEAST (Drummond & Rambaut, 2007) | 45 | LASER (Rabosky, 2006); MEDUSA (Alfaro *et al.*, 2009) | 0.0158-1.52 | NO | NO |
| Santini, F., et al. (2009). Did genome duplication drive the origin of teleosts? A comparative study of diversification in ray-finned fishes. BMC Evolutionary Biology, 9(1), 194. | 1497 | 1 | 225 | BEAST (Drummond & Rambaut, 2007) | 44 | MEDUSA (Alfaro *et al.*, 2009) | 0.011-0.081 | NO | NO |
| Magallón, S., & Castillo, A. (2009). Angiosperm diversification through time. American Journal of Botany, 96(1), 349-365. | - | 5 | 265 | r8s (Sanderson, 2003) | 3 | Net speciation minus extinction (Magallón & Sanderson, 2001); SymmeTree (Chan & Moore, 2005) | 0.01-0.149 | NO | YES |
| Wiens, J. J., et al. (2007). Phylogenetic history underlies elevational biodiversity patterns in tropical salamanders. Proceedings of the Royal Society B: Biological Sciences, 274(1612), 919-928. | 3002 | 2 | 137 | r8s (Sanderson, 2003) | 1 | Net speciation minus extinction (Magallón & Sanderson, 2001); Relative cladogensis statistic (Nee, 1992) | 0.04-0.24 | NO | YES |
| FitzJohn, R. G., et al. (2009). Estimating trait-dependent speciation and extinction rates from incompletely resolved phylogenies. Systematic Biology, 58(6), 595-611. | - | - | 134 | Supertree from (Thomas *et al.*, 2004) | - | BiSSE, estimation of trait-dependent diversification rates | 0.04-0.1 | NO | NO |
| Alfaro, M. E., et al. (2009). Nine exceptional radiations plus high turnover explain species diversity in jawed vertebrates. Proceedings of the National Academy of Sciences, 106(32), 13410-13414. | 1445 | 1 | 217 | BEAST (Drummond & Rambaut, 2007) | 41 | MEDUSA (Alfaro *et al.*, 2009) | 0.03 | NO | NO |
| Arnold, A. E., et al. (2009). A phylogenetic estimation of trophic transition networks for ascomycetous fungi: are lichens cradles of symbiotrophic fungal diversification?. Systematic Biology, 58(3), 283-297. | 2412 | 2 | 359 | r8s (Sanderson, 2003) | 0 | Lineages through time plot | - | YES | NO |
| Cardillo, M., et al. (2005). Testing for latitudinal bias in diversification rates: an example using New World birds. Ecology, 86(9), 2278-2287. | - | - | 37 clades at the genus-level | Clade ages from Sibley & Ahlquist, (1990); and Barker et al. (2004) | - | Log(N)/t (Stanley, 1979) | 0.001-0.6 | NO | YES |
| Morlon, H., et al. (2011). Reconciling molecular phylogenies with the fossil record. Proceedings of the National Academy of Sciences, 108(39), 16327-16332. | - | 10 | 87 | r8s (Sanderson, 2003); phylogeny from Steeman et al. (2009) | 7 | Likelihood expression accommodating for declining diversity and time-variable diversification rates | 0.1-0.2 | NO | NO |
| Goldberg, E. E., et al. (2011). Phylogenetic inference of reciprocal effects between geographic range evolution and diversification. Systematic Biology, 60(4), 451-465. | 511 | 2 | 40 | BEAST (Drummond & Rambaut, 2007) | 1 | GeoSSE (Goldberg *et al.*, 2011) | 0.08-0.22 | NO | NO |
| Jetz, W., et al. (2012). The global diversity of birds in space and time. Nature, 491(7424), 444-448. | 13277 | 15 | 9993 | BEAST (Drummond & Rambaut, 2007) | 10 | TreePar (Stadler 2011); Inverse of mean equal splits (Redding & Mooers, 2006) | 0.05-0.75 | NO | YES |
| FitzJohn, R. G. (2010). Quantitative traits and diversification. Systematic Biology, 59(6) 619-633. | - | - | 233 | BEAST (Drummond & Rambaut, 2007) | - | QuaSSE, rates of diversification informed by quantitative traits | 0.13-0.29 | NO | NO |
| Esselstyn, J. A., et al. (2009). Do geological or climatic processes drive speciation in dynamic archipelagos? The tempo and mode of diversification in Southeast Asian shrews. Evolution, 63(10), 2595-2610. | 4055 | 5 | 227 | PAUP 4.0 (constant molecular rates assumed; Swofford, 1998) | 1 | LASER (Rabosky, 2006) | - | NO | NO |
| Adams, D. C., et al. (2009). Are rates of species diversification correlated with rates of morphological evolution?. Proceedings of the Royal Society B: Biological Sciences, rspb-20090543 | 5590 | 4 | 190 | r8s (Sanderson, 2003) | 1 | Net speciation minus extinction (Magallón & Sanderson, 2001) | 0.01-0.175 | NO | YES |
| Crisp, M. D., & Cook, L. G. (2009). Explosive radiation or cryptic mass extinction? Interpreting signatures in molecular phylogenies. Evolution, 63(9), 2257-2265. | - | 3 | 350 | r8s (Sanderson, 2003) | 14 | Gamma statistic (Pybus & Harvey, 2000); LASER (Rabosky, 2006) | - | NO | NO |
| Thacker, C. E. (2009). Phylogeny of Gobioidei and placement within Acanthomorpha, with a new classification and investigation of diversification and character evolution. Copeia, 2009(1), 93-104. | 3254 | 4 | 196 | - | 0 | Gamma statistic (Pybus & Harvey, 2000); LASER (Rabosky, 2006) | - | YES | NO |
| Sauquet, H., et al. (2009). Contrasted patterns of hyperdiversification in Mediterranean hotspots. Proceedings of the National Academy of Sciences, 106(1), 221-225. | 9914 | 8 | 97 | r8s (Sanderson, 2003) and BEAST (Drummond & Rambaut, 2007) | 6 | Net speciation minus extinction (Magallón & Sanderson, 2001) | 0.001-0.3 | NO | YES |
| Hardman, M., & Hardman, L. M. (2008). The relative importance of body size and paleoclimatic change as explanatory variables influencing lineage diversification rate: an evolutionary analysis of bullhead catfishes (Siluriformes: Ictaluridae). Systematic Biology, 57(1), 116-130. | 1466 | 2 | 38 | BEAST (Drummond & Rambaut, 2007) | 5 | Relative cladogenesis statistic; SymmeTree (Chan & Moore, 2005) | - | NO | NO |
| Wood, T. E., et al. (2009). The frequency of polyploid speciation in vascular plants. Proceedings of the national Academy of sciences, 106(33), 13875-13879. | - | - | 123 trees with 3-163 species | Trees taken from the literature | - | SymmeTree (Chan & Moore, 2005) | - | NO | NO |
| Near, T. J., et al. (2013). Phylogeny and tempo of diversification in the superradiation of spiny-rayed fishes. Proceedings of the National Academy of Sciences, 110(31), 12738-12743. | 8577 | 10 | 520 | BEAST (Drummond & Rambaut, 2007) | 37 | MEDUSA (Alfaro *et al.*, 2009) | 0.01-0.03 | NO | NO |
| Valente, L. M., et al. (2010). Unparalleled rates of species diversification in Europe. Proceedings of the Royal Society B: Biological Sciences, rspb20092163. | 2870 | 4 | 104 | BEAST (Drummond & Rambaut, 2007) | 1 | Net speciation minus extinction (Magallón & Sanderson, 2001); LASER (Rabosky, 2006) | 2.2-5.4 | NO | YES |
| Phillimore, A. B., & Price, T. D. (2008). Density-dependent cladogenesis in birds. PLoS Biology, 6(3), e71. | 1000-2000 | - | 45 trees with 7-139 | BEAST (Drummond & Rambaut, 2007) | 0 | Gamma statistic (Pybus & Harvey, 2000) | - | YES | NO |
| Jones, K. E., et al. (2005). Bats, clocks, and rocks: diversification patterns in Chiroptera. Evolution, 59(10), 2243-2255. | 6782 | 3 | 430 | Local clocks | 98 | SymmeTree (Chan & Moore, 2005) | - | NO | NO |
| Couvreur, et al. (2011). Origin and global diversification patterns of tropical rain forests: inferences from a complete genus-level phylogeny of palms. BMC Biology, 9(1), 44. | 4733 | 4 | 183 | BEAST (Drummond & Rambaut, 2007) | 4 | Gamma statistic (Pybus & Harvey, 2000); LASER (Rabosky, 2006) | - | NO | NO |
| Ricklefs, R. E., et al. (2007). Evolutionary diversification of clades of squamate reptiles. Journal of Evolutionary Biology, 20(5), 1751-1762. | 3174 | 1 | 69 | r8s (Sanderson, 2003) | 1 | Log(N)/t (Stanley, 1979) | 0.04 | NO | YES |
| Fiz-Palacios, et al. (2011) Diversification of land plants: insights from a family-level phylogenetic analysis. BMC Evolutionary Biology, 11(1), 341. | 6950 | 5 | 699 | r8s (Sanderson, 2003) | 16 | Net speciation minus extinction (Magallón & Sanderson, 2001); apTreeshape (Bortolussi et al 2006); LASER (Rabosky, 2006); MEDUSA (Alfaro *et al.*, 2009) | 0.0001-0.298 | NO | YES |
| Wiens, J. J. (2007). Global patterns of diversification and species richness in amphibians. The American Naturalist, 170(2), S86-S106. | 1525 | 1 | 66 | r8s (Sanderson, 2003) | 11 | Net speciation minus extinction (Magallón & Sanderson, 2001) | 0.02-0.14 | NO | YES |
| Etienne, R. S., et al. (2011). Diversity-dependence brings molecular phylogenies closer to agreement with the fossil record. Proceedings of the Royal Society B: Biological Sciences, rspb20111439. | - | - | - | Trees from Steeman et al. (2009) and Rabosky & Lovette (2008) | - | DDD (Etienne *et al.*, 2012); LASER (Rabosky, 2006) | 0.2-0.7 | NO | NO |
| McKenna, D. D., & Farrell, B. D. (2006). Tropical forests are both evolutionary cradles and museums of leaf beetle diversity. Proceedings of the National Academy of Sciences, 103(29), 10947-10951. | 2200 | 2 | 133 | r8s (Sanderson, 2003) | 3 | Gamma statistic (Pybus & Harvey, 2000); SymmeTree (Chan & Moore, 2005); Relative cladogenesis test (Harmon *et al.*, 2008) | - | NO | NO |
| Morlon, H., et al. (2010). Inferring the dynamics of diversification: a coalescent approach. PLoS Biology, 8(9), e1000493. | - | - | - | Trees from Phillimore & Price (2008) and McPeek, (2008) | - | Coalescent model-testing | - | YES | NO |
| Becerra, J. X. (2005). Timing the origin and expansion of the Mexican tropical dry forest. Proceedings of the National Academy of Sciences of the United States of America, 102(31), 10919-10923. | 1315 | 3 | 41 | r8s (Sanderson, 2003) | 3 | Gamma statistic (Pybus & Harvey, 2000) | - | NO | YES |
| Kozak, K. H., & Wiens, J. J. (2010). Accelerated rates of climatic‐niche evolution underlie rapid species diversification. Ecology Letters, 13(11), 1378-1389. | - | 5 | 235 | r8s (Sanderson, 2003); tree from Adams et al. (2009; Proc. Roy. Soc. B) | 5 | Net speciation minus extinction (Magallón & Sanderson, 2001); gamma statistic (Pybus & Harvey, 2000); LASER (Rabosky, 2006) | 0.03-0.18 | NO | YES |
| Verdú, M., et al. (2007). Burning phylogenies: fire, molecular evolutionary rates, and diversification. Evolution, 61(9), 2195-2204. | - | 13 | 91 | r8s (Sanderson, 2003) | 0 | SymmeTree (Chan & Moore, 2005); KIT (Ree, 2005) | - |  |  |
| Wiens, J. J., et al. (2011). Phylogenetic origins of local‐scale diversity patterns and the causes of Amazonian megadiversity. Ecology Letters, 14(7), 643-652. | - | 11 | 362 | BEAST (Drummond & Rambaut, 2007) | 10 | Net speciation minus extinction (Magallón & Sanderson, 2001); BiSSE (FitzJohn *et al.*, 2009) | 0.03-0.066 | NO | YES |
| Valente, L. M., et al. (2010). Diversification of the African genus Protea (Proteaceae) in the Cape biodiversity hotspot and beyond: equal rates in different biomes. Evolution, 64(3), 745-760. | - | 6 | 87 | BEAST (Drummond & Rambaut, 2007) | 1 | BiSSE (FitzJohn *et al.*, 2009) | - | NO | NO |
| De‐Nova, J. A., et al. (2012). Insights into the historical construction of species‐rich Mesoamerican seasonally dry tropical forests: the diversification of Bursera (Burseraceae, Sapindales). New Phytologist, 193(1), 276-287. | - | 4 | 93 | BEAST (Drummond & Rambaut, 2007) | 18 | Net speciation minus extinction (Magallón & Sanderson, 2001); SymmeTree (Chan & Moore, 2005); LASER (Rabosky, 2006) | 0.03-0.21 | NO | YES |
| Derryberry, E. P., et al. (2011). Lineage diversification and morphological evolution in a large-scale continental radiation: The neotropical ovenbirds and woodpeckers (Aves: Furnariidae). Evolution, 65(10), 2973-2986. | 6972 | 4 | 285 | BEAST (Drummond & Rambaut, 2007) | 12 | LASER (Rabosky 2006); MEDUSA (Alfaro et al. 2009) | - | NO | NO |
| Near, T. J., et al. (2012). Ancient climate change, antifreeze, and the evolutionary diversification of Antarctic fishes. Proceedings of the National Academy of Sciences, 109(9), 3434-3439. | 6431 | 6 | 83 | BEAST (Drummond & Rambaut, 2007) | 4 | MEDUSA (Alfaro *et al.*, 2009); Net speciation minus extinction (Magallón & Sanderson, 2001); gamma statistic (Pybus & Harvey, 2000) | 0.075-0.2 | NO | YES |
| Aguirre-Planter, É., et al. (2012). Phylogeny, diversification rates and species boundaries of Mesoamerican firs (*Abies*, Pinaceae) in a genus-wide context. Molecular phylogenetics and evolution, 62(1), 263-274. | 1284 | 3 | 35 | r8s (Sanderson, 2003) | 2 | Net speciation minus extinction (Magallón & Sanderson, 2001) | 0.004-0.054 | NO | YES |
| Heikkilä, M., et al. (2012). Cretaceous origin and repeated tertiary diversification of the redefined butterflies. Proceedings of the Royal Society B: Biological Sciences, 279(1731), 1093-1099. | 6165 | 8 | 52 | BEAST (Drummond & Rambaut, 2007) | 3 | MEDUSA (Alfaro *et al.*, 2009) | - | NO | NO |
| Wiegmann, B. M., et al. (2011). Episodic radiations in the fly tree of life. Proceedings of the National Academy of Sciences, 108(14), 5690-5695. | 7000 | 5 | 202 | r8s (Sanderson, 2003) | 1 | MEDUSA (Alfaro *et al.*, 2009) | - | NO | NO |
| Burbrink, F. T., & Pyron, R. A. (2011). The impact of gene‐tree/species‐tree discordance on diversification‐rate estimation. Evolution, 65(7), 1851-1861. | 3320 | 4 | 21 | r8s (Sanderson, 2003) | 0 | Gamma statistic (Pybus & Harvey, 2000) | - | YES | NO |
| Rüber, L., & Zardoya, R. (2005). Rapid cladogenesis in marine fishes revisited. Evolution, 59(5), 1119-1127. | 521-1651 | 1 | 34 trees with between 9 and 102 species | r8s (Sanderson, 2003) | 0 | Gamma statistic (Pybus & Harvey, 2000) | - | YES | NO |
| Ribera, I., et al. (2008). Phylogeny and diversification of diving beetles (Coleoptera: Dytiscidae). Cladistics, 24(4), 563-590. | 4708 | 4 | 222 | r8s (Sanderson, 2003) | 0 | SymmeTree (Chan & Moore, 2005) | - | YES | NO |
| Patel, S., et al. (2011). Temporal and spatial diversification of *Pteroglossus* *araçaris* (Aves: Ramphastidae) in the neotropics: Constant rate of diversification does not support an increase in radiation during the Pleistocene. Molecular Phylogenetics and Evolution, 58(1), 105-115. | 3215 | 2 | 35 | BEAST (Drummond & Rambaut, 2007) | 2 | Gamma statistic (Pybus & Harvey, 2000); LASER (Rabosky, 2006) | - | NO | NO |
| Hou, Z., et al. (2011). Eocene habitat shift from saline to freshwater promoted Tethyan amphipod diversification. Proceedings of the National Academy of Sciences, 108(35), 14533-14538. | 5088 | 2 | 305 | r8s (Sanderson, 2003) and BEAST(Drummond & Rambaut, 2007) | 3 | Gamma statistic (Pybus & Harvey, 2000); LASER (Rabosky, 2006) | - | NO | NO |
| Fabre, P. H., et al. (2012). A glimpse on the pattern of rodent diversification: a phylogenetic approach. BMC Evolutionary Biology, 12(1), 88. | 15563 | 11 | 1265 | RAxML (Stamatakis, 2014), no timetree | - | SymmeTree (Chan & Moore, 2005) | - | NO | NO |
| Catalano, S. A., t al. (2008). Molecular phylogeny and diversification history of Prosopis (Fabaceae: Mimosoideae). Biological Journal of the Linnean Society, 93(3), 621-640. | 6710 | 5 | 30 | r8s (Sanderson, 2003) | 2 | Lineages through time plot | - | NO | NO |
| Cusimano, N., et al. (2012). A new method for handling missing species in diversification analysis applicable to randomly or nonrandomly sampled phylogenies. Systematic Biology, 61(5), 785-792. | 4352 | 4 | 112 | BEAST (Drummond & Rambaut, 2007) | 1 | Gamma statistic (Pybus & Harvey, 2000); LASER (Rabosky, 2006); TreePar (Stadler, 2013) | 0.01-0.17 | NO | NO |
| Alfaro, M. E., et al. (2009). Does evolutionary innovation in pharyngeal jaws lead to rapid lineage diversification in labrid fishes?. BMC Evolutionary Biology, 9(1), 255. | - | 3 | 147 | BEAST (Drummond & Rambaut, 2007) | 4 | MEDUSA (Alfaro *et al.*, 2009) | 0.053-0.199 | NO | NO |
| Hines, H. M. (2008). Historical biogeography, divergence times, and diversification patterns of bumble bees (Hymenoptera: Apidae: Bombus). Systematic Biology, 57(1), 58-75. | 3745 | 5 | 218 | r8s (Sanderson, 2003) and MLTIDIVTIME (Thorne & Kishino, 2002) | 4 | Gamma statistic (Pybus & Harvey, 2000); DIVERSI (Paradis, 1998; survival models) | - | NO | NO |
| Dumont, E. R., et al. (2011). Morphological innovation, diversification and invasion of a new adaptive zone. Proceedings of the Royal Society B: Biological Sciences, rspb20112005. | 4840 | 2 | 150 | BEAST (Drummond & Rambaut, 2007) | 10 | LASER (Rabosky, 2006); BiSSE (FitzJohn *et al.*, 2009) | 0.1-0.35 | NO | YES |
| Vieites, D. R., et al. (2007). Rapid diversification and dispersal during periods of global warming by plethodontid salamanders. Proceedings of the National Academy of Sciences, 104(50), 19903-19907. | 2707 | 3 | 51 | MULTIDIVTIME (Thorne & Kishino, 2002) | 7 | LAGRANGE (Ree & Smith, 2008) | - | NO | NO |
| Couvreur, T. L., et al. (2011). Early evolutionary history of the flowering plant family Annonaceae: steady diversification and boreotropical geodispersal. Journal of Biogeography, 38(4), 664-680. | 8823 | 7 | 100 | r8s (Sanderson, 2003) and BEAST (Drummond & Rambaut, 2007) | 2 | LASER (Rabosky, 2006) | - | NO | NO |
| Bouchenak‐Khelladi, Y.A., et al. (2009). The origins and diversification of C4 grasses and savanna‐adapted ungulates. Global Change Biology, 15(10), 2397-2417. | 5060 | 2 | 90 | MULTIDIVTIME (Thorne & Kishino, 2002) | 5 | SymmeTree (Chan & Moore, 2005) | - | NO | NO |
| Fordyce, J. A. (2010). Host shifts and evolutionary radiations of butterflies. Proceedings of the Royal Society B: Biological Sciences, 277(1701), 3735-3743. | - | 2 | 15 butterfly trees analyzed | r8s (Sanderson, 2003) | 0 | Gamma statistic (Pybus & Harvey, 2000); LASER (Rabosky, 2006) | - | YES | NO |
| Smith, B. T., & Klicka, J. (2010). The profound influence of the Late Pliocene Panamanian uplift on the exchange, diversification, and distribution of New World birds. Ecography, 33(2), 333-342. | - | 1 | 64 phylogenies copiled from the literature | BEAST (Drummond & Rambaut, 2007) | 1 | Simulations compared to empirical data | - | NO | NO |
| Smith, C. I., et al. (2008). Pattern and timing of diversification in Yucca (Agavaceae): specialized pollination does not escalate rates of diversification. Proceedings of the Royal Society B: Biological Sciences, 275(1632), 249-258. | 3785 | 6 | 34 | r8s (Sanderson, 2003) | 1 | SymmeTree (Chan & Moore, 2005); Gamma statistic (Pybus & Harvey, 2000) | 0.21-0.33 | NO | YES |
| Harmon, L. J., et al. (2008). The role of geography and ecological opportunity in the diversification of day geckos (Phelsuma). Systematic Biology, 57(4), 562-573. | 2818 | 2 | 35 | r8s (Sanderson, 2003) | 1 | Net speciation minus extinction (Magallón & Sanderson, 2001); gamma statistic | 0.25-3.14 | NO | YES |
| Day, J. J., et al. (2008). Tempo and mode of diversification of Lake Tanganyika cichlid fishes. PloS one, 3(3), e1730. | 1384 | 1 | 161 | BEAST (Drummond & Rambaut, 2007) | 1 | BEAST speciation rate estimate (Drummond & Rambaut, 2007); gamma statistic (Pybus & Harvey, 2000) | 0.25-0.6 | NO | YES |
| Jansson, R., & Davies, T. J. (2008). Global variation in diversification rates of flowering plants: energy vs. climate change. Ecology Letters, 11(2), 173-183. | - | - | 172 families from the phylogeny by Soltis et al. (2000; Bot J Lin Soc) | - | - | Net speciation minus extinction (Magallón & Sanderson, 2001) | - | NO | YES |
| Lopez‐Vaamonde, C., et al. (2006). Fossil‐calibrated molecular phylogenies reveal that leaf‐mining moths radiated millions of years after their host plants. Journal of Evolutionary Biology, 19(4), 1314-1326. | 1000 | 1 | 110 | r8s (Sanderson, 2003) | 1 | Net speciation minus extinction (Magallón & Sanderson, 2001) | 0.03-0.04 | NO | YES |
| Burbrink, F. T., & Pyron, R. A. (2010). How does ecological opportunity influence rates of speciation, extinction, and morphological diversification in New World ratsnakes (tribe Lampropeltini)?. Evolution, 64(4), 934-943. | 4298 | 5 | 36 | BEAST (Drummond & Rambaut, 2007) | 5 | Gamma statistic (Pybus & Harvey, 2000); LASER (Rabosky, 2006) | 0.04-0.26 | NO | NO |
| Wilson, R., et al. (2007). Steady diversification of derived liverworts under Tertiary climatic fluctuations. Biology Letters, 3(5), 566-569. | 3773 | 4 | 135 | r8s (Sanderson, 2003) | 21 | Log(N)/t (Stanley, 1979) | 0.021 | NO | YES |
| Svenning, J. C., et al. (2008). High tropical net diversification drives the New World latitudinal gradient in palm (Arecaceae) species richness. Journal of Biogeography, 35(3), 394-406. | - | 4 | 161 | - | - | Mean root distance (Kerr & Currie, 1999) | - | NO | NO |
| Schuettpelz, E., & Pryer, K. M. (2009). Evidence for a Cenozoic radiation of ferns in an angiosperm-dominated canopy. Proceedings of the National Academy of Sciences, 106(27), 11200-11205. | 4000 | 3 | 400 | r8s (Sanderson, 2003) | 24 | Magallón & Sanderson, (2001) | 0.023-0.028 | NO | YES |
| Mayrose, I., et al. (2011). Recently formed polyploid plants diversify at lower rates. Science, 333(6047), 1257-1257. | - | 39 (mean) | 63 inferred phylogenies | r8s (Sanderson, 2003) | 0 | BiSSE (FitzJohn *et al.*, 2009) | - | YES | NO |
| Winkler, I. S., et al. (2009). Repeated climate-linked host shifts have promoted diversification in a temperate clade of leaf-mining flies. Proceedings of the National Academy of Sciences, 106(43), 18103-18108. | 2965 | 3 | 86 | r8s (Sanderson, 2003) and BEAST (Drummond & Rambaut, 2007) | 3 | Net speciation minus extinction (Magallón & Sanderson, 2001); and LASER (Rabosky, 2006) | 0.05-0.15 | NO | YES |
| Pennington, R. T., et al. (2010). Contrasting plant diversification histories within the Andean biodiversity hotspot. Proceedings of the National Academy of Sciences, 107(31), 13783-13787. | 3387 | 2 | 52 | r8s (Sanderson, 2003) | 1 | Time for speciation (inverse of Log(N)/t) | - | NO | NO |
| McLeish, M. J., et al. (2007). Host-driven diversification of gall-inducing Acacia thrips and the aridification of Australia. BMC Biology, 5(1), 3. | 2710 | 4 | 49 | r8s (Sanderson, 2003) | 2 | SymmeTree (Chan & Moore, 2005) | - | NO | NO |
| Mao, K., et al. (2010). Diversification and biogeography of Juniperus (Cupressaceae): variable diversification rates and multiple intercontinental dispersals. New Phytologist, 188(1), 254-272. | - | 9 | 116 | r8s (Sanderson, 2003), MLTIDIVTIME (Thorne & Kishino, 2002) and BEAST (Drummond et al., 2006) | 8 | Survival analysis and relative cladogenesis test (GEIGER; Harmon et al., 2008; Nee et al., 1994) | 0.025-0.11 | NO | YES |
| Slater, G. J., et al. (2010). Diversity versus disparity and the radiation of modern cetaceans. Proceedings of the Royal Society B: Biological Sciences, 277(1697), 3097-3104. | 1400 | 1 | 84 | BEAST (Drummond & Rambaut, 2007) | 7 | Gamma statistic (Pybus & Harvey, 2000), LASER (Rabosky, 2006); MEDUSA (Alfaro *et al.*, 2009) | - | NO | NO |
| Burleigh, J. G., et al. (2012). Exploring diversification and genome size evolution in extant gymnosperms through phylogenetic synthesis. Journal of Botany, 2012. | 4500000 | 5 | 739 | r8s (Sanderson, 2003) | 8 | apTreeshape (Bortolussi *et al.*, 2006) | - | NO | NO |
| Price, S. A., et al. (2012). Tempo of trophic evolution and its impact on mammalian diversification. Proceedings of the National Academy of Sciences, 109(18), 7008-7012. | - | - | 1538 | 100 trees from (Fritz *et al.*, 2009), based on (Bininda-Emonds *et al.*, 2007) | - | MuSSE (FitzJohn, 2012) | 0.03-0.14 | NO | YES |
| Merckx, V., et al. (2008). Diversification of myco-heterotrophic angiosperms: evidence from Burmanniaceae. BMC Evolutionary Biology, 8(1), 178. | 3937 | 3 | 51 | BEAST (Drummond & Rambaut, 2007) | 2 | Gamma statistic (Pybus & Harvey, 2000); SymmeTree (Chan & Moore, 2005) | - | NO | NO |
| Arakaki, M., et al. (2011). Contemporaneous and recent radiations of the world's major succulent plant lineages. Proceedings of the National Academy of Sciences, 108(20), 8379-8384. | 75643 | 83 | 102 | MULTIDIVTIME (Thorne & Kishino, 2002) | 1 | MEDUSA (Alfaro *et al.*, 2009) | - | NO | NO |
| Wahlberg, N., et al. (2009). Nymphalid butterflies diversify following near demise at the Cretaceous/Tertiary boundary. Proceedings of the Royal Society B: Biological Sciences, 276(1677), 4295-4302. | 7733 | 10 | 429 | BEAST (Drummond & Rambaut, 2007) | 6 | Lineages through time plot | - | NO | NO |
| Rabosky, D. L., & Glor, R. E. (2010). Equilibrium speciation dynamics in a model adaptive radiation of island lizards. Proceedings of the National Academy of Sciences, 107(51), 22178-22183. | 1500 | 1 | 189 | BEAST (Drummond & Rambaut, 2007) | 0 | Diversification model fitting of 12 models. | 1.1-3.2 | YES | NO |
| Balke, M., et al. (2005). The systematic position of Aspidytidae, the diversification of Dytiscoidea (Coleoptera, Adephaga) and the phylogenetic signal of third codon positions. Journal of Zoological Systematics and Evolutionary Research, 43(3), 223-242. | 4426 | 2 | 35 | - | - | Equal rates random branching model (Nee *et al.*, 1994) | - | NO | NO |
| Hearn, D. J. (2006). Adenia (Passifloraceae) and its adaptive radiation: phylogeny and growth form diversification. Systematic Botany, 31(4), 805-821. | - | 2 | 67 | r8s (Sanderson, 2003) | 3 | Log(N)/t (Stanley, 1979) | 0.42 | NO | YES |
| Steeman, M. E., et al. (2009). Radiation of extant cetaceans driven by restructuring of the oceans. Systematic Biology, 58(6), 573-585. | 16175 | 10 | 90 | r8s (Sanderson, 2003) | 7 | SymmeTree (Chan & Moore, 2005); gamma statistic (Pybus & Harvey, 2000); LASER (Rabosky, 2006) | - | NO | NO |
| Alfaro, M. E., et al. (2008). Phylogeny, evolutionary history, and biogeography of Oriental–Australian rear-fanged water snakes (Colubroidea: Homalopsidae) inferred from mitochondrial and nuclear DNA sequences. Molecular Phylogenetics and Evolution, 46(2), 576-593. | 2896 | 2 | 181 | BEAST (Drummond & Rambaut, 2007) | 2 | Net speciation minus extinction (Magallón & Sanderson, 2001); gamma statistic (Pybus & Harvey, 2000); Relative cladogensis statistic (Nee *et al.*, 1994) | - | NO | YES |

**Table S2.** Characteristics of datasets used for phylogenetic studies of diversification rate, based on a sample of 100 studies from 2005-2015 (See Table S1). Note that not all information was available for every study (see Supplementary methods for details).

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  | Min. | 1st Quartile | Median | Mean | 3rd  Quartile | Max. |
| Number of loci | 1 | 2 | 4 | 5 | 5 | 83 |
| Combined number of alignment sites | 511 | 2412 | 3773 | 71100 | 6431 | 4500000 |
| Number of taxa | 21 | 69 | 133 | 990 | 227 | 55470 |
| Number of calibrations | 0 | 1 | 3 | 8 | 7 | 98 |
| Net diversification rate estimates (rate of speciation minus rate of extinction) | 0.019 | 0.07 | 0.14 | 0.46 | 0.42 | 3.80 |

**Figure S1.** Methods used for inference of branch lengths in sampled studies. “Number of studies” represents the number of studies from a sample of 100 studies of macroevolution from a 10-year period (2005-2015). Where a study used more than one method, each was recorded.

../Trial0317/FigS1.pdf

**Figure S2.** Lineages through time plots of 10k posterior samples from three BEAST analyses of simulated data. An example is shown for data sets diversification rates are either constant, undergoing slowdown, or undergoing speedup. Analyses with and without a link between the rate of diversification and the rate of molecular evolution produced similar amounts of uncertainty. Uncertainties are likely to be low compared with many empirical data sets, due to the highly informative nature of the simulated data.

../plot.beast.unc.pdf

**Figure S3.** Number of studies using macroevolutionary methods for detecting changes in diversification rate in a sample of 100 from a 10-year period (2005-2015). Some studies used multiple methods.

FigS2.pdf

**Figure S4.** ROC analyses across thresholds for rejecting the null model across all phylogenies from (a) simulated data, (b) NPRS estimates, and (c) BEAST estimates. Simulated data and macroevolutionary estimates using TESS tend to have higher area under the curve (AUC), suggesting that these are the test conditions with the best compromise between the sensitivity and the specificity.

**../plot.roc.pdf**

**Figure S5.** Posterior probability densities estimated by TESS for two example simulation cases where the software TESS and LASER behave differently. The first two cases (a and b) are parameter estimates under a model that assumes speciation rate slowdown. In the first, (a) both TESS and LASER correctly identify diversification rate slowdown. In the second, (b) LASER correctly identifies diversification rate slowdown, while TESS does not. The third and fourth cases (c and d) are parameter estimates under a model that assumes speciation rate speedup. In the third case, (c) both TESS and LASER correctly identify diversification rate speedup. In the fourth case, (d) TESS correctly identifies speciation speedup, while LASER does not.

**../Trial0317/tess.example.plot.2.pdf**

**Supplementary References**

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