

Appendix

Reproducible computation: A diversification rate analysis

This appendix illustrates the diversification rate analysis discussed in the main text. For completeness we begin by executing the code discussed in the manuscript which locates, downloads, and imports the relevant data:

Different diversification models make different assumptions about the rate of speciation, extinction, and how these rates may be changing over time. The original authors consider eight different models, implemented in the laser package (Rabosky 2006). This code fits each of the eight models to that data:

```
library(ape)
library(laser)
models <- list(
  yule = pureBirth(bt),
  birth_death = bd(bt),
  yule.2.rate = yule2rate(bt),
  linear.diversity.dependent = DDL(bt),
  exponential.diversity.dependent = DDX(bt),
  varying.speciation_rate = fitSPVAR(bt),
  varying.extinction_rate = fitEXVAR(bt),
  varying_both = fitBOTHVAR(bt))
```

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12 Each of the model estimate includes an Akaike Information Criterion (AIC) score indicating the good-
13 ness of fit, penalized by model complexity (lower scores indicate better fits) We ask R to tell us which
14 model has the lowest AIC score,

```
aics <- sapply(models, function(model) model$aic)
best_fit <- names(models[which.min(aics)])
```

15 and confirm the result presented in E. P. Derryberry et al. (2011); that the best-fit model in the laser
16 analysis was a Yule (net diversification rate) model with two separate rates.

17 We can ask TreePar to see if a model with more rate shifts is favoured over this single shift, a ques-
18 tion that was not possible to address using the tools provided in laser. The previous analysis also
19 considers a birth-death model that allowed speciation and extinction rates to be estimated separately,
20 but did not allow for a shift in the rate of such a model. In the main text we introduced a model from
21 Stadler (2011) that permitted up to 3 change-points in the speciation rate of the Yule model,

```
yule_models <- bd.shifts.optim(x, sampling = c(1,1,1,1),
  grid = 5, start = 0, end = 60, yule = TRUE)[[2]]
```

22 We can also compare the performance of models which allow up to three shifts while estimating
23 extinction and speciation rates separately:

```
birth_death_models <- bd.shifts.optim(x, sampling = c(1,1,1,1),
  grid = 5, start = 0, end = 60, yule = FALSE)[[2]]
```

24 The models output by these functions are ordered by increasing number of shifts. We can select the
25 best-fitting model by AIC score, which is slightly cumbersome in TreePar syntax. First, we compute
26 the AIC scores of both the yule_models and the birth_death_models we fitted above,

```
yule_aic <-
sapply(yule_models, function(pars)
  2 * (length(pars) - 1) + 2 * pars[1] )
```

```

birth_death_aic <-
sapply(birth_death_models, function(pars)
      2 * (length(pars) - 1) + 2 * pars[1] )

```

27 Then we generate a list identifying which model has the best (lowest) AIC score among the Yule
 28 models and which has the best AIC score among the birth-death models,

```

best_no_of_rates <- list(Yule = which.min(yule_aic),
      birth.death = which.min(birth_death_aic))

```

29 The best model is then whichever of these has the smaller AIC value.

```

best_model <- which.min(c(min(yule_aic), min(birth_death_aic)))

```

30 which still confirms that the Yule 2-rate model is still the best choice based on AIC score. Of the eight
 31 models in this second analysis, only three were in the original set considered (Yule 1-rate and 2-rate,
 32 and birth-death without a shift), so we could by no means have been sure ahead of time that a birth
 33 death with a shift, or a Yule model with a greater number of shifts, would not have fitted better.

34 References

35 Derryberry, Elizabeth P., Santiago Claramunt, Graham Derryberry, R. Terry Chesser, Joel Cracraft,
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39 Rabosky, Daniel L. 2006. "LASER: a maximum likelihood toolkit for detecting temporal shifts in di-
 40 versification rates from molecular phylogenies." *Evolutionary bioinformatics online* 2 (Jan): 273–6.

41 Stadler, Tanja. 2011. "Mammalian phylogeny reveals recent diversification rate shifts." *Proceedings of*
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