Appendix S2

Metabolic differentiation facilitates coexistence in two coral reef fish species

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*Data processing and statistical analysis*

We performed the analyses using the software *R* (R Core Team 2019) and the following packages: *drake* (Landau 2018), *tidyverse* (Wickham et al. 2019), *rstan* (Stan Development Team 2016), *brms* (Bürkner 2017), *bipartite* (Dormann et al. 2008), *iNEXT* (Hsieh et al. 2016), (Pollock et al. 2014), and *fishualize* (Schiettekatte et al. 2019). All code and data necessary to fully reproduce the results presented in this paper are available with the submission (*Brandletal\_MetabolicNicheSandgobies\_RCode.zip*) and will be made publicly available via a public repository and the lead author’s GitHub page (<https://github.com/simonjbrandl>). The appended .zip file contains the full coding framework assembled via the *drake* pipeline. A README.md document that provides guidance on how to reproduce the results is included. The supplementary tables below are output from the analyses and can also be found as separate documents in the “outputs” folder.

Table S1: Model summary for standard metabolic rate. The model was run for 5,000 iterations using the default brms priors.



Table S2: Model summary for maximum metabolic rate. The model was run for 5,000 iterations using the default brms priors. 

Table S3: Model summary for horizontal gape. The model was run for 2,000 iterations using the default brms priors.



Table S4: Model summary for vertical gape. The model was run for 2,000 iterations using the default brms priors.



Table S5: Model summary for girth. The model was run for 2,000 iterations using the default brms priors.



Table S6: Model summary for gastrointestinal tract. The model was run for 2,000 iterations using the default brms priors.

Table S7: Model summary for number of bites. The model was run for 2,000 iterations using the default brms priors and a negative binomial error distribution with a log link-function.



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