

Supplement to: *Intermediate abundance promotes speciation when dispersal is limited*

S1 Computation set-up

We created a make use of a custom R package *abundolism* which can be installed from github.

```
devtools::install_github("ajrominger/abundolism")
```

The following R computing environment is used for all simulations and analyses:

```
library(abundolism)
library(dplyr)
```

Attaching package: 'dplyr'

The following objects are masked from 'package:stats':

filter, lag

The following objects are masked from 'package:base':

intersect, setdiff, setequal, union

```
library(ggplot2)
library(ggpointdensity)
library(knitr)

sessionInfo() |>
  print(locale = FALSE)
```

```
R version 4.5.2 (2025-10-31)
Platform: aarch64-apple-darwin20
Running under: macOS Sequoia 15.0.1

Matrix products: default
BLAS:   /System/Library/Frameworks/Accelerate.framework/Versions/A/Frameworks/vecLib.framework/Versions/A/Libraries/libBLAS.dylib
LAPACK: /Library/Frameworks/R.framework/Versions/4.5-arm64/Resources/lib/libRlapack.dylib;
```

attached base packages:

```
[1] stats      graphics  grDevices  utils      datasets  methods    base
```

other attached packages:

```
[1] knitr_1.50          ggpointdensity_0.2.1 ggplot2_4.0.1
[4] dplyr_1.1.4         abundolism_0.1.0
```

loaded via a namespace (and not attached):

```
[1] vctrs_0.6.5      cli_3.6.5        rlang_1.1.6      xfun_0.52
[5] generics_0.1.4   S7_0.2.1         jsonlite_2.0.0   glue_1.8.0
[9] htmltools_0.5.8.1 scales_1.4.0     rmarkdown_2.29   grid_4.5.2
[13] evaluate_1.0.4   tibble_3.3.0     MASS_7.3-65      fastmap_1.2.0
[17] yaml_2.3.10      lifecycle_1.0.4  compiler_4.5.2   RColorBrewer_1.1-3
[21] Rcpp_1.1.0       pkgconfig_2.0.3  rstudioapi_0.17.1 farver_2.1.2
[25] digest_0.6.39    R6_2.6.1         tidyselect_1.2.1 pillar_1.11.0
[29] magrittr_2.0.4   withr_3.0.2      tools_4.5.2      gtable_0.3.6
```

The quarto (Allaire et al. 2025) document used to generate this supplement can be found with the R command `system.file("ab_supp.qmd", package = "abundolism")`.

S2 Simulation details

Foo foo foo

S3 Simulation experiment details

Simulation parameters are drawn from uniform distributions with the following minimum and maximum limits:

```

par_range <- data.frame(
  param = c("la", "mu", "g", "m_prop", "nu", "tau", "xi"),
  min    = c(1,    1,    0,    0,    0,    0,    0.5),
  max    = c(10,   10,   0.1, 0.1,   0.001, 4,    2)
)

# fixed params
np <- 2
nstep <- 100000

# number of simulation replicates
nrep <- 1000

# format param names for printing
mutate(par_range,
  param = sprintf("%s", param)) |>
  kable(format.args = list(scientific = FALSE))

```

param	min	max
la	1.0	10.000
mu	1.0	10.000
g	0.0	0.100
m_prop	0.0	0.100
nu	0.0	0.001
tau	0.0	4.000
xi	0.5	2.000

The parameters governing number of populations (**np**) and number of time steps (**nstep**) do not vary across simulations and are set to **np** = 2 and **nstep** = 10^5 . We simulate a total of **nrep** = 1000 replicates, each with a unique, randomly sampled set of parameter values.

S3.1 Running the simulation experiment

Parameter values for each simulation replicate are stored in a **data.frame** with one column for each parameter.

```

# change or remove for different results
set.seed(123)

```

```
# data.frame of randomly sampled param values
# one param per column
pars <- sapply(par_range$param, function(p) {
  runif(nrep,
        par_range[par_range$param == p, "min"],
        par_range[par_range$param == p, "max"])
}) |>
  as.data.frame()
```

```
# now run the simulation, see `?sim_BDI_spec` for details
# on input and output
sim_dat <- sim_BDI_spec(la = pars$la, mu = pars$mu, g = pars$g,
                       m_prop = pars$m_prop, nu = pars$nu,
                       tau = pars$tau, xi = pars$xi,
                       np = np, nstep = nstep)
```

Now we can plot the results and find out how abundance relates to speciation in this model

```
ggplot(sim_dat,
       aes(x = tau, speciation)) +
  geom_pointdensity(method = "kde2d") +
  scale_shape_binned() +
  scale_color_viridis_c() +
  # scale_x_log10() +
  geom_smooth(method = "glm",
             method.args = list(family = "binomial"),
             color = "black")

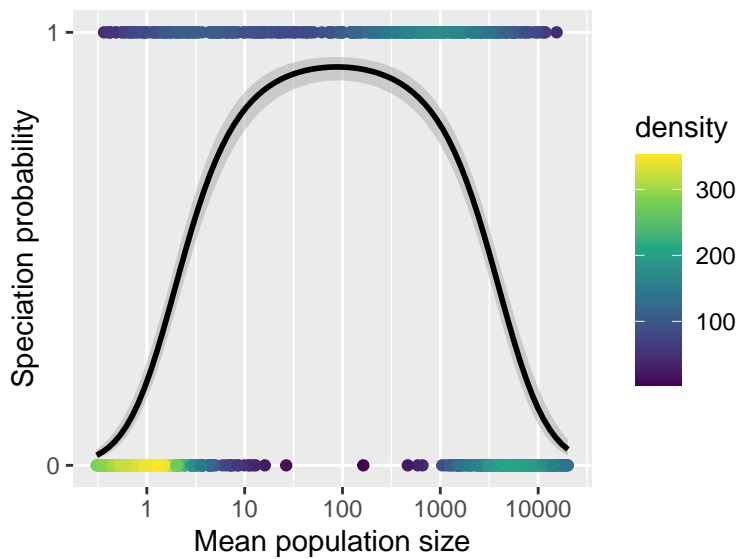
ggplot(sim_dat, aes(time, mean_pop_size)) +
  geom_point(data = select(sim_dat, !speciation),
            mapping = aes(time, mean_pop_size), color = "gray50") +
  geom_pointdensity() +
  facet_wrap(vars(speciation)) +
  scale_x_log10() +
  scale_y_log10() +
  scale_color_viridis_c(trans = "log10")

ggplot(sim_dat, aes(mean_pop_size)) +
  geom_histogram() +
  scale_x_log10()
```

This is the main figure

```
sim_fig <- ggplot(sim_dat,
                  aes(x = mean_pop_size, y = speciation)) +
  geom_pointdensity() +
  scale_color_viridis_c() +
  scale_x_log10() +
  scale_y_continuous(breaks = c(0, 1)) +
  xlab("Mean population size") +
  ylab("Speciation probability") +
  theme(panel.grid.minor.y = element_blank()) +
  geom_smooth(method = glm, formula = y ~ x + I(x^2),
             method.args = list(family = "binomial"), color = "black")
```

sim_fig



References

Allaire, J. J., Teague, C., Scheidegger, C., Xie, Y., Dervieux, C. and Woodhull, G. 2025. [Quarto](#).