

# **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/
LAPACK:   /Library/Frameworks/R.framework/Versions/4.5-arm64/Resources/lib/libRlapack.dylib; 1

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(0.1, 0.1, 0, 0, 0, 0, 1),
  max   = c(10, 10, 0.1, 0.1, 0.001, 2, 1)
)

# fixed params
np <- 2
nstep <- 10000

# number of simulation replicates
nrep <- 10000

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

```

	param	min	max
la	0.1	10.000	
mu	0.1	10.000	
g	0.0	0.100	
m_prop	0.0	0.100	
nu	0.0	0.001	
tau	0.0	2.000	
xi	1.0	1.000	

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 = 104`. We simulate a total of `nrep = 104` 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()

# pars$tau <- 10 / (pars$la + pars$mu + runif(nrep, 0, 1))

# 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(niter, time)) +
  geom_pointdensity(method = "kde2d") +
  scale_color_viridis_c() +
  # scale_x_log10() +
  scale_y_log10() +
  facet_wrap(vars(speciation))

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(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[sim_dat$time < 100, ], aes(time, mean_pop_size)) +
  geom_pointdensity() +
  facet_wrap(vars(speciation)) +
  scale_x_log10() +
  scale_y_log10() +
  scale_color_viridis_c(trans = "log10")

ggplot(sim_dat, aes(time)) +
  geom_histogram() +
  facet_wrap(vars(speciation), ncol = 1) +
  scale_x_log10()

```

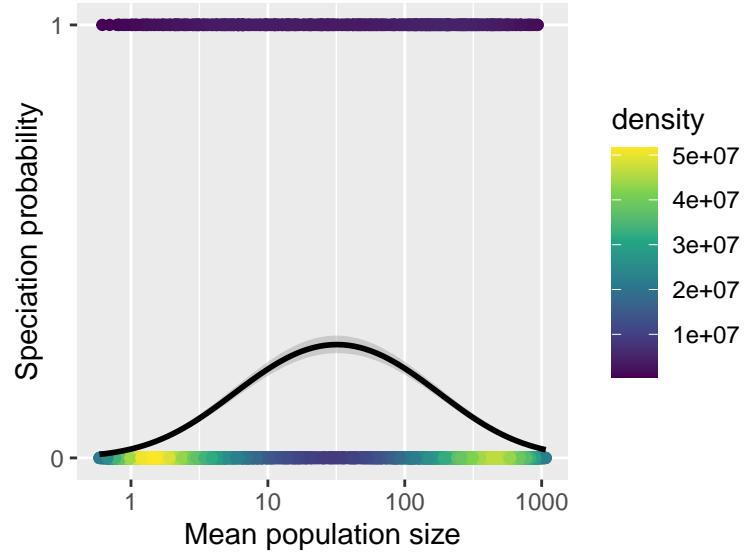
This is the main figure

```

sim_fig <- ggplot(sim_dat,
                    aes(x = mean_pop_size, y = speciation)) +
  geom_pointdensity(method = "kde2d") +
  scale_color_viridis_c() +
#  scale_size_continuous(range = c(0.001, 4)) +
  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](#).