

Playing with abundance and speciation

Birth-death-immigration model with speciation

We simulate a birth-death-immigration model (BDI) with speciation (BDIS) in a metapopulation setting. This is the set-up

- There are **np** number of local populations in the metapopulation
- There is a global source pool

Here are the biological process steps:

1. Birth, death, immigration, and speciation all happen independently and are determined by respective rates (see params below)
2. Speciation has 2 steps:
 - i. incipient speciation happens by turning one local population into an incipient new species
 - ii. if the incipient species lasts long enough it becomes a new species
3. Immigration between local communities and from the global source pool slows the progress toward speciation (technically if an incipient species has to wait τ time (in the absence of immigration) until it's a full species, each immigration event adds an increment to τ of ξ/n_i where ξ is a parameter we can set and n_i is the population size of the incipient species)
4. Once full speciation occurs the simulation is stopped; if the simulation reaches the maximum designated number of iterations (**nstep**) without full speciation, then the simulation stops anyway

Here are the parameters:

- λ (**la**): birth rate
- μ (**mu**): death rate
- γ (**g**): immigration rate from global source pool
- m_p (**m_prop**): proportional immigration rate between local populations; immigration rate $m = \gamma \times m_p$

- ν (nu): incipient speciation rate
- τ (tau): wait time to full speciation in the absence of immigration
- ξ (xi): amount each immigrant sets back the progression toward speciation
- (np): number of local populations
- (nstep): number of iterations to run simulation for

And we can now actually run this thing and see what happens

```
library(abundolism)

nrep <- 1000 # number of different parameter combos to look at
la = runif(nrep, 0.1, 10)
mu = runif(nrep, 0.1, 10)
g = la * runif(nrep, 0, 0.1)
m_prop = runif(nrep, 0, 0.1)
nu = runif(nrep, 0, 0.1)
tau = 10 / (la + mu + runif(nrep, 0, 1))
xi = rep(1, nrep)
np = 2
nstep = 10000

# `sim_BDI_spec` is the workhorse function
sim_dat <- sim_BDI_spec(la = la, mu = mu, g = g, m_prop = m_prop,
                        nu = nu, tau = tau, xi = xi, np = np,
                        nstep = nstep)
```

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

```
library(ggplot2)
library(hexbin)

# make a quadratic logistic model
sim_dat$log_pop <- log(sim_dat$mean_pop_size, 10)
mod <- glm(speciation ~ log_pop + I(log_pop^2), data = sim_dat,
           family = "binomial")

# add to data
sim_dat$mod_pred <- predict(mod, type = "response")

p <- ggplot(sim_dat, aes(x = mean_pop_size, y = speciation)) +
  geom_hex(bins = 40) +
```

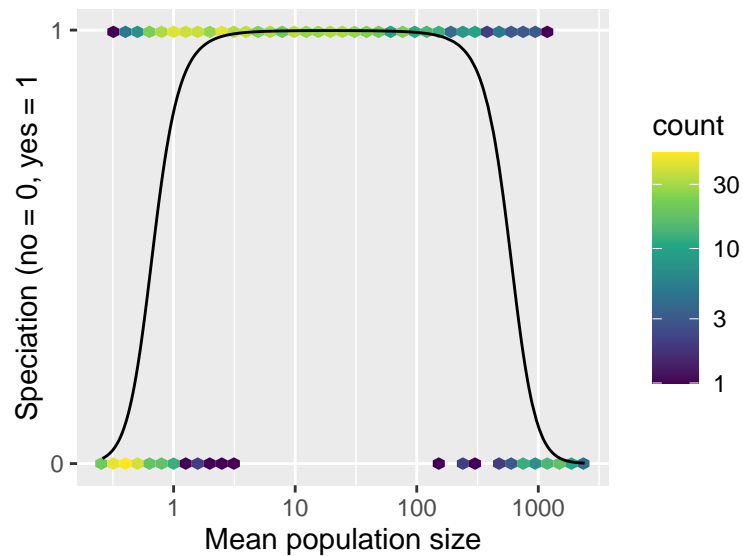
```

scale_x_log10()

pdat <- ggplot_build(p)$data[[1]]
tk <- round(10^seq(floor(min(log(pdat$count, 10))),
                    ceiling(max(log(pdat$count, 10))),
                    by = 0.5))
for(i in c(10, 100, 1000)) {
  tk[tk > i] <- round(tk[tk > i] / i) * i
}

p + scale_fill_viridis_c(trans = "log", breaks = tk) +
  geom_line(aes(x = mean_pop_size, y = mod_pred)) +
  scale_y_continuous(breaks = c(0, 1)) +
  xlab("Mean population size") +
  ylab("Speciation (no = 0, yes = 1)") +
  theme(panel.grid.minor.y = element_blank())

```



So we see there is a sweet spot of intermediate abundance where speciation is most likely to take place!