

equations

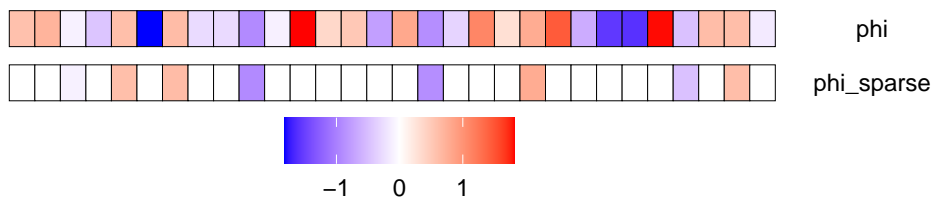
$$F = \sum_i \phi_i N_i$$

$$\phi_i \sim \text{Normal}(0, 1)$$

$$\phi_i \sim \text{Normal}(0, 1) \times \text{Bernoulli}(0.2)$$

```
sn = 30
set.seed(12345)
species <- tibble(x = 1:sn, y = 1, phi = rnorm(sn, mean = 0, sd = 1)) %>%
  mutate(phi_sparse = phi * rbernoulli(sn, p = 0.2))

species %>%
  pivot_longer(cols = starts_with("phi")) %>%
  ggplot() +
  geom_tile(aes(x = x, y = y, fill = value), color = 1) +
  scale_fill_gradient2(low = "blue", mid = "white", high = "red") +
  facet_grid(name~.) +
  theme_void() +
  theme(legend.position = "bottom", legend.title = element_blank())
```



$$F = \sum_i \sum_j \epsilon_{ij} N_i N_j$$

$$\epsilon_{ij} \sim \text{Normal}(0, 1)$$

$$\text{species } i$$

$$\text{species } j$$

$$\epsilon_{ij} \sim \text{Normal}(0, 1) \times \text{Bernoulli}(0.2)$$

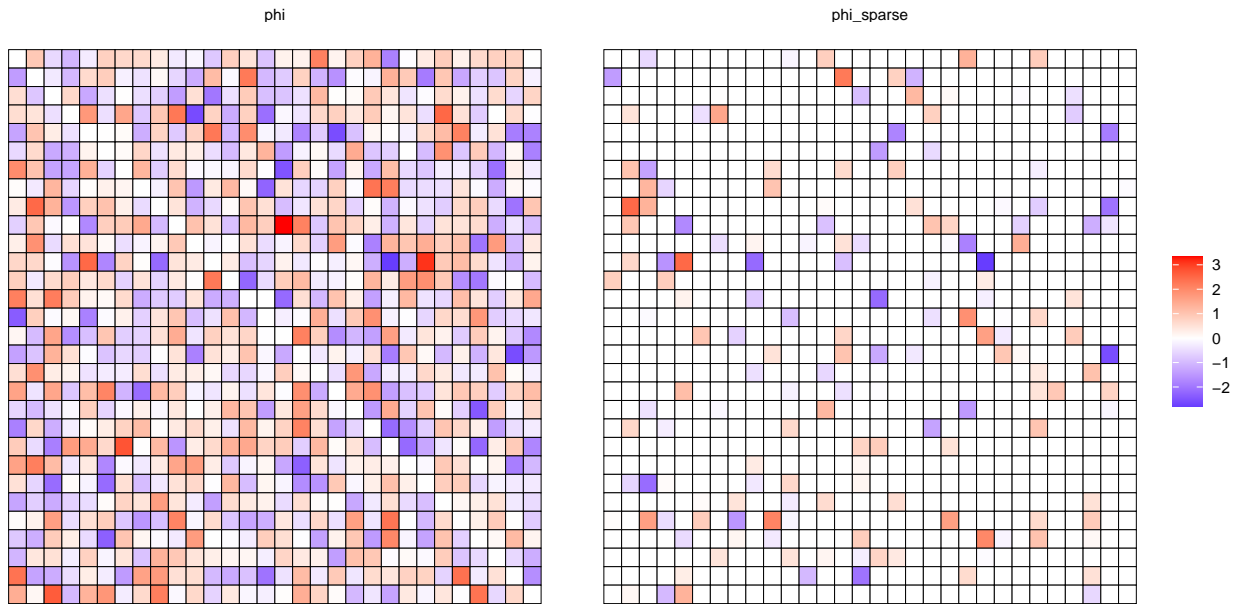
```
species <- tibble(x = rep(1:sn, each = sn), y = rep(1:sn, sn), phi = rnorm(sn^2)) %>%
  mutate(phi_sparse = phi * rbernoulli(sn^2, p = 0.2))
species$phi[species$x==species$y] <- 0
species$phi_sparse[species$x==species$y] <- 0

species %>%
  pivot_longer(cols = starts_with("phi")) %>%
  ggplot() +
  geom_tile(aes(x = x, y = y, fill = value), color = 1) +
```

```

scale_y_reverse() +
scale_fill_gradient2(low = "blue", mid = "white", high = "red") +
facet_grid(.~name) +
theme_void() +
theme(legend.position = "right", legend.title = element_blank())

```



$$F = \sum_i (1 - g_i) N_i$$

$$g_i \sim Uniform(0, 1)$$

$$g_i$$

$$1 - g_i$$

$$F = -R_{target}$$

$$F = -N_{invader}$$

Functional response

$$\sigma_I(R_\alpha) = c_i R_\alpha$$

$$\sigma_{II}(R_\alpha) = \frac{c_i R_\alpha}{1 + \frac{c_i R_\alpha}{\sigma_{max}}}$$

$$\sigma_{III}(R_\alpha) = \frac{(c_i R_\alpha)^n}{1 + \frac{(c_i R_\alpha)^n}{\sigma_{max}}}$$

Metacommunitiy sampling

$$P_{power}(x) = ax^{a-1}$$

$$P_{log-normal}(x) = \frac{1}{x\sigma\sqrt{2\pi}} e^{-\frac{(\ln x - \mu)^2}{2\sigma^2}}$$