Appendix 7: Supplementary Information for Chapter 4
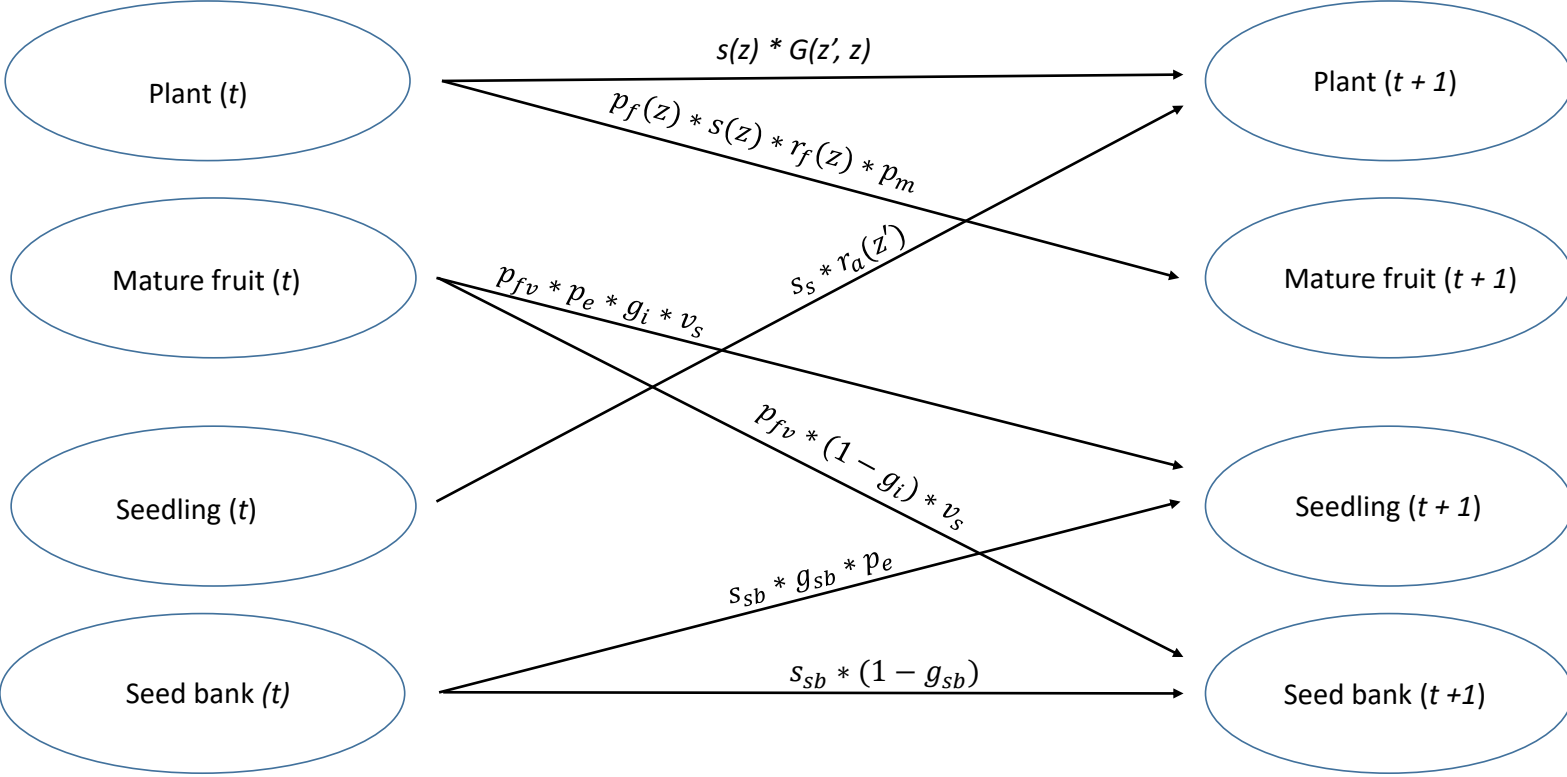
Model diagram

The following diagram describes a single iteration of the IPM.

Plant (t)

Mature fruit (t)

Seedling (t)

Seed bank (t)

Plant ($t + 1$)

Mature fruit ($t + 1$)

Seedling ($t + 1$)

Seed bank ($t + 1$)

$s(z) * G(z', z)$

$p_f(z) * s(z) * r_f(z) * p_m$

$s_s * r_a(z')$

$p_{fv} * p_e * g_i * v_s$

$p_{fv} * (1 - g_i) * v_s$

$s_{sb} * g_{sb} * p_e$

$s_{sb} * (1 - g_{sb})$

See the next section for a complete description of each vital rate parameter.

IPM Equations

IPMs describe how the abundance and distribution of a continuously distributed trait changes in a population through discrete time. Vital rates are combined in projection kernels that describe state-dependent per-capita contributions of existing individuals to the population trait distribution in the following time step via survival and development (denoted $(P(z', z))$) and sexual and asexual reproduction (denoted $F(z', z)$ and $C(z', z)$ respectively).

$$n(z', t+1) = \int_L^U [G(z'|z, \sigma, \theta) * s_a(z, \theta)]n(z, t)dz + s_s * r_a(z')sdl(t), \tag{4.1.1}$$

$$mf(t+1) = \int_L^U [p_f(z, \theta) * s_a(z, \theta) * r_f(z, \theta) * p_m * p_{fv}]n(z, t)dz, \tag{4.1.2}$$

$$sdl(t+1) = p_e * g_i * v_s * mf(t) + s_{sb} * g_{sb} * p_e * sb(t), \tag{4.1.3}$$

and

$$sb(t+1) = s_{sb} * (1 - g_{sb}) * sb(t) + (1 - g_i) * v_s * mf(t). \tag{4.1.4}$$

The survival probability of non-seedlings function, $s_a(z, \theta)$, is given by:

$$Logit(s_a(z, \theta)) = \beta_{0,s,i} + \beta_{s,z} * z+ \tag{4.1.5}$$

$$\beta_{s,\theta_t,dry} * \theta_{t,dry,i} + \beta_{s,\theta_t,wet} * \theta_{t,wet,i}+$$

$$\beta_{s,\theta_p,dry} * \theta_{p,dry,i} + \beta_{s,\theta_p,wet} * \theta_{p,wet,i}+$$

$$\beta_{s,\theta_{s3},dry} * \theta_{s3,dry,i} + \beta_{s,\theta_{s3},wet} * \theta_{s3,wet,i}+$$

$$\beta_{s,\theta_t \times z,dry} * \theta_{t,dry,i} * z + \beta_{s,\theta_t \times z,wet} * \theta_{t,wet,i} * z+$$

$$\beta_{s,\theta_p \times z,dry} * \theta_{p,dry,i} * z + \beta_{s,\theta_p \times z,wet} * \theta_{p,wet,i} * z+$$

$$\beta_{s,\theta_{s3} \times z,dry} * \theta_{s3,dry,i} * z + \beta_{s,\theta_{s3} \times z,wet} * \theta_{s3,wet,i} * z+$$

$$\beta_{s,native} * g(i) + \beta_{s,i},$$

where wet and dry denote wet season and dry seasons covariation values, i indexes each site in Table 4.1, and the function $g()$ takes a site i and returns 0 for sites in the invaded range and 1 for sites in the native range. The development function, $G(z'|z, \sigma, \theta)$ is given by:

$$G(z'|z, \sigma, \theta) = f_G(z'|\mu_G(z, \theta), \sigma_G(z, i)), \tag{4.1.6}$$

where f_G denotes a normal probability density function, $\mu_G(z, \theta)$ is given by:

$$\mu_G(z, \theta) = \beta_{0,G,i}+ \tag{4.1.7}$$

$$\beta_{G,\theta_t,dry} * \theta_{t,dry,i} + \beta_{G,\theta_t,wet} * \theta_{t,wet,i}+$$

$$\beta_{G,\theta_p,dry} * \theta_{p,dry,i} + \beta_{G,\theta_p,wet} * \theta_{p,wet,i}+$$

$$\beta_{G,\theta_{s3},dry} * \theta_{s3,dry,i} + \beta_{G,\theta_{s3},wet} * \theta_{s3,wet,i}+$$

$$\beta_{G,\theta_t \times z,dry} * \theta_{t,dry,i} * z + \beta_{G,\theta_t \times z,wet} * \theta_{t,wet,i} * z +$$
$$\beta_{G,\theta_p \times z,dry} * \theta_{p,dry,i} * z + \beta_{G,\theta_p \times z,wet} * \theta_{p,wet,i} * z +$$
$$\beta_{G,\theta_{s3} \times z,dry} * \theta_{s3,dry,i} * z + \beta_{G,\theta_{s3} \times z,wet} * \theta_{s3,wet,i} * z,$$
$$\beta_{G,native} * g(i) + \beta_{G,i},$$

$\sigma_G(z, i)$ is given by:

$$\sigma_G(z, \theta) = \beta_{0,\sigma_G,i} + \tag{4.1.8}$$
$$\beta_{\sigma_G,\theta_t,dry} * \theta_{t,dry,i} + \beta_{\sigma_G,\theta_t,wet} * \theta_{t,wet,i} +$$
$$\beta_{\sigma_G,\theta_p,dry} * \theta_{p,dry,i} + \beta_{\sigma_G,\theta_p,wet} * \theta_{p,wet,i} +$$
$$\beta_{\sigma_G,\theta_{s3},dry} * \theta_{s3,dry,i} + \beta_{\sigma_G,\theta_{s3},wet} * \theta_{s3,wet,i} +$$
$$\beta_{\sigma_G,native} * g(i) + \beta_{\sigma_G,i},$$

The probability of flowering function, $p_f(z, \theta)$, is given by:

$$Logit(p_f(z, \theta)) = \beta_{0,p_f,i} + \beta_{z,p_f} * z + \tag{4.1.9}$$
$$\beta_{p_f,\theta_t,dry} * \theta_{t,dry,i} + \beta_{p_f,\theta_t,wet} * \theta_{t,wet,i} +$$
$$\beta_{p_f,\theta_p,dry} * \theta_{p,dry,i} + \beta_{p_f,\theta_p,wet} * \theta_{p,wet,i} +$$
$$\beta_{p_f,\theta_{s1},dry} * \theta_{s1,dry,i} + \beta_{p_f,\theta_{s1},wet} * \theta_{s1,wet,i} +$$
$$\beta_{p_f,\theta_t \times z,dry} * \theta_{t,dry,i} * z + \beta_{p_f,\theta_t \times z,wet} * \theta_{t,wet,i} * z +$$
$$\beta_{p_f,\theta_p \times z,dry} * \theta_{p,dry,i} * z + \beta_{p_f,\theta_p \times z,wet} * \theta_{p,wet,i} * z +$$
$$\beta_{p_f,\theta_{s1} \times z,dry} * \theta_{s1,dry,i} * z + \beta_{p_f,\theta_{s1} \times z,wet} * \theta_{s1,wet,i} * z,$$
$$\beta_{p_f,native} * g(i) + \beta_{p_f,native \times z} * g(i) * z + \beta_{p_f,i},$$

The number of flowers produced conditional on flowering function, $r_f(z, \theta)$, is given by:

$$Log(r_f(z, \theta)) = \beta_{0,r_f,i} + \beta_{z,r_f} * z + \tag{4.1.10}$$
$$\beta_{r_f,\theta_t,mean} * \theta_{t,mean,i} + \beta_{r_f,\theta_t,seas} * \theta_{t,seas,i} +$$
$$\beta_{r_f,\theta_p,total} * \theta_{p,total,i} + \beta_{r_f,\theta_p,seas} * \theta_{p,seas,i} +$$
$$\beta_{r_f,\theta_{s3},mean} * \theta_{s3,mean,i} + \beta_{r_f,\theta_{s3},seas} * \theta_{s3,seas,i} +$$
$$\beta_{r_f,\theta_t \times z,mean} + \theta_{t,mean,i} * z + \beta_{r_f,\theta_t \times z,seas} * \theta_{t,seas,i} * z +$$
$$\beta_{r_f,\theta_p \times z,total} + \theta_{p,total,i} * z + \beta_{r_f,\theta_p \times z,seas} * \theta_{p,seas,i} * z +$$
$$\beta_{r_f,\theta_{s3} \times z,mean} + \theta_{s3,mean,i} * z + \beta_{r_f,\theta_s3 \times z,seas} * \theta_{s3,seas,i} * z +$$
$$\beta_{r_f,native} * g(i) + \beta_{r_f,native \times z} * g(i) * z.$$

$g(i)$ is a function that returns 1 if site i in the native range (South Africa) and 0 when site i is located elsewhere. Finally, the size distribution of newly observed non-seedling plants, $r_a(z')$, is given by:

$$r_a(z') = f_{r_a}(z'|\mu_{r_a}, \sigma_{r_a}), \tag{4.1.11}$$

where f_{r_a} is a Gaussian probability density function.

Vital rate model summaries

Survival model

```
summary(surv_mod)
```

```
##  Family: bernoulli
##   Links: mu = logit
## Formula: alive ~ log_size + temp_dry_t * log_size + temp_wet_t * log_size + prec_dry_t * log_size + prec_wet_t * log_size + sw3_dry_t *
##    Data: data (Number of observations: 5958)
##   Draws: 4 chains, each with iter = 2000; warmup = 1000; thin = 1;
##          total post-warmup draws = 4000
##
## Group-Level Effects:
## ~site (Number of levels: 13)
##               Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## sd(Intercept)     0.23      0.18     0.01     0.69 1.00     1157     1632
##
## Population-Level Effects:
##                     Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## Intercept               2.45      0.60     1.31     3.71 1.00     1224     1661
## log_size                0.23      0.13    -0.02     0.49 1.00     1292     1963
## temp_dry_t             -0.84      0.38    -1.60    -0.05 1.00     1383     1440
## temp_wet_t             -0.43      0.52    -1.49     0.57 1.00     1700     1880
## prec_dry_t             -2.92      0.50    -3.92    -1.90 1.00     1384     1678
## prec_wet_t              1.64      0.62     0.36     2.88 1.00     1193     1547
## sw3_dry_t               1.95      0.78     0.35     3.44 1.00     1167     1591
## sw3_wet_t              -2.00      1.05    -4.01     0.18 1.00     1251     1706
## native                  0.13      0.57    -1.05     1.30 1.00     2530     2167
## log_size:temp_dry_t    -0.38      0.08    -0.52    -0.22 1.00     2060     2461
## log_size:temp_wet_t     0.11      0.10    -0.08     0.30 1.00     2575     2853
## log_size:prec_dry_t    -1.04      0.12    -1.28    -0.81 1.00     1495     2215
## log_size:prec_wet_t     0.84      0.14     0.57     1.12 1.00     1256     1832
## log_size:sw3_dry_t      1.05      0.17     0.71     1.39 1.00     1265     1735
## log_size:sw3_wet_t     -1.11      0.23    -1.57    -0.66 1.00     1428     1971
##
## Draws were sampled using sample(hmc). For each parameter, Bulk_ESS
## and Tail_ESS are effective sample size measures, and Rhat is the potential
## scale reduction factor on split chains (at convergence, Rhat = 1).
```

Growth model

```
summary(grow_mod)
```

```
##  Family: gaussian
##   Links: mu = identity; sigma = log
## Formula: log_size_next ~ log_size + temp_dry_t * log_size + temp_wet_t * log_size + prec_dry_t * log_size + prec_wet_t * log_size + sw3
##          sigma ~ log_size + temp_dry_t + temp_wet_t + prec_dry_t + prec_wet_t + sw3_dry_t + sw3_wet_t + native + (1 | site)
##     Data: data (Number of observations: 4280)
##   Draws: 4 chains, each with iter = 2000; warmup = 1000; thin = 1;
##          total post-warmup draws = 4000
##
## Group-Level Effects:
## ~site (Number of levels: 13)
##                     Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## sd(Intercept)           0.46      0.21     0.21     1.02 1.01     1210     1625
## sd(sigma_Intercept)     0.21      0.12     0.09     0.50 1.00      967      932
##
## Population-Level Effects:
##                     Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## Intercept               0.05      0.68    -1.30     1.41 1.00     1806     1599
## sigma_Intercept        -0.50      0.31    -1.16     0.10 1.00     1844     1386
## log_size                0.85      0.03     0.79     0.92 1.00     1898     2330
## temp_dry_t              0.06      0.51    -0.95     1.02 1.00     2139     1514
## temp_wet_t             -0.24      0.68    -1.56     1.16 1.00     2313     1630
## prec_dry_t             -0.40      0.55    -1.54     0.68 1.00     1813     1343
## prec_wet_t              0.15      0.74    -1.34     1.65 1.00     1554     1560
## sw3_dry_t              -0.10      0.91    -1.93     1.73 1.00     1604     1501
## sw3_wet_t               0.24      1.25    -2.28     2.77 1.00     1682     1524
## native                  0.25      0.83    -1.44     1.98 1.00     2605     1933
## log_size:temp_dry_t    -0.08      0.02    -0.11    -0.04 1.00     2477     2803
## log_size:temp_wet_t     0.05      0.02     0.01     0.10 1.00     3051     2866
## log_size:prec_dry_t    -0.14      0.03    -0.20    -0.09 1.00     1838     2660
## log_size:prec_wet_t     0.12      0.04     0.04     0.21 1.00     1876     2457
## log_size:sw3_dry_t      0.20      0.05     0.11     0.29 1.00     1938     2312
## log_size:sw3_wet_t     -0.19      0.06    -0.30    -0.07 1.00     2116     2460
## sigma_log_size         -0.12      0.01    -0.13    -0.10 1.00     7536     3177
## sigma_temp_dry_t        0.22      0.23    -0.24     0.68 1.00     2154     1600
## sigma_temp_wet_t       -0.34      0.32    -0.98     0.29 1.00     2396     1582
```

```
## sigma_prec_dry_t         0.05      0.25    -0.49      0.54 1.00      1752      1395
## sigma_prec_wet_t         0.23      0.34    -0.44      0.94 1.00      1693      1388
## sigma_sw3_dry_t          0.07      0.42    -0.76      0.94 1.00      1682      1234
## sigma_sw3_wet_t         -0.26      0.59    -1.49      0.87 1.00      1743      1297
## sigma_native            0.49      0.41    -0.32      1.31 1.00      2558      1790
##
## Draws were sampled using sample(hmc). For each parameter, Bulk_ESS
## and Tail_ESS are effective sample size measures, and Rhat is the potential
## scale reduction factor on split chains (at convergence, Rhat = 1).
```

Pr(Flowering) model

```
summary(repr_mod)
```

```
##  Family: bernoulli
##   Links: mu = logit
## Formula: repro ~ log_size + temp_dry_t_1 * log_size + temp_wet_t_1 * log_size + prec_dry_t_1 * log_size + prec_wet_t_1 * log_size + sw1
##    Data: data (Number of observations: 6581)
##   Draws: 4 chains, each with iter = 2000; warmup = 1000; thin = 1;
##          total post-warmup draws = 4000
##
## Group-Level Effects:
## ~site (Number of levels: 13)
##               Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## sd(Intercept)     2.58      0.99     1.35      5.06 1.00      1536      2058
##
## Population-Level Effects:
##                    Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS
## Intercept             -0.97      1.72    -4.26      2.45 1.00      3793
## log_size               1.59      0.14     1.33      1.87 1.00      2421
## temp_dry_t_1          -0.87      2.80    -6.57      4.55 1.00      2473
## temp_wet_t_1           1.23      3.89    -6.63      9.35 1.00      2426
## prec_dry_t_1           0.08      4.35    -8.91      8.89 1.00      2433
## prec_wet_t_1          -0.49      2.75    -6.05      4.94 1.00      2309
## sw1_dry_t_1           -0.14      6.29   -12.89     12.90 1.00      2342
## sw1_wet_t_1           -0.32      5.05   -10.74      9.89 1.00      2336
## native                -1.92      3.88   -10.23      5.54 1.00      2644
## log_size:temp_dry_t_1  0.39      0.27    -0.14      0.93 1.00      2085
```

```
## log_size:temp_wet_t_1    -0.56      0.33     -1.23      0.10 1.00      1742
## log_size:prec_dry_t_1    -0.96      0.29     -1.55     -0.41 1.00      2016
## log_size:prec_wet_t_1     0.61      0.24      0.16      1.10 1.00      1774
## log_size:sw1_dry_t_1      1.37      0.45      0.50      2.31 1.00      1709
## log_size:sw1_wet_t_1     -0.67      0.33     -1.33     -0.03 1.00      1916
## log_size:native           0.21      0.41     -0.63      1.00 1.00      2119
##                       Tail_ESS
## Intercept                 2636
## log_size                  2590
## temp_dry_t_1              2066
## temp_wet_t_1              2340
## prec_dry_t_1              1659
## prec_wet_t_1              2071
## sw1_dry_t_1               2113
## sw1_wet_t_1               2371
## native                    1988
## log_size:temp_dry_t_1     2866
## log_size:temp_wet_t_1     2470
## log_size:prec_dry_t_1     2425
## log_size:prec_wet_t_1     2277
## log_size:sw1_dry_t_1      2005
## log_size:sw1_wet_t_1      2342
## log_size:native           2547
##
## Draws were sampled using sample(hmc). For each parameter, Bulk_ESS
## and Tail_ESS are effective sample size measures, and Rhat is the potential
## scale reduction factor on split chains (at convergence, Rhat = 1).
```

Flower number model

```
summary(flow_mod)
```

```
##  Family: negbinomial
##   Links: mu = log; shape = identity
## Formula: flower_n ~ log_size + temp_dry_t_1 * log_size + temp_wet_t_1 * log_size + prec_dry_t_1 * log_size + prec_wet_t_1 * log_size +
##    Data: data (Number of observations: 1093)
##   Draws: 4 chains, each with iter = 2000; warmup = 1000; thin = 1;
##          total post-warmup draws = 4000
```

```
## 
## Group-Level Effects:
## ~site (Number of levels: 13)
##                         Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS
## sd(Intercept)               0.53      0.29     0.15     1.24 1.00     1322
## sd(log_size)                0.25      0.15     0.05     0.65 1.00      982
## cor(Intercept,log_size)     0.01      0.54    -0.92     0.93 1.00     1215
##                         Tail_ESS
## sd(Intercept)               1283
## sd(log_size)                1769
## cor(Intercept,log_size)     1916
## 
## Population-Level Effects:
##                      Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS
## Intercept                1.25      0.41     0.37     2.03 1.00     2700
## log_size                 0.64      0.20     0.21     1.02 1.00     2174
## temp_dry_t_1            -1.28      0.88    -3.14     0.34 1.00     1407
## temp_wet_t_1             2.90      1.46     0.15     6.04 1.00     1423
## prec_dry_t_1            -0.07      0.32    -0.75     0.58 1.00     1765
## prec_wet_t_1            -1.69      0.90    -3.59     0.15 1.00     1242
## sw3_dry_t_1             -3.25      1.78    -6.94     0.28 1.00     1206
## sw3_wet_t_1              5.19      2.92    -0.78    11.30 1.00     1170
## native                  -0.43      1.19    -2.67     1.74 1.00     1409
## log_size:temp_dry_t_1   -0.46      0.34    -1.27     0.13 1.00     1100
## log_size:temp_wet_t_1    1.01      0.72    -0.22     2.63 1.00     1025
## log_size:prec_dry_t_1   -0.17      0.15    -0.50     0.11 1.00     1389
## log_size:prec_wet_t_1   -0.62      0.45    -1.63     0.21 1.00      917
## log_size:sw3_dry_t_1    -1.30      0.89    -3.34     0.23 1.00      914
## log_size:sw3_wet_t_1     2.12      1.44    -0.36     5.39 1.00      891
##                      Tail_ESS
## Intercept                2376
## log_size                 1927
## temp_dry_t_1             1979
## temp_wet_t_1             1744
## prec_dry_t_1             2067
## prec_wet_t_1             1652
## sw3_dry_t_1              1520
## sw3_wet_t_1              1360
## native                   2485
```

```
## log_size:temp_dry_t_1       1209
## log_size:temp_wet_t_1       1060
## log_size:prec_dry_t_1       1676
## log_size:prec_wet_t_1       1269
## log_size:sw3_dry_t_1        1088
## log_size:sw3_wet_t_1        1152
##
## Family Specific Parameters:
##       Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## shape     2.36      0.14     2.10     2.65 1.00     6013     2820
##
## Draws were sampled using sample(hmc). For each parameter, Bulk_ESS
## and Tail_ESS are effective sample size measures, and Rhat is the potential
## scale reduction factor on split chains (at convergence, Rhat = 1).
```

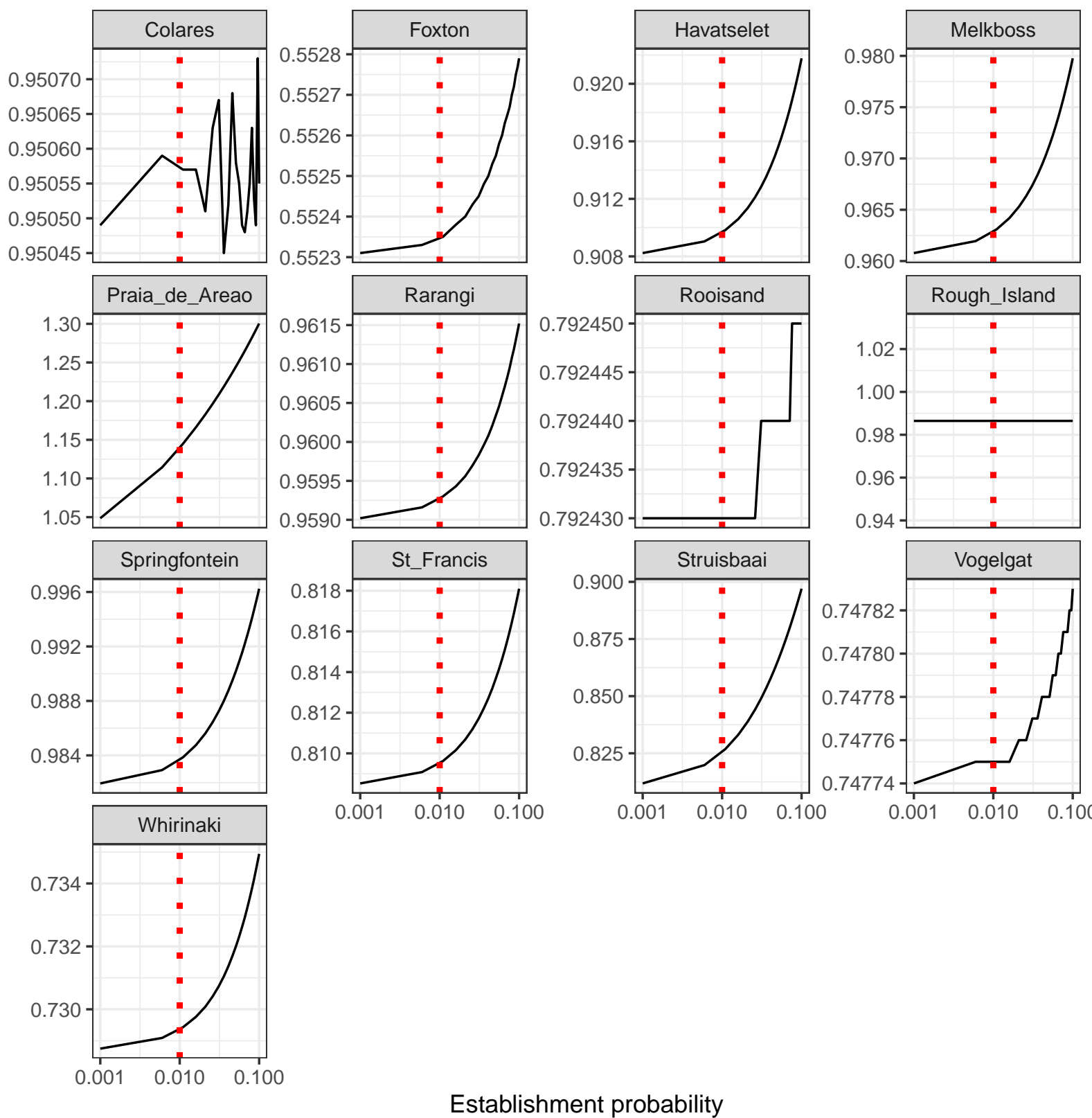## Recruit size model

```
summary(recr_mod)
```

```
##  Family: gaussian
##   Links: mu = identity; sigma = identity
## Formula: log_size_next ~ 1
##    Data: recruits (Number of observations: 15)
##   Draws: 4 chains, each with iter = 2000; warmup = 1000; thin = 1;
##          total post-warmup draws = 4000
##
## Population-Level Effects:
##           Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## Intercept    -8.62      0.14    -8.91    -8.34 1.00     1685     1566
##
## Family Specific Parameters:
##       Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## sigma     0.54      0.12     0.37     0.84 1.00     1800     1777
##
## Draws were sampled using sample(hmc). For each parameter, Bulk_ESS
## and Tail_ESS are effective sample size measures, and Rhat is the potential
## scale reduction factor on split chains (at convergence, Rhat = 1).
```

Sensitivity of site-level λs to simulated parameter values

We could not find parameter values for establishment probability (p_e) or seedbank survival rate (s_{sb}). Therefore, we simulated a range of values from 0-1 for each (incrementing by 0.05), re-building the model, and then computing λ. The results are reported here. Dotted, red vertical lines how the parameter value we used in the results reported in the main text.

p_e

s_{sb}

Per-capita Growth Rate (λ)

Seedbank Survival rate