

Codes to generate Fig.3

```
library(VBRobM)
library(lmerTest)
#> Loading required package: lme4
#> Loading required package: Matrix
#> Warning: package 'Matrix' was built under R version 4.3.2
#>
#> Attaching package: 'lmerTest'
#> The following object is masked from 'package:lme4':
#>
#>     lmer
#> The following object is masked from 'package:stats':
#>
#>     step
library(piecewiseSEM)
#> Warning: package 'piecewiseSEM' was built under R version 4.3.2
#>
#>   This is piecewiseSEM version 2.3.0.
#>
#>
#>   Questions or bugs can be addressed to <LefcheckJ@si.edu>.
#>
#> Attaching package: 'piecewiseSEM'
#> The following object is masked from 'package:VBRobM':
#>
#>     coefs
library(brms)
#> Warning: package 'brms' was built under R version 4.3.2
#> Loading required package: Rcpp
#> Loading 'brms' package (version 2.20.4). Useful instructions
#> can be found by typing help('brms'). A more detailed introduction
#> to the package is available through vignette('brms_overview').
#>
#> Attaching package: 'brms'
#> The following object is masked from 'package:lme4':
#>
#>     ngrps
#> The following object is masked from 'package:stats':
#>
#>     ar
```

Results of Figure 3

```
## 3b-3e
```

```

trophic$Treat <- 1

set.seed(123)

fit.3b <- psem(lmer(smd_herbivore ~ -1+Treat+(-1+Treat|Code),
  data = trophic,
  weights = 1/vi_herbivore),
  lmer(smd_plant ~ -1+Treat+smd_herbivore+(-1+Treat|Code),
  data = trophic,
  weights = 1/vi_plant),
  trophic)

fit.3b
#> Structural Equations of x :
#> lmerModLmerTest: smd_herbivore ~ -1 + Treat
#> lmerModLmerTest: smd_plant ~ -1 + Treat + smd_herbivore
#>
#> Data:
#>      Code Latitude wd lc          pm Year Lat_low      ecosystem diversity
#> 1 Paper1   38.767  0  1 intercropping    2      0 Agroecosystem      0
#> 2 Paper2   38.750  0  1 intercropping    1      0 Agroecosystem      1
#> 3 Paper3   39.500  0  1 intercropping    2      0 Agroecosystem      0
#> 4 Paper3   39.500  0  1 intercropping    2      0 Agroecosystem      0
#> 5 Paper3   39.500  0  1 intercropping    2      0 Agroecosystem      0
#> 6 Paper3   39.500  0  1 intercropping    2      0 Agroecosystem      0
#>      smd_enemy  vi_enemy smd_herbivore vi_herbivore smd_plant vi_plant Treat
#> 1 -0.9167564  0.4669089   -1.657739    0.6187803  0.6865371  0.7678156    1
#> 2  1.0224805  0.4832312   -1.226826    0.5198236  2.0634066  0.7389578    1
#> 3  9.3008576 19.2310030   -1.967156    1.4971122  1.7448444  1.3200181    1
#> 4  6.1226686  8.7114609   -1.967156    1.4971122  1.7448444  1.3200181    1
#> 5  9.3008576 19.2310030   -4.178354    4.4133226  1.7448444  1.3200181    1
#> 6  6.1226686  8.7114609   -4.178354    4.4133226  1.7448444  1.3200181    1
#> ...with 256 more rows
#>
#> [1] "class(psem)"

## Suppressed for fast building vignettes.
# bf_plant <- bf(smd_plant ~ 1 + smd_herbivore + (1/p|Code) + fcor(v_plant))
# bf_herbivore <- bf(smd_herbivore ~ 1 + (1/p|Code) + fcor(v_herbivore))
# prior <- c(set_prior('normal(0, 10)', class = 'Intercept', resp = 'smdplant'),
#            set_prior('normal(0, 10)', class = 'Intercept', resp = 'smdherbivore'),
#            set_prior('normal(0, 10)', class = 'b', resp = 'smdplant'),
#            set_prior('student_t(3, 0, 5)', class = 'sd', group = 'Code', resp = 'smdplant'),
#            set_prior('student_t(3, 0, 5)', class = 'sd', group = 'Code', resp = 'smdherbivore'))
# v_plant <- diag(trophic$vi_plant)
# v_herbivore <- diag(trophic$vi_herbivore)
# fit.3c <- brm(bf_plant + bf_herbivore + set_rescor(rescor = FALSE),
#              data = trophic,
#              data2 = list(v_plant = v_plant, v_herbivore = v_herbivore),
#              prior = prior)
# fit.3c

fit.3d <- vbrobm(bcrREML(smd_herbivore ~ 1+(1|Code),

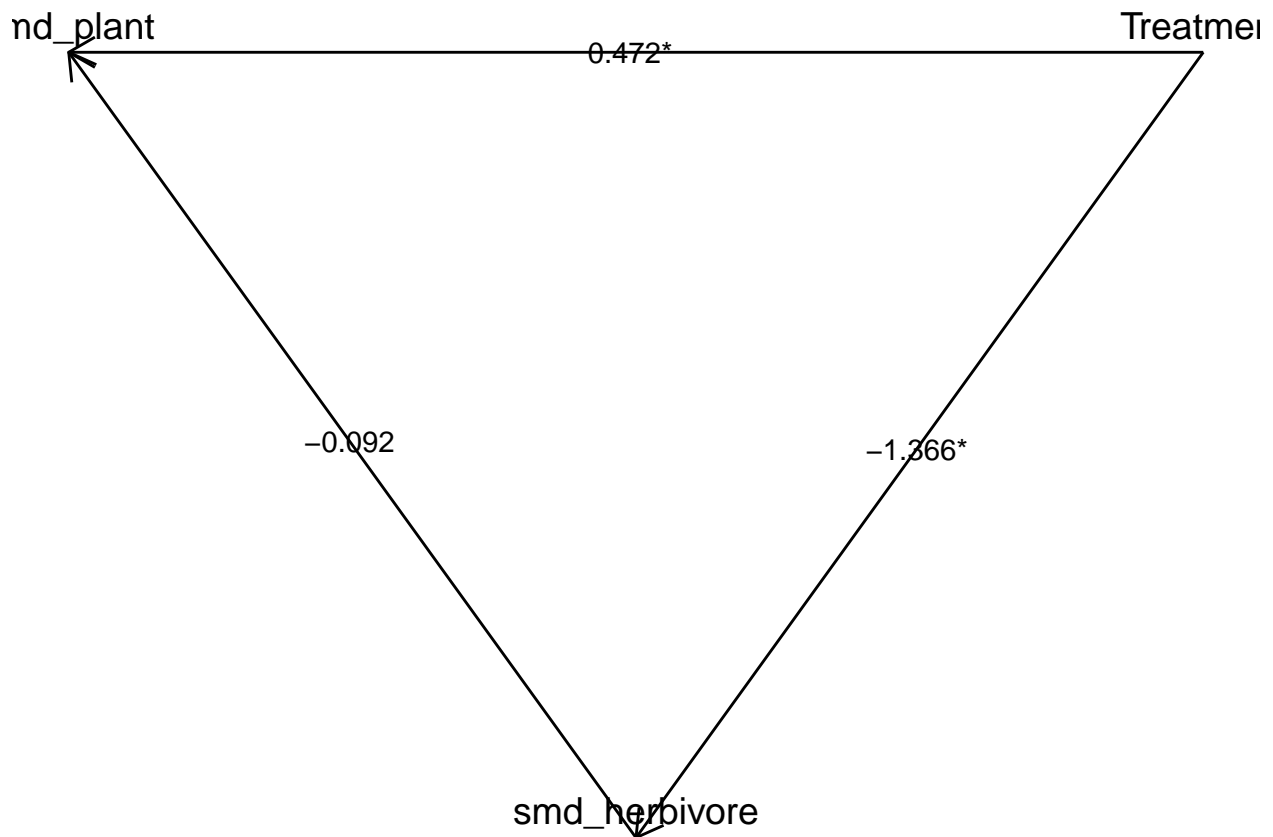
```

```

data = trophic,
vi = trophic$vi_herbivore,
maxit = 1000),
bcrREML(smd_plant ~ 1+smd_herbivore+(1|Code),
data = trophic,
vi = trophic$vi_plant,
maxit = 1000))

fit.3d
#> Path coefficients:
#>      Predictor      Response Coefficient Std.Error      z      p.value
#> 1 Treatment smd_herbivore -1.36632359 0.1813227 -7.535314 4.871598e-14
#> 2 Treatment smd_plant 0.47245032 0.1773778 2.663526 7.732642e-03
#> 3 smd_herbivore smd_plant -0.09192819 0.0541168 -1.698700 8.937577e-02
#>
#> Mediation analysis:
#> [[1]]
#>      Exposure Outcome Mediators Effect type Mean effect      Sd
#> 1 Treatment smd_plant smd_herbivore Indirect effect 0.1237544 0.07623444
#> 2 Treatment smd_plant <NA> Direct effect 0.4792931 0.17495511
#> 3 Treatment smd_plant <NA> Total effect 0.6030475 0.15283987
#>      Lower bound Upper bound
#> 1 -0.01920071 0.2849098
#> 2 0.13900194 0.8144244
#> 3 0.31678743 0.8979351
plot(fit.3d)

```



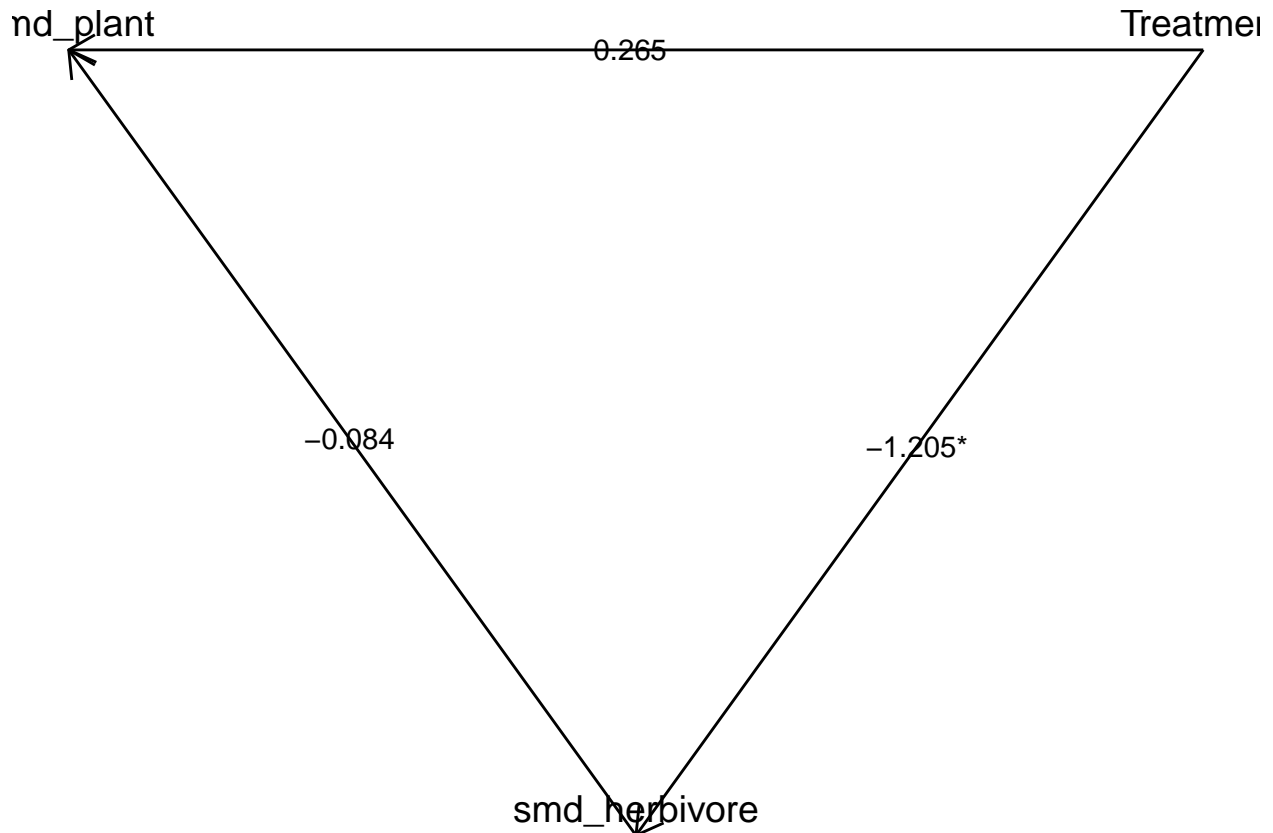
```

fit.3e <- vbrobm(vbrob(smd_herbivore ~ 1+(1|Code),
  data = trophic,
  vi = trophic$vi_herbivore,
  maxit = 1000),
vbrob(smd_plant ~ 1+smd_herbivore+(1|Code),
  data = trophic,
  vi = trophic$vi_plant,
  maxit = 1000))

fit.3e
#> Path coefficients:
#>      Predictor      Response Coefficient Std.Error      z      p.value
#> 1 Treatment smd_herbivore -1.20475044 0.17381355 -6.931280 4.170486e-12
#> 2 Treatment smd_plant 0.26455893 0.17324953 1.527040 1.267511e-01
#> 3 smd_herbivore smd_plant -0.08352151 0.05349159 -1.561395 1.184305e-01
#>
#> Mediation analysis:
#> [[1]]
#> Exposure Outcome Mediators Effect type Mean effect Sd
#> 1 Treatment smd_plant smd_herbivore Indirect effect 0.0999740 0.06487618
#> 2 Treatment smd_plant <NA> Direct effect 0.2645019 0.17366876
#> 3 Treatment smd_plant <NA> Total effect 0.3644759 0.15187672
#> Lower bound Upper bound

```

```
#> 1  -0.0212860  0.2293167
#> 2  -0.0893569  0.6137113
#> 3   0.0581423  0.6536598
plot(fit.3e)
```



```
## 3f-3i
fit.3f <- psem(lmer(smd_enemy ~ -1+Treat+(-1+Treat|Code),
  data = trophic,
  weights = 1/vi_enemy),
  lmer(smd_herbivore ~ -1+Treat+smd_enemy+(-1+Treat|Code),
  data = trophic,
  weights = 1/vi_herbivore),
  lmer(smd_plant ~ -1+Treat+smd_herbivore+(-1+Treat|Code),
  data = trophic,
  weights = 1/vi_plant),
  trophic)

fit.3f
#> Structural Equations of x :
#> lmerModLmerTest: smd_enemy ~ -1 + Treat
#> lmerModLmerTest: smd_herbivore ~ -1 + Treat + smd_enemy
#> lmerModLmerTest: smd_plant ~ -1 + Treat + smd_herbivore
#>
#> Data:
#>      Code Latitude wd lc      pm Year Lat_low      ecosystem diversity
```

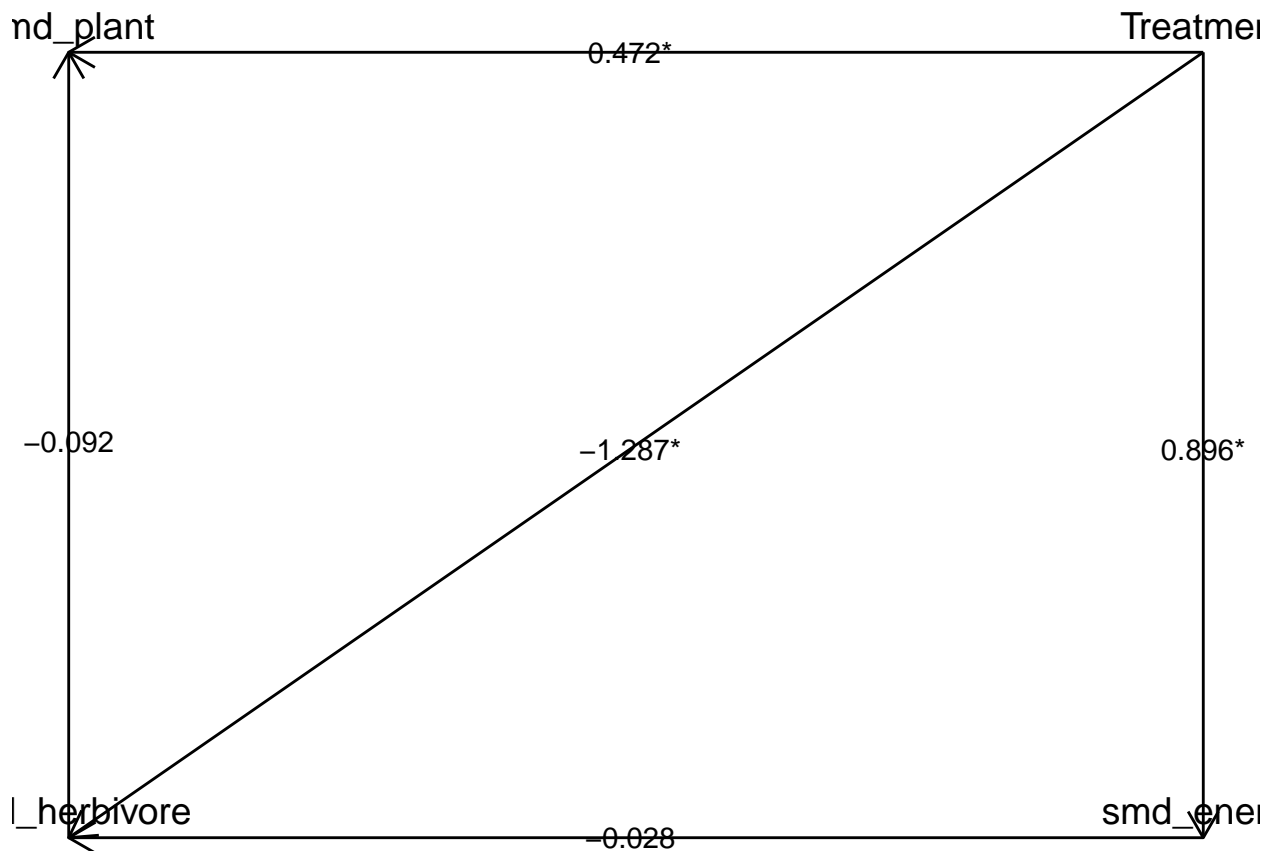
```

#> 1 Paper1 38.767 0 1 intercropping 2 0 Agroecosystem 0
#> 2 Paper2 38.750 0 1 intercropping 1 0 Agroecosystem 1
#> 3 Paper3 39.500 0 1 intercropping 2 0 Agroecosystem 0
#> 4 Paper3 39.500 0 1 intercropping 2 0 Agroecosystem 0
#> 5 Paper3 39.500 0 1 intercropping 2 0 Agroecosystem 0
#> 6 Paper3 39.500 0 1 intercropping 2 0 Agroecosystem 0
#> smd_enemy vi_enemy smd_herbivore vi_herbivore smd_plant vi_plant Treat
#> 1 -0.9167564 0.4669089 -1.657739 0.6187803 0.6865371 0.7678156 1
#> 2 1.0224805 0.4832312 -1.226826 0.5198236 2.0634066 0.7389578 1
#> 3 9.3008576 19.2310030 -1.967156 1.4971122 1.7448444 1.3200181 1
#> 4 6.1226686 8.7114609 -1.967156 1.4971122 1.7448444 1.3200181 1
#> 5 9.3008576 19.2310030 -4.178354 4.4133226 1.7448444 1.3200181 1
#> 6 6.1226686 8.7114609 -4.178354 4.4133226 1.7448444 1.3200181 1
#> ...with 256 more rows
#>
#> [1] "class(psem)"

fit.3g <- vbrobm(bcrREML(smd_enemy ~ 1+(1|Code),
                        data = trophic,
                        vi = trophic$vi_enemy,
                        maxit = 1000),
bcrREML(smd_herbivore ~ 1+smd_enemy+(1|Code),
        data = trophic,
        vi = trophic$vi_herbivore,
        maxit = 1000),
bcrREML(smd_plant ~ 1+smd_herbivore+(1|Code),
        data = trophic,
        vi = trophic$vi_plant,
        maxit = 1000))

fit.3g
#> Path coefficients:
#> Predictor Response Coefficient Std.Error z p.value
#> 1 Treatment smd_enemy 0.89616231 0.11708217 7.6541314 1.946232e-14
#> 2 Treatment smd_herbivore -1.28705641 0.17558242 -7.3302122 2.297886e-13
#> 3 smd_enemy smd_herbivore -0.02778882 0.03066899 -0.9060885 3.648890e-01
#> 4 Treatment smd_plant 0.47245032 0.17737777 2.6635261 7.732642e-03
#> 5 smd_herbivore smd_plant -0.09192819 0.05411680 -1.6986997 8.937577e-02
#>
#> Mediation analysis:
#> [[1]]
#> Exposure Outcome Mediators Effect type Mean effect
#> 1 Treatment smd_plant smd_enemy&smd_herbivore Indirect effect 0.002392059
#> 2 Treatment smd_plant smd_herbivore Indirect effect 0.120013516
#> 3 Treatment smd_plant <NA> Direct effect 0.473783989
#> 4 Treatment smd_plant <NA> Total effect 0.596189563
#> Sd Lower bound Upper bound
#> 1 0.00339399 -0.002873366 0.01090441
#> 2 0.07050185 -0.022276220 0.26467825
#> 3 0.17984268 0.116913945 0.82302361
#> 4 0.16016324 0.278292810 0.90998606
plot(fit.3g)

```



```
## Suppressed for fast building vignettes.
# bf_plant <- bf(smd_plant ~ 1 + smd_herbivore + (1|p|Code) + fcor(v_plant))
# bf_herbivore <- bf(smd_herbivore ~ 1 + smd_enemy + (1|p|Code) + fcor(v_herbivore))
# bf_enemy <- bf(smd_enemy ~ 1 + (1|p|Code) + fcor(v_enemy))
# prior <- c(set_prior('normal(0, 10)', class = 'Intercept', resp = 'smdplant'),
#            set_prior('normal(0, 10)', class = 'Intercept', resp = 'smdherbivore'),
#            set_prior('normal(0, 10)', class = 'Intercept', resp = 'smdenemy'),
#            set_prior('normal(0, 10)', class = 'b', resp = 'smdplant'),
#            set_prior('normal(0, 10)', class = 'b', resp = 'smdherbivore'),
#            set_prior('student_t(3, 0, 5)', class = 'sd', group = 'Code', resp = 'smdplant'),
#            set_prior('student_t(3, 0, 5)', class = 'sd', group = 'Code', resp = 'smdherbivore'),
#            set_prior('student_t(3, 0, 5)', class = 'sd', group = 'Code', resp = 'smdenemy'))
# v_plant <- diag(trophic$vi_plant)
# v_herbivore <- diag(trophic$vi_herbivore)
# v_enemy <- diag(trophic$vi_enemy)
# fit.3h <- brm(bf_plant + bf_herbivore + bf_enemy + set_rescor(rescor = FALSE),
#              data = trophic,
#              data2 = list(v_plant = v_plant, v_herbivore = v_herbivore, v_enemy = v_enemy),
#              prior = prior)
# fit.3h

fit.3i <- vbrobm(vbrob(smd_enemy ~ 1+(1|Code),
                     data = trophic,
                     vi = trophic$vi_enemy,
                     maxit = 1000),
```

```

vbrob(smd_herbivore ~ 1+smd_enemy+(1|Code),
      data = trophic,
      vi = trophic$vi_herbivore,
      maxit = 1000),
vbrob(smd_plant ~ 1+smd_herbivore+(1|Code),
      data = trophic,
      vi = trophic$vi_plant,
      maxit = 1000))

fit.3i
#> Path coefficients:
#>      Predictor      Response Coefficient Std.Error      z      p.value
#> 1 Treatment      smd_enemy  0.70840057 0.10205427  6.941410 3.882048e-12
#> 2 Treatment smd_herbivore -1.05299330 0.16546920 -6.363682 1.969742e-10
#> 3 smd_enemy smd_herbivore -0.13646259 0.03005728 -4.540085 5.623149e-06
#> 4 Treatment      smd_plant  0.26455893 0.17324953  1.527040 1.267511e-01
#> 5 smd_herbivore      smd_plant -0.08352151 0.05349159 -1.561395 1.184305e-01
#>
#> Mediation analysis:
#> [[1]]
#>      Exposure Outcome      Mediators      Effect type Mean effect
#> 1 Treatment smd_plant smd_enemy&smd_herbivore Indirect effect 0.008481238
#> 2 Treatment smd_plant      smd_herbivore Indirect effect 0.089767686
#> 3 Treatment smd_plant      <NA> Direct effect 0.258367683
#> 4 Treatment smd_plant      <NA> Total effect 0.356616606
#>
#>      Sd Lower bound Upper bound
#> 1 0.00590143 -0.001270235 0.02084576
#> 2 0.05767976 -0.013197750 0.21154736
#> 3 0.17172160 -0.088154826 0.58445742
#> 4 0.14885573 0.051820141 0.64337503
plot(fit.3i)

```