Model for attack-fruits

> sem4<-list(#with fitness, attack

+ lm(phen\_int~meanT\*moist\_per,allplants),

+ glm.nb(Mrub\_sch\_s~meanT\*moist\_per,allplants),

+ lm(suit\_neigh~meanT\*moist\_per,allplants),

+ glm(attack~phen\_int\*Mrub\_sch\_s+suit\_neigh+meanT+moist\_per,allplants,family="binomial"),

+ glm(cbind(fr\_in,n\_fl)~phen\_int+meanT+moist\_per+attack,allplants,family="binomial")

+ )

> sem.fit(sem4, data=allplants,

+ corr.errors=c("phen\_int~~Mrub\_sch\_s","phen\_int~~suit\_neigh","suit\_neigh~~Mrub\_sch\_s"))

$missing.paths

missing.path estimate std.error df crit.value p.value

1 attack ~ meanT\*moist\_per + ... -0.0022 0.0089 8840 -0.2510 0.8018

2 cbind(fr\_in,n\_fl) ~ meanT\*moist\_per + ... -0.0024 0.0066 521 -0.3594 0.7193

3 cbind(fr\_in,n\_fl) ~ Mrub\_sch\_s\*phen\_int + ... -0.0181 0.0149 520 -1.2133 0.2250

4 cbind(fr\_in,n\_fl) ~ Mrub\_sch\_s + ... -0.0020 0.0066 520 -0.2984 0.7654

5 cbind(fr\_in,n\_fl) ~ suit\_neigh + ... -0.0024 0.0066 520 -0.3624 0.7171

$Fisher.C

fisher.c df p.value

1 5.28 10 0.871

$AIC

AIC AICc K n

1 59.28 62.31 27 527

> sem.model.fits(sem4)

Class Family Link n R.squared

1 lm gaussian identity 8848 0.1150905

2 negbin Negative Binomial log 8852 0.2089349

3 lm gaussian identity 8852 0.3702739

4 glm binomial logit 8848 0.3774603

5 glm binomial logit 527 0.1807202

> sem.coefs(sem4, data=allplants,

+ corr.errors=c("phen\_int~~Mrub\_sch\_s","phen\_int~~suit\_neigh","suit\_neigh~~Mrub\_sch\_s"))

response predictor estimate std.error p.value

1 phen\_int meanT -1.583246e+00 0.252059807 0.0000 \*\*\*

2 phen\_int moist\_per -3.254147e-01 0.058171568 0.0000 \*\*\*

3 phen\_int meanT:moist\_per 1.670082e-02 0.003555492 0.0000 \*\*\*

4 Mrub\_sch\_s moist\_per -1.843120e+00 0.079656232 0.0000 \*\*\*

5 Mrub\_sch\_s meanT:moist\_per 1.091834e-01 0.004855336 0.0000 \*\*\*

6 Mrub\_sch\_s meanT -6.279957e+00 0.324828375 0.0000 \*\*\*

7 suit\_neigh meanT:moist\_per 2.877139e+00 0.077902194 0.0000 \*\*\*

8 suit\_neigh moist\_per -4.494631e+01 1.274535797 0.0000 \*\*\*

9 suit\_neigh meanT -1.803224e+02 5.522417433 0.0000 \*\*\*

10 attack suit\_neigh -4.596958e-02 0.002176858 0.0000 \*\*\*

11 attack phen\_int 8.155260e-01 0.052724034 0.0000 \*\*\*

12 attack meanT 1.522937e+00 0.125876522 0.0000 \*\*\*

13 attack moist\_per 4.279806e-02 0.005372010 0.0000 \*\*\*

14 attack phen\_int:Mrub\_sch\_s 3.705436e-02 0.014883112 0.0128 \*

15 attack Mrub\_sch\_s -1.372672e-01 0.074491626 0.0654

16 cbind(fr\_in, n\_fl) attack -5.715453e-01 0.072892189 0.0000 \*\*\*

17 cbind(fr\_in, n\_fl) phen\_int 1.267448e-01 0.039492386 0.0013 \*\*

18 cbind(fr\_in, n\_fl) moist\_per -2.895526e-03 0.003433458 0.3990

19 cbind(fr\_in, n\_fl) meanT 3.892632e-03 0.088428827 0.9649

20 ~~ phen\_int ~~ suit\_neigh -2.217326e-02 NA 0.9815

21 ~~ phen\_int ~~ Mrub\_sch\_s -2.470386e-02 NA 0.9899

22 ~~ suit\_neigh ~~ Mrub\_sch\_s -1.153325e-01 NA 1.0000

Model for number of eggs-fruits

> sem5<-list(#with fitness, number of eggs (only pls w eggs)

+ lm(phen\_int~meanT\*moist\_per,allplants),

+ glm.nb(Mrub\_sch\_s~meanT\*moist\_per,allplants),

+ lm(suit\_neigh~meanT\*moist\_per,allplants),

+ glm.nb(n\_eggs\_max~phen\_int\*Mrub\_sch\_s+suit\_neigh+meanT+moist\_per,subset(allplants,n\_eggs\_max>0)),

+ glm(cbind(fr\_in,n\_fl)~phen\_int+meanT+moist\_per+n\_eggs\_max,subset(allplants,n\_eggs\_max>0),family="binomial")

+ )

> sem.fit(sem5, data=allplants,

+ corr.errors=c("phen\_int~~Mrub\_sch\_s","phen\_int~~suit\_neigh","suit\_neigh~~Mrub\_sch\_s"))

$missing.paths

missing.path estimate std.error df crit.value p.value

1 n\_eggs\_max ~ meanT\*moist\_per + ... -0.0079 0.0094 8840 -0.8358 0.4033

2 cbind(fr\_in,n\_fl) ~ meanT\*moist\_per + ... -0.0024 0.0066 521 -0.3652 0.7150

3 cbind(fr\_in,n\_fl) ~ Mrub\_sch\_s\*phen\_int + ... -0.0119 0.0151 520 -0.7858 0.4320

4 cbind(fr\_in,n\_fl) ~ Mrub\_sch\_s + ... -0.0022 0.0066 520 -0.3386 0.7349

5 cbind(fr\_in,n\_fl) ~ suit\_neigh + ... -0.0024 0.0066 520 -0.3550 0.7226

$Fisher.C

fisher.c df p.value

1 5.43 10 0.861

$AIC

AIC AICc K n

1 61.43 70.763 28 203

> sem.model.fits(sem5)

Class Family Link n R.squared

1 lm gaussian identity 8848 0.1150905

2 negbin Negative Binomial log 8852 0.2089349

3 lm gaussian identity 8852 0.3702739

4 negbin Negative Binomial log 731 0.1585786

5 glm binomial logit 203 0.1907027

> sem.coefs(sem5, data=allplants,

+ corr.errors=c("phen\_int~~Mrub\_sch\_s","phen\_int~~suit\_neigh","suit\_neigh~~Mrub\_sch\_s"))

response predictor estimate std.error p.value

1 phen\_int meanT -1.583246e+00 0.252059807 0.0000 \*\*\*

2 phen\_int moist\_per -3.254147e-01 0.058171568 0.0000 \*\*\*

3 phen\_int meanT:moist\_per 1.670082e-02 0.003555492 0.0000 \*\*\*

4 Mrub\_sch\_s moist\_per -1.843120e+00 0.079656232 0.0000 \*\*\*

5 Mrub\_sch\_s meanT:moist\_per 1.091834e-01 0.004855336 0.0000 \*\*\*

6 Mrub\_sch\_s meanT -6.279957e+00 0.324828375 0.0000 \*\*\*

7 suit\_neigh meanT:moist\_per 2.877139e+00 0.077902194 0.0000 \*\*\*

8 suit\_neigh moist\_per -4.494631e+01 1.274535797 0.0000 \*\*\*

9 suit\_neigh meanT -1.803224e+02 5.522417433 0.0000 \*\*\*

10 n\_eggs\_max suit\_neigh -1.260109e-02 0.001758187 0.0000 \*\*\*

11 n\_eggs\_max phen\_int 2.857857e-01 0.045184872 0.0000 \*\*\*

12 n\_eggs\_max meanT 3.691620e-01 0.090443533 0.0000 \*\*\*

13 n\_eggs\_max moist\_per 1.566458e-02 0.003925759 0.0001 \*\*\*

14 n\_eggs\_max phen\_int:Mrub\_sch\_s 4.199724e-03 0.009256085 0.6500

15 n\_eggs\_max Mrub\_sch\_s 2.396161e-05 0.048065341 0.9996

16 cbind(fr\_in, n\_fl) n\_eggs\_max -5.737336e-02 0.010367165 0.0000 \*\*\*

17 cbind(fr\_in, n\_fl) phen\_int 1.313114e-01 0.088650553 0.1385

18 cbind(fr\_in, n\_fl) meanT 1.604185e-01 0.152963284 0.2943

19 cbind(fr\_in, n\_fl) moist\_per -4.367945e-04 0.006048926 0.9424

20 ~~ phen\_int ~~ suit\_neigh -2.217326e-02 NA 0.9815

21 ~~ phen\_int ~~ Mrub\_sch\_s -2.470386e-02 NA 0.9899

22 ~~ suit\_neigh ~~ Mrub\_sch\_s -1.153325e-01 NA 1.0000

Seed data

> head(seeds)

pl\_id P\_m UP\_m P\_i UP\_i status n\_fl fr\_in fr\_pr seeds\_per\_fl

1 2 NA 360 NA NA Both\_m 3 1 0 120.00000

2 3 NA NA NA 290 UP\_i 4 3 0 217.50000

3 4 50 NA NA 268 UP\_i 11 1 2 33.45455

4 6 NA NA NA 610 UP\_i 2 2 0 610.00000

5 7 NA NA NA 640 UP\_i 4 4 0 640.00000

6 8 NA 660 NA NA Both\_m 5 5 0 660.00000

Models for attack-seeds

> sem6<-list(#with fitness, attack

+ lm(phen\_int~meanT\*moist\_per,allplants),

+ glm.nb(Mrub\_sch\_s~meanT\*moist\_per,allplants),

+ lm(suit\_neigh~meanT\*moist\_per,allplants),

+ glm(attack~phen\_int\*Mrub\_sch\_s+suit\_neigh+meanT+moist\_per,allplants,family="binomial"),

+ lm(seeds\_per\_fl~phen\_int+meanT+moist\_per+attack,allplants)

+ )

> sem.fit(sem6, data=allplants,

+ corr.errors=c("phen\_int~~Mrub\_sch\_s","phen\_int~~suit\_neigh","suit\_neigh~~Mrub\_sch\_s"))

$Fisher.C

fisher.c df p.value

1 10.5 10 0.398

$AIC

AIC AICc K n

1 66.5 70.321 28 454

> sem.model.fits(sem6)

Class Family Link n R.squared

1 lm gaussian identity 8848 0.1150905

2 negbin Negative Binomial log 8852 0.2089349

3 lm gaussian identity 8852 0.3702739

4 glm binomial logit 8848 0.3774603

5 lm gaussian identity 454 0.1883276

> sem.coefs(sem6, data=allplants,

+ corr.errors=c("phen\_int~~Mrub\_sch\_s","phen\_int~~suit\_neigh","suit\_neigh~~Mrub\_sch\_s"))

response predictor estimate std.error p.value

1 phen\_int meanT -1.58324603 0.252059807 0.0000 \*\*\*

2 phen\_int moist\_per -0.32541471 0.058171568 0.0000 \*\*\*

3 phen\_int meanT:moist\_per 0.01670082 0.003555492 0.0000 \*\*\*

4 Mrub\_sch\_s moist\_per -1.84311995 0.079656232 0.0000 \*\*\*

5 Mrub\_sch\_s meanT:moist\_per 0.10918338 0.004855336 0.0000 \*\*\*

6 Mrub\_sch\_s meanT -6.27995740 0.324828375 0.0000 \*\*\*

7 suit\_neigh meanT:moist\_per 2.87713912 0.077902194 0.0000 \*\*\*

8 suit\_neigh moist\_per -44.94631258 1.274535797 0.0000 \*\*\*

9 suit\_neigh meanT -180.32238027 5.522417433 0.0000 \*\*\*

10 attack suit\_neigh -0.04596958 0.002176858 0.0000 \*\*\*

11 attack phen\_int 0.81552604 0.052724034 0.0000 \*\*\*

12 attack meanT 1.52293721 0.125876522 0.0000 \*\*\*

13 attack moist\_per 0.04279806 0.005372010 0.0000 \*\*\*

14 attack phen\_int:Mrub\_sch\_s 0.03705436 0.014883112 0.0128 \*

15 attack Mrub\_sch\_s -0.13726717 0.074491626 0.0654

16 seeds\_per\_fl attack -197.74492087 20.692221174 0.0000 \*\*\*

17 seeds\_per\_fl phen\_int 14.77029442 9.603402084 0.1247

18 seeds\_per\_fl meanT -26.39084403 23.910346200 0.2703

19 seeds\_per\_fl moist\_per -0.46269965 0.905025548 0.6094

20 ~~ phen\_int ~~ suit\_neigh -0.02217326 NA 0.9815

21 ~~ phen\_int ~~ Mrub\_sch\_s -0.02470386 NA 0.9899

22 ~~ suit\_neigh ~~ Mrub\_sch\_s -0.11533255 NA 1.0000

Model for number of eggs-seeds

> sem7<-list(#with fitness, number of eggs (only pls w eggs)

+ lm(phen\_int~meanT\*moist\_per,allplants),

+ glm.nb(Mrub\_sch\_s~meanT\*moist\_per,allplants),

+ lm(suit\_neigh~meanT\*moist\_per,allplants),

+ glm.nb(n\_eggs\_max~phen\_int\*Mrub\_sch\_s+suit\_neigh+meanT+moist\_per,allplants),

+ lm(seeds\_per\_fl~phen\_int+meanT+moist\_per+n\_eggs\_max,allplants)

+ )

> sem.fit(sem7, data=allplants,

+ corr.errors=c("phen\_int~~Mrub\_sch\_s","phen\_int~~suit\_neigh","suit\_neigh~~Mrub\_sch\_s"))

$missing.paths

missing.path estimate std.error df crit.value p.value

1 n\_eggs\_max ~ meanT\*moist\_per + ... -0.0079 0.0094 8840 -0.8358 0.4033

2 seeds\_per\_fl ~ meanT\*moist\_per + ... -1.9825 1.7275 448 -1.1476 0.2518

3 seeds\_per\_fl ~ Mrub\_sch\_s\*phen\_int + ... -1.8994 3.6999 447 -0.5134 0.6080

4 seeds\_per\_fl ~ Mrub\_sch\_s + ... -1.7271 1.7229 447 -1.0024 0.3167

5 seeds\_per\_fl ~ suit\_neigh + ... -1.8322 1.7365 447 -1.0551 0.2919

$Fisher.C

fisher.c df p.value

1 10.33 10 0.412

$AIC

AIC AICc K n

1 68.33 72.434 29 454

> sem.model.fits(sem7)

Class Family Link n R.squared

1 lm gaussian identity 8848 0.1150905

2 negbin Negative Binomial log 8852 0.2089349

3 lm gaussian identity 8852 0.3702739

4 negbin Negative Binomial log 8848 0.6011241

5 lm gaussian identity 454 0.1448934

> sem.coefs(sem7, data=allplants,

+ corr.errors=c("phen\_int~~Mrub\_sch\_s","phen\_int~~suit\_neigh","suit\_neigh~~Mrub\_sch\_s"))

response predictor estimate std.error p.value

1 phen\_int meanT -1.58324603 0.252059807 0.0000 \*\*\*

2 phen\_int moist\_per -0.32541471 0.058171568 0.0000 \*\*\*

3 phen\_int meanT:moist\_per 0.01670082 0.003555492 0.0000 \*\*\*

4 Mrub\_sch\_s moist\_per -1.84311995 0.079656232 0.0000 \*\*\*

5 Mrub\_sch\_s meanT:moist\_per 0.10918338 0.004855336 0.0000 \*\*\*

6 Mrub\_sch\_s meanT -6.27995740 0.324828375 0.0000 \*\*\*

7 suit\_neigh meanT:moist\_per 2.87713912 0.077902194 0.0000 \*\*\*

8 suit\_neigh moist\_per -44.94631258 1.274535797 0.0000 \*\*\*

9 suit\_neigh meanT -180.32238027 5.522417433 0.0000 \*\*\*

10 n\_eggs\_max suit\_neigh -0.04966937 0.001923348 0.0000 \*\*\*

11 n\_eggs\_max phen\_int 0.94640288 0.049085251 0.0000 \*\*\*

12 n\_eggs\_max meanT 1.67063959 0.125659397 0.0000 \*\*\*

13 n\_eggs\_max moist\_per 0.05328452 0.005562871 0.0000 \*\*\*

14 n\_eggs\_max phen\_int:Mrub\_sch\_s 0.03518298 0.014227901 0.0134 \*

15 n\_eggs\_max Mrub\_sch\_s -0.10912583 0.069596512 0.1169

16 seeds\_per\_fl n\_eggs\_max -17.19076701 2.150843913 0.0000 \*\*\*

17 seeds\_per\_fl meanT -34.29677319 24.492229298 0.1621

18 seeds\_per\_fl phen\_int 11.11823135 9.846449546 0.2594

19 seeds\_per\_fl moist\_per -0.44744678 0.929372082 0.6304

20 ~~ phen\_int ~~ suit\_neigh -0.02217326 NA 0.9815

21 ~~ phen\_int ~~ Mrub\_sch\_s -0.02470386 NA 0.9899

22 ~~ suit\_neigh ~~ Mrub\_sch\_s -0.11533255 NA 1.0000

+ Check autocorrelation in residuals of all models / add eigenvectors?