Veg h 🡪 Soil T

Temperature decreases and is less variable with higher vegetation – no interaction veg h\*pop





Soil T 🡪 Phen

Plants in warmer microsites have an earlier phenology (significative temp\*pop only for min T)









BUT: Phenology and vegetation height



Call:

glm(formula = phen\_index ~ meanT + veg\_h\_mean + population, family = "gaussian",

data = data3)

Estimate Std. Error t value Pr(>|t|)

(Intercept) -1.203243 0.582494 -2.066 0.03973 \*

meanT 0.130341 0.032077 4.063 6.20e-05 \*\*\*

veg\_h\_mean 0.012866 0.003101 4.149 4.37e-05 \*\*\*

populationRemmene 0.244110 0.084439 2.891 0.00412 \*\*

populationTånga Hed 1.044814 0.088497 11.806 < 2e-16 \*\*\*

Interaction meant x Veg h not significant

glm(formula = phen\_index ~ meanT + population, family = "gaussian",

data = data3)

Estimate Std. Error t value Pr(>|t|)

(Intercept) -0.02730 0.52260 -0.052 0.95838

meanT 0.08675 0.03112 2.787 0.00566 \*\*

populationRemmene 0.14204 0.08295 1.712 0.08788 .

populationTånga Hed 0.90896 0.08443 10.766 < 2e-16 \*\*\*

Veg h and Soil T 🡪 Ants

Ant abundance increases with vegetation height and decreases with temperature in all 3 populations





|  |  |
| --- | --- |
|  |  |

Interaction effect?

glm.nb(formula = n\_redants ~ veg\_h\_mean \* meanT + population,

data = data3, na.action = "na.fail", init.theta = 0.4779976853,

link = log)

Estimate Std. Error z value Pr(>|z|)

(Intercept) 12.298417 3.690266 3.333 0.00086 \*\*\*

veg\_h\_mean -0.218548 0.106595 -2.050 0.04034 \*

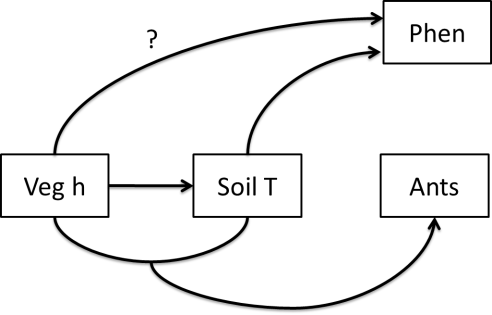
meanT -0.694061 0.212771 -3.262 0.00111 \*\*

populationRemmene -0.966343 0.247299 -3.908 9.32e-05 \*\*\*

populationTånga Hed 1.568307 0.253605 6.184 6.25e-10 \*\*\*

veg\_h\_mean:meanT 0.014407 0.006255 2.303 0.02126 \*

SEMs



#1 Effects of temperature and vegetation height on phenology

> sem1<-list(

+ glm.nb(n\_redants~meanT+veg\_h\_mean+meanT:veg\_h\_mean+pop,data=data3),

+ glm(meanT~veg\_h\_mean+pop,family="gaussian",data=data3),

+ glm(phen\_index~meanT+veg\_h\_mean+pop,family="gaussian",data=data3)

+ )

> sem.fit(sem1,data3,corr.errors=c("meanT:veg\_h\_mean~~meanT",

+ "meanT:veg\_h\_mean~~veg\_h\_mean"))#p=0.297

> sem.coefs(sem1,data3)

response predictor estimate std.error p.value

1 n\_redants popT 1.56830732 0.253604788 0.0000 \*\*\*

2 n\_redants popR -0.96634317 0.247298733 0.0001 \*\*\*

3 n\_redants meanT -0.69406081 0.212771197 0.0011 \*\*

4 n\_redants meanT:veg\_h\_mean 0.01440749 0.006255013 0.0213 \*

5 n\_redants veg\_h\_mean -0.21854803 0.106595191 0.0403 \*

6 meanT popR -0.91563058 0.143207350 0.0000 \*\*\*

7 meanT veg\_h\_mean -0.03166011 0.005300288 0.0000 \*\*\*

8 meanT popT 0.60639226 0.156171144 0.0001 \*\*\*

9 phen\_index popT 1.04481351 0.088496595 0.0000 \*\*\*

10 phen\_index veg\_h\_mean 0.01286648 0.003101044 0.0000 \*\*\*

11 phen\_index meanT 0.13034093 0.032077101 0.0001 \*\*\*

12 phen\_index popR 0.24411021 0.084438713 0.0041 \*\*

#2 Only effect of temperature on phenology

> sem.fit(sem1,data3,corr.errors=c("meanT:veg\_h\_mean~~meanT",

+"meanT:veg\_h\_mean~~veg\_h\_mean","phen\_index~~veg\_h\_mean"))#p=0.191

> sem.coefs(sem1,data3)

#Considered as a correlated error rather than a directed causal path (parallel responses to unmeasured variables – Duffy et al. 2015)

response predictor estimate std.error p.value

1 n\_redants popT 1.56830732 0.253604788 0.0000 \*\*\*

2 n\_redants popR -0.96634317 0.247298733 0.0001 \*\*\*

3 n\_redants meanT -0.69406081 0.212771197 0.0011 \*\*

4 n\_redants meanT:veg\_h\_mean 0.01440749 0.006255013 0.0213 \*

5 n\_redants veg\_h\_mean -0.21854803 0.106595191 0.0403 \*

6 meanT popR -0.91563058 0.143207350 0.0000 \*\*\*

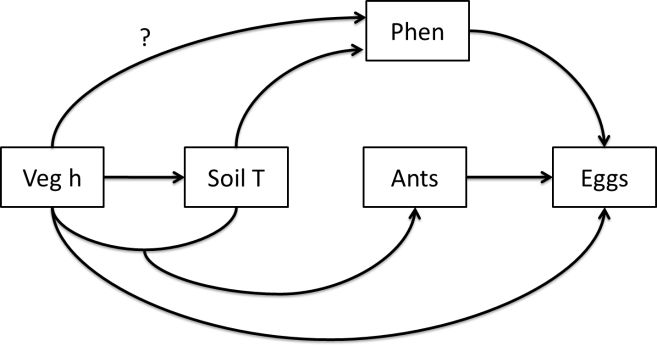
7 meanT veg\_h\_mean -0.03166011 0.005300288 0.0000 \*\*\*

8 meanT popT 0.60639226 0.156171144 0.0001 \*\*\*

9 phen\_index popT 0.90896355 0.084431271 0.0000 \*\*\*

10 phen\_index meanT 0.08675499 0.031124536 0.0057 \*\*

11 phen\_index popR 0.14204195 0.082951468 0.0879



glm.nb(formula = n\_eggs\_max ~ phen\_index + veg\_h\_mean + n\_redants +

pop, data = data3, init.theta = 0.4642244756, link = log)

Estimate Std. Error z value Pr(>|z|)

(Intercept) -0.13235 0.37904 -0.349 0.727

phen\_index 0.73160 0.16275 4.495 6.95e-06 \*\*\*

veg\_h\_mean 0.00234 0.00869 0.269 0.788

n\_redants 0.01706 0.01041 1.638 0.101

popR 0.21235 0.23045 0.921 0.357

popT -0.05810 0.32448 -0.179 0.858

glm.nb(formula = n\_eggs\_max ~ phen\_index + veg\_h\_mean + n\_redants +

meanT + pop, data = data3, init.theta = 0.5060063245, link = log)

Estimate Std. Error z value Pr(>|z|)

(Intercept) 6.543892 1.657310 3.949 7.86e-05 \*\*\*

phen\_index 0.857630 0.161693 5.304 1.13e-07 \*\*\*

veg\_h\_mean -0.010782 0.009065 -1.189 0.2343

n\_redants 0.018578 0.010119 1.836 0.0664 .

meanT -0.395687 0.093832 -4.217 2.48e-05 \*\*\*

popR 0.093138 0.240960 0.387 0.6991

popT 0.204362 0.318250 0.642 0.5208

> sem1<-list(

+ glm.nb(n\_eggs\_max~phen\_index+veg\_h\_mean+n\_redants+pop,data=data3),

+ glm.nb(n\_redants~meanT+veg\_h\_mean+meanT:veg\_h\_mean+pop,data=data3),

+ glm(meanT~veg\_h\_mean+pop,family="gaussian",data=data3),

+ glm(phen\_index~meanT+pop,family="gaussian",data=data3)

+ )

> sem.fit(sem1,data3,corr.errors=c("meanT:veg\_h\_mean~~meanT",

+ "phen\_index~~veg\_h\_mean","meanT:veg\_h\_mean~~veg\_h\_mean"))#p=0

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

1 n\_eggs\_max ~ meanT\*veg\_h\_mean + ... 0.0010 0.0063 293 0.1528 0.8786

2 n\_eggs\_max ~ meanT + ... -0.3957 0.0938 294 -4.2170 0.0000 \*\*\*

3 n\_redants ~ phen\_index + ... 0.0140 0.0062 294 2.2516 0.0243 \*

$Fisher.C

fisher.c df p.value

1 28.9 6 0

sem.fit(sem1,data3,corr.errors=c("meanT:veg\_h\_mean~~meanT","phen\_index~~veg\_h\_mean","meanT:veg\_h\_mean~~veg\_h\_mean","meanT~~n\_eggs\_max"))#p=0.024

> sem.coefs(sem1,data3)

response predictor estimate std.error p.value

1 n\_eggs\_max phen\_index 0.731601543 0.162751945 0.0000 \*\*\*

2 n\_eggs\_max n\_redants 0.017060102 0.010414109 0.1014

3 n\_eggs\_max popR 0.212353910 0.230446989 0.3568

4 n\_eggs\_max veg\_h\_mean 0.002339562 0.008690180 0.7878

5 n\_eggs\_max popT -0.058105385 0.324483672 0.8579

6 n\_redants popT 1.568307318 0.253604788 0.0000 \*\*\*

7 n\_redants popR -0.966343166 0.247298733 0.0001 \*\*\*

8 n\_redants meanT -0.694060806 0.212771197 0.0011 \*\*

9 n\_redants meanT:veg\_h\_mean 0.014407488 0.006255013 0.0213 \*

10 n\_redants veg\_h\_mean -0.218548026 0.106595191 0.0403 \*

11 meanT popR -0.915630584 0.143207350 0.0000 \*\*\*

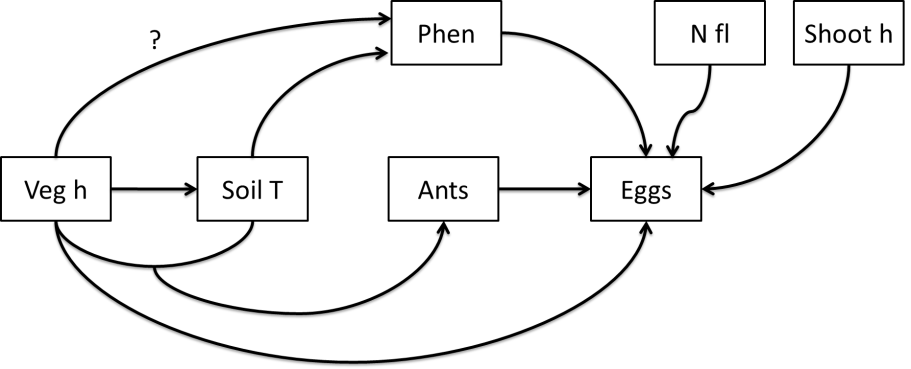
12 meanT veg\_h\_mean -0.031660109 0.005300288 0.0000 \*\*\*

13 meanT popT 0.606392258 0.156171144 0.0001 \*\*\*

14 phen\_index popT 0.908963545 0.084431271 0.0000 \*\*\*

15 phen\_index meanT 0.086754994 0.031124536 0.0057 \*\*

16 phen\_index popR 0.142041950 0.082951468 0.0879



> sem1<-list(

+ glm.nb(n\_eggs\_max~phen\_index+shoot\_h+n\_fl\_corrected+veg\_h\_mean+n\_redants+pop,data=data3),

+ glm.nb(n\_redants~meanT+veg\_h\_mean+meanT:veg\_h\_mean+pop,data=data3),

+ glm(meanT~veg\_h\_mean+pop,family="gaussian",data=data3),

+ glm(phen\_index~meanT+pop,family="gaussian",data=data3)

+ )

> sem.fit(sem1,data3,corr.errors=c("meanT:veg\_h\_mean~~meanT","n\_eggs\_max~~meanT",

+ "phen\_index~~shoot\_h","phen\_index~~n\_fl\_corrected","shoot\_h~~n\_fl\_corrected",

+ "phen\_index~~veg\_h\_mean","meanT:veg\_h\_mean~~veg\_h\_mean"))

$missing.paths

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

1 meanT ~ shoot\_h + ... -0.0465 0.0095 296 -4.8761 0.0000 \*\*\*

2 n\_redants ~ shoot\_h + ... 0.0146 0.0063 294 2.3403 0.0193 \*

3 meanT ~ n\_fl\_corrected + ... -0.0336 0.0239 296 -1.4038 0.1614

4 n\_redants ~ n\_fl\_corrected + ... 0.0158 0.0063 294 2.5249 0.0116 \*

5 n\_redants ~ phen\_index + ... 0.0140 0.0062 294 2.2516 0.0243 \*

$Fisher.C

fisher.c df p.value

1 54.39 10 0

> sem.coefs(sem1,data3)

response predictor estimate std.error p.value

1 n\_eggs\_max n\_fl\_corrected 0.18884570 0.040647246 0.0000 \*\*\*

2 n\_eggs\_max popT -0.97275903 0.332498189 0.0034 \*\*

3 n\_eggs\_max phen\_index 0.42880524 0.149784984 0.0042 \*\*

4 n\_eggs\_max shoot\_h 0.04052294 0.016847912 0.0162 \*

5 n\_eggs\_max n\_redants 0.02068132 0.009372690 0.0273 \*

6 n\_eggs\_max veg\_h\_mean -0.01975782 0.008966298 0.0276 \*

7 n\_eggs\_max popR 0.14815214 0.208833960 0.4781

8 n\_redants popT 1.56830732 0.253604788 0.0000 \*\*\*

9 n\_redants popR -0.96634317 0.247298733 0.0001 \*\*\*

10 n\_redants meanT -0.69406081 0.212771197 0.0011 \*\*

11 n\_redants meanT:veg\_h\_mean 0.01440749 0.006255013 0.0213 \*

12 n\_redants veg\_h\_mean -0.21854803 0.106595191 0.0403 \*

13 meanT popR -0.91563058 0.143207350 0.0000 \*\*\*

14 meanT veg\_h\_mean -0.03166011 0.005300288 0.0000 \*\*\*

15 meanT popT 0.60639226 0.156171144 0.0001 \*\*\*

16 phen\_index popT 0.90896355 0.084431271 0.0000 \*\*\*

17 phen\_index meanT 0.08675499 0.031124536 0.0057 \*\*

18 phen\_index popR 0.14204195 0.082951468 0.0879

Include missing paths as correlated errors🡪p>0.05

> sem.fit(sem1,data3,corr.errors=c("meanT:veg\_h\_mean~~meanT","n\_eggs\_max~~meanT",

+"phen\_index~~shoot\_h","phen\_index~~n\_fl\_corrected","shoot\_h~~n\_fl\_corrected",

+"phen\_index~~veg\_h\_mean","meanT:veg\_h\_mean~~veg\_h\_mean",

+"meanT~~shoot\_h","n\_redants~~shoot\_h","n\_redants~~n\_fl\_corrected","n\_redants~~phen\_index")) #p=0.161

Tests of correlations

18 ~~ n\_eggs\_max ~~ meanT -0.21703399 NA 0.9999

19 ~~ phen\_index ~~ n\_fl\_corrected 0.26517390 NA 0.0000 \*\*\*

20 ~~ phen\_index ~~ shoot\_h 0.25416534 NA 0.0000 \*\*\*

21 ~~ phen\_index ~~ veg\_h\_mean 0.23443939 NA 0.0000 \*\*\*

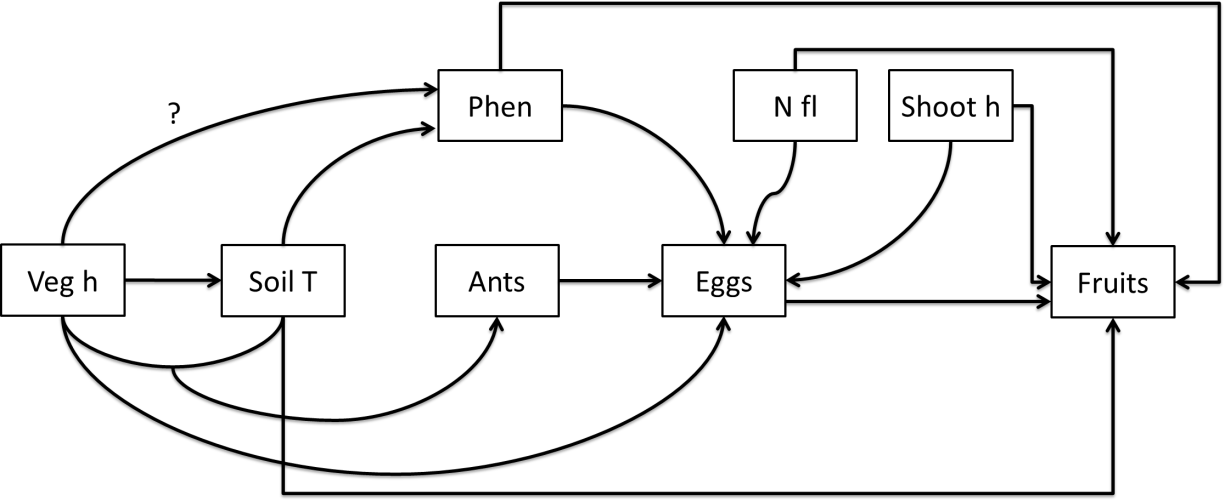
22 ~~ shoot\_h ~~ n\_fl\_corrected 0.58465538 NA 0.0000 \*\*\*

23 ~~ meanT ~~ shoot\_h -0.27267898 NA 1.0000

24 ~~ n\_redants ~~ shoot\_h 0.02451139 NA 0.3359

25 ~~ n\_redants ~~ n\_fl\_corrected -0.06069005 NA 0.8530

26 ~~ n\_redants ~~ phen\_index -0.13502868 NA 0.9905



> sem1<-list(

+ glm(n\_intact\_fruits~phen\_index+n\_fl\_corrected+shoot\_h+meanT+n\_eggs\_max+pop,family="poisson",data=data3),

+ glm.nb(n\_eggs\_max~phen\_index+n\_fl\_corrected+shoot\_h+veg\_h\_mean+n\_redants+pop,data=data3),

+ glm.nb(n\_redants~meanT+veg\_h\_mean+meanT:veg\_h\_mean+pop,data=data3),

+ glm(meanT~veg\_h\_mean+pop,family="gaussian",data=data3),

+ glm(phen\_index~meanT+pop,family="gaussian",data=data3)

+ )

> sem.fit(sem1,data3,corr.errors=c("meanT:veg\_h\_mean~~meanT","n\_eggs\_max~~meanT",

"phen\_index~~n\_redants","phen\_index~~veg\_h\_mean","meanT:veg\_h\_mean~~veg\_h\_mean",

+"phen\_index~~n\_fl\_corrected","shoot\_h~~phen\_index"shoot\_h~~n\_fl\_corrected"))#p=0

$missing.paths

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

1 meanT ~ n\_fl\_corrected + ... -0.0336 0.0239 296 -1.4038 0.1614

2 n\_redants ~ n\_fl\_corrected + ... 0.0158 0.0063 294 2.5249 0.0116 \*

3 meanT ~ shoot\_h + ... -0.0465 0.0095 296 -4.8761 0.0000 \*\*\*

4 n\_redants ~ shoot\_h + ... 0.0146 0.0063 294 2.3403 0.0193 \*

5 n\_intact\_fruits ~ veg\_h\_mean + ... -0.0093 0.0067 292 -1.3874 0.1653

6 n\_intact\_fruits ~ meanT\*veg\_h\_mean + ... -0.0009 0.0054 291 -0.1686 0.8661

7 n\_redants ~ n\_intact\_fruits + ... 0.0148 0.0062 290 2.3951 0.0166 \*

> sem.fit(sem1,data3,corr.errors=c("meanT:veg\_h\_mean~~meanT","n\_eggs\_max~~meanT",

"phen\_index~~n\_redants","phen\_index~~veg\_h\_mean","meanT:veg\_h\_mean~~veg\_h\_mean","phen\_index~~n\_fl\_corrected","shoot\_h~~phen\_index","shoot\_h~~n\_fl\_corrected","meanT~~shoot\_h",

"n\_redants~~n\_fl\_corrected","n\_redants~~shoot\_h","n\_redants~~n\_intact\_fruits"))#p=0.274

> sem.coefs

response predictor estimate std.error p.value

1 n\_intact\_fruits n\_fl\_corrected 0.13149329 0.017657121 0.0000 \*\*\*

2 n\_intact\_fruits n\_eggs\_max -0.05969457 0.008837357 0.0000 \*\*\*

3 n\_intact\_fruits popT 1.30496484 0.218525189 0.0000 \*\*\*

4 n\_intact\_fruits shoot\_h 0.02899276 0.010798151 0.0073 \*\*

5 n\_intact\_fruits phen\_index 0.21111870 0.088907448 0.0176 \*

6 n\_intact\_fruits meanT 0.16610428 0.075236132 0.0273 \*

7 n\_intact\_fruits popR -0.56972417 0.311358614 0.0673

8 n\_eggs\_max n\_fl\_corrected 0.18884570 0.040647246 0.0000 \*\*\*

9 n\_eggs\_max popT -0.97275903 0.332498189 0.0034 \*\*

10 n\_eggs\_max phen\_index 0.42880524 0.149784984 0.0042 \*\*

11 n\_eggs\_max shoot\_h 0.04052294 0.016847912 0.0162 \*

12 n\_eggs\_max n\_redants 0.02068132 0.009372690 0.0273 \*

13 n\_eggs\_max veg\_h\_mean -0.01975782 0.008966298 0.0276 \*

14 n\_eggs\_max popR 0.14815214 0.208833960 0.4781

15 n\_redants popT 1.56830732 0.253604788 0.0000 \*\*\*

16 n\_redants popR -0.96634317 0.247298733 0.0001 \*\*\*

17 n\_redants meanT -0.69406081 0.212771197 0.0011 \*\*

18 n\_redants meanT:veg\_h\_mean 0.01440749 0.006255013 0.0213 \*

19 n\_redants veg\_h\_mean -0.21854803 0.106595191 0.0403 \*

20 meanT popR -0.91563058 0.143207350 0.0000 \*\*\*

21 meanT veg\_h\_mean -0.03166011 0.005300288 0.0000 \*\*\*

22 meanT popT 0.60639226 0.156171144 0.0001 \*\*\*

23 phen\_index popT 0.90896355 0.084431271 0.0000 \*\*\*

24 phen\_index meanT 0.08675499 0.031124536 0.0057 \*\*

25 phen\_index popR 0.14204195 0.082951468 0.0879

26 ~~ n\_eggs\_max ~~ meanT -0.17617706 NA 0.9989

27 ~~ phen\_index ~~ n\_fl\_corrected 0.26517390 NA 0.0000 \*\*\*

28 ~~ phen\_index ~~ veg\_h\_mean 0.23443939 NA 0.0000 \*\*\*

29 ~~ phen\_index ~~ n\_redants -0.11858201 NA 0.9801

30 ~~ shoot\_h ~~ n\_fl\_corrected 0.58465538 NA 0.0000 \*\*\*

31 ~~ shoot\_h ~~ phen\_index 0.26060414 NA 0.0000 \*\*\*

32 ~~ meanT ~~ shoot\_h -0.27267898 NA 1.0000

33 ~~ n\_redants ~~ shoot\_h 0.02451139 NA 0.3359

34 ~~ n\_redants ~~ n\_fl\_corrected -0.06069005 NA 0.8530

35 ~~ n\_redants ~~ n\_intact\_fruits -0.08930343 NA 0.9389