RESULTS FROM FIELD DATA 2015

Summary of the data available

3 populations, approx. 100 plants marked per population (+ some data from the Spanish population not used by now)

Variables calculated for each plant:

|  |  |  |
| --- | --- | --- |
| **Short name variable** | | **Long name / comments** |
| bud\_h | | Bud height (mm) |
| shoot\_h | | Shoot height (cm) |
| veg\_h\_min | | Minimum height of surrounding vegetation (cm) |
| veg\_h\_max | | Maximum height of surrounding vegetation (cm) |
| veg\_h\_mean | Mean height of surrounding vegetation (cm, mean of two previous) | |
| diff\_veg\_h\_max\_shoot\_h | veg\_h\_max- shoot\_h (negative values indicate that shoot is higher than vegetation) | |
| diff\_veg\_h\_mean\_shoot\_h | veg\_h\_mean- shoot\_h (negative values indicate that shoot is higher than vegetation) | |
| higher\_veg\_max | binary variable indicating if plant shoot is higher than max. vegetation (1) or not (0) | |
| higher\_veg\_mean | binary variable indicating if plant shoot is higher than mean vegetation (1) or not (0) | |
| phen\_index | | phenology index (as in last paper) |
| most\_adv | | state of the most advanced bud (as in last paper) |
| fr\_int\_h\_max | | height of intact fruit (mm) |
| fr\_pred\_h\_max | | height of predated fruit (mm) |
| n\_intact\_fruits\_max | | number of intact fruits |
| n\_fruits\_total\_max | | total number of fruits (intact + predated) |
| n\_predated | | number of predated (fruits + flowers + buds with signs of larvae attack) |
| prop\_pred | | n\_predated / n\_fl\_corrected |
| n\_fl\_corrected | | total number of flowers (including buds that did not open into flowers) |
| fruit\_set | | n\_fruits\_total\_max/ n\_fl\_corrected (proportion of flowers setting fruit) |
| n\_eggs\_max | | máximum number of eggs observed |
| attack | | binary variable indicating if the plant was attacked (1, at least one egg observed) or not (0, no eggs observed) |
| n\_redants | | máximum number of *Myrmica* ants observed |
| redants\_pres | | binary variable indicating if *Myrmica* ants were observed (1) or not (0) |
| n\_blackants | | máximum number of ants from other genera observed |
| dist\_closest\_redants | | distance to the closes plant with *Myrmica* ants observed at least once (BIASED because it only takes into account the marked plants) |
| avg\_d\_mean | | average value of the daily mean temperature |
| avg\_d\_sd | | average value of the daily standard deviation of temperature |
| avg\_d\_min | | average value of the daily minimum temperature |
| avg\_d\_max | | average value of the daily máximum temperature |

Correlations (highlighted values>0.6)

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | bud\_h | shoot\_h | diff\_veg\_h\_mean\_shoot\_h | phen\_index | most\_adv | fr\_int\_h\_max | fr\_pred\_h\_max | n\_intact\_fruits\_max | n\_fruits\_total\_max | n\_predated | fruit\_set | n\_fl\_corrected | n\_eggs\_max | n\_redants | avg\_d\_mean |
| bud\_h | 1,00 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| shoot\_h | 0,40 | 1,00 |  |  |  |  |  |  |  |  |  |  |  |  |  |
| diff\_veg\_h\_mean\_shoot\_h | -0,42 | -0,18 | 1,00 |  |  |  |  |  |  |  |  |  |  |  |  |
| phen\_index | 0,87 | 0,26 | -0,34 | 1,00 |  |  |  |  |  |  |  |  |  |  |  |
| most\_adv | 0,93 | 0,34 | -0,38 | 0,92 | 1,00 |  |  |  |  |  |  |  |  |  |  |
| fr\_int\_h\_max | 0,41 | 0,13 | -0,07 | 0,38 | 0,37 | 1,00 |  |  |  |  |  |  |  |  |  |
| fr\_pred\_h\_max | 0,44 | 0,04 | -0,23 | 0,44 | 0,43 | 0,30 | 1,00 |  |  |  |  |  |  |  |  |
| n\_intact\_fruits\_max | 0,59 | 0,33 | -0,39 | 0,53 | 0,56 | 0,27 | 0,27 | 1,00 |  |  |  |  |  |  |  |
| n\_fruits\_total\_max | 0,69 | 0,40 | -0,43 | 0,62 | 0,65 | 0,33 | 0,31 | 0,93 | 1,00 |  |  |  |  |  |  |
| n\_predated | 0,51 | 0,48 | -0,27 | 0,38 | 0,48 | 0,15 | 0,09 | 0,11 | 0,35 | 1,00 |  |  |  |  |  |
| fruit\_set | 0,47 | 0,19 | -0,28 | 0,51 | 0,45 | 0,24 | 0,23 | 0,70 | 0,74 | 0,07 | 1,00 |  |  |  |  |
| n\_fl\_corrected | 0,74 | 0,57 | -0,44 | 0,53 | 0,69 | 0,24 | 0,18 | 0,70 | 0,77 | 0,60 | 0,35 | 1,00 |  |  |  |
| n\_eggs\_max | 0,47 | 0,41 | -0,24 | 0,33 | 0,43 | 0,20 | -0,03 | 0,06 | 0,20 | 0,75 | -0,06 | 0,56 | 1,00 |  |  |
| n\_redants | 0,16 | 0,13 | -0,08 | 0,11 | 0,14 | -0,06 | 0,05 | 0,14 | 0,11 | 0,05 | 0,08 | 0,16 | 0,11 | 1,00 |  |
| avg\_d\_mean | 0,51 | -0,05 | -0,40 | 0,53 | 0,51 | 0,28 | 0,32 | 0,51 | 0,52 | 0,03 | 0,51 | 0,37 | 0,01 | 0,22 | 1,00 |

Objectives / questions (this is just something to start with!)

1) What are the effects of plant traits (phenology, flower production, height), environmental context (soil temperature, surrounding vegetation) and community context (ants) on predispersal seed predation (probability of attack, intensity)?

H1: Plants are more prone to be attacked by the butterfly (and the interaction is more intense) when they show an early phenology and a high number of flowers, when they are taller than the surrounding vegetation and when ants are present in the proximity of the plant. Can we expect any direct effect of soil temperature?

2) What are the (direct / indirect) effects of plant traits and context on fitness (fruit / seed production) / (fruit / seed set)?

H2: Higher soil temperatures (speeding up fruit maturation?) and higher flower production directly increase fitness. The effects of phenology, height and ants are indirect effects through seed predation (plants flowering early, being higher than the surrounding vegetation and having high ant abundance have higher seed predation and therefore lower fitness).

3) What is the relative importance of plant traits vs. context for explaining the variation in predispersal seed predation? What is the relative importance of plant traits, context and seed predation for explaining the variation in plant fitness? (variation partitioning)

H3: … We could hypothesize that the context where the interaction occurs is (nearly) as important as plant traits for explaining variation in seed predation.

4) Does temperature (environmental context) determine plant traits (e.g. phenology) and ant abundance (community context)?

H4: When soil temperature is higher, plants flower earlier and ants are more abundant.

There are differences between the three study populations in all the variables (tests not shown, but the effect of population was significant in all of them)



1) Effects of plant traits, environmental and community context on seed predation

First constructed a model (GLM) including the interactions of all variables \* population (results not shown), then a model were only the significant interactions were kept, and finally a mixed model (GLMM) where population was included as a random effect. The best model was chosen using AIC.

Explanatory variables were standardized before including them in the model (z.) in order to improve the interpretation of model coefficients.

I also fitted SEM/path models in order to distinguish between direct / indirect effects (just shown a couple of examples below). But I was thinking if it makes sense to use data from 3 populations in this kind of models, as interactions or random effects cannot be included. It seems right if there are no interactions between population and other variables, but I am not sure about other cases. I think that you can at least include random effects using some more advanced methods (e.g. piecewise SEM), but I still don’t know how to do this.

1.1) Models for probability of attack (none of the interactions were significant so using mixed model with population as a random effect).

> summary(model2c)

Generalized linear mixed model fit by maximum likelihood (Laplace Approximation) ['glmerMod']

Family: binomial ( logit )

Formula: attack ~ z.shoot\_h + z.diff\_veg\_h\_mean\_shoot\_h + z.most\_adv +

z.n\_fl\_corrected + z.n\_redants + z.avg\_d\_mean + (1 | population)

AIC BIC logLik deviance df.resid

326.1 355.8 -155.0 310.1 295

Scaled residuals:

Min 1Q Median 3Q Max

-12.4808 -0.6932 0.2653 0.6376 3.5744

Random effects:

Groups Name Variance Std.Dev.

population (Intercept) 0 0

Number of obs: 303, groups: population, 3

Fixed effects:

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

(Intercept) 0.54563 0.14634 3.729 0.000193 \*\*\*

z.shoot\_h -0.03885 0.18430 -0.211 0.833052

z.diff\_veg\_h\_mean\_shoot\_h -0.87003 0.19809 -4.392 1.12e-05 \*\*\*

z.most\_adv 0.69724 0.22491 3.100 0.001934 \*\*

z.n\_fl\_corrected 0.72785 0.29464 2.470 0.013499 \*

z.n\_redants 0.13257 0.15169 0.874 0.382142

z.avg\_d\_mean -1.04448 0.20091 -5.199 2.01e-07 \*\*\*

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Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

> r.squaredLR(model2c,null.RE=T) #R2 for fixed factors

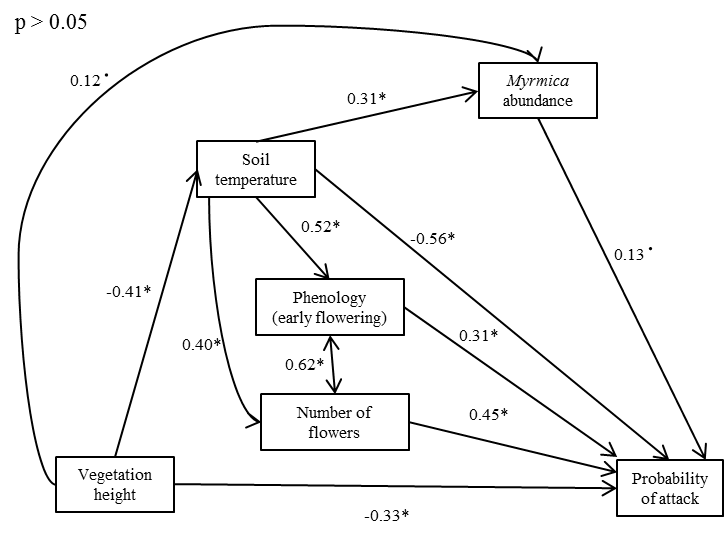
[1] 0.256324

attr(,"adj.r.squared")

[1] 0.3498212

According to this model, the probability of attack decreases with the difference between height of surrounding vegetation and shoot height (i.e. increases when the shoot protrudes out of the vegetation). The probability of attack increases with early flowering and with number of flowers, and decreases with soil temperature (not sure how to explain this effect!). There is no effect of *Myrmica* abundance and of shoot height. These effects are constant among the 3 populations studied (although if the model is fitted separately for each population, different effects turn out to be significant in each case – effect of sample size?).

SEM model



1.2) Models for interaction intensity (measured as number of eggs per plant)

Model with significant interactions (observation-level random effect “id” included to avoid overdispersion)

> summary(model2eg\_b)

Generalized linear mixed model fit by maximum likelihood (Laplace Approximation) ['glmerMod']

Family: poisson ( log )

Formula: n\_eggs\_max ~ z.shoot\_h + z.diff\_veg\_h\_mean\_shoot\_h + z.most\_adv +

z.n\_fl\_corrected + z.n\_redants + z.avg\_d\_mean + population +

population:z.diff\_veg\_h\_mean\_shoot\_h + population:z.n\_redants + population:z.avg\_d\_mean + (1 | id)

Control: glmerControl(optimizer = "bobyqa")

AIC BIC logLik deviance df.resid

1406.6 1466.1 -687.3 1374.6 287

Scaled residuals:

Min 1Q Median 3Q Max

-1.4463 -0.6225 -0.1114 0.2226 2.6411

Random effects:

Groups Name Variance Std.Dev.

id (Intercept) 1.238 1.113

Number of obs: 303, groups: id, 303

Fixed effects:

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

(Intercept) 0.86205 0.19498 4.421 9.82e-06 \*\*\*

z.shoot\_h 0.04383 0.11290 0.388 0.697869

z.diff\_veg\_h\_mean\_shoot\_h -1.37586 0.27465 -5.009 5.46e-07 \*\*\*

z.most\_adv 0.63901 0.12848 4.973 6.58e-07 \*\*\*

z.n\_fl\_corrected 0.39215 0.13114 2.990 0.002788 \*\*

z.n\_redants 0.60193 0.19015 3.166 0.001548 \*\*

z.avg\_d\_mean -1.19987 0.20300 -5.911 3.41e-09 \*\*\*

populationRemmene 0.54950 0.45376 1.211 0.225902

populationTånga Hed -0.10506 0.45532 -0.231 0.817526

z.diff\_veg\_h\_mean\_shoot\_h:populationRemmene 0.89966 0.33048 2.722 0.006483 \*\*

z.diff\_veg\_h\_mean\_shoot\_h:populationTånga Hed 1.10345 0.33067 3.337 0.000847 \*\*\*

z.n\_redants:populationRemmene -0.02753 0.42343 -0.065 0.948156

z.n\_redants:populationTånga Hed -0.53188 0.21434 -2.481 0.013086 \*

z.avg\_d\_mean:populationRemmene 1.41520 0.39750 3.560 0.000370 \*\*\*

z.avg\_d\_mean:populationTånga Hed 0.36233 0.37431 0.968 0.333052

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Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

> r.squaredLR(model2eg\_b,null.RE=T) #R2 for fixed factors

[1] 0.4279207

attr(,"adj.r.squared")

[1] 0.4305583

GLMM with population as a random effect (observation-level random effect “id” also included)

> summary(model2eg\_c)

Generalized linear mixed model fit by maximum likelihood (Laplace Approximation) ['glmerMod']

Family: poisson ( log )

Formula: n\_eggs\_max ~ z.shoot\_h + z.diff\_veg\_h\_mean\_shoot\_h + z.most\_adv +

z.n\_fl\_corrected + z.n\_redants + z.avg\_d\_mean + (1 | population) + (1 | id)

Control: glmerControl(optimizer = "bobyqa")

AIC BIC logLik deviance df.resid

1421.3 1454.7 -701.6 1403.3 294

Scaled residuals:

Min 1Q Median 3Q Max

-1.41272 -0.59011 -0.07325 0.24262 1.31300

Random effects:

Groups Name Variance Std.Dev.

id (Intercept) 1.469 1.212

population (Intercept) 0.000 0.000

Number of obs: 303, groups: id, 303; population, 3

Fixed effects:

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

(Intercept) 0.432467 0.105354 4.105 4.05e-05 \*\*\*

z.shoot\_h 0.003174 0.113286 0.028 0.977648

z.diff\_veg\_h\_mean\_shoot\_h -0.517654 0.120010 -4.313 1.61e-05 \*\*\*

z.most\_adv 0.620472 0.125915 4.928 8.32e-07 \*\*\*

z.n\_fl\_corrected 0.455813 0.135997 3.352 0.000803 \*\*\*

z.n\_redants 0.184710 0.084908 2.175 0.029600 \*

z.avg\_d\_mean -0.785035 0.120616 -6.509 7.59e-11 \*\*\*

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Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

> r.squaredLR(model2eg\_c,null.RE=T) #R2 for fixed factors

[1] 0.3544446

attr(,"adj.r.squared")

[1] 0.3566879

> AIC(model2eg\_b,model2eg\_c)

df AIC

model2eg\_b 16 1406.631 #AIC is lower for the model with interactions

model2eg\_c 9 1421.277

The model with interactions seems to be better. According to this model, earlier flowering phenologies and higher numbers of flowers increase interaction intensity measured as number of eggs per plant (and these effects do not differ between populations). Not sure how to interpret the significant interactions with population for the other effects though, as population “Högjsön” is used as a reference level for the categorical factor “population”. So as I understand, these effects should be interpreted as the difference in the slopes of each variable between a certain population and the reference population? And then should we ignore the significance of the main effects?

1.3) Models for interaction intensity (measured as number of predated fruits, flowers and buds)

Model with significant interactions (GLM)

> summary(model2pred\_b)

Call:

glm(formula = n\_predated ~ z.shoot\_h + z.diff\_veg\_h\_mean\_shoot\_h +

z.most\_adv + z.n\_fl\_corrected + z.n\_redants + z.avg\_d\_mean +

population + population:z.avg\_d\_mean, family = "poisson",

na.action = "na.fail")

Deviance Residuals:

Min 1Q Median 3Q Max

-3.9582 -0.9319 -0.2290 0.5150 3.3239

Coefficients:

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

(Intercept) 0.006148 0.145660 0.042 0.96634

z.shoot\_h 0.228932 0.071854 3.186 0.00144 \*\*

z.diff\_veg\_h\_mean\_shoot\_h -0.249440 0.078796 -3.166 0.00155 \*\*

z.most\_adv 0.531982 0.079828 6.664 2.66e-11 \*\*\*

z.n\_fl\_corrected 0.203166 0.066461 3.057 0.00224 \*\*

z.n\_redants 0.050188 0.052928 0.948 0.34302

z.avg\_d\_mean -0.633319 0.151018 -4.194 2.74e-05 \*\*\*

populationRemmene 0.063640 0.300064 0.212 0.83204

populationTånga Hed -0.061155 0.298630 -0.205 0.83774

z.avg\_d\_mean:populationRemmene 0.501455 0.282350 1.776 0.07573 .

z.avg\_d\_mean:populationTånga Hed 0.010105 0.253139 0.040 0.96816

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Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for poisson family taken to be 1)

Null deviance: 593.09 on 302 degrees of freedom

Residual deviance: 300.96 on 292 degrees of freedom

AIC: 771.64

Number of Fisher Scoring iterations: 5

> r.squaredLR(model2pred\_b)

[1] 0.6186784

attr(,"adj.r.squared")

[1] 0.6392124

The interaction z.avg\_d\_mean\*population was significant in the model with all interactions, but not here. Still this model gets a lower AIC than the GLMM (see below)

GLMM with population as a random effect

> summary(model2pred\_c)

Generalized linear mixed model fit by maximum likelihood (Laplace Approximation) ['glmerMod']

Family: poisson ( log )

Formula: n\_predated ~ z.shoot\_h + z.diff\_veg\_h\_mean\_shoot\_h + z.most\_adv +

z.n\_fl\_corrected + z.n\_redants + z.avg\_d\_mean + (1 | population)

AIC BIC logLik deviance df.resid

774.6 804.3 -379.3 758.6 295

Scaled residuals:

Min 1Q Median 3Q Max

-2.8112 -0.6998 -0.2286 0.5746 4.7714

Random effects:

Groups Name Variance Std.Dev.

population (Intercept) 0 0

Number of obs: 303, groups: population, 3

Fixed effects:

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

(Intercept) -0.12594 0.06727 -1.872 0.061198 .

z.shoot\_h 0.23178 0.06795 3.411 0.000647 \*\*\*

z.diff\_veg\_h\_mean\_shoot\_h -0.19977 0.07127 -2.803 0.005064 \*\*

z.most\_adv 0.48084 0.07153 6.722 1.79e-11 \*\*\*

z.n\_fl\_corrected 0.22519 0.06416 3.510 0.000449 \*\*\*

z.n\_redants 0.05415 0.04905 1.104 0.269694

z.avg\_d\_mean -0.44752 0.07335 -6.101 1.05e-09 \*\*\*

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Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

> r.squaredLR(model2pred\_c,null.RE=T) #R2 for fixed factors

[1] 0.5578141

attr(,"adj.r.squared")

[1] 0.5787419

> AIC(model2pred\_b,model2pred\_c)

df AIC

model2pred\_b 11 771.6353 #AIC is lower for the model with interactions

model2pred\_c 8 774.6377

According to this model, predation intensity increases with shoot height, early flowering phenology and number of flowers, and decreases with the difference between height of surrounding vegetation and shoot height (i.e. increases when the shoot protrudes out of the vegetation) and with soil temperature. There is no effect of *Myrmica* abundance. These effects are constant among the 3 populations studied (although if the model is fitted separately for each population, different effects turn out to be significant in each case – effect of sample size?).

1.4) Models for interaction intensity (measured as proportion of predated fruits, flowers and buds)

Model with significant interactions (observation-level random effect “id” included to avoid overdispersion)

> summary(model2pred\_prop\_b)

Generalized linear mixed model fit by maximum likelihood (Laplace Approximation) ['glmerMod']

Family: binomial ( logit )

Formula: prop\_pred ~ z.shoot\_h + z.diff\_veg\_h\_mean\_shoot\_h + z.most\_adv +

z.n\_fl\_corrected + z.n\_redants + z.avg\_d\_mean + population + population:z.avg\_d\_mean + (1 | id)

AIC BIC logLik deviance df.resid

649.7 694.2 -312.8 625.7 291

Scaled residuals:

Min 1Q Median 3Q Max

-2.3343 -0.6612 -0.2202 0.5258 3.2603

Random effects:

Groups Name Variance Std.Dev.

id (Intercept) 8.264e-17 9.091e-09

Number of obs: 303, groups: id, 303

Fixed effects:

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

(Intercept) -1.05832 0.16276 -6.502 7.92e-11 \*\*\*

z.shoot\_h 0.11229 0.08448 1.329 0.18377

z.diff\_veg\_h\_mean\_shoot\_h -0.23839 0.09260 -2.574 0.01004 \*

z.most\_adv 0.44919 0.09375 4.791 1.66e-06 \*\*\*

z.n\_fl\_corrected -0.16257 0.08079 -2.012 0.04419 \*

z.n\_redants 0.02104 0.06075 0.346 0.72904

z.avg\_d\_mean -0.47493 0.16824 -2.823 0.00476 \*\*

populationRemmene -0.10054 0.35443 -0.284 0.77666

populationTånga Hed -0.13025 0.32453 -0.401 0.68816

z.avg\_d\_mean:populationRemmene 0.29427 0.33499 0.878 0.37971

z.avg\_d\_mean:populationTånga Hed -0.28917 0.27779 -1.041 0.29789

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Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

> r.squaredLR(model2pred\_prop\_b,null.RE=T)

[1] 0.1784855

attr(,"adj.r.squared")

[1] 0.1992467

The interaction z.avg\_d\_mean\*population was significant in the model with all interactions, but not here. Still this model gets a lower AIC than the GLMM (see below)

GLMM with population as a random effect (observation-level random effect “id” also included)

> summary(model2pred\_prop\_c)

Generalized linear mixed model fit by maximum likelihood (Laplace Approximation) ['glmerMod']

Family: binomial ( logit )

Formula: prop\_pred ~ z.shoot\_h + z.diff\_veg\_h\_mean\_shoot\_h + z.most\_adv +

z.n\_fl\_corrected + z.n\_redants + z.avg\_d\_mean + (1 | population) + (1 | id)

AIC BIC logLik deviance df.resid

651.2 684.6 -316.6 633.2 294

Scaled residuals:

Min 1Q Median 3Q Max

-2.2972 -0.6723 -0.2955 0.4844 2.8873

Random effects:

Groups Name Variance Std.Dev.

id (Intercept) 3.955e-22 1.989e-11

population (Intercept) 0.000e+00 0.000e+00

Number of obs: 303, groups: id, 303; population, 3

Fixed effects:

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

(Intercept) -1.32285 0.07697 -17.187 < 2e-16 \*\*\*

z.shoot\_h 0.14202 0.08066 1.761 0.0783 .

z.diff\_veg\_h\_mean\_shoot\_h -0.17792 0.08510 -2.091 0.0366 \*

z.most\_adv 0.37246 0.08407 4.430 9.41e-06 \*\*\*

z.n\_fl\_corrected -0.15311 0.07872 -1.945 0.0518 .

z.n\_redants 0.02108 0.05670 0.372 0.7101

z.avg\_d\_mean -0.46802 0.08685 -5.389 7.09e-08 \*\*\*

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Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

> r.squaredLR(model2pred\_prop\_c,null.RE=T)

[1] 0.1542574

attr(,"adj.r.squared")

[1] 0.1722851

> AIC(model2pred\_prop\_b,model2pred\_prop\_c)

df AIC

model2pred\_prop\_b 12 649.6502 #AIC is lower for the model with interactions

model2pred\_prop\_c 9 651.1789

According to this model, predation intensity increases with early flowering phenology and number of flowers, and decreases with the difference between height of surrounding vegetation and shoot height (i.e. increases when the shoot protrudes out of the vegetation) and with soil temperature. There is no effect of *Myrmica* abundance or shoot height. These effects are constant among the 3 populations studied (although if the model is fitted separately for each population, different effects turn out to be significant in each case – effect of sample size?).

The effect of the number of flowers is less important here than in the models with n\_predated (as that depended directly on the number of flowers), so maybe prop\_pred is a better measure of the intensity of predation?

2) Effects of plant traits, environmental and community context on fitness

Same procedure as above: first constructed a model including the interactions of all variables \* population (results not shown), then a model were only the significant interactions were kept, and finally a mixed model (GLMM) where population was included as a random effect. The best model was chosen using AIC.

Explanatory variables were standardized before including them in the model (z.) in order to improve the interpretation of model coefficients. Number of intact fruits was used as a measure of fitness by now (although I did not perform classic selection analyses – i.e. fitness is not relativized). I also run models with fruit set as a response variable because I thought that could be also interesting. I still have to count the seeds in the fruits but when this is done I could run similar models using number of seeds as the fitness variable.

2.1) Models for number of intact fruits

Model with significant interactions

> summary(model1fr\_b)

Call:

glm(formula = n\_intact\_fruits\_max ~ z.shoot\_h + z.diff\_veg\_h\_mean\_shoot\_h +

z.most\_adv + z.n\_fl\_corrected + z.n\_redants + attack + population \*

z.avg\_d\_mean, family = "poisson", na.action = "na.fail")

Deviance Residuals:

Min 1Q Median 3Q Max

-2.6959 -0.7274 -0.5238 0.3648 2.6134

Coefficients:

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

(Intercept) -1.22915 0.21085 -5.829 5.56e-09 \*\*\*

z.shoot\_h 0.23438 0.08002 2.929 0.003399 \*\*

z.diff\_veg\_h\_mean\_shoot\_h 0.02052 0.08010 0.256 0.797768

z.most\_adv 0.04930 0.08817 0.559 0.576034

z.n\_fl\_corrected 0.30166 0.06119 4.930 8.22e-07 \*\*\*

z.n\_redants -0.03352 0.04950 -0.677 0.498293

attack.L -0.30979 0.09004 -3.440 0.000581 \*\*\*

populationRemmene -0.65232 0.60214 -1.083 0.278659

populationTånga Hed 1.41707 0.32244 4.395 1.11e-05 \*\*\*

z.avg\_d\_mean 0.62626 0.24675 2.538 0.011147 \*

populationRemmene:z.avg\_d\_mean -1.12790 0.54261 -2.079 0.037649 \*

populationTånga Hed:z.avg\_d\_mean -0.12114 0.29058 -0.417 0.676746

---

Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for poisson family taken to be 1)

Null deviance: 775.13 on 302 degrees of freedom

Residual deviance: 262.39 on 291 degrees of freedom

AIC: 638.13

Number of Fisher Scoring iterations: 5

> r.squaredLR(model1fr\_b)

[1] 0.8158838

attr(,"adj.r.squared")

[1] 0.8361676

GLMM with population as a random effect

> summary(model1fr\_c)

Generalized linear mixed model fit by maximum likelihood (Laplace Approximation) ['glmerMod']

Family: poisson ( log )

Formula: n\_intact\_fruits\_max ~ z.shoot\_h + z.diff\_veg\_h\_mean\_shoot\_h +

z.most\_adv + z.n\_fl\_corrected + z.n\_redants + z.avg\_d\_mean + attack + (1 | population)

AIC BIC logLik deviance df.resid

649.0 682.5 -315.5 631.0 294

Scaled residuals:

Min 1Q Median 3Q Max

-2.1919 -0.5269 -0.3914 0.4067 4.8326

Random effects:

Groups Name Variance Std.Dev.

population (Intercept) 0.3278 0.5726

Number of obs: 303, groups: population, 3

Fixed effects:

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

(Intercept) -0.631462 0.345305 -1.829 0.067443 .

z.shoot\_h 0.246529 0.078475 3.141 0.001681 \*\*

z.diff\_veg\_h\_mean\_shoot\_h 0.002662 0.081320 0.033 0.973887

z.most\_adv 0.064753 0.087769 0.738 0.460658

z.n\_fl\_corrected 0.297333 0.060815 4.889 1.01e-06 \*\*\*

z.n\_redants -0.025830 0.049508 -0.522 0.601851

z.avg\_d\_mean 0.517334 0.139471 3.709 0.000208 \*\*\*

attack.L -0.315828 0.089925 -3.512 0.000445 \*\*\*

---

Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

> r.squaredLR(model1fr\_c,null.RE=T)

[1] 0.2866938

attr(,"adj.r.squared")

[1] 0.3146598

> AIC(model1fr\_b,model1fr\_c)

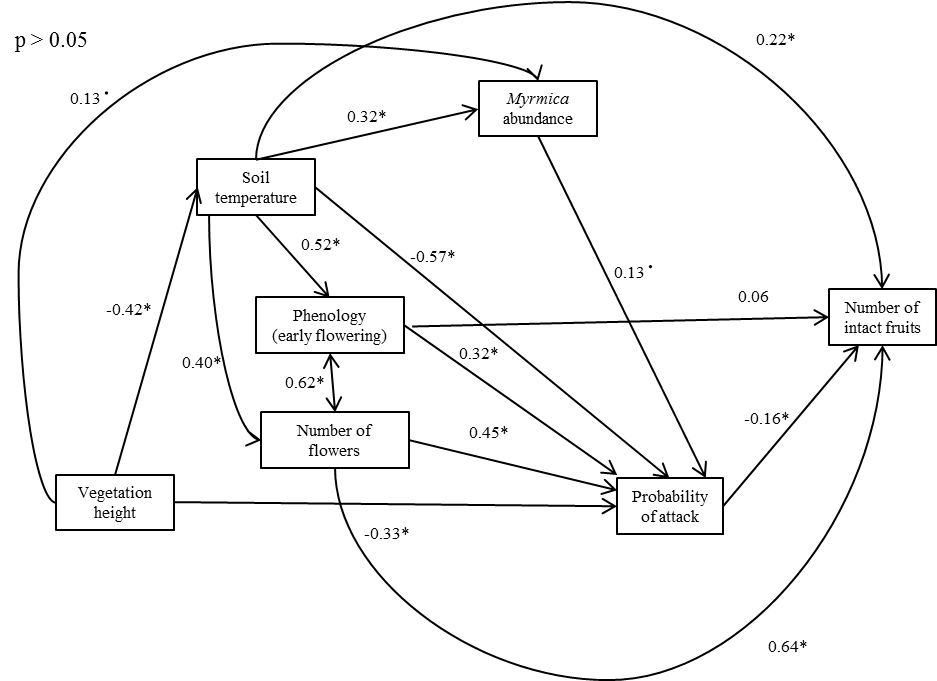
df AIC

model1fr\_b 12 638.1258 #AIC is lower for the model with interactions

model1fr\_c 9 649.0455

The model with interactions is better, and according to this model, plants with higher numbers of flowers and higher shoots have higher fitness (measured as number of intact fruits). Attack by the butterfly decreases plant fitness. There is an effect of population, with plants in Tånga Hed having higher fitness. There is a positive effect of soil temperature, but this effect differs between populations… (again having trouble to interpret interactions here).

SEM model – I think this one is interesting to show the indirect effects through seed predation!



2.2) Models for fruit set

Model with significant interactions

> summary(model1frs\_b)

Call:

glm(formula = fruit\_set1 ~ z.shoot\_h + z.diff\_veg\_h\_mean\_shoot\_h +

z.most\_adv + z.n\_fl\_corrected + z.n\_redants + z.avg\_d\_mean \*

population + attack, family = "binomial", na.action = "na.fail")

Deviance Residuals:

Min 1Q Median 3Q Max

-2.2856 -0.6773 -0.4291 0.3649 2.3464

Coefficients:

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

(Intercept) -2.02438 0.21085 -9.601 < 2e-16 \*\*\*

z.shoot\_h 0.19799 0.08629 2.294 0.021769 \*

z.diff\_veg\_h\_mean\_shoot\_h -0.01862 0.08929 -0.209 0.834824

z.most\_adv 0.19998 0.09421 2.123 0.033772 \*

z.n\_fl\_corrected -0.12000 0.06938 -1.730 0.083675 .

z.n\_redants -0.07423 0.05480 -1.354 0.175596

z.avg\_d\_mean 0.79549 0.24540 3.242 0.001189 \*\*

populationRemmene -0.37703 0.51841 -0.727 0.467055

populationTånga Hed 1.20933 0.33902 3.567 0.000361 \*\*\*

attack.L -0.32346 0.10357 -3.123 0.001789 \*\*

z.avg\_d\_mean:populationRemmene -1.19465 0.48807 -2.448 0.014377 \*

z.avg\_d\_mean:populationTånga Hed -0.59814 0.29833 -2.005 0.044967 \*

---

Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for binomial family taken to be 1)

Null deviance: 371.37 on 302 degrees of freedom

Residual deviance: 207.76 on 291 degrees of freedom

AIC: 574.08

Number of Fisher Scoring iterations: 5

> r.squaredLR(model1frs\_b)

[1] 0.4172277

attr(,"adj.r.squared")

[1] 0.460952

GLMM with population as a random effect

> summary(model1frs\_c)

Generalized linear mixed model fit by maximum likelihood (Laplace Approximation) ['glmerMod']

Family: binomial ( logit )

Formula: fruit\_set1 ~ z.shoot\_h + z.diff\_veg\_h\_mean\_shoot\_h + z.most\_adv +

z.n\_fl\_corrected + z.n\_redants + z.avg\_d\_mean + attack + (1 | population)

AIC BIC logLik deviance df.resid

585.0 618.5 -283.5 567.0 294

Scaled residuals:

Min 1Q Median 3Q Max

-1.8915 -0.5504 -0.3556 0.3562 3.4324

Random effects:

Groups Name Variance Std.Dev.

population (Intercept) 0.09472 0.3078

Number of obs: 303, groups: population, 3

Fixed effects:

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

(Intercept) -1.53208 0.20118 -7.615 2.63e-14 \*\*\*

z.shoot\_h 0.23011 0.08432 2.729 0.00635 \*\*

z.diff\_veg\_h\_mean\_shoot\_h -0.06712 0.09288 -0.723 0.46989

z.most\_adv 0.21703 0.09620 2.256 0.02407 \*

z.n\_fl\_corrected -0.11180 0.06928 -1.614 0.10658

z.n\_redants -0.04626 0.05528 -0.837 0.40270

z.avg\_d\_mean 0.43173 0.13977 3.089 0.00201 \*\*

attack.L -0.33740 0.10315 -3.271 0.00107 \*\*

---

Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Correlation of Fixed Effects:

(Intr) z.sht\_ z.\_\_\_\_ z.mst\_ z.n\_f\_ z.n\_rd z.vg\_\_

z.shoot\_h -0.095

z.dff\_v\_\_\_\_ -0.019 0.311

z.most\_adv -0.025 -0.102 -0.346

z.n\_fl\_crrc -0.008 -0.511 0.032 -0.317

z.n\_redants 0.007 -0.124 -0.200 0.246 0.090

z.avg\_d\_men -0.070 0.325 0.111 -0.150 0.054 0.147

attack.L -0.044 -0.075 0.170 -0.262 0.046 -0.016 0.172

> r.squaredLR(model1frs\_c,null.RE=T)

[1] 0.1068191

attr(,"adj.r.squared")

[1] 0.1238437

> AIC(model1frs\_b,model1frs\_c)

df AIC

model1frs\_b 12 574.0761 #AIC is lower for the model with interactions

model1frs\_c 9 585.0338

The model with interactions is better, and according to this model, early-flowering plants and plants with higher shoots have higher fruit set. Attack by the butterfly decreases fruit set. The effect of number of flowers is not significant in this case. There is an effect of population, with plants in Tånga Hed having higher fruit set. There is a positive effect of soil temperature, but this effect differs between populations…

3) Relative importance of plant traits vs. context for explaining the variation in predispersal seed predation and in plant fitness

Variation partitioning analyses using GLMMs with population always as a random effect. I have used this kind of analysis and graphs before and I think they are quite visual and informative. Values shown inside the ellipses in the figures below are percentages of the total variation explained by fixed factors (R2 fixed of the model including all the variables). The calculations are made so that the percentages sum to 100%.

3.1) Predispersal seed predation

3 variable groups:

Traits: z.shoot\_h + z.most\_adv + z.n\_fl\_corrected

Environmental context: z.diff\_veg\_h\_mean\_shoot\_h + z.avg\_d\_mean

Community context: z.n\_redants

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Plant traits and the environmental context explain similar amounts of variation in the probability of the plant being attacked, the % of variation explained by the context being only slightly lower (I think this could be a nice result, stressing the importance of the context!). This changes if we look at the intensity of the interaction measured either as number of eggs or number of predated fruits, flowers and buds, as in these cases plant traits explain most of the variation (this seems logical, as for example the number of flowers sets an upper limit to the number of predated fruits, flowers and buds). If we look at the variation on the proportion of predated fruits, flowers and buds, again the contribution of plant traits and the environmental context is fairly similar. The community context explains low percentages of variation in all cases.

3.2) Plant fitness

3 variable groups:

Traits: z.shoot\_h + z.most\_adv + z.n\_fl\_corrected

Context: z.diff\_veg\_h\_mean\_shoot\_h + z.avg\_d\_mean + z.n\_redants (environmental + community context merged together here because it is tricky to present this analysis with more than 3 variable groups!)

Interaction: attack

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Plant traits explain a very high amount of the variation on the number of intact fruits (this could also be due to the number of flowers setting an upper limit to the number of fruits). However, if we look at the variation in fruit set, although plant traits explain the highest percentage of variation, there are fairly high amounts of variation explained also by the context and by the interaction with the seed predator.

4) Effects of temperature on plant traits (phenology) and ant abundance

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Plants located in (micro)sites where soil temperature is higher flower earlier. Warmer (micro)sites have higher abundance of *Myrmica* (but the relations with ants are negative if we look at them for each population!).

\* Differences in temperature could be due to differences in vegetation height? (relation included in path models)

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