Things to add

Phenology was only related to temperature when not considering differences among populations



> with(data1comp,summary(glm(most\_adv~avg\_d\_min\_ja,family="poisson")))

Call:

glm(formula = most\_adv ~ avg\_d\_min\_ja, family = "poisson")

Deviance Residuals:

Min 1Q Median 3Q Max

-1.2678 -0.6106 -0.1902 0.4396 1.5937

Coefficients:

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

(Intercept) -0.40405 0.47046 -0.859 0.39043

avg\_d\_min\_ja 0.09627 0.03534 2.724 0.00645 \*\*

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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: 173.44 on 302 degrees of freedom

Residual deviance: 165.90 on 301 degrees of freedom

AIC: 978.36

Number of Fisher Scoring iterations: 4

> with(data1comp,summary(glm(most\_adv~avg\_d\_min\_ja\*population,family="poisson")))

Call:

glm(formula = most\_adv ~ avg\_d\_min\_ja \* population, family = "poisson")

Deviance Residuals:

Min 1Q Median 3Q Max

-1.56006 -0.55997 0.07049 0.27053 1.81411

Coefficients:

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

(Intercept) -0.04915 1.16493 -0.042 0.966

avg\_d\_min\_ja 0.04221 0.08438 0.500 0.617

populationRemmene 0.45737 1.64246 0.278 0.781

populationTånga Hed 0.10778 1.85990 0.058 0.954

avg\_d\_min\_ja:populationRemmene -0.02115 0.12789 -0.165 0.869

avg\_d\_min\_ja:populationTånga Hed 0.04493 0.13550 0.332 0.740

(Dispersion parameter for poisson family taken to be 1)

Null deviance: 173.441 on 302 degrees of freedom

Residual deviance: 95.491 on 297 degrees of freedom

AIC: 915.96

Number of Fisher Scoring iterations: 4

> with(data1comp,summary(glm(most\_adv~avg\_d\_min\_ja+population,family="poisson")))

Call:

glm(formula = most\_adv ~ avg\_d\_min\_ja + population, family = "poisson")

Deviance Residuals:

Min 1Q Median 3Q Max

-1.5662 -0.5578 0.1032 0.2721 1.7925

Coefficients:

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

(Intercept) -0.12232 0.75252 -0.163 0.871

avg\_d\_min\_ja 0.04752 0.05433 0.875 0.382

populationRemmene 0.21228 0.14143 1.501 0.133

populationTånga Hed 0.72220 0.09210 7.842 4.44e-15 \*\*\*

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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: 173.441 on 302 degrees of freedom

Residual deviance: 95.711 on 299 degrees of freedom

AIC: 912.18

Number of Fisher Scoring iterations: 4

> with(subset(data1comp,population=="Högsjön"),summary(glm(most\_adv~avg\_d\_min\_ja,family="poisson")))

Call:

glm(formula = most\_adv ~ avg\_d\_min\_ja, family = "poisson")

Deviance Residuals:

Min 1Q Median 3Q Max

-0.6511 -0.5389 0.1903 0.2481 0.8469

Coefficients:

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

(Intercept) -0.04915 1.16493 -0.042 0.966

avg\_d\_min\_ja 0.04221 0.08438 0.500 0.617

(Dispersion parameter for poisson family taken to be 1)

Null deviance: 15.203 on 103 degrees of freedom

Residual deviance: 14.953 on 102 degrees of freedom

AIC: 271.52

Number of Fisher Scoring iterations: 4

> with(subset(data1comp,population=="Remmene"),summary(glm(most\_adv~avg\_d\_min\_ja,family="poisson")))

Call:

glm(formula = most\_adv ~ avg\_d\_min\_ja, family = "poisson")

Deviance Residuals:

Min 1Q Median 3Q Max

-0.80930 -0.74178 0.02816 0.27257 1.81411

Coefficients:

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

(Intercept) 0.40822 1.15784 0.353 0.724

avg\_d\_min\_ja 0.02107 0.09611 0.219 0.826

(Dispersion parameter for poisson family taken to be 1)

Null deviance: 50.332 on 95 degrees of freedom

Residual deviance: 50.284 on 94 degrees of freedom

AIC: 291.67

Number of Fisher Scoring iterations: 4

> with(subset(data1comp,population!="Högsjön"&population!="Remmene"),summary(glm(most\_adv~avg\_d\_min\_ja,family="poisson")))

Call:

glm(formula = most\_adv ~ avg\_d\_min\_ja, family = "poisson")

Deviance Residuals:

Min 1Q Median 3Q Max

-1.5601 -0.3172 -0.1348 0.3103 0.8692

Coefficients:

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

(Intercept) 0.05863 1.44988 0.040 0.968

avg\_d\_min\_ja 0.08714 0.10602 0.822 0.411

(Dispersion parameter for poisson family taken to be 1)

Null deviance: 30.947 on 102 degrees of freedom

Residual deviance: 30.254 on 101 degrees of freedom

AIC: 352.77

Number of Fisher Scoring iterations: 4

The same happened with relationship among soil temperature and vegetation height.

These relationships were tested in the path model, but resulted to be not significant.

