**PPM OUTPUT EXPLAINED**

Given the following model…

* dim(spxyz) = 28 13
* dim(ppmxyz) = 200028 14
* names(ppmxyz) = "X" "Y" "landuse" "bio1" "bio12" "bio15" "bulkdens" "pawc" "soilcarb" "srtm" "slope" "aspect" "Pres" "wt"
* # covariates = 12 (landuse, bio1, bio12, bio15, bulkdens, pawc, soilcarb, srtm, slope, aspect) + (X, Y)
* # interaction terms = X:Y
* ppmform = ~poly(X, Y, degree = 2, raw = FALSE) + poly(landuse, degree = 2, raw = FALSE)
* mod <- try(ppmlasso(formula = ppmform, data = ppmxyz, n.fits = n.fits, criterion = "bic",standardise = FALSE), silent=TRUE)

The output is…

> str(mod)

List of 27

$ betas : num [1:8, 1:51] -5.29 0 0 0 0 ...

$ lambdas : num [1:51] 0.1215 0.1034 0.088 0.0749 0.0638 ...

$ likelihoods : num [1:51] -244 -243 -226 -210 -201 ...

$ pen.likelihoods : num [1:51] -244 -244 -243 -238 -233 ...

$ lambda : num 4.54e-05

$ beta : num [1:8] -7.39 412.62 551.34 -612.07 0 ...

$ mu : num [1:200028, 1] 0.108 0.108 0.108 0.108 0.108 ...

..- attr(\*, "dimnames")=List of 2

.. ..$ : chr [1:200028] "687" "688" "689" "690" ...

.. ..$ : NULL

$ likelihood : num -158

$ criterion : chr "bic"

$ family : chr "poisson"

$ gamma : num 0

$ alpha : num 1

$ init.coef : logi NA

$ criterion.matrix:'data.frame': 51 obs. of 5 variables:

..$ AIC : num [1:51] 490 491 459 429 410 ...

..$ BIC : num [1:51] 491 493 465 434 415 ...

..$ HQC : num [1:51] 490 491 461 431 411 ...

..$ GCV : num [1:51] 11.38 11.33 10.2 9.25 8.66 ...

..$ NLGCV: num [1:51] 10.58 10.53 9.27 8.18 7.5 ...

$ data : num [1:200028, 1:8] 1 1 1 1 1 1 1 1 1 1 ...

..- attr(\*, "dimnames")=List of 2

.. ..$ : chr [1:200028] "687" "688" "689" "690" ...

.. ..$ : chr [1:8] "(Intercept)" "poly(X, Y, degree = 2, raw = FALSE)1.0" "poly(X, Y, degree = 2, raw = FALSE)2.0" "poly(X, Y, degree = 2, raw = FALSE)0.1" ...

$ pt.interactions : logi NA

$ wt : num [1:200028] 1e-06 1e-06 1e-06 1e-06 1e-06 1e-06 1e-06 1e-06 1e-06 1e-06 ...

$ pres : num [1:200028] 1 1 1 1 1 1 1 1 1 1 ...

$ x : num [1:200028] 146 146 146 146 146 ...

$ y : num [1:200028] -17.1 -17.1 -17.1 -17.1 -17.1 ...

$ r : logi NA

$ call : language ppmlasso(formula = ppmform, data = ppmxyz, n.fits = n.fits, criterion = "bic", standardise = FALSE)

$ formula :Class 'formula' language ~poly(X, Y, degree = 2, raw = FALSE) + poly(landuse, degree = 2, raw = FALSE)

.. ..- attr(\*, ".Environment")=<environment: R\_GlobalEnv>

$ s.means : NULL

$ s.sds : NULL

$ cv.group : num [1:200028] 0 0 0 0 0 0 0 0 0 0 ...

$ n.blocks : logi NA

- attr(\*, "class")= chr [1:2] "ppmlasso" "list"

**NUMBER OF COEFFICIENTS (mod$beta)**

* If no categorical covariates (i.e. landuse): Number of covariates \* number of degrees of freedom + + 2 spatial covariates (X & Y) + 1 interaction term (only between X & Y)
* If categorical covariate is used (i.e. landuse): (Number of covariates – Number of categorical covariates) \* number of degrees of freedom + + 2 spatial covariates (X & Y) + 1 interaction term (only between X & Y) + sum over number of categorical covariates (number of classes in categorical covariate)

**Example: ~ poly(X, Y, degree = 2, raw = FALSE) + poly(landuse, degree = 2, raw = FALSE)**

1. (Intercept)
2. X poly(X, Y, degree = 2, raw = FALSE)1.0
3. X^2 poly(X, Y, degree = 2, raw = FALSE)2.0
4. Y poly(X, Y, degree = 2, raw = FALSE)0.1
5. Y^2 poly(X, Y, degree = 2, raw = FALSE)0.2
6. X:Y poly(X, Y, degree = 2, raw = FALSE)1.1
7. landuse poly(landuse, degree = 2, raw = FALSE)1
8. laduse^2 poly(landuse, degree = 2, raw = FALSE)2"

**Example: *~poly(X, Y, srtm, degree = 2, raw = FALSE) + poly(bio1, degree = 2, raw = FALSE)***

1. (Intercept)
2. X poly(X, Y, srtm, degree = 2, raw = FALSE)1.0.0
3. X^2 poly(X, Y, srtm, degree = 2, raw = FALSE)2.0.0
4. Y poly(X, Y, srtm, degree = 2, raw = FALSE)0.1.0
5. Y^2 poly(X, Y, srtm, degree = 2, raw = FALSE)0.2.0
6. srtm poly(X, Y, srtm, degree = 2, raw = FALSE)0.0.1
7. srtm^2 poly(X, Y, srtm, degree = 2, raw = FALSE)0.0.2
8. X:Y:srtm poly(X, Y, srtm, degree = 2, raw = FALSE)1.1.0
9. poly(X, Y, srtm, degree = 2, raw = FALSE)1.0.1
10. poly(X, Y, srtm, degree = 2, raw = FALSE)0.1.1
11. bio1 poly(bio1, degree = 2, raw = FALSE)1
12. bio1^2 poly(bio1, degree = 2, raw = FALSE)2

Error in models

Class 'try-error' atomic [1:1] Error in glm.fit(x = structure(c(1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, :

NA/NaN/Inf in 'x'

..- attr(\*, "condition")=List of 2

.. ..$ message: chr "NA/NaN/Inf in 'x'"

.. ..$ call : language glm.fit(x = c(1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, | \_\_truncated\_\_ ...

.. ..- attr(\*, "class")= chr [1:3] "simpleError" "error" "condition"

(see notes in notebook)

This may be happening for species that are spatially restricted, so there isn’t much (or any) variability in the predictors for these species. As a result, coeff would be very small (indicating species does not occur anywhere in space irrespective of predictors) and coeffs might be very small indicating that predictors do not tell us anything. BUT we don’t get a model output, so we can’t see this. The error might be a result of the fact that R is dealing with very small numbers and therefore reads them as NA…perhaps.

OR see: <https://stats.idre.ucla.edu/other/mult-pkg/faq/general/faqwhat-is-complete-or-quasi-complete-separation-in-logisticprobit-regression-and-how-do-we-deal-with-them/>

Figure out what to do to fix this with Skip…

Some solutions here: <https://support.minitab.com/en-us/minitab-express/1/help-and-how-to/modeling-statistics/regression/supporting-topics/regression-models/what-are-complete-separation-and-quasi-complete-separation/>

Warnings after model fitting

Warning messages:

1: step size truncated due to divergence

2: glm.fit: algorithm did not converge

3: glm.fit: algorithm stopped at boundary value

4: glm.fit: fitted rates numerically 0 occurred

5: glm.fit: algorithm did not converge

6: glm.fit: fitted rates numerically 0 occurred

7: step size truncated due to divergence

8: glm.fit: fitted rates numerically 0 occurred

9: step size truncated due to divergence

10: glm.fit: algorithm did not converge