Variable selection in individual patient data meta-analysis - stent dataset

Michael Seo

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## glmm\_null

## Generalized linear mixed model fit by maximum likelihood (Laplace  
## Approximation) [glmerMod]  
## Family: binomial ( logit )  
## Formula: y ~ studyid + treat + (-1 + treat | studyid)  
## Data: mydata  
##   
## AIC BIC logLik deviance df.resid   
## 4285.6 4358.7 -2132.8 4265.6 11096   
##   
## Scaled residuals:   
## Min 1Q Median 3Q Max   
## -0.3634 -0.2931 -0.2288 -0.1224 10.4429   
##   
## Random effects:  
## Groups Name Variance Std.Dev.  
## studyid treat 0 0   
## Number of obs: 11106, groups: studyid, 8  
##   
## Fixed effects:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) -4.58259 0.32021 -14.311 < 2e-16 \*\*\*  
## studyid2 0.93318 0.35853 2.603 0.00925 \*\*   
## studyid3 1.18835 0.78536 1.513 0.13025   
## studyid4 1.74166 0.33903 5.137 2.79e-07 \*\*\*  
## studyid5 2.12812 0.34713 6.131 8.75e-10 \*\*\*  
## studyid6 0.49172 0.36076 1.363 0.17287   
## studyid7 2.19284 0.32634 6.720 1.82e-11 \*\*\*  
## studyid8 2.55808 0.32753 7.810 5.71e-15 \*\*\*  
## treat -0.10926 0.08704 -1.255 0.20938   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Correlation of Fixed Effects:  
## (Intr) stdyd2 stdyd3 stdyd4 stdyd5 stdyd6 stdyd7 stdyd8  
## studyid2 -0.878   
## studyid3 -0.401 0.358   
## studyid4 -0.923 0.830 0.379   
## studyid5 -0.907 0.810 0.370 0.857   
## studyid6 -0.868 0.780 0.356 0.827 0.805   
## studyid7 -0.965 0.862 0.393 0.912 0.890 0.857   
## studyid8 -0.961 0.859 0.392 0.908 0.887 0.854 0.943   
## treat -0.128 -0.001 -0.003 -0.043 0.000 -0.041 -0.002 -0.002  
## convergence code: 0  
## boundary (singular) fit: see ?isSingular

## (Intercept) studyid2 studyid3 studyid4 studyid5 studyid6 studyid7  
## 1 -4.582585 0.9331798 1.188349 1.741656 2.128118 0.4917237 2.192844  
## studyid8 treat  
## 1 2.558076 -0.1092571

## [1] 0.7558980 0.8964999 1.0632547

## glmm\_full

## Generalized linear mixed model fit by maximum likelihood (Laplace  
## Approximation) [glmerMod]  
## Family: binomial ( logit )  
## Formula:   
## y ~ studyid + (age + gender + diabetes + stable\_cad + multivessel +   
## ladtreated + overlap + m\_dia\_above\_3 + num\_stent) \* treat +   
## (-1 + treat | studyid)  
## Data: mydata  
##   
## AIC BIC logLik deviance df.resid   
## 4107.3 4312.1 -2025.7 4051.3 11078   
##   
## Scaled residuals:   
## Min 1Q Median 3Q Max   
## -1.0069 -0.2692 -0.1763 -0.1087 23.0529   
##   
## Random effects:  
## Groups Name Variance Std.Dev.  
## studyid treat 4e-14 2e-07   
## Number of obs: 11106, groups: studyid, 8  
##   
## Fixed effects:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) -4.299408 0.326641 -13.162 < 2e-16 \*\*\*  
## studyid2 0.524606 0.365267 1.436 0.150937   
## studyid3 1.071342 0.795260 1.347 0.177929   
## studyid4 1.059063 0.346325 3.058 0.002228 \*\*   
## studyid5 0.807254 0.361000 2.236 0.025341 \*   
## studyid6 0.298375 0.365188 0.817 0.413903   
## studyid7 1.355898 0.337663 4.016 5.93e-05 \*\*\*  
## studyid8 1.786975 0.334612 5.340 9.27e-08 \*\*\*  
## age 0.697817 0.088616 7.875 3.42e-15 \*\*\*  
## gender -0.009563 0.060064 -0.159 0.873499   
## diabetes 0.202784 0.056544 3.586 0.000335 \*\*\*  
## stable\_cad -0.264425 0.071444 -3.701 0.000215 \*\*\*  
## multivessel 0.148957 0.072012 2.068 0.038594 \*   
## ladtreated 0.098352 0.065133 1.510 0.131035   
## overlap 0.146446 0.064927 2.256 0.024099 \*   
## m\_dia\_above\_3 -0.051418 0.047019 -1.094 0.274153   
## num\_stent 0.017515 0.070713 0.248 0.804373   
## treat 0.044368 0.118005 0.376 0.706930   
## age:treat -0.084909 0.114654 -0.741 0.458957   
## gender:treat 0.021694 0.084673 0.256 0.797793   
## diabetes:treat -0.033872 0.078758 -0.430 0.667143   
## stable\_cad:treat 0.054410 0.096454 0.564 0.572688   
## multivessel:treat -0.087968 0.093551 -0.940 0.347053   
## ladtreated:treat -0.184145 0.089987 -2.046 0.040723 \*   
## overlap:treat -0.015321 0.091473 -0.167 0.866983   
## m\_dia\_above\_3:treat 0.094494 0.073102 1.293 0.196138   
## num\_stent:treat -0.081490 0.102641 -0.794 0.427233   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
## convergence code: 0  
## boundary (singular) fit: see ?isSingular

## [1] 0.1094305 0.2821936 0.7277059

## [1] 0.9833844 1.8416560 3.4490040

## naive step

##   
## Call:  
## glm(formula = y ~ studyid + age + diabetes + stable\_cad + multivessel +   
## ladtreated + overlap + num\_stent + treat + ladtreated:treat +   
## num\_stent:treat, family = binomial(link = "logit"), data = mydata)  
##   
## Deviance Residuals:   
## Min 1Q Median 3Q Max   
## -1.1169 -0.3752 -0.2471 -0.1529 3.4772   
##   
## Coefficients:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) -4.24918 0.32353 -13.134 < 2e-16 \*\*\*  
## studyid2 0.52315 0.36516 1.433 0.15195   
## studyid3 1.06017 0.79501 1.334 0.18236   
## studyid4 1.06262 0.34605 3.071 0.00214 \*\*   
## studyid5 0.81161 0.36083 2.249 0.02450 \*   
## studyid6 0.31342 0.36489 0.859 0.39037   
## studyid7 1.35939 0.33742 4.029 5.61e-05 \*\*\*  
## studyid8 1.78766 0.33452 5.344 9.10e-08 \*\*\*  
## age 0.65122 0.06211 10.486 < 2e-16 \*\*\*  
## diabetes 0.18495 0.03951 4.681 2.85e-06 \*\*\*  
## stable\_cad -0.23557 0.04916 -4.792 1.65e-06 \*\*\*  
## multivessel 0.10385 0.05295 1.962 0.04982 \*   
## ladtreated 0.10422 0.06467 1.612 0.10705   
## overlap 0.13918 0.04728 2.943 0.00325 \*\*   
## num\_stent 0.03766 0.06328 0.595 0.55174   
## treat -0.04704 0.09069 -0.519 0.60398   
## ladtreated:treat -0.19639 0.08943 -2.196 0.02810 \*   
## num\_stent:treat -0.12341 0.07996 -1.543 0.12272   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for binomial family taken to be 1)  
##   
## Null deviance: 4565.3 on 11105 degrees of freedom  
## Residual deviance: 4055.4 on 11088 degrees of freedom  
## AIC: 4091.4  
##   
## Number of Fisher Scoring iterations: 7

## [1] 0.3173741 0.5229361 0.8616398

## [1] 0.9422707 1.2390903 1.6294095

## naive lasso

## 27 x 1 sparse Matrix of class "dgCMatrix"  
## 1  
## (Intercept) -4.228479338  
## studyid2 0.521844203  
## studyid3 1.055691469  
## studyid4 1.056579469  
## studyid5 0.811519784  
## studyid6 0.317113237  
## studyid7 1.355425489  
## studyid8 1.781785784  
## age 0.649305785  
## gender 0.001074054  
## diabetes 0.184294165  
## stable\_cad -0.236285330  
## multivessel 0.109658650  
## ladtreated 0.055680484  
## overlap 0.137056452  
## m\_dia\_above\_3 -0.023342371  
## num\_stent 0.004604541  
## treat -0.070295390  
## age:treat .   
## gender:treat .   
## diabetes:treat .   
## stable\_cad:treat .   
## multivessel:treat -0.011282951  
## ladtreated:treat -0.103428992  
## overlap:treat .   
## m\_dia\_above\_3:treat 0.032085143  
## num\_stent:treat -0.049038776

## glmmLasso

## Bayes Lasso

## SSVS