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

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## glmm\_null

## Generalized linear mixed model fit by maximum likelihood (Laplace  
## Approximation) [glmerMod]  
## Family: binomial ( logit )  
## Formula: y ~ -1 + 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 4e-14 2e-07   
## Number of obs: 11106, groups: studyid, 8  
##   
## Fixed effects:  
## Estimate Std. Error z value Pr(>|z|)   
## studyid1 -4.58259 0.32042 -14.302 < 2e-16 \*\*\*  
## studyid2 -3.64941 0.17153 -21.276 < 2e-16 \*\*\*  
## studyid3 -3.39424 0.71959 -4.717 2.39e-06 \*\*\*  
## studyid4 -2.84093 0.13030 -21.804 < 2e-16 \*\*\*  
## studyid5 -2.45447 0.14615 -16.794 < 2e-16 \*\*\*  
## studyid6 -4.09086 0.17934 -22.810 < 2e-16 \*\*\*  
## studyid7 -2.38974 0.08599 -27.792 < 2e-16 \*\*\*  
## studyid8 -2.02451 0.09040 -22.396 < 2e-16 \*\*\*  
## treat -0.10926 0.08704 -1.255 0.209   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Correlation of Fixed Effects:  
## stdyd1 stdyd2 stdyd3 stdyd4 stdyd5 stdyd6 stdyd7 stdyd8  
## studyid2 0.031   
## studyid3 0.008 0.015   
## studyid4 0.055 0.104 0.026   
## studyid5 0.036 0.068 0.017 0.120   
## studyid6 0.040 0.076 0.019 0.133 0.088   
## studyid7 0.062 0.117 0.029 0.207 0.136 0.151   
## studyid8 0.059 0.112 0.028 0.197 0.130 0.144 0.223   
## treat -0.128 -0.242 -0.060 -0.427 -0.282 -0.312 -0.484 -0.461  
## convergence code: 0  
## boundary (singular) fit: see ?isSingular

## glmm\_full

## Generalized linear mixed model fit by maximum likelihood (Laplace  
## Approximation) [glmerMod]  
## Family: binomial ( logit )  
## Formula:   
## y ~ -1 + 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 0 0   
## Number of obs: 11106, groups: studyid, 8  
##   
## Fixed effects:  
## Estimate Std. Error z value Pr(>|z|)   
## studyid1 -4.24680 0.44258 -9.596 < 2e-16 \*\*\*  
## studyid2 -3.72219 0.35186 -10.578 < 2e-16 \*\*\*  
## studyid3 -3.17546 0.79820 -3.978 6.94e-05 \*\*\*  
## studyid4 -3.18774 0.32764 -9.729 < 2e-16 \*\*\*  
## studyid5 -3.43955 0.35097 -9.800 < 2e-16 \*\*\*  
## studyid6 -3.94842 0.35499 -11.123 < 2e-16 \*\*\*  
## studyid7 -2.89090 0.31913 -9.059 < 2e-16 \*\*\*  
## studyid8 -2.45982 0.32052 -7.674 1.66e-14 \*\*\*  
## age 0.69780 0.08861 7.874 3.42e-15 \*\*\*  
## gender -0.02156 0.13541 -0.159 0.873500   
## diabetes 0.47900 0.13357 3.586 0.000335 \*\*\*  
## stable\_cad -0.55839 0.15087 -3.701 0.000215 \*\*\*  
## multivessel 0.29874 0.14442 2.068 0.038594 \*   
## ladtreated 0.19714 0.13055 1.510 0.131032   
## overlap 0.40622 0.18010 2.256 0.024099 \*   
## m\_dia\_above\_3 -0.28613 0.26164 -1.094 0.274123   
## num\_stent 0.01664 0.06719 0.248 0.804373   
## treat -0.13118 0.46924 -0.280 0.779809   
## age:treat -0.08491 0.11465 -0.741 0.458964   
## gender:treat 0.04891 0.19089 0.256 0.797795   
## diabetes:treat -0.08001 0.18604 -0.430 0.667144   
## stable\_cad:treat 0.11490 0.20368 0.564 0.572683   
## multivessel:treat -0.17642 0.18762 -0.940 0.347051   
## ladtreated:treat -0.36910 0.18037 -2.046 0.040721 \*   
## overlap:treat -0.04250 0.25374 -0.167 0.866983   
## m\_dia\_above\_3:treat 0.52584 0.40678 1.293 0.196121   
## num\_stent:treat -0.07743 0.09752 -0.794 0.427231   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
## convergence code: 0  
## boundary (singular) fit: see ?isSingular

## naive step

##   
## Call:  
## glm(formula = y ~ 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   
## -1.0062 -0.3717 -0.2657 -0.1836 3.4074   
##   
## Coefficients:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) -3.50570 0.14098 -24.867 < 2e-16 \*\*\*  
## age 0.80568 0.05549 14.520 < 2e-16 \*\*\*  
## diabetes 0.50648 0.09200 5.505 3.69e-08 \*\*\*  
## stable\_cad -0.47178 0.10081 -4.680 2.87e-06 \*\*\*  
## multivessel 0.15495 0.09274 1.671 0.094751 .   
## ladtreated 0.24448 0.12826 1.906 0.056637 .   
## overlap 0.48461 0.12567 3.856 0.000115 \*\*\*  
## num\_stent 0.05435 0.05721 0.950 0.342126   
## treat 0.25083 0.17809 1.408 0.159006   
## ladtreated:treat -0.33647 0.17769 -1.894 0.058279 .   
## num\_stent:treat -0.11165 0.07431 -1.503 0.132948   
## ---  
## 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: 4176.2 on 11095 degrees of freedom  
## AIC: 4198.2  
##   
## Number of Fisher Scoring iterations: 6

## 20 x 1 sparse Matrix of class "dgCMatrix"  
## 1  
## (Intercept) -2.7827729  
## age .   
## gender .   
## diabetes .   
## stable\_cad .   
## multivessel .   
## ladtreated .   
## overlap .   
## m\_dia\_above\_3 .   
## num\_stent .   
## treat -0.2104127  
## age:treat .   
## gender:treat .   
## diabetes:treat .   
## stable\_cad:treat .   
## multivessel:treat .   
## ladtreated:treat .   
## overlap:treat .   
## m\_dia\_above\_3:treat .   
## num\_stent:treat .

## [1] "Iteration 1"  
## [1] "Iteration 2"  
## [1] "Iteration 3"  
## [1] "Iteration 4"  
## [1] "Iteration 5"  
## [1] "Iteration 6"  
## [1] "Iteration 7"  
## [1] "Iteration 8"  
## [1] "Iteration 9"  
## [1] "Iteration 10"  
## [1] "Iteration 11"  
## [1] "Iteration 12"  
## [1] "Iteration 13"  
## [1] "Iteration 14"  
## [1] "Iteration 15"  
## [1] "Iteration 16"  
## [1] "Iteration 17"  
## [1] "Iteration 18"  
## [1] "Iteration 19"  
## Warning:  
## Algorithm did not converge!  
## [1] "Iteration 20"  
## [1] "Iteration 21"  
## [1] 7679.918 7613.524 7622.148 7865.139 6779.865 7372.107 7077.315  
## [8] 6532.467 6314.481 6643.799 7275.259 7538.815 7994.287 7948.349  
## [15] 7580.335 8346.291 8469.076 9088.079 13160.079 9569.288 7773.873  
## [1] "optimal lambda value is 60"

## Call:  
## glmmLasso(fix = form.fixed, rnd = form.rnd, data = data\_glmmLasso\_train,   
## lambda = lambda[opt2], family = family, final.re = FALSE,   
## control = list(index = c(NA, 1:((dim(data\_glmmLasso)[2] -   
## 3)), NA)))  
##   
##   
## Fixed Effects:  
##   
## Coefficients:  
## Estimate StdErr z.value p.value  
## (Intercept) -3.1270338 NA NA NA  
## age 0.3089560 NA NA NA  
## gender -0.0217220 NA NA NA  
## diabetes 0.1479460 NA NA NA  
## stable\_cad -0.1791584 NA NA NA  
## multivessel 0.0353541 NA NA NA  
## ladtreated 0.0187194 NA NA NA  
## overlap 0.2278921 NA NA NA  
## m\_dia\_above\_3 0.0000000 NA NA NA  
## num\_stent 0.0158728 NA NA NA  
## age\_treat 0.0477836 NA NA NA  
## gender\_treat 0.0057484 NA NA NA  
## diabetes\_treat 0.0000000 NA NA NA  
## stable\_cad\_treat -0.0368493 NA NA NA  
## multivessel\_treat 0.0000000 NA NA NA  
## ladtreated\_treat 0.0000000 NA NA NA  
## overlap\_treat 0.0000000 NA NA NA  
## m\_dia\_above\_3\_treat 0.0000000 NA NA NA  
## num\_stent\_treat 0.0000000 NA NA NA  
## as.factor(studyid)2 -0.2851762 NA NA NA  
## as.factor(studyid)3 -0.3682810 NA NA NA  
## as.factor(studyid)4 0.1658545 NA NA NA  
## as.factor(studyid)5 0.2334019 NA NA NA  
## as.factor(studyid)6 -0.6267369 NA NA NA  
## as.factor(studyid)7 0.4687527 NA NA NA  
## as.factor(studyid)8 0.8618851 NA NA NA  
## treat -0.1454213 NA NA NA  
##   
## Random Effects:  
##   
## StdDev:  
## treat:studyid  
## treat:studyid 0.1014203