

# This is a note for Golden Gate Association analysis

## R Markdown

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This project is led by Ms. Jacqui Marzec. Our objectives are to find any significant association between SNPs (Golden Gate SNP candidate pool) in RSV positive patients.

## GWAS on mitochondrial variants

In this analysis, we tried three different cases as following. Each setting will help to answer different hypothesis. The Analysis will be done with each case independently.

Case1, all three genotypes are kept: AA/AB/BB Case2, two genotypes are kept: AA AB/BB Case3, two genotypes are kept: AA/AB BB

## Analysis set up and load necessary functions

```
library(HardyWeinberg)

## Warning: package 'HardyWeinberg' was built under R version 3.2.5
## Warning: package 'mice' was built under R version 3.2.5
library(XLConnect)

## Warning: package 'XLConnect' was built under R version 3.2.5
## Warning: package 'XLConnectJars' was built under R version 3.2.5
source("helperScripts/analysisFuncs.R")
```

## Load up preprocessed data

```
## Phenotype data
dt <- read.table("data/RSV_cohort_data_ASCII.txt", header = TRUE, sep = "\t")

## ONLY use for RSV positive candidates
row2use <- which(dt[,5] == 1)

## This is for reading Excel file
## We need to set memory at 24 GB
options(java.parameters = "-Xmx24g" )

snpsFiles <- "data/ASCII_genotype_data_GoldenGate_for_JYL_07122015.xlsx"

## There are five sheets of data
sheets <- c(seq(1,5))
```

## Analysis results on disease severity – logistic regression model

```
sig.asso.SAT      <- c(list())
results.logit <- logisticAnalysis (sig.asso.SAT, snpFiles, sheets, dt, 6, row2use)
results.logit
```

```
## [[1]]
## [[1]]$`Case-I`
##           SNP           pval
## 1  seq.rs3806496 0.03249843
## 2  seq.rs2066843 0.03161207
## 3  seq.rs17244587 0.04618051
##
## [[1]]$`Case-II`
##           SNP           pval
## 1  seq.rs12987402 0.03525483
## 2  seq.rs469390 0.02409298
## 3  seq.rs3806265 0.03776518
## 4  seq.rs2066843 0.03371025
##
## [[1]]$`Case-III`
##           SNP           pval
## 1  seq.rs17189298 0.04594427
## 2  seq.rs2770146 0.01637843
##
##
## [[2]]
## [[2]]$`Case-I`
##           SNP           pval
## 1  seq.rs2252930 0.0123745940
## 2  seq.rs2243592 0.0005072162
## 3  seq.rs2257167 0.0016167643
## 4  seq.rs2243599 0.0006175882
## 5  seq.rs2254180 0.0054136510
## 6  seq.rs2254315 0.0042648958
## 7  seq.rs1474347 0.0233376514
## 8  seq.rs8193036 0.0138688712
##
## [[2]]$`Case-II`
##           SNP           pval
## 1  seq.rs2243592 0.003018021
## 2  seq.rs2257167 0.006062165
## 3  seq.rs2243599 0.006208847
## 4  seq.rs2254180 0.021865717
## 5  seq.rs2254315 0.015360578
## 6  seq.rs1800795 0.025821513
## 7  seq.rs2069832 0.012473056
## 8  seq.rs1474347 0.011935878
## 9  seq.rs1800893 0.048201983
## 10 seq.rs8193036 0.019022066
##
## [[2]]$`Case-III`
##           SNP           pval
## 1  seq.rs2280789 0.026207189
```

```

## 2 seq.rs2252930 0.010498389
## 3 seq.rs2243592 0.006836451
## 4 seq.rs2257167 0.011030534
## 5 seq.rs2243599 0.004429888
## 6 seq.rs2254180 0.019988072
## 7 seq.rs2254315 0.022174971
## 8 seq.rs9376268 0.042321508
## 9 seq.rs9376267 0.029287461
## 10 seq.rs369908 0.023580640
##
##
## [[3]]
## [[3]]$`Case-I`
##          SNP          pval
## 1 seq.rs1293749 0.041542545
## 2 seq.rs15895 0.034259581
## 3 seq.rs7966314 0.030823898
## 4 seq.rs2072133 0.007942976
## 5 seq.rs1041981 0.024407218
##
## [[3]]$`Case-II`
##          SNP          pval
## 1 seq.rs7966314 0.02788702
## 2 seq.rs2072133 0.01039301
##
## [[3]]$`Case-III`
##          SNP          pval
## 1 seq.rs1293755 0.04087340
## 2 seq.rs15895 0.04041382
## 3 seq.rs12693591 0.01505629
## 4 seq.rs3771300 0.03111144
## 5 seq.rs1800693 0.01013580
##
##
## [[4]]
## [[4]]$`Case-I`
##          SNP          pval
## 1 seq.rs3769823 0.0402697
##
## [[4]]$`Case-II`
## NULL
##
## [[4]]$`Case-III`
##          SNP          pval
## 1 seq.rs3769823 0.01005097
## 2 seq.rs4844590 0.03257378
##
##
## [[5]]
## [[5]]$`Case-I`
##          SNP          pval
## 1 rs3761624 0.02619375
##
## [[5]]$`Case-II`

```

```
##          SNP          pval
## 1 rs3761624 0.02858216
##
## [[5]]$`Case-III`
## NULL
```

## Analysis results on disease severity – logistic with gender as covariate

```
sig.asso.SAT      <- c(list())
results.logit <- logisticAnalysisWCorrV (sig.asso.SAT, snpFiles, sheets, dt, 6, row2use, params$corCol)
results.logit
```

```
## [[1]]
## [[1]]$`Case-I`
##          SNP          pval
## 1 seq.rs4925659 0.04857201
## 2 seq.rs7502875 0.02966858
## 3 seq.rs5030725 0.03166908
##
## [[1]]$`Case-II`
##          SNP          pval
## 1 seq.rs11795343 0.03356908
## 2 seq.rs10813831 0.03897348
## 3 seq.rs7502875 0.04425052
## 4 seq.rs5030725 0.03166908
##
## [[1]]$`Case-III`
##          SNP          pval
## 1 seq.rs469012 0.02343009
## 2 seq.rs469390 0.01958672
##
##
## [[2]]
## [[2]]$`Case-I`
##          SNP          pval
## 1 seq.rs11063084 0.045638507
## 2 seq.rs2107538 0.009151977
## 3 seq.rs2257167 0.017594107
## 4 seq.rs2275913 0.013270682
## 5 seq.rs8193038 0.014041868
## 6 seq.rs7744 0.026364135
##
## [[2]]$`Case-II`
##          SNP          pval
## 1 seq.rs2107538 0.018246758
## 2 seq.rs2275913 0.008774505
## 3 seq.rs8193038 0.006582946
##
## [[2]]$`Case-III`
##          SNP          pval
## 1 seq.rs2257167 0.02022729
## 2 seq.rs2250889 0.04664627
##
```

```
##
## [[3]]
## [[3]]$`Case-I`
##          SNP          pval
## 1 seq.rs16824035 0.005067530
## 2 seq.rs1800692 0.003280719
##
## [[3]]$`Case-II`
##          SNP          pval
## 1 seq.rs10199181 0.042982420
## 2 seq.rs16824035 0.006314110
## 3 seq.rs1800692 0.009707555
##
## [[3]]$`Case-III`
## NULL
##
##
## [[4]]
## [[4]]$`Case-I`
##          SNP          pval
## 1 seq.rs11208545 0.03037701
##
## [[4]]$`Case-II`
##          SNP          pval
## 1 seq.rs310202 0.01642526
## 2 seq.rs11208545 0.02557307
##
## [[4]]$`Case-III`
##          SNP          pval
## 1 seq.rs310247 0.03893488
## 2 seq.rs12743599 0.01310665
##
##
## [[5]]
## [[5]]$`Case-I`
## NULL
##
## [[5]]$`Case-II`
## NULL
##
## [[5]]$`Case-III`
## NULL
```

## Analysis results on disease severity – chi-square test based model

```
sig.asso.SAT      <- c(list())
results.chisquare <- AssoAnalysis      (sig.asso.SAT, snpFiles, sheets, dt, 6, row2use)
results.chisquare
```

```
## [[1]]
## [[1]]$`Case-I`
##          SNP          pval
## 1 seq.rs469390 0.03553412
```

```

## 2 seq.rs2770146 0.03031926
##
## [[1]]$`Case-II`
##          SNP          pval
## 1 seq.rs12987402 0.04484957
## 2   seq.rs469390 0.03136834
## 3   seq.rs3806265 0.04864552
## 4   seq.rs2066843 0.04292077
##
## [[1]]$`Case-III`
##          SNP          pval
## 1 seq.rs2770146 0.02269727
##
##
## [[2]]
## [[2]]$`Case-I`
##          SNP          pval
## 1   seq.rs2252930 0.032963115
## 2   seq.rs2243592 0.002065785
## 3   seq.rs2257167 0.004097110
## 4   seq.rs2243599 0.002391277
## 5   seq.rs2254180 0.016497081
## 6   seq.rs2254315 0.014203726
## 7   seq.rs2069832 0.026046287
## 8   seq.rs1474347 0.040922019
## 9   seq.rs8193036 0.046061333
## 10  seq.rs8193038 0.049507445
##
## [[2]]$`Case-II`
##          SNP          pval
## 1 seq.rs2243592 0.003973553
## 2 seq.rs2257167 0.007940527
## 3 seq.rs2243599 0.008163886
## 4 seq.rs2254180 0.028029801
## 5 seq.rs2254315 0.019873260
## 6 seq.rs1800795 0.033217808
## 7 seq.rs2069832 0.016223152
## 8 seq.rs1474347 0.015568224
## 9 seq.rs8193036 0.024515805
##
## [[2]]$`Case-III`
##          SNP          pval
## 1   seq.rs2280789 0.037358791
## 2   seq.rs2252930 0.013686847
## 3   seq.rs2243592 0.009214950
## 4   seq.rs2257167 0.014382366
## 5   seq.rs2243599 0.005967165
## 6   seq.rs2254180 0.027873558
## 7   seq.rs2254315 0.030957836
## 8   seq.rs9376268 0.033497757
## 9   seq.rs9376267 0.035090018
## 10  seq.rs369908 0.033457931
##
##

```

```

## [[3]]
## [[3]]$`Case-I`
##           SNP           pval
## 1 seq.rs2072133 0.02734773
## 2 seq.rs12693591 0.01358428
## 3 seq.rs361525 0.02179245
## 4 seq.rs1800693 0.01481453
##
## [[3]]$`Case-II`
##           SNP           pval
## 1 seq.rs7966314 0.03569512
## 2 seq.rs2072133 0.01355917
##
## [[3]]$`Case-III`
##           SNP           pval
## 1 seq.rs12693591 0.02004173
## 2 seq.rs3771300 0.03990646
## 3 seq.rs361525 0.02179672
## 4 seq.rs1800693 0.01382160
##
##
## [[4]]
## [[4]]$`Case-I`
##           SNP           pval
## 1 seq.rs3769823 0.03369201
##
## [[4]]$`Case-II`
## NULL
##
## [[4]]$`Case-III`
##           SNP           pval
## 1 seq.rs3769823 0.01319883
## 2 seq.rs4844590 0.04305651
##
##
## [[5]]
## [[5]]$`Case-I`
## NULL
##
## [[5]]$`Case-II`
##           SNP           pval
## 1 rs3761624 0.03637326
##
## [[5]]$`Case-III`
## NULL

```