

# The APOE locus

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*December 31, 2015*

In this short note, I demonstrated how the priors affected bayes-glmm's posterior estimations of variant effects by inspecting the APOE locus of ADSP dataset. The priors came from IGAP's meta-analysis. APOE genotypes were removed from the covariate matrix of the GLMM.

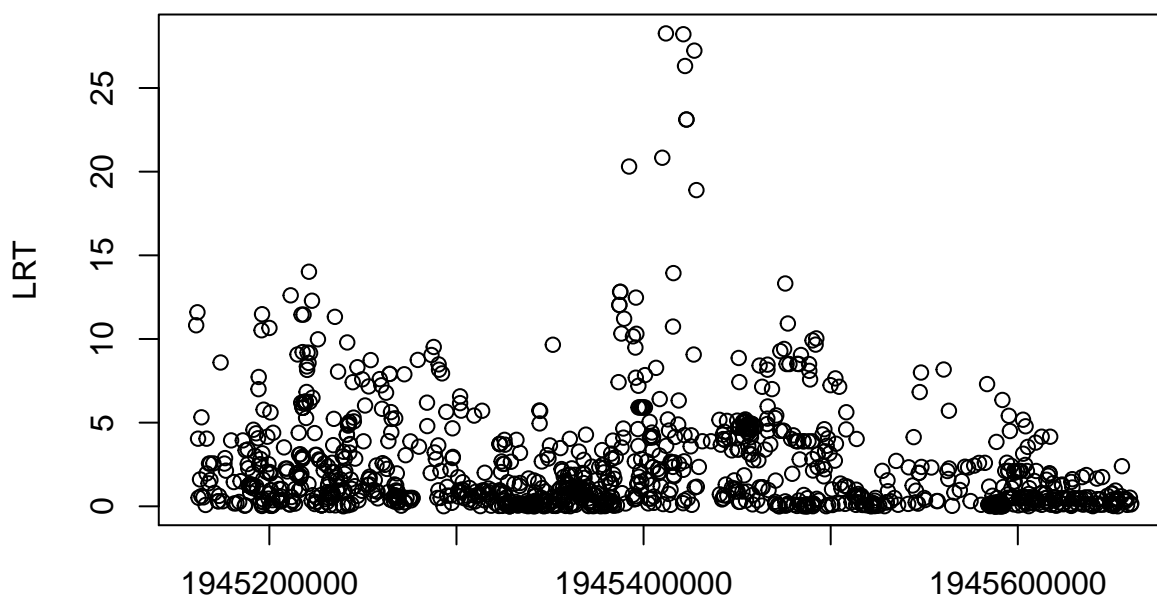
```
library(dplyr)
```

```
##  
## Attaching package: 'dplyr'  
##  
## The following objects are masked from 'package:stats':  
##  
##   filter, lag  
##  
## The following objects are masked from 'package:base':  
##  
##   intersect, setdiff, setequal, union
```

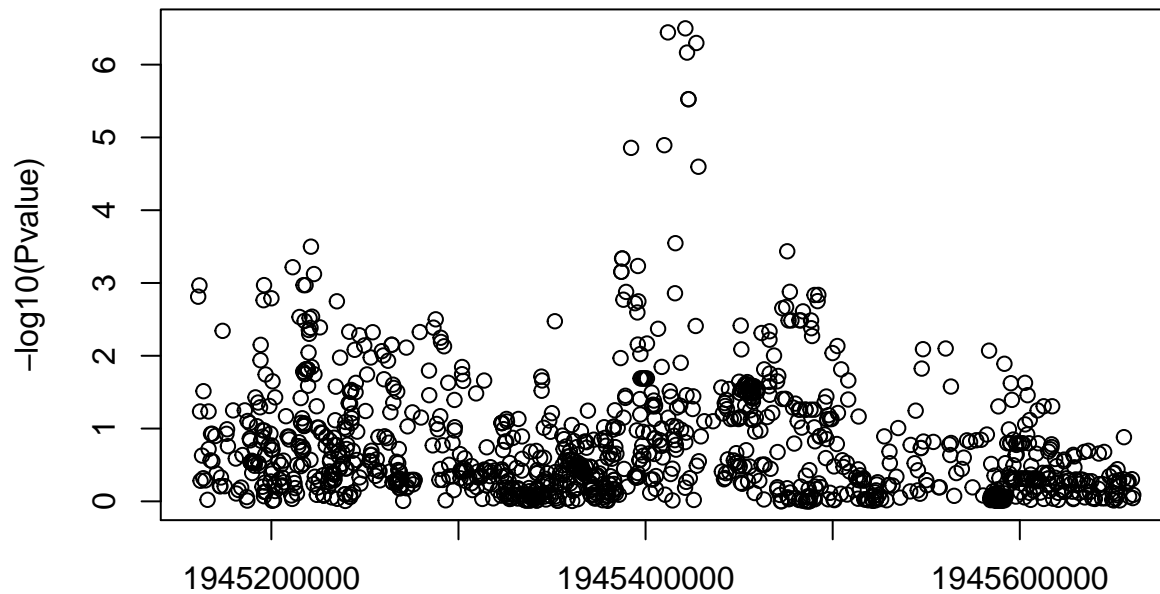
```
rm(list = ls())  
setwd("~/GitHub/byglmm")  
load("./ApoE/md.rdt")
```

As a change, p-value of the variant's effect size was taken as the significance metric, as opposed to the likelihood ratio test (LRT) that we used before. Do the two statistics agree with each other?

## ADSP w/o prior



## ADSP w/o prior



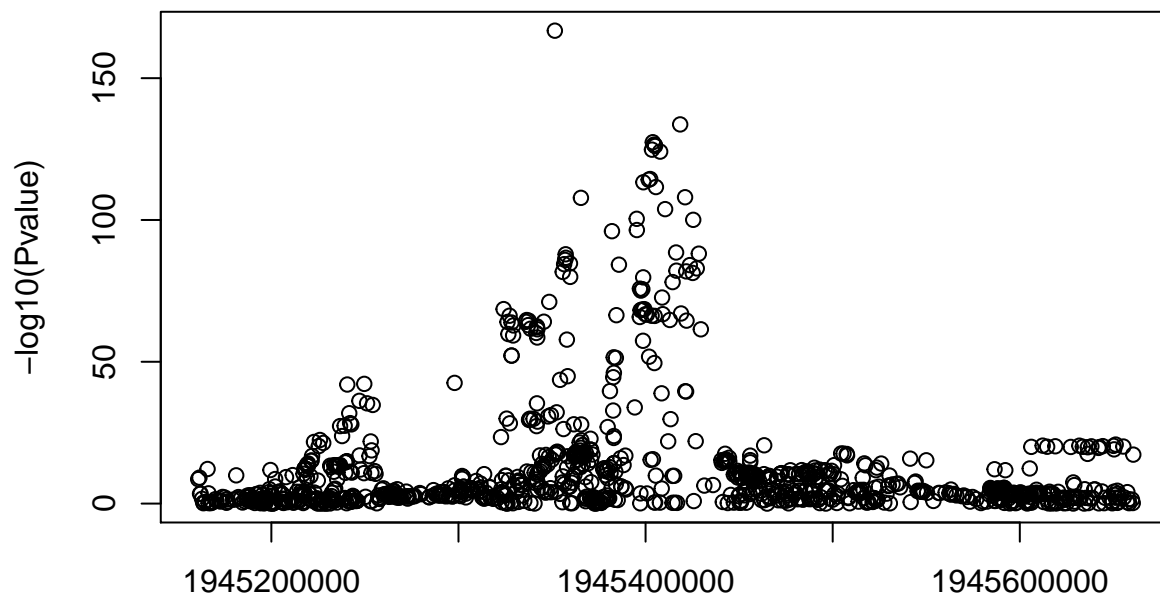
```
## [1] 0.9912165
```

The two statistics agreed with each other well, with pearson's 0.99. Noticed that the APOE locus did not pass the genome-wide significance threshold  $5e-8$ , which equaled 7.3 in  $-\log_{10}(\text{Pvalue})$  unit. How would this result change by including the IGAP results into the prior?

IGAP's results on the APOE locus by P-values.

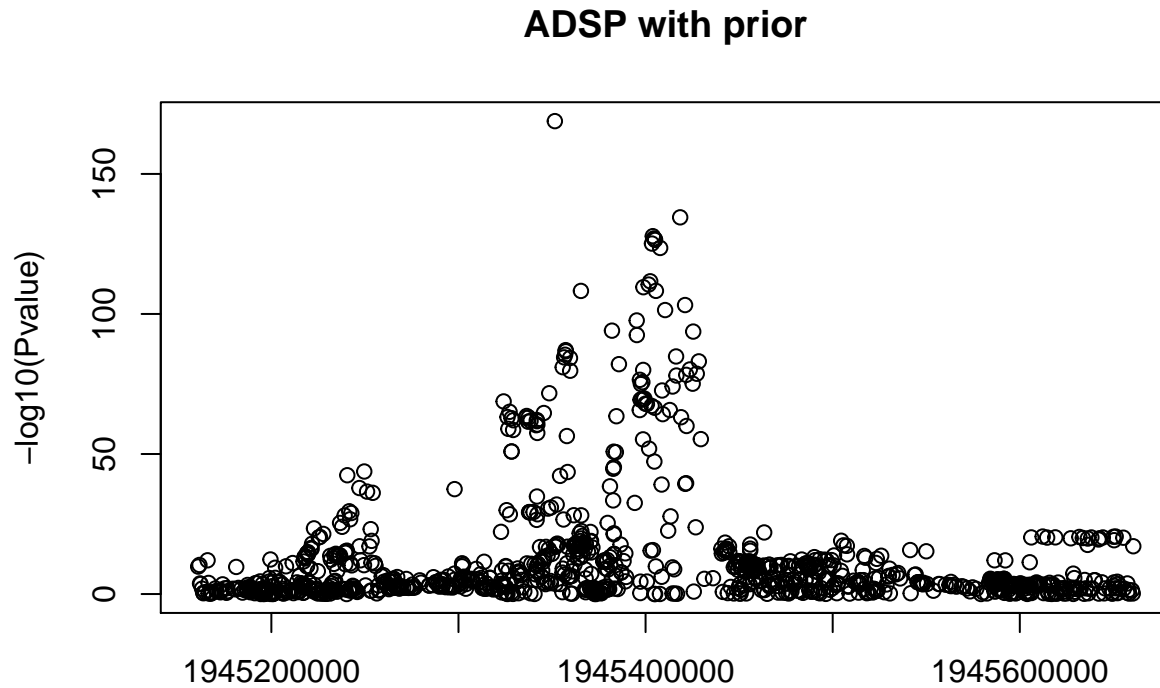
```
p_igap_prior = pnorm(abs(p1[, "Beta"]), sd = p1[, "SE"], lower.tail = F) * 2
plot(pos, -log10(p_igap_prior), main = "IGAP", xlab = "", ylab = "-log10(Pvalue)")
```

## IGAP



ADSP results by taking IGAP results into the prior.

```
p_adsp_prior = pnorm(abs(fit_prior$p), sd = fit_prior$se_p, lower.tail = F) * 2  
plot(pos, -log10(p_adsp_prior), main = "ADSP with prior", xlab = "", ylab = "-log10(Pvalue)")
```



APOE locus became significant with the help of the IGAP results.