Setting prior distributions for variant effects using IGAP results

Xulong Wang

December 11, 2015

Reference: Meta-analysis of 74,046 individuals identifies 11 new susceptibility loci for Alzheimer's disease

```
rm(list = ls())
load("~/GitHub/bgwas/igap/igap.rdt")
```

6.76 million and 96% of IGAP variants appeared in ADSP

```
nrow(glmm)
```

```
## [1] 6757220
```

```
nrow(igap_s1)
```

```
## [1] 7055881
```

```
nrow(glmm) / nrow(igap_s1)
```

```
## [1] 0.957672
```
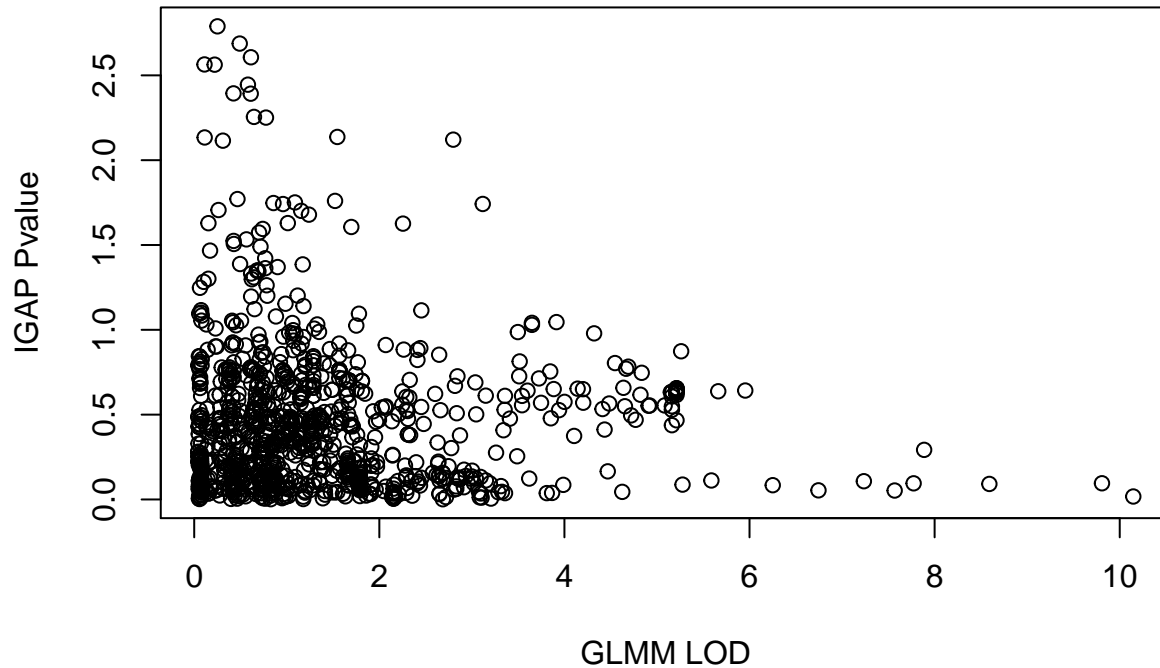
Correlation between ADSP and IGAP was poor

```
igap = igap_s1[match(glmm$UID, igap_s1$UID), ]

all(igap$UID == glmm$UID)
```

```
## [1] TRUE
```

```
plot(glmm$LOD[1:1e3], -log10(igap$Pvalue)[1:1e3], xlab = "GLMM LOD", ylab = "IGAP Pvalue", main = "First
```

First 1000 SNP

Build the reported "beta" and "se" as priors of variant effects

IGAP reported for each variant (1) effect size, (2) standard error of effect size, and (3) P-value. The P-value represented the probability to get more extrme values than the observed effect size from a normal distribution with expected mean zero and standard deviation the standard error.

```
head(igap)
```

```
##   Chromosome Position  MarkerName Effect_allele Non_Effect_allele    Beta
## 1          1   751343  rs28544273             A                 T -0.0146
## 2          1   751756 rs143225517             C                 T -0.0146
## 3          1   752566   rs3094315             G                 A -0.0122
## 4          1   753405  rs61770173             C                 A -0.0126
## 5          1   768253   rs2977608             A                 C -0.0394
## 6          1   768448  rs77786510             A                 G -0.0385
##       SE Pvalue        UID
## 1 0.0338 0.6651 1-751343
## 2 0.0338 0.6651 1-751756
## 3 0.0294 0.6773 1-752566
## 4 0.0339 0.7104 1-753405
## 5 0.0261 0.1308 1-768253
## 6 0.0303 0.2034 1-768448
```

```
pvalue = pnorm(abs(igap$Beta), sd = igap$SE, lower.tail = F) * 2
plot(pvalue[1:1e3], igap$Pvalue[1:1e3], xlab = "Craft", ylab = "Report")
```
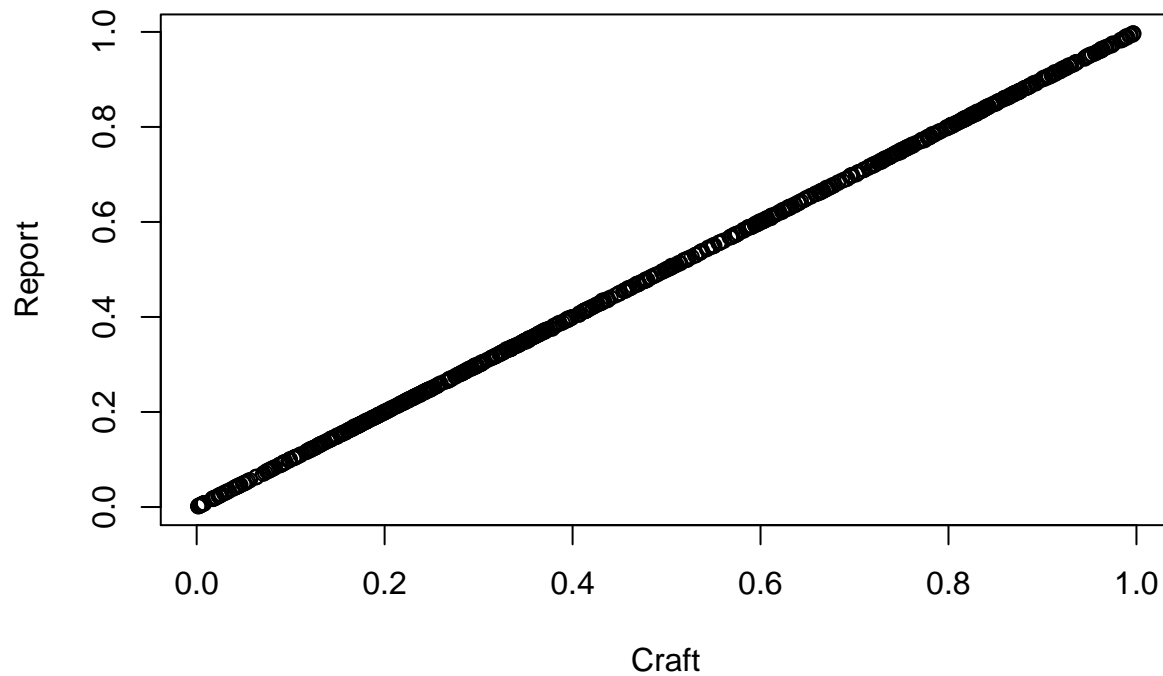
To integrate this inforamtion into the current GWAS for a given variant, prior distribution of variant effect size was set as normal with mean the effect size, and standard deviation the standard error.
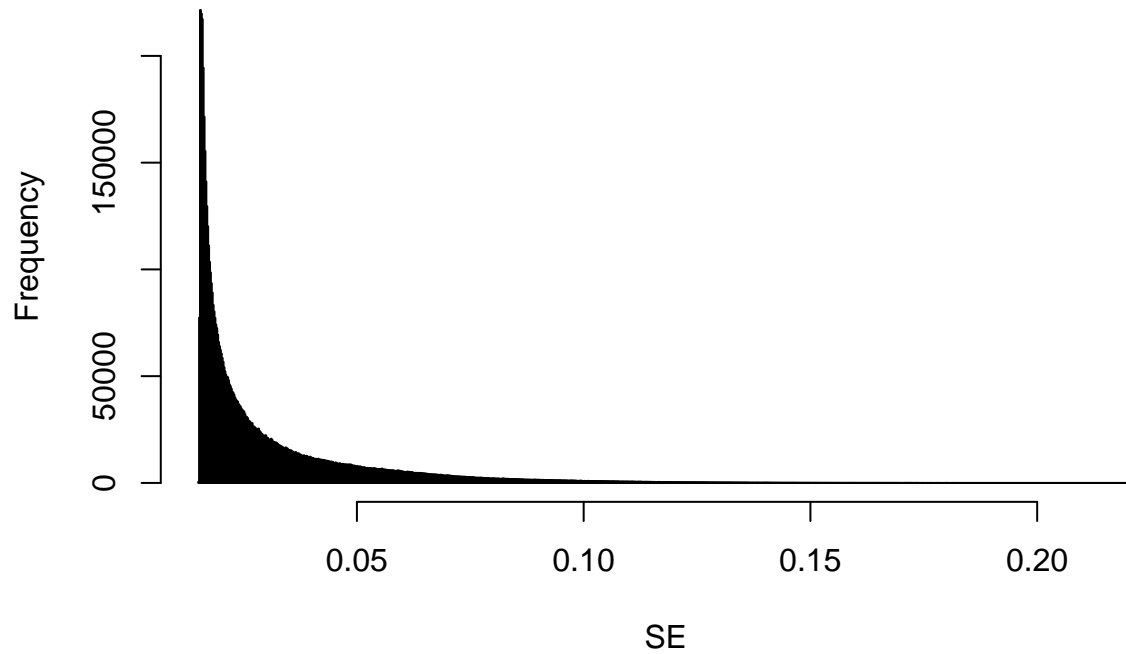
```
hist(igap$Beta, n = 1e3, xlab = "Effect size")
```

Histogram of igap$Beta
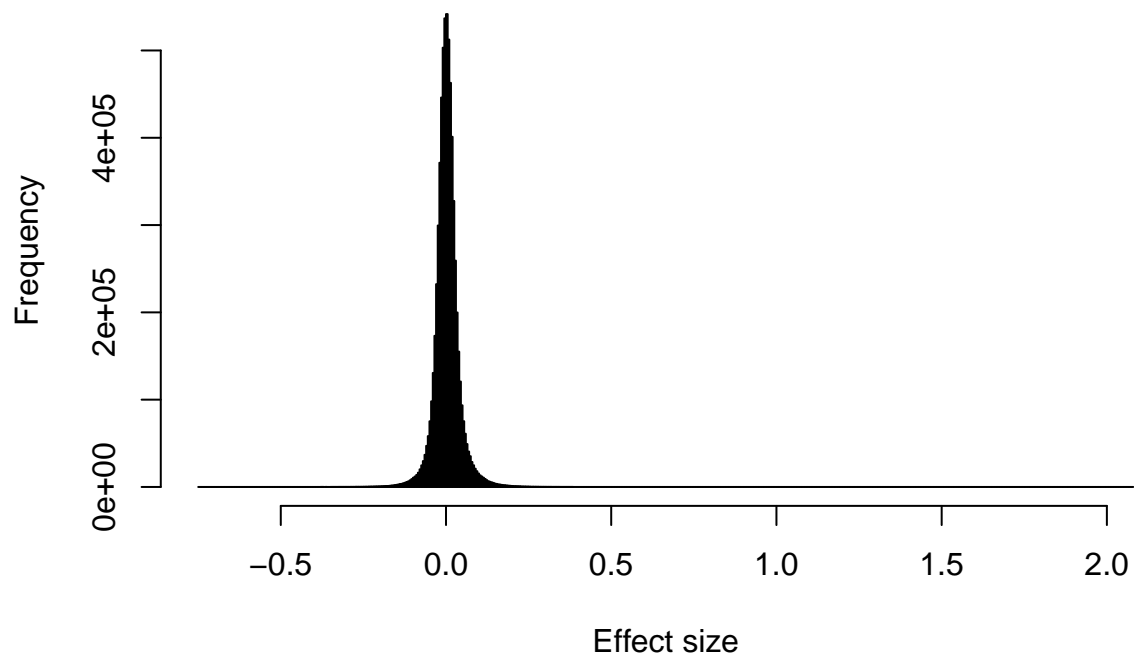

```
hist(igap$SE, n = 1e3, xlab = "SE")
```

Histogram of igap$SE


```r
table(igap$Beta > 1)
```

```
## 
##    FALSE      TRUE
## 6757184        36
```

```r
table(igap$Beta < -1)
```

```
## 
##    FALSE
## 6757220
```

```r
head(sort(igap$SE), n = 10)
```

```
##  [1] 0.0151 0.0151 0.0151 0.0151 0.0151 0.0151 0.0152 0.0152 0.0152 0.0152
```

```r
tail(sort(igap$SE), n = 10)
```

```
##  [1] 0.2049 0.2053 0.2062 0.2080 0.2085 0.2106 0.2125 0.2127 0.2130 0.2211
```

END