

# Generate plot in Figure 2

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Load the relevant libraries:

```
library(ggplot2)

## Warning: package 'ggplot2' was built under R version 3.3.3

library(reshape2)
library(dplyr)
library(scales)

## Warning: package 'scales' was built under R version 3.3.3

library(qvalue)
library(xtable)
```

Load the data and the results and add them to the data object:

```
load("BMI_GIANT_GWAS.RData")

tot <- BMI_GIANT_GWAS

load("BMI_GIANT_GWAS_results_logistic.RData")

tot$fitted0.8 <- fitted0.8
tot$fitted0.9 <- fitted0.9
tot$fitted.final.smooth <- fitted.final.smooth

load("BMI_GIANT_GWAS_results_Scott_theoretical.RData")

tot$ScottT <- pi0EstScott

load("BMI_GIANT_GWAS_results_Scott.RData")

tot$ScottE <- pi0EstScott

load("BMI_GIANT_GWAS_bootstrap_CIs_logistic.RData")

dim(tot)

## [1] 2500573      14

dim(perc.05.95)

## [1] 2500573      2

head(tot)

## Source: local data frame [6 x 14]
##
##       SNP     A1     A2 Freq_MAF_Hapmap      b      se      p      N
##       (chr) (chr) (chr)          (dbl)   (dbl)   (dbl)   (dbl)   (dbl)
## 1 rs10000000      G      A      0.3667 -0.0001  0.0043  0.98140 233572
```

```

## 2 rs10000010      T      C      0.4250  0.0022 0.0029 0.43840 339148
## 3 rs10000012      G      C      0.1917 -0.0096 0.0053 0.07009 236095
## 4 rs10000013      A      C      0.1667  0.0096 0.0043 0.02558 236048
## 5 rs10000017      C      T      0.2333  0.0038 0.0045 0.39840 235308
## 6 rs10000023      G      T      0.4083  0.0023 0.0037 0.53420 236022
## Variables not shown: Freq_MAF_Int_Hapmap (fctr), fitted0.8 (dbl),
##   fitted0.9 (dbl), fitted.final.smooth (dbl), ScottT (dbl), ScottE (dbl)
head(perc.05.95)

##          [,1]      [,2]
## 1 0.8946947 0.9062979
## 2 0.6841069 0.7169933
## 3 0.8973993 0.9056517
## 4 0.8976166 0.9070543
## 5 0.9038571 0.9139008
## 6 0.8667469 0.8766078

head(rownames(perc.05.95))

## [1] "1" "2" "3" "4" "5" "6"
identical(as.integer(rownames(perc.05.95)), 1:nrow(perc.05.95))

## [1] TRUE
tot$lower.CI <- perc.05.95[,1]
tot$upper.CI <- perc.05.95[,2]

```

Get range of estimates:

```

range(tot$fitted.final.smooth)

## [1] 0.6966151 1.0000000

range(tot$fitted0.8)

## [1] 0.7042345 1.0000000

range(tot$fitted0.9)

## [1] 0.6890391 1.0000000

```

Only use random sample of 50,000 SNPs in plot:

```

##get random sample of 50,000 SNPs
set.seed(310841)
d1 = tot %>% sample_n(5e4)

```

Create long data frame (for ggplot):

```

colnames(d1)[colnames(d1)=="ScottT"] <- "fitted.ScottT"
colnames(d1)[colnames(d1)=="ScottE"] <- "fitted.ScottE"

d3 <- melt(d1,
            id.vars=colnames(d1)[-grep("fitted", colnames(d1))],
            value.name = "pi0", variable.name = "lambda")
d3$lambda <- as.character(d3$lambda)
d3$lambda[d3$lambda=="fitted0.8"] <- "lambda=0.8"
d3$lambda[d3$lambda=="fitted0.9"] <- "lambda=0.9"
d3$lambda[d3$lambda=="fitted.final.smooth"] <- "final smoothed pi0(x)"

```

```

d3$lambda[d3$lambda=="fitted.ScottT"] <- "Scott theoretical"
d3$lambda[d3$lambda=="fitted.ScottE"] <- "Scott empirical"

d3$Freq_MAF_Int_Hapmap <- paste("MAF in", d3$Freq_MAF_Int_Hapmap)

head(d3)

##          SNP A1 A2 Freq_MAF_Hapmap      b      se      p      N
## 1 rs10510371 T  C       0.0250  0.0147  0.0152  0.3335 212965
## 2 rs918232   A  G       0.3417 -0.0034  0.0037  0.3581 236084
## 3 rs4816764  A  C       0.0083  0.0163  0.0131  0.2134 221771
## 4 rs17630047 A  G       0.1667  0.0004  0.0048  0.9336 236177
## 5 rs4609437  C  G       0.2500  0.0011  0.0042  0.7934 236028
## 6 rs11130746 G  A       0.2333 -0.0006  0.0042  0.8864 235634
##          Freq_MAF_Int_Hapmap lower.CI upper.CI      lambda      pi0
## 1 MAF in [0.000,0.127) 1.0000000 1.0000000 lambda=0.8 1.0000000
## 2 MAF in [0.302,0.500] 0.8662131 0.8766112 lambda=0.8 0.8838673
## 3 MAF in [0.000,0.127) 1.0000000 1.0000000 lambda=0.8 1.0000000
## 4 MAF in [0.127,0.302) 0.8976483 0.9073273 lambda=0.8 0.9101864
## 5 MAF in [0.127,0.302) 0.8975774 0.9070475 lambda=0.8 0.9101274
## 6 MAF in [0.127,0.302) 0.8999862 0.9096028 lambda=0.8 0.9118310

```

Function to change the way labels are displayed:

```

display_thousands <- function(l) {
  ##divide by 1000
  l1 <- l/1000
  ##add k afterwards
  l11 <- paste(l1, "k", sep="")

  l11
}

```

Generate Figure 2:

```

ggplot(d3, aes(x=N, y=pi0))+
  geom_vline(xintercept=median(tot$N), colour="grey50")+
  geom_ribbon(aes(ymin=lower.CI, ymax=upper.CI, group=Freq_MAF_Int_Hapmap), fill="grey50")+
  geom_line(aes(linetype=lambda)) +
  facet_grid(. ~ Freq_MAF_Int_Hapmap) +
  scale_x_continuous(labels=comma) +
  ylab("Estimated proportion of nulls") +
  scale_linetype_discrete(labels =
    c(expression(paste("Final smoothed ",
                      hat(pi)[0](x))),
      expression(paste(hat(pi)[0], "``^lambda",
                      (x),
                      " for ", lambda, "=",
                      0.8)),
      expression(paste(hat(pi)[0], "``^lambda",
                      (x),
                      " for ", lambda, "=",
                      0.9)),
      "Scott empirical",
      "Scott theoretical")) +

```

```

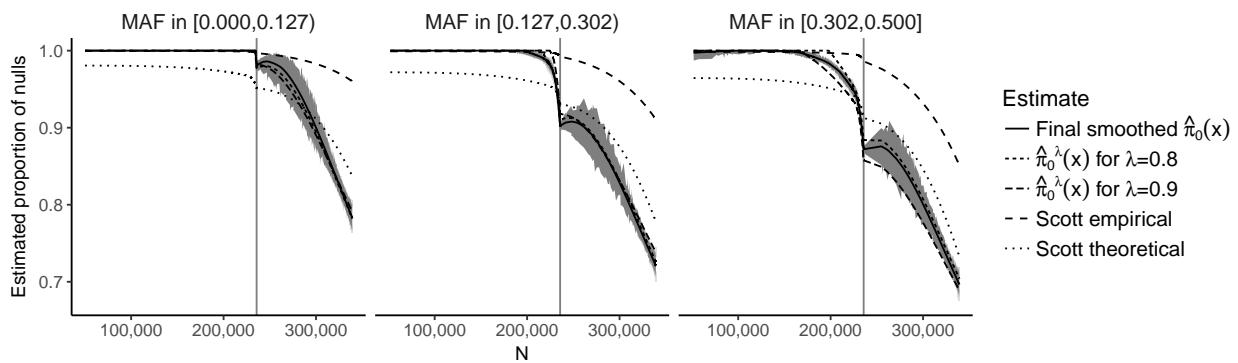
theme(axis.line = element_line(colour = "black"),
      plot.title = element_text(size = 16, hjust = 0.5),
      panel.grid.major = element_blank(),
      panel.grid.minor = element_blank(),
      panel.border = element_blank(),
      panel.background = element_blank(),
      legend.key = element_blank(),
      legend.text.align = 0,
      legend.title=element_text(size=13),
      legend.text=element_text(size=12),
      strip.background = element_blank(),
      strip.text.x = element_text(size = 12),
      axis.text.x = element_text(size=10),
      axis.text.y = element_text(size=10))+  

      ##axis.line.x = element_line(color="black", size = 0.5), ##this is to show axes - bug in this v  

      ##axis.line.y = element_line(color="black", size = 0.5)) +  

guides(linetype=guide_legend(title="Estimate"))

```



Get FDR for our method:

```

##first get BH q-values
qValsBH <- p.adjust(tot$p, method="BH")
##also get Storey q-values
qValsStorey <- qvalue(tot$p)$qvalues
##what is their difference
head(qValsStorey/qValsBH)

## [1] 0.9486617 0.9486617 0.9486617 0.9486617 0.9486617 0.9486617

qValsReg <- qValsBH*tot$fitted.smooth

tot$qValsBH <- qValsBH
tot$qValsStorey <- qValsStorey
tot$qValsReg <- qValsReg

sum(tot$qValsBH < 0.05)

## [1] 12500

sum(tot$qValsStorey < 0.05)

## [1] 12771

```

```

sum(tot$qValsReg < 0.05)

## [1] 13384

sum(FDRScott_emp < 0.05)

## [1] 7636

sum(FDRScott_theo < 0.05)

## [1] 16697

mean(tot$qValsBH < 0.05)

## [1] 0.004998854

mean(tot$qValsStorey < 0.05)

## [1] 0.005107229

mean(tot$qValsReg < 0.05)

## [1] 0.005352373

mean(FDRScott_emp < 0.05)

## [1] 0.0030537

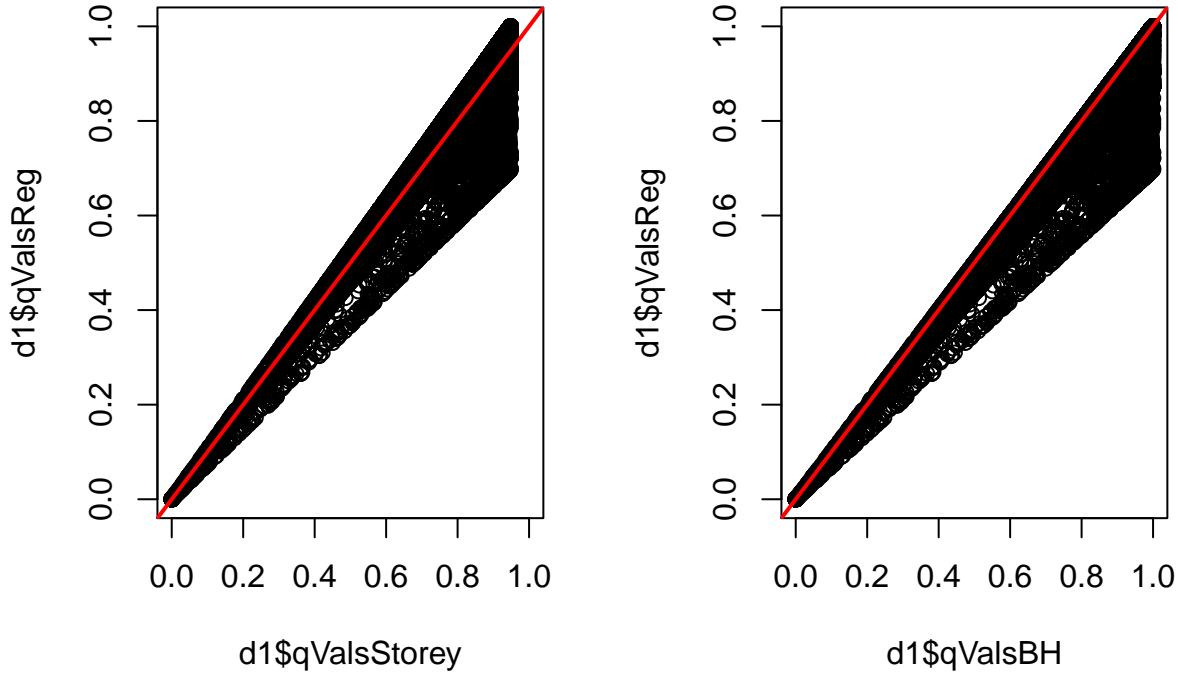
mean(FDRScott_theo < 0.05)

## [1] 0.00667727

set.seed(310841)
d1 = tot %>% sample_n(5e4)

par(mfrow=c(1,2))
plot(d1$qValsReg ~ d1$qValsStorey, xlim=c(0,1), ylim=c(0,1))
abline(a=0,b=1, col="red", lwd=2)
plot(d1$qValsReg ~ d1$qValsBH, xlim=c(0,1), ylim=c(0,1))
abline(a=0,b=1, col="red", lwd=2)

```



Make nice table for summary results:

```
xtable(data.frame(BL = sum(tot$qValsReg <= 0.05),
                  Scott_T = sum(FDRScott_theo <= 0.05),
                  Scott_E = sum(FDRScott_emp <= 0.05),
                  Storey = sum(tot$qValsStorey <= 0.05),
                  BH = sum(tot$qValsBH <= 0.05)))

## % latex table generated in R 3.3.1 by xtable 1.8-2 package
## % Thu Jun 22 11:23:44 2017
## \begin{table}[ht]
## \centering
## \begin{tabular}{rrrrrr}
##   \hline
##   & BL & Scott\_T & Scott\_E & Storey & BH \\
##   \hline
##   1 & 13384 & 16697 & 7636 & 12771 & 12500 \\
##   \hline
## \end{tabular}
## \end{table}
```

How many are in common between all the methods?

```
length(Reduce(intersect, list(which(tot$qValsReg <= 0.05),
                             which(FDRScott_theo <= 0.05),
                             which(FDRScott_emp <= 0.05),
                             which(tot$qValsStorey <= 0.05),
                             which(tot$qValsBH <= 0.05))))
```

```
[1] 6892
length(Reduce(intersect, list(which(tot$qValsReg <= 0.05),
                                which(tot$qValsStorey <= 0.05),
                                which(tot$qValsBH <= 0.05))))
```

```
[1] 12500
length(Reduce(intersect, list(which(tot$qValsStorey <= 0.05),
                                which(tot$qValsReg <= 0.05))))
```

```
[1] 12740
length(Reduce(intersect, list(which(FDRScott_theo <= 0.05),
                                which(tot$qValsReg <= 0.05))))
```

```
[1] 13119
length(Reduce(intersect, list(which(FDRScott_theo <= 0.05),
                                which(FDRScott_emp <= 0.05),
                                which(tot$qValsBH <= 0.05))))
```

```
[1] 6892
length(Reduce(intersect, list(which(FDRScott_emp <= 0.05),
                                which(tot$qValsBH <= 0.05))))
```

```
[1] 6892
length(Reduce(intersect, list(which(FDRScott_theo <= 0.05),
                                which(tot$qValsBH <= 0.05))))
```

```
[1] 12251
```

## Session Information

```
devtools::session_info()

## Session info -----
## setting  value
## version R version 3.3.1 (2016-06-21)
## system   x86_64, mingw32
## ui        RTerm
## language (EN)
## collate  English_United States.1252
## tz       America/New_York
## date     2017-06-22

## Packages -----
## package    * version date      source
## assertthat  0.1     2013-12-06 CRAN (R 3.3.1)
## backports   1.0.4   2016-10-24 CRAN (R 3.3.1)
## BiocStyle   * 2.0.3   2016-08-04 Bioconductor
## codetools   0.2-14  2015-07-15 CRAN (R 3.3.1)
## colorspace  1.2-6   2015-03-11 CRAN (R 3.3.1)
## DBI        0.4-1   2016-05-08 CRAN (R 3.3.1)
## devtools    1.12.0  2016-06-24 CRAN (R 3.3.3)
```

```
## digest      0.6.9  2016-01-08 CRAN (R 3.3.1)
## dplyr       * 0.4.3  2015-09-01 CRAN (R 3.3.1)
## evaluate     0.10   2016-10-11 CRAN (R 3.3.1)
## ggplot2      * 2.2.1  2016-12-30 CRAN (R 3.3.3)
## gtable       0.2.0   2016-02-26 CRAN (R 3.3.1)
## htmltools    0.3.5   2016-03-21 CRAN (R 3.3.1)
## knitr        1.15.1  2016-11-22 CRAN (R 3.3.1)
## labeling     0.3     2014-08-23 CRAN (R 3.3.0)
## lazyeval     0.2.0   2016-06-12 CRAN (R 3.3.1)
## magrittr     1.5     2014-11-22 CRAN (R 3.3.1)
## memoise      1.0.0   2016-01-29 CRAN (R 3.3.1)
## munsell      0.4.3   2016-02-13 CRAN (R 3.3.1)
## plyr         1.8.4   2016-06-08 CRAN (R 3.3.1)
## qvalue       * 2.4.2  2016-05-16 Bioconductor
## R6            2.1.2   2016-01-26 CRAN (R 3.3.1)
## Rcpp          0.12.10 2017-03-19 CRAN (R 3.3.3)
## reshape2      * 1.4.1  2014-12-06 CRAN (R 3.3.1)
## rmarkdown     1.2     2016-11-21 CRAN (R 3.3.1)
## rprojroot    1.1     2016-10-29 CRAN (R 3.3.1)
## scales        * 0.4.1  2016-11-09 CRAN (R 3.3.3)
## stringi       1.1.1   2016-05-27 CRAN (R 3.3.0)
## stringr       1.0.0   2015-04-30 CRAN (R 3.3.1)
## tibble        1.2     2016-08-26 CRAN (R 3.3.2)
## withr         1.0.2   2016-06-20 CRAN (R 3.3.1)
## xtable        * 1.8-2  2016-02-05 CRAN (R 3.3.1)
## yaml          2.1.13  2014-06-12 CRAN (R 3.3.1)
```