Generate plot in Figure 4

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Load the relevant libraries:

```
library(ggplot2)
library(reshape2)
library(dplyr)
```

Load the data and the results:

```
load("BMI_GIANT_GWAS.RData")
load("BMI_GIANT_GWAS_results.RData")
load("BMI_GIANT_GWAS_results_Scott.RData")

tot <- BMI_GIANT_GWAS
```

Add the results to the data object:

```
##add the estimates from Scott
tot$Scott <- pi0EstScott

##add the estimates from our approach
##add the estimates for lambda=0.8, lambda=0.9, final smoothed value
tot$fitted0.8 <- fitted0.8
tot$fitted0.9 <- fitted0.9
tot$fitted.final.smooth <- fitted.final.smooth
```

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)
```
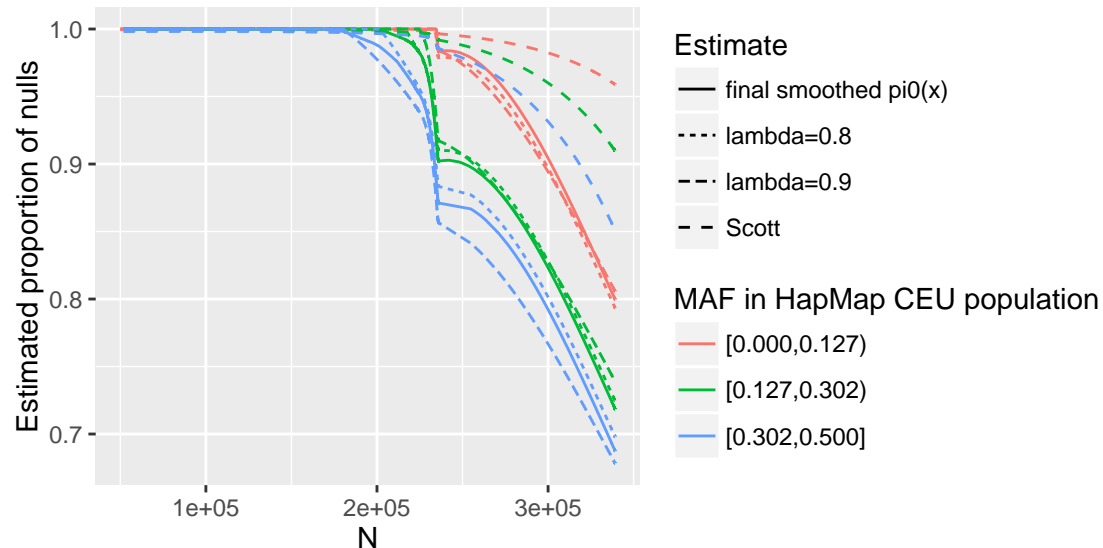
Create long data frame (for ggplot):

```
colnames(d1)[colnames(d1)=="Scott"] <- "fitted.Scott"

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.Scott"] <- "Scott"
```

Generate Figure 4:

```
ggplot(d3, aes(x=N, y=pi0))+
  geom_line(aes(col=Freq_MAF_Int_Hapmap, linetype=lambda)) +
  ylab("Estimated proportion of nulls") +
  guides(color=guide_legend(title="MAF in HapMap CEU population"),
         linetype=guide_legend(title="Estimate"))
```


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     2016-10-28

## Packages ---------------------------------------------------------------

##   package    * version date       source
##   assertthat   0.1     2013-12-06 CRAN (R 3.3.1)
##   BiocStyle  * 2.0.2   2016-05-16 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 3.3.1)
##   digest       0.6.9   2016-01-08 CRAN (R 3.3.1)
```

```
## dplyr      * 0.5.0   2016-06-24 CRAN (R 3.3.1)
## evaluate     0.9     2016-04-29 CRAN (R 3.3.1)
## formatR      1.4     2016-05-09 CRAN (R 3.3.1)
## ggplot2    * 2.1.0   2016-03-01 CRAN (R 3.3.1)
## 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        1.13    2016-05-09 CRAN (R 3.3.1)
## labeling     0.3     2014-08-23 CRAN (R 3.3.0)
## 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)
## R6           2.1.2   2016-01-26 CRAN (R 3.3.1)
## Rcpp         0.12.6  2016-07-19 CRAN (R 3.3.1)
## reshape2   * 1.4.1   2014-12-06 CRAN (R 3.3.1)
## rmarkdown    1.0     2016-07-08 CRAN (R 3.3.1)
## scales       0.4.0   2016-02-26 CRAN (R 3.3.1)
## 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       1.1     2016-07-04 CRAN (R 3.3.1)
## withr        1.0.2   2016-06-20 CRAN (R 3.3.1)
## yaml         2.1.13  2014-06-12 CRAN (R 3.3.1)
```