

Generate plot in Figure 4

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2016-10-27

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)
```

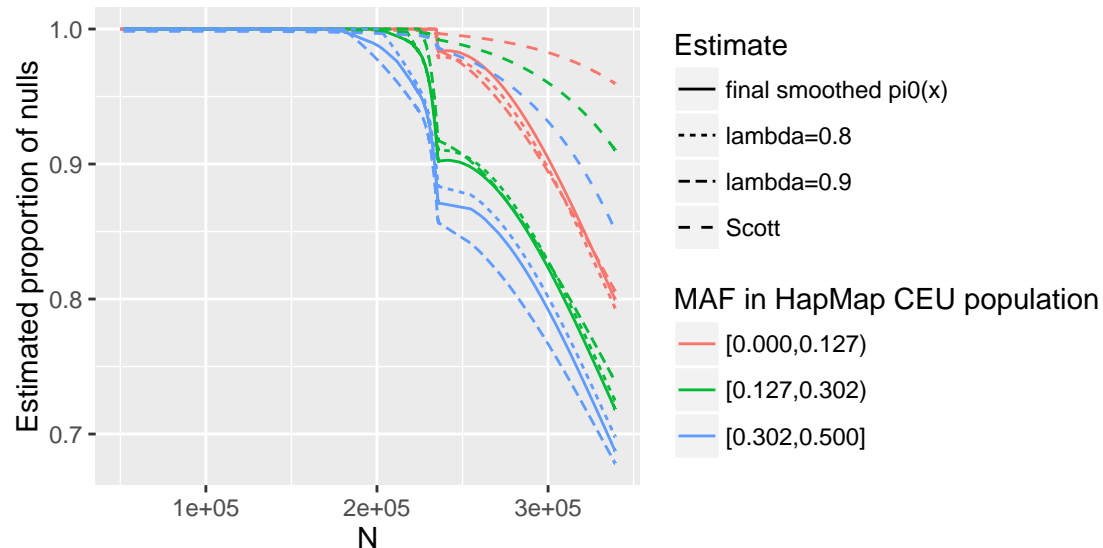
Create long data frame (for ggplot):

```
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     2016-10-27

## 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)