

Generate plot in Figure 4

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2017-01-06

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)
```

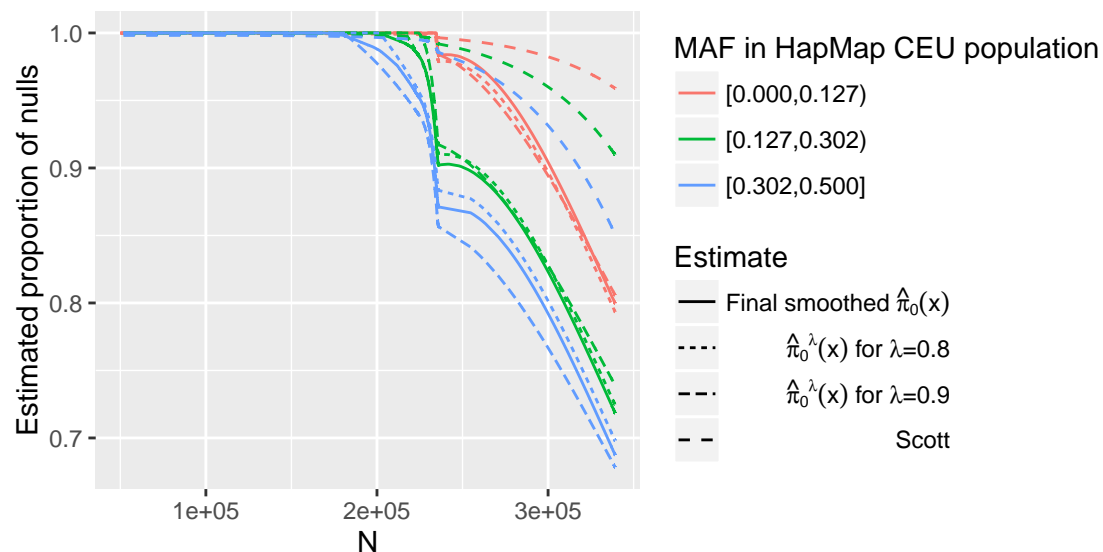
Create long data frame (for ggplot):

```
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") +
  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")) +
  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 2017-01-06
```

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 3.3.2)
##	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	0.10	2016-10-11	CRAN (R 3.3.2)
##	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	1.15.1	2016-11-22	CRAN (R 3.3.2)
##	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	1.2.9000	2016-11-28	Github (rstudio/rmarkdown@c46d1d1)
##	rprojroot	1.1	2016-10-29	CRAN (R 3.3.2)
##	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	2.1.14	2016-11-12	CRAN (R 3.3.2)