

Figure 2 of Deleterious Alleles paper

```
#setwd("~/Documents/Github/pvpDiallel/")
knitr::opts_knit$set(root.dir=normalizePath('..'))
```

To reproduce the figures, we should set `pvpDiallel` as the root path, i.e. `setwd("~/Documents/Github/pvpDiallel/")`. And then use `knitr` package to get a pdf file. Or simply click Knit PDF icon on RStudio. Note, to produce panels into separate pdf files, we should set `getpdf` into `TRUE` (i.e. `getpdf=TRUE`) when calling the plotting functions.

First of all, determine font size and set the `getpdf` option:

```
#par(mar=c(5,4,4,2))
#par(font=2, font.lab=2, font.axis=2)
fs = 1.4 # times bigger than default
fsize = 16 # absolute font size
getpdf = FALSE # get figures in separated pdf [TRUE] or not [FALSE]
```

Figure 2a

```
plot_fig2a <- function(outfile, getpdf){
  library("beanplot")

  avar5 <- read.csv("cache/rsnp_var_nf5.csv")
  ### Note: 0.15 is missing from the analysis for the random samples
  ### therefore, concatenate 0.1 and 0.15 into a single category
  myd <- subset(avar5, sample != 0)
  myd[myd$frq==0.10, ]$frq <- 0.15

  myd0 <- subset(avar5, sample == 0)
  myd0[myd0$frq==0.15, ]$totvar <- sum(myd0[myd0$frq==0.15, ]$totvar)
  myd0 <- myd0[-1,]

  ##### for trait perse
  beanplot(totvar ~ frq, data = myd, ll = 0.04, border = NA, cex.axis=fs, cex.names=fs, cex.lab=fs,
    what=c(0, 1, 0, 1), col=c(c("grey", "black")), cex=1.3, xlab="Allele Frequency", ylab="Variance Explained")
  for(i in 1:nrow(myd0)){
    lines(x=c(i-0.3, i+0.3), y=c(myd0$totvar[i], myd0$totvar[i]), lwd=2, col="red")
  }

  if(getpdf == TRUE){
    pdf(outfile, width=6, height=5)
    ##### for trait perse
    beanplot(totvar ~ frq, data = myd, ll = 0.04, border = NA, cex.axis=fs, cex.names=fs, cex.lab=fs,
      what=c(0, 1, 0, 1), col=c(c("grey", "black")), xlab="Allele Frequency", ylab="Variance Explained")
    for(i in 1:nrow(myd0)){
      lines(x=c(i-0.3, i+0.3), y=c(myd0$totvar[i], myd0$totvar[i]), lwd=2, col="red")
    }
  }
}
```

```

    }
    dev.off()
  }
}

#####
plot_fig2a(outfile="graphs/Fig2a_del_snps.pdf", getpdf)

```

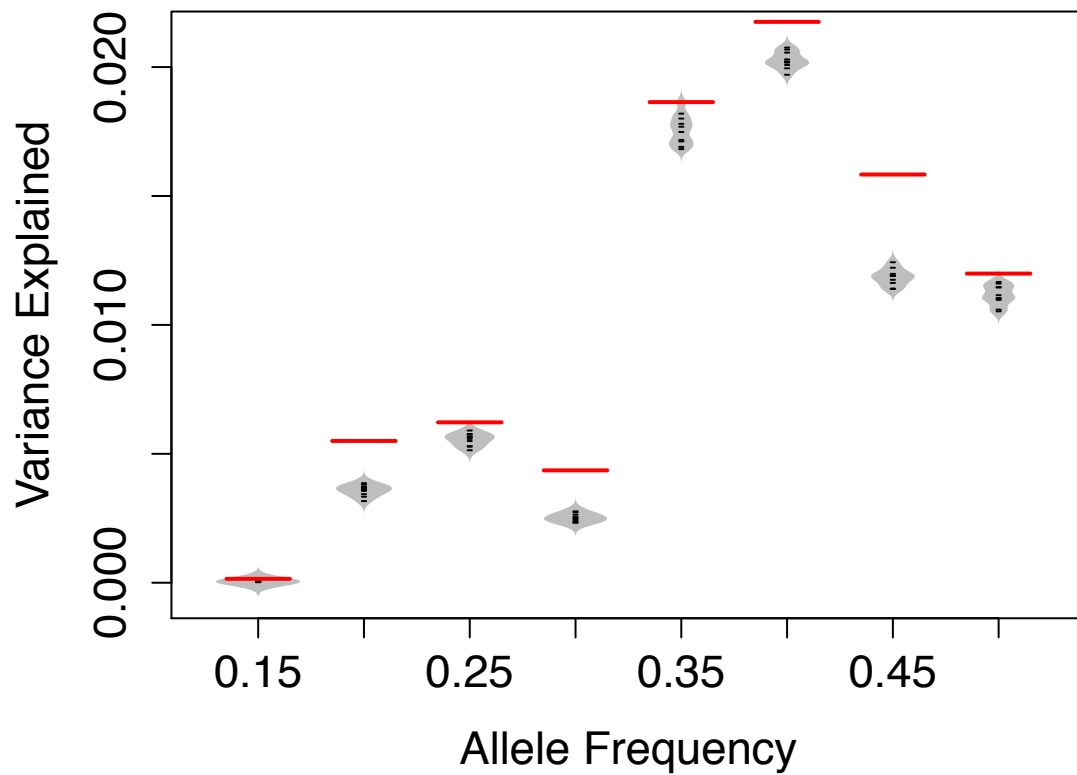


Figure 2b

```

library(ggplot2)

## Warning: package 'ggplot2' was built under R version 3.2.4

library(reshape2)
source("lib/multiplot.R")

plot_eff <- function(outfile, getpdf){
  res1 <- read.csv("cache/gblup_var.csv")
  res2 <- read.csv("cache/kval_perse_5x.csv")
  med <- read.csv("cache/loh_pBPHmax_median.csv")
  bymed <- med[order(med$h),]

  #####
  theme_set(theme_grey(base_size = 18))

```

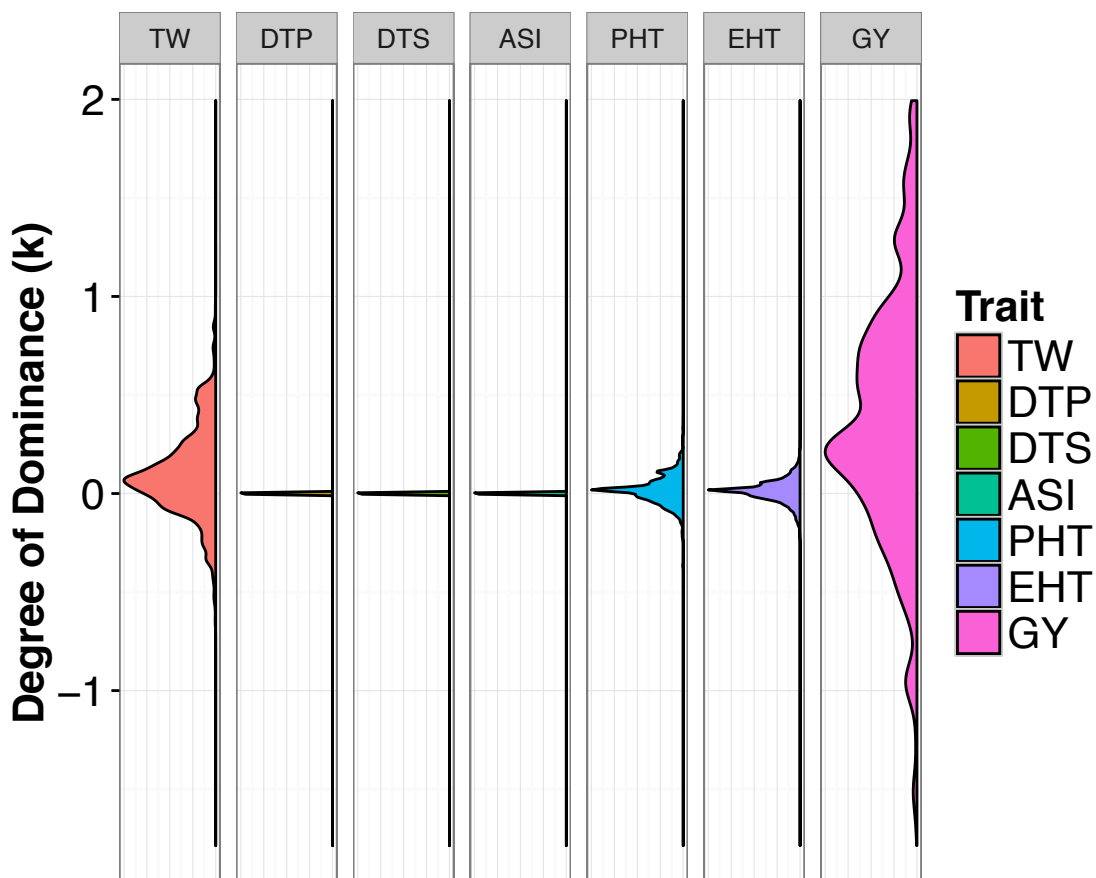
```

res2$trait <- toupper(res2$trait)
res2$trait <- factor(res2$trait, levels=bymed$trait)
p2 <- ggplot(data=res2) +
  geom_density(aes(x= k, y=-..scaled.., fill= as.factor(trait)) ) +
  #guides(fill=FALSE) +
  labs(y=NULL, fill="Trait") + theme_bw() +
  theme(axis.text.x=element_blank(), axis.ticks.x=element_blank(),
        axis.text=element_text(size=fsize),
        axis.title=element_text(size=fsize, face="bold"),
        legend.title = element_text(size=fsize, face="bold"),
        legend.text = element_text(size=fsize)) +
  coord_flip() + xlab("Degree of Dominance (k)") + ylab("") + facet_grid(~ trait)

return(p2)
}

#####
p <- plot_eff(outfile="graphs/Fig2b_var.pdf", getpdf)
p

```



```

if(getpdf == TRUE){
  pdf("graphs/Fig2b_var.pdf", width=6, height=4)
}

```

```

    p
    dev.off()
}

```

Figure 2c-e

```

library(wesanderson)
library(data.table)

##
## Attaching package: 'data.table'

## The following objects are masked from 'package:reshape2':
##
##      dcast, melt

source("lib/multiplot.R")

plot_adk_gerp <- function(outfile, getpdf){

  dat <- fread("largedata/gerpdata1x.csv", data.table=FALSE)
  dat$trait <- toupper(dat$trait)
  med2 <- read.csv("cache/loh_pBPHmax_median.csv")
  out <- read.csv("cache/eff_adk_1x.csv")
  #cols <- wes_palette(7, name = "Zissou", type = "continuous")
  cols <- c("#f6546a", "#daa520", "#00ff00", "#66cdaa", "#3b5998", "#8a2be2", "#ff00ff")
  theme_set(theme_grey(base_size = 18))

  getlty <- function(df, eff, cutoff=0.05){
    df$l <- 2
    if(nrow(df[df[, eff] < cutoff, ]) > 0) df[df[, eff] < cutoff, ]$l <- 1
    return(df)
  }

  lty1 <- getlty(df=out, eff="effa", cutoff=0.05)$l
  p1 <- ggplot(dat, aes(x=RS, y=Effect_A, colour=factor(trait, levels=med2$trait),
                      linetype=factor(trait, levels=med2$trait))) +
    labs(colour="Traits") +
    theme_bw() +
    xlab("GERP Score") +
    ylab("Additive Effect") +
    scale_color_manual(values=cols) +
    scale_linetype_manual(values=lty1) +
    guides(colour=FALSE, linetype=FALSE) +
    geom_smooth(method="gam", size=1.3) +
    theme(axis.text.y = element_text(angle = 90, hjust = 1),
          axis.text.x=element_blank(), axis.ticks.x=element_blank(),
          axis.text=element_text(size=fsize),
          axis.title=element_text(size=fsize, face="bold"),
          legend.title = element_text(size=fsize, face="bold"),

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        legend.text = element_text(size=fsize))

lty2 <- getlty(df=out, eff="effd", cutoff=0.05)$l
p2 <- ggplot(dat, aes(x=RS, y=Effect_D, colour=factor(trait, levels=med2$trait),
                    linetype=factor(trait, levels=med2$trait))) +
  labs(colour="Traits") +
  theme_bw() +
  xlab("GERP Score") +
  ylab("Dominant Effect") +
  scale_color_manual(values=cols) +
  scale_linetype_manual(values=lty2) +
  guides(colour=FALSE, linetype=FALSE) +
  geom_smooth(method="gam", size=1.3) + # Add linear regression line
  theme(axis.text.y = element_text(angle = 90, hjust = 1),
        axis.text.x=element_blank(), axis.ticks.x=element_blank(),
        axis.text=element_text(size=fsize),
        axis.title=element_text(size=fsize, face="bold"),
        legend.title = element_text(size=fsize, face="bold"),
        legend.text = element_text(size=fsize))

lty3 <- getlty(df=out, eff="effk", cutoff=0.05)$l
p3 <- ggplot(dat, aes(x=RS, y=k, colour=factor(trait, levels=med2$trait),
                    linetype=factor(trait, levels=med2$trait))) +
  labs(colour="Traits") +
  theme_bw() +
  xlab("GERP Score") +
  ylab("Degree of Domiance (k)") +
  scale_color_manual(values=cols) +
  scale_linetype_manual(values=lty3) +
  guides(colour=FALSE, linetype=FALSE) +
  theme(axis.text.y = element_text(angle = 90, hjust = 1),
        axis.text.x=element_blank(), axis.ticks.x=element_blank(),
        axis.text=element_text(size=fsize),
        axis.title=element_text(size=fsize, face="bold"),
        legend.title = element_text(size=fsize, face="bold"),
        legend.text = element_text(size=fsize)) +
  geom_smooth(method="gam", size=1.3) # Add linear regression line

multiplot(p1, p2, p3, cols=3)
if(getpdf == TRUE){
  pdf(outfile, width=13, height=4)
  multiplot(p1, p2, p3, cols=3)
  dev.off()
}

}

####
plot_adk_gerp(outfile="graphs/Fig2c-e_adk.pdf", getpdf)

```

