

manhattan_plots

The aim of this notebook is to demonstrate a way to create custom Manhattan plots for BLUPf90 (https://masuday.github.io/blupf90_tutorial/) output

```
library(tidyverse)

## — Attaching packages —
tidyverse 1.3.0 —

## ✓ ggplot2 3.3.2      ✓ purrr  0.3.4
## ✓ tibble  3.0.3      ✓ dplyr  1.0.0
## ✓ tidyr   1.1.0      ✓ stringr 1.4.0
## ✓ readr   1.3.1      ✓ forcats 0.5.0

## — Conflicts —
tidyverse_conflicts() —
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()    masks stats::lag()
```

Loading data for first plot

```
dfvar <- read.table("~/macierz/ch4_ppm/models/Sped/chrsnpvar")
dfvar <- dfvar %>% filter(V2 == 6 & V1 == 1)
x <- dfvar$V4
y <- dfvar$V3
```

Manhattan plot for % variance explained by each SNP

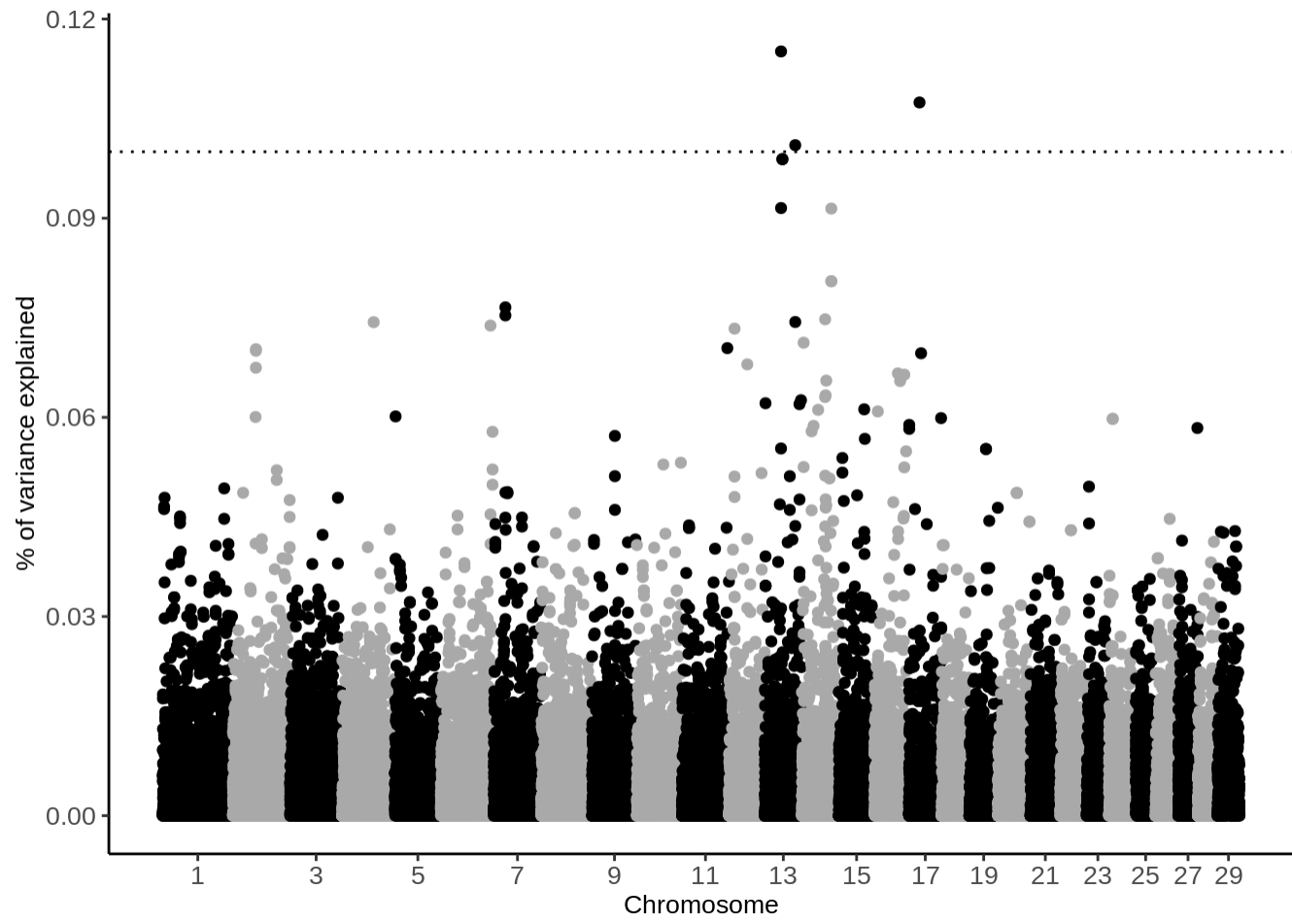
```
chrlist <- c()

for (i in 1:max(unique(dfvar$V5))) {
  chrlist[i] <- median(dfvar$V4[dfvar$V5 == i])
}

dfvar %>% ggplot(aes(x = x, y = y, col = as.factor(dfvar$V5))) + geom_point() + theme_classic() +
  theme(
    legend.position = "none",
    axis.title = element_text(size = 14),
    axis.text = element_text(size = 14)) +
    scale_x_continuous(labels = seq(1,29,2), breaks = chrlist[seq(1,29,2)]) +
    scale_color_manual(values = rep(c("#000000", "#A9A9A9"), length(unique(dfvar$V5)))) +
    ylab('% of variance explained') +
    xlab('Chromosome') +

    geom_hline(yintercept = 0.1, linetype = 'dotted') +
    theme(plot.title = element_text(size = 10, hjust=0.5), axis.title.x = element_text(size = 10), axis.title.y = e
    lement_text(size = 10), axis.text.x = element_text(size = 10), axis.text.y = element_text(size = 10))

## Warning: Use of `dfvar$V5` is discouraged. Use `V5` instead.
```



Loading data for second plot

```
dfvar <- read.table("~/macierz/ch4_ppm/models/Sped/chrsnp_pval")
dfvar <- dfvar %>% filter(V2 == 6 & V1 == 1)
x <- dfvar$V4
y <- dfvar$V3
```

Classic Manhattan plot of -log10 pvalues for each SNP

```
chrlist <- c()

for (i in 1:max(unique(dfvar$V5))) {
  chrlist[i] <- median(dfvar$V4[dfvar$V5 == i])
}

dfvar %>% ggplot(aes(x = x, y = y, col = as.factor(dfvar$V5))) + geom_point() + theme_classic() +

  theme(
    legend.position = "none",
    plot.title = element_text(size = 20, hjust=0.5),
    axis.text = element_text(size = 20)) +
    scale_x_continuous(labels = seq(1,29,2), breaks = chrlist[seq(1,29,2)]) +
    scale_color_manual(values = rep(c("#000000", "#A9A9A9"), length(unique(dfvar$V5)))) +
    ylab(expression('-log'[10]'(p-value)')) +
    xlab('Chromosome') +
    theme(plot.title = element_text(size = 10, hjust=0.5), axis.title.x = element_text(size = 10), axis.title.y = e
    lement_text(size = 10), axis.text.x = element_text(size = 10), axis.text.y = element_text(size = 10))

## Warning: Use of `dfvar$V5` is discouraged. Use `V5` instead.
```

