

FQ2

2025-11-07

```
library(lme4)

## Loading required package: Matrix

library(tibble)
library(dplyr)

##
## Attaching package: 'dplyr'

## The following objects are masked from 'package:stats':
## 
##     filter, lag

## The following objects are masked from 'package:base':
## 
##     intersect, setdiff, setequal, union

library(tidyverse)

## -- Attaching core tidyverse packages ----- tidyverse 2.0.0 --
## vforcats    1.0.0    vreadr      2.1.5
## vggplot2    3.5.2    vstringr   1.5.1
## vlubridate  1.9.4    vtidyrm   1.3.1
## vpurrr      1.0.4

## -- Conflicts ----- tidyverse_conflicts() --
## xtidyrm::expand() masks Matrix::expand()
## xdplyr::filter() masks stats::filter()
## xdplyr::lag()    masks stats::lag()
## xtidyrm::pack()  masks Matrix::pack()
## xtidyrm::unpack() masks Matrix::unpack()
## i Use the conflicted package (<http://conflicted.r-lib.org/>) to force all conflicts to become errors

library(ggthemes)
library(ggrepel)
library(lfmm)
library(RSpectra)
load("growth_light_time.lmer.RData")
source("manhattan_plot.R")
```

```

## 
## Attaching package: 'scales'
## 
## The following object is masked from 'package:purrr':
## 
##     discard
## 
## The following object is masked from 'package:readr':
## 
##     col_factor

pheno_2023 <- ranef(growth_light_time.lmer)$parent_pop %>%
  as_tibble(rownames = "parent_pop", .name_repair = "unique") %>%
  rename(blup_intercept = `Intercept)...1`,
         blup_light = `weekly_avg_SlrW2`) %>%
  mutate(model = "Y2023")

```

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## New names:
## * '(Intercept)' -> '(Intercept)...1'
## * '(Intercept)' -> '(Intercept)...3'

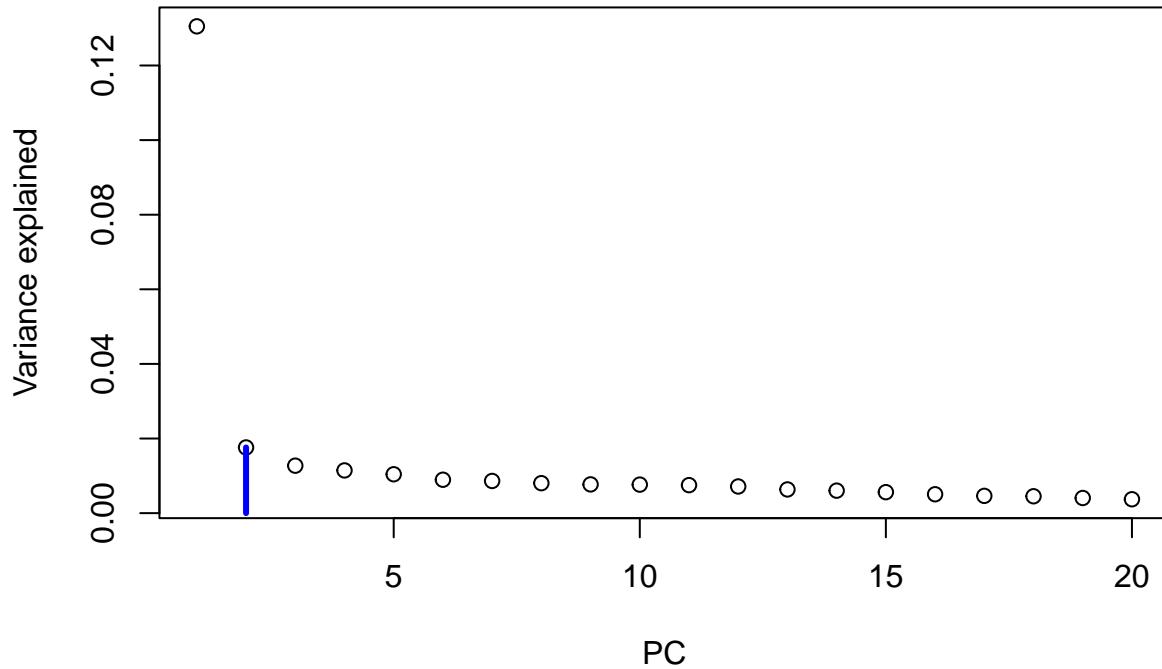
```

```
geno_23 <- read.delim("Data/merged_maf_common_WL2_2023.tsv", header = TRUE)
```

```

Y <- as.matrix(geno_23[,-1])
pc <- prcomp(Y)
plot(pc$sdev[1:20]^2, xlab = 'PC', ylab = "Variance explained")
points(2,pc$sdev[2]^2, type = "h", lwd = 3, col = "blue")

```



```

Y <- as.matrix(geno_23[, -1])
Y <- t(Y)
X <- matrix(scale(pheno_2023$blup_light), ncol = 1)
rownames(X) <- pheno_2023$parent_pop
colnames(X) <- "blup_light"
common <- intersect(rownames(X), rownames(Y))
Y <- Y[common,]
X <- X[common, , drop = FALSE]
mod.lfmm <- lfmm_ridge(Y = Y,
                         X = X,
                         K = 2)

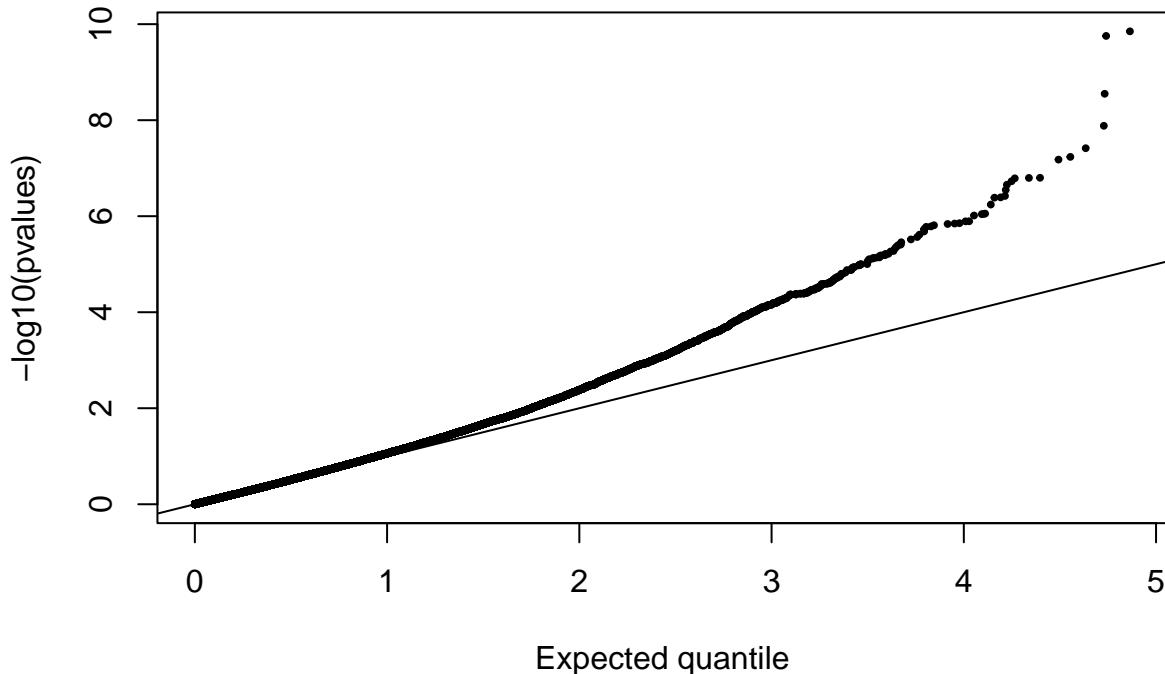
```

```

pv <- lfmm_test(Y = Y,
                  X = X,
                  lfmm = mod.lfmm,
                  calibrate = "gif")
pvalues <- pv$calibrated.pvalue

#QQ plot
qqplot(rexp(length(pvalues), rate = log(10)),
       -log10(pvalues), xlab = "Expected quantile",
       pch = 19, cex = .4)
abline(0,1)

```



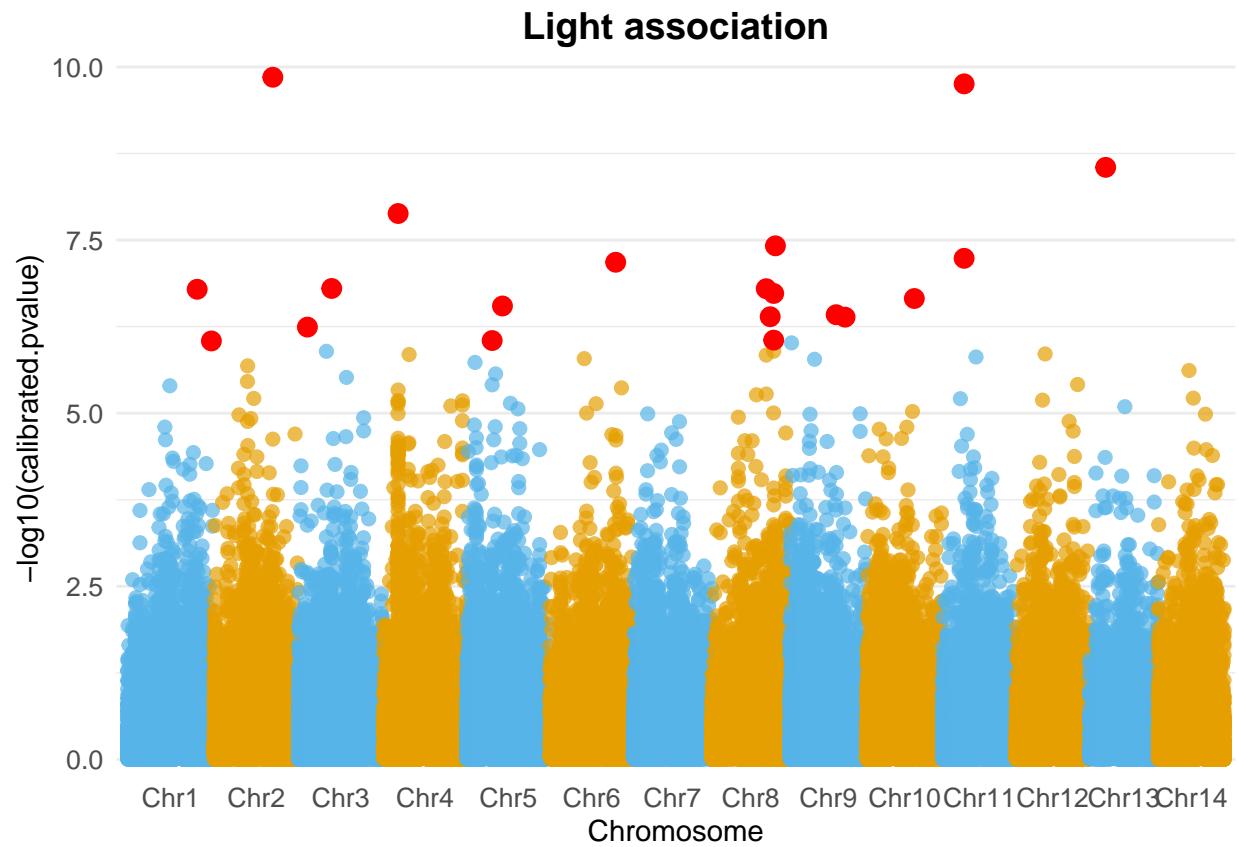
```

plot_data = tibble(loci = geno_23[,1], p_val = pv$pvalue[,1], calibrated.pvalue = pv$calibrated.pvalue[,
separate_wider_delim(loci, delim = ":" , names = c("chr", "bp")) |>
filter(str_detect(chr, "Chr")) |>
mutate(p.bonf = p.adjust(p_val, method = "bonferroni"),
bp = as.numeric(bp))

light_manhattan = plot_manhattan(plot_data,
                                chr_col = "chr",
                                pos_col = "bp",
                                value_col = "calibrated.pvalue",
                                transform = "neglog10",
                                title = "Light association",
                                highlight_top_n = 20)

print(light_manhattan)

```



```
# Save plot  
ggsave("light_interaction23.png", light_manhattan, width = 12, height = 6, dpi = 300)
```