

Genetic mapping with the Oregon Wolfe Barley population using R/qt12

PBG621

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```
setwd("C://PBG621_2022/Labs/Rqt12")
```

Install R/qt12

```
install.packages("qt12")  
library(qt12)
```

Read in data using a control file

Information about input file formats is here https://kbroman.org/qt12/assets/vignettes/input_files.html.

```
owb <- read_cross2("OWB_82_SpikeLen.yaml")
```

Look at a summary of the data

```
summary(owb)
```

Insert pseudomarkers into the genetic map

These are equivalent to the “Q” markers used in lecture examples to signify QTL whose precise positions are unknown relative to marker positions.

```
map <- insert_pseudomarkers(owb$gmap, step=1)
```

Calculate conditional genotype probabilities

```
pr <- calc_genoprob(owb, map, error_prob=0.002)
```

Calculate a kinship matrix

```
kinship <- calc_kinship(pr)
```

Perform a basic genome scan, then plot the results

```
out <- scan1(pr, owb$pheno)

par(mar=c(5.1, 4.1, 1.1, 1.1))
ymx <- maxlod(out) # overall maximum LOD score
plot(out, map, lodcolumn=1, col="slateblue", ylim=c(0, ymx*1.02))
legend("topleft", lwd=2, col=c("slateblue"), colnames(out), bg="gray90")
```

Perform a genome scan using a linear mixed model including kinship

```
out_mlm <- scan1(pr, owb$pheno, kinship)
par(mar=c(5.1, 4.1, 1.1, 1.1))
ymx <- maxlod(out_mlm) # overall maximum LOD score
plot(out_mlm, map, lodcolumn=1, col="slateblue", ylim=c(0, ymx*1.02))
legend("topleft", lwd=2, col=c("slateblue"), colnames(out_mlm), bg="gray90")
```

Perform a genome scan using the binary phenotypes option

```
out_bn <- scan1(pr, owb$pheno, model = "binary")
par(mar=c(5.1, 4.1, 1.1, 1.1))
ymx <- maxlod(out) # overall maximum LOD score
plot(out_bn, map, lodcolumn=1, col="slateblue", ylim=c(0, ymx*1.02))
legend("topleft", lwd=2, col=c("slateblue"), colnames(out), bg="gray90")
```

```
operm <- scan1perm(pr, owb$pheno, n_perm=1000)
summary(operm)
```

Estimate QTL effects

```
c2eff_Nud <- scan1coef(pr[, "2H"], owb$pheno)
par(mar=c(4.1, 4.1, 1.1, 2.6), las=1)
col <- c("slateblue", "darkgreen")
plot(c2eff_Nud, map["2H"], columns=1:2, col=col)
last_coef <- unclass(c2eff_Nud)[nrow(c2eff_Nud),] # pull out last coefficients
for(i in seq(along=last_coef))
  axis(side=4, at=last_coef[i], names(last_coef)[i], tick=FALSE, col.axis=col[i])
```