Rqtl_code V.3

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1 Works for me dx.doi.org/10.17504/protocols.io.bmwtk7en

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```
##Install_rqtl
install.packages("qtl")
##load_package
library(qtl)

##Trait_data
mycross <- read.cross("csv", file = "trait_data.csv")
mycross <- jittermap(mycross)
mycross <- calc.genoprob(mycross, step=1.0, off.end=0.0, error.prob=1.0e-4, map.function ="haldane", stepwidth = "fixed")
mycross <-sim.geno(mycross, n.draws=10000, step =1.0, off.end=0.0, error.prob=1.0e-4, map.function="haldane", stepwidth
="fixed")

##Covariate_sex
ac <- pull.pheno(mycross, c("sex"))
#Main_effect_sex
out.covar<- scanone(mycross, addcovar=ac, pheno.col=1, model ="normal", method ="hk")
out.covar.perm <- scanone(mycross,addcovar=ac, model="normal", method="hk", n.perm=10000)
summary(out.covar, perms=out.covar.perm, pvalues=TRUE)

#Epistatic_effect_sex
out.covar<- scantwo(mycross, addcovar=ac, pheno.col=1, model ="normal", method ="em")
out.covar.perm <- scantwo(mycross,addcovar=ac, model="normal", method="em", n.perm=10000)
summary(out.covar, perms=out.covar.perm, pvalues=TRUE)
##RNA_Seq
```

```
mycross <- read.cross("csv", file = "RNA_SEQ.csv")
mycross <- calc.genoprob(mycross, step=1.0, off.end=0.0, error.prob=1.0e-4, map.function ="haldane", stepwidth = "fixed")
mycross <-sim.geno(mycross, n.draws=10000, step =1.0, off.end=0.0, error.prob=1.0e-4, map.function="haldane", stepwidth
="fixed")
##Covariate_sex
ac <- pull.pheno(mycross, c("sex"))

##Main_effect
operm1 <- scanone(mycross, addcovar=ac, method="hk", n.perm=10000)
n=1
c<-a <- scanone(mycross, pheno.col = 1, method = "hk")
for (n in 1:2180){
 a <- scanone(mycross, pheno.col = n, method = "hk")
 c <- append(c,a)
 n+1}
print(c)

##Epistatic_effect
operm2 <- scantwo(mycross, addcovar= ac, method="em", n.perm=10000)
n=1
c<-a <- scantwo(mycross, pheno.col = 1, method = "em")
for (n in 1:2180){
 a <- scantwo(mycross, pheno.col = n, method = "em")
 c <- append(c,a)
 n+1}
print(c)

##Visualizations
mname1 <- find.marker(mycross, chr=X, pos=X)
mname2 <- find.marker(mycross, chr=Y, pos=Y)

###Genotype Plot 1
plotPXG(mycross, pheno.col=1, c(mname1))

##Genotype Plot 2
plotPXG(mycross, pheno.col=1, c(mname2))

###Main Effect
thresh1 <- summary(out.covar.perm, alpha=c(0.05))
plot(out.covar, main= "Mainscan plot of GENE", ylim = c(0,6))
abline(h=thresh1, lty="dotted", lwd=1)

###Genotype Interactions
chr <- c("chrx", "chry")
pos <- c(posx,posy)
qtl <- makeqtl(mycross, chr, pos, what="prob")
rqtl <- refineqtl(mycross, qtl=qtl, formula = y~Q1+Q2+Q1:Q2)
plotLodProfile(rqtl)

###Interaction effects
plotPXG(mycross, pheno.col=1, c(mname1, mname2))

###Context Dependent Genotype Effects
effectplot(mycross, pheno.col=1, mname1=mname1, mname2=mname2)

##LOD intervals
lodint(rqtl, qtl.index=2)

##Overall interaction RNA-Seq
```


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```
library(tidyverse)
library(car)
library(rgl)
ggplot(data = RNA_SEQ_Plot) +
 geom_point(aes(x = RNA_SEQ_Plot$`Main 1`, y = RNA_SEQ_Plot$Epistatic), col = "midnightblue") +
 theme_bw() + xlim(0, 15) + ylim(0, 15) +
 labs( x= "Main Effect 1", y = "Epistatic")
ggplot(data = RNA_SEQ_Plot) +
 geom_point(aes(x = RNA_SEQ_Plot$`Main 2`, y = RNA_SEQ_Plot$Epistatic), col = "midnightblue") +
 theme_bw() + xlim(0, 15) + ylim(0, 15) +
 labs( x= "Main Effect 2", y = "Epistatic")
ggplot(data = RNA_SEQ_MAIN_EFFECTS_FOR_PLOTS_4_2) +
 geom_point(aes(x = RNA_SEQ_MAIN_EFFECTS_FOR_PLOTS_4_2$main_LOD, y =
RNA_SEQ_MAIN_EFFECTS_FOR_PLOTS_4_2$`Epistatic P`), col = "midnightblue") +
 theme_bw() + xlim(0, 15) + ylim(0, 15) + labs( x= "Main Effect", y = "Epistatic")

##Circos Plot
library(circlize)
df <- circose_inr
circos.par("track.height" = 0.1)
circos.initialize(factors = df$chr, x = df$pos)
circos.track(factors = df$chr, y = df$pos, bg.col=c("blue", "red"),
        panel.fun = function(x, y) {
          circos.text(CELL_META$xcenter, CELL_META$cell.ylim[2] + uy(5, "mm"),
                CELL_META$sector.index)
          circos.axis(labels.cex = 0.6) })
circos.link(chr1,position,chr2,position,col = "color")
circos.link(chr1,position,chr2,position,col = "color")
```


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