rPlasmo tools, Tools for viewing and analyzing malaria data.

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Code for computing mQTL

Read input files

markerList <- readMark() # QTL_genotype.csv file
pheno <- readPeak() # QTL_phenotype.csv file
covar <- c(1, 2, 5, 6, 5, 1, 6, 1, 6, 2, 2, 4, 2, 5, 3, 4, 1, 5, 1,
         6, 2, 2, 4, 3, 1, 5, 3, 5, 3, 1, 4, 3, 1, 3, 4, 3)

Compute QTLs

final <- mzQTL(pheno = pheno, markerList = markerList, covar = covar)
mzAlpha <- c(0.05, 0.01, 0.001, 0.05 / (nrow(pheno) - 2))
alphaT <- matrix(NA, nrow = nrow(pheno), ncol = length(mzAlpha))
for(i in 1:length(mzAlpha)) {
  alphaT[,i] <- sapply(final[[2]], function(x) summary(x, alpha = mzAlpha[i]))
}
alphaT <- data.frame(alphaT)
names(alphaT) <- mzAlpha
row.names(alphaT) <- pheno$compound
chr <- as.numeric(as.vector(unlist(sapply(final[[1]],
           function(x) max(x)[1]))))
pos <- as.numeric(as.vector(unlist(sapply(final[[1]],
           function(x) max(x)[2]))))
lod <- as.numeric(as.vector(unlist(sapply(final[[1]],
           function(x) max(x)[3]))))
pVal <- rep(NA, length(lod))
for(i in 1:length(final[[1]]))
  pVal[i] <- min(summary(final[[1]][[i]], perms = final[[2]][[i]], pvalues = T)$pval)

Generate summary

cpdSummary <- data.frame(
  compound = names(final[[1]]),
  chr, pos, lod, pVal, stringsAsFactors = F)

Code for modeling parasite growth
dat <- readPeak()  # population_summary.csv file

fitR <- fitComp(obs = dat$S_1, pop1 = .5, syncC = F, N = 50000)

fitF1 <- fitComp(obs = dat$S_1, pop1 = .5, lc1 = 47, lc2 = 49, t0 = 43, r1 = .065, sc = 8, pSync = 1, rSample = F, syncC = T)

fitF2 <- fitComp(obs = dat$S_2, pop1 = .25, lc1 = 47, lc2 = 49, t0 = 43, r1 = .065, sc = 8, pSync = 1, rSample = F, syncC = T)