

File S12

Harvest maximum QTL peaks

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# Harvest the QTL by taking the maximum peak and determining if it it
over
# the 0.05 treshold.
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#####
#####
options(stringsAsFactors = FALSE)
library(DOQTL)

setwd("/hpcdata/dgatti/RNAediting/QTL/")

load("_9_RNAediting_QTL_mapping.Rdata")

files = dir(pattern = "_RNAediting_QTL.Rdata$")

# Get the chromosome lengths.
chrLen = get.chr.lengths()
chrLen = c(0, chrLen)

result = NULL

for(i in 1:length(files)) {

  # Get the site.
  site = sites[sub("_RNAediting_QTL.Rdata$", "", files[i])]

  # Add the DO editing ratio to the end of the site.
  site$DO.total = mean(total[,names(site)], na.rm = TRUE)
  site$DO.ratio = mean(edit[,names(site)] / total[,names(site)], na.rm
= TRUE)

  # Load in the QTL and perms.
  load(files[i])
  # Get the 0.05 threshold.
  thr = quantile(perms, 0.95)

  # Plot the genome scan.
  png(sub("\\.Rdata$", ".png", files[i]), width = 1000, height = 800,
res = 128)
  plot(qtl, sig.thr = thr, main = names(site))
  site.chr = as.character(sub("^chr", "", seqnames(site)))
  if(site.chr == "X") {
    site.pos = start(site) * 1e-6 + sum(chrLen[1:20])
  }
}
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} else if(site.chr == "Y") {
  site.pos = -100
} else {
  site.pos = start(site) * 1e-6 +
sum(chrlen[1:as.numeric(site.chr)])
} # else
points(site.pos, 0, pch = 17, cex = 2, col = 2)
dev.off()

spl = split(qtl$lod$A, qtl$lod$A[,2])
spl$X = qtl$lod$X
max.lod = lapply(spl, function(z) { z[which.max(z[,7]),] })
max.lod = unsplit(max.lod, names(spl))

# Only keep cis-QTL on X.
if(as.character(seqnames(site)) == "chrX") {
  if(max.lod[max.lod[,2] == "X",7] < 2 * thr) {
    max.lod = max.lod[max.lod[,2] != "X",]
  } # if(max.lod[max.lod[,2] == "X",7] < 2 * thr)
} else if(as.character(seqnames(site)) == "chrY") {
  # Nothing
} else {
  max.lod = max.lod[max.lod[,2] != "X",]
} # else

# max.lod = max.lod[max.lod[,7] >= thr,,drop = FALSE]
max.lod = max.lod[which.max(max.lod[,7]),,drop = FALSE]
max.lod = cbind(max.lod, p.gw = mean(perms >= max.lod[,7]))
result = rbind(result, cbind(as.data.frame(site), max.lod))

for(j in 1:nrow(max.lod)) {

  png(sub("_QTL\\.Rdata$", paste0("_coef_chr", max.lod[j,2],
".png")), files[i]),
      width = 1000, height = 800, res = 128)
  if(max.lod[j,2] == "X") {
#     coefplot(qtl, chr = max.lod[j,2], sex = "F", main =
names(site))
  } else {
    coefplot(qtl, chr = max.lod[j,2], main = names(site))
  } # else
  dev.off()

} # for(j)

} # for(i)

result = cbind(result, p.adj = p.adjust(p = result$p.gw, method =
"BH"))

save(result, file = "_11_RNAediting_qtl_results.Rdata")
write.csv(result, file = "_11_RNAediting_qtl_results.csv")

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