fMRI_Analysis

2022-11-27

Import data

```r
# Change file extension
# path <- "./data/data/"
# old_names <- list.files(path)
# new_names <- gsub(".1D", ".csv", old_names)
# file.rename(paste0(path, file_names), paste0(path, new_names))

# Import data
diag <- read_csv("./data/phenotypic_CMU.csv") %>% janitor::clean_names()
```

Single-subject analysis

```r
path <- "./data/data/"
indepTest <- gaussCItest

# Set asd vs. control
df_file_names <- inner_join(data.frame(name = list.files("./data/data/"),
                                       sub_id = as.numeric(substring(list.files("./data/data/"), 7, 13))
                            diag, by = "sub_id")
asd_files <- df_file_names %>% filter(dx_group == 1) %>%
  select(1) %>% mutate(name = paste(path, name, sep = ""))
tc_files <- df_file_names %>% filter(dx_group == 2) %>%
  select(1) %>% mutate(name = paste(path, name, sep = ""))

normalize_val <- function(x){
  t_x <- (x - min(x))/(max(x) - min(x))
  return(t_x)
}

# --- ASD ---
# Randomly select one asd sample
set.seed(202212)
asd_sel <- sample(as.matrix(asd_files), 1)
asd_dat <- fread(asd_sel, select = c(1:160))
suffStat_asd <- list(C = cor(asd_dat), n = nrow(asd_dat))

# Corr
asd_corr <- cor(asd_dat)
t_asd_corr <- normalize_val(asd_corr)
diag(t_asd_corr) <- 0
```
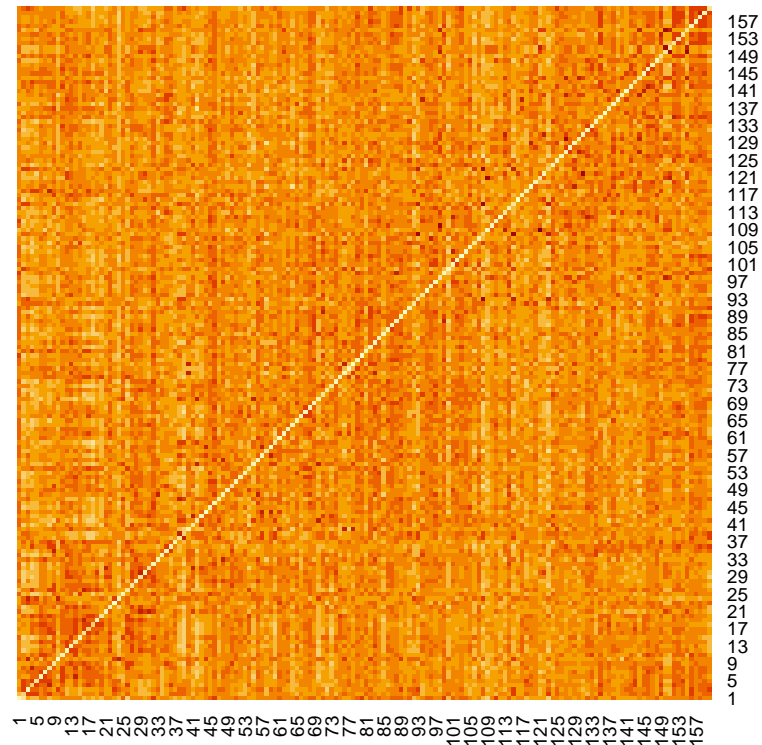
```
colnames(t_asd_corr) <- seq(160)
rownames(t_asd_corr) <- seq(160)

heatmap(t_asd_corr, Rowv = NA, Colv = NA)
```
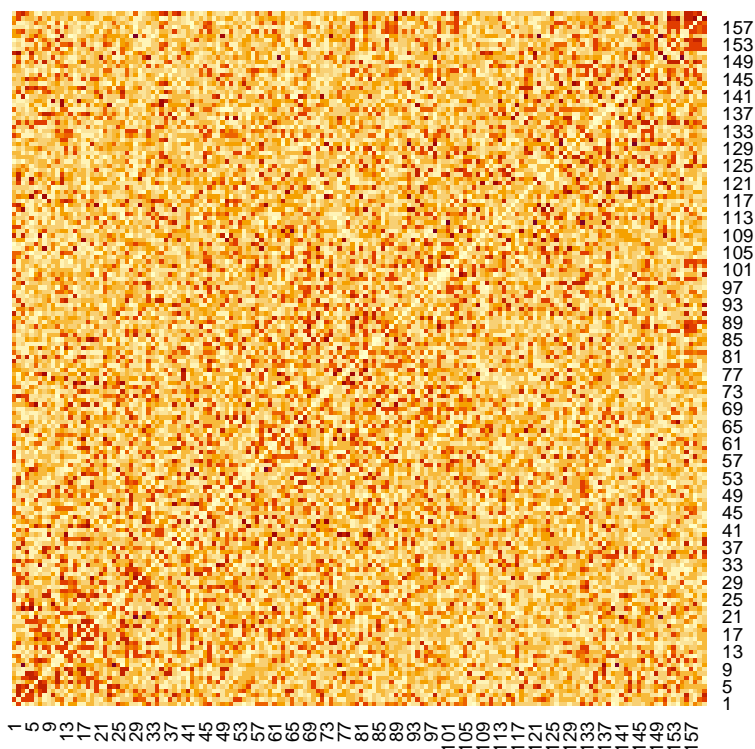


```
# fig_asd_1 <- melt(t_asd_corr) %>%
#   ggplot(aes(x = Var1, y = Var2, fill = value)) +
#   geom_tile() + theme_bw() + scale_fill_distiller(palette = "YlGnBu") +
#   theme(axis.title = element_blank(), axis.text = element_blank()) +
#   labs(title = "Pearson Correlation")

# PC
asd_pc <- pc(suffStat_asd, indepTest, alpha = 0.5, m.max = 1,
             p = ncol(asd_dat), verbose = FALSE)

heatmap(1 - asd_pc@pMax, Rowv = NA, Colv = NA)
```
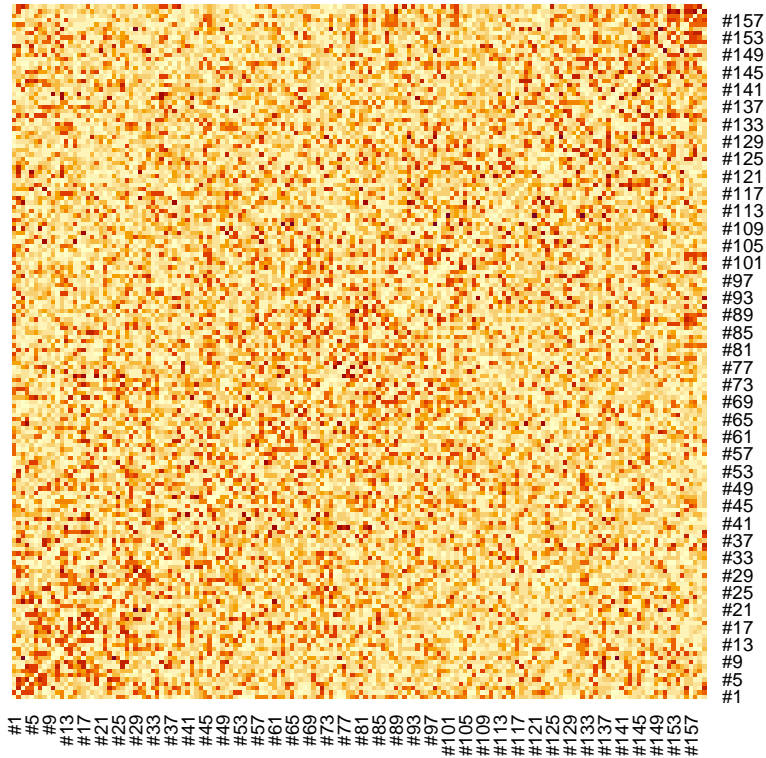
```
# fig_asd_2 <- melt(1 - asd_pc@pMax) %>%
#   ggplot(aes(x = Var1, y = Var2, fill = value)) +
#   geom_tile() + theme_bw() + scale_fill_distiller(palette = "YlGnBu") +
#   theme(axis.title = element_blank(), axis.text = element_blank()) +
#   labs(title = "PC Algorithm")

# FCI
asd_fci <- fci(suffStat_asd, indepTest, alpha = 0.5, m.max = 1,
               p = ncol(asd_dat), verbose = FALSE)

heatmap(1 - asd_fci@pMax, Rowv = NA, Colv = NA)
# fig_asd_3 <- melt(1 - asd_fci@pMax) %>%
#   ggplot(aes(x = Var1, y = Var2, fill = value)) +
#   geom_tile() + theme_bw() + scale_fill_distiller(palette = "YlGnBu") +
#   theme(axis.title = element_blank(), axis.text = element_blank()) +
#   labs(title = "FCI Algorithm")

# MMHC
asd_mmhc <- mmhc(as.matrix(asd_dat), alpha = 0.5, max_k = 1)

heatmap(1 - exp(asd_mmhc$ini$pvalue), Rowv = NA, Colv = NA)
```
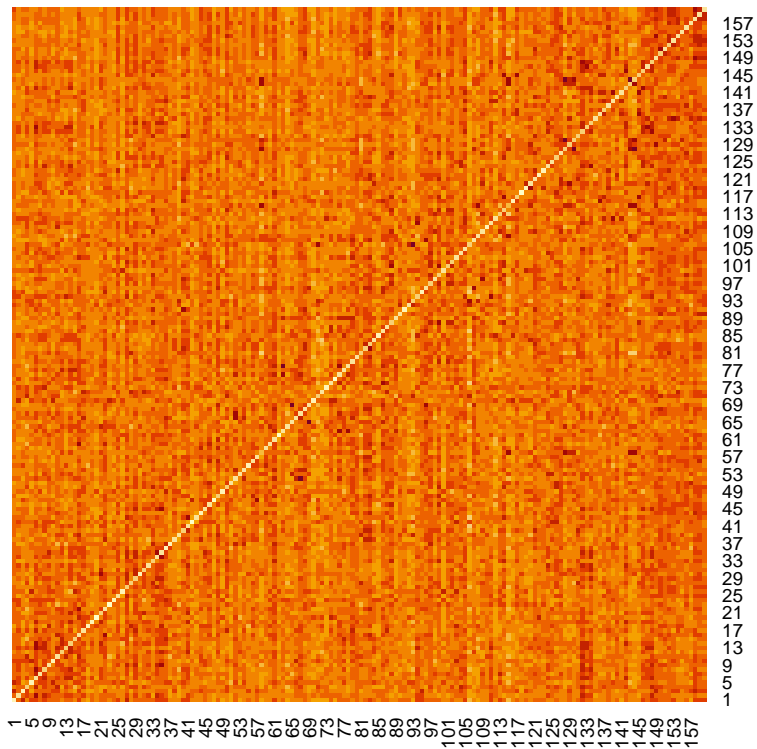
```
# fig_asd_4 <- melt(1 - exp(asd_mmhc$ini$pvalue)) %>%
#   ggplot(aes(x = Var1, y = Var2, fill = value)) +
#   geom_tile() + theme_bw() + scale_fill_distiller(palette = "YlGnBu") +
#   theme(axis.title = element_blank(), axis.text = element_blank()) +
#   labs(title = "MMHC Algorithm")


# --- TC ---
# Randomly select one tc sample
set.seed(202212)
tc_sel <- sample(as.matrix(tc_files), 1)
tc_dat <- fread(tc_sel, select = c(1:160))
suffStat_tc <- list(C = cor(tc_dat), n = nrow(tc_dat))

# Corr
tc_corr <- cor(tc_dat)
t_tc_corr <- normalize_val(tc_corr)
diag(t_tc_corr) <- 0
colnames(t_tc_corr) <- seq(160)
rownames(t_tc_corr) <- seq(160)

heatmap(t_tc_corr, Rowv = NA, Colv = NA)
```
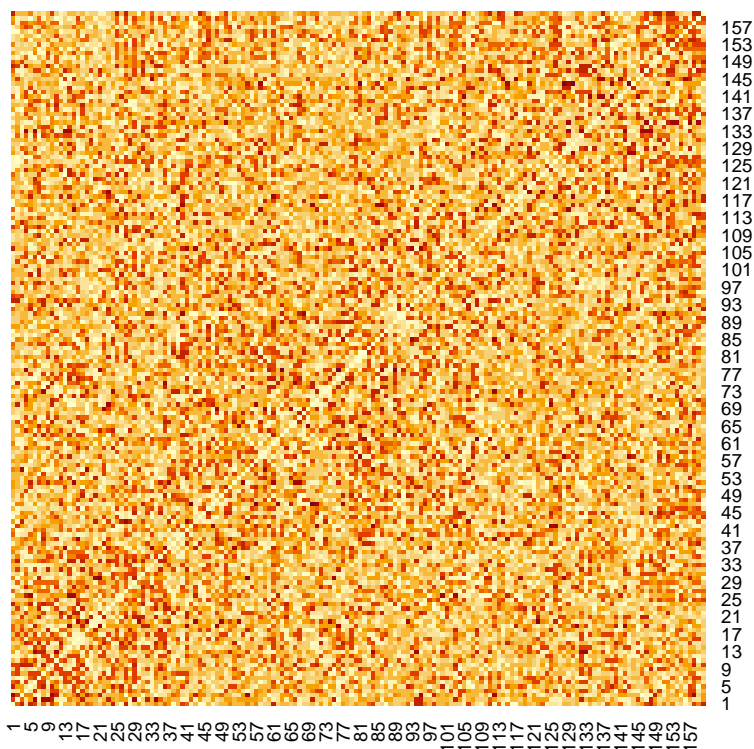
4

```
# fig_tc_1 <- melt(t_tc_corr) %>%
#   ggplot(aes(x = Var1, y = Var2, fill = value)) +
#   geom_tile() + theme_bw() + scale_fill_distiller(palette = "YlGnBu") +
#   theme(axis.title = element_blank(), axis.text = element_blank()) +
#   labs(title = "Pearson Correlation")

# PC
tc_pc <- pc(suffStat_tc, indepTest, alpha = 0.5, m.max = 1,
            p = ncol(tc_dat), verbose = FALSE)
heatmap(1 - tc_pc@pMax, Rowv = NA, Colv = NA)
```
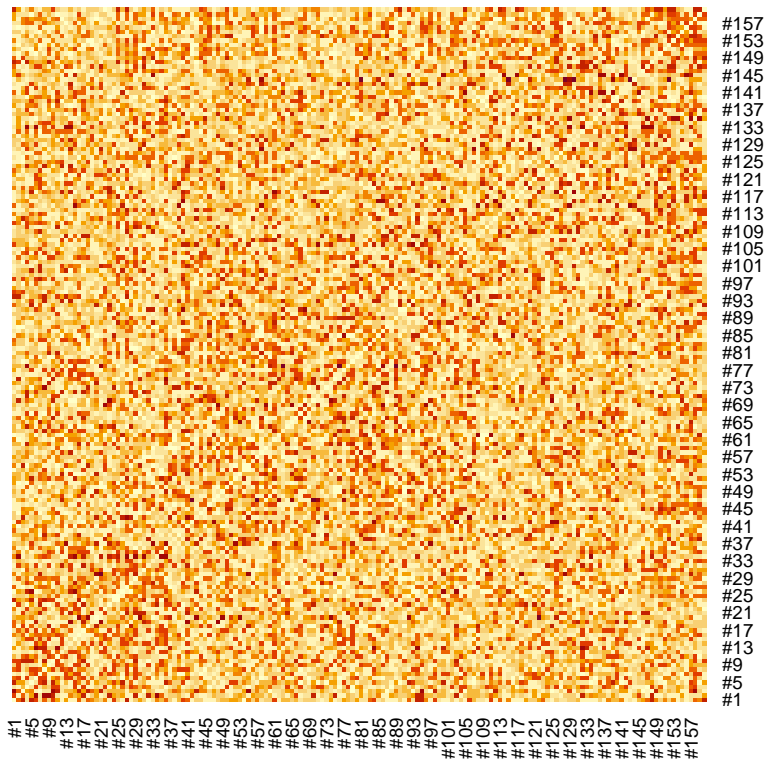
```
# fig_tc_2 <- melt(1 - tc_pc@pMax) %>%
#   ggplot(aes(x = Var1, y = Var2, fill = value)) +
#   geom_tile() + theme_bw() + scale_fill_distiller(palette = "YlGnBu") +
#   theme(axis.title = element_blank(), axis.text = element_blank()) +
#   labs(title = "PC Algorithm")

# FCI
tc_fci <- fci(suffStat_tc, indepTest, alpha = 0.5, m.max = 1,
              p = ncol(tc_dat), verbose = FALSE)
heatmap(1 - tc_fci@pMax, Rowv = NA, Colv = NA)

# fig_tc_3 <- melt(1 - tc_fci@pMax) %>%
#   ggplot(aes(x = Var1, y = Var2, fill = value)) +
#   geom_tile() + theme_bw() + scale_fill_distiller(palette = "YlGnBu") +
#   theme(axis.title = element_blank(), axis.text = element_blank()) +
#   labs(title = "FCI Algorithm")

# MMHC
tc_mmhc <- mmhc(as.matrix(tc_dat), alpha = 0.5, max_k = 1)
heatmap(1 - exp(tc_mmhc$ini$pvalue), Rowv = NA, Colv = NA)
```

```
# fig_tc_4 <- melt(1 - exp(tc_mmhc$ini$pvalue)) %>%
#   ggplot(aes(x = Var1, y = Var2, fill = value)) +
#   geom_tile() + theme_bw() + scale_fill_distiller(palette = "YlGnBu") +
#   theme(axis.title = element_blank(), axis.text = element_blank()) +
#   labs(title = "MMHC Algorithm")
#
# # Make plots
# ggarrange(fig_asd_1, fig_asd_2, fig_asd_4, fig_tc_1, fig_tc_2, fig_tc_4,
#         nrow = 2, ncol = 3, common.legend = TRUE, legend = "bottom") %>%
#   annotate_figure(top = text_grob(paste("ASD (ID=", substring(asd_sel, 19, 25),
#                   ") &", "(Down) Typical Control (ID=", substring(tc_sel, 19, 25),
#                   ")", sep = "")))
```

Group analysis

```
# # ASD
# all_asd <- lapply(seq(nrow(asd_files)), function(x) {
#   file_path <- paste(path, asd_files[x ,], sep = "")
#   dat <- fread(file_path, select = c(1:160))
#
#   cor_dat <- cor(dat, method = "pearson")
# })
#
# # average correlations
# mean_asd <- apply(simplify2array(all_asd), 1:2, mean)
#
# # PC algorithm
```

```
# indepTest <- gaussCItest
#
# suffStat_2 <- list(C = cor(dat2), n = nrow(dat2))
# pc_est_21 <- pc(suffStat_2, indepTest, alpha = 0.5, p = 160,
#                    m.max = 1, verbose = FALSE)
# a <- pc_est_21@pMax
# b <- 1 - (a - min(a))/(max(a) - min(a))
# heatmap(b)
```