

Transporter Colocalization Analysis (ImageJ Coloc2)

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```
filelist <- list.files(path="../data/coloc2_results_mrp2/", pattern="*.txt", full.names = TRUE)
cols <- c("sample", "m1", "m2", "r_pearson", "Pval", "r_rand", "sd_rand")
coloc2 <- as.data.frame(matrix(,1,length(cols)))
names(coloc2) <- cols

for (i in filelist) {
  test <- read_lines(i)
  sample <- str_subset(test, "Working on") %>% str_extract(., "(?<=[[:space:]]).*")
  r_pearson <- str_subset(test, "no threshold") %>% str_extract(., "(?<=[[:space:]]).*")
  m1 <- str_subset(test, "tM1") %>% str_extract(., "(?<=[[:space:]]).*")
  m2 <- str_subset(test, "tM2") %>% str_extract(., "(?<=[[:space:]]).*")
  Pval <- str_subset(test, "P-Value") %>% str_extract(., "(?<=[[:space:]]).*")
  r_rand <- str_subset(test, "Costes Shuffled Mean") %>% str_extract(., "(?<=[[:space:]]).*")
  sd_rand <- str_subset(test, "Costes Shuffled Std") %>% str_extract(., "(?<=[[:space:]]).*")
  res <- c(all_of(sample), all_of(m1), all_of(m2), all_of(r_pearson), all_of(Pval), all_of(r_rand), all_of(sd_rand))
  coloc2 <- rbind(coloc2, res)
}

coloc2 <- coloc2 %>% na.omit(coloc2) %>%
  mutate(sex = as.factor(str_sub(sample, start=1L, end=1L)),
         mouseID = as.factor(str_extract(sample, "(?<=-)[[:digit:]]+")),
         image = str_extract(sample, "s.*(?=_)"),
         roi = str_extract(sample, "(?<=_)ate"), .before=m1)

coloc2 <- coloc2 %>% select(-sample) %>%
  mutate(m1 = as.double(m1),
         m2 = as.double(m2),
         r_pearson = as.double(r_pearson),
         Pval = as.double(Pval),
         r_rand = as.double(r_rand),
         sd_rand = as.double(sd_rand),
         coloc = Pval>0.95)

#write.xlsx(coloc2, "../data/coloc2-mrp2-totals.xlsx")

head(coloc2)
```

##	sex	mouseID	image	roi	m1	m2	r_pearson	Pval	r_rand	sd_rand
## 2	F	22	section2-40x-1	gcl1	0.063	0.360	0.12	1.00	-0.01	0.04
## 3	F	22	section2-40x-1	inl1	0.000	0.087	-0.01	0.34	0.00	0.02
## 4	F	22	section2-40x-1	inl2	0.000	0.097	-0.03	0.12	0.00	0.02

```
## 5 F 22 section2-40x-2 gcl1 0.111 0.001 0.01 0.77 0.00 0.01
## 6 F 22 section2-40x-2 inl1 0.000 0.183 -0.02 0.18 0.00 0.03
## 7 F 22 section2-40x-3 gcl1 0.000 0.181 -0.02 0.14 0.00 0.02
## coloc
## 2 TRUE
## 3 FALSE
## 4 FALSE
## 5 FALSE
## 6 FALSE
## 7 FALSE
```

```
sumstats <- coloc2 %>% summarise(m1_mean = mean(m1),
  m1_sd = sd(m1),
  m2_mean = mean(m2),
  m2_sd = sd(m2),
  r_mean = mean(r_pearson),
  r_sd = sd(r_pearson),
  n_total = n(),
  n_coloc = sum(coloc)
)
sumstats
```

```
## m1_mean m1_sd m2_mean m2_sd r_mean r_sd n_total n_coloc
## 1 0.1098828 0.1436731 0.2081172 0.1569569 0.03496552 0.07127923 145 55
```

```
sumstats_animals <- coloc2 %>% group_by(mouseID) %>%
  summarise(m1_mean = mean(m1),
    m1_sd = sd(m1),
    m2_mean = mean(m2),
    m2_sd = sd(m2),
    r_mean = mean(r_pearson),
    r_sd = sd(r_pearson),
    n_total = n(),
    n_coloc = sum(coloc)
  )
sumstats_animals
```

```
## # A tibble: 8 x 9
## mouseID m1_mean m1_sd m2_mean m2_sd r_mean r_sd n_total n_coloc
## <fct> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <int> <int>
## 1 22 0.0253 0.0476 0.207 0.118 -0.0144 0.0541 18 2
## 2 40 0.0654 0.0608 0.124 0.0956 0.0281 0.0232 16 7
## 3 62 0.0655 0.0959 0.0723 0.0747 -0.0174 0.0254 19 0
## 4 77 0.101 0.131 0.156 0.0518 0.0318 0.0472 22 7
## 5 81 0.0127 0.0241 0.430 0.245 0.00944 0.0284 18 5
## 6 82 0.257 0.193 0.199 0.115 0.102 0.0759 20 15
## 7 92 0.122 0.152 0.231 0.107 0.0238 0.0737 13 4
## 8 98 0.212 0.141 0.260 0.0856 0.105 0.0864 19 15
```

```
sumstats_sex <- coloc2 %>% group_by(sex) %>%
  summarise(m1_mean = mean(m1),
    m1_sd = sd(m1),
```

```

      m2_mean = mean(m2),
      m2_sd = sd(m2),
      r_mean = mean(r_pearson),
      r_sd = sd(r_pearson),
      n_total = n(),
      n_coloc = sum(coloc)
    )
sumstats_sex

```

```

## # A tibble: 2 x 9
##   sex    m1_mean m1_sd m2_mean m2_sd r_mean  r_sd n_total n_coloc
##   <fct>   <dbl> <dbl>   <dbl> <dbl> <dbl> <dbl>   <int>   <int>
## 1 F      0.104 0.124   0.201 0.113 0.0411 0.0794    53     24
## 2 M      0.113 0.154   0.212 0.178 0.0314 0.0664    92     31

```

```

sumstats_coloc <- coloc2 %>% group_by(coloc) %>%
  summarise(m1_mean = mean(m1),
            m1_sd = sd(m1),
            m2_mean = mean(m2),
            m2_sd = sd(m2),
            r_mean = mean(r_pearson),
            r_sd = sd(r_pearson),
            n_total = n(),
            mean_P = mean(Pval)
  )
sumstats_coloc

```

```

## # A tibble: 2 x 9
##   coloc m1_mean m1_sd m2_mean m2_sd  r_mean  r_sd n_total mean_P
##   <lgl>   <dbl> <dbl>   <dbl> <dbl>   <dbl> <dbl>   <int>   <dbl>
## 1 FALSE  0.0393 0.0672   0.187 0.166 -0.00622 0.0329    90  0.431
## 2 TRUE   0.225 0.160   0.243 0.136  0.102   0.0656    55  0.996

```

M1 = occludin overlapping mrp2 M2 = mrp2 overlapping occludin

```

coloc2$coloc <- as.factor(coloc2$coloc)

#coin::wilcox_test(coloc2$r_pearson ~ coloc2$coloc, conf.int=TRUE)
coin::wilcox_test(coloc2$r_pearson ~ coloc2$coloc, conf.int=TRUE, distribution="exact")

```

```

##
## Exact Wilcoxon-Mann-Whitney Test
##
## data:  coloc2$r_pearson by coloc2$coloc (FALSE, TRUE)
## Z = -9.665, p-value < 2.2e-16
## alternative hypothesis: true mu is not equal to 0
## 95 percent confidence interval:
##  -0.11 -0.08
## sample estimates:
## difference in location
##                -0.1

```

```
#coin::wilcox_test(coloc2$m1 ~ coloc2$coloc, conf.int=TRUE)
coin::wilcox_test(coloc2$m1 ~ coloc2$coloc, conf.int=TRUE, distribution="exact")
```

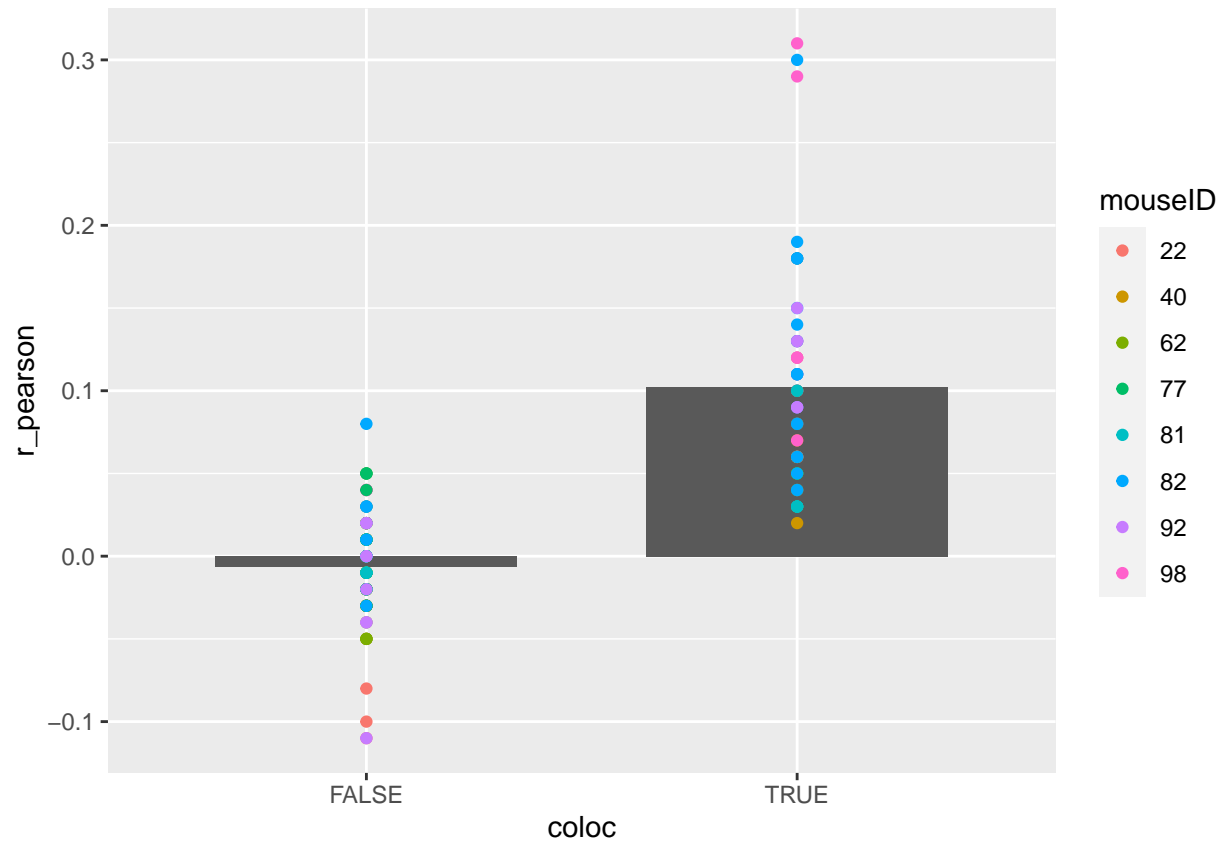
```
##
## Exact Wilcoxon-Mann-Whitney Test
##
## data: coloc2$m1 by coloc2$coloc (FALSE, TRUE)
## Z = -7.9711, p-value < 2.2e-16
## alternative hypothesis: true mu is not equal to 0
## 95 percent confidence interval:
## -0.226 -0.125
## sample estimates:
## difference in location
## -0.183
```

```
#coin::wilcox_test(coloc2$m2 ~ coloc2$coloc, conf.int=TRUE)
coin::wilcox_test(coloc2$m2 ~ coloc2$coloc, conf.int=TRUE, distribution="exact")
```

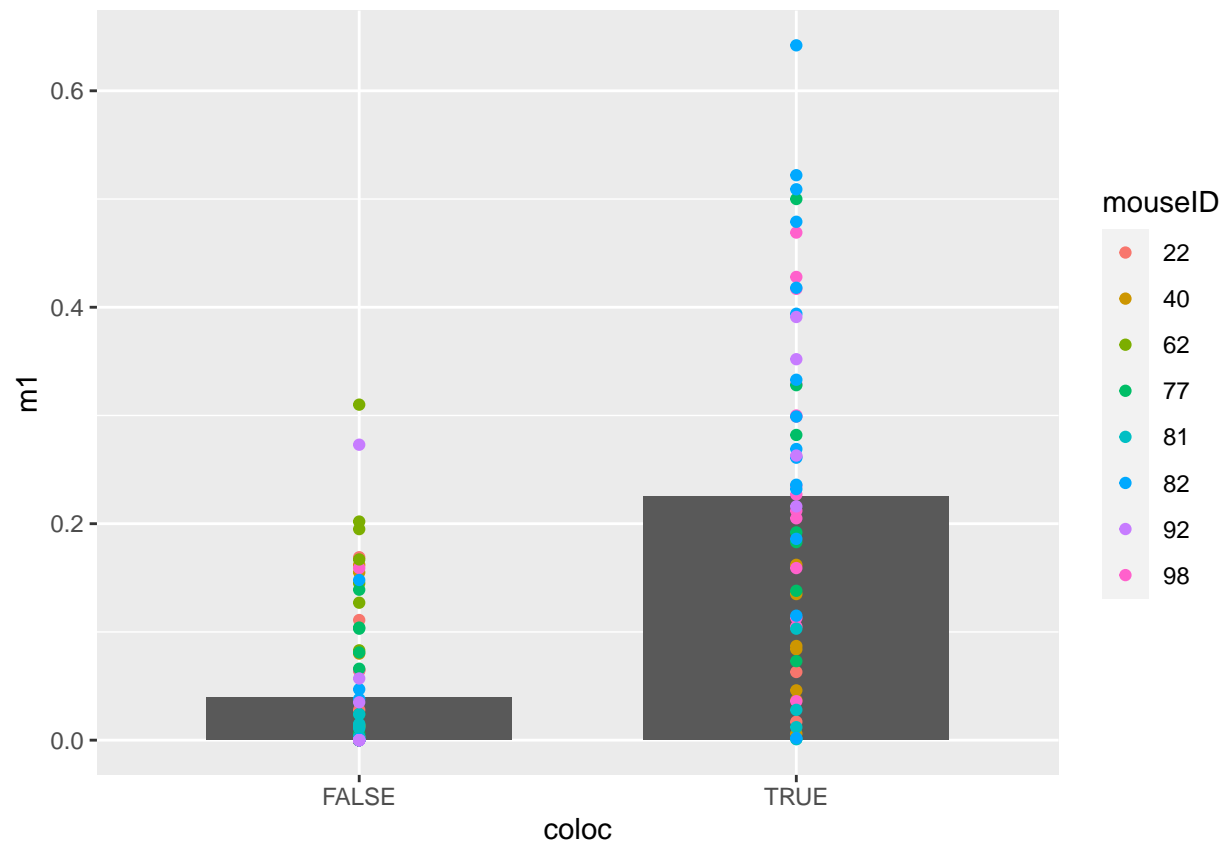
```
##
## Exact Wilcoxon-Mann-Whitney Test
##
## data: coloc2$m2 by coloc2$coloc (FALSE, TRUE)
## Z = -3.0646, p-value = 0.002026
## alternative hypothesis: true mu is not equal to 0
## 95 percent confidence interval:
## -0.111 -0.028
## sample estimates:
## difference in location
## -0.071
```

```
#coin::wilcox_test(coloc2$r_pearson ~ coloc2$sex, conf.int=TRUE)
#coin::wilcox_test(coloc2$m1 ~ coloc2$sex, conf.int=TRUE)
#coin::wilcox_test(coloc2$m2 ~ coloc2$sex, conf.int=TRUE)
```

```
coloc2 %>% ggplot(aes(x=coloc, y=r_pearson)) +
  stat_summary(fun = 'mean', geom="bar", width=0.7) +
  geom_point(aes(color=mouseID))
```



```
coloc2 %>% ggplot(aes(x=coloc, y=m1)) +
  stat_summary(fun = 'mean', geom="bar", width=0.7) +
  geom_point(aes(color=mouseID))
```



```
coloc2 %>% ggplot(aes(x=coloc, y=m2)) +
  stat_summary(fun = 'mean', geom="bar", width=0.7) +
  geom_point(aes(color=mouseID))
```

