

# Transporter Colocalization Analysis (ImageJ Coloc2)

CT Berezin

2022-08-18

```
filelist <- list.files(path="../data/coloc2_results_pgp/", 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:]]+")),
         prep = as.factor(str_extract(sample, "[[:lower:]]{2,}")),
         image = str_extract(sample, "[[:alpha:]]{2,}.*", .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-pgp-totals.xlsx")

head(coloc2)
```

##	sex	mouseID	prep	image	m1	m2	r_pearson	Pval	r_rand	sd_rand	coloc
## 2	F	87	wm	wm-20x-1	0.010	0.047	0.21	1	0.01	0	TRUE
## 3	F	87	wm	wm-20x-2	0.021	0.044	0.28	1	-0.01	0	TRUE
## 4	F	87	wm	wm-20x-3	0.655	0.585	0.33	1	0.00	0	TRUE

```
## 5 F 87 wm wm-20x-4 0.719 0.479 0.38 1 -0.01 0 TRUE
## 6 F 87 wm wm-20x-5 0.674 0.331 0.30 1 0.00 0 TRUE
## 7 M 10 wm GFP-wm-20x-1 0.012 0.040 0.13 1 -0.01 0 TRUE
```

```
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 0.2532927 0.294287 0.195439 0.2355011 0.2804878 0.1387795      41      41
```

```
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 10      0.01    0.00784 0.043 0.0168 0.128 0.0295      5      5
## 2 11      0.0258 0.0409 0.0503 0.0192 0.145 0.0191      4      4
## 3 80      0.320 0.282 0.246 0.290 0.37 0.140      6      6
## 4 81      0.283 0.251 0.204 0.286 0.377 0.0838      6      6
## 5 82      0.381 0.325 0.208 0.270 0.352 0.183      6      6
## 6 83      0.430 0.373 0.368 0.274 0.328 0.0804      5      5
## 7 87      0.416 0.366 0.297 0.247 0.3 0.0628      5      5
## 8 9       0.0265 0.0155 0.0812 0.0538 0.138 0.0419      4      4
```

```
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      0.416 0.366    0.297 0.247 0.3    0.0628     5     5
## 2 M      0.231 0.282    0.181 0.234 0.278 0.147    36    36
```

```
sumstats_prep <- coloc2 %>% group_by(prepare) %>%
  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_prep
```

```
## # A tibble: 2 x 9
##   prep    m1_mean m1_sd m2_mean m2_sd r_mean  r_sd n_total mean_P
##   <fct>    <dbl> <dbl>    <dbl> <dbl> <dbl>  <dbl>   <int>   <dbl>
## 1 section  0.328 0.273    0.219 0.266 0.366 0.133     18     1
## 2 wm      0.195 0.303    0.177 0.213 0.213 0.103     23     1
```

M1 = occludin overlapping p-gp M2 = p-gp overlapping occludin

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

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

```
##
## Asymptotic Wilcoxon-Mann-Whitney Test
##
## data: coloc2$r_pearson by coloc2$sex (F, M)
## Z = 0.51834, p-value = 0.6042
## alternative hypothesis: true mu is not equal to 0
## 95 percent confidence interval:
## -0.11 0.16
## sample estimates:
## difference in location
## 0.03
```

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

```
##
## Asymptotic Wilcoxon-Mann-Whitney Test
##
## data: coloc2$m1 by coloc2$sex (F, M)
## Z = 0.67733, p-value = 0.4982
## alternative hypothesis: true mu is not equal to 0
## 95 percent confidence interval:
## -0.09200001 0.63199999
```

```
## sample estimates:
## difference in location
##          0.02931474
```

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

```
##
## Asymptotic Wilcoxon-Mann-Whitney Test
##
## data: coloc2$m2 by coloc2$sex (F, M)
## Z = 1.1954, p-value = 0.2319
## alternative hypothesis: true mu is not equal to 0
## 95 percent confidence interval:
## -0.062 0.430
## sample estimates:
## difference in location
##          0.03536466
```

```
coin::wilcox_test(coloc2$r_pearson ~ coloc2$prep, conf.int=TRUE)
```

```
##
## Asymptotic Wilcoxon-Mann-Whitney Test
##
## data: coloc2$r_pearson by coloc2$prep (section, wm)
## Z = 3.4573, p-value = 0.0005457
## alternative hypothesis: true mu is not equal to 0
## 95 percent confidence interval:
## 0.08999999 0.23000001
## sample estimates:
## difference in location
##          0.16
```

```
coin::wilcox_test(coloc2$m1 ~ coloc2$prep, conf.int=TRUE)
```

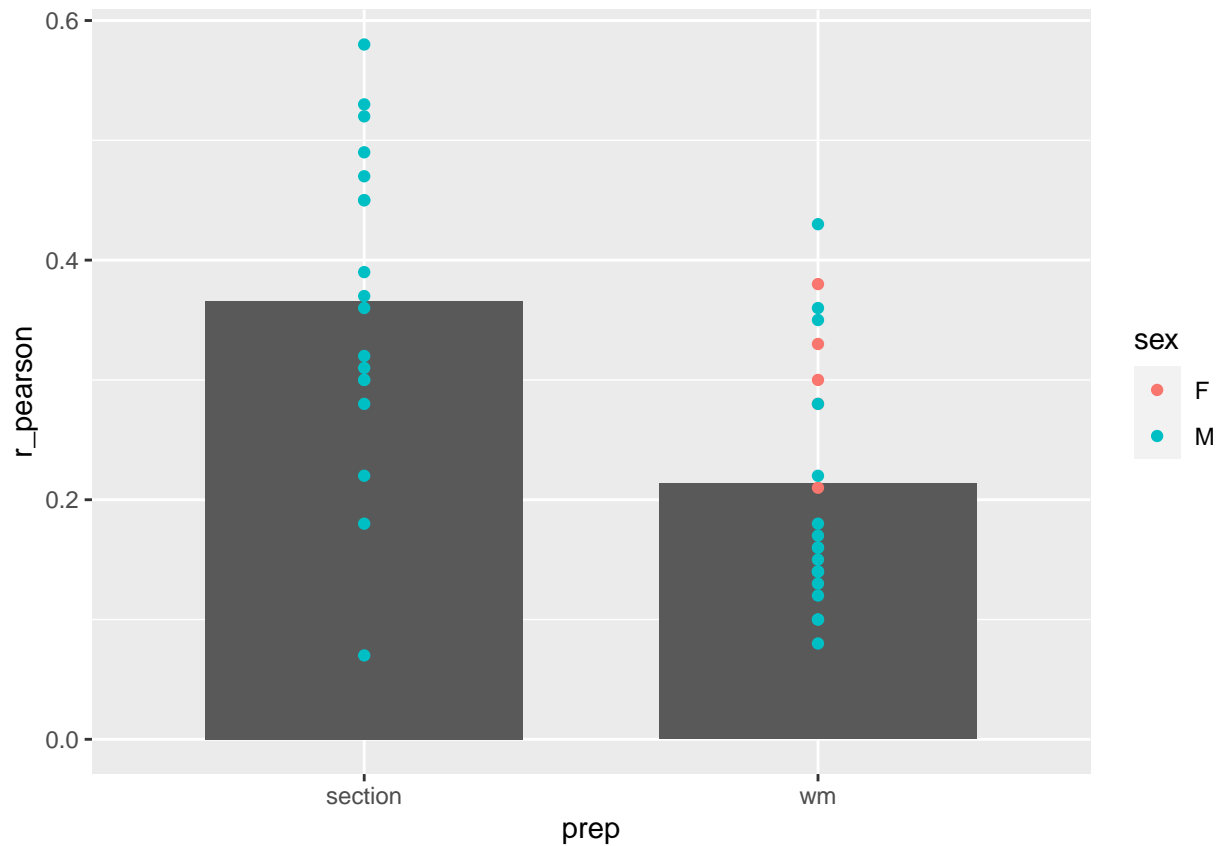
```
##
## Asymptotic Wilcoxon-Mann-Whitney Test
##
## data: coloc2$m1 by coloc2$prep (section, wm)
## Z = 3.1, p-value = 0.001935
## alternative hypothesis: true mu is not equal to 0
## 95 percent confidence interval:
## 0.064 0.200
## sample estimates:
## difference in location
##          0.1432319
```

```
coin::wilcox_test(coloc2$m2 ~ coloc2$prep, conf.int=TRUE)
```

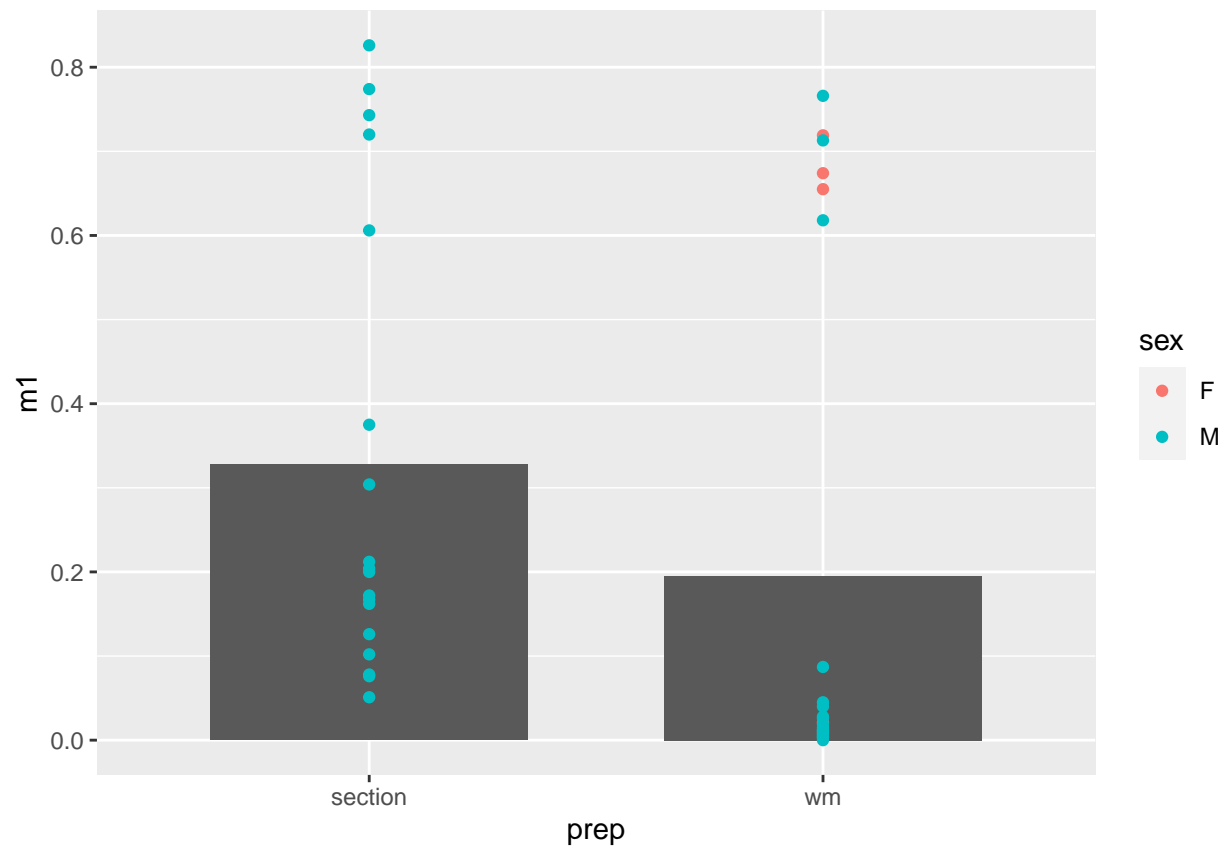
```
##
## Asymptotic Wilcoxon-Mann-Whitney Test
##
```

```
## data: coloc2$m2 by coloc2$prep (section, wm)
## Z = -1.0904, p-value = 0.2756
## alternative hypothesis: true mu is not equal to 0
## 95 percent confidence interval:
## -0.048 0.128
## sample estimates:
## difference in location
## -0.02323714
```

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



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



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

