

main

November 24, 2021

1 Generate Rank-Rank Hypergeometric Overlap (RRHO) plots

```
[1]: library(RRHO)
library(dplyr)
library(lattice)
```

Loading required package: grid

Attaching package: 'dplyr'

The following objects are masked from 'package:stats':

filter, lag

The following objects are masked from 'package:base':

intersect, setdiff, setequal, union

```
[2]: get_deg_df <- function(sex, tissue){
  if(tolower(sex) == 'female'){
    fn = paste0(".././.././", tolower(tissue), "/female_analysis/_m/genes/
    ↪diffExpr_szVctl_full.txt")
  } else {
    fn = paste0(".././.././", tolower(tissue), "/male_analysis/_m/genes/
    ↪diffExpr_szVctl_full.txt")
  }
  if(tolower(tissue) == 'cmc_dlpfc'){
    df = data.table::fread(fn) %>% mutate(metric=-log10(P.Value)*sign(t),
    ↪gencodeID=gene_id) %>%
      select('gencodeID', 'metric')
  } else {
```

```

    df = data.table::fread(fn) %>% mutate(metric=-log10(P.Value)*sign(t))
    ↪%>%
      select('gencodeID', 'metric')
  }
  return(df)
}

within_tissue_rrho_plot <- function(tissue){
  defaultW <- getOption("warn")
  options(warn = -1)
  f.list = get_deg_df('female', tolower(tissue)) %>% distinct(gencodeID, .
    ↪keep_all = TRUE)
  m.list = get_deg_df('male', tolower(tissue)) %>% distinct(gencodeID, .
    ↪keep_all = TRUE)
  rrho_df <- RRHO(f.list, m.list, BY=TRUE, labels=c("Female", "Male"),
    alternative='enrichment', log10.ind=TRUE)
  rrho_df$hypermat[is.na(rrho_df$hypermat)] <- 0 # for NA, correct to 0
  options(warn = defaultW)
  plt = levelplot(rrho_df$hypermat, col.regions=viridis::viridis(100),
    xlab="Female", ylab="Male", at=seq(0, 1000, 100))
  print(plt)
  label = paste("rrho_sex_compare", tolower(tissue), sep='_')
  R.devices::devEval(c("pdf", "png"), name=label, print(plt))
  #return(rrho_df)
}

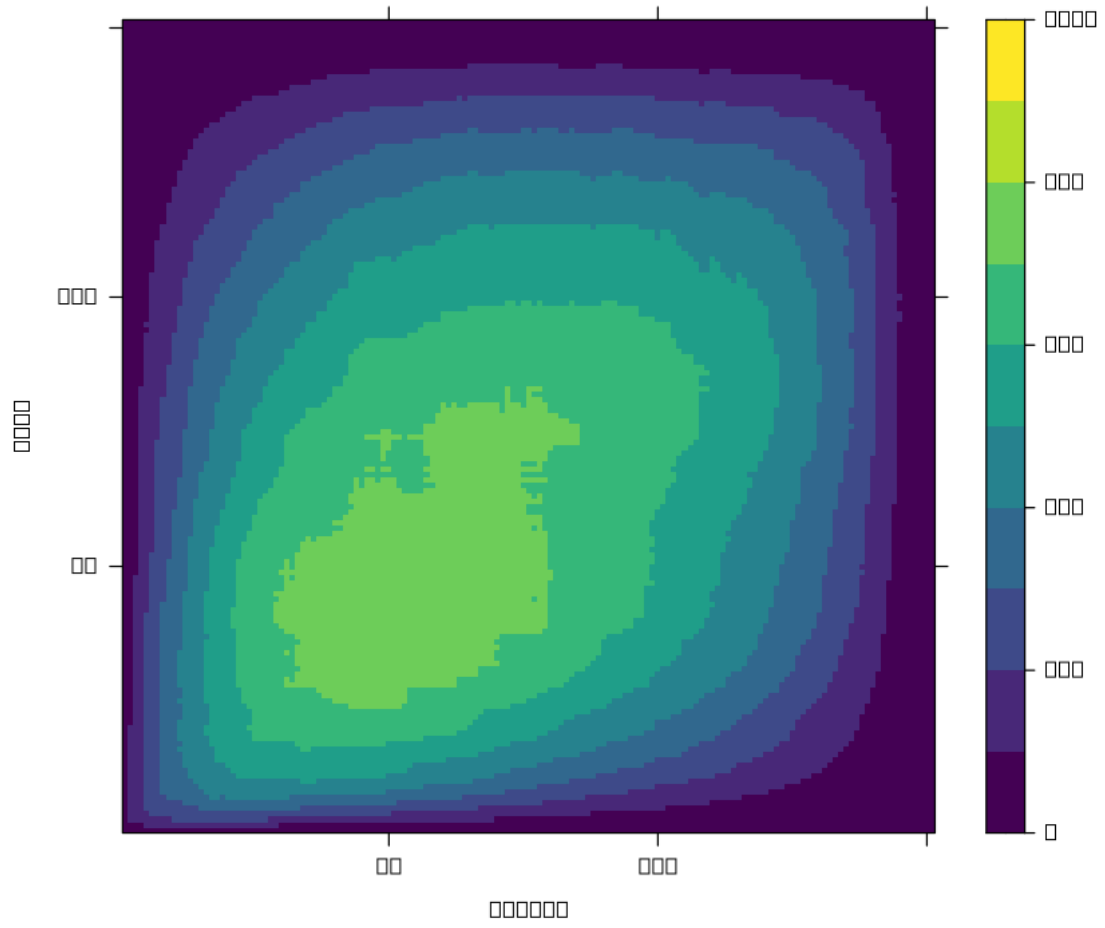
```

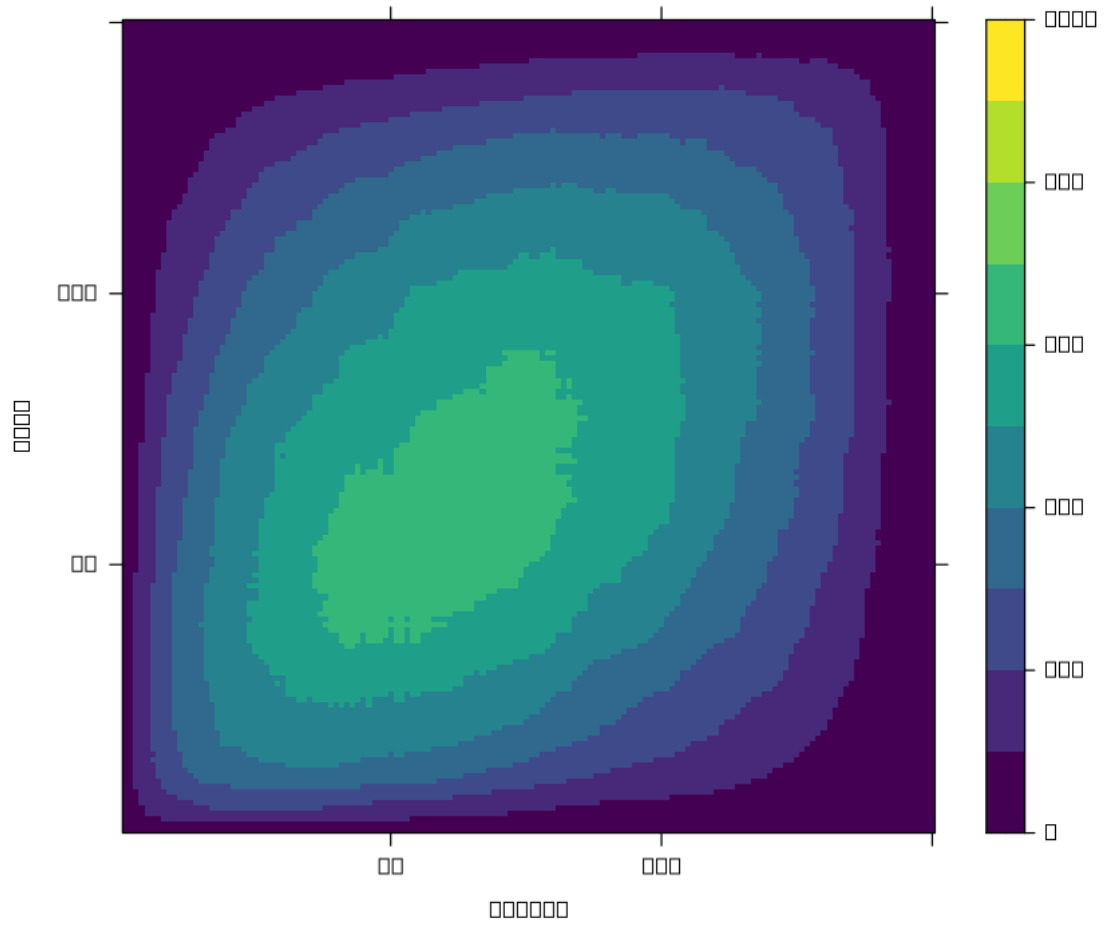
1.1 Within tissue comparison

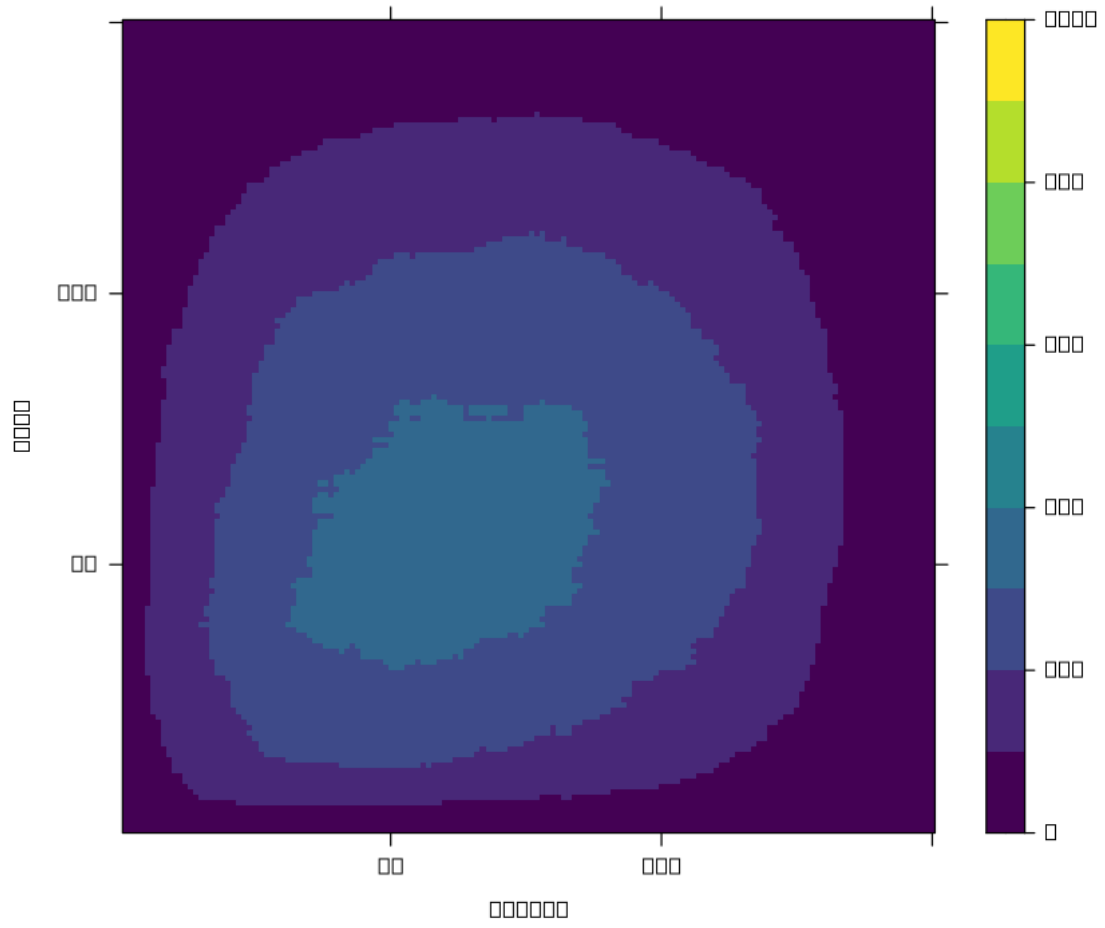
```

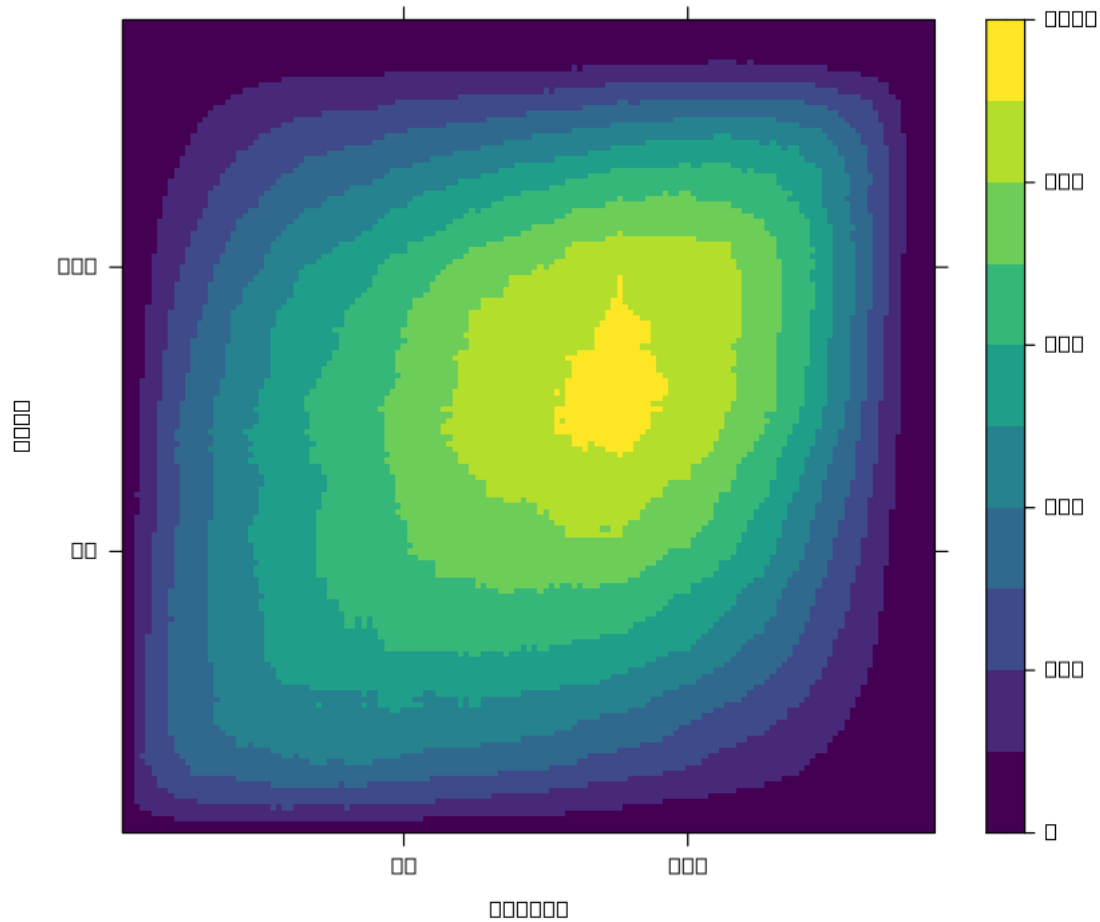
[3]: for(tissue in c('caudate', 'dlpfc', 'hippocampus', 'cmc_dlpfc')){
      within_tissue_rrho_plot(tissue)
    }

```









1.2 Female comparison across tissues

```
[4]: compare_tissue_plot <- function(sex, tissue1, tissue2){
  list1 = get_deg_df(sex, tissue1) %>% distinct(gencodeID, .keep_all = TRUE)
  list2 = get_deg_df(sex, tissue2) %>% distinct(gencodeID, .keep_all = TRUE)
  gene_overlap = intersect(list1$gencodeID, list2$gencodeID)
  list1 = list1 %>% filter(gencodeID %in% gene_overlap)
  list2 = list2 %>% filter(gencodeID %in% gene_overlap)
  rrho_df <- RRHO(list1, list2, BY=TRUE, labels=c(tissue1, tissue2),
    alternative='enrichment', log10.ind=TRUE)
  rrho_df$hypermat[is.na(rrho_df$hypermat)] <- 0 # for NA, correct to 0
  rrho_plot = levelplot(rrho_df$hypermat, col.regions=viridis::viridis,
    xlab=tissue1, ylab=tissue2, at=seq(0, 800, 100))
}
```

```

R.devices::devEval(c("pdf", "png"),
                    name=paste("rrho",sex,tissue1,tissue2, sep='_'),
                    print(rrho_plot))
}

```

1.2.1 Female

```

[5]: compare_tissue_plot("female", "Caudate", "DLPFC")
      compare_tissue_plot("female", "Caudate", "Hippocampus")
      compare_tissue_plot("female", "DLPFC", "Hippocampus")

```

\$pdf 'figures/rrho_female_Caudate_DLPFC.pdf'

\$png 'figures/rrho_female_Caudate_DLPFC.png'

\$pdf 'figures/rrho_female_Caudate_Hippocampus.pdf'

\$png 'figures/rrho_female_Caudate_Hippocampus.png'

\$pdf 'figures/rrho_female_DLPFC_Hippocampus.pdf'

\$png 'figures/rrho_female_DLPFC_Hippocampus.png'

```

[6]: compare_tissue_plot("female", "CMC_DLPFC", "Caudate")
      compare_tissue_plot("female", "CMC_DLPFC", "DLPFC")
      compare_tissue_plot("female", "CMC_DLPFC", "Hippocampus")

```

\$pdf 'figures/rrho_female_CMC_DLPFC_Caudate.pdf'

\$png 'figures/rrho_female_CMC_DLPFC_Caudate.png'

\$pdf 'figures/rrho_female_CMC_DLPFC_DLPFC.pdf'

\$png 'figures/rrho_female_CMC_DLPFC_DLPFC.png'

\$pdf 'figures/rrho_female_CMC_DLPFC_Hippocampus.pdf'

\$png 'figures/rrho_female_CMC_DLPFC_Hippocampus.png'

1.2.2 Male

```

[7]: compare_tissue_plot("male", "Caudate", "DLPFC")
      compare_tissue_plot("male", "Caudate", "Hippocampus")
      compare_tissue_plot("male", "DLPFC", "Hippocampus")

```

\$pdf 'figures/rrho_male_Caudate_DLPFC.pdf'

\$png 'figures/rrho_male_Caudate_DLPFC.png'

\$pdf 'figures/rrho_male_Caudate_Hippocampus.pdf'

\$png 'figures/rrho_male_Caudate_Hippocampus.png'

\$pdf 'figures/rrho_male_DLPFC_Hippocampus.pdf'

\$png 'figures/rrho_male_DLPFC_Hippocampus.png'

```
[8]: compare_tissue_plot("male", "CMC_DLPFC", "Caudate")
      compare_tissue_plot("male", "CMC_DLPFC", "DLPFC")
      compare_tissue_plot("male", "CMC_DLPFC", "Hippocampus")
```

```
$pdf 'figures/rrho_male_CMC_DLPFC_Caudate.pdf'
```

```
$png 'figures/rrho_male_CMC_DLPFC_Caudate.png'
```

```
$pdf 'figures/rrho_male_CMC_DLPFC_DLPFC.pdf'
```

```
$png 'figures/rrho_male_CMC_DLPFC_DLPFC.png'
```

```
$pdf 'figures/rrho_male_CMC_DLPFC_Hippocampus.pdf'
```

```
$png 'figures/rrho_male_CMC_DLPFC_Hippocampus.png'
```

1.3 Reproducibility Information

```
[9]: Sys.time()
      proc.time()
      options(width = 120)
      sessioninfo::session_info()
```

```
[1] "2021-11-24 10:26:38 EST"
```

```
      user    system elapsed
1001.511    3.407   992.448
```

```
$platform $version 'R version 4.1.2 (2021-11-01)'
```

```
$os 'Arch Linux'
```

```
$system 'x86_64, linux-gnu'
```

```
$ui 'X11'
```

```
$language '(EN)'
```

```
$collate 'en_US.UTF-8'
```

```
$ctype 'en_US.UTF-8'
```

```
$tz 'America/New_York'
```

```
$date '2021-11-24'
```

```
$pandoc '2.14.1 @ /usr/bin/pandoc'
```


	package <chr>	ondiskversion <chr>	loadedversion <chr>	path <chr>
	assertthat	0.2.1	0.2.1	/home/jb
	base64enc	0.1.3	0.1-3	/home/jb
	cli	3.1.0	3.1.0	/home/jb
	colorspace	2.0.2	2.0-2	/home/jb
	crayon	1.4.2	1.4.2	/home/jb
	data.table	1.14.2	1.14.2	/home/jb
	DBI	1.1.1	1.1.1	/home/jb
	digest	0.6.28	0.6.28	/home/jb
	dplyr	1.0.7	1.0.7	/home/jb
	ellipsis	0.3.2	0.3.2	/home/jb
	evaluate	0.14	0.14	/home/jb
	fansi	0.5.0	0.5.0	/home/jb
	fastmap	1.1.0	1.1.0	/home/jb
	formatR	1.11	1.11	/home/jb
	futile.logger	1.4.3	1.4.3	/home/jb
	futile.options	1.0.1	1.0.1	/home/jb
	generics	0.1.1	0.1.1	/home/jb
	ggplot2	3.3.5	3.3.5	/home/jb
	glue	1.5.0	1.5.0	/home/jb
	gridExtra	2.3	2.3	/home/jb
	gtable	0.3.0	0.3.0	/home/jb
	htmltools	0.5.2	0.5.2	/home/jb
	IRdisplay	1.0	1.0	/home/jb
	IRkernel	1.2	1.2	/home/jb
\$packages	jsonlite	1.7.2	1.7.2	/home/jb
	lambda.r	1.2.4	1.2.4	/home/jb
	lattice	0.20.45	0.20-45	/usr/lib/
	lifecycle	1.0.1	1.0.1	/home/jb
	magrittr	2.0.1	2.0.1	/home/jb
	munsell	0.5.0	0.5.0	/home/jb
	pbdBZMQ	0.3.6	0.3-6	/home/jb
	pillar	1.6.4	1.6.4	/home/jb
	pkgconfig	2.0.3	2.0.3	/home/jb
	purrr	0.3.4	0.3.4	/home/jb
	R.devices	2.17.0	2.17.0	/home/jb
	R.methodsS3	1.8.1	1.8.1	/home/jb
	R.oo	1.24.0	1.24.0	/home/jb
	R.utils	2.11.0	2.11.0	/home/jb
	R6	2.5.1	2.5.1	/home/jb
	repr	1.1.3	1.1.3	/home/jb
	rlang	0.4.12	0.4.12	/home/jb
	RRHO	1.34.0	1.34.0	/home/jb
	scales	1.1.1	1.1.1	/home/jb
	sessioninfo	1.2.1	1.2.1	/home/jb
	tibble	3.1.6	3.1.6	/home/jb
	tidyselect	1.1.1	1.1.1	/home/jb
	utf8	1.2.2	1.2.2	/home/jb
	uuid	1.0.3	1.0-3	/home/jb
	vctrs	0.3.8	0.3.8	/home/jb
	VennDiagram	1.7.0	1.7.0	/home/jb
	viridis	0.6.2	0.6.2	/home/jb

\$hash \$emoji 1. ' ' 2. ' ' 3. ' '

\$emo_text 1. 'baby angel: light skin tone' 2. 'pig face' 3. 'person facepalming: light skin tone'

[]: