

# BioDomain analysis for FXS and CTRL

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2025-07-24

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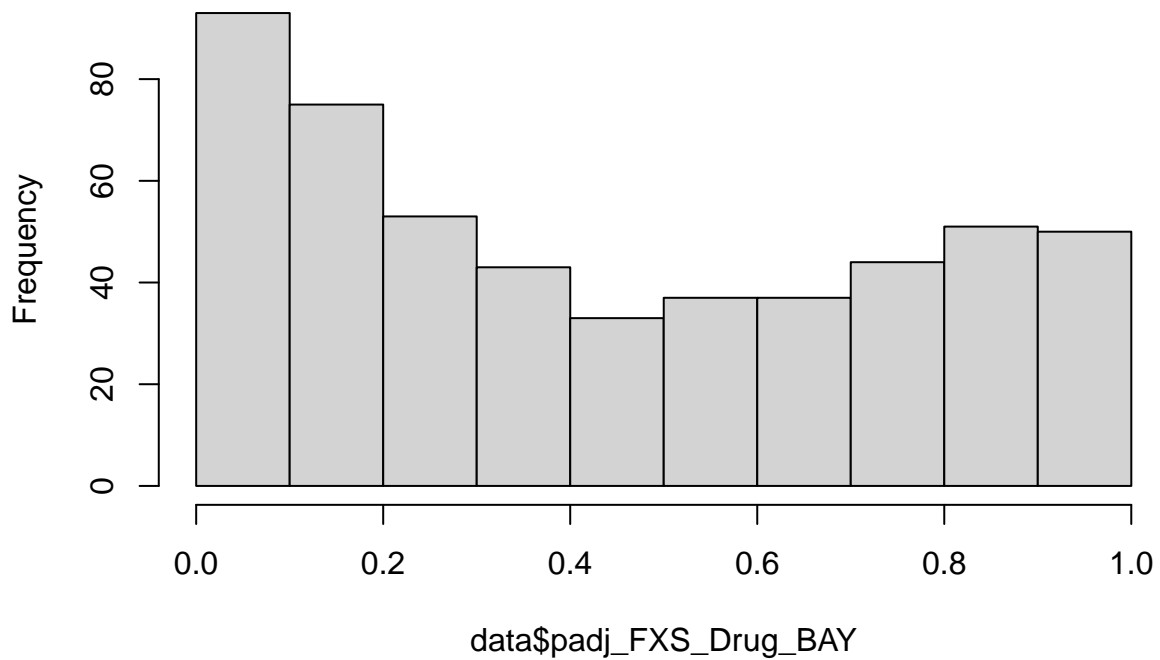
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## 1. BioDomain analysis

Load the GSVA analysis

## 2. Load GSVA result

**Histogram of data\$padj\_FXS\_Drug\_BAY**



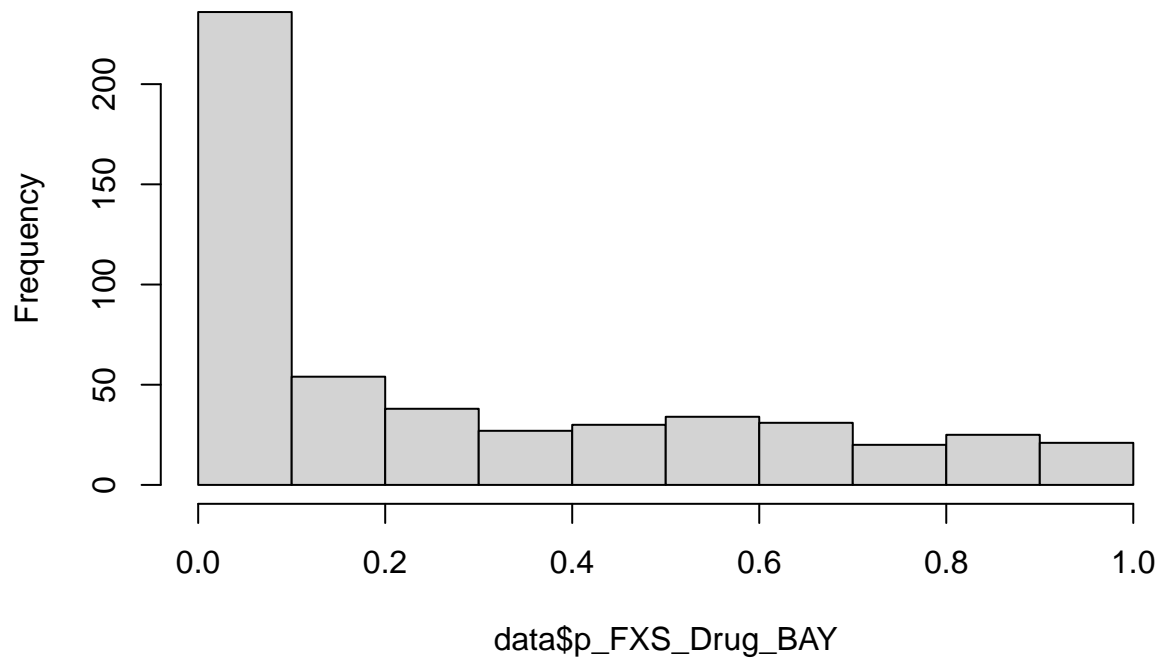
```
## [1] "padj_FXS_Drug_BAY < 0.05"
```

```
##
```

```
## FALSE TRUE
```

```
## 477 39
```

**Histogram of data\$p\_FXS\_Drug\_BAY**



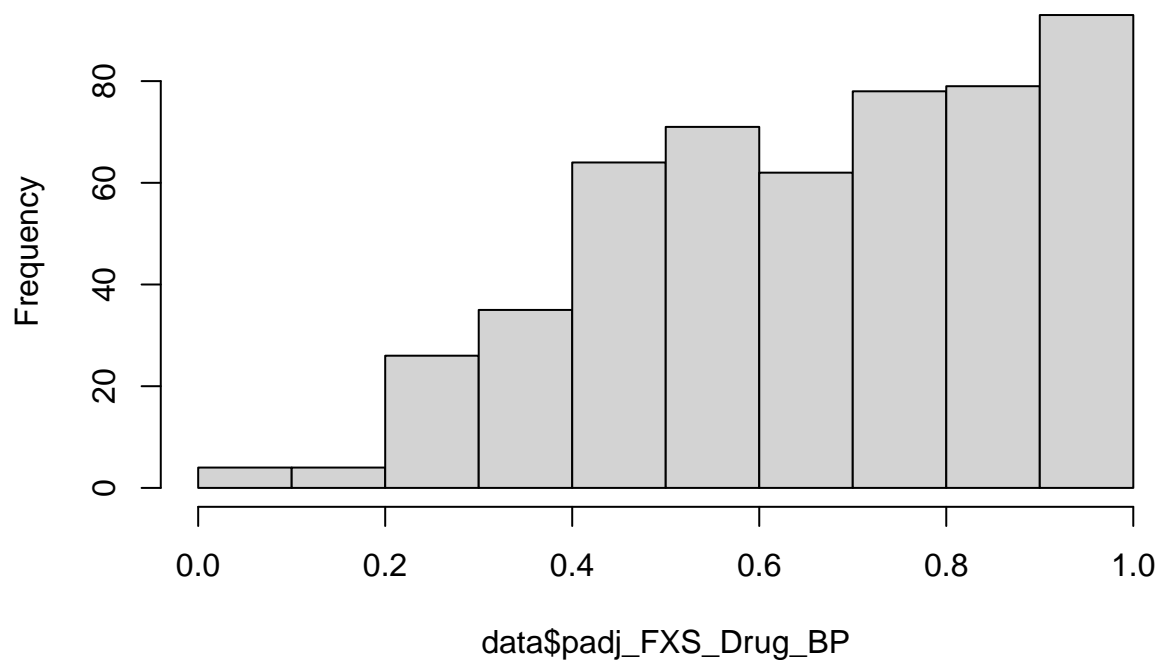
```
## [1] "p_FXS_Drug_BAY < 0.05"
```

```
##
```

```
## FALSE TRUE
```

```
## 324 192
```

**Histogram of data\$padj\_FXS\_Drug\_BP**



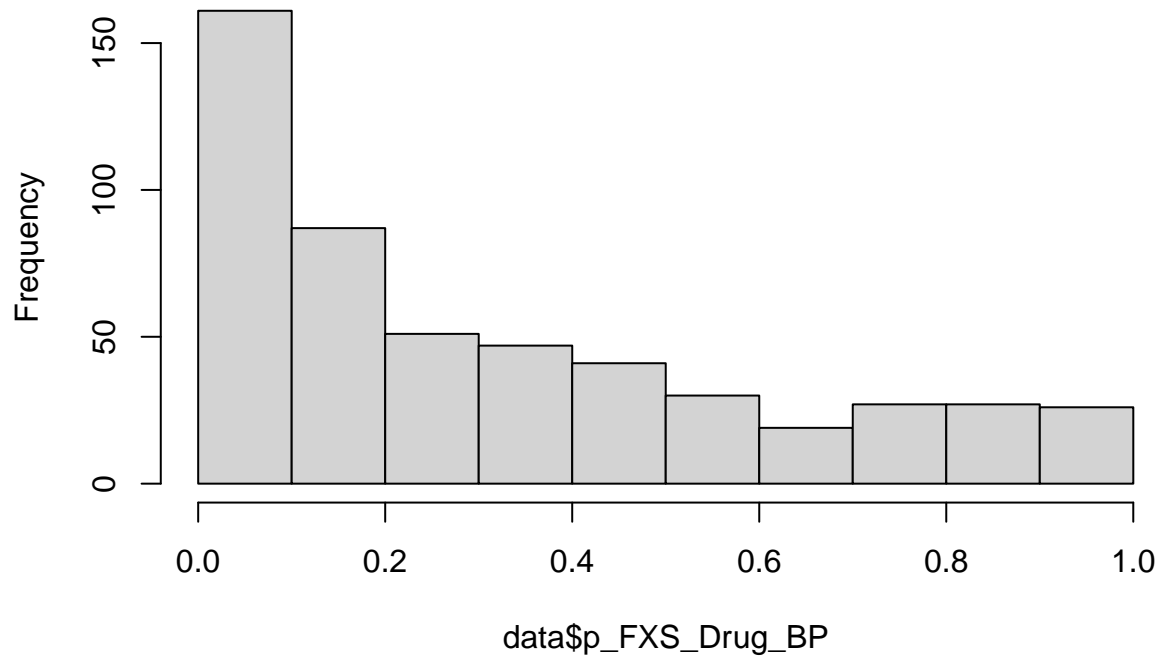
```
## [1] "p_adj_FXS_Drug_BP < 0.05"
```

```
##
```

```
## FALSE TRUE
```

```
## 515 1
```

### Histogram of data\$p\_FXS\_Drug\_BP



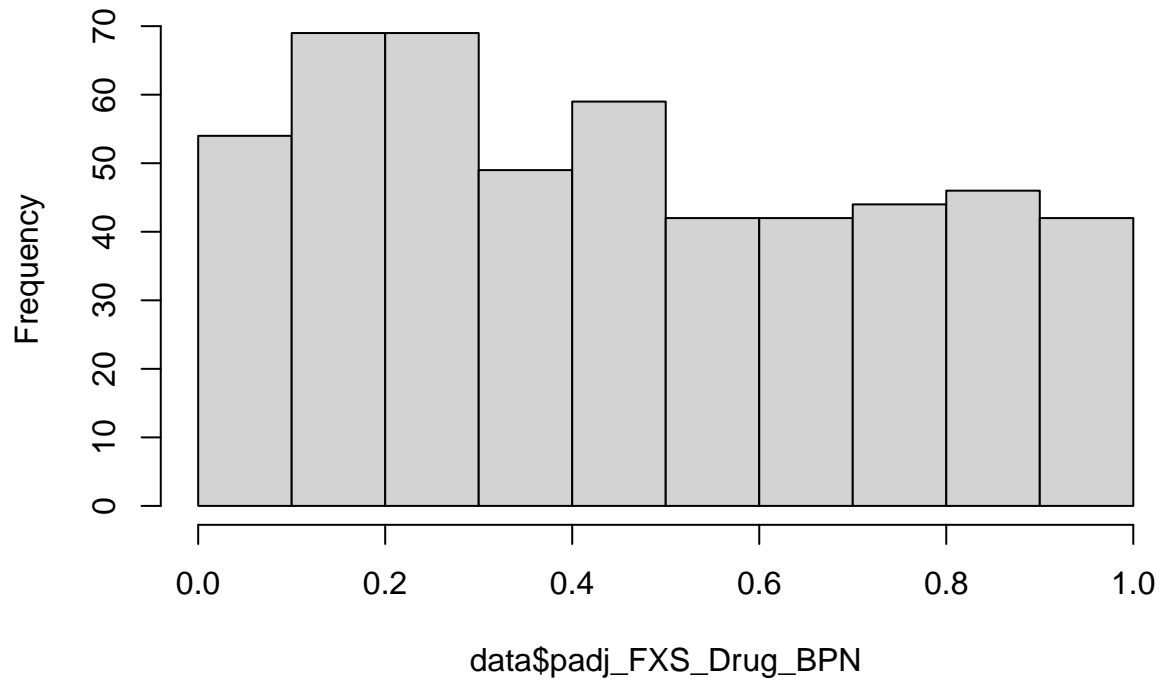
```
## [1] "p_FXS_Drug_BP < 0.05"
```

```
##
```

```
## FALSE TRUE
```

```
## 423 93
```

**Histogram of data\$padj\_FXS\_Drug\_BPN**



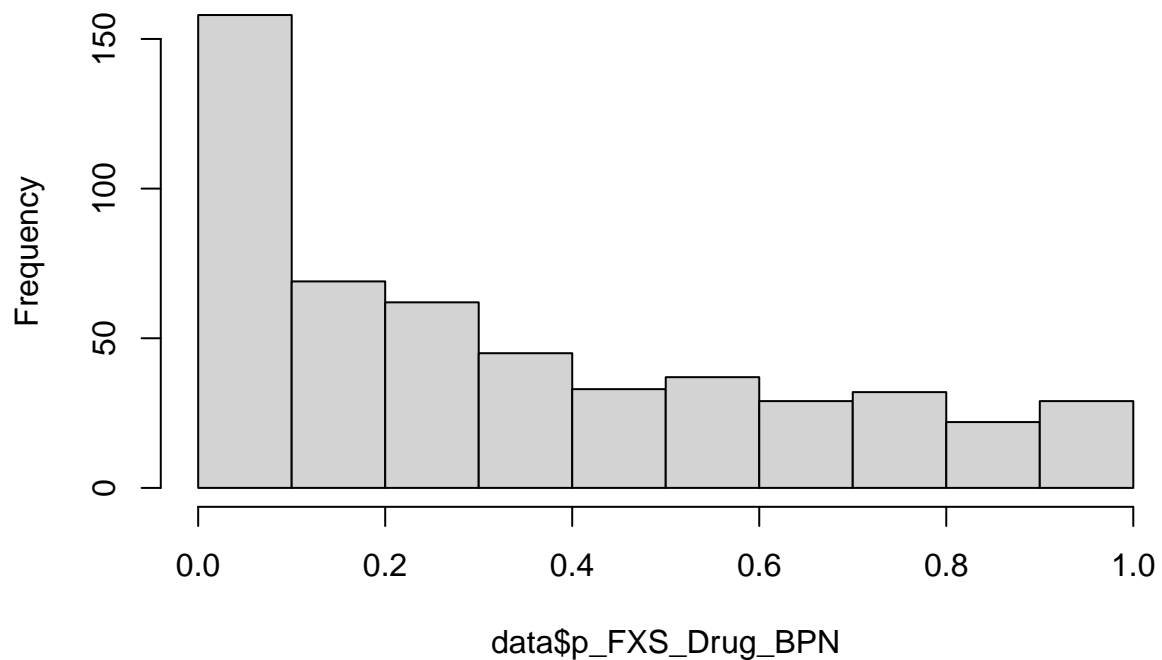
```
## [1] "padj_FXS_Drug_BPN < 0.05"
```

```
##
```

```
## FALSE TRUE
```

```
## 513 3
```

**Histogram of data\$p\_FXS\_Drug\_BPN**



```
## [1] "p_FXS_Drug_BPN < 0.05"  
##  
## FALSE TRUE  
## 412 104
```

### 3. Define the fully rescue and partical rescue

```
## [1] "BAY"
```

```
##
```

```
## No Side Effect    Side Effect
##           439           77
```

```
##
```

```
##    Full Rescue    No Rescue Partial Rescue    Side Effect
##           40           307           92           77
```

```
## [1] "BP"
```

```
##
```

```
## No Side Effect    Side Effect
##           253           263
```

```
##
```

```
##    Full Rescue    No Rescue Partial Rescue    Side Effect
##           8           227           18           263
```

```
## [1] "BPN"
```

```
##
```

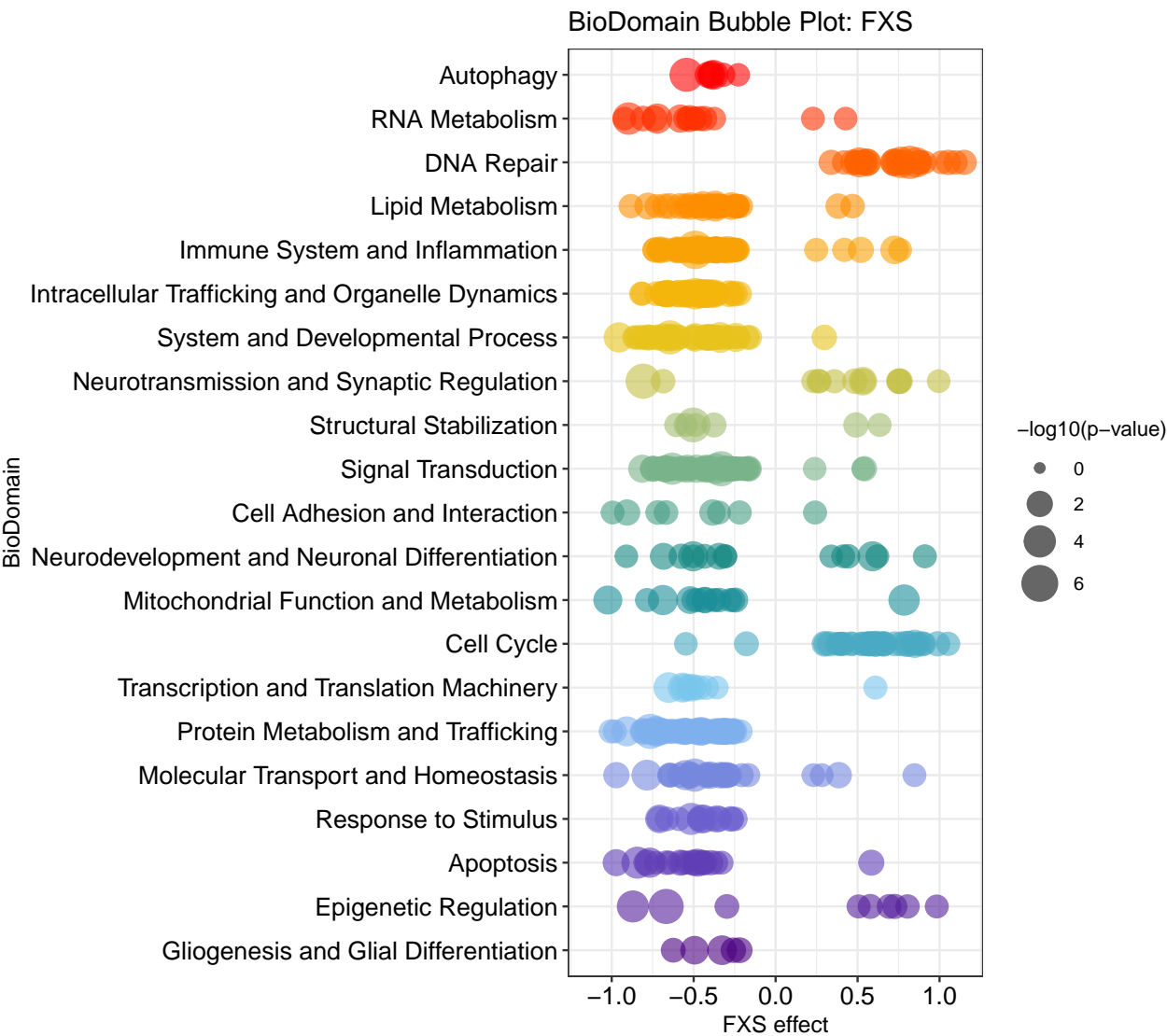
```
## No Side Effect    Side Effect
##           452           64
```

```
##
```

```
##    Full Rescue    No Rescue Partial Rescue    Side Effect
##           28           378           46           64
```

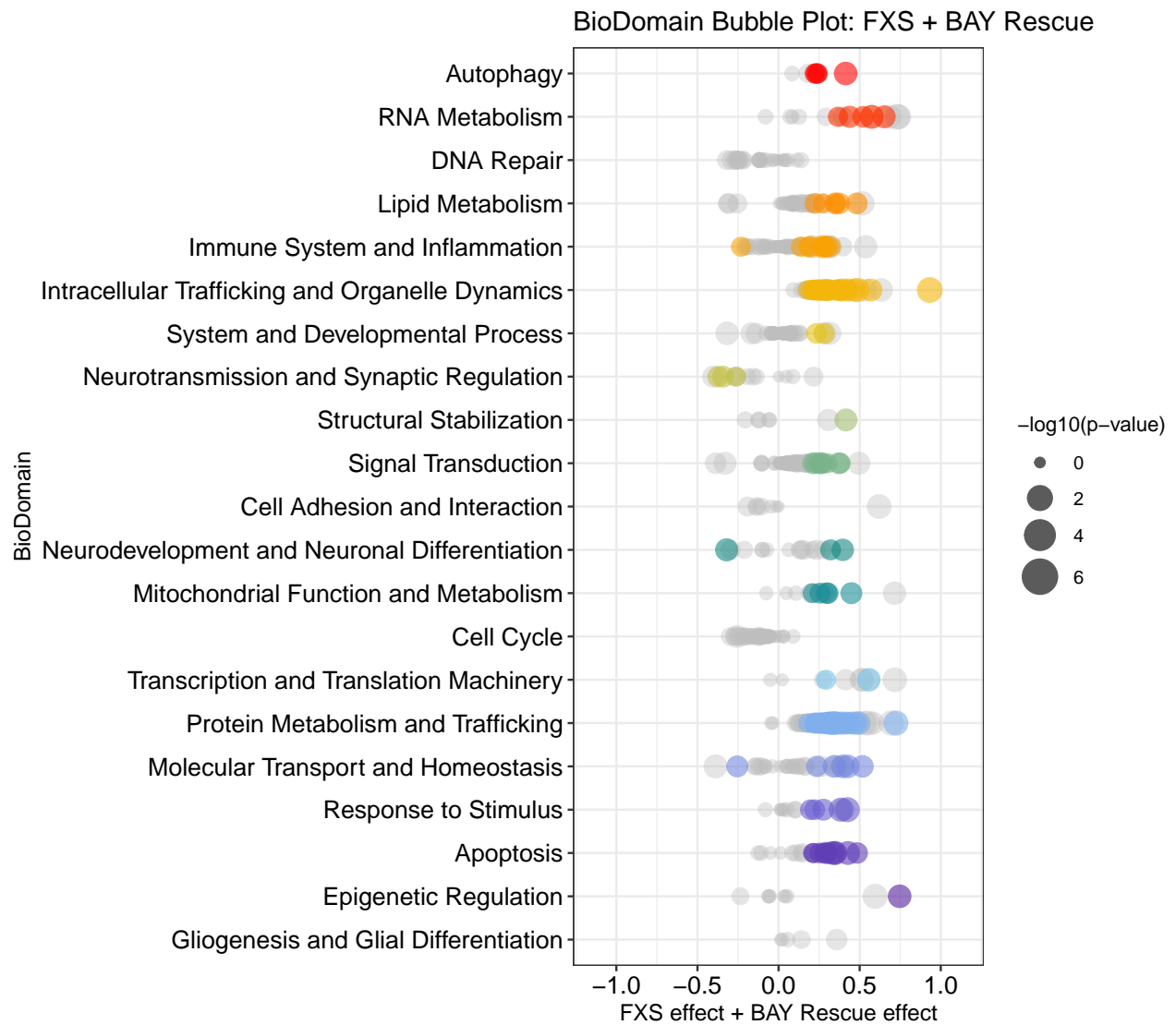
4. Bubble plot for the BioDomain

## [1] "FXS"

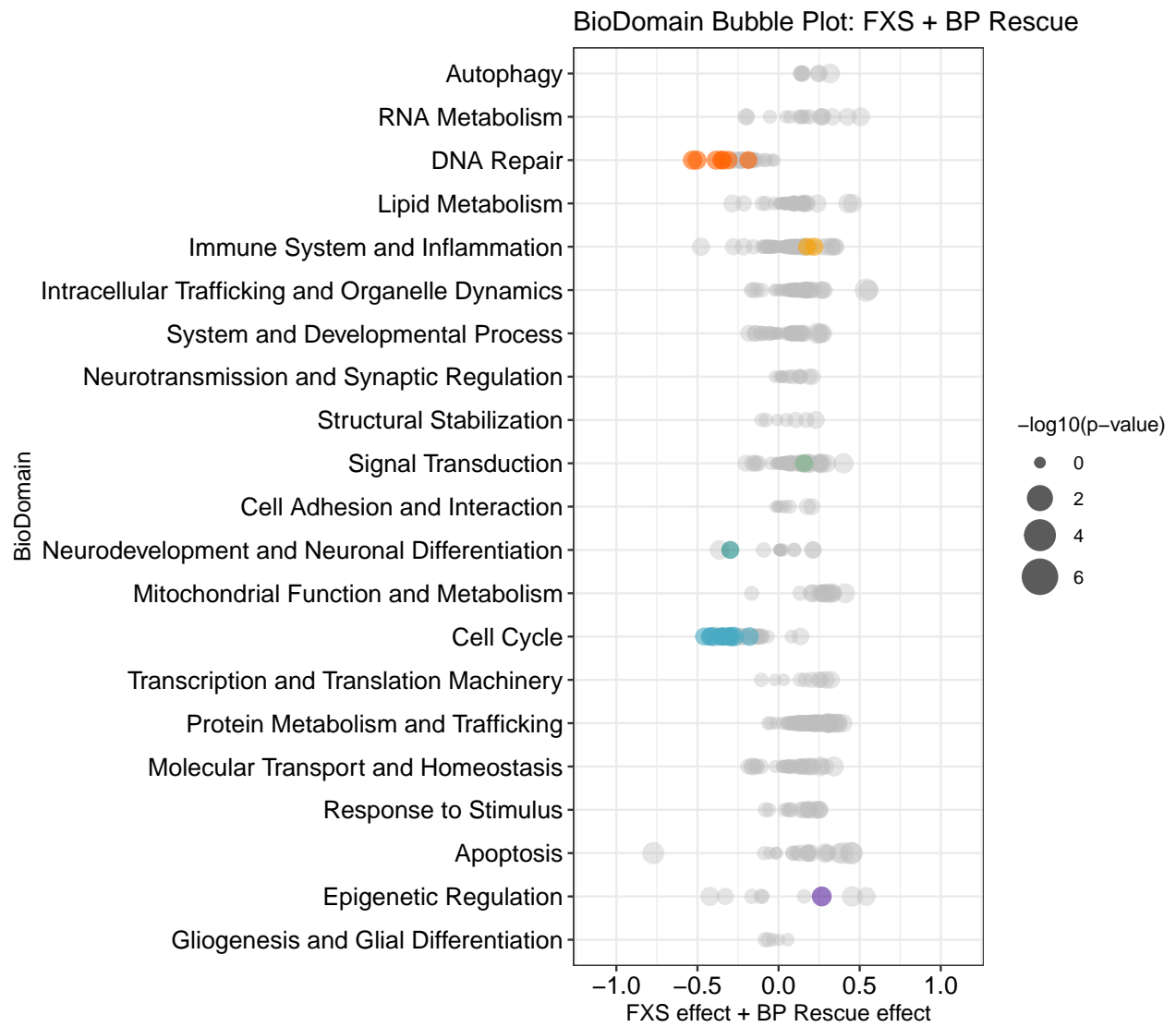


## [1] "FXS\_+\_BAY\_Rescue"

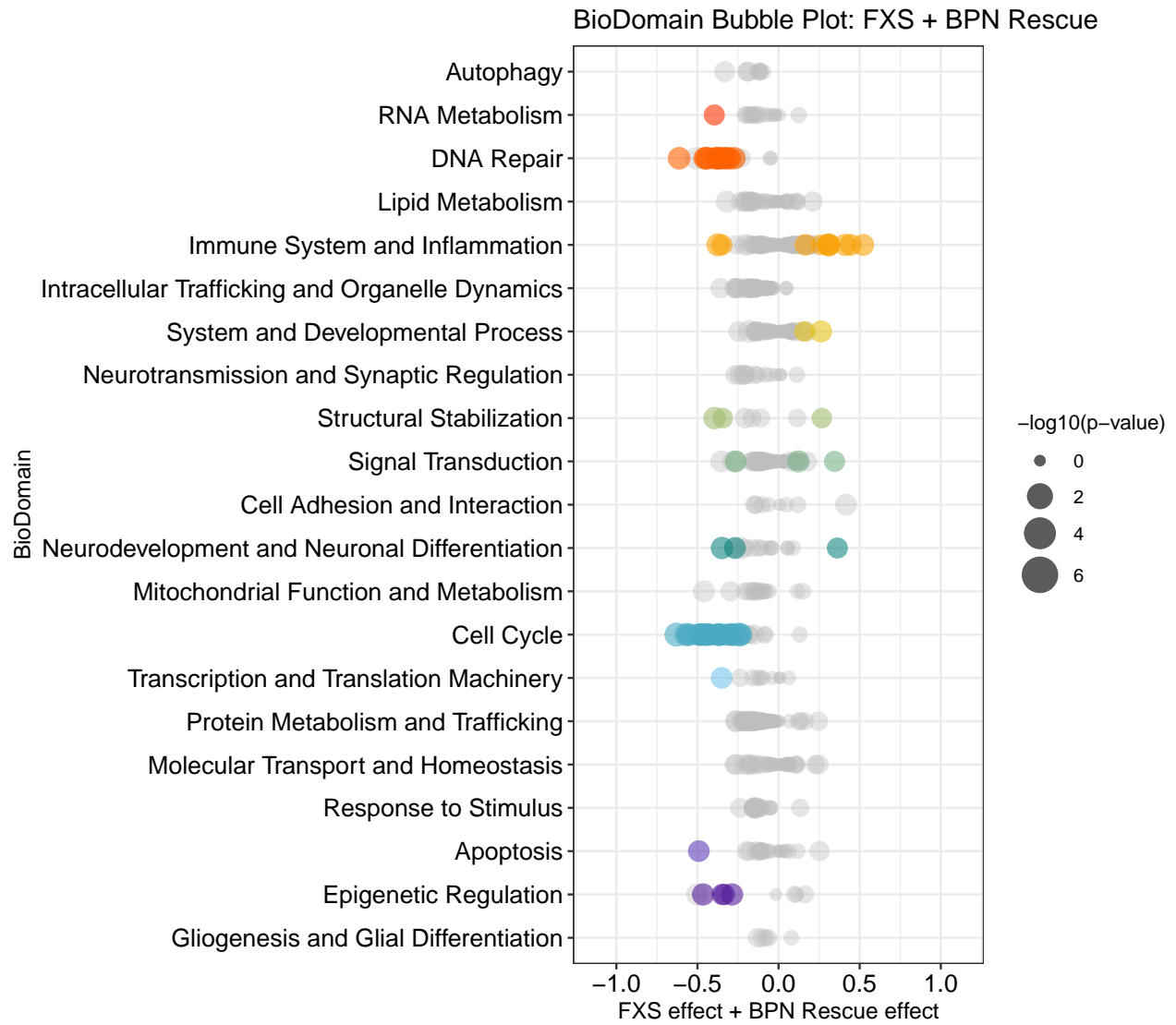




```
## [1] "FXS_+_BP_Rescue"
```



```
## [1] "FXS+_BPN_Rescue"
```



## Plot the gene heatmap

```
## [1] "Durg : BAY, BioDomain : Autophagy"
## [1] "Durg : BAY, BioDomain : RNA Metabolism"
## [1] "Durg : BAY, BioDomain : Lipid Metabolism"
## [1] "Durg : BAY, BioDomain : Immune System and Inflammation"
## [1] "Durg : BAY, BioDomain : Intracellular Trafficking and Organelle Dynamics"
## [1] "Durg : BAY, BioDomain : System and Developmental Process"
## [1] "Durg : BAY, BioDomain : Neurotransmission and Synaptic Regulation"
## [1] "Durg : BAY, BioDomain : Structural Stabilization"
## [1] "Durg : BAY, BioDomain : Signal Transduction"
## [1] "Durg : BAY, BioDomain : Neurodevelopment and Neuronal Differentiation"
## [1] "Durg : BAY, BioDomain : Mitochondrial Function and Metabolism"
## [1] "Durg : BAY, BioDomain : Transcription and Translation Machinery"
## [1] "Durg : BAY, BioDomain : Protein Metabolism and Trafficking"
## [1] "Durg : BAY, BioDomain : Molecular Transport and Homeostasis"
## [1] "Durg : BAY, BioDomain : Response to Stimulus"
## [1] "Durg : BAY, BioDomain : Apoptosis"
## [1] "Durg : BP, BioDomain : DNA Repair"
## [1] "Durg : BP, BioDomain : Immune System and Inflammation"
## [1] "Durg : BP, BioDomain : Signal Transduction"
## [1] "Durg : BP, BioDomain : Neurodevelopment and Neuronal Differentiation"
## [1] "Durg : BP, BioDomain : Cell Cycle"
## [1] "Durg : BP, BioDomain : Epigenetic Regulation"
## [1] "Durg : BPN, BioDomain : RNA Metabolism"
## [1] "Durg : BPN, BioDomain : DNA Repair"
## [1] "Durg : BPN, BioDomain : Immune System and Inflammation"
## [1] "Durg : BPN, BioDomain : System and Developmental Process"
## [1] "Durg : BPN, BioDomain : Structural Stabilization"
## [1] "Durg : BPN, BioDomain : Signal Transduction"
## [1] "Durg : BPN, BioDomain : Neurodevelopment and Neuronal Differentiation"
## [1] "Durg : BPN, BioDomain : Cell Cycle"
## [1] "Durg : BPN, BioDomain : Transcription and Translation Machinery"
## [1] "Durg : BPN, BioDomain : Apoptosis"
```

## Session information

```
## R version 4.4.0 (2024-04-24)
## Platform: aarch64-apple-darwin20
## Running under: macOS 15.5
##
## Matrix products: default
## BLAS:   /Library/Frameworks/R.framework/Versions/4.4-arm64/Resources/lib/libRblas.0.dylib
## LAPACK: /Library/Frameworks/R.framework/Versions/4.4-arm64/Resources/lib/libRlapack.dylib; LAPACK v
##
## locale:
## [1] en_US.UTF-8/en_US.UTF-8/en_US.UTF-8/C/en_US.UTF-8/en_US.UTF-8
##
## time zone: America/New_York
## tzcode source: internal
##
## attached base packages:
## [1] grid      parallel stats4      stats      graphics  grDevices utils
## [8] datasets  methods   base
##
## other attached packages:
## [1] msigdbr_10.0.2      GSEABase_1.66.0
## [3] graph_1.82.0        annotate_1.82.0
## [5] XML_3.99-0.18       extrafont_0.19
## [7] ggsignif_0.6.4      patchwork_1.3.0
## [9] decoupleR_2.10.0    GSVA_1.52.3
## [11] BiocParallel_1.38.0 edgeR_4.2.2
## [13] limma_3.60.6        GenomicFeatures_1.56.0
## [15] biomaRt_2.60.1      gprofiler2_0.2.3
## [17] RColorBrewer_1.1-3  data.table_1.17.4
## [19] org.Hs.eg.db_3.19.1 AnnotationDbi_1.66.0
## [21] clusterProfiler_4.12.6 ggfortify_0.4.17
## [23] pheatmap_1.0.12     EnhancedVolcano_1.22.0
## [25] ggrepel_0.9.6       apegglm_1.26.1
## [27] DESeq2_1.44.0       SummarizedExperiment_1.34.0
## [29] Biobase_2.64.0      MatrixGenerics_1.16.0
## [31] matrixStats_1.5.0   reshape2_1.4.4
## [33] Matrix_1.7-3        Signac_1.14.0
## [35] Seurat_5.3.0        SeuratObject_5.1.0
## [37] sp_2.2-0            rtracklayer_1.64.0
## [39] GenomicRanges_1.56.2 GenomeInfoDb_1.40.1
## [41] IRanges_2.38.1      S4Vectors_0.42.1
## [43] BiocGenerics_0.50.0 knitr_1.50
## [45] lubridate_1.9.4     forcats_1.0.0
## [47] stringr_1.5.1       dplyr_1.1.4
## [49] purrr_1.0.4         readr_2.1.5
## [51] tidyr_1.3.1         tibble_3.2.1
## [53] ggplot2_3.5.2       tidyverse_2.0.0
##
## loaded via a namespace (and not attached):
## [1] SpatialExperiment_1.14.0 R.methodsS3_1.8.2
## [3] dichromat_2.0-0.1      progress_1.2.3
## [5] goftest_1.2-3          HDF5Array_1.32.1
## [7] Biostrings_2.72.1      vctrs_0.6.5
```

## [9] spatstat.random_3.4-1	digest_0.6.37
## [11] png_0.1-8	deldir_2.0-4
## [13] parallelly_1.44.0	magick_2.8.6
## [15] MASS_7.3-65	httpuv_1.6.16
## [17] qvalue_2.36.0	withr_3.0.2
## [19] xfun_0.52	ggfun_0.1.8
## [21] survival_3.8-3	memoise_2.0.1
## [23] gson_0.1.0	systemfonts_1.2.3
## [25] ragg_1.4.0	tidytree_0.4.6
## [27] zoo_1.8-14	pbapply_1.7-2
## [29] R.oo_1.27.1	prettyunits_1.2.0
## [31] KEGGREST_1.44.1	promises_1.3.3
## [33] httr_1.4.7	restfulr_0.0.15
## [35] rhdf5filters_1.16.0	globals_0.18.0
## [37] fitdistrplus_1.2-2	rhdf5_2.48.0
## [39] rstudioapi_0.17.1	UCSC.utils_1.0.0
## [41] miniUI_0.1.2	generics_0.1.4
## [43] DOSE_3.30.5	babelgene_22.9
## [45] curl_6.2.3	zlibbioc_1.50.0
## [47] ScaledMatrix_1.12.0	ggraph_2.2.1
## [49] polyclip_1.10-7	GenomeInfoDbData_1.2.12
## [51] SparseArray_1.4.8	xtable_1.8-4
## [53] evaluate_1.0.3	S4Arrays_1.4.1
## [55] BiocFileCache_2.12.0	hms_1.1.3
## [57] irlba_2.3.5.1	colorspace_2.1-1
## [59] filelock_1.0.3	ROCR_1.0-11
## [61] reticulate_1.42.0	spatstat.data_3.1-6
## [63] magrittr_2.0.3	lmtest_0.9-40
## [65] later_1.4.2	viridis_0.6.5
## [67] ggtree_3.12.0	lattice_0.22-7
## [69] spatstat.geom_3.4-1	future.apply_1.11.3
## [71] scattermore_1.2	shadowtext_0.1.4
## [73] cowplot_1.1.3	RcppAnnoy_0.0.22
## [75] pillar_1.10.2	nlme_3.1-168
## [77] compiler_4.4.0	beachmat_2.20.0
## [79] RSpectra_0.16-2	stringi_1.8.7
## [81] tensor_1.5	GenomicAlignments_1.40.0
## [83] plyr_1.8.9	crayon_1.5.3
## [85] abind_1.4-8	BiocIO_1.14.0
## [87] gridGraphics_0.5-1	emdbbook_1.3.13
## [89] locfit_1.5-9.12	graphlayouts_1.2.2
## [91] bit_4.6.0	fastmatch_1.1-6
## [93] textshaping_1.0.1	codetools_0.2-20
## [95] BiocSingular_1.20.0	plotly_4.10.4
## [97] mime_0.13	splines_4.4.0
## [99] Rcpp_1.0.14	fastDummies_1.7.5
## [101] sparseMatrixStats_1.16.0	dbplyr_2.5.0
## [103] Rttf2pt1_1.3.12	blob_1.2.4
## [105] here_1.0.1	fs_1.6.6
## [107] listenv_0.9.1	ggplotify_0.1.2
## [109] statmod_1.5.0	tzdb_0.5.0
## [111] tweenr_2.0.3	pkgconfig_2.0.3
## [113] tools_4.4.0	cachem_1.1.0
## [115] RSQLite_2.3.11	viridisLite_0.4.2

## [117] DBI_1.2.3	numDeriv_2016.8-1.1
## [119] fastmap_1.2.0	rmarkdown_2.29
## [121] scales_1.4.0	ica_1.0-3
## [123] Rsamtools_2.20.0	coda_0.19-4.1
## [125] dotCall64_1.2	RANN_2.6.2
## [127] farver_2.1.2	tidygraph_1.3.1
## [129] scatterpie_0.2.4	yaml_2.3.10
## [131] msigdbdf_24.1.1	cli_3.6.5
## [133] lifecycle_1.0.4	uwot_0.2.3
## [135] mvtnorm_1.3-3	timechange_0.3.0
## [137] gtable_0.3.6	rjson_0.2.23
## [139] gggridges_0.5.6	progressr_0.15.1
## [141] ape_5.8-1	jsonlite_2.0.0
## [143] RcppHNSW_0.6.0	bitops_1.0-9
## [145] assertthat_0.2.1	bit64_4.6.0-1
## [147] Rtsne_0.17	yulab.utils_0.2.0
## [149] spatstat.utils_3.1-4	bdsmatrix_1.3-7
## [151] GOSemSim_2.30.2	spatstat.univar_3.1-3
## [153] R.utils_2.13.0	lazyeval_0.2.2
## [155] shiny_1.10.0	htmltools_0.5.8.1
## [157] enrichplot_1.24.4	GO.db_3.19.1
## [159] sctransform_0.4.2	rappdirs_0.3.3
## [161] tinytex_0.57	glue_1.8.0
## [163] spam_2.11-1	httr2_1.1.2
## [165] XVector_0.44.0	RCurl_1.98-1.17
## [167] rprojroot_2.0.4	treeio_1.28.0
## [169] gridExtra_2.3	extrafontdb_1.0
## [171] igraph_2.1.4	R6_2.6.1
## [173] SingleCellExperiment_1.26.0	labeling_0.4.3
## [175] RcppRoll_0.3.1	cluster_2.1.8.1
## [177] bbmle_1.0.25.1	Rhdf5lib_1.26.0
## [179] aplot_0.2.5	DelayedArray_0.30.1
## [181] tidyselect_1.2.1	ggforce_0.4.2
## [183] xml2_1.3.8	future_1.49.0
## [185] rsvd_1.0.5	KernSmooth_2.23-26
## [187] htmlwidgets_1.6.4	fgsea_1.30.0
## [189] rlang_1.1.6	spatstat.sparse_3.1-0
## [191] spatstat.explore_3.4-3	