00_prettyNet

zagor

2022-10-26

```r
library(crayon)
```

```
## Warning: package 'crayon' was built under R version 4.1.3
```

```r
fp = file.path('..', 'input')
(fl = list.files(fp, pattern = '2022-10-26'))
```

```
## [1] "pss-dinar-edges-restricted_2022-10-26.tsv"
## [2] "pss-dinar-nodes-restricted_2022-10-26.tsv"
```

```r
nodes = data.table::fread(file.path(fp, fl[2]), header = TRUE)
data.table::setDF(nodes)
head(nodes)
```

```
##                                                                   name short_name
## 1                                                          HC-Pro|vsiRNA
## 2 AHP[AT1G03430,AT1G80100,AT3G16360,AT3G21510,AT3G29350,AT5G39340]        AHP
## 3                                                               Drought
## 4                                                           Waterlogging
## 5                                              MKD1[AT5G11850]          MKD1
## 6                  ARF[AT1G19850,AT2G33860,AT5G60450,AT5G62000]          ARF
##   family                                                 description
## 1        In viral suppression of RNA-Silencing, Hc-Pro binds to vsiRNAs.
## 2    AHP               histidine-containing phosphotransfer protein
## 3
## 4
## 5                                 Protein kinase superfamily protein
## 6    ARF                              auxin response transcription factor
##                             pathway
## 1          Regulation - Silencing
## 2        Hormone - Cytokinins (CK)
## 3
## 4
## 5 Signalling - MAP kinases (MAPKs)
## 6            Hormone - Auxins (AUX)
##                                                           ath_homologues
## 1
## 2 ["AT1G03430","AT1G80100","AT3G16360","AT3G21510","AT3G29350","AT5G39340"]
## 3
## 4
```

```
## 5                                                         ["AT5G11850"]
## 6                       ["AT1G19850","AT2G33860","AT5G60450","AT5G62000"]
##         node_type
## 1       Complex
## 2     PlantCoding
## 3 ForeignAbiotic
## 4 ForeignAbiotic
## 5     PlantCoding
## 6     PlantCoding
```

```
edges = data.table::fread(file.path(fp, fl[1]), header = TRUE)
data.table::setDF(edges)
head(edges)
```

```
##                 source
## 1         NAC072[]
## 2 NAC019[AT1G52890]
## 3 NAC055[AT3G15500]
## 4         NAC072[]
## 5               GA
## 6   WRKY6[AT1G62300]
##                                                         target directed
## 1                                   ICS[AT1G18870,AT1G74710]     TRUE
## 2                                 SAGT[AT2G43820,AT2G43840]     TRUE
## 3                                 SAGT[AT2G43820,AT2G43840]     TRUE
## 4                                 SAGT[AT2G43820,AT2G43840]     TRUE
## 5 MYB33,44,65[AT3G11440,AT5G06100,AT5G67300,SOTUB06G030530.1.1]     TRUE
## 6                                   NPR1[AT1G64280]     TRUE
##                   reaction_type reaction_effect reaction_id
## 1 transcriptional/translational activation     activation   rx00256
## 2 transcriptional/translational activation     activation   rx00257
## 3 transcriptional/translational activation     activation   rx00258
## 4 transcriptional/translational activation     activation   rx00259
## 5 transcriptional/translational activation     activation   rx00302
## 6 transcriptional/translational activation     activation   rx00309
##   source_edge_type     source_location     source_form target_edge_type
## 1         ACTIVATES             nucleus protein_active         SUBSTRATE
## 2         ACTIVATES             nucleus protein_active         SUBSTRATE
## 3         ACTIVATES             nucleus protein_active         SUBSTRATE
## 4         ACTIVATES             nucleus protein_active         SUBSTRATE
## 5         ACTIVATES putative:cytoplasm    metabolite         SUBSTRATE
## 6         ACTIVATES             nucleus protein_active         SUBSTRATE
##   target_location target_form
## 1         nucleus        gene
## 2         nucleus        gene
## 3         nucleus        gene
## 4         nucleus        gene
## 5         nucleus        gene
## 6         nucleus        gene
```

```
(m = max(stringr::str_count(nodes$name, pattern = '\\['))+1)
```

```
## [1] 2
```

```r
tmp = stringr::str_split_fixed(nodes$name, '\\[', m)
tmp[, 2] = gsub('\\]', '', tmp[,2])

nodes$name = tmp[, 1]
ind = which(nodes$short_name == '')
nodes$short_name[ind] = nodes$name[ind]

max(stringr::str_count(tmp[, 2], pattern = '\\['))
```

```
## [1] 0
```

```r
max(stringr::str_count(tmp[, 2], pattern = '\\]'))
```

```
## [1] 0
```

```r
max(stringr::str_count(tmp[, 1], pattern = '\\['))
```

```
## [1] 0
```

```r
max(stringr::str_count(tmp[, 1], pattern = '\\]'))
```

```
## [1] 0
```

```r
(m = max(stringr::str_count(tmp[, 2], pattern = ',')) + 1)
```

```
## [1] 29
```

```r
temp = stringr::str_split_fixed(tmp[,2], ',', m)

translate = as.data.frame(cbind(tmp, temp))
translate[translate == ''] = NA
colnames(translate)
```

```
##  [1] "V1"  "V2"  "V3"  "V4"  "V5"  "V6"  "V7"  "V8"  "V9"  "V10" "V11" "V12"
## [13] "V13" "V14" "V15" "V16" "V17" "V18" "V19" "V20" "V21" "V22" "V23" "V24"
## [25] "V25" "V26" "V27" "V28" "V29" "V30" "V31"
```

```r
translate.long = tidyr::gather(translate,
                               group, athID,
                               colnames(translate)[3]:colnames(translate)[ncol(translate)],
                               factor_key=FALSE)

colnames(translate.long)[1:2] = c('nodeID', 'genesID')
translate.long = translate.long[, -3]
translate.long = translate.long[!is.na(translate.long$athID), ]
translate.long = translate.long[, -2]
translate.long$athID = gsub('\\.1\\.1', '', translate.long$athID)
translate.long = translate.long[translate.long$athID != 'unknown', ]
head(translate.long)
```

```
##    nodeID       athID
## 2     AHP AT1G03430
## 5    MKD1 AT5G11850
## 6     ARF AT1G19850
## 7     ASK AT1G06390
## 8    CHY1 AT5G65940
## 9     CAT AT1G20620
```

```
tail(translate.long)
```

```
##         nodeID       athID
## 12125 AUX/IAA AT4G29080
## 12635 AUX/IAA AT4G32280
## 13145 AUX/IAA AT5G25890
## 13655 AUX/IAA AT5G43700
## 14165 AUX/IAA AT5G57420
## 14675 AUX/IAA AT5G65670
```

```
ind = grep('^AT', translate.long$athID)
translate.long.ath = translate.long[ind,]
ind = grep('^SOTUB', translate.long$athID)
translate.long.stu = translate.long[ind,]
```

```
translate.long.stu$athID = tolower(translate.long.stu$athID)
translate.long.stu$athID = gsub('s', 'S', translate.long.stu$athID)
```

```
fp = file.path('..', '..', '_A_01_networkExpress-R', 'input')
list.files(fp)
```

```
##  [1] "!README.MD"
##  [2] "AT1G55860-PGSC0003DMP400038590.html"
##  [3] "AT1G55860-PGSC0003DMP400038590_files"
##  [4] "EXP2-geneIDs.txt"
##  [5] "MERGED_conversion-table_2019-12-19_1_within-gene-model_per-gene_ITAG.txt.zip"
##  [6] "MERGED_conversion-table_2019-12-19_2_between-gene-models_per-gene_ITAG.txt.zip"
##  [7] "MERGED_conversion-table_2019-12-19_2_between-gene-models_per-gene_ITAG_untranslatable.txt.zip"
##  [8] "mixedEXP2_AND_monoEXP1_logFC_padj_TMMcpm_narrow.txt"
##  [9] "ortholog_OCD_all_genes.tsv.gz"
## [10] "PSS_2021-12-22"
## [11] "rbb_ath-vs-stuGFF_5_rbb-translation_filtered-long.txt"
## [12] "rbb_ath-vs-stuGFF_5_rbb-translation_filtered-long.txt.gz"
## [13] "Solanum_tuberosum_PGSC_DM_v3.4_converterWithDescriptions.txt"
## [14] "Solanum_tuberosum_PGSC_DM_v3.4_converterWithDescriptions.txt.zip"
```

```
fn = 'rbb_ath-vs-stuGFF_5_rbb-translation_filtered-long.txt'
```

```
rbb = data.table::fread(file.path(fp, fn), header = TRUE)
data.table::setDF(rbb)
head(rbb)
```

```
##            rbbID      athID 1               tarID
```

```
## 1 RBB_hvu_00003 AT1G01040 1          Sotub10g006390
## 2 RBB_hvu_00004 AT1G01050 4          Sotub12g024490
## 3 RBB_hvu_00004 AT1G01050 4          Sotub08g026940
## 4 RBB_hvu_00004 AT1G01050 4 PGSC0003DMP400006264
## 5 RBB_hvu_00004 AT1G01050 4          Sotub08g009140
## 6 RBB_hvu_00005 AT1G01060 1 PGSC0003DMP400020008
##                           athDescription positives athCoverage tarCoverage
## 1                         dicer-like 1          81          97          98
## 2                   pyrophosphorylase 1          93         100         100
## 3                   pyrophosphorylase 1          95          95          98
## 4                   pyrophosphorylase 1          94          92          91
## 5                   pyrophosphorylase 1          95          52          99
## 6 Homeodomain-like superfamily protein          98           9          85
```

```r
fn = 'Solanum_tuberosum_PGSC_DM_v3.4_converterWithDescriptions.txt'
pgsc = data.table::fread(file.path(fp, fn), header = FALSE)
data.table::setDF(pgsc)
head(pgsc)
```

```
##                    V1                   V2                   V3
## 1 PGSC0003DMG400000001 PGSC0003DMT400000001 PGSC0003DMC400000001
## 2 PGSC0003DMG400000001 PGSC0003DMT400000002 PGSC0003DMC400000002
## 3 PGSC0003DMG400000001 PGSC0003DMT400000003 PGSC0003DMC400000003
## 4 PGSC0003DMG400000002 PGSC0003DMT400000004 PGSC0003DMC400000004
## 5 PGSC0003DMG400000002 PGSC0003DMT400000005 PGSC0003DMC400000005
## 6 PGSC0003DMG400000003 PGSC0003DMT400000009 PGSC0003DMC400000009
##                    V4                                              V5
## 1 PGSC0003DMP400000001 Adenosine 3'-phospho 5'-phosphosulfate transporter
## 2 PGSC0003DMP400000002 Adenosine 3'-phospho 5'-phosphosulfate transporter
## 3 PGSC0003DMP400000003 Adenosine 3'-phospho 5'-phosphosulfate transporter
## 4 PGSC0003DMP400000004                   Vacuolar iron family transporter
## 5 PGSC0003DMP400000005                   Vacuolar iron family transporter
## 6 PGSC0003DMP400000009         SPX domain-containing membrane protein
##       V6    V7
## 1 nonred     -
## 2 nonred repres
## 3 nonred     -
## 4 nonred repres
## 5 nonred     -
## 6 nonred repres
```

```r
colnames(pgsc)[4] = colnames(rbb)[4]
colnames(pgsc)[1] = 'geneID'
```

```r
rbb = merge(rbb, pgsc[, c(4, 1)], by = colnames(pgsc)[4], all.x = TRUE, all.y = FALSE)
ind = which(is.na(rbb$geneID))
rbb$geneID[ind] = rbb$tarID[ind]
```

```r
patterns = c("athID", "geneID", "athDescription")
ind = which(grepl(paste(patterns, collapse = "|"), colnames(rbb)))
rbb = rbb[, ind]
head(rbb)
```

```
##        athID
## 1 AT1G12600
## 2 AT4G22990
## 3 AT2G45500
## 4 AT2G45500
## 5 AT2G24190
## 6 AT4G11610
##                                                                   athDescription
## 1                               UDP-N-acetylglucosamine (UAA) transporter family
## 2 Major Facilitator Superfamily with SPX (SYG1/Pho81/XPR1) domain-containing protein
## 3                                                     AAA-type ATPase family protein
## 4                                                     AAA-type ATPase family protein
## 5                                 NAD(P)-binding Rossmann-fold superfamily protein
## 6            C2 calcium/lipid-binding plant phosphoribosyltransferase family protein
##                geneID
## 1 PGSC0003DMG400000001
## 2 PGSC0003DMG400000003
## 3 PGSC0003DMG401000018
## 4 PGSC0003DMG402000018
## 5 PGSC0003DMG400000022
## 6 PGSC0003DMG401000029
```

Chr Un

PGSC0003DMT402...

PGSC0003DMG406...

PGSC0003DMC402...

```
rbb[grep('DMP402', rbb$geneID), ]
```

```
##          athID
## 2349 AT5G57660
## 2350 AT2G40840
## 2351 AT2G40320
## 2352 AT1G23800
## 2353 AT3G05170
## 2354 AT4G38840
## 2355 AT3G45080
## 2356 AT3G12260
## 2357 AT5G47010
## 2358 AT4G25550
## 2359 AT4G37870
## 2360 AT1G43800
## 2361 AT4G36670
## 2362 AT1G19835
## 2363 AT1G55020
## 2364 AT3G53260
## 2365 AT3G63110
## 2366 AT2G24370
## 2367 AT4G25310
## 2368 AT2G37040
## 2369 AT2G47990
## 2370 AT4G14430
```

```
## 2371 AT3G63110
## 2372 AT5G23660
## 2373 AT1G63030
## 2374 AT1G66410
## 2375 AT5G17330
## 2376 AT2G23180
## 2377 AT4G13420
## 2378 AT3G45660
## 2379 AT4G08950
## 2380 AT2G36870
## 2381 AT1G29930
## 2382 AT2G28230
## 2383 AT5G58390
## 2384 AT2G30210
## 2385 AT3G20650
## 2386 AT1G15520
## 2387 AT1G32910
## 2388 AT2G36310
## 2389 AT3G22910
## 2390 AT2G20340
## 2391 AT5G15490
## 2392 AT4G15200
## 2393 AT3G44990
## 2394 AT5G10810
## 2395 AT3G11980
## 2396 AT2G21210
## 2397 AT5G39160
## 2398 AT1G55290
## 2399 AT1G43800
## 2400 AT5G54650
## 2401 AT1G53720
## 2402 AT5G28950
## 2403 AT1G60500
## 2404 AT4G16260
## 2405 AT3G16180
## 2406 AT4G11050
## 2407 AT4G12570
## 2408 AT4G08570
## 2409 AT2G37040
## 2410 AT1G50920
## 2411 AT2G23620
## 2412 AT2G23620
## 2413 AT3G21460
## 2414 AT1G67680
## 2415 AT1G28220
## 2416 AT4G19810
## 2417 AT3G18280
## 2418 AT1G26910
## 2419 AT1G72900
## 2420 AT3G28580
## 2421 AT4G18550
## 2422 AT5G19040
## 2423 AT2G28490
## 2424 AT1G60530
```

```
## 2425 AT2G40110
## 2426 AT3G12500
## 2427 AT3G14640
## 2428 AT3G62450
## 2429 AT4G34570
##                                                                              athDescription
## 2349                                                                        CONSTANS-like 5
## 2350                                                              disproportionating enzyme 2
## 2351                                                               TRICHOME BIREFRINGENCE-LIKE 33
## 2352                                                                  aldehyde dehydrogenase 2B7
## 2353                                                       Phosphoglycerate mutase family protein
## 2354                                                    SAUR-like auxin-responsive protein family
## 2355              P-loop containing nucleoside triphosphate hydrolases superfamily protein
## 2356                                          LYR family of Fe/S cluster biogenesis protein
## 2357                                                                               RNA helicase
## 2358                                        Cleavage/polyadenylation specificity factor%2C 25kDa subunit
## 2359                                                        phosphoenolpyruvate carboxykinase 1
## 2360                                  Plant stearoyl-acyl-carrier-protein desaturase family protein
## 2361                                                      Major facilitator superfamily protein
## 2362                                                           filament-like protein (DUF869)
## 2363                                                                             lipoxygenase 1
## 2364                                                          phenylalanine ammonia-lyase 2
## 2365                                                             isopentenyltransferase 3
## 2366            kinase with adenine nucleotide alpha hydrolases-like domain-containing protein
## 2367             2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein
## 2368                                                                        PHE ammonia lyase 1
## 2369                                       transducin family protein / WD-40 repeat family protein
## 2370                                                          indole-3-butyric acid response 10
## 2371                                                             isopentenyltransferase 3
## 2372                                         bidirectional sugar transporter SWEET12-like protein
## 2373                                            Integrase-type DNA-binding superfamily protein
## 2374                                                                               calmodulin 4
## 2375                                                                   glutamate decarboxylase
## 2376                              cytochrome P450%2C family 96%2C subfamily A%2C polypeptide 1
## 2377                                                            high affinity K+ transporter 5
## 2378                                                      Major facilitator superfamily protein
## 2379                                                    Phosphate-responsive 1 family protein
## 2380                                         xyloglucan endotransglucosylase/hydrolase 32
## 2381                                                          chlorophyll A/B binding protein 1
## 2382                      TATA-binding related factor (TRF) of subunit 20 of Mediator complex
## 2383                                                            Peroxidase superfamily protein
## 2384                                                                                 laccase 3
## 2385                                                     mRNA capping enzyme family protein
## 2386                                                            pleiotropic drug resistance 12
## 2387                                                 HXXXD-type acyl-transferase family protein
## 2388                                                              uridine-ribohydrolase 1
## 2389    ATPase E1-E2 type family protein / haloacid dehalogenase-like hydrolase family protein
## 2390                    Pyridoxal phosphate (PLP)-dependent transferases superfamily protein
## 2391                                             UDP-glucose 6-dehydrogenase family protein
## 2392                                                                                  formin 3
## 2393                                            xyloglucan endo-transglycosylase-related 8
## 2394                                                         enhancer of rudimentary protein
## 2395                                  Jojoba acyl CoA reductase-related male sterility protein
## 2396                                                    SAUR-like auxin-responsive protein family
```

```
## 2397                                                RmlC-like cupins superfamily protein
## 2398            2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein
## 2399                      Plant stearoyl-acyl-carrier-protein desaturase family protein
## 2400                                                               formin homology5
## 2401                                                                 cyclophilin 59
## 2402                                                                       nuclease
## 2403                                                      Dynamin related protein 4C
## 2404                                       Glycosyl hydrolase superfamily protein
## 2405                                       Major facilitator superfamily protein
## 2406                                                         glycosyl hydrolase 9C3
## 2407                                                      ubiquitin protein ligase 5
## 2408                      Heavy metal transport/detoxification superfamily protein
## 2409                                                           PHE ammonia lyase 1
## 2410                                                   Nucleolar GTP-binding protein
## 2411                                                              methyl esterase 1
## 2412                                                              methyl esterase 1
## 2413                                                      Glutaredoxin family protein
## 2414                                   SRP72 RNA-binding domain-containing protein
## 2415                                                               purine permease 3
## 2416      Glycosyl hydrolase family protein with chitinase insertion domain-containing protein
## 2417 Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein
## 2418                                          Ribosomal protein L16p/L10e family protein
## 2419                         Toll-Interleukin-Resistance (TIR) domain-containing protein
## 2420            P-loop containing nucleoside triphosphate hydrolases superfamily protein
## 2421                                           alpha/beta-Hydrolases superfamily protein
## 2422                                                        isopentenyltransferase 5
## 2423                                                RmlC-like cupins superfamily protein
## 2424                                                      Dynamin related protein 4A
## 2425                                   Yippee family putative zinc-binding protein
## 2426                                                                 basic chitinase
## 2427                        cytochrome P450%2C family 72%2C subfamily A%2C polypeptide 10
## 2428                                                     DNA mismatch repair protein
## 2429                                                          thymidylate synthase 2
##                       geneID
## 2349 PGSC0003DMP402000005
## 2350 PGSC0003DMP402000010
## 2351 PGSC0003DMP402000022
## 2352 PGSC0003DMP402000026
## 2353 PGSC0003DMP402000029
## 2354 PGSC0003DMP402000031
## 2355 PGSC0003DMP402000032
## 2356 PGSC0003DMP402000044
## 2357 PGSC0003DMP402000053
## 2358 PGSC0003DMP402000055
## 2359 PGSC0003DMP402000057
## 2360 PGSC0003DMP402000058
## 2361 PGSC0003DMP402000059
## 2362 PGSC0003DMP402000065
## 2363 PGSC0003DMP402000070
## 2364 PGSC0003DMP402000072
## 2365 PGSC0003DMP402000076
## 2366 PGSC0003DMP402000087
## 2367 PGSC0003DMP402000091
## 2368 PGSC0003DMP402000097
```

```
## 2369 PGSC0003DMP402000099
## 2370 PGSC0003DMP402000106
## 2371 PGSC0003DMP402000110
## 2372 PGSC0003DMP402000116
## 2373 PGSC0003DMP402000120
## 2374 PGSC0003DMP402000122
## 2375 PGSC0003DMP402000123
## 2376 PGSC0003DMP402000130
## 2377 PGSC0003DMP402000134
## 2378 PGSC0003DMP402000137
## 2379 PGSC0003DMP402000138
## 2380 PGSC0003DMP402000142
## 2381 PGSC0003DMP402000144
## 2382 PGSC0003DMP402000150
## 2383 PGSC0003DMP402000151
## 2384 PGSC0003DMP402000153
## 2385 PGSC0003DMP402000154
## 2386 PGSC0003DMP402000156
## 2387 PGSC0003DMP402000165
## 2388 PGSC0003DMP402000167
## 2389 PGSC0003DMP402000171
## 2390 PGSC0003DMP402000187
## 2391 PGSC0003DMP402000193
## 2392 PGSC0003DMP402000194
## 2393 PGSC0003DMP402000203
## 2394 PGSC0003DMP402000209
## 2395 PGSC0003DMP402000215
## 2396 PGSC0003DMP402000221
## 2397 PGSC0003DMP402000224
## 2398 PGSC0003DMP402000228
## 2399 PGSC0003DMP402000232
## 2400 PGSC0003DMP402000233
## 2401 PGSC0003DMP402000236
## 2402 PGSC0003DMP402000237
## 2403 PGSC0003DMP402000244
## 2404 PGSC0003DMP402000245
## 2405 PGSC0003DMP402000256
## 2406 PGSC0003DMP402000257
## 2407 PGSC0003DMP402000258
## 2408 PGSC0003DMP402000269
## 2409 PGSC0003DMP402000271
## 2410 PGSC0003DMP402000284
## 2411 PGSC0003DMP402000285
## 2412 PGSC0003DMP402000290
## 2413 PGSC0003DMP402000295
## 2414 PGSC0003DMP402000297
## 2415 PGSC0003DMP402000301
## 2416 PGSC0003DMP402000309
## 2417 PGSC0003DMP402000313
## 2418 PGSC0003DMP402000323
## 2419 PGSC0003DMP402000325
## 2420 PGSC0003DMP402000328
## 2421 PGSC0003DMP402000335
## 2422 PGSC0003DMP402000337
```

```
## 2423 PGSC0003DMP402000343
## 2424 PGSC0003DMP402000350
## 2425 PGSC0003DMP402000357
## 2426 PGSC0003DMP402000376
## 2427 PGSC0003DMP402000377
## 2428 PGSC0003DMP402000389
## 2429 PGSC0003DMP402000400
```

```r
rbb$geneID = gsub('DMP402', 'DMG406', rbb$geneID)
```

```r
translate.long.ath = merge(translate.long.ath, rbb, by = 'athID', all.x = TRUE, all.y = FALSE)
colnames(translate.long.stu)[2] = 'geneID'
translate.long.stu$athID = NA
translate.long.stu$athDescription = NA

ind = match(colnames(translate.long.ath), colnames(translate.long.stu))
translate.long.stu = translate.long.stu[, ind]

translate.long = rbind(translate.long.ath, translate.long.stu)

translate.long = translate.long[order(translate.long$geneID), ]

translate.long[grep('Sotub12g027890', translate.long$geneID, ignore.case = TRUE), ]
```

```
##          athID nodeID athDescription          geneID
## 766  AT4G35090    CAT      catalase 2 Sotub12g027890
## 1539      <NA>    CAT            <NA> Sotub12g027890
```

```r
table(duplicated(translate.long$geneID))
```

```
##
## FALSE   TRUE
##   671    326
```

```r
dup = translate.long$geneID[intersect(setdiff(which(duplicated(translate.long$geneID)),
                                              which(is.na(translate.long$geneID))),
                             which(duplicated(translate.long$nodeID)))]
translate.long[translate.long$geneID %in% dup, c(1:2, 4)]
```

```
##          athID  nodeID          geneID
## 714  AT4G25420   GA20ox Sotub01g031210
## 2670      <NA>   GA20ox Sotub01g031210
## 301  AT2G23620      MES Sotub02g012040
## 3416      <NA>      MES Sotub02g012040
## 487  AT3G23240     ERF1 Sotub02g020180
## 493  AT3G23240  ERF/EDF Sotub02g020180
## 486  AT3G23240     ERF1 Sotub03g005750
## 492  AT3G23240  ERF/EDF Sotub03g005750
## 705  AT4G25420   GA20ox Sotub03g007160
## 3180      <NA>   GA20ox Sotub03g007160
## 484  AT3G23240     ERF1 Sotub03g030820
```

```
## 490  AT3G23240 ERF/EDF Sotub03g030820
## 81   AT1G17420     LOX Sotub03g034620
## 3411     <NA>      LOX Sotub03g034620
## 526  AT3G49500    RDR6 Sotub04g012000
## 528  AT3G49500  RDR1,6 Sotub04g012000
## 485  AT3G23240    ERF1 Sotub05g023530
## 491  AT3G23240 ERF/EDF Sotub05g023530
## 187  AT1G65480    SP5G Sotub05g026730
## 1035     <NA>     SP5G Sotub05g026730
## 71   AT1G15550   GA3ox Sotub06g023360
## 2161     <NA>    GA3ox Sotub06g023360
## 907  AT5G47910    RBOH Sotub06g025550
## 5232     <NA>     RBOH Sotub06g025550
## 908  AT5G47910    RBOH Sotub06g025580
## 5742     <NA>     RBOH Sotub06g025580
## 729  AT4G29010    AIM1 Sotub07g011920
## 734  AT4G29010     MFP Sotub07g011920
## 27   AT1G05010     ACO Sotub07g018820
## 2806     <NA>      ACO Sotub07g018820
## 728  AT4G29010    AIM1 Sotub08g019780
## 733  AT4G29010     MFP Sotub08g019780
## 731  AT4G29010    AIM1 Sotub08g019790
## 736  AT4G29010     MFP Sotub08g019790
## 483  AT3G23240    ERF1 Sotub09g019380
## 489  AT3G23240 ERF/EDF Sotub09g019380
## 488  AT3G23240    ERF1 Sotub09g026020
## 494  AT3G23240 ERF/EDF Sotub09g026020
## 35   AT1G06290     ACX Sotub10g008540
## 2550     <NA>      ACX Sotub10g008540
## 703  AT4G25420   GA20ox Sotub11g029030
## 4710     <NA>    GA20ox Sotub11g029030
## 730  AT4G29010    AIM1 Sotub12g009260
## 735  AT4G29010     MFP Sotub12g009260
## 766  AT4G35090     CAT Sotub12g027890
## 1539     <NA>      CAT Sotub12g027890
```

```r
fp = file.path('..', 'intermediate')
dir.create(fp)
```

```
## Warning in dir.create(fp): '..\intermediate' already exists
```

```r
fn = 'FC_Ath_Stu_combo-redundant.txt'

write.table(x = translate.long,
            file = file.path(fp, fn),
            append = FALSE,
            quote = FALSE,
            sep = "\t",
            eol = "\n",
            na = "-",
            dec = ".",
            row.names = FALSE,
            col.names = TRUE,
```

```
            qmethod = c("escape"),
            fileEncoding = "UTF-8")
```

```
translate.long = translate.long[, c(2:4)]
translate.long = translate.long[!is.na(translate.long$geneID), ]

dup = translate.long$geneID[intersect(setdiff(which(duplicated(translate.long$geneID)),
                                              which(is.na(translate.long$geneID))),
                                      which(duplicated(translate.long$nodeID)))]
translate.long[translate.long$geneID %in% dup, ]
```

```
##          nodeID
## 714      GA20ox
## 2670     GA20ox
## 301         MES
## 3416        MES
## 487        ERF1
## 493     ERF/EDF
## 486        ERF1
## 492     ERF/EDF
## 705      GA20ox
## 3180     GA20ox
## 484        ERF1
## 490     ERF/EDF
## 81          LOX
## 3411        LOX
## 526        RDR6
## 528       RDR1,6
## 485        ERF1
## 491     ERF/EDF
## 187        SP5G
## 1035       SP5G
## 71        GA3ox
## 2161      GA3ox
## 907        RBOH
## 5232       RBOH
## 908        RBOH
## 5742       RBOH
## 729       AIM1
## 734        MFP
## 27         ACO
## 2806       ACO
## 728       AIM1
## 733        MFP
## 731       AIM1
## 736        MFP
## 483       ERF1
## 489    ERF/EDF
## 488       ERF1
## 494    ERF/EDF
## 35         ACX
## 2550       ACX
## 703     GA20ox
```

```
## 4710  GA20ox
## 730     AIM1
## 735      MFP
## 766      CAT
## 1539     CAT
##                                                              athDescription
## 714  2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein
## 2670                                                                   <NA>
## 301                                                       methyl esterase 1
## 3416                                                                   <NA>
## 487                                                 ethylene response factor 1
## 493                                                 ethylene response factor 1
## 486                                                 ethylene response factor 1
## 492                                                 ethylene response factor 1
## 705  2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein
## 3180                                                                   <NA>
## 484                                                 ethylene response factor 1
## 490                                                 ethylene response factor 1
## 81                                                           lipoxygenase 3
## 3411                                                                   <NA>
## 526                                               RNA-dependent RNA polymerase 6
## 528                                               RNA-dependent RNA polymerase 6
## 485                                                 ethylene response factor 1
## 491                                                 ethylene response factor 1
## 187          PEBP (phosphatidylethanolamine-binding protein) family protein
## 1035                                                                   <NA>
## 71                                                        gibberellin 3-oxidase 1
## 2161                                                                   <NA>
## 907                                          respiratory burst oxidase homologue D
## 5232                                                                   <NA>
## 908                                          respiratory burst oxidase homologue D
## 5742                                                                   <NA>
## 729                                           Enoyl-CoA hydratase/isomerase family
## 734                                           Enoyl-CoA hydratase/isomerase family
## 27                                                        ethylene-forming enzyme
## 2806                                                                   <NA>
## 728                                           Enoyl-CoA hydratase/isomerase family
## 733                                           Enoyl-CoA hydratase/isomerase family
## 731                                           Enoyl-CoA hydratase/isomerase family
## 736                                           Enoyl-CoA hydratase/isomerase family
## 483                                                 ethylene response factor 1
## 489                                                 ethylene response factor 1
## 488                                                 ethylene response factor 1
## 494                                                 ethylene response factor 1
## 35                                                          acyl-CoA oxidase 3
## 2550                                                                   <NA>
## 703  2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein
## 4710                                                                   <NA>
## 730                                           Enoyl-CoA hydratase/isomerase family
## 735                                           Enoyl-CoA hydratase/isomerase family
## 766                                                                 catalase 2
## 1539                                                                   <NA>
##              geneID
## 714  Sotub01g031210
```

```
## 2670 Sotub01g031210
## 301  Sotub02g012040
## 3416 Sotub02g012040
## 487  Sotub02g020180
## 493  Sotub02g020180
## 486  Sotub03g005750
## 492  Sotub03g005750
## 705  Sotub03g007160
## 3180 Sotub03g007160
## 484  Sotub03g030820
## 490  Sotub03g030820
## 81   Sotub03g034620
## 3411 Sotub03g034620
## 526  Sotub04g012000
## 528  Sotub04g012000
## 485  Sotub05g023530
## 491  Sotub05g023530
## 187  Sotub05g026730
## 1035 Sotub05g026730
## 71   Sotub06g023360
## 2161 Sotub06g023360
## 907  Sotub06g025550
## 5232 Sotub06g025550
## 908  Sotub06g025580
## 5742 Sotub06g025580
## 729  Sotub07g011920
## 734  Sotub07g011920
## 27   Sotub07g018820
## 2806 Sotub07g018820
## 728  Sotub08g019780
## 733  Sotub08g019780
## 731  Sotub08g019790
## 736  Sotub08g019790
## 483  Sotub09g019380
## 489  Sotub09g019380
## 488  Sotub09g026020
## 494  Sotub09g026020
## 35   Sotub10g008540
## 2550 Sotub10g008540
## 703  Sotub11g029030
## 4710 Sotub11g029030
## 730  Sotub12g009260
## 735  Sotub12g009260
## 766  Sotub12g027890
## 1539 Sotub12g027890
```

```r
translate.long$athDescription = zoo::na.locf(translate.long$athDescription)

translate.long[translate.long$geneID %in% dup, ]
```

```
##      nodeID
## 714  GA20ox
## 2670 GA20ox
## 301     MES
```

```
## 3416       MES
## 487       ERF1
## 493   ERF/EDF
## 486       ERF1
## 492   ERF/EDF
## 705    GA20ox
## 3180   GA20ox
## 484       ERF1
## 490   ERF/EDF
## 81        LOX
## 3411      LOX
## 526      RDR6
## 528    RDR1,6
## 485       ERF1
## 491   ERF/EDF
## 187      SP5G
## 1035     SP5G
## 71      GA3ox
## 2161    GA3ox
## 907      RBOH
## 5232     RBOH
## 908      RBOH
## 5742     RBOH
## 729      AIM1
## 734       MFP
## 27        ACO
## 2806      ACO
## 728      AIM1
## 733       MFP
## 731      AIM1
## 736       MFP
## 483       ERF1
## 489   ERF/EDF
## 488       ERF1
## 494   ERF/EDF
## 35        ACX
## 2550      ACX
## 703    GA20ox
## 4710   GA20ox
## 730      AIM1
## 735       MFP
## 766       CAT
## 1539      CAT
##                                                      athDescription
## 714  2-oxoglutarate (20G) and Fe(II)-dependent oxygenase superfamily protein
## 2670 2-oxoglutarate (20G) and Fe(II)-dependent oxygenase superfamily protein
## 301                                               methyl esterase 1
## 3416                                              methyl esterase 1
## 487                                          ethylene response factor 1
## 493                                          ethylene response factor 1
## 486                                          ethylene response factor 1
## 492                                          ethylene response factor 1
## 705  2-oxoglutarate (20G) and Fe(II)-dependent oxygenase superfamily protein
## 3180 2-oxoglutarate (20G) and Fe(II)-dependent oxygenase superfamily protein
```

```
## 484                                              ethylene response factor 1
## 490                                              ethylene response factor 1
## 81                                                           lipoxygenase 3
## 3411                                                         lipoxygenase 3
## 526                                           RNA-dependent RNA polymerase 6
## 528                                           RNA-dependent RNA polymerase 6
## 485                                              ethylene response factor 1
## 491                                              ethylene response factor 1
## 187          PEBP (phosphatidylethanolamine-binding protein) family protein
## 1035         PEBP (phosphatidylethanolamine-binding protein) family protein
## 71                                                     gibberellin 3-oxidase 1
## 2161                                                   gibberellin 3-oxidase 1
## 907                                     respiratory burst oxidase homologue D
## 5232                                    respiratory burst oxidase homologue D
## 908                                     respiratory burst oxidase homologue D
## 5742                                    respiratory burst oxidase homologue D
## 729                                      Enoyl-CoA hydratase/isomerase family
## 734                                      Enoyl-CoA hydratase/isomerase family
## 27                                                      ethylene-forming enzyme
## 2806                                                    ethylene-forming enzyme
## 728                                      Enoyl-CoA hydratase/isomerase family
## 733                                      Enoyl-CoA hydratase/isomerase family
## 731                                      Enoyl-CoA hydratase/isomerase family
## 736                                      Enoyl-CoA hydratase/isomerase family
## 483                                              ethylene response factor 1
## 489                                              ethylene response factor 1
## 488                                              ethylene response factor 1
## 494                                              ethylene response factor 1
## 35                                                          acyl-CoA oxidase 3
## 2550                                                        acyl-CoA oxidase 3
## 703   2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein
## 4710 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein
## 730                                      Enoyl-CoA hydratase/isomerase family
## 735                                      Enoyl-CoA hydratase/isomerase family
## 766                                                                catalase 2
## 1539                                                               catalase 2
##              geneID
## 714  Sotub01g031210
## 2670 Sotub01g031210
## 301  Sotub02g012040
## 3416 Sotub02g012040
## 487  Sotub02g020180
## 493  Sotub02g020180
## 486  Sotub03g005750
## 492  Sotub03g005750
## 705  Sotub03g007160
## 3180 Sotub03g007160
## 484  Sotub03g030820
## 490  Sotub03g030820
## 81   Sotub03g034620
## 3411 Sotub03g034620
## 526  Sotub04g012000
## 528  Sotub04g012000
## 485  Sotub05g023530
```

```
## 491  Sotub05g023530
## 187  Sotub05g026730
## 1035 Sotub05g026730
## 71   Sotub06g023360
## 2161 Sotub06g023360
## 907  Sotub06g025550
## 5232 Sotub06g025550
## 908  Sotub06g025580
## 5742 Sotub06g025580
## 729  Sotub07g011920
## 734  Sotub07g011920
## 27   Sotub07g018820
## 2806 Sotub07g018820
## 728  Sotub08g019780
## 733  Sotub08g019780
## 731  Sotub08g019790
## 736  Sotub08g019790
## 483  Sotub09g019380
## 489  Sotub09g019380
## 488  Sotub09g026020
## 494  Sotub09g026020
## 35   Sotub10g008540
## 2550 Sotub10g008540
## 703  Sotub11g029030
## 4710 Sotub11g029030
## 730  Sotub12g009260
## 735  Sotub12g009260
## 766  Sotub12g027890
## 1539 Sotub12g027890
```

```
translate.long = translate.long[!duplicated(translate.long), ]
```

```
table(duplicated(translate.long$geneID))
```

```
##
## FALSE  TRUE
##   670    13
```

```
dup = translate.long[which(duplicated(translate.long$geneID)), ]$geneID
translate.long[translate.long$geneID %in%  dup, ]
```

```
##       nodeID                   athDescription                geneID
## 732   AIM1 Enoyl-CoA hydratase/isomerase family PGSC0003DMG400003906
## 737    MFP Enoyl-CoA hydratase/isomerase family PGSC0003DMG400003906
## 527   RDR6        RNA-dependent RNA polymerase 6 PGSC0003DMG400030859
## 529 RDR1,6        RNA-dependent RNA polymerase 6 PGSC0003DMG400030859
## 487   ERF1           ethylene response factor 1      Sotub02g020180
## 493 ERF/EDF           ethylene response factor 1      Sotub02g020180
## 486   ERF1           ethylene response factor 1      Sotub03g005750
## 492 ERF/EDF           ethylene response factor 1      Sotub03g005750
## 484   ERF1           ethylene response factor 1      Sotub03g030820
## 490 ERF/EDF           ethylene response factor 1      Sotub03g030820
```

```
## 526     RDR6         RNA-dependent RNA polymerase 6        Sotub04g012000
## 528   RDR1,6         RNA-dependent RNA polymerase 6        Sotub04g012000
## 485     ERF1              ethylene response factor 1        Sotub05g023530
## 491 ERF/EDF              ethylene response factor 1        Sotub05g023530
## 729     AIM1 Enoyl-CoA hydratase/isomerase family          Sotub07g011920
## 734      MFP Enoyl-CoA hydratase/isomerase family          Sotub07g011920
## 728     AIM1 Enoyl-CoA hydratase/isomerase family          Sotub08g019780
## 733      MFP Enoyl-CoA hydratase/isomerase family          Sotub08g019780
## 731     AIM1 Enoyl-CoA hydratase/isomerase family          Sotub08g019790
## 736      MFP Enoyl-CoA hydratase/isomerase family          Sotub08g019790
## 483     ERF1              ethylene response factor 1        Sotub09g019380
## 489 ERF/EDF              ethylene response factor 1        Sotub09g019380
## 488     ERF1              ethylene response factor 1        Sotub09g026020
## 494 ERF/EDF              ethylene response factor 1        Sotub09g026020
## 730     AIM1 Enoyl-CoA hydratase/isomerase family          Sotub12g009260
## 735      MFP Enoyl-CoA hydratase/isomerase family          Sotub12g009260
```

```r
fn = 'FC_Stu_combo.txt'

write.table(x = translate.long,
            file = file.path(fp, fn),
            append = FALSE,
            quote = FALSE,
            sep = "\t",
            eol = "\n",
            na = "-",
            dec = ".",
            row.names = FALSE,
            col.names = TRUE,
            qmethod = c("escape"),
            fileEncoding = "UTF-8")
```

```r
tmp = stringr::str_split_fixed(edges$source, '\\[', m)
edges$source = tmp[, 1]

tmp = stringr::str_split_fixed(edges$target, '\\[', m)
edges$target = tmp[, 1]

eid = sort(unique(c(edges$source, edges$target)))

table(eid %in% nodes$name)
```

```
##
## TRUE
##  509
```

```r
table(nodes$name %in% eid)
```

```
##
## FALSE  TRUE
##     1   509
```

```
nodes[which(!nodes$name %in% eid),]
```

```
##    name short_name family          description pathway ath_homologues
## 92 CAU1      CAU1      Calcium Underaccumulation 1          ["AT4G31120"]
##    node_type
## 92 PlantCoding
```

for https://nib-si.shinyapps.io/pre-processing/

need cols:

geneID shortName shortDescription MapManBin

geneID1 geneID2 reactionType

```
table(duplicated(nodes$name))
```

```
##
## FALSE
##   510
```

```
dup = nodes$name[which(duplicated(nodes$name))]
nodes[nodes$name %in% dup, ]
```

```
## [1] name          short_name    family        description    pathway
## [6] ath_homologues node_type
## <0 rows> (or 0-length row.names)
```

```
tmp = translate.long[, 1:2]
colnames(tmp)[1] = 'name'
nodes = merge(nodes, tmp, by = 'name', all.x = TRUE, all.y = FALSE)

ind = which(nodes$description == '')
nodes$description[ind] = nodes$athDescription[ind]


nodes = nodes[, c(1, 2, 4, 5)]
colnames(nodes)
```

```
## [1] "name"        "short_name"  "description" "pathway"
```

```
colnames(nodes) = c('geneID', 'shortName', 'shortDescription', 'MapManBin')

nodes = nodes[!duplicated(nodes), ]

cat(red('due to translation description'))
```

```
## due to translation description
```

```
table(duplicated(nodes$geneID))
```

```
##
## FALSE  TRUE
##   510     4
```

```
dup = nodes$geneID[which(duplicated(nodes$geneID))]
nodes[nodes$geneID %in% dup, ]
```

```
##    geneID shortName                                    shortDescription
## 9     4CL       4CL                            4-coumarate:CoA ligase 3
## 10    4CL       4CL                            4-coumarate:CoA ligase 2
## 11    4CL       4CL AMP-dependent synthetase and ligase family protein
## 14    4CL       4CL                            4-coumarate:CoA ligase 1
## 16    4CL       4CL                                 acyl-CoA synthetase 5
##                        MapManBin
## 9  Hormone - Salicylic acid (SA)
## 10 Hormone - Salicylic acid (SA)
## 11 Hormone - Salicylic acid (SA)
## 14 Hormone - Salicylic acid (SA)
## 16 Hormone - Salicylic acid (SA)
```

```
nodes[nodes$geneID %in% dup, ]$shortDescription = '4-coumarate:CoA ligase'

nodes = nodes[!duplicated(nodes), ]

table(duplicated(nodes$geneID))
```

```
##
## FALSE
##   510
```

```
dup = nodes$geneID[which(duplicated(nodes$geneID))]
nodes[nodes$geneID %in% dup, ]
```

```
## [1] geneID          shortName        shortDescription MapManBin
## <0 rows> (or 0-length row.names)
```

```
fn = 'nodes_to_preprocess.txt'
write.table(x = nodes,
            file = file.path(fp, fn),
            append = FALSE,
            quote = FALSE,
            sep = "\t",
            eol = "\n",
            na = "NA",
            dec = ".",
            row.names = FALSE,
            col.names = TRUE,
            qmethod = c("escape"),
            fileEncoding = "UTF-8")
```

```
myedges = data.frame(matrix(ncol = 3, nrow = nrow(edges)))
colnames(myedges) = c('geneID1', 'geneID2', 'reactionType')
table(edges$reaction_effect)
```

```
##
##                                   activation depletion of substrates
##                 27                          932                    3
##           inhibition
##                 90
```

```
myedges$geneID1 = edges$source
myedges$geneID2 = edges$target
ind = which(edges$reaction_effect == '')
myedges$reactionType = paste(edges$reaction_effect, edges$reaction_type, sep = '_')
myedges$reactionType[ind] = edges$reaction_type[ind]

table(myedges$reactionType)
```

```
##
##                 activation_binding/oligomerisation
##                                                285
##                 activation_binding_oligomerisation
##                                                  3
##                              activation_catalysis
##                                                403
##               activation_cleavage/auto-cleavage
##                                                 64
##                 activation_degradation/secretion
##                                                  2
##                            activation_dissociation
##                                                  3
##                     activation_protein activation
##                                                 66
## activation_transcriptional/translational activation
##                                                 98
##                            activation_translocation
##                                                  7
##                                 activation_unknown
##                                                  1
##                             binding/oligomerisation
##                                                  6
##                                           catalysis
##                                                 21
##     depletion of substrates_binding/oligomerisation
##                                                  3
##               inhibition_binding/oligomerisation
##                                                  9
##               inhibition_binding_oligomerisation
##                                                  3
##                 inhibition_degradation/secretion
##                                                 31
##                     inhibition_protein deactivation
```

22

```
##                                                            17
## inhibition_transcriptional/translational repression
##                                                            22
##                               inhibition_undefined
##                                                             8
```

```r
fn = 'edges_to_preprocess.txt'
write.table(x = myedges,
            file = file.path(fp, fn),
            append = FALSE,
            quote = FALSE,
            sep = "\t",
            eol = "\n",
            na = "NA",
            dec = ".",
            row.names = FALSE,
            col.names = TRUE,
            qmethod = c("escape"),
            fileEncoding = "UTF-8")
```

```r
devtools::session_info()
```

```
## - Session info ---------------------------------------------------------------
##  setting  value
##  version  R version 4.1.2 (2021-11-01)
##  os       Windows 10 x64 (build 19044)
##  system   x86_64, mingw32
##  ui       RTerm
##  language (EN)
##  collate  English_United Kingdom.1252
##  ctype    English_United Kingdom.1252
##  tz       Europe/Prague
##  date     2022-10-26
##  pandoc   2.17.1.1 @ C:/mzInstall/RStudio/bin/quarto/bin/ (via rmarkdown)
##
## - Packages -------------------------------------------------------------------
##  package      * version date (UTC) lib source
##  assertthat     0.2.1   2019-03-21 [1] CRAN (R 4.1.3)
##  cachem         1.0.6   2021-08-19 [1] CRAN (R 4.1.2)
##  callr          3.7.2   2022-08-22 [1] CRAN (R 4.1.3)
##  cli            3.3.0   2022-04-25 [1] CRAN (R 4.1.3)
##  crayon       * 1.5.1   2022-03-26 [1] CRAN (R 4.1.3)
##  data.table     1.14.2  2021-09-27 [1] CRAN (R 4.1.2)
##  DBI            1.1.3   2022-06-18 [1] CRAN (R 4.1.3)
##  devtools       2.4.4   2022-07-20 [1] CRAN (R 4.1.3)
##  digest         0.6.29  2021-12-01 [1] CRAN (R 4.1.2)
##  dplyr          1.0.9   2022-04-28 [1] CRAN (R 4.1.3)
##  ellipsis       0.3.2   2021-04-29 [1] CRAN (R 4.1.2)
##  evaluate       0.16    2022-08-09 [1] CRAN (R 4.1.3)
##  fansi          1.0.3   2022-03-24 [1] CRAN (R 4.1.3)
##  fastmap        1.1.0   2021-01-25 [1] CRAN (R 4.1.2)
##  fs             1.5.2   2021-12-08 [1] CRAN (R 4.1.2)
##  generics       0.1.3   2022-07-05 [1] CRAN (R 4.1.2)
```

```
##  glue         1.6.2   2022-02-24 [1] CRAN (R 4.1.2)
##  htmltools    0.5.2   2021-08-25 [1] CRAN (R 4.1.2)
##  htmlwidgets  1.5.4   2021-09-08 [1] CRAN (R 4.1.2)
##  httpuv       1.6.5   2022-01-05 [1] CRAN (R 4.1.3)
##  knitr        1.39    2022-04-26 [1] CRAN (R 4.1.3)
##  later        1.3.0   2021-08-18 [1] CRAN (R 4.1.3)
##  lattice      0.20-45 2021-09-22 [1] CRAN (R 4.1.2)
##  lifecycle    1.0.1   2021-09-24 [1] CRAN (R 4.1.2)
##  magrittr     2.0.3   2022-03-30 [1] CRAN (R 4.1.3)
##  memoise      2.0.1   2021-11-26 [1] CRAN (R 4.1.2)
##  mime         0.12    2021-09-28 [1] CRAN (R 4.1.1)
##  miniUI       0.1.1.1 2018-05-18 [1] CRAN (R 4.1.3)
##  pillar       1.8.1   2022-08-19 [1] CRAN (R 4.1.3)
##  pkgbuild     1.3.1   2021-12-20 [1] CRAN (R 4.1.2)
##  pkgconfig    2.0.3   2019-09-22 [1] CRAN (R 4.1.2)
##  pkgload      1.3.0   2022-06-27 [1] CRAN (R 4.1.3)
##  prettyunits  1.1.1   2020-01-24 [1] CRAN (R 4.1.2)
##  processx     3.7.0   2022-07-07 [1] CRAN (R 4.1.3)
##  profvis      0.3.7   2020-11-02 [1] CRAN (R 4.1.3)
##  promises     1.2.0.1 2021-02-11 [1] CRAN (R 4.1.3)
##  ps           1.7.1   2022-06-18 [1] CRAN (R 4.1.3)
##  purrr        0.3.4   2020-04-17 [1] CRAN (R 4.1.2)
##  R6           2.5.1   2021-08-19 [1] CRAN (R 4.1.2)
##  Rcpp         1.0.8.3 2022-03-17 [1] CRAN (R 4.1.3)
##  remotes      2.4.2   2021-11-30 [1] CRAN (R 4.1.2)
##  rlang        1.0.5   2022-08-31 [1] CRAN (R 4.1.3)
##  rmarkdown    2.16    2022-08-24 [1] CRAN (R 4.1.3)
##  rstudioapi   0.14    2022-08-22 [1] CRAN (R 4.1.3)
##  sessioninfo  1.2.2   2021-12-06 [1] CRAN (R 4.1.2)
##  shiny        1.7.2   2022-07-19 [1] CRAN (R 4.1.3)
##  stringi      1.7.6   2021-11-29 [1] CRAN (R 4.1.2)
##  stringr      1.4.1   2022-08-20 [1] CRAN (R 4.1.3)
##  tibble       3.1.7   2022-05-03 [1] CRAN (R 4.1.3)
##  tidyr        1.2.0   2022-02-01 [1] CRAN (R 4.1.3)
##  tidyselect   1.1.2   2022-02-21 [1] CRAN (R 4.1.2)
##  urlchecker   1.0.1   2021-11-30 [1] CRAN (R 4.1.3)
##  usethis      2.1.6   2022-05-25 [1] CRAN (R 4.1.3)
##  utf8         1.2.2   2021-07-24 [1] CRAN (R 4.1.2)
##  vctrs        0.4.1   2022-04-13 [1] CRAN (R 4.1.3)
##  xfun         0.31    2022-05-10 [1] CRAN (R 4.1.3)
##  xtable       1.8-4   2019-04-21 [1] CRAN (R 4.1.2)
##  yaml         2.3.5   2022-02-21 [1] CRAN (R 4.1.2)
##  zoo          1.8-11  2022-09-17 [1] CRAN (R 4.1.3)
##
##  [1] C:/mzInstall/R/R-4.1.2/library
##
## -------------------------------------------------------------------------------
```