

STRING edgelist

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Intro

Coletar e filtrar as interações PPI dos genes obtidos via STRING.

```
library(RCurl)
library(dplyr)
library(readr)
library(magrittr)

combine_scores <- function(string_interactions, sources){
  #sources = nscore,fscore,pscore,ascore,escore,dscore,tscore
  cs <- 1 - string_interactions[, sources, drop = FALSE]
  cs <- apply(X = cs, MARGIN = 1, FUN = function(x) 1 - prod(x))
  return(cs)
}
```

Data

```
data(gene_ids, package = "neurotransmission")
```

STRING API

Baixamos a tabela de interações pela API do string

```
identifiers <- gene_ids[["string_id"]] %>% na.omit %>% substring(6) %>% paste(collapse="%0d",sep="")

string_edgelist <- read_tsv(
  postForm("http://string-db.org/api/tsv/network", identifiers = identifiers, species = "9606")
)

string_edgelist
```

```
## # A tibble: 9,408 x 13
##   stringId_A stringId_B preferredName_A preferredName_B ncbiTaxonId score
##   <chr>      <chr>      <chr>          <chr>          <dbl> <dbl>
## 1 ENSP00000~ ENSP00000~ MAPK12         MAPK13          9606 0.948
## 2 ENSP00000~ ENSP00000~ MAPK1          CREB3L3          9606 0.609
## 3 ENSP00000~ ENSP00000~ MAPK1          PPP2R5B          9606 0.935
## 4 ENSP00000~ ENSP00000~ MAPK1          MAPK13           9606 0.814
## 5 ENSP00000~ ENSP00000~ MAPK1          MAPK12           9606 0.836
## 6 ENSP00000~ ENSP00000~ ATP6V1D         MAPK1            9606 0.442
## 7 ENSP00000~ ENSP00000~ SLC32A1         STX1B            9606 0.461
## 8 ENSP00000~ ENSP00000~ SLC6A2          DRD4             9606 0.604
## 9 ENSP00000~ ENSP00000~ SLC6A2          STX1B            9606 0.435
## 10 ENSP00000~ ENSP00000~ PPP2CB          PPP2R5B           9606 0.983
## # ... with 9,398 more rows, and 7 more variables: nscore <dbl>,
## #   fscore <dbl>, pscore <dbl>, ascore <dbl>, escore <dbl>, dscore <dbl>,
## #   tscore <dbl>
```

Recalculating scores

Recalculamos o combinedscore apenas com as colunas `escore` (experimental) e `dscore` (database)

```
string_edgelist[, "cs"] <- combine_scores(string_edgelist, c("escore", "dscore"))
string_edgelist %<>% filter(cs >= 0.7) %>% select(stringId_A, stringId_B)

# exporting for package use
usethis::use_data(string_edgelist, overwrite = TRUE)
```

```
## <U+2714> Setting active project to 'C:/R/neurotransmission'
## <U+2714> Saving 'string_edgelist' to 'data/string_edgelist.rda'
```