

Supplementary Material

Ionotropic receptors as the driving force behind human synapse establishment

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Abstract

Model uncertainty and limited data are fundamental challenges to robust management of human intervention in a natural system. These challenges are acutely highlighted by concerns that many ecological systems may contain tipping points, such as Allee population sizes. Before a collapse, we do not know where the tipping points lie, if they exist at all. Hence, we know neither a complete model of the system dynamics nor do we have access to data in some large region of state-space where such a tipping point might exist.

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Project structure

This is the title page

Preprocessing

Preprocessing

Eukaryota species tree

Explanation

NCBI Taxonomy tree

Explanation

Duplicated Genera

Hybrid tree

Explanation

Gene selection and annotation

Gene selection and annotation

Neuroexclusivity

Explanation

Expression

Pathways

COG data

Network

Analysis

Analysis

```
library(here)
```

```
## here() starts at /home/danilo/R/neuro
```

```
library(purrr)
library(tibble)

# download_if_missing <- function(filename, url) {
#   if (!file.exists(here("data-raw", "download", filename))) {
```

```

#   download.file(url, filename)
# }
# }

# files <- tribble(
#   ~filename,      ~url,
#   "species.v11.0.txt", "https://stringdb-static.org/download/species.v11.0.txt",
#   # "download/taxonomy", "https://ftp.ncbi.nlm.nih.gov/pub/taxonomy/new_taxdump/new_taxdump.tar.gz",
#   # "x",                "y",
#   # "x",                "y",
# )

files <- tribble(
  ~url,
  ~filename,

  "https://stringdb-static.org/download/species.v11.0.txt",
  "species.v11.0.txt",

  "https://ftp.ncbi.nlm.nih.gov/pub/taxonomy/new_taxdump/new_taxdump.tar.gz",
  "new_taxdump.tar.gz",

  "http://rest.kegg.jp/link/pathway/hsa",
  "link_pathway_entrez.tsv",

  "https://string-db.org/mapping_files/entrez/human.entrez_2_string.2018.tsv.gz",
  "human.entrez_2_string.2018.tsv.gz",

  "https://string-db.org/mapping_files/STRING_display_names/human.name_2_string.tsv.gz",
  "human.name_2_string.tsv.gz",

  "https://ftp.ncbi.nlm.nih.gov/gene/DATA/GENE_INFO/Mammalia/Homo_sapiens.gene_info.gz",
  "Homo_sapiens.gene_info.gz",

  "http://rest.genome.jp/link/ensembl/hsa",
  "link_ensembl_entrez.tsv",

  # "https://ftp.ncbi.nlm.nih.gov/gene/DATA/GENE_INFO/Mammalia/Homo_sapiens.gene_info.gz",
  # "Homo_sapiens.gene_info.gz",
)

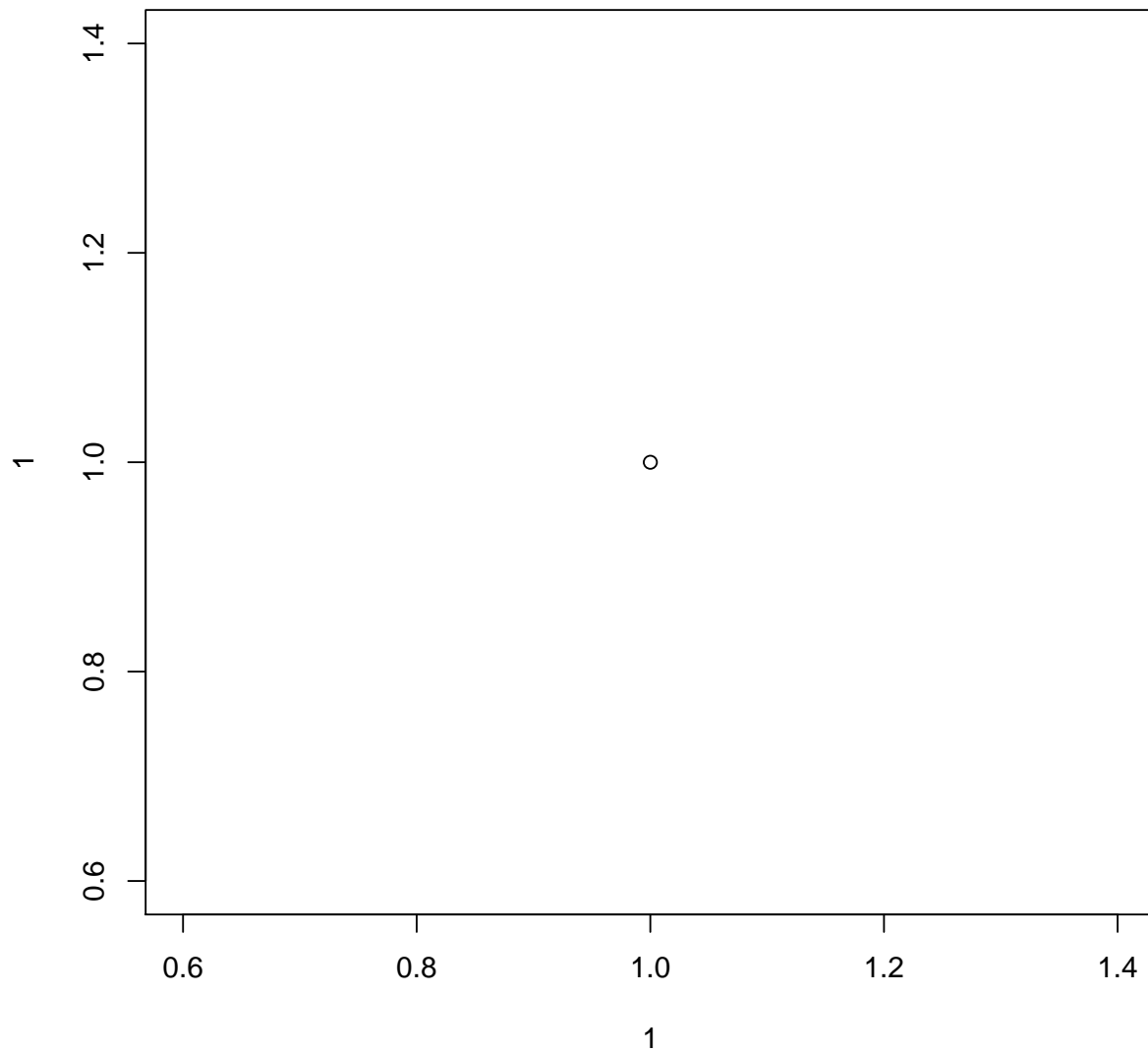
knitr::kable(files, "markdown", booktabs = F)

```

url	filename
https://stringdb-static.org/download/species.v11.0.txt	species.v11.0.txt
https://ftp.ncbi.nlm.nih.gov/pub/taxonomy/new_taxdump/new_taxdump.tar.gz	new_taxdump.tar.gz
http://rest.kegg.jp/link/pathway/hsa	link_pathway_entrez.tsv
https://string-db.org/mapping_files/entrez/human.entrez_2_string.2018.tsv.gz	human.entrez_2_string.2018.tsv.gz
https://string-db.org/mapping_files/STRING_display_names/human.name_2_string.tsv.gz	human.name_2_string.tsv.gz

url	filename
https://ftp.ncbi.nlm.nih.gov/gene/DATA/GENE_INFO/Mammalia/Homo_sapiens.gene_info.gz	Homo_sapiens.gene_info.gz
http://rest.genome.jp/link/ensembl/hsa	link_ensembl_entrez.tsv

```
# pwalk(files, download_if_missing)
plot(1,1)
```



Special cases

```
# if (!file.exists("download/taxonomy")) {  
#   tmp <- tempfile()  
#   download.file("https://ftp.ncbi.nlm.nih.gov/pub/taxonomy/new_taxdump/new_taxdump.tar.gz", tmp)  
#   untar(tmp, exdir = "download/taxonomy")  
#   unlink(tmp)  
# }
```