hpAnnot

Marta R. Hidalgo *[1], **Francisco Salavert** [2], **Alicia Amadoz** [3], **Çankut Cubuk** [4], **José Carbonell-Caballero** [5], **and Joaquín Dopazo** [4,6,7]

[1]Unidad de Bioinformática y Bioestadística, Centro de Investigación Príncipe Felipe (CIPF), Valencia, 46012, Spain
[2]BioBam Bioinformatics S.L., Valencia, 46012, Spain
[3]Department of Bioinformatics, Igenomix S.A., Valencia, 46980, Spain
[4]Clinical Bioinformatics Area, Fundación Progreso y Salud (FPS), Hospital Virgen del Rocio, Sevilla, 41013, Spain
[5]Chromatin and Gene expression Lab, Gene Regulation, Stem Cells and Cancer Program, Centre de Regulació Genòmica (CRG), The Barcelona Institute of Science and Technology, PRBB, Barcelona, 08003, Spain
[6]Functional Genomics Node (INB), FPS, Hospital Virgen del Rocio, Sevilla, 41013, Spain.
[7]Bioinformatics in Rare Diseases (BiER), Centro de Investigación Biomédica en Red de Enfermedades Raras (CIBERER), FPS, Hospital Virgen del Rocio, Sevilla, 41013, Spain

*`marta.hidalgo@outlook.es`

2025-10-15

Abstract

HpAnnot is the annotation and data package of the *hipathia* package. *Hipathia* is a method for the computation of signal transduction along signaling pathways. The method is based on an iterative algorithm which is able to compute the signal intensity passing through the nodes of a network by taking into account the level of expression of each gene and the intensity of the signal arriving to it.

Contents

1 Usage

In order to access to the files stored in *AnnotationHub*, type:

```
library(AnnotationHub)
ah <- AnnotationHub()
hp <- query(ah, "hpAnnot")
hp
## AnnotationHub with 64 records
## # snapshotDate(): 2025-10-10
## # $dataprovider: BioMart, KEGG, GeneOntology
## # $species: Rattus norvegicus, Mus musculus, Homo sapiens, NA
## # $rdataclass: data.frame, list, igraph
## # additional mcols(): taxonomyid, genome, description,
## #   coordinate_1_based, maintainer, rdatadateadded, preparerclass, tags,
## #   rdatapath, sourceurl, sourcetype
## # retrieve records with, e.g., 'object[["AH60887"]]'
##
##             title
##   AH60887 | annofuns_GO_hsa.rda
##   AH60888 | annofuns_GO_mmu.rda
##   AH60889 | annofuns_GO_rno.rda
##   AH60890 | annofuns_uniprot_hsa.rda
##   AH60891 | annofuns_uniprot_mmu.rda
##   ...       ...
##   AH69121 | pmgi_rno_GO_v2.rda
##   AH69122 | pmgi_rno_uniprot_v2.rda
##   AH69123 | xref_hsa_v2.rda
##   AH69124 | xref_mmu_v2.rda
##   AH69125 | xref_rno_v2.rda
mcols(hp)[,c("title", "description")]
## DataFrame with 64 rows and 2 columns
##                          title            description
##                    <character>            <character>
## AH60887    annofuns_GO_hsa.rda Annotations from pat..
## AH60888    annofuns_GO_mmu.rda Annotations from pat..
## AH60889    annofuns_GO_rno.rda Annotations from pat..
## AH60890 annofuns_uniprot_hsa.. Annotations from pat..
## AH60891 annofuns_uniprot_mmu.. Annotations from pat..
## ...                        ...                    ...
## AH69121     pmgi_rno_GO_v2.rda Pseudo-pathways topo..
## AH69122 pmgi_rno_uniprot_v2... Pseudo-pathways topo..
## AH69123        xref_hsa_v2.rda XRef transformation ..
## AH69124        xref_mmu_v2.rda XRef transformation ..
## AH69125        xref_rno_v2.rda XRef transformation ..
xtabs(~dataprovider + species, mcols(hp))
##               species
## dataprovider   Homo sapiens Mus musculus Rattus norvegicus
##   BioMart                12           12                12
##   GeneOntology            0            0                 0
##   KEGG                    8            8                 8
```

hpAnnot

```
head(hp[["AH60887"]])
##                           effector.nodes         paths
## hsa03320.N-hsa03320-37   N-hsa03320-37 P-hsa03320-37
## hsa03320.N-hsa03320-611  N-hsa03320-61 P-hsa03320-61
## hsa03320.N-hsa03320-612  N-hsa03320-61 P-hsa03320-61
## hsa03320.N-hsa03320-613  N-hsa03320-61 P-hsa03320-61
## hsa03320.N-hsa03320-614  N-hsa03320-61 P-hsa03320-61
## hsa03320.N-hsa03320-615  N-hsa03320-61 P-hsa03320-61
##                                                                                             funs
## hsa03320.N-hsa03320-37                                                                      <NA>
## hsa03320.N-hsa03320-611 negative regulation of very-low-density lipoprotein particle remodeling
## hsa03320.N-hsa03320-612                            high-density lipoprotein particle remodeling
## hsa03320.N-hsa03320-613                                                     phospholipid efflux
## hsa03320.N-hsa03320-614                         regulation of Cdc42 protein signal transduction
## hsa03320.N-hsa03320-615                                                      cholesterol efflux
hp$title
##  [1] "annofuns_GO_hsa.rda"         "annofuns_GO_mmu.rda"
##  [3] "annofuns_GO_rno.rda"         "annofuns_uniprot_hsa.rda"
##  [5] "annofuns_uniprot_mmu.rda"    "annofuns_uniprot_rno.rda"
##  [7] "annot_GO_hsa.rda"            "annot_GO_mmu.rda"
##  [9] "annot_GO_rno.rda"            "annot_uniprot_hsa.rda"
## [11] "annot_uniprot_mmu.rda"       "annot_uniprot_rno.rda"
## [13] "entrez_hgnc_hsa.rda"         "entrez_hgnc_mmu.rda"
## [15] "entrez_hgnc_rno.rda"         "go_bp_frame.rda"
## [17] "go_bp_net.rda"               "meta_graph_info_hsa.rda"
## [19] "meta_graph_info_mmu.rda"     "meta_graph_info_rno.rda"
## [21] "pmgi_hsa_genes.rda"          "pmgi_hsa_GO.rda"
## [23] "pmgi_hsa_uniprot.rda"        "pmgi_mmu_genes.rda"
## [25] "pmgi_mmu_GO.rda"             "pmgi_mmu_uniprot.rda"
## [27] "pmgi_rno_genes.rda"          "pmgi_rno_GO.rda"
## [29] "pmgi_rno_uniprot.rda"        "xref_hsa.rda"
## [31] "xref_mmu.rda"                "xref_rno.rda"
## [33] "annofuns_GO_hsa_v2.rda"      "annofuns_GO_mmu_v2.rda"
## [35] "annofuns_GO_rno_v2.rda"      "annofuns_uniprot_hsa_v2.rda"
## [37] "annofuns_uniprot_mmu_v2.rda" "annofuns_uniprot_rno_v2.rda"
## [39] "annot_GO_hsa_v2.rda"         "annot_GO_mmu_v2.rda"
## [41] "annot_GO_rno_v2.rda"         "annot_uniprot_hsa_v2.rda"
## [43] "annot_uniprot_mmu_v2.rda"    "annot_uniprot_rno_v2.rda"
## [45] "entrez_hgnc_hsa_v2.rda"      "entrez_hgnc_mmu_v2.rda"
## [47] "entrez_hgnc_rno_v2.rda"      "go_bp_frame_v2.rda"
## [49] "go_bp_net_v2.rda"            "meta_graph_info_hsa_v2.rda"
## [51] "meta_graph_info_mmu_v2.rda"  "meta_graph_info_rno_v2.rda"
## [53] "pmgi_hsa_genes_v2.rda"       "pmgi_hsa_GO_v2.rda"
## [55] "pmgi_hsa_uniprot_v2.rda"     "pmgi_mmu_genes_v2.rda"
## [57] "pmgi_mmu_GO_v2.rda"          "pmgi_mmu_uniprot_v2.rda"
## [59] "pmgi_rno_genes_v2.rda"       "pmgi_rno_GO_v2.rda"
## [61] "pmgi_rno_uniprot_v2.rda"     "xref_hsa_v2.rda"
## [63] "xref_mmu_v2.rda"             "xref_rno_v2.rda"
```

For further information on this please refer to *AnnotationHub*.