

hpAnnot

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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.

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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(): 2025-11-14
## # $dataprovder: BioMart, KEGG, GeneOntology
## # $species: Rattus norvegicus, Mus musculus, Homo sapiens, NA
## # $rdataclass: data.frame, list, igrph
## # 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(~dataprovder + species, mcols(hp))
##           species
## dataprovder  Homo sapiens Mus musculus Rattus norvegicus
## BioMart      12           12           12
## GeneOntology  0            0            0
## KEGG         8            8            8
```

```

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](#).