

# 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 32 records
## # snapshotDate(): 2018-10-24
## # $dataprovder: BioMart, KEGG, GeneOntology
## # $species: Homo sapiens, Mus musculus, Rattus norvegicus, 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
## ...
## AH60914 | pmgi_rno_GO.rda
## AH60915 | pmgi_rno_uniprot.rda
## AH60916 | xref_hsa.rda
## AH60917 | xref_mmu.rda
## AH60918 | xref_rno.rda
mcols(hp)[,c("title", "description")]
## DataFrame with 32 rows and 2 columns
##           title
##           <character>
## 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
## ...
## AH60914   pmgi_rno_GO.rda
## AH60915   pmgi_rno_uniprot.rda
## AH60916   xref_hsa.rda
## AH60917   xref_mmu.rda
## AH60918   xref_rno.rda
##
##           description
##           <character>
## AH60887   Annotations from pathways to GO terms for HSA species
## AH60888   Annotations from pathways to GO terms for MMU species
## AH60889   Annotations from pathways to GO terms for RNO species
## AH60890   Annotations from pathways to Uniprot keywords for HSA species
```

## hpAnnot

```
## AH60891      Annotations from pathways to Uniprot keywords for MMU species
## ...
## AH60914      Pseudo-pathways topologies grouped by GO terms for RNO species
## AH60915      Pseudo-pathways topologies grouped by Uniprot keywords for RNO species
## AH60916      XRef transformation of genes for HSA species
## AH60917      XRef transformation of genes for MMU species
## AH60918      XRef transformation of genes for RNO species
xtabs(~dataprovder + species, mcols(hp))
##          species
## dataprovder Homo sapiens Mus musculus Rattus norvegicus
##      BioMart          6          6          6
##      KEGG            4          4          4
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"
```

For further information on this please refer to [AnnotationHub](#).