cMAP

November 11, 2026

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cMAP *Bioconductor annotation data package*

Description

The annotation package was built using a downloadable R package - AnnBuilder (download and build your own) from www.bioconductor.org using the following public data sources:

cMAP: http://cmap.nci.nih.gov/PW/Download. Build: Unavailable. Downloaded:Tue Sep 12 16:52:56 2006

Tue Sep 12 16:52:56 2006

cMAP

KEGG

The function cMAP() provides information about the binary data files

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cMAPCARTAINTERACTION *An annotation data file that maps cMAP molecule identifiers to data concerning the interactions between molecules*

Description

cMAPCARTAINTERACTION maps cMAP (NCICB Pathway Interaction Database) molecule identifiers to data about the interactions of the molecule represented by the identifiers and other molecules

Details

This is an environment object containing key and value pairs. Keys are molecule identifiers and values are lists of vectors and sublists. Each molecule identifier is mapped to a list that has a source, process, reversible, condition, and component element.

The source element is a character string indicating whether the interactions between molecules are from a BioCarta or KEGG pathway.

The process is a character string describing the process the key molecule is involved. Potential values include "reaction", "modification", "transcription", "translocation", "macroprocess" or a more specific subtype of macroprocess including any term from the GO Biological Process vocabulary.

The reversible element is a boolean indicating whether the interaction is reversible.

The condition element is a character string indicating the biological process the interactions take place. Potential values include any term from the GO Biological Process vocabulary.

The component element contains sublists of vectors. Each key molecule identifier has a sequence of component represented by elements of the sublist. Each sublist has an identifier (molecule identifier of the interacting molecule), edge (indicating the way two molecule interact. Potential values include "input", "agent", "inhibitor", and "output"), role (the function of the key molecule. Potential values include any term from the GO Molecular Function vocabulary), location (a GO Cellular Component vocabulary indicating the location of the interaction), and activity (an abstract term that can be "inactive", "active", "active1", "active2") elements.

Mappings were based on data provided by:

cMAP: http://cmap.nci.nih.gov/PW/Download. Build: Unavailable. Downloaded:Tue Sep 12 16:52:56 2006

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References

cMAP http://cmap.nci.nih.gov/PW

Examples

```
require(cMAP) || stop(paste(cMAP, "unavailable"))
xx <- as.list(cMAPCARTAINTERACTION)
if(length(xx) > 0){
    # Get the value of the first key
    xx[[1]]
    # Get the values for multiget for a few keys
    if(length(xx) >= 3){
    xx[1:3]
    }
}
```

cMAPCARTAMOLECULE *An annotation data file that maps cMAP molecule identifiers to data concerning the molecule*

Description

cMAPCARTAMOLECULE maps cMAP (NCICB Pathway Interaction Database) molecule identifiers to data about the molecules

Details

This is an environment object containing key and value pairs. Keys are molecule identifiers and values are lists of vectors and sublists. Each molecule identifier is mapped to a list that has a type, extid, component, and member element.

The type element is a character string describing what type of molecule the key molecule identifier corresponds to. Potential values for type include "protein", "complex", "compound", and "rna".

The extid element is a named vector of character strings. values of the vector are external identifiers corresponding to the key molecule identifier. Names of the vector are abbreviations of the external public data sources from which the external identifiers are obtained. Potential values for vector names include "LL" (Entrez Gene identifier), "CA" (CAChemical Abstract number), "GO" (Gene Ontology), "KG" (KEGG), etc.

The component element is a sublist with an identifier (molecule id of the component molecule), location (a GO Cellular Component vocabulary indicating the location of the molecule), and activity (an abstract term that can be "inactive", "active", "active1", "active2") elements. The component element only applies to complex molecules. Each complex molecule has a sequence of component molecules represented by elements of the sublist.

The member element is a named vector of molecule identifiers for molecules that belong to the same protein family as the key molecule identifier. Names of the vector are the key molecule identifier.

Mappings were based on data provided by:

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Package built: Tue Sep 12 16:52:56 2006

References

cMAP http://cmap.nci.nih.gov/PW

Examples

```
require(cMAP) || stop(paste(cMAP, "unavailable"))
xx <- as.list(cMAPCARTAMOLECULE)
if(length(xx) > 0){
    # Get the value of the first key
    xx[[1]]
    # Get the values for multiget for a few keys
```

```
    if(length(xx) >= 3){
    xx[1:3]
    }
}
```

---

cMAPCARTAPATHWAY *An annotation data file that maps cMAP short pathway names to descriptive data about the pathway*

Description

cMAPCARTAPATHWAY maps cMAP (NCICB Pathway Interaction Database) abbreviated pathway names to descriptive data about the pathway

Details

This is an environment object containing key and value pairs. Keys are short pathway names and values are lists of vectors. Each pathway name is mapped to a list that has an identifier. name, organism, source, and component element.

The identifier element is an integer for NCICB Pathway Interaction Database identifier.

The name element is the full length of textual descriptive name for the pathway.

The organism is a character string for an abbreviation of organism name (e. g. Hs = human)

The source element is a character string indicating whether the interaction is a BioCarta or KEGG pathway.

The type element is a character string describing what type of molecule the key molecule identifier corresponds to. Potential values for type include "protein", "complex", "compound", and "rna".

The component element is a vector of integers for the identifiers of molecules that are involved in the pathway.

Mappings were based on data provided by:

cMAP: http://cmap.nci.nih.gov/PW/Download. Build: Unavailable. Downloaded:Tue Sep 12 16:52:56 2006

Package built: Tue Sep 12 16:52:56 2006

References

cMAP http://cmap.nci.nih.gov/PW

Examples

```
require(cMAP) || stop(paste(cMAP, "unavailable"))
xx <- as.list(cMAPCARTAPATHWAY)
if(length(xx) > 0){
    # Get the value of the first key
    xx[[1]]
    # Get the values for multiget for a few keys
```

```
    if(length(xx) >= 3){
    xx[1:3]
    }
}
```

---

cMAPKEGGINTERACTION *An annotation data file that maps cMAP molecule identifiers to data concerning the interactions between molecules*

Description

cMAPKEGGINTERACTION maps cMAP (NCICB Pathway Interaction Database) molecule identifiers to data about the interactions of the molecule represented by the identifiers and other molecules

Details

This is an environment object containing key and value pairs. Keys are molecule identifiers and values are lists of vectors and sublists. Each molecule identifier is mapped to a list that has a source, process, reversible, condition, and component element.

The source element is a character string indicating whether the interactions between molecules are from a BioCarta or KEGG pathway.

The process is a character string describing the process the key molecule is involved. Potential values include "reaction", "modification", "transcription", "translocation", "macroprocess" or a more specific subtype of macroprocess including any term from the GO Biological Process vocabulary.

The reversible element is a boolean indicating whether the interaction is reversible.

The condition element is a character string indicating the biological process the interactions take place. Potential values include any term from the GO Biological Process vocabulary.

The component element contains sublists of vectors. Each key molecule identifier has a sequence of component represented by elements of the sublist. Each sublist has an identifier (molecule identifier of the interacting molecule), edge (indicating the way two molecule interact. Potential values include "input", "agent", "inhibitor", and "output"), role (the function of the key molecule. Potential values include any term from the GO Molecular Function vocabulary), location (a GO Cellular Component vocabulary indicating the location of the interaction), and activity (an abstract term that can be "inactive", "active", "active1", "active2") elements.

Mappings were based on data provided by:

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Package built: Tue Sep 12 16:52:56 2006

References

cMAP http://cmap.nci.nih.gov/PW

Examples

```
require(cMAP) || stop(paste(cMAP, "unavailable"))
xx <- as.list(cMAPKEGGINTERACTION)
if(length(xx) > 0){
    # Get the value of the first key
    xx[[1]]
    # Get the values for multiget for a few keys
    if(length(xx) >= 3){
    xx[1:3]
    }
}
```

---

cMAPKEGGMOLECULE *An annotation data file that maps cMAP molecule identifiers to data concerning the molecule*

Description

cMAPKEGGMOLECULE maps cMAP (NCICB Pathway Interaction Database) molecule identifiers to data about the molecules

Details

This is an environment object containing key and value pairs. Keys are molecule identifiers and values are lists of vectors and sublists. Each molecule identifier is mapped to a list that has a type, extid, component, and member element.

The type element is a character string describing what type of molecule the key molecule identifier corresponds to. Potential values for type include "protein", "complex", "compound", and "rna".

The extid element is a named vector of character strings. values of the vector are external identifiers corresponding to the key molecule identifier. Names of the vector are abbreviations of the external public data sources from which the external identifiers are obtained. Potential values for vector names include "LL" (Entrez Gene identifier), "CA" (CAChemical Abstract number), "GO" (Gene Ontology), "KG" (KEGG), etc.

The component element is a sublist with an identifier (molecule id of the component molecule), location (a GO Cellular Component vocabulary indicating the location of the molecule), and activity (an abstract term that can be "inactive", "active", "active1", "active2") elements. The component element only applies to complex molecules. Each complex molecule has a sequence of component molecules represented by elements of the sublist.

The member element is a named vector of molecule identifiers for molecules that belong to the same protein family as the key molecule identifier. Names of the vector are the key molecule identifier.

Mappings were based on data provided by:

cMAP: http://cmap.nci.nih.gov/PW/Download. Build: Unavailable. Downloaded:Tue Sep 12 16:52:56 2006

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References

cMAP http://cmap.nci.nih.gov/PW

Examples

```
require(cMAP) || stop(paste(cMAP, "unavailable"))
xx <- as.list(cMAPKEGGMOLECULE)
if(length(xx) > 0){
    # Get the value of the first key
    xx[[1]]
    # Get the values for multiget for a few keys
    if(length(xx) >= 3){
    xx[1:3]
    }
}
```

---

cMAPKEGGPATHWAY *An annotation data file that maps cMAP short pathway names to descriptive data about the pathway*

Description

cMAPKEGGPATHWAY maps cMAP (NCICB Pathway Interaction Database) abbreviated pathway names to descriptive data about the pathway

Details

This is an environment object containing key and value pairs. Keys are short pathway names and values are lists of vectors. Each pathway name is mapped to a list that has an identifier. name, organism, source, and component element.

The identifier element is an integer for NCICB Pathway Interaction Database identifier.

The name element is the full length of textual descriptive name for the pathway.

The organism is a character string for an abbreviation of organism name (e. g. Hs = human)

The source element is a character string indicating whether the interaction is a BioCarta or KEGG pathway.

The type element is a character string describing what type of molecule the key molecule identifier corresponds to. Potential values for type include "protein", "complex", "compound", and "rna".

The component element is a vector of integers for the identifiers of molecules that are involved in the pathway.

Mappings were based on data provided by:

cMAP: http://cmap.nci.nih.gov/PW/Download. Build: Unavailable. Downloaded:Tue Sep 12 16:52:56 2006

Package built: Tue Sep 12 16:52:56 2006

References

cMAP http://cmap.nci.nih.gov/PW

Examples

```
require(cMAP) || stop(paste(cMAP, "unavailable"))
xx <- as.list(cMAPKEGGPATHWAY)
if(length(xx) > 0){
    # Get the value of the first key
    xx[[1]]
    # Get the values for multiget for a few keys
    if(length(xx) >= 3){
    xx[1:3]
    }
}
```

---

cMAPQC *Quality control information for cMAP*

Description

cMAPQC is an R environment that provides quality control information for cMAP

Details

This file contains quality control information that can be displayed by typing cMAP() after loading the package using library(cMAP). The follow items are included:

Date built: Date when the package was built.

Number of probes: total number of probes included

Probe number missmatch: if the total number of probes of any of the data file is different from a base file used to check the data files the name of the data file will be listed

Probe missmatch: if any of probes in a data file missmatched that of the base file, the name of the data file will be listed

Mappings found for probe based files: number of mappings obtained for the total number of probes

Mappings found for non-probe based files: total number of mappings obtained

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