

ontoTools

April 19, 2009

`A.csr` *~~data-name / kind ...*

Description

demonstration sparse matrix matrix.csr form

Usage

```
data(A.csr)
```

Format

The format is: list() - attr(*, "ra")= num [1:27] 2.894 -0.610 -0.714 0.546 0.901 ... - attr(*, "ja")= int [1:27] 3 4 5 2 4 1 3 4 5 3 ... - attr(*, "ia")= int [1:11] 1 4 6 10 11 14 18 21 22 26 ... - attr(*, "dimension")= int [1:2] 10 5 - attr(*, "class")= atomic [1:1] matrix.csr ..- attr(*, "package")= chr ".GlobalEnv"

Source

SparseM library matrix.csr example generated it

`GDI_NCIThesaurus` *Structures for working with formal nomenclatures*

Description

Structures for working with formal nomenclatures

Usage

```
data(GDI_NCIThesaurus)
parents(term, nom)
children(term, nom)
getDefs(term, nom)
```

Arguments

term	character string, term
nom	instance of class <code>taggedHierNomenclature</code>

Details

DAG-structured nomenclatures are in wide use. For any term, one can seek parents (generalizations) or children (specializations). These resources prototype tools for dealing with such structures, including provenance information.

Author(s)

Vince Carey <stvjc@channing.harvard.edu>

Examples

```
data(GDI_NCIThesaurus)
parents("Mesna", GDI_NCIThesaurus)
parents("Actinomycin_Antibiotic", GDI_NCIThesaurus)
```

LLGOMFcp

resources saved for computation of concept probabilities for GO MF terms applied to human LocusLink entries

Description

concept probabilities for GO MF terms applied to human LocusLink entries

Usage

```
data(LLGOMFcp)
```

Format

The format is: Named num [1:5399] 0 0 0 0 0 ... - attr(*, "names")= chr [1:5399] "GO:0000005" "GO:0000006" "GO:0000007" "GO:0000008" ...

Source

derived from Bioconductor packages humanLLMappings and GO

OOC-class

*Class "OOC" object-ontology complex***Description**

Object that binds ontology (structured vocabulary) with an object-term map.

Objects from the Class

Objects can be created by calls of the form `new("OOC", ...)`.

Slots

ontology: Object of class "ontology" instance of `ontoTools::ontology`

Oomap: Object of class "namedSparse" `SparseM::matrix.csr` bound with `dimnames` facilities

Methods

coverageMat signature(x = "OOC"): return a `namedSparse` incidence matrix with r,c element indicating whether term c covers object r

ontology signature(x = "OOC"): accessor

Oomap signature(x = "OOC"): accessor

show signature(object = "OOC"): concise printer

Author(s)

VJ Carey <stvjc@channing.harvard.edu>

Examples

```
data(litOnto)
g1 <- new("rootedDAG", DAG=litOnto, root="A")
o1 <- new("ontology", name="demo", version="0.1",
        rDAG=g1)
kvlist <- list(W="E", X="K", Y="B", Z=c("D","G"))
litMap <- otkvList2namedSparse( names(kvlist), LETTERS[1:12], kvlist )
print(litMap)
ooc1 <- makeOOC( o1, litMap )
show(ooc1)
print(coverageMat(ooc1))
# note the following will be slow with large OOCs
print(conceptProbs(ooc1))
# for larger OOCs it is useful to precompute the accessibility
# matrix of the ontology and the map from objects to terms -- these
# can be supplied as additional arguments to conceptProbs
```

 SGDIvocab

Vocabulary for genomic data integration

Description

Vocabulary for genomic data integration

Usage

```
data(SGDIvocab)
```

Details

Currently unites some english terms with a formal tag to NCI Metathesaurus. Additional content to be added, with bridges to NCI EVS.

Value

This is an instance of a [taggedHierNomenclature](#) derived from an informal specification of terms about breast cancer provided by S. Ramaswamy.

Author(s)

Vince Carey <stvjc@channing.harvard.edu>

Examples

```
data(SGDIvocab)
SGDIvocab
grep("differ", SGDIvocab)
getTerms(SGDIvocab)
```

STMA

Vocabulary from statistics theory and methods abstracts

Description

Vocabulary from statistics theory and methods abstracts

Usage

```
data(STMA)
```

Author(s)

Vince Carey <stvjc@channing.harvard.edu>

Examples

```
data(STMA)
grep("exponential", STMA)
parents("Exponential families", STMA)
children("PROBABILITY DISTRIBUTIONS", STMA)
```

accessMat *matrix utilities for ontoTools.*

Description

A variety of matrix utilities used in ontoTools

Usage

```
accessMat (object)
```

Arguments

```
object                    object
```

Author(s)

Vince Carey <stvjc@channing.harvard.edu>

buildGOgraph *build graphNEL corresponding to bioc GO environment*

Description

build graphNEL corresponding to bioc GO environment

Usage

```
buildGOgraph (useenv=GOMFPARENTS)
```

Arguments

```
useenv                    useenv: environment to be used
```

Details

all GO MF tags are nodes, edges drawn from node to parent

Value

graphNEL instance

Author(s)

Vince Carey <stvjc@channing.harvard.edu>

See Also

Biograph package

Examples

```
# takes a while; trivial invocation
```

compoundGraph-class

Class "compoundGraph" list representation of multiple graph::graph objects

Description

Class "compoundGraph" list+list representation of multiple graph::graph objects

Objects from the Class

Objects can be created by calls of the form `new("compoundGraph", ...)`.

Slots

grList: Object of class "list" list of graph::graph objects

between: Object of class "list" list of node-to-node connections across graphs

Methods

adjMat signature(`cg = "compoundGraph"`):...

between signature(`object = "compoundGraph"`):...

grList signature(`object = "compoundGraph"`):...

toDot signature(`G = "compoundGraph"`, `outDotFile = "character"`, `renderList = "list"`, `optList = "missing"`):...

toDot signature(`G = "compoundGraph"`, `outDotFile = "character"`, `renderList = "list"`, `optList = "list"`):...

toDot signature(`G = "compoundGraph"`, `outDotFile = "missing"`, `renderList = "list"`, `optList = "missing"`):...

Note

Should be supplanted by Rgraphviz facilities before too long.

Author(s)

VJ Carey <stvjc@channing.harvard.edu>

References

~put references to the literature/web site here ~

See Also

Rgraphviz::subgraph

`depthStruct`*tools for manipulating depth concepts for rooted DAGs*

Description

return a list of environments giving mapping from node name to rooted DAG depth and from depth to vector of names of nodes at that depth

Usage

```
depthStruct(rg)
ontoDepth(rg)
DMdepth(g, maxd)
```

Arguments

<code>rg</code>	<code>rg</code> : instance of class <code>rootedDAG</code>
<code>g</code>	<code>rg</code> : instance of class <code>depth</code>
<code>maxd</code>	<code>maxd</code> : bound on depth to be measured

Value

`depthStruct`: a list of two environments (see examples).

Note

`ontoDepth` is the workhorse for `depthStruct`. `DMdepth` is a function that works on a plain graph, creating the 'daughter matrix' and computing depths.

Author(s)

Vince Carey <stvjc@channing.harvard.edu>

Examples

```
data(litOnto)
print(litOnto)
g1 <- new("rootedDAG", DAG=litOnto, root="A")
o1 <- new("ontology", name="demo", version="0.1",
         rDAG=g1)
print(ds <- depthStruct(g1))
ds$tag2depth("A")
ds$tag2depth("H")
ds$depth2tag(2)
```

gomfAmat	<i>sparse matrix representing accessibilities of terms in GO MF graph; graph also documented here</i>
----------	---

Description

sparse matrix representing accessibilities of terms in GO MF graph

Usage

```
data(gomfAmat); data(goMFgraphDemo)
```

Format

The format is: list() - attr(*, "Dimnames")=List of 2 ..: chr[1 : 5399]"GO : 0000005""GO : 0000006""GO : 0000007""GO : 0000008"..... : chr [1:5399] "GO:0000005" "GO:0000006" "GO:0000007" "GO:0000008" ... - attr(*, "mat")= list() ..- attr(*, "ra")= num [1:33263] 0 1 1 1 1 1 1 1 1 1- attr(*, "ja")= int [1:33263] 1 261 203 3073 1741 1744 2820 5367 2035 5356- attr(*, "ia")= int [1:5400] 1 4 14 22 24 30 34 45 50 56- attr(*, "dimension")= int [1:2] 5399 5399 ..- attr(*, "class")= atomic [1:1] matrix.csr- attr(*, "package")= chr ".GlobalEnv" - attr(*, "rowindex")=List of 2 ..n2i : length0 < environment > .. i2n:length 0 <environment> - attr(*, "colindex")=List of 2 ..n2i : length0 < environment > .. i2n:length 0 <environment> - attr(*, "class")= atomic [1:1] namedSparse ..- attr(*, "package")= chr ".GlobalEnv"

Source

built from bioconductor graph, GO and ontoTools package tools

litOnto	<i>litOnto: graph illustrating the ontology concept; litObj: matrix illustrating the object-ontology mapping</i>
---------	--

Description

litOnto: graph illustrating the ontology concept; litObj: matrix illustrating the object-ontology mapping

Usage

```
data(litOnto)
```

Format

The format is: list() - attr(*, "nodes")= chr [1:12] "A" "B" "C" "D" ... - attr(*, "edgeL")=List of 12 ..A : Listof1.... edge: NULL ..B : Listof1.... edges: int 1 ..C : Listof1.... edges: int 1 ..D : Listof1.... edges: int 2 ..E : Listof1.... edges: int 2 ..F : Listof1.... edges: int 3 ..G : Listof1.... edges: int 3 ..H : Listof1.... edges: int [1:2] 4 5 ..I : Listof1.... edges: int [1:3] 4 3 5 ..J : Listof1.... edges: int 6 ..K : Listof1.... edges: int 6 ..L : Listof1.... edges: int 7 - attr(*, "edgemode")= chr "directed" - attr(*, "class")= chr "graphNEL"

namedSparse-class *Class "namedSparse" adds margin names to sparse matrices*

Description

manages margin names for sparse matrices

Objects from the Class

Objects can be created by calls of the form `new("namedSparse", ...)`. These are S4 objects that include a `SparseM::matrix.csr`, associated `dimnames` in the customary form, and two lists of name-to-index mapping environments (for row and column name resolution, with `forward` (name to index) and `backward` (index to name) mapping).

Slots

Dimnames: Object of class "list" ordinary dimnames matrix metadata

mat: Object of class "matrix.csr" sparse matrix

Methods

Arith signature(e1 = "namedSparse", e2 = "namedSparse"):...

show signature(object = "namedSparse"):...

Note

A constructor `makeNamedSparse` is illustrated in the example.

Author(s)

VJ Carey <stvjc@channing.harvard.edu>

Examples

```
data(A.csr)
namedA <- mkNS(A.csr) # installs default dimnames R{1:nrow}, C{1:ncol}
print(namedA)
print(colSums(namedA))
dimnames(namedA) <- list(paste("A", 1:10, sep=""), paste("B", 1:5, sep=""))
print(namedA)
print(namedA %*% t(namedA))
```

ontology-class *Class "ontology" wraps a rooted DAG with some ontology metadata*

Description

instances of class ontology are used to represent things like Gene Ontology

Objects from the Class

Objects can be created by calls of the form `new("ontology", ...)`. This simply possesses information on name and version of ontology.

Slots

name: Object of class "character" name of ontology

version: Object of class "character" version tag

rDAG: Object of class "rootedDAG" the rooted DAG representing the terminology hierarchy

Methods

accessMat signature(object = "ontology"): returns square matrix with 1 in element `r,c` if term corresponding to `r` can be reached from term corresponding to `c`

name signature(x = "ontology"): access name

OVersion signature(x = "ontology"): access version

rDAG signature(x = "ontology"): access the rooted DAG

show signature(object = "ontology"): concise report

Note

This class was written to deal with ontologies that are representable as rooted DAGs. It is not clear that this is a good use of the term 'ontology', which has broader implications. However this does work for Gene Ontology.

Author(s)

~~who you are~~

Examples

```
data(litOnto)
print(litOnto)
g1 <- new("rootedDAG", DAG=litOnto, root="A")
o1 <- new("ontology", name="demo", version="0.1",
        rDAG=g1)
# can also use
o1b <- makeOntology( name="demo", version="0.1",
                    graph=litOnto, root="A")
show(o1)
print(accessMat(o1))
print(OVersion(o1))
```

ooMapLL2GOMFdemo *object-term mapping for human locuslink entries and GO MF*

Description

object-term mapping for human locuslink entries and GO MF

Usage

```
data(ooMapLL2GOMFdemo)
```

Format

The format is: list() - attr(*, "Dimnames")=List of 2 ..: chr[1 : 10776]"1""10""100""1000"
: chr [1:5399] "GO:0000005" "GO:0000006" "GO:0000007" "GO:0000008" ... - attr(*, "mat")=
list() ..- attr(*, "ra")= num [1:19679] 0 1 1 1 1 1 1 1 1 1- attr(*, "ja")= int [1:19679] 1 1842
541 3528 3753 485 3799 1594 1804 1098- attr(*, "ia")= int [1:10777] 1 3 6 8 10 13 14 17
23 28- attr(*, "dimension")= int [1:2] 10776 5399 ..- attr(*, "class")= chr "matrix.csr" - attr(*,
"rowindex")=List of 2 ..n2i : length0 < environment > .. i2n:length 0 <environment> - attr(*,
"colindex")=List of 2 ..n2i : length0 < environment > .. i2n:length 0 <environment> - attr(*,
"class")= chr "namedSparse"

Source

bioconductor GO, humanLLMapping and ontoTools otkv tools.

otkvEnv2namedSparse

obtain sparse matrix representation of key-value structures

Description

obtain sparse matrix representation of key-value structures

Usage

```
otkvEnv2namedSparse(obs, tms, otkvEnv)
otkvList2namedSparse(obs, tms, otkvlist)
```

Arguments

obs	obs: vector of object tags
tms	tms: vector of terms to which objects are mapped
otkvEnv	otkvEnv: environment encoding the key-value mapping
otkvlist	otkvlist: list encoding the key-value mapping

Author(s)

Vince Carey <stvjc@channing.harvard.edu>

Examples

```
otkvList2namedSparse(c("A","B","D","E"), letters[1:7],
  list("A"=c("a","b"), "B"=c("b","d"), "E"="c"))
```

```
rootedDAG-class      Class "rootedDAG"
```

Description

wraps a graph that can be shown to be a DAG and has a root (one node with no ancestor)

Objects from the Class

Objects can be created by calls of the form `new("rootedDAG", ...)`. Does not extend graph but probably should.

Slots

root: Object of class "character" name of root

DAG: Object of class "graph" DAG

Methods

DAG signature(x = "rootedDAG"): extract the graph

getMatrix signature(g = "rootedDAG", type = "character", mode = "character"): Currently only 'child2parent' can be used for type, meaning that row corresponds to child, column corresponds to ancestor and `mat[row,column]` is 1 if node corresponding to row is a child of node corresponding to ancestor. Type can be 'sparse' (return sparse representation) or 'dense'.

root signature(x = "rootedDAG"): extract name of root

Author(s)

VJ Carey <stvjc@channing.harvard.edu>

```
semsim              Compute semantic similarity measure for terms in an object-ontology
                    complex
```

Description

Compute semantic similarity measure for terms in an object-ontology complex

Usage

```
semsim(c1, c2, ooc, acc=NULL, pc=NULL)
conceptProbs(ooc, acc=NULL, inds=NULL)
subsumers(c1, c2, ont, acc=NULL)
pms(c1, c2, ooc, acc=NULL, pc=NULL)
usageCount(map, acc, inds)
```

Arguments

c1	c1, c2: "character" terms to be compared
c2	c1, c2: "character" terms to be compared
ooc	ooc: an object of class "OOC": object-ontology complex
ont	ont: an object of class "ontology": annotated rooted DAG
acc	acc: optional (sparse) accessibility matrix for the ontology
pc	pc: optional vector of concept probabilities, if pre-computed
map	map: OOmap component of an ooc
inds	inds: vector of numeric indices, row indices of object-ontology map to be processed

Details

For large ontologies, computation of the term accessibility relationships and term probabilities can be costly. Once these are computed to support one semsim calculation, they should be saved. The acc and pc parameters allow use of this saved information.

Value

semsim returns the measure of semantic similarity cited by Lord et al (2003).

Author(s)

Vince Carey <stvjc@channing.harvard.edu>

References

PW Lord et al, Bioinformatics, 19(10)2003:1275

Examples

```
#
# we are given a graph of GOMF and the OOmap between LL and GOMF
# derived from humanLLMappings and stored as data resources in
# ontoTools -- these will have to be updated regularly
#
data(goMFgraph.1.15)
data(LL2GOMFooMap.1.15)
#
# build the rooted DAG, the ontology, and the OOC objects
#
gomfrDAG <- new("rootedDAG", root="GO:0003674", DAG=goMFgraph.1.15)
GOMFonto <- new("ontology", name="GOMF", version="bioc GO 1.15", rDAG=gomfrDAG)
LLGOMFOOC <- makeOOC(GOMFonto, LL2GOMFooMap.1.15)
#
# we are given the accessibility matrix for the GO MF graph as a
# data resource, and we can compute some term probabilities
#
data(goMFamat.1.15)
pc <- conceptProbs(LLGOMFOOC, goMFamat.1.15, inds=1:20)
#
# now we will get a sample of GO MF terms and compute the
# semantic similarities of pairs of terms in the sample
```

```

#
data(LL2GOMFcp.1.15) # full set of precomputed concept probabilities
library(GO.db)
library(Biobase)
library(combinat)
library(annotate)
GO() # get the GO environments
GOTags <- ls(GOTERM)
GOLabs <- mget(GOTags, GOTERM, ifnotfound=NA)
GOMFtags <- GOTags[ sapply(GOLabs,Ontology)=="MF" ]
GOMFtags <- GOMFtags[!is.na(GOMFtags)]
GOMFtermObs <- mget(GOMFtags,env=GOTERM)
GOMFterms <- sapply(GOMFtermObs, Term )
nTags <- length(GOMFtags)
if (any(duplicated(GOMFterms)))
{
  dups <- (1:nTags)[duplicated(GOMFterms)]
  GOMFterms[dups] <- paste(GOMFterms[dups],".2",sep="")
}
#names(GOMFterms) <- GOMFtags
set.seed(1234)
# does not lead to common samples across platforms...
st <- sample(names(GOMFterms),size=50) # take the sample
st <- intersect(st, names(LL2GOMFcp.1.15))[1:10] # use only those terms available in bio
# thus ...
st = c("GO:0004397", "GO:0030215", "GO:0042802", "GO:0008504", "GO:0008640",
"GO:0008528", "GO:0008375", "GO:0005436", "GO:0004756", "GO:0003729"
)
pst <- combn(st,2) # get a matrix with the pairs of terms in columns
bad = c(4L, 12L, 19L, 25L, 31L, 32L, 33L, 34L, 35L) # can't use 8640
pst = pst[,-bad]
npst <- ncol(pst)
ss <- rep(NA,npst)
for (i in 1:npst) # compute semantic similarities
{
  cat(i)
  ss[i] <- semsim( pst[1,i], pst[2,i], ooc=LLGOMFOOC, acc=goMFamat.1.15, pc=LL2GOMFcp.1.1
}
print(summary(ss))
top <- (1:npst)[ss==max(ss,na.rm=TRUE)][1] # index of the most similar pair
# note -- must come to an understanding of the NAs
print( GOMFterms[ as.character(pst[,top]) ] )
pen <- (1:npst)[ss==max(ss[-top],na.rm=TRUE)][1] # second most similar
print( GOMFterms[ as.character(pst[,pen]) ] )

```

taggedHierNomenclature-class

Class "taggedHierNomenclature" ~~~

Description

representation of a DAG-structured nomenclature

Objects from the Class

Objects can be created by calls of the form `new ("taggedHierNomenclature", ...)`. See example

Slots

tags: Object of class "character" ; formal tags, often semantically opaque
parents: Object of class "character"; terms regarded as generalizations of the given term
delim: Object of class "character"; the parent strings are decomposed using this delimiter
rootToken: Object of class "character"; token used to indicate root of DAG
name: Object of class "character" name of nomenclature
provenance: Object of class "provStruct" information on origins of vocabulary
inMappings: Object of class "character" list of mappings in which the term is employed
terms: Object of class "character" actual subject matter terms being organized
definitions: Object of class "character" verbal definitions of terms

Extends

Class "nomenclature", directly.

Methods

children signature(term = "character", nom = "taggedHierNomenclature"): ...
parents signature(term = "character", nom = "taggedHierNomenclature"): ...
show signature(object = "taggedHierNomenclature"): ...

Author(s)

VJ Carey <stvjc@channing.harvard.edu>

See Also

[GDI_NCIThesaurus](#)

Examples

```
data(GDI_NCIThesaurus)
GDI_NCIThesaurus
```

toDot-methods

Methods for Function toDot in Package 'ontoTools' – should be replaced by Rgraphviz facilities soon

Description

These methods write graphviz dot language for various graph structures encountered with ontologies. This activity should be moved to Rgraphviz ASAP, but there are aspects of representation and portability that need to be resolved.

Methods

G = "graphNEL", outDotFile = "character", renderList = "list", optList = "list" create dot language description of graph

G = "graphNEL", outDotFile = "character", renderList = "missing", optList = "missing" create dot language description of graph

G = "graphNEL", outDotFile = "character", renderList = "missing", optList = "list" create dot language description of graph

G = "graphNEL", outDotFile = "missing", renderList = "missing", optList = "missing" create dot language description of graph

G = "graphNEL", outDotFile = "missing", renderList = "missing", optList = "list" create dot language description of graph

G = "graphNEL", outDotFile = "missing", renderList = "character", optList = "missing" create dot language description of graph

G = "graphNEL", outDotFile = "missing", renderList = "list", optList = "list" create dot language description of graph

G = "graphNEL", outDotFile = "missing", renderList = "list", optList = "missing" create dot language description of graph

G = "compoundGraph", outDotFile = "character", renderList = "list", optList = "missing" create dot language description of graph

G = "compoundGraph", outDotFile = "character", renderList = "list", optList = "list" create dot language description of graph

G = "compoundGraph", outDotFile = "missing", renderList = "list", optList = "missing" create dot language description of graph

Examples

```
example(randomGraph)
tmp <- tempfile()
toDot(g1, tmp)
readLines(tmp)
unlink(tmp)
```


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