

Package: visATC (via r-universe)

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Type Package

Title Visualise the Anatomical Therapeutic Chemical (ATC) Hierarchy

Version 1.0.0.9000

Description Visualisation and subsetting of the World Health Organisation Anatomical Therapeutic Chemical (ATC) classification system.

License GPL (>= 3)

Encoding UTF-8

LazyData true

Imports tidyr, dplyr, rlang, igraph, methods, plotly, graphlayouts, purrr

RoxygenNote 7.3.2

Suggests knitr, rmarkdown

Depends R (>= 4.1.0)

URL <https://jnm212.github.io/visATC/>

Config/pak/sysreqs cmake libglib-dev make libicu-dev libuv1-dev libxml2-dev libssl-dev

Repository <https://jnm212.r-universe.dev>

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[,atctree-method	<i>find a subset of the tree</i>
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Description

find a subset of the tree

Usage

```
## S4 method for signature 'atctree'
x[i, j = 1L]
```

Arguments

- x object of class atctree
- i label (ATC code) of focal node
- j generation (integer). 0: siblings, -1: children, -2: grandchildren, 1: parents etc

Details

The subset method for objects of class atctree uses a focal node and a specification of how many generations to accrue. The focal node is specified by an ATC code at any of the five levels (e.g. i="A01"). The generation is specified by integer j, signed positive for ancestors and negative for descendants.

Value

an object of class atctree

Examples

```
h <- atctree(schema="full")
#more useful to use the full tree with this approach
# plot descendents of P01 (as far as grandchildren):
h["P01",-2] |> plot(stem_label=TRUE, leaf_label=TRUE)
# plot descendents of P01 (as far as great grandchildren):
h["P01",-3] |> plot(stem_label=TRUE, leaf_label=FALSE)
# plot descendents of parent of P01A:
```

```
h["P01A",1] |> plot(stem_label=TRUE, leaf_label=TRUE)
# plot descendents of grandparent of P01A:
h["P01A",2] |> plot(stem_label=TRUE, leaf_label=TRUE)
```

ATCdata

nodes of the ATC hierarchy

Description

This contains nodes of the ATC hierarchy at all 5 levels (e.g. A, A01, A01A ...), and associated descriptive text (eg. for A: ALIMENTARY TRACT AND METABOLISM), used here for visualisation.

Usage

```
ATCdata
```

Format

A named character vector for each node, where each entry is an ATC code and the name is a textual description

Source

The ATC data can be perused at <https://atcddd.fhi.no/atc_ddd_index/>.

This data is from the repository at <<https://github.com/fabkury/atcd>> and this release is at <<https://github.com/fabkury/atcd/re>>

The first two columns from the .csv file were selected to produce the named character vector

atctree

constructor for atctree objects

Description

constructor for atctree objects

Usage

```
atctree(
  whichlevs = NULL,
  schema = c("none", "full", "anatomical", "therapeutic", "chemical")
)
```

Arguments

whichlevs	subset of levels to use from integers 1:5
schema	a conceptual subset of the ATC hierarchy, or all of it ('full'), or something bespoke ('none')

Details

either schema or whichlevs should be specified; (e.g. 'schema=full' corresponds to 'whichlevs=1:5')

Value

an object of class atctree

Examples

```
h <- atctree(schema="anatomical")
# tree will contain levels 1 and 5
h <- atctree(whichlevs=c(1,2,5))
# bespoke structure
```

atctree-class

class to represent a tree from the ATC hierarchy

Description

class to represent a tree from the ATC hierarchy

Slots

node node id
 pnode parent node id
 lab ATC code
 plab parent ATC code
 text ATC textual info
 drugnames common names for drugs where known
 lev level of each node (root node is 0)
 schema one of 'none', 'full', 'anatomical', 'therapeutic', 'chemical'
 whichlevs subset of integers 1:5; should correspond to schema
 Nnode number of nodes in the tree excluding root node
 Nlev number of levels in the tree excluding root node

cutting,atctree-method	
	<i>cutting from an ATC tree</i>

Description

Cut out a branch with just the descendants of the specified node.

This will include the direct parent of the specified node as information - this is also useful for grafting.

Usage

```
## S4 method for signature 'atctree'
cutting(h, nodelabel = NULL)
```

Arguments

h	an object of class atctree
nodelabel	identify node of interest

Value

returns a (smaller) object of class atctree

Examples

```
h <- atctree(schema="therapeutic")
# Suppose we are interested in a branch of this tree; take a cutting and plot it:
cutting(h, "P01") |> plot()

# a different look:
cutting(h, "P01") |> plot(text_angle=0, circle=TRUE)
```

drugnames	<i>display drug name for ATC codes</i>
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Description

display drug name for ATC codes

Usage

```
drugnames(x)
```

Arguments

x vector of ATC codes

Value

character vector of drug names

graft,atctree,atctree-method
graft (combine) trees

Description

graft (combine) trees

Usage

```
## S4 method for signature 'atctree,atctree'
graft(h1, h2, ...)
```

Arguments

h1 an atctree
h2 an atctree
... more atctree objects

Details

Trees are grafted together at the root so they can be displayed on the same figure. At the moment the branches need to be of the same schema/have the same levels.

Value

an object of class atctree

Examples

```
# some nodes involving inflammation from look(h, "inflamm")
h <- atctree(schema="full")
h1 <- cutting(h, "M01")
h2 <- cutting(h, "A07")
graft(h1,h2) |> plot(circle=TRUE, leaf=FALSE)

h1 <- h["P01",-3] #P01 to great grandchildren
h2 <- h["C01",-1] #C01 to children
h3 <- cutting(h, "G01A") #descendents of G01A
graft(h1, h2, h3) |> plot(stem_label=TRUE)
```

look,atctree-method	<i>search the node texts for an expression</i>
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Description

search the node texts for an expression

Usage

```
## S4 method for signature 'atctree'  
look(h, txt)
```

Arguments

h	an object of class atctree
txt	word or part of a word or regular expression to search for

Value

returns a vector of nodes whose text matches

Examples

```
h <- atctree(schema="full")  
nds <- look(h, "inflamm")  
# a search for inflammatory substances and families  
  
# plot element nds[1] which is "A07E":  
cutting(h, nds[1]) |> plot()
```

parents,atctree-method	<i>show the parents for the specified node(s) in the tree</i>
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Description

show the parents for the specified node(s) in the tree

Usage

```
## S4 method for signature 'atctree'  
parents(h, node, anc = 1)
```

Arguments

h	tree the node belongs to
node	a node e.g. A01AX
anc	level of ancestry (default 1). How many generations back or forward?

Value

atctree object

parents,character-method
<i>show the parents for the specified node(s) in the full tree</i>

Description

show the parents for the specified node(s) in the full tree

Usage

```
## S4 method for signature 'character'
parents(h)
```

Arguments

h	node(s)
---	---------

Value

parent node(s)

Examples

```
parents(c("A01AA", "A01", "A"))
```

plot,atctree-method *plot the tree as a network graph*

Description

plot the tree as a network graph

Usage

```
## S4 method for signature 'atctree'
plot(
  x,
  circle = NULL,
  ATC_text = NULL,
  leaf_label = NULL,
  stem_label = NULL,
  include_names = F,
  text_size = 10,
  text_angle = 45,
  width = 500,
  height = 500,
  hover_msg = TRUE
)
```

Arguments

x	an object of class atctree
circle	whether or not to arrange graph over a circle
ATC_text	whether or not to label with ATC textual info
leaf_label	whether or not leaf nodes will be labelled
stem_label	whether or not stem nodes will be labelled
include_names	whether or not to include common names in text
text_size	annotation text size
text_angle	annotation text angle
width	graph width
height	graph height
hover_msg	whether to remind the user that they can hover over nodes

Details

Each node is labelled with its ATC code, and by hovering the cursor over any node the ATC description is displayed. The ATC tree can be displayed as a network in layers or on a circle (with radii corresponding to ATC level). It is evident that a plot the full ATC tree is too cluttered. Some subsetting (link), pruning (link) or cutting (link) of the tree is likely to help visualisation.

Value

No return value, called for side effects

Examples

```
# create an ATC tree and plot the whole thing:
h <- atctree(schema="full")
# you could plot this with plot(h) but it takes a while
# large network so not easy to read

# take cutting above node B ; plot all its descendants:
cutting(h,"B") |> plot()

# plot node B down to its grandchildren:
h["B",-2] |> plot()
# or use a circular layout
h["B",-2] |> plot(circle=TRUE, stem_label=TRUE)
```

pruning,atctree-method

prune an ATC tree

Description

Pruning is specifying the removal of some unwanted branch of the tree (in contrast to taking a cutting, where it is the branch which is kept).

Usage

```
## S4 method for signature 'atctree'
pruning(h, nodelabels = NULL)
```

Arguments

h	an object of class atctree
nodelabels	character vector of nodes of interest

Value

a (smaller) object of class atctree

Examples

```
library(visATC)
h1 <- atctree(whichlevs=1:3)
h1A <- cutting(h1, "C")
# make a subtree cut at node C
plot(h1A, circle=TRUE)
# suppose we decide not to display some nodes:
pruning(h1A, c("C01", "C05", "C10")) |> plot(circle=TRUE)
```

show,atctree-method *summarise atctree object*

Description

shows schema, number of nodes and levels and a cross-table, excluding the root node.

Usage

```
## S4 method for signature 'atctree'
show(object)
```

Arguments

object of class atctree

Value

prints summary to console

Examples

```
h <- atctree(whichlevs=1:4)
(h)
```

treelevs,atctree-method *helper functions for atctrees*

Description

treelevs: return levels within tree (excluding 0)
 leaves: return labels of terminal elements (leaves) of tree
 nlevs: number of levels in tree (excluding 0)

Usage

```
## S4 method for signature 'atctree'  
treelevs(h)
```

```
## S4 method for signature 'atctree'  
leaves(h)
```

```
## S4 method for signature 'atctree'  
nlevs(h)
```

Arguments

h an object of class atctree

Value

a vector of the level of each node
vector of labels of the leaf nodes
vector of number of levels in the tree

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