Package 'rsml'

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Type Package

Title Plant Root System Markup Language (RSML) File Processing

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Description Read and analyse Root System Markup Language (RSML) files, used to
store plant root system architecture data. More information can be found
at the address <http://rootsystemml.github.io/>.

License GPL-2

Imports XML,rgl

NeedsCompilation no

Repository CRAN

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R topics documented:

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addChildToRoot   *Add a child root (lateral) to an existing root*

Description

Add a child root (lateral) to an existing root

Usage

```
addChildToRoot(current, child)
```

Arguments

current   = the current root

child   = the child root to attach

Value

the current root, with the additional child attached

Author(s)

Guillaume Lobet - guillaume.lobet(at)ulg.ac.be

Examples

```
data(lupin)
current <- lupin$roots[[1]]
child <- current$children[[1]]
current <- addChildToRoot(current, child)
```

---

addNodeToRoot   *Add a node to an existing root*

Description

Add a node to an existing root

Usage

```
addNodeToRoot(ro, no)
```

Arguments

ro	= the current root
no	= the current node

Value

the root, with the added node

Author(s)

Guillaume Lobet - guillaume.lobet(at)ulg.ac.be

Examples

```
n <- node(1, 1)
r <- root()
r <- addNodeToRoot(r, n)
```

---

addRootToPlant | *Add a root to an existing plant. Returns the plant with the added root*

Description

Add a root to an existing plant. Returns the plant with the added root

Usage

```
addRootToPlant(pl, ro)
```

Arguments

pl   the plant to add the root to

ro   the root object to add to the plant.

Value

the new plant, with the added root

Author(s)

Guillaume Lobet - guillaume.lobet(at)ulg.ac.be

Examples

```
data(lupin)
r <- root()
lupin <- addRootToPlant(lupin, r)
```

---

anagallis | *Root system of a anagallis plant in 3D*

Description

Root system of a anagallis plant in 3D

Usage

```
data(anagallis)
```

---

coords   *Get the coordinates of the root nodes*

Description

Get the coordinates of the root nodes

Usage

```
coords(obj)
```

Arguments

obj   of class root

Value

a dataframe containing the node coordinates (x, y, z)

Author(s)

Guillaume Lobet - guillaume.lobet(at)ulg.ac.be

---

getInsertionAngle   *Compute the insertion angle of the root on its parent*

Description

Compute the insertion angle of the root on its parent

Usage

```
getInsertionAngle(parent, current)
```

Arguments

parent   = the parent root

current   = the current root

Value

the insertion angle, in degree

Examples

```
data(lupin)
r <- lupin$roots[[1]]
r1 <- r$children[[1]]
getInsertionAngle(r, r1)
```

---

getInsertionPosition   *Compute the insertion of the root on its parent*

Description

Compute the insertion of the root on its parent

Usage

```
getInsertionPosition(parent, current)
```

Arguments

parent	= the parent root
current	= the current root

Value

the insertion position

Examples

```
data(lupin)
r <- lupin$roots[[1]]
r1 <- r$children[[1]]
getInsertionPosition(r, r1)
```

---

latLength   *Compute the length of the lateral root based on the coordinates of its nodes*

Description

Compute the length of the lateral root based on the coordinates of its nodes

Usage

```
latLength(obj)
```

Arguments

obj   of class plant

Value

the total length of the lateral roots

Examples

```
data(lupin)
latLength(lupin)
```

---

length.plant   *Compute the length of the root based on the coordinates of its nodes*

Description

Compute the length of the root based on the coordinates of its nodes

Usage

```
## S3 method for class 'plant'
length(x)
```

Arguments

x   object of class plant

Value

the total length of the plant roots

Examples

```
data(lupin)
length(lupin)
```

---

length.root   *Compute the length of the root based on the coordinatres of its nodes*

Description

Compute the length of the root based on the coordinatres of its nodes

Usage

```
## S3 method for class 'root'
length(x)
```

Arguments

x   object of class root

Value

the length of the root

Author(s)

Guillaume Lobet - guillaume.lobet(at)ulg.ac.be

Examples

```
data(lupin)
r <- lupin$roots[[1]]
length(r)
```

---

lupin   *Root system of a lupin plant in 2D*

Description

Root system of a lupin plant in 2D

Usage

```
data(lupin)
```

---

maize   *Root system of a maize plant in 3D*

Description

Root system of a maize plant in 3D

Usage

```
data(maize)
```

---

meanInsertionAngle   *Compute the mean insertion angle of the children (lateral) roots*

Description

Compute the mean insertion angle of the children (lateral) roots

Usage

```
meanInsertionAngle(obj)
```

Arguments

obj   of class root

Value

the mean lateral angle

Author(s)

Guillaume Lobet - guillaume.lobet(at)ulg.ac.be

Examples

```
data(lupin)
r <- lupin$roots[[1]]
meanInsertionAngle(r)
```

---

meanInsertionAnglePlant

Compute the mean insertion angle of all the laterals in the plant

---

Description

Compute the mean insertion angle of all the laterals in the plant

Usage

```
meanInsertionAnglePlant(obj)
```

Arguments

obj   of class plant

Value

the mean insertion angle of the root system

Author(s)

Guillaume Lobet - guillaume.lobet(at)ulg.ac.be

Examples

```
data(lupin)
meanInsertionAnglePlant(lupin)
```

---

meanInterbranch   *Compute the mean interbranch distance of the children (lateral) roots*

Description

Compute the mean interbranch distance of the children (lateral) roots

Usage

```
meanInterbranch(obj, allroot = F)
```

Arguments

obj   of class root

allroot   if true, compute the interbanch distance on the whole root

Value

the mean interbranch distance

Author(s)

Guillaume Lobet - guillaume.lobet(at)ulg.ac.be

Examples

```
data(lupin)
r <- lupin$roots[[1]]
meanInterbranch(r)
```

---

meanInterbranchPlant	*Compute the mean interbranch distance of all the primary roots in the image*

Description

Compute the mean interbranch distance of all the primary roots in the image

Usage

```
meanInterbranchPlant(obj, allroot = F)
```

Arguments

obj	of class plant
allroot	if true, compute the interbanch distance on the whole root

Value

the mean interbranch distance of the root system

Author(s)

Guillaume Lobet - guillaume.lobet(at)ulg.ac.be

Examples

```
data(lupin)
meanInterbranchPlant(lupin)
```

---

nChild   *Get the number of children in a root*

Description

Get the number of children in a root

Usage

```
nChild(obj)
```

Arguments

obj   of class root

Value

the number of child root in the current root

Author(s)

Guillaume Lobet - guillaume.lobet(at)ulg.ac.be

Examples

```
data(lupin)
r <- lupin$roots[[1]]
nChild(r)
```

---

nLatRoot   *Compute the number of lateral roots in the plant*

Description

Compute the number of lateral roots in the plant

Usage

```
nLatRoot(obj)
```

Arguments

obj   of class plant

Value

the number of lateral root in the plant

Examples

```
data(lupin)
nLatRoot(lupin)
```

---

nNode   *Get the number of nodes in a root*

Description

Get the number of nodes in a root

Usage

```
nNode(obj)
```

Arguments

obj   of class root

Value

the number of nodes in the root

Author(s)

Guillaume Lobet - guillaume.lobet(at)ulg.ac.be

Examples

```
data(lupin)
r <- lupin$roots[[1]]
nNode(r)
```

---

node   *Node constructor*

Description

Node constructor

Usage

```
node(x, y, z = 0, diameter = 0, orientation = 0, bLength = 0)
```

Arguments

x	= x coordinate of the node. Mandatory
y	= y coordinate of the node. Mandatory
z	= z coordinate of the root. Optional
diameter	= diameter of the node. Optional
orientation	= orientation of the node. Optional
bLength	= lenght from the node position in the root from the base of the root. Optional

Value

the node

Author(s)

Guillaume Lobet - guillaume.lobet(at)ulg.ac.be

Examples

```
n <- node(1, 1)
```

---

nPrimRoot   *Compute the number of primary roots in the plant*

Description

Compute the number of primary roots in the plant

Usage

```
nPrimRoot(obj)
```

Arguments

obj	of class plant

Value

the number of primary root in the plant

Author(s)

Guillaume Lobet - guillaume.lobet(at)ulg.ac.be

Examples

```
data(lupin)
nPrimRoot(lupin)
```

---

nRoot   *Compute the total number of roots in the plant*

Description

Compute the total number of roots in the plant

Usage

```
nRoot(obj)
```

Arguments

obj   of class plant

Value

the number of root in the plant

Author(s)

Guillaume Lobet - guillaume.lobet(at)ulg.ac.be

Examples

```
data(lupin)
nRoot(lupin)
```

---

plant   *Plant object, containing a root system, composed of roots*

Description

Plant object, containing a root system, composed of roots

Usage

```
plant(roots = NULL)
```

Arguments

roots   the root object contained in the plant. Can be null and incremented afterward

Value

the plant

Author(s)

Guillaume Lobet - guillaume.lobet(at)ulg.ac.be

Examples

```
pl <- plant()
```

```
plot.plant          Plot the root system
```

Description

Plot the root system

Usage

```
## S3 method for class 'plant'
plot(x, threed = F, ...)
```

Arguments

x	object of class plant
threed	make a 3D plot for the plant
...	plot options

Value

null

Examples

```
# Plot 2D plant
data(lupin)
plot(lupin, threed=FALSE)

# Plot 3D plant
data(anagallis)
plot(anagallis, threed=TRUE)
```

---

primLength *Compute the length of the primary root based on the coordinates of its nodes*

Description

Compute the length of the primary root based on the coordinates of its nodes

Usage

```
primLength(obj)
```

Arguments

obj   of class plant

Value

the total length of the primary roots

Examples

```
data(lupin)
primLength(lupin)
```

---

print.node *Print the node*

Description

Print the node

Usage

```
## S3 method for class 'node'
print(x, ...)
```

Arguments

x   object of class node

...   print options

Author(s)

Guillaume Lobet - guillaume.lobet(at)ulg.ac.be

Examples

```
n <- node(1, 1)
print(n)
```

---

print.plant	*Print the plant*

Description

Print the plant

Usage

```
## S3 method for class 'plant'
print(x, ...)
```

Arguments

x	object of class node
...	print options

Author(s)

Guillaume Lobet - guillaume.lobet(at)ulg.ac.be

Examples

```
data(lupin)
print(lupin)
```

---

root	*Root constructor*

Description

Root constructor

Usage

```
root(nodes = NULL, parent = "", children = NULL, id = "",
  insertion = NULL, insertion_angle = NULL)
```

Arguments

`nodes`	= the nodes composing the root. Can be null
`parent`	= the identifier of the root parent. Can be null
`children`	= vector of children roots (root objects)
`id`	= root unique identifier
`insertion`	= insertion position of the root on its parent. Can be null is no parent
`insertion_angle`	
	= insertion angle of the root on its parent. Can be null is no parent

Value

the root

Author(s)

Guillaume Lobet - guillaume.lobet(at)ulg.ac.be

Examples

```
r <- root()

n <- node(1, 1)
r <- root(n)
```

---

rsmlToList	*Import a single RSML file into a List. Work only if the roots in the rsml file have properties associated with them.*

Description

Import a single RSML file into a List. Work only if the roots in the rsml file have properties associated with them.

Usage

```
rsmlToList(rsml.path)
```

Arguments

`rsml.path`	The path to the .rsml file. Mandatory.

Examples

```
path <- "http://rootsystemml.github.io/images/examples/arabidopsis-simple.rsml"
pl.list <- rsmlToList(path) # import the file as a list
write.csv(pl.list$processed, "rsml-table.csv") # save it as a csv table
```

rsmlToPlant *Import a single RSML file into a Plant object*

Description

Import a single RSML file into a Plant object

Usage

```
rsmlToPlant(rsml.path, threed = FALSE)
```

Arguments

rsml.path	The path to the .rsml file. Mandatory.
threed	Does the RSML file contains a 3D root system?

Examples

```
# 2D example
path <- "http://rootsystemml.github.io/images/examples/arabidopsis-simple.rsml"
pl <- rsmlToPlant(path) # import the file as a 2D plant
plot(pl) # plot the plant

# 3D example
path <- "http://rootsystemml.github.io/images/examples/anagallis.rsml"
pl <- rsmlToPlant(path, threed=TRUE) # import the file as a 2D plant
plot(pl, threed=TRUE) # plot the plant
```

summary.plant *Summary of the plant*

Description

Summary of the plant

Usage

```
## S3 method for class 'plant'
summary(object, ...)
```

Arguments

object	object of class node
...	summary options

Author(s)

Guillaume Lobet - guillaume.lobet(at)ulg.ac.be

Examples

```
data(lupin)
sum.lup <- summary(lupin)
sum.lup$total.length$value # Get total length
```

---

totalLength	*Compute the length of the root and its children based on the coordinates of its nodes*

Description

Compute the length of the root and its children based on the coordinates of its nodes

Usage

```
totalLength(obj)
```

Arguments

obj   of class root

Value

the total lenght of the root and children

Author(s)

Guillaume Lobet - guillaume.lobet(at)ulg.ac.be

Examples

```
data(lupin)
r <- lupin$roots[[1]]
totalLength(r)
```

---

xrange *Compute the xrange of the root*

Description

Compute the xrange of the root

Usage

```
xrange(obj)
```

Arguments

obj   of class root

Value

c(x1,x2) where x1 and x2 are the x limits of the root

Examples

```
data(lupin)
r <- lupin$roots[[1]]
xrange(r)
```

---

xrangePlant *Compute the xrange of the plant*

Description

Compute the xrange of the plant

Usage

```
xrangePlant(obj)
```

Arguments

obj   of class plant

Value

c(x1,x2) where x1 and x2 are the x limits of the plant

Examples

```
data(lupin)
xrangePlant(lupin)
```

---

yrange *Compute the xrange of the root*

Description

Compute the xrange of the root

Usage

```
yrange(obj)
```

Arguments

obj   of class root

Value

c(y1,y2) where y1 and y2 are the y limits of the root

Examples

```
data(lupin)
r <- lupin$roots[[1]]
yrange(r)
```

---

yrangePlant *Compute the yrange of the plant*

Description

Compute the yrange of the plant

Usage

```
yrangePlant(obj)
```

Arguments

obj   of class plant

Value

c(y1,y2) where y1 and y2 are the y limits of the plant

Examples

```
data(lupin)
yrangePlant(lupin)
```

---

zrange *Compute the xrange of the root*

Description

Compute the xrange of the root

Usage

```
zrange(obj)
```

Arguments

obj   of class root

Value

c(y1,y2) where y1 and y2 are the y limits of the root

Examples

```
data(lupin)
r <- lupin$roots[[1]]
zrange(r)
```

---

zrangePlant *Compute the zrange of the plant*

Description

Compute the zrange of the plant

Usage

```
zrangePlant(obj)
```

Arguments

obj   of class plant

Value

c(z1,z2) where z1 and z2 are the z limits of the plant

Examples

```
data(lupin)
zrangePlant(lupin)
```

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