

# Package ‘RCX’

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**Type** Package

**Title** R package implementing the Cytoscape Exchange (CX) format

**Version** 1.17.0

**Description** Create, handle, validate, visualize and convert networks in the Cytoscape exchange (CX) format to standard data types and objects.  
The package also provides conversion to and from objects of iGraph and graphNEL.  
The CX format is also used by the NDEx platform, a online commons for biological networks, and the network visualization software Cytoscape.

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## Contents

.addAspectNameToJson . . . . .	3
.addAttributeData . . . . .	4
.aspectClass . . . . .	5
.convertRawList . . . . .	6
.createAttributeAspect . . . . .	6
.createCyVpPorD . . . . .	7
.errorCodes . . . . .	8
.filterBy . . . . .	10
.format . . . . .	11
.infer . . . . .	12
.json2RDataType . . . . .	13
.jsonL . . . . .	14
.jsonV . . . . .	15
.log . . . . .	15
.mergeAttributesAspect . . . . .	16
.mergeIdAspect . . . . .	17
.modClass . . . . .	18
.pasteC . . . . .	19
.renameDF . . . . .	20
.stop . . . . .	20
.summaryAspect . . . . .	23
.transformListLength<- . . . . .	23
.transformVLD . . . . .	24
.validateAttributesAspect . . . . .	25
.validateCyVisualPropertyPandD . . . . .	25
aspectClasses . . . . .	26
CartesianLayout . . . . .	27
checks . . . . .	28
convert-data-types-and-values . . . . .	32
Convert-Names-and-Classes . . . . .	32
convert2json . . . . .	34
countElements . . . . .	35
custom-print . . . . .	36
CyGroups . . . . .	37
CyHiddenAttributes . . . . .	39
CyNetworkRelations . . . . .	41
CySubNetworks . . . . .	42
CyTableColumn . . . . .	43
CyVisualProperties . . . . .	45
CyVisualProperty . . . . .	47
CyVisualPropertyDependencies . . . . .	49
CyVisualPropertyMappings . . . . .	51
CyVisualPropertyProperties . . . . .	53
dot_test . . . . .	55
EdgeAttributes . . . . .	58
Edges . . . . .	60
getCyVisualProperty . . . . .	61
graphNEL . . . . .	63
hasIds . . . . .	65
idProperty . . . . .	66

Igraph	67
jsonToRCX	69
markAttributeColumn	71
markRefColumn	72
maxId	72
Meta-data	73
NetworkAttributes	75
NodeAttributes	77
Nodes	79
RCX	80
RCX-object	81
rcxToJson	84
readCX	86
referredBy	88
refersTo	89
setExtension	90
summary	91
toCX	93
updateCartesianLayout	94
updateCyGroups	96
updateCyHiddenAttributes	99
updateCyNetworkRelations	101
updateCySubNetworks	104
updateCyTableColumn	107
updateCyVisualProperties	109
updateCyVisualProperty	113
updateEdgeAttributes	116
updateEdges	119
updateMetaProperties	120
updateNetworkAttributes	121
updateNodeAttributes	124
updateNodes	127
validate	128
visualize	131
writeCX	132
writeHTML	133

**Index** **136**

---

.addAspectNameToJson *Add the aspect name to the JSON*

---

**Description**

Add the aspect name to the JSON

**Usage**

.addAspectNameToJson(json, name)

**Arguments**

<code>json</code>	character; preformatted json
<code>name</code>	character; name of the aspect

**Value**

character; character of json object

**Note**

Internal function only for convenience

**Examples**

```
json = '{bla:"BLA", blubb:"BLUBB"}'
RCX:::addAspectNameToJson(json, "foo")
```

---

<code>.addAttributeData</code>	<i>Add attribute data to an igraph object</i>
--------------------------------	---

---

**Description**

Not only simply add the name-value pairs, but also:

- unlist lists if indicated by `isList` column
- renames `name="name"` to `"attribute$name"`
- puts subnetwork id at the end of the attribute name
- adds a data type as `attribute$dataType` if not string, boolean or double

**Usage**

```
.addAttributeData(ig, attributeRef, attribute)
```

**Arguments**

<code>ig</code>	igraph object
<code>attributeRef</code>	reference name; "node", "edge" or "network"
<code>attribute</code>	an attribute aspect

**Value**

igraph object

**Note**

Internal function only for convenience

**Examples**

NULL

---

<code>.aspectClass</code>	<i>Get the class of aspects</i>
---------------------------	---------------------------------

---

### Description

Get the class of aspects

### Usage

```
.aspectClass(x)
```

### Arguments

`x` a potential aspect

### Value

The aspect class name or NA if it's not an aspect

### Note

Internal function only for convenience

### Examples

```
x = list(a="foo", b="bar")
class(x)
# [1] "list"
## Not run:
.addClass(x) <- .CLS$nodes
class(x)
# [1] "NodesAspect" "list"

.aspectClass(x)
# [1] "NodesAspect"

.removeClass(x) <- "NodesAspect"

.aspectClass(x)
# [1] "NA"

## End(Not run)
```

---

```
.convertRawList            Convert a list of vectors to a character vector with pasted elements
```

---

**Description**

Convert a list of vectors to a character vector with pasted elements

**Usage**

```
.convertRawList(1, keepNa = TRUE)
```

**Arguments**

<code>1</code>	unnamed list
<code>keepNa</code>	logical; whether to keep NA values or replace it with an empty list

**Value**

character

**Note**

Internal function only for convenience

**Examples**

```
l = list(NA,c(2,3), 5)
RCX:::.convertRawList(l)
```

---

```
.createAttributeAspect
                          Create a default *AttributeAspect
```

---

**Description**

Some aspects like *NodeAttributesAspect* or *EdgeAttributesAspect* use a key-value scheme. This function helps in constructing while avoiding repetition.

**Usage**

```
.createAttributeAspect(
  propertyOf,
  name,
  value,
  dataType,
  isList,
  subnetworkId = NULL,
  .log = ""
)
```

**Arguments**

propertyOf	integer; refers to the IDs of an other aspect
name	character; key of the attribute
value	character; value of the attribute
dataType	character (optional);
isList	logical (optional);
subnetworkId	integer (optional); CySubNetworks

**Value**

\*AttributeAspect prototype object

**Note**

Internal function only for convenience

**See Also**

[.mergeIdAspect](#), [.mergeAttributesAspect](#), [CySubNetworks](#)

**Examples**

NULL

---

.createCyVpPorD	<i>Helper to create structure for classes CyVisualPropertyProperties and CyVisualPropertyDependencies</i>
-----------------	---

---

**Description**

Helper to create structure for classes CyVisualPropertyProperties and CyVisualPropertyDependencies

**Usage**

```
.createCyVpPorD(name = NULL, value, .log = "")
```

**Arguments**

name	character, optional; name of the properties
value	character or named character; value of the properties
.log	character (optional); name of the calling function used in logging

**Value**

data.frame

**Note**

Internal function only for convenience

**See Also**

Used in [CyVisualPropertyProperties](#), [CyVisualPropertyDependencies](#) and [CyVisualPropertyMappings](#)

**Examples**

```
## Not run:
data1 = c(NODE_BORDER_STROKE="SOLID", NODE_BORDER_WIDTH="1.5")
.createCyVpPorD(value=data1)

key1 = c("NODE_BORDER_STROKE", "NODE_BORDER_WIDTH")
value1 = c("SOLID", "1.5")
.createCyVpPorD(key1, value1)

# Result for either:
#           name value
# 1 NODE_BORDER_STROKE SOLID
# 2 NODE_BORDER_WIDTH  1.5

## End(Not run)
```

---

.errorCodes

*Error codes used in this package*

---

**Description**

This function returns the error message to a given (internal) error code. For some codes, additional information for the message is needed.

**Usage**

```
.errorCodes(code, info = c("<info[1]>", "<info[2]>"))
```

**Arguments**

code            character; Error code.  
info            character; Additional information used in some error codes.

**Value**

Full text for a given error code.

**Details****List of error codes::**

*ErrorCodeNotFound:*

```
#####
## !!ERROR CODE NOT FOUND!! ##
#####
requested error code:
<info[1]>
```

*e404:*

THIS ERROR SHOULD NEVER HAPPEN!!!

*graphNELEdgesRequired:*  
RCX object requires edges to be converted to an graphNEL object!

*idNonNeg:*  
Provided IDs (<info[1]>) must be non-negative!

*idNotNum:*  
Provided IDs (<info[1]>) must be numeric!

*idRefNotFound:*  
Provided IDs of <info[1]> don't exist in <info[2]>

*idRefNotPresent:*  
<info[1]> not present as <info[2]>

*igraphEdgesRequired:*  
RCX object requires edges to be converted to an igraph object!

*paramAllNull:*  
At least one argument of <info[1]> must be set!

*paramDifferentLength:*  
Arguments must have the same length!  
<info[1]>

*paramListAllWrongClass:*  
Not all elements of the list <info[1]> are of class "<info[2]>!"

*paramMissing:*  
Missing arguments: <info[1]>

*paramMissingRCX:*  
RCX object is missing!

*paramNa:*  
Argument <info[1]> must not contain any NA values!

*paramNonNeg:*  
All elements of <info[1]> must be non-negative!

*paramNotChar:*  
All elements of <info[1]> must be characters!

*paramNotList:*  
Argument <info[1]> must be a list!

*paramNotLog:*  
All elements of <info[1]> must be logical!

*paramNotNamed:*  
Object <info[1]> must have names!

*paramNotNum:*  
All elements of <info[1]> must be numeric!

*paramNotUnique:*  
Elements of <info[1]> must not contain duplicates!

*paramWrongValue:*  
Argument <info[1]> only can take following values: <info[2]>

*validationFail:*

Aspect (<info[1]>) failed validation!  
Check if the aspect is valid: validate(<info[1]>)

*wrongClass:*

Class of object <info[1]> is not "<info[2]>"!

*wrongClassOf:*

Class of object <info[1]> is not one of <info[2]>!

## Note

Internal function only for convenience

---

<code>.filterBy</code>	<i>Filter several parameters for elements, that match to a given name in a given param</i>
------------------------	--

---

## Description

Filter several parameters for elements, that match to a given name in a given param

## Usage

```
.filterBy(name, param, ...)
```

## Arguments

name	character; matching value
param	character; in which param in ...
...	several parameters

## Value

list with only matching elements of all parameters

## Note

Internal function only for convenience

## Examples

```
po=c("match","not","some","other","match")
prop=c(1,2,3,4,5)
dep=c("bla","blubb","bla","blubb","bla")
map=list("BLA","BLUBB","BLA","BLUBB","BLA")

RCX:::filterBy("match", "po", po, prop, dep, map)
```

---

.format *Format objects for error logging*

---

### Description

Format objects for error logging

### Usage

```
.formatQuote(v)
.formatComma(v)
.formatParams(v, con = "and")
.formatData(v)
.formatLog(v, fname = c())
.formatO(v, fname)
```

### Arguments

v	character vector; just some strings
fname	character; function name

### Value

character

### Functions

- .formatQuote(): add quotes to the vector elements: "<v[i]>"
- .formatComma(): add commas between the vector elements: <v[1]>, <v[2]>, <v[3]>
- .formatParams(): format the vector: "<v[1]>", "<v[2]>" and "<v[3]>"
- .formatData(): format the vector: <v[1]>\$<v[2]>\$<v[3]>
- .formatLog(): format the vector: "<v[1]>", "<v[2]>" and "<v[3]>" (in <fname>)
- .formatO(): format a object name with its calling function

### Note

Internal function only for convenience

### Examples

```
## Not run:
v <- c("one", "two", "three")
fname <- "foo"

.formatQuote(v)
```

```

#[1] "\"one\""  "\"two\""  "\"three\""

.formatComma(v)
#[1] "one, two, three"

.formatParams(v)
#[1] "\"one\"", \"two\" and \"three\""

.formatData(v)
#[1] "one$two$three"

.formatLog(v)
#[1] "\"one\"", \"two\" and \"three\""

.formatLog(v, fname)
#[1] "\"one\"", \"two\" and \"three\" (in foo)"

.format0(.formatLog(v), fname)
#[1] "\"\"one\"", \"two\" and \"three\"\"" (foo)"

## End(Not run)

```

---

<code>.infer</code>	<i>Infer the data type from values and check if the value elements are a list</i>
---------------------	---

---

## Description

Each element has an R data type (i.e. class). If more than one element are present in one list element, it is marked as list

## Usage

```

.inferDataType(values)

.inferIsList(values)

```

## Arguments

values                    vector or list of R data values

## Details

`.inferDataType` infers the data type of the elements in the vector or list. `.inferIsList` infers for each element if it is a list. For a vector, the return therefore is FALSE for each element!

## Value

character vector of data types or logical vector of list status

## Functions

- `.inferIsList()`: Infer, if the values are lists

**Note**

Internal function only for convenience

**Examples**

NULL

---

.json2RDataType      *Get the data type and isList from JSON data*

---

**Description**

Get the data type and isList from JSON data

**Usage**

```
.json2RDataType(dataType, default = "string")
```

**Arguments**

dataType	data type column from jsonToRCX => .jsonV
default	default value for NA values (by default the values remain NA)

**Value**

```
list(type=<character vector>, isList=<logical vector>)
```

**Note**

Internal function only for convenience

**Examples**

```
jsonD = c("boolean", "double", "integer", "long", "string",  
          "list_of_boolean", "list_of_double", "list_of_integer",  
          "list_of_long", "list_of_string")  
  
RCX:::json2RDataType(jsonD)
```

---

.jsonL *Return data as a list from a JSON list*

---

### Description

Return data as a list from a JSON list

### Usage

```
.jsonL(  
  data,  
  acc,  
  default = as.character(NA),  
  unList = TRUE,  
  returnAllDefault = TRUE  
)
```

### Arguments

data	json list
acc	accession name
default	default return value
unList	logical; whether to unlist the list elements (e.g. for a list of lists return a list of vectors)
returnAllDefault	whether to return the vector if all values are the default value (or NULL instead)

### Value

list

### Note

Internal function only for convenience

### Examples

```
testData = list(list(n="CDKN1B"),  
               list(n="ROCK1", r="BLA"),  
               list(n="SHC1", r="BLUBB"),  
               list(n="IRS1"))  
RCX:::jsonL(testData, "r")
```

---

.jsonV *Return data as a vector from a JSON list*

---

### Description

Return data as a vector from a JSON list

### Usage

```
.jsonV(data, acc, default = NA, returnAllDefault = TRUE)
```

### Arguments

data	json list
acc	accession name
default	default return value
returnAllDefault	whether to return the vector if all values are the default value (or NULL instead)

### Value

vector

### Note

Internal function only for convenience

### Examples

```
testData = list(list(n="CDKN1B"),
                list(n="ROCK1", r="BLA"),
                list(n="SHC1", r="BLUBB"),
                list(n="IRS1"))
RCX:::jsonV(testData, "r")
```

---

.log *Logging (printing) the results of test cases*

---

### Description

Logging (printing) the results of test cases

### Usage

```
.log(info, pass, sep = "...", spaceLine = FALSE)
```

**Arguments**

info	character; description of the test case.
pass	boolean; was the test passed?
sep	character (default="..."); separates description from result.
spaceLine	boolean (default=FALSE); should a blank line be added after.

**Value**

NULL, only prints the log

**Note**

Internal function only for convenience

**Examples**

```
testPassed <- TRUE
testFailed <- FALSE
## Not run:
.log('testing something', testPassed)
#testing something..OK
.log('testing other stuff', testFailed, spaceLine=TRUE)
#testing other stuff...FAIL
#
.log('testing more', testPassed, " ", TRUE)
#testing more OK

## End(Not run)
```

---

```
.mergeAttributesAspect
```

*Merge two \*AttributeAspects*

---

**Description**

Some aspects like *NodeAttributesAspect* or *EdgeAttributesAspect* use a key-value scheme. This function helps in merging while avoiding repetition.

**Usage**

```
.mergeAttributesAspect(
  firstAspect,
  secondAspect,
  replace = TRUE,
  stopOnDuplications = FALSE,
  required = c("propertyOf", "name"),
  optional = "subnetworkId",
  .log = c()
)
```

**Arguments**

<code>firstAspect</code>	<code>*AttributeAspect</code> object; first aspect.
<code>secondAspect</code>	<code>*AttributeAspect</code> object; second aspect.
<code>replace</code>	logical (default: TRUE); should duplicate keys be replaced with values of the <code>secondAspect</code>
<code>stopOnDuplicates</code>	logical (default: FALSE); whether to stop, if duplicate keys are found
<code>required</code>	character (optional); names of required column names
<code>optional</code>	character (optional); names of optional column names
<code>.log</code>	character (optional); origin of the data used for error logging

**Value**

`*AttributeAspect` object

**Note**

Internal function only for convenience

**See Also**

[.mergeIdAspect](#), [.createAttributeAspect](#)

**Examples**

```
NULL
```

---

<code>.mergeIdAspect</code>	<i>Merge two aspects (data.frames)</i>
-----------------------------	--

---

**Description**

Merges two aspects, that are both `data.frames` and of the same aspect class. If the `idCol` contains duplicates new ids (for `secondAspect`) are created (ids of `firstAspect` are kept), unless it is specified otherwise by `saveOldIds`.

**Usage**

```
.mergeIdAspect(  
  firstAspect,  
  secondAspect,  
  idCol,  
  uniqCols,  
  stopOnDuplicates = FALSE,  
  saveOldIds = TRUE,  
  .log = c()  
)
```

**Arguments**

firstAspect	data.frame; first aspect.
secondAspect	data.frame; second aspect.
idCol	character; name of the column to merge on.
uniqCols	character; name of the column to be checked for uniqueness.
stopOnDuplicates	boolean (default=FALSE); whether to stop, if duplicates in uniqCols column are found.
saveOldIds	boolean (default=TRUE); whether to keep the IDs from secondAspect, if duplicates in uniqCols column are found.
.log	character (optional); name of the calling function used in logging

**Value**

data.frame of the merged aspects.

**Note**

The two aspects must be the same type of aspect (same aspect class)!  
Internal function only for convenience

**See Also**

[.mergeAttributesAspect](#), [.createAttributeAspect](#)

**Examples**

NULL

---

.modClass

*Add or remove a class name from an object*

---

**Description**

Add or remove a class name from an object

**Usage**

```
.addClass(x) <- value
```

```
.removeClass(x) <- value
```

**Arguments**

x	an R object.
value	character vector of length 1.

**Value**

an R object.

**Note**

Internal function only for convenience

**Examples**

```
x = list(a="foo", b="bar")
class(x)
# [1] "list"
## Not run:
.addClass(x) <- "blubb"
class(x)
# [1] "blubb" "list"

.addClass(x) <- "blubb"
class(x)
# [1] "blubb" "list"

.removeClass(x) <- "blubb"
class(x)
# [1] "list"

## End(Not run)
```

---

`.pasteC`*Concatenate as comma separated character vector*

---

**Description**

Concatenate as comma separated character vector

**Usage**

```
.pasteC(x)
```

**Arguments**

x                    character vector.

**Value**

character vector of length 1.

**Note**

Internal function only for convenience

**Examples**

```
## Not run:
a <- c("one", "two", "three")
.pasteC(a)
#[1] "one, two, three"

## End(Not run)
```

`.renameDF`*Rename data.frame columns by key-value pairs in rnames*

---

**Description**

Rename data.frame columns by key-value pairs in rnames

**Usage**

```
.renameDF(df, rnames)
```

**Arguments**

<code>df</code>	data.frame
<code>rnames</code>	named character vector; <code>names(rnames)=colnames(df)</code>

**Value**

df with new colnames; or NULL on error

**Note**

Internal function only for convenience

**Examples**

```
nodes = data.frame(id=c(0,1,2),
                   name=c("CDK1",NA,"CDK3"),
                   represents=c(NA,"bla",NA))
rnames = c(id="@id", name="n", represents="r")
RCX:::renameDF(nodes, rnames)
```

---

`.stop`*Customized stop() function*

---

**Description**

Customized stop() function

**Usage**

```
.stop(code, info = NULL, msg = NULL)
```

**Arguments**

<code>code</code>	character; Error code.
<code>info</code>	character; Additional information used in some error codes.
<code>msg</code>	character;

**Value**

Does not have any return value, simply throws an error!

**Details**

**List of error codes::**

*ErrorCodeNotFound:*

```
#####  
## !!ERROR CODE NOT FOUND!! ##  
#####  
requested error code:  
<info[1]>
```

*e404:*

THIS ERROR SHOULD NEVER HAPPEN!!!

*graphNELEdgesRequired:*

RCX object requires edges to be converted to an graphNEL object!

*idNonNeg:*

Provided IDs (<info[1]>) must be non-negative!

*idNotNum:*

Provided IDs (<info[1]>) must be numeric!

*idRefNotFound:*

Provided IDs of <info[1]> don't exist in <info[2]>

*idRefNotPresent:*

<info[1]> not present as <info[2]>

*igraphEdgesRequired:*

RCX object requires edges to be converted to an igraph object!

*paramAllNull:*

At least one argument of <info[1]> must be set!

*paramDifferentLength:*

Arguments must have the same length!  
<info[1]>

*paramListAllWrongClass:*

Not all elements of the list <info[1]> are of class "<info[2]>"!

*paramMissing:*

Missing arguments: <info[1]>

*paramMissingRCX:*

RCX object is missing!

*paramNa:*

Argument <info[1]> must not contain any NA values!

*paramNonNeg:*

All elements of <info[1]> must be non-negative!

*paramNotChar:*

All elements of <info[1]> must be characters!

*paramNotList:*

Argument <info[1]> must be a list!

*paramNotLog:*

All elements of <info[1]> must be logical!

*paramNotNamed:*

Object <info[1]> must have names!

*paramNotNum:*

All elements of <info[1]> must be numeric!

*paramNotUnique:*

Elements of <info[1]> must not contain duplicates!

*paramWrongValue:*

Argument <info[1]> only can take following values: <info[2]>

*validationFail:*

Aspect (<info[1]>) failed validation!

Check if the aspect is valid: validate(<info[1]>)

*wrongClass:*

Class of object <info[1]> is not "<info[2]>!"

*wrongClassOf:*

Class of object <info[1]> is not one of <info[2]>!

**Note**

Internal function only for convenience

**Examples**

```
## Not run:
.stop("paramMissingRCX")
#Error: .stop
#   RCX object is missing!

.stop("paramNotUnique", "idParamName")
#Error: .stop
#   Provided IDs (idParamName) contain duplicates!

.stop("wrongClass", c("nodesAspect", "NodesAspect"))
#Error: .stop
#   Class of object "nodesAspect" is not "NodesAspect"!

## End(Not run)
```

---

.summaryAspect                    *Helper function to mark columns that are ids or reference ids*

---

**Description**

Helper function to mark columns that are ids or reference ids

**Usage**

```
.summaryAspect(aspect)
```

**Arguments**

aspect                    an aspect (data.frame)

**Value**

the aspect (data.frame)

**Note**

Internal function only for convenience

**Examples**

```
edges = createEdges(source=c(1,1), target=c(2,3))
edges = RCX:::.summaryAspect(edges)
class(edges$id)
```

---

.transformListLength<-  
                                  *Transform an aspect with a list as column*

---

**Description**

Transforms an aspect with a column, that is a list to force a custom format in summary generation. Only show the number of elements in the list elements.

**Usage**

```
.transformListLength(aspect) <- value
```

**Arguments**

aspect                    an aspect (data.frame)  
value                    character; property

**Value**

the aspect (data.frame)

**Note**

Internal function only for convenience

**Examples**

```
df = data.frame(bla=c("a", "b", "c"))
df$blubb=list(c("a", "b", "c"),
             c(1,2),
             c(TRUE, FALSE, FALSE, TRUE, TRUE))

RCX:::transformListLength(df) = "blubb"

summary(df)
```

---

<code>.transformVLD</code>	<i>Transform an aspect with data type</i>
----------------------------	---

---

**Description**

Transforms an aspect with value, dataType and isList columns to force a custom format in summary generation.

**Usage**

```
.transformVLD(aspect)
```

**Arguments**

aspect            an aspect (data.frame)

**Value**

the aspect (data.frame)

**Note**

Internal function only for convenience

**Examples**

```
df = data.frame(bla=c("a", "b", "c"),
               value=list("a", 2, TRUE),
               dataType=c("string", "integer", "boolean"),
               isList=c(FALSE, FALSE, FALSE))
df = RCX:::transformVLD(df)

summary(df)
```

---

.validateAttributesAspect

*Helper for validating node- and edge-attributes aspects*

---

### Description

Helper for validating node- and edge-attributes aspects

### Usage

```
.validateAttributesAspect(aspect, verbose = TRUE)
```

### Arguments

aspect	an RCX aspect
verbose	logical; whether to print the test results.

### Value

logical; whether the test passed

### Note

Internal function only for convenience

---

.validateCyVisualPropertyPandD

*Cytoscape visual property: List of property and dependency*

---

### Description

For both properties the checks are the same.

### Usage

```
.validateCyVisualPropertyPandD(aspect, property, verbose = TRUE)
```

```
.validateListOfCyVisualPropertyPandD(aspect, property, verbose = TRUE)
```

### Arguments

aspect	either <a href="#">CyVisualPropertyProperties</a> or <a href="#">CyVisualPropertyDependencies</a> object
property	character; name of the property
verbose	logical; whether to print the test results.

### Value

logical; whether the object passed all tests.

**Functions**

- `.validateListOfCyVisualPropertyPandD()`: List of property and dependency objects

**Note**

Internal function only for convenience

---

aspectClasses	<i>aspectClasses and subAspectClasses</i>
---------------	---

---

**Description**

To get the aspect classes it is advised to always use the `getAspectClasses()` function to ensure the correct functionality. `aspectClasses` and `subAspectClasses` contain the default [RCX](#) accession name and the classes of the corresponding (sub)aspect. The `getAspectClasses()` function standardizes access to the accession names and classes, and also allows to include installed extensions of the [RCX](#) data model. Only installed and loaded extensions are included in the result: New extensions should register on load using the [setExtension](#) function to be added to `options()$RCX.options$extensions`, and therefore to `getAspectClasses()`.

**Usage**

```

aspectClasses

getAspectClasses(extensions = TRUE)

subAspectClasses

updateAspectClasses(aspectClasses = aspectClasses)

```

**Arguments**

`extensions`      logical; whether to include aspect classes from extensions  
`aspectClasses`    named character; accession names and aspect classes

**Format**

An object of class character of length 14.  
 An object of class character of length 4.

**Details**

`updateAspectClasses` sets the default aspect classes in `options()$RCX.options`, either from `aspectClasses` or manually provided options.

**Value**

named character; accession names and aspect classes

**See Also**

[setExtension](#)

**Examples**

```

## default aspect classes
aspectClasses

## get set aspect classes from options()
aspectClasses = getAspectClasses()

## get aspect classes without extensions
aspectClasses = getAspectClasses(extensions=FALSE)

## set default updateClasses
updateAspectClasses(
  aspectClasses = aspectClasses
)

## default sub aspect classes
subAspectClasses

```

---

CartesianLayout

*Cartesian layout*


---

**Description**

This function creates a cartesian layout aspect, that stores coordinates of nodes.

**Usage**

```
createCartesianLayout(node, x, y, z = NULL, view = NULL)
```

**Arguments**

node	integer; reference to <a href="#">node ids</a>
x	numeric; x coordinate
y	numeric; y coordinate
z	numeric (optional); z coordinate
view	integer (optional); reference to <a href="#">subnetwork id</a> of type view ( <a href="#">CyNetworkRelations</a> )

**Details**

The layout of networks can be influenced by setting the [node](#) position manually. While x and y coordinates are mandatory, the z coordinates are optional and can, for example, be used to define the vertical stacking order of overlapping nodes.

Similar to Cytoscape <https://cytoscape.org/>, it is possible to define different views of the same network. The views itself are defined in [CySubNetworks](#) and [CyNetworkRelations](#), and only referenced by a unique subnetwork id.

**Value**

*CartesianLayoutAspect* object

**See Also**

[updateCartesianLayout](#);

**Examples**

```
## a minimal example
cartesianLayout = createCartesianLayout(
  node=0,
  x=5.5,
  y=200.3
)

## defining several coordinates at once
cartesianLayout = createCartesianLayout(
  node=c(0, 1),
  x=c(5.5, 110.1),
  y=c(200.3, 210.2)
)

## with all parameters
cartesianLayout = createCartesianLayout(
  node=c(0, 1, 0),
  x=c(5.5, 110.1, 7.2),
  y=c(200.3, 210.2, 13.9),
  z=c(-1, 3.1, NA),
  view=c(NA, NA, 1476)
)
```

---

checks

*Checks*

---

**Description**

Different functions to check parameters, ids, elements and lists

**Usage**

```
.paramClass(param, cls)

.checkClass(param, cls, name, cname = c())

.checkAllClass(L, cls, name, cname = c())

.checkClassOneOf(param, class, name, cname = c())

.checkCharacter(param, name, cname = c())

.checkNumeric(param, name, cname = c())

.checkLogical(param, name, cname = c())

.checkList(param, name, cname = c())
```

```
.paramNamed(param)
.checkNamed(param, name, cname = c())
.checkNamedCharacter(param, name, cname = c())
.checkNamedNumeric(param, name, cname = c())
.checkNamedLogical(param, name, cname = c())
.checkNamedList(param, name, cname = c())
.paramNonNeg(param)
.checkNonNeg(param, name, cname = c())
.paramNoNa(param)
.checkNoNa(param, name, cname = c())
.checkIsUniqueId(param, name, cname = c())
.checkIsId(param, name, cname = c())
.paramIsOptionalId(param, name)
.checkSameLength(cname, ...)
.paramAnyNotNull(name, ...)
.checkAnyNotNull(name, cname = c(), ...)
.elementsUnique(A)
.checkUnique(A, name, cname = c())
.elementsUniqueDF(DF, cols)
.checkUniqueDF(DF, cols, cname = c())
.elementsInDict(A, key)
.elementsBContainsAllA(A, B)
.checkBContainsAllA(A, B, name, cname = c())
.checkRefs(A, B, name, cname = c())
.checkRefPresent(A, key, cls, name, cname = c())
.listAllNumeric(L)
```

```
.checkAllNumeric(L, name, cname = c())
.listAllNumericOrInDict(L, key)
.checkAllNumericOrInDict(L, key, name, cname = c())
```

### Arguments

param	some parameter.
cls	character; class name.
name	character; for logging the used name for the parameter.
cname	character; for logging the name of the calling function.
L	list.
class	character vector; list of class names.
...	list of some vectors.
A, B	vectors.
DF	data.frame.
cols	column names.
key	name of the dictionary entry in <code>.DICT</code> .

### Details

The `.check*` functions perform a test and stop with a custom error on fail. All other functions perform a test and return the result.

The used **.DICT**: looks as follows:

- `VPpropertiesOf`: network, nodes, edges, nodes:default, edges:default
- `VPpropertyFields`: properties, dependencies, mappings
- `SN`: all
- `TCappliesTo`: nodes, edges, networks

### Value

logical

### Functions

- `.paramClass()`: checks if the object `param` is of class `cls`.
- `.checkClass()`: checks if the object `param` is of class `cls`.
- `.checkAllClass()`: checks if all elements of the list `L` are of class `cls`.
- `.checkClassOneOf()`: checks if `param` is any class of `class`.
- `.checkCharacter()`: checks if `param` is character.
- `.checkNumeric()`: checks if `param` is numeric.
- `.checkLogical()`: checks if `param` is logical.
- `.checkList()`: checks if `param` is a list.
- `.paramNamed()`: checks if `param` has names.

- `.checkNamed()`: checks if param has names.
- `.checkNamedCharacter()`: checks if param has names and is character.
- `.checkNamedNumeric()`: checks if param has names and is numeric.
- `.checkNamedLogical()`: checks if param has names and is logical.
- `.checkNamedList()`: checks if param has names and is a list.
- `.paramNonNeg()`: checks if param is greater than 0 if not NA.
- `.checkNonNeg()`: checks if param is greater than 0 if not NA.
- `.paramNoNa()`: checks if param is not NA.
- `.checkNoNa()`: checks if param is not NA.
- `.checkIsUniqueId()`: checks if param is an unique id.
- `.checkIsId()`: checks if param is an id.
- `.paramIsOptionalId()`: checks if param is an optional id.
- `.checkSameLength()`: checks if all elements in ... have the same number of elements.
- `.paramAnyNotNull()`: checks if any element in ... is not NULL.
- `.checkAnyNotNull()`: checks if any element in ... is not NULL.
- `.elementsUnique()`: checks if the elements in A are unique.
- `.checkUnique()`: checks if the elements in A are unique.
- `.elementsUniqueDF()`: checks if the elements in the columns cols of DF are unique.
- `.checkUniqueDF()`: checks if the elements in the columns cols of DF are unique.
- `.elementsInDict()`: checks if the elements of A are in `.DICT[[key]]`.
- `.elementsBContainsAllA()`: checks if all elements of A are present in B.
- `.checkBContainsAllA()`: checks if all elements of A are present in B.
- `.checkRefs()`: checks if B contains all elements of A, aka. references.
- `.checkRefPresent()`: checks if a referred aspect of class cls is accessible by key in A.
- `.listAllNumeric()`: checks if all elements of a list L are numeric.
- `.checkAllNumeric()`: checks if all elements of a list L are numeric.
- `.listAllNumericOrInDict()`: checks if all elements of a list L are numeric or in `.DICT[[key]]`.
- `.checkAllNumericOrInDict()`: checks if all elements of a list L are numeric or in `.DICT[[key]]`.

**Note**

Internal function only for convenience

**Examples**

NULL

---

convert-data-types-and-values

*Convert data types in data.frame(dataType, isList) to character of NDEx data types*

---

### Description

Convert data types in data.frame(dataType, isList) to character of NDEx data types

### Usage

```
.convertDataTypes(df, cols = c(dataType = "dataType", isList = "isList"))
.convertValues(df, cols = c(value = "value", isList = "isList"))
```

### Arguments

df	data.frame with dataType and isList: data.frame(dataType, isList)
cols	named character; column names of dataType and isList in df

### Value

character; NDEx data types (e.g. "string" or "list\_of\_integer")

### Note

Internal function only for convenience

### Examples

```
df = data.frame(dataType=c("string", "boolean", "double", "integer", "long",
                          "string", "boolean", "double", "integer", "long"),
               isList=c(FALSE, FALSE, FALSE, FALSE, FALSE,
                        TRUE, TRUE, TRUE, TRUE, TRUE))
df$value = list("string", TRUE, 3.14, 314, 314,
               c("str", "ing"), c(TRUE, FALSE), c(3.14, 1.0), c(314, 666), c(314, 666))
RCX:::.convertDataTypes(df)
RCX:::.convertValues(df)
```

---

Convert-Names-and-Classes

*Convert aspect class name to RCX accession*

---

### Description

The aspects in an RCX object are accessed by a name and return the aspect as an object of c1s. To simplify the conversion between those, these functions return the corresponding name.

**Usage**

```
aspectName2Class(name)
```

```
aspectClass2Name(cls)
```

**Arguments**

name                    character; name of the RCX accession of the Aspect

cls                     character; name of the aspect class

**Details**

The following accessions/classes are available within the standard RCX implementation:

**accession name <=> class name**

```
metaData <=> MetaDataAspect
nodes <=> NodesAspect
edges <=> EdgesAspect
nodeAttributes <=> NodeAttributesAspect
edgeAttributes <=> EdgeAttributesAspect
networkAttributes <=> NetworkAttributesAspect
cartesianLayout <=> CartesianLayoutAspect
cyGroups <=> CyGroupsAspect
cyVisualProperties <=> CyVisualPropertiesAspect
cyHiddenAttributes <=> CyHiddenAttributesAspect
cyNetworkRelations <=> CyNetworkRelationsAspect
cySubNetworks <=> CySubNetworksAspect
cyTableColumn <=> CyTableColumnAspect```
```

**Value**

accession or class name

**Examples**

```
aspectName2Class("nodes")
##[1] "NodesAspect"

aspectClass2Name("NodesAspect")
##[1] "nodes"

aspectClasses

subAspectClasses
```

---

convert2json                      *Convert data to json by R class*

---

### Description

Convert data to json by R class

### Usage

```
.convert2json(x, ...)  
  
## S3 method for class 'character'  
.convert2json(x, ...)  
  
## S3 method for class 'numeric'  
.convert2json(x, ...)  
  
## S3 method for class 'integer'  
.convert2json(x, ...)  
  
## S3 method for class 'logical'  
.convert2json(x, ...)  
  
## S3 method for class 'list'  
.convert2json(x, raw = c(), byElement = FALSE, skipNa = TRUE, ...)  
  
## S3 method for class 'data.frame'  
.convert2json(x, raw = c(), skipNa = TRUE, ...)
```

### Arguments

x	data element
raw	character; names of columns not to format (e.g. because it is already converted)

### Value

character; json

### Note

Internal function only for convenience

### Examples

```
NULL
```

---

countElements	<i>Number of elements in aspect</i>
---------------	-------------------------------------

---

## Description

This function returns the number of elements in an aspect.

## Usage

```
countElements(x)

## Default S3 method:
countElements(x)

## S3 method for class 'RCX'
countElements(x)

## S3 method for class 'CyVisualPropertiesAspect'
countElements(x)

## S3 method for class 'MetaDataAspect'
countElements(x)
```

## Arguments

x                    an object of one of the aspect classes (e.g. [Nodes](#)) or [RCX](#) class.

## Details

Uses method dispatch, so the default methods already returns the correct number for the most aspect classes. This way it is easier to extend the data model.

There are only two exceptions in the core and Cytoscape aspects: [Meta-data](#) and [CyVisualProperties](#).

[Meta-data](#) is a meta-aspect and therefore not included in [Meta-data](#), and so its return is NA.

[CyVisualProperties](#) is the only aspect with a complex data structure beneath. Therefore its number of elements is just the number of how many of the following properties are set: network, nodes, edges, defaultNodes or defaultEdges.

## Value

integer; number of elements. For RCX objects all counts are returned in the vector named by the aspect class.

## See Also

[hasIds\(\)](#), [idProperty\(\)](#), [refersTo\(\)](#), [referredBy\(\)](#), [maxId\(\)](#)

## Examples

```
nodes = createNodes(name = c("CDK1", "CDK2", "CDK3"))
edges = createEdges(source = c(0,0), target = c(1,2))
rcx = createRCX(nodes = nodes, edges = edges)

countElements(nodes)

countElements(rcx)
```

---

custom-print

*Print functions for RCX and aspect classes*

---

## Description

These functions attempt to print [RCX](#) and aspect objects in a more readable form.

## Usage

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

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

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

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

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

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

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

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

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

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

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

```

## S3 method for class 'CyVisualProperty'
print(x, fields = c("all"), ...)

## S3 method for class 'CyVisualPropertiesAspect'
print(x, propertyOf = "all", fields = "all", ...)

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

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

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

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

## S3 method for class 'RCX'
print(x, inofficial = TRUE, ...)

```

### Arguments

x	aspect or <a href="#">RCX</a> object
...	further arguments passed to or from other methods. See <a href="#">base::print()</a>
fields	character; Which fields should be shown, one of properties, dependencies, mappings or all
propertyOf	character; Which properties should be shown, one of network, nodes, edges, nodes:default, edges:default or all
inofficial	logical; if FALSE only the official aspects are printed

### Value

prints the object and returns it invisibly ([invisible](#))

### See Also

[summary](#)

### Examples

```

rcx = createRCX(createNodes())
print(rcx)

```

---

CyGroups

*Cytoscape Groups*

---

### Description

This function is used to create Cytoscape "groups" aspects.

**Usage**

```
createCyGroups(
  id = NULL,
  name,
  nodes = NULL,
  externalEdges = NULL,
  internalEdges = NULL,
  collapsed = NULL
)
```

**Arguments**

id	integer (optional); Cytoscape group ids; reference to <a href="#">node ids</a>
name	character; names of the groups
nodes	list of integers (optional); reference to <a href="#">node ids</a>
externalEdges	list of integers (optional); the external edges making up the group; reference to <a href="#">edge ids</a>
internalEdges	list of integers (optional); the internal edges making up the group; reference to <a href="#">edge ids</a>
collapsed	logical (optional); whether the group is displayed as a single node

**Details**

Cytoscape contributes aspects that organize subnetworks, attribute tables, and visual attributes for use by its own layout and analysis tools. Furthermore are the aspects used in web-based visualizations like within the NDEx platform.

Cytoscape groups allow to group a set of [Nodes](#) and corresponding internal and external [Edges](#) together, and represent a group as a single node in the visualization. A group is defined by its unique id, which must be an (positive) integer, which serves as reference to other aspects. If no ids are provided, they are created automatically. When adding the CyGroups aspect to an [RCX](#) object, its ids **must** be present as [Nodes](#) ids, in the [RCX](#) object, otherwise an error is raised (i.e. a CyGroup is represented as an additional Node in the [Nodes](#) aspect).

**Value**

*CyGroupsAspect* object

**See Also**

[updateCyGroups](#);

**Examples**

```
## a minimal example
cyGroups = createCyGroups(
  name = "Group One",
  nodes = list(c(1,2,3)),
  internalEdges = list(c(0,1))
)

## defining several groups at once
cyGroups = createCyGroups(
```

```

    name = c("Group One", "Group Two"),
    nodes = list(c(1,2,3), 0),
    internalEdges = list(c(0,1),NA)
  )

  ## with all parameters
  cyGroups = createCyGroups(
    id = c(0,1),
    name = c("Group One", "Group Two"),
    nodes = list(c(1,2,3), 0),
    internalEdges = list(c(0,1),NA),
    externalEdges = list(NA,c(1,3)),
    collapsed = c(TRUE,NA)
  )

```

---

CyHiddenAttributes      *Cytoscape hidden attributes*

---

## Description

This function is used to create Cytoscape hidden attributes aspects.

## Usage

```

createCyHiddenAttributes(
  name,
  value,
  dataType = NULL,
  isList = NULL,
  subnetworkId = NULL
)

```

## Arguments

name	character; key of the attribute
value	character or list of character; value of the attribute
dataType	character (optional); data type of the attribute
isList	logical (optional); a value should be considered as list
subnetworkId	integer (optional); refers to the IDs of a subnetwork aspect, but left blank (or NA) if root-network

## Details

Cytoscape contributes aspects that organize subnetworks, attribute tables, and visual attributes for use by its own layout and analysis tools. Furthermore are the aspects used in web-based visualizations like within the NDEx platform.

Besides network attributes, networks may have additional describing attributes originated from and used by Cytoscape. They are also defined in a key-value like manner, with the name of the attribute as key. The same attribute can also be defined for different [subnetworks](#) with different values. The

values itself may differ in their data types, therefore it is necessary to provide the values as a list of the single values instead of a vector.

With *isList* it can be set, if a value should be considered as a list. This is of minor significance while working solely with **RCX** objects, unless it will be transformed to JSON. For some attributes it might be necessary that the values are encoded as lists, even if they contain only one element (or even zero elements). To force an element to be encoded correctly, this parameter can be used, for example: `name="A", value=a, isList=T` will be encoded in JSON as `A=["a"]`.

## Value

*CyHiddenAttributesAspect* object

## See Also

[updateCyHiddenAttributes;](#)

## Examples

```
## a minimal example
hiddenAttributes = createCyHiddenAttributes(
  name="A",
  value="a"
)

## defining several properties at once
hiddenAttributes = createCyHiddenAttributes(
  name=c("A", "B"),
  value=c("a", "b")
)

## with characters and numbers mixed
hiddenAttributes = createCyHiddenAttributes(
  name=c("A", "B"),
  value=list("a", 3.14)
)

## force the number to be characters
hiddenAttributes = createCyHiddenAttributes(
  name=c("A", "B"),
  value=list("a", 3.14),
  dataType=c("character", "character")
)

## with a list as input for one value
hiddenAttributes = createCyHiddenAttributes(
  name=c("A", "B"),
  value=list(c("a1", "a2"),
            "b")
)

## force "B" to be a list as well
hiddenAttributes = createCyHiddenAttributes(
  name=c("A", "B"),
  value=list(c("a1", "a2"),
            "b"),
  isList=c(TRUE, TRUE)
```

```

)

## with a subnetwork
hiddenAttributes = createCyHiddenAttributes(
  name=c("A", "A"),
  value=c("a", "a with subnetwork"),
  subnetworkId=c(NA,1)
)

## with all parameters
hiddenAttributes = createCyHiddenAttributes(
  name=c("A", "A", "B", "B"),
  value=list(c("a1", "a2"),
            "a with subnetwork",
            "b",
            "b with subnetwork"),
  isList=c(TRUE, FALSE, TRUE, FALSE),
  subnetworkId=c(NA, 1, NA, 1)
)

```

---

CyNetworkRelations      *Cytoscape network relations*

---

## Description

This function is used to create Cytoscape network relations aspects.

## Usage

```
createCyNetworkRelations(child, parent = NULL, name = NULL, isView = FALSE)
```

## Arguments

child	integer; reference to <a href="#">subnetwork id</a>
parent	integer (optional); reference to <a href="#">subnetwork id</a> , but left blank (or NA) for root-network
name	character (optional); name of the subnetwork or view
isView	logical (optional); TRUE for views, else the network defines a subnetwork

## Details

Cytoscape contributes aspects that organize subnetworks, attribute tables, and visual attributes for use by its own layout and analysis tools. Furthermore are the aspects used in web-based visualizations like within the NDEx platform.

Cytoscape network relations define the relationship between the main network, subnetworks and views and also a name can be assigned to the relationship. Both, subnetworks and views are defined as [subnetworks](#) aspect, but their type is defined here by the *isView* property. The parent of a subnetwork or view can be an other subnetwork or the root network.

## Value

*CyNetworkRelationsAspect* object

**See Also**

[updateCyNetworkRelations](#);

**Examples**

```
## a minimal example
cyNetworkRelations = createCyNetworkRelations(
  child = 1
)

## with all parameters
cyNetworkRelations = createCyNetworkRelations(
  child = c(1,2),
  parent = c(NA,1),
  name = c("Network A",
           "View A"),
  isView = c(FALSE, TRUE)
)
```

---

CySubNetworks

*Cytoscape subnetworks*

---

**Description**

This function is used to create Cytoscape subnetwork aspects.

**Usage**

```
createCySubNetworks(id, nodes = NULL, edges = NULL)
```

**Arguments**

<code>id</code>	integer; subnetwork IDs
<code>nodes</code>	integer; reference to <a href="#">node id</a> OR character "all" to refer to all nodes
<code>edges</code>	integer; reference to <a href="#">edge id</a> OR character "all" to refer to all edges

**Details**

Cytoscape contributes aspects that organize subnetworks, attribute tables, and visual attributes for use by its own layout and analysis tools. Furthermore are the aspects used in web-based visualizations like within the NDEx platform.

A group is defined by its unique *id*, which must be an (positive) integer, which serves as reference to other aspects. If no IDs are provided, they are created automatically.

Nodes and edges are referred by the IDs of the corresponding aspect. Unlike other aspects referring those IDs, the Cytoscape subnetwork aspect allows to refer to all nodes and edges using the keyword `all`.

The relationship between (sub-)networks and views, and also the type (subnetwork or view) is defined in [CyNetworkRelations](#).

**Value**

*CySubNetworksAspect* object

**See Also**

[updateCySubNetworks;](#)

**Examples**

```
## a minimal example
cySubNetworks = createCySubNetworks(
  nodes = "all",
  edges = "all"
)

## defining several subnetworks at once
cySubNetworks = createCySubNetworks(
  nodes = list("all",
              c(1,2,3)),
  edges = list("all",
              c(0,2))
)

## with all parameters
cySubNetworks = createCySubNetworks(
  id = c(0,1),
  nodes = list("all",
              c(1,2,3)),
  edges = list("all",
              c(0,2))
)
```

---

CyTableColumn

*Cytoscape table column properties*

---

**Description**

This function is used to create Cytoscape table column aspects.

**Usage**

```
createCyTableColumn(
  appliesTo,
  name,
  dataType = NULL,
  isList = NULL,
  subnetworkId = NULL
)
```

**Arguments**

appliesTo	character; indicates whether this applies to "nodes", "edges" or "networks" table columns
name	character; key of the attribute
dataType	character (optional); data type of the attribute
isList	logical (optional); a value should be considered as list
subnetworkId	integer (optional); reference to <a href="#">subnetwork id</a> , but left blank (or NA) if root-network

**Details**

Cytoscape contributes aspects that organize subnetworks, attribute tables, and visual attributes for use by its own layout and analysis tools. Furthermore are the aspects used in web-based visualizations like within the NDEx platform.

These elements are used to represent Cytoscape table column labels and types. Its main use is to disambiguate empty table columns. The same attribute can also be defined for different [subnetworks](#) with different values. Cytoscape does not currently support table columns for the root network, but this is option is included here for consistency.

With *isList* it can be set, if a value should be considered as a list. This is of minor significance while working solely with [RCX](#) objects, unless it will be transformed to JSON.

**Value**

*CyTableColumnAspect* object

**See Also**

[updateCyTableColumn](#); [CyNetworkRelations](#)

**Examples**

```
## a minimal example
tableColumn = createCyTableColumn(
  appliesTo="nodes",
  name="weight"
)

## defining several properties at once
tableColumn = createCyTableColumn(
  appliesTo=c("nodes", "edges"),
  name=c("weight", "weight")
)

## with all parameters
tableColumn = createCyTableColumn(
  appliesTo=c("nodes", "edges", "networks"),
  name=c("weight", "weight", "collapsed"),
  dataType=c("numeric", "numeric", "logical"),
  isList=c(FALSE, FALSE, TRUE),
  subnetworkId=c(NA, NA, 1)
)
```

---

CyVisualProperties      *Cytoscape visual properties (aspect)*

---

## Description

This function is used to create Cytoscape visual properties aspects, that consists of [CyVisualProperty](#) objects for networks, nodes, edges, and default nodes and edges.

## Usage

```
createCyVisualProperties(
  network = NULL,
  nodes = NULL,
  edges = NULL,
  defaultNodes = NULL,
  defaultEdges = NULL
)
```

## Arguments

network	<a href="#">CyVisualProperty</a> object (optional); the visual properties of networks
nodes	<a href="#">CyVisualProperty</a> object (optional); the visual properties of nodes
edges	<a href="#">CyVisualProperty</a> object (optional); the visual properties of edges
defaultNodes	<a href="#">CyVisualProperty</a> object (optional); the default visual properties of nodes
defaultEdges	<a href="#">CyVisualProperty</a> object (optional); the default visual properties of edges

## Details

Cytoscape contributes aspects that organize subnetworks, attribute tables, and visual attributes for use by its own layout and analysis tools. Furthermore are the aspects used in web-based visualizations like within the NDEx platform.

The visual properties aspect is the only aspect ([CyVisualProperties](#)) with a complex structure. It is composed of several sub-property classes and consists of [CyVisualProperty](#) objects, that belong to, or more precisely describe one of the following network elements: *network*, *nodes*, *edges*, *defaultNodes* or *defaultEdges*.

A single visual property (i.e. [CyVisualProperty](#) object) organizes the information as *properties*, *dependencies* and *mappings*, as well as the single values *appliesTo* and *view*, that define the subnetwork or view to which the IDs apply.

Properties are [CyVisualPropertyProperties](#) objects, that hold information like "NODE\_FILL\_COLOR" : "#26CCC9" or "NODE\_LABEL\_TRANSPARENCY" : "255" in a key-value like manner.

Dependencies are [CyVisualPropertyDependencies](#) objects, that hold information about dependencies between visual properties. Currently there are only three dependencies supported:

- Lock Node with and height: nodeSizeLocked = "false"
- Fit Custom Graphics to node: nodeCustomGraphicsSizeSync = "true"
- Edge color to arrows: arrowColorMatchesEdge = "false"



```

## Create a visual properties aspect
## (using the same visual property object for simplicity)
createCyVisualProperties(network=vpProperty1,
                        nodes=vpProperty1,
                        edges=vpProperty1,
                        defaultNodes=vpProperty1,
                        defaultEdges=vpProperty1)

```

---

CyVisualProperty	<i>Cytoscape visual property (object used in CyVisualProperties aspect)</i>
------------------	---

---

## Description

This function is used to create Cytoscape visual property objects, that define networks, nodes, edges, and default nodes and edges in a [CyVisualProperties](#) aspect.

## Usage

```

createCyVisualProperty(
  properties = NULL,
  dependencies = NULL,
  mappings = NULL,
  appliesTo = NULL,
  view = NULL
)

```

## Arguments

<code>properties</code>	a single or a list of <a href="#">CyVisualPropertyProperties</a> object (optional);
<code>dependencies</code>	a single or a list of <a href="#">CyVisualPropertyDependencies</a> object (optional);
<code>mappings</code>	a single or a list of <a href="#">CyVisualPropertyMappings</a> object (optional);
<code>appliesTo</code>	integer (optional); might refer to the IDs of a <a href="#">subnetwork</a> aspect, but CX documentation is unclear
<code>view</code>	integer (optional); might refer to the IDs of a <a href="#">subnetwork</a> aspect that is a view, but CX documentation is unclear

## Details

Cytoscape contributes aspects that organize subnetworks, attribute tables, and visual attributes for use by its own layout and analysis tools. Furthermore are the aspects used in web-based visualizations like within the NDEx platform.

The visual properties aspect is the only aspect ([CyVisualProperties](#)) with a complex structure. It is composed of several sub-property classes and consists of [CyVisualProperty](#) objects, that belong to, or more precisely describe one of the following network elements: *network*, *nodes*, *edges*, *defaultNodes* or *defaultEdges*.

A single visual property (i.e. [CyVisualProperty](#) object) organizes the information as *properties*, *dependencies* and *mappings*, as well as the single values *appliesTo* and *view*, that define the subnetwork or view to which the IDs apply.

Properties are [CyVisualPropertyProperties](#) objects, that hold information like "NODE\_FILL\_COLOR" : "#26CCC9" or "NODE\_LABEL\_TRANSPARENCY" : "255" in a key-value like manner.

Dependencies are [CyVisualPropertyDependencies](#) objects, that hold information about dependencies between visual properties. Currently there are only three dependencies supported:

- Lock Node with and height: nodeSizeLocked = "false"
- Fit Custom Graphics to node: nodeCustomGraphicsSizeSync = "true"
- Edge color to arrows: arrowColorMatchesEdge = "false"

Mappings are [CyVisualPropertyMappings](#) objects, that hold information as a triplet consisting of name, type and definition, like "NODE\_FILL\_COLOR" : "DISCRETE" : "COL=molecule\_type,T=string,K=0=miRNA,V=0" "NODE\_FILL\_COLOR" : "CONTINUOUS" : "COL=gal1RGexp,T=double..." or "NODE\_LABEL" : "PASSTHROUGH" : "COL=COMMON,T=string".

For further information about Cytoscape visual properties see the Styles topic of the official Cytoscape documentation: <http://manual.cytoscape.org/en/stable/Styles.html>

### Structure of Cytoscape Visual Properties:

```
CyVisualProperties
|---network = CyVisualProperty
|---nodes = CyVisualProperty
|---edges = CyVisualProperty
|---defaultNodes = CyVisualProperty
|---defaultEdges = CyVisualProperty

CyVisualProperty
|---properties = CyVisualPropertyProperties
|  |--name
|  |--value
|---dependencies = CyVisualPropertyDependencies
|  |--name
|  |--value
|---mappings = CyVisualPropertyMappings
|  |--name
|  |--type
|  |--definition
|---appliesTo = <reference to subnetwork id>
|---view = <reference to subnetwork id>
```

### Value

[CyVisualProperty](#) object

### See Also

[updateCyVisualProperty](#), [updateCyVisualProperties](#)

### Examples

```
## Prepare used properties
## Visual property: Properties
vpPropertyNamedValue = c(NODE_BORDER_STROKE="SOLID",
                        NODE_BORDER_WIDTH="1.5")
vpPropertyP = createCyVisualPropertyProperties(vpPropertyNamedValue)
```

```

## Visual property: Dependencies
vpDependencyNamedValue = c(nodeSizeLocked="false",
                           arrowColorMatchesEdge="true")
vpPropertyD = createCyVisualPropertyDependencies(vpDependencyNamedValue)

## Visual property: Mappings
vpMappingNamedType = c(NODE_FILL_COLOR="CONTINUOUS",
                       EDGE_TARGET_ARROW_SHAPE="DISCRETE")
vpMappingDefinition = c("COL=gal1RGexp,T=double,...",
                        "COL=directed,T=boolean,K=0=true,V=0=ARROW")
vpPropertyM = createCyVisualPropertyMappings(vpMappingNamedType,
                                             vpMappingDefinition)

## Create visual property object
createCyVisualProperty(properties=vpPropertyP,
                      dependencies=vpPropertyD,
                      mappings=vpPropertyM)

## Create visual property object with different subnetworks
createCyVisualProperty(properties=list(vpPropertyP,
                                     vpPropertyP),
                      dependencies=list(vpPropertyD,
                                       NA),
                      mappings=list(NA,
                                    vpPropertyM),
                      appliesTo = c(NA,
                                    1),
                      view = c(1,
                              NA))

```

---

CyVisualPropertyDependencies

*Create a object for dependency of Cytoscape Visual Properties (object used in CyVisualProperty)*

---

## Description

This function is used to create aspects for mappings in [Cytoscape visual properties](#). Networks, nodes, edges, and default nodes and edges mappings are realized as [CyVisualProperty](#) objects, that each consist of properties ([CyVisualPropertyProperties](#) objects), dependencies (**this here**) and mappings ([CyVisualPropertyMappings](#) objects).

## Usage

```
createCyVisualPropertyDependencies(value, name = NULL)
```

## Arguments

value	character or named character; value of the dependencies
name	character (optional); name of the dependencies

## Details

Cytoscape contributes aspects that organize subnetworks, attribute tables, and visual attributes for use by its own layout and analysis tools. Furthermore are the aspects used in web-based visualizations like within the NDEx platform.

The visual properties aspect is the only aspect ([CyVisualProperties](#)) with a complex structure. It is composed of several sub-property classes and consists of [CyVisualProperty](#) objects, that belong to, or more precisely describe one of the following network elements: *network*, *nodes*, *edges*, *defaultNodes* or *defaultEdges*.

A single visual property (i.e. [CyVisualProperty](#) object) organizes the information as *properties*, *dependencies* and *mappings*, as well as the single values *appliesTo* and *view*, that define the subnetwork or view to which the IDs apply.

Properties are [CyVisualPropertyProperties](#) objects, that hold information like "NODE\_FILL\_COLOR" : "#26CCC9" or "NODE\_LABEL\_TRANSPARENCY" : "255" in a key-value like manner.

Dependencies are [CyVisualPropertyDependencies](#) objects, that hold information about dependencies between visual properties. Currently there are only three dependencies supported:

- Lock Node with and height: `nodeSizeLocked = "false"`
- Fit Custom Graphics to node: `nodeCustomGraphicsSizeSync = "true"`
- Edge color to arrows: `arrowColorMatchesEdge = "false"`

Mappings are [CyVisualPropertyMappings](#) objects, that hold information as a triplet consisting of name, type and definition, like "NODE\_FILL\_COLOR" : "DISCRETE" : "COL=molecule\_type,T=string,K=0=miRNA,V=0" or "NODE\_FILL\_COLOR" : "CONTINUOUS" : "COL=gal1RGexp,T=double... or "NODE\_LABEL" : "PASSTHROUGH" : "COL=COMMON,T=string".

For further information about Cytoscape visual properties see the Styles topic of the official Cytoscape documentation: <http://manual.cytoscape.org/en/stable/Styles.html>

## Value

CyVisualPropertyDependencies object

## Note

If *name* is not provided, the *names(value)* is used instead to infer the names.

## See Also

[updateCyVisualProperty](#), [updateCyVisualProperties](#)

## Examples

```
## Using a named vector
vpDependencyNamedValue = c(nodeSizeLocked="false",
                           arrowColorMatchesEdge="true")
createCyVisualPropertyDependencies(vpDependencyNamedValue)

## Using two separate vectors
vpDependencyName = c("nodeSizeLocked",
                    "arrowColorMatchesEdge")
vpDependencyValue = c("false",
                     "true")
createCyVisualPropertyDependencies(vpDependencyValue,
```

```
vpDependencyName)
```

```
# Result for either:
#           name value
# 1       nodeSizeLocked false
# 2 arrowColorMatchesEdge true
```

---

## CyVisualPropertyMappings

*Create an object for mappings of Cytoscape Visual Properties (object used in CyVisualProperty)*

---

### Description

This function is used to create objects for mappings in [Cytoscape visual properties](#). Networks, nodes, edges, and default nodes and edges mappings are realized as [CyVisualProperty](#) objects, that each consist of properties ([CyVisualPropertyProperties](#) objects), dependencies ([CyVisualPropertyDependencies](#) objects) and mappings (**this here**).

### Usage

```
createCyVisualPropertyMappings(type, definition, name = NULL)
```

### Arguments

type	character or named character; value of the mappings
definition	character; definitions of the mappings
name	character (optional); names of the mappings

### Details

Cytoscape contributes aspects that organize subnetworks, attribute tables, and visual attributes for use by its own layout and analysis tools. Furthermore are the aspects used in web-based visualizations like within the NDEx platform.

The visual properties aspect is the only aspect ([CyVisualProperties](#)) with a complex structure. It is composed of several sub-property classes and consists of [CyVisualProperty](#) objects, that belong to, or more precisely describe one of the following network elements: *network*, *nodes*, *edges*, *defaultNodes* or *defaultEdges*.

A single visual property (i.e. [CyVisualProperty](#) object) organizes the information as *properties*, *dependencies* and *mappings*, as well as the single values *appliesTo* and *view*, that define the subnetwork or view to which the IDs apply.

Properties are [CyVisualPropertyProperties](#) objects, that hold information like "NODE\_FILL\_COLOR" : "#26CCC9" or "NODE\_LABEL\_TRANSPARENCY" : "255" in a key-value like manner.

Dependencies are [CyVisualPropertyDependencies](#) objects, that hold information about dependencies between visual properties. Currently there are only three dependencies supported:

- Lock Node with and height: nodeSizeLocked = "false"
- Fit Custom Graphics to node: nodeCustomGraphicsSizeSync = "true"
- Edge color to arrows: arrowColorMatchesEdge = "false"

Mappings are `CyVisualPropertyMappings` objects, that hold information as a triplet consisting of name, type and definition, like `"NODE_FILL_COLOR" : "DISCRETE" : "COL=molecule_type,T=string,K=0=miRNA,V=0=ARROW"` or `"NODE_FILL_COLOR" : "CONTINUOUS" : "COL=gal1RGexp,T=double..."` or `"NODE_LABEL" : "PASSTHROUGH" : "COL=COMMON,T=string"`.

For further information about Cytoscape visual properties see the Styles topic of the official Cytoscape documentation: <http://manual.cytoscape.org/en/stable/Styles.html>

### Structure of Cytoscape Visual Properties:

```
CyVisualProperties
|---network = CyVisualProperty
|---nodes = CyVisualProperty
|---edges = CyVisualProperty
|---defaultNodes = CyVisualProperty
|---defaultEdges = CyVisualProperty

CyVisualProperty
|---properties = CyVisualPropertyProperties
|   |--name
|   |--value
|---dependencies = CyVisualPropertyDependencies
|   |--name
|   |--value
|---mappings = CyVisualPropertyMappings
|   |--name
|   |--type
|   |--definition
|---appliesTo = <reference to subnetwork id>
|---view = <reference to subnetwork id>
```

### Value

`CyVisualPropertyMappings` object

### Note

If *name* is not provided, the *names(type)* is used instead to infer the names.

### See Also

[updateCyVisualProperty](#), [updateCyVisualProperties](#)

### Examples

```
## Using a named vector
vpMappingNamedType = c(NODE_FILL_COLOR="CONTINUOUS",
                      EDGE_TARGET_ARROW_SHAPE="DISCRETE")
vpMappingDefinition = c("COL=gal1RGexp,T=double,...",
                       "COL=directed,T=boolean,K=0=true,V=0=ARROW")
createCyVisualPropertyMappings(vpMappingNamedType,
                              vpMappingDefinition)

## Using three separate vectors
vpMappingName = c("NODE_FILL_COLOR",
                 "EDGE_TARGET_ARROW_SHAPE")
```

```

vpMappingType = c("CONTINUOUS",
                  "DISCRETE")
createCyVisualPropertyMappings(vpMappingType,
                              vpMappingDefinition,
                              vpMappingName)

# Result for either:
#           name           type           definition
# 1  NODE_FILL_COLOR CONTINUOUS COL=gal1RGexp,T=double,...
# 2 EDGE_TARGET_ARROW_SHAPE DISCRETE COL=directed,T=boolean,K=0=true,V=0=ARROW

```

---

## CyVisualPropertyProperties

*Create a object for properties of Cytoscape Visual Properties (object used in CyVisualProperty)*

---

### Description

This function is used to create aspects for mappings in [Cytoscape visual properties](#). Networks, nodes, edges, and default nodes and edges mappings are realized as [CyVisualProperty](#) objects, that each consist of properties (**this here**), dependencies ([CyVisualPropertyDependencies](#) objects) and mappings ([CyVisualPropertyMappings](#) objects).

### Usage

```
createCyVisualPropertyProperties(value, name = NULL)
```

### Arguments

value	character or named character; value of the property
name	character (optional); name of the property

### Details

Cytoscape contributes aspects that organize subnetworks, attribute tables, and visual attributes for use by its own layout and analysis tools. Furthermore are the aspects used in web-based visualizations like within the NDEx platform.

The visual properties aspect is the only aspect ([CyVisualProperties](#)) with a complex structure. It is composed of several sub-property classes and consists of [CyVisualProperty](#) objects, that belong to, or more precisely describe one of the following network elements: *network*, *nodes*, *edges*, *defaultNodes* or *defaultEdges*.

A single visual property (i.e. [CyVisualProperty](#) object) organizes the information as *properties*, *dependencies* and *mappings*, as well as the single values *appliesTo* and *view*, that define the subnetwork or view to which the IDs apply.

Properties are [CyVisualPropertyProperties](#) objects, that hold information like "NODE\_FILL\_COLOR" : "#26CCC9" or "NODE\_LABEL\_TRANSPARENCY" : "255" in a key-value like manner.

Dependencies are [CyVisualPropertyDependencies](#) objects, that hold information about dependencies between visual properties. Currently there are only three dependencies supported:

- Lock Node with and height: nodeSizeLocked = "false"

- Fit Custom Graphics to node: `nodeCustomGraphicsSizeSync = "true"`
- Edge color to arrows: `arrowColorMatchesEdge = "false"`

Mappings are `CyVisualPropertyMappings` objects, that hold information as a triplet consisting of name, type and definition, like `"NODE_FILL_COLOR" : "DISCRETE" : "COL=molecule_type,T=string,K=0=miRNA,V=0"`, `"NODE_FILL_COLOR" : "CONTINUOUS" : "COL=gal1RGexp,T=double..."` or `"NODE_LABEL" : "PASSTHROUGH" : "COL=COMMON,T=string"`.

For further information about Cytoscape visual properties see the Styles topic of the official Cytoscape documentation: <http://manual.cytoscape.org/en/stable/Styles.html>

### Structure of Cytoscape Visual Properties:

```
CyVisualProperties
|---network = CyVisualProperty
|---nodes = CyVisualProperty
|---edges = CyVisualProperty
|---defaultNodes = CyVisualProperty
|---defaultEdges = CyVisualProperty

CyVisualProperty
|---properties = CyVisualPropertyProperties
|  |--name
|  |--value
|---dependencies = CyVisualPropertyDependencies
|  |--name
|  |--value
|---mappings = CyVisualPropertyMappings
|  |--name
|  |--type
|  |--definition
|---appliesTo = <reference to subnetwork id>
|---view = <reference to subnetwork id>
```

### Value

`CyVisualPropertyProperties` object

### Note

If *name* is not provided, the *names(value)* is used instead to infer the names.

### See Also

[updateCyVisualProperty](#), [updateCyVisualProperties](#)

### Examples

```
## Using a named vector
vpPropertyNamedValue = c(NODE_BORDER_STROKE="SOLID",
                        NODE_BORDER_WIDTH="1.5")
createCyVisualPropertyProperties(vpPropertyNamedValue)

## Using two separate vectors
vpPropertyName = c("NODE_BORDER_STROKE",
```

```

        "NODE_BORDER_WIDTH")
vpPropertyValue = c("SOLID",
                  "1.5")
createCyVisualPropertyProperties(vpPropertyValue,
                               vpPropertyName)

# Result for either:
#           name value
# 1 NODE_BORDER_STROKE SOLID
# 2 NODE_BORDER_WIDTH 1.5

```

---

dot\_test

*Helping tests*


---

## Description

Tests for validating RCX objects and its aspects.

## Usage

```

.test_RequiredColumnsPresent(aspect, columns, verbose = FALSE)
.test_ListRequiredColumnsPresent(aspect, columns, verbose = FALSE)
.test_AllowedColumnsPresent(aspect, columns, verbose = FALSE)
.test_ListAllowedColumnsPresent(aspect, columns, verbose = FALSE)
.test_NoMergeColumn(aspect, column, verbose = FALSE)
.test_AtLeastOneColumnPresent(aspect, columns, verbose = FALSE)
.test_AtLeastOneElementPresent(aspect, element, verbose = FALSE)
.test_OneNodePresent(nodesAspect, column, verbose = FALSE)
.test_IsUnique(aspect, column, verbose = FALSE)
.test_ListAllUnique(aspect, column, verbose = FALSE)
.test_IsUniqueInLists(aspect, column, verbose = FALSE)
.test_ListAllUniqueInLists(aspect, column, verbose = FALSE)
.test_IsLogical(aspect, column, verbose = FALSE)
.test_IsNumeric(aspect, column, verbose = FALSE)
.test_ElementIsNumeric(aspect, element, verbose = FALSE)
.test_IsCharacter(aspect, column, verbose = FALSE)

```

```

.test_ListAllCharacter(aspect, element, verbose = FALSE)
.test_IsList(aspect, column, verbose = FALSE)
.test_ElementIsList(aspect, element, verbose = FALSE)
.test_IsPos(aspect, column, verbose = FALSE)
.test_IsClass(x, cls, verbose = FALSE)
.test_IsNamedList(aspect, names, verbose = FALSE)
.test_IsCVPclass(x, cls, verbose = FALSE)
.test_ListOfCVPclass(x, cls, verbose = FALSE)
.test_ContainsNA(aspect, column, verbose = FALSE)
.test_ListAllContainsNA(aspect, element, verbose = FALSE)
.test_ListAllNumeric(aspect, column, verbose = FALSE)
.test_ListAllNumericOrInDict(aspect, column, dic, verbose = FALSE)
.test_ListAllOfClass(aspect, cls, verbose = FALSE)
.test_AspectExist(rcx, aspect, verbose = FALSE)
.test_IdsInAspect(ids, aspect, column, info = "", verbose = FALSE)
.test_ValuesInSet(aspect, column, set, ignoreNA = TRUE, verbose = FALSE)
.test_DataTypeColumn(aspect, column, verbose = FALSE)

```

### Arguments

aspect	one RCX aspect
columns	character; list of columns
verbose	logical (default=FALSE); also log the results
column	character; column name
cls	character; class name in .CLS or .CLSvp
names	character; names of list
dic	character; key in .DICT
rcx	RCX object
ids	numeric; ids
info	character (default=""); additional message for verbose
ignoreNA	logical (default=TRUE); ignore NA values

### Value

logical; pass or fail the test

## Functions

- `.test_RequiredColumnsPresent()`: checks if aspect has all required columns
- `.test_ListRequiredColumnsPresent()`: checks if all list elements have all required columns
- `.test_AllowedColumnsPresent()`: checks if only allowed columns are set
- `.test_ListAllowedColumnsPresent()`: checks if all list elements have only allowed columns
- `.test_NoMergeColumn()`: checks if column with old ids is not present (would be a merge artefact)
- `.test_AtLeastOneColumnPresent()`: checks if at least one specified column is present
- `.test_AtLeastOneElementPresent()`: checks if at least one specified element is present
- `.test_OneNodePresent()`: checks if at least one element (node) is present in the specified column
- `.test_IsUnique()`: checks if all elements in specified column are unique
- `.test_ListAllUnique()`: checks for all list elements if all elements in specified column are unique
- `.test_IsUniqueInLists()`: checks if all elements in specified column are unique
- `.test_ListAllUniqueInLists()`: checks if all elements in specified column are unique
- `.test_IsLogical()`: checks if the specified column is of type logical
- `.test_IsNumeric()`: checks if the specified column is of type numeric
- `.test_ElementIsNumeric()`: checks if the specified column is of type numeric
- `.test_IsCharacter()`: checks if the specified column is of type character
- `.test_ListAllCharacter()`: checks if the specified list element are all of type character
- `.test_IsList()`: checks if the specified column is of type list
- `.test_ElementIsList()`: checks if the specified column is of type list
- `.test_IsPos()`: checks if the specified column are positive integers
- `.test_IsClass()`: checks if the specified column is of the specified class in `.CLS`
- `.test_IsNamedList()`: checks if the aspect is a list with specified names
- `.test_IsCVPclass()`: checks if the specified column is of the specified class in `.CLSvp`
- `.test_ListOfCVPclass()`: checks if the all elements in the list are of class in `.CLSvp`
- `.test_ContainsNA()`: checks if the specified column contains any NA values
- `.test_ListAllContainsNA()`: checks if the specified list element contains any NA values
- `.test_ListAllNumeric()`: checks if the specified column is a list with only numeric values (NAs and NULLs are not considered)
- `.test_ListAllNumericOrInDict()`: checks if the specified column is a list with only numeric values (NAs and NULLs are not considered) or in `.DICT`
- `.test_ListAllOfClass()`: checks if the specified column is a list with only numeric values (NAs and NULLs are not considered) or in `.DICT`
- `.test_AspectExist()`: checks if the rx object contains the specified aspect
- `.test_IdsInAspect()`: checks if all provided ids are present in the specified column of an aspect
- `.test_ValuesInSet()`: checks if the specified column of an aspect only contains values of the provided set
- `.test_DataTypeColumn()`: checks if the dataType column of an aspect only contains JSON data types.

**Note**

Internal function only for convenience

---

EdgeAttributes	<i>Edge attributes</i>
----------------	------------------------

---

**Description**

This function creates an aspect for additional attributes of edges.

**Usage**

```
createEdgeAttributes(
  propertyOf,
  name,
  value,
  dataType = NULL,
  isList = NULL,
  subnetworkId = NULL
)
```

**Arguments**

propertyOf	integer; reference to <a href="#">edge ids</a>
name	character; key of the attribute
value	character; value of the attribute
dataType	character (optional); data type of the attribute
isList	logical (optional); a value should be considered as list
subnetworkId	integer (optional); reference to <a href="#">subnetwork id</a>

**Details**

Edges may have additional attributes besides a name and a representation. Those additional attributes reference a edge by its id and are defined in a key-value like manner, with the name of the attribute as key. The same attribute can also be defined for different [subnetworks](#) with different values. The values itself may also differ in their data types, therefore it is necessary to provide the values as a list of the single values instead of a vector.

With *isList* it can be set, if a value should be considered as a list. This is of minor significance while working solely with [RCX](#) objects, unless it will be transformed to JSON. For some attributes it might be necessary that the values are encoded as lists, even if they contain only one element (or even zero elements). To force an element to be encoded correctly, this parameter can be used, for example: name="A", value=a, isList=T will be encoded in JSON as A=["a"].

**Value**

*EdgeAttributesAspect* object

**Note**

The *propertyOf* parameter references the edge ids to which the attributes belong to. When adding an EdgeAttributesAspect object to an RCX object, those ids must be present in the Edges aspect, otherwise an error is raised.

**See Also**

[updateEdgeAttributes](#)

**Examples**

```
## a minimal example
edgeAttributes = createEdgeAttributes(
  propertyOf=1,
  name="A",
  value="a"
)

## defining several properties at once
edgeAttributes = createEdgeAttributes(
  propertyOf=c(1,1),
  name=c("A", "B"),
  value=c("a", "b")
)

## with characters and numbers mixed
edgeAttributes = createEdgeAttributes(
  propertyOf=c(1,1),
  name=c("A", "B"),
  value=list("a", 3.14)
)

## force the number to be characters
edgeAttributes = createEdgeAttributes(
  propertyOf=c(1,1),
  name=c("A", "B"),
  value=list("a", 3.14),
  dataType=c("character", "character")
)

## with a list as input for one value
edgeAttributes = createEdgeAttributes(
  propertyOf=c(1,1),
  name=c("A", "B"),
  value=list(c("a1", "a2"),
            "b")
)

## force "B" to be a list as well
edgeAttributes = createEdgeAttributes(
  propertyOf=c(1,1),
  name=c("A", "B"),
  value=list(c("a1", "a2"),
            "b"),
  isList=c(TRUE, TRUE)
)
```

```

## with a subnetwork
edgeAttributes = createEdgeAttributes(
  propertyOf=c(1,1),
  name=c("A", "A"),
  value=c("a", "a with subnetwork"),
  subnetworkId=c(NA,1)
)

## with all parameters
edgeAttributes = createEdgeAttributes(
  propertyOf=c(1,1,1,1),
  name=c("A", "A", "B", "B"),
  value=list(c("a1", "a2"),
            "a with subnetwork",
            "b",
            "b with subnetwork"),
  isList=c(TRUE, FALSE, TRUE, FALSE),
  subnetworkId=c(NA, 1, NA, 1)
)

```

---

Edges

*Edges*


---

## Description

This function creates edges between nodes in networks.

## Usage

```
createEdges(id = NULL, source, target, interaction = NULL)
```

## Arguments

<code>id</code>	integer (optional); edge IDs
<code>source</code>	integer; reference to <a href="#">node id</a>
<code>target</code>	integer; reference to <a href="#">node id</a>
<code>interaction</code>	character (optional); type of interaction, eg. "binds" or "activates"

## Details

Edges are represented by *EdgesAspect* objects. Edges connect two nodes, which means that *source* and *target* must reference the IDs of nodes in a [Nodes](#) object. On creation, the IDs don't matter yet, but at least while adding the *EdgesAspect* object to an [RCX-object](#), the *IDs* must be present in the nodes aspect of the [RCX-object](#).

Similar to nodes, an edge also has a unique *id*, which must be an (positive) integer, which serves as reference to other aspects. If no IDs are provided, those are assigned automatically. Optionally, edges can have an interaction attribute to define the type of interaction between the nodes.

## Value

*EdgesAspect* object

**See Also**

[updateEdges](#) for adding a *EdgesAspect* object to an *EdgesAspect* or *RCX* object

**Examples**

```
## create some simple edges
edges1 = createEdges(source=1, target=2)

## create edges with more information
edges2 = createEdges(id=c(3,2,4),
                     source=c(0,0,1),
                     target=c(1,2,2),
                     interaction=c("activates", "inhibits", NA))
```

---

getCyVisualProperty	<i>Get a Cytoscape visual property (object used in CyVisualProperties aspect) by appliesTo and view</i>
---------------------	---

---

**Description**

This function helps filtering [CyVisualProperty](#) objects by `appliesTo` and `view` attributes (i.e. a unique combination of both). If nothing matches the searched pattern NULL is returned.

**Usage**

```
getCyVisualProperty(cyVisualProperty, appliesTo = NA, view = NA)
```

**Arguments**

<code>cyVisualProperty</code>	<a href="#">CyVisualProperty</a> object
<code>appliesTo</code>	integer (optional); value of <code>appliesTo</code> to filter for
<code>view</code>	integer (optional); value of <code>view</code> to filter for

**Details**

Cytoscape contributes aspects that organize subnetworks, attribute tables, and visual attributes for use by its own layout and analysis tools. Furthermore are the aspects used in web-based visualizations like within the NDEx platform.

The visual properties aspect is the only aspect ([CyVisualProperties](#)) with a complex structure. It is composed of several sub-property classes and consists of [CyVisualProperty](#) objects, that belong to, or more precisely describe one of the following network elements: *network*, *nodes*, *edges*, *defaultNodes* or *defaultEdges*.

A single visual property (i.e. [CyVisualProperty](#) object) organizes the information as *properties*, *dependencies* and *mappings*, as well as the single values *appliesTo* and *view*, that define the subnetwork or view to which the IDs apply.

Properties are [CyVisualPropertyProperties](#) objects, that hold information like "NODE\_FILL\_COLOR" : "#26CCC9" or "NODE\_LABEL\_TRANSPARENCY" : "255" in a key-value like manner.

Dependencies are [CyVisualPropertyDependencies](#) objects, that hold information about dependencies between visual properties. Currently there are only three dependencies supported:

- Lock Node with and height: nodeSizeLocked = "false"
- Fit Custom Graphics to node: nodeCustomGraphicsSizeSync = "true"
- Edge color to arrows: arrowColorMatchesEdge = "false"

Mappings are [CyVisualPropertyMappings](#) objects, that hold information as a triplet consisting of name, type and definition, like "NODE\_FILL\_COLOR" : "DISCRETE" : "COL=molecule\_type,T=string,K=0=miRNA,V=0" or "NODE\_FILL\_COLOR" : "CONTINUOUS" : "COL=gal1RGexp,T=double... or "NODE\_LABEL" : "PASSTHROUGH" : "COL=COMMON,T=string".

For further information about Cytoscape visual properties see the Styles topic of the official Cytoscape documentation: <http://manual.cytoscape.org/en/stable/Styles.html>

### Structure of Cytoscape Visual Properties:

```

CyVisualProperties
|---network = CyVisualProperty
|---nodes = CyVisualProperty
|---edges = CyVisualProperty
|---defaultNodes = CyVisualProperty
|---defaultEdges = CyVisualProperty

CyVisualProperty
|---properties = CyVisualPropertyProperties
|   |--name
|   |--value
|---dependencies = CyVisualPropertyDependencies
|   |--name
|   |--value
|---mappings = CyVisualPropertyMappings
|   |--name
|   |--type
|   |--definition
|---appliesTo = <reference to subnetwork id>
|---view = <reference to subnetwork id>

```

### Value

[CyVisualProperty](#) object containing only one element, or NULL

### See Also

[updateCyVisualProperty](#), [updateCyVisualProperties](#)

### Examples

```

## Visual property: Properties
vpPropertyP1 = createCyVisualPropertyProperties(c(NODE_BORDER_STROKE="SOLID"))

## Visual property: Dependencies
vpPropertyD1 = createCyVisualPropertyDependencies(c(nodeSizeLocked="false"))

## Visual property: Mappings
vpPropertyM1 = createCyVisualPropertyMappings(c(NODE_FILL_COLOR="CONTINUOUS"),
                                              "COL=directed,T=boolean,K=0=true,V=0=ARROW")

```

```

## Create visual property object
vpProperty = createCyVisualProperty(properties=list(vpPropertyP1,
                                                    vpPropertyP1,
                                                    vpPropertyP1),
                                   dependencies=list(vpPropertyD1,
                                                    vpPropertyD1,
                                                    NA),
                                   mappings=list(vpPropertyM1,
                                                NA,
                                                vpPropertyM1),
                                   appliesTo = c(NA,
                                                NA,
                                                1),
                                   view = c(NA,
                                           1,
                                           1))

## Get VP for no subnetwork an no view
getCyVisualProperty(vpProperty)

getCyVisualProperty(vpProperty,
                    appliesTo = 1,
                    view = 1)

```

---

graphNEL

---

*Convert an RCX object from and to an graphNEL object*


---

## Description

Convert an [RCX](#) object to an [graphNEL](#) object

## Usage

```

toGraphNEL(rcx, directed = FALSE)

fromGraphNEL(
  graphNEL,
  nodeId = "id",
  nodeName = "nodeName",
  nodeIgnore = c("name"),
  edgeId = "id",
  edgeInteraction = "edgeInteraction",
  edgeIgnore = c(),
  suppressWarning = FALSE
)

```

## Arguments

rcx	<a href="#">RCX</a> object
directed	logical; whether the graph is directed
graphNEL	<a href="#">graphNEL</a> object
nodeId	character; igraph attribute name used for <a href="#">node</a> ids

nodeName	character; igraph attribute name used for <a href="#">node</a> names
nodeIgnore	character; igraph attribute names that should be ignored
edgeId	character; igraph attribute name used for <a href="#">edge</a> ids
edgeInteraction	character; igraph attribute name used for <a href="#">edge</a> interaction
edgeIgnore	character; igraph attribute names that should be ignored
suppressWarning	logical; whether to suppress a warning message, if the validation of the <a href="#">RCX</a> object fails

## Details

In the [graphNEL](#) object the attributes are not separated from the graph like in [RCX](#). Therefore, for converting an [RCX](#) object to an [graphNEL](#) object, and back, some adjustments in the naming of the attributes have to be made.

For nodes the name can be present in the [nodes](#) aspect, as name in the [nodeAttributes](#) aspect. Also name is used in [graphNEL](#) for naming the vertices. To avoid collisions in the conversion, the [nodes](#) name is saved in [graphNEL](#) as nodeName, while the [nodeAttributes](#) property name is saved as "attribute...name". These names are also used for the conversion back to [RCX](#), but here the name used in the [nodes](#) aspect can be changed by the nodeName parameter.

Similar to the node name, if "represents" is present as property in [nodeAttributes](#) its name is changed to "attribute...represents".

The conversion of [edges](#) works analogously: If "interaction" is present as property in [edgeAttributes](#) its name is changed to "attribute...interaction".

[Nodes](#) and [edges](#) must have IDs in the [RCX](#), but not in the [graphNEL](#) object. To define an [vertex](#) or [edge](#) attribute to be used as ID, the parameters nodeId and edgeId can be used to define either an attribute name (default:"id") or set it to NULL to generate ID automatically.

The attributes also may have a special data type assigned. The data type then is saved by adding "...dataType" to the attribute name.

The [cartesian layout](#) is also stored in the [graphNEL](#) object. To make those [graph vertex attributes](#) distinguishable from [nodeAttributes](#) they are named "cartesianLayout...x", "cartesianLayout...y" and "cartesianLayout...z".

In the [RCX](#) attributes it is also possible to define a [subnetwork](#), to which an attribute applies. Those attributes are added with "...123" added to its name, where "123" is the [subnetwork id](#). The [subnetwork id](#) itself are added as graph graph attributes, and are named subnetwork...123...nodes" and "subnetwork...123...edges", where "123" is the [subnetwork id](#).

Altogether, the conventions look as follows: "[attribute...]<name>[...<subnetwork>][...dataType]"

## Value

[graphNEL](#) or [RCX](#) object

## See Also

[Igraph](#), [igraph::as\\_graphnel\(\)](#)

**Examples**

```

## Read from a CX file
## reading the provided example network of the package
cxFile <- system.file(
  "extdata",
  "Imatinib-Inhibition-of-BCR-ABL-66a902f5-2022-11e9-bb6a-0ac135e8bacf.cx",
  package = "RCX"
)

rcx = readCX(cxFile)

## graphNEL can handle multi-edges, but only if the graph is directed and the
## source and target start and end not between the same nodes.
## Unfortunately this is the case in our sample network.
## A quick fix is simply switching the direction of source and target
## for the multi-edges:
dubEdges = duplicated(rcx$edges[c("source", "target")])

s = rcx$edges$source
rcx$edges$source[dubEdges] = rcx$edges$target[dubEdges]
rcx$edges$target[dubEdges] = s[dubEdges]

## convert the network to graphNEL
gNel = toGraphNEL(rcx, directed = TRUE)

## convert it back
rcxFromGraphNel = fromGraphNEL(gNel)

```

---

hasIds

*IDs of an aspect*


---

**Description**

This function checks, if an aspect has IDs that may be referenced by other aspects.

By default aspects don't have IDs, so only the implemented classes have IDs. Aspects with IDs will be considered in the meta-data aspect to determine properties like: *idCounter* and *elementCount*.

**Usage**

```

hasIds(aspect)

## Default S3 method:
hasIds(aspect)

## S3 method for class 'NodesAspect'
hasIds(aspect)

## S3 method for class 'EdgesAspect'
hasIds(aspect)

## S3 method for class 'CyGroupsAspect'
hasIds(aspect)

```

```
## S3 method for class 'CySubNetworksAspect'
hasIds(aspect)
```

### Arguments

aspect                    an object of one of the aspect classes (e.g. NodesAspect, EdgesAspect, etc.)

### Details

Uses method dispatch, so the default return is *FALSE* and only aspect classes with IDs are implemented. This way it is easier to extend the data model.

### Value

logical

### See Also

[idProperty\(\)](#), [refersTo\(\)](#), [referredBy\(\)](#), [maxId\(\)](#)

### Examples

```
edges = createEdges(source = c(0,0), target = c(1,2))
hasIds(edges)
```

---

idProperty

*Name of the property of an aspect that is an ID*

---

### Description

This function returns the name of the property, if an aspect uses IDs for its elements. As example, the aspect *NodesAspect* has the property *id* that represents the IDs of the aspect.

### Usage

```
idProperty(aspect)

## Default S3 method:
idProperty(aspect)

## S3 method for class 'NodesAspect'
idProperty(aspect)

## S3 method for class 'EdgesAspect'
idProperty(aspect)

## S3 method for class 'CyGroupsAspect'
idProperty(aspect)

## S3 method for class 'CySubNetworksAspect'
idProperty(aspect)
```

## Arguments

aspect                    an object of one of the aspect classes (e.g. NodesAspect, EdgesAspect, etc.)

## Details

By default aspects don't have IDs, so only the implemented classes have IDs. Aspects with IDs will be considered in the meta-data aspect to determine properties like: *idCounter* and *elementCount*.

Uses method dispatch, so the default return is *NULL* and only aspect classes with IDs are implemented. This way it is easier to extend the data model.

## Value

character; Name of the ID property or *NULL*

## See Also

[hasIds\(\)](#), [refersTo\(\)](#), [referredBy\(\)](#), [maxId\(\)](#)

## Examples

```
edges = createEdges(source = c(0,0), target = c(1,2))
idProperty(edges)
```

---

Igraph

*Convert an RCX object from and to an igraph object*

---

## Description

Convert an [RCX](#) object to an [igraph](#) object

## Usage

```
toIgraph(rcx, directed = FALSE)

fromIgraph(
  ig,
  nodeId = "id",
  nodeName = "nodeName",
  nodeIgnore = c("name"),
  edgeId = "id",
  edgeInteraction = "edgeInteraction",
  edgeIgnore = c(),
  suppressWarning = FALSE
)
```

**Arguments**

rcx	RCX object
directed	logical; whether the graph is directed
ig	igraph object
nodeId	character; igraph attribute name used for <b>node</b> ids
nodeName	character; igraph attribute name used for <b>node</b> names
nodeIgnore	character; igraph attribute names that should be ignored
edgeId	character; igraph attribute name used for <b>edge</b> ids
edgeInteraction	character; igraph attribute name used for <b>edge</b> interaction
edgeIgnore	character; igraph attribute names that should be ignored
suppressWarning	logical; whether to suppress a warning message, if the validation of the RCX object fails

**Details**

In the **igraph** object the attributes are not separated from the graph like in **RCX**. Therefore, for converting an **RCX** object to an **igraph** object, and back, some adjustments in the naming of the attributes have to be made.

For nodes the name can be present in the **nodes** aspect, as name in the **nodeAttributes** aspect. Also name is used in **igraph** for naming the vertices. To avoid collisions in the conversion, the **nodes** name is saved in **igraph** as **nodeName**, while the **nodeAttributes** property name is saved as "attribute...name". These names are also used for the conversion back to **RCX**, but here the name used in the **nodes** aspect can be changed by the **nodeName** parameter.

Similar to the node name, if "represents" is present as property in **nodeAttributes** its name is changed to "attribute...represents".

The conversion of **edges** works analogously: If "interaction" is present as property in **edgeAttributes** its name is changed to "attribute...interaction".

**Nodes** and **edges** must have IDs in the **RCX**, but not in the **igraph** object. To define an **vertex** or **edge** attribute to be used as ID, the parameters **nodeId** and **edgeId** can be used to define either an attribute name (default:"id") or set it to NULL to generate ID automatically.

The attributes also may have a special data type assigned. The data type then is saved by adding "...dataType" to the attribute name.

The **cartesian layout** is also stored in the **igraph** object. To make those **igraph vertex attributes** distinguishable from **nodeAttributes** they are named "cartesianLayout...x", "cartesianLayout...y" and "cartesianLayout...z".

In the **RCX** attributes it is also possible to define a **subnetwork**, to which an attribute applies. Those attributes are added with "...123" added to its name, where "123" is the **subnetwork id**. The **subnetwork id** itself are added as **igraph graph attributes**, and are named **subnetwork...123...nodes** and "subnetwork...123...edges", where "123" is the **subnetwork id**.

Altogether, the conventions look as follows: "[attribute...]<name>[...<subnetwork>][...dataType]"

**Value**

**igraph** or **RCX** object

**See Also**[graphNEL](#)**Examples**

```
## Read from a CX file
## reading the provided example network of the package
cxFile <- system.file(
  "extdata",
  "Imatinib-Inhibition-of-BCR-ABL-66a902f5-2022-11e9-bb6a-0ac135e8bacf.cx",
  package = "RCX"
)

rcx = readCX(cxFile)

## convert the network to igraph
ig = toIgraph(rcx)

## convert it back
rcxFromIg = fromIgraph(ig)
```

---

`jsonToRCX`*Convert parsed JSON aspects to RCX*

---

**Description**

Functions to handle parsed JSON for the different aspects.

**Usage**

```
jsonToRCX(jsonData, verbose)

## Default S3 method:
jsonToRCX(jsonData, verbose)

## S3 method for class 'status'
jsonToRCX(jsonData, verbose)

## S3 method for class 'numberVerification'
jsonToRCX(jsonData, verbose)

## S3 method for class 'metaData'
jsonToRCX(jsonData, verbose)

## S3 method for class 'nodes'
jsonToRCX(jsonData, verbose)

## S3 method for class 'edges'
jsonToRCX(jsonData, verbose)

## S3 method for class 'nodeAttributes'
jsonToRCX(jsonData, verbose)
```

```

## S3 method for class 'edgeAttributes'
jsonToRCX(jsonData, verbose)

## S3 method for class 'networkAttributes'
jsonToRCX(jsonData, verbose)

## S3 method for class 'cartesianLayout'
jsonToRCX(jsonData, verbose)

## S3 method for class 'cyGroups'
jsonToRCX(jsonData, verbose)

## S3 method for class 'cyHiddenAttributes'
jsonToRCX(jsonData, verbose)

## S3 method for class 'cyNetworkRelations'
jsonToRCX(jsonData, verbose)

## S3 method for class 'cySubNetworks'
jsonToRCX(jsonData, verbose)

## S3 method for class 'cyTableColumn'
jsonToRCX(jsonData, verbose)

## S3 method for class 'cyVisualProperties'
jsonToRCX(jsonData, verbose)

```

### Arguments

jsonData	nested list from parsed JSON
verbose	logical; whether to print what is happening

### Details

These functions will be used in [processCX](#) to process the JSON data for every aspect. Each aspect is accessible in the CX-JSON by a particular accession name (i.e. its aspect name; see NDEx documentation: <https://home.ndexbio.org/data-model/>). This name is used as class to handle different aspects by method dispatch. This simplifies the extension of RCX for non-standard or self-defined aspects.

The CX-JSON is parsed to R data types using the [jsonlite](#) package as follows:

```
jsonlite::fromJSON(cx, simplifyVector = FALSE)
```

This results in a list of lists (of lists...) to avoid automatic data type conversions, which affect the correctness and usability of the data. Simplified JSON data for example [NodeAttributes](#) would be coerced into a data.frame, therefore the value column loses the format for data types other than string.

The *jsonData* will be a list with only one element named by the aspect: `jsonData$<accessionName>`

To access the parsed data for example nodes, this can be done by `jsonData$nodes`. The single aspects are then created using the corresponding **create** functions and combined to an **RCX** object using the corresponding **update** functions.

**Value**

created aspect or NULL

**See Also**

[rcxToJson](#), [toCX](#), [readCX](#), [writeCX](#)

**Examples**

```
nodesJD = list(nodes=list(list("@id"=6, name="EGFR"),
                           list("@id"=7, name="CDK3")))
class(nodesJD) = c("nodes", class(nodesJD))

jsonToRCX(nodesJD, verbose=TRUE)
```

---

markAttributeColumn     *Mark attribute name columns within a data.frame*

---

**Description**

Assigns a class to a data.frame column to force a custom format in summary generation.

**Usage**

```
.markAttributeColumn(aspect) <- value
```

**Arguments**

aspect	an aspect (data.frame)
value	character; property

**Value**

the aspect (data.frame)

**Note**

Internal function only for convenience

**Examples**

```
df = data.frame(name=c("a", "b", "c"),
                 value=c("a", "b", "c"))
RCX:::markRefColumn(df) = "name"

summary(df)
```

---

markRefColumn	<i>Mark required and optional references within a data.frame</i>
---------------	--

---

**Description**

Assigns a class to a data.frame column to force a custom format in summary generation.

**Usage**

```
.markRefColumn(aspect) <- value
.markReqRefColumn(aspect) <- value
```

**Arguments**

aspect	an aspect (data.frame)
value	character; property

**Value**

the aspect (data.frame)

**Note**

Internal function only for convenience

**Examples**

```
df = data.frame(bla=c("a", "b", "c"),
                blubb=c("a", "b", "c"))
RCX:::markRefColumn(df) = "bla"

summary(df)
```

---

maxId	<i>Highest ID of an aspect</i>
-------	--------------------------------

---

**Description**

This function returns the highest id used in an aspect, that has ids. As example, the aspect *Node-Aspect* has the property *id* that must be a unique positive integer.

**Usage**

```
maxId(x)

## Default S3 method:
maxId(x)

## S3 method for class 'RCX'
maxId(x)
```

## Arguments

x an object of one of the aspect classes (e.g. NodesAspect, EdgesAspect, etc.) or [RCX](#) class.

## Details

Uses method dispatch, so the default return is *NULL* and only aspect classes that have ids are implemented. This way it is easier to extend the data model.

## Value

integer; Highest id. For [RCX](#) objects all highest ids are returned in the vector named by the aspect class.

## See Also

[hasIds\(\)](#), [idProperty\(\)](#), [refersTo\(\)](#), [referredBy\(\)](#), [maxId\(\)](#)

## Examples

```
nodes = createNodes(name = c("CDK1", "CDK2", "CDK3"))
maxId(nodes)
```

---

Meta-data

*Update RCX meta-data*

---

## Description

The meta-data aspect contains meta-data about the aspects in the [RCX](#) object. It can be generated automatically based on the aspects present in a [RCX](#) object:

- for *version* and *consistencyGroup* default values are used
- *idCounter* is inferred with [hasIds](#) and [maxId](#) of an aspect
- *elementCount* is inferred from [countElements](#)
- *properties* is left out by default

## Usage

```
updateMetaData(  
  x,  
  version = NULL,  
  consistencyGroup = NULL,  
  properties = NULL,  
  aspectClasses = getAspectClasses()  
)
```

```
## S3 method for class 'RCX'  
updateMetaData(  
  x,  
  version = NULL,  
  consistencyGroup = NULL,
```

```

    properties = NULL,
    aspectClasses = getAspectClasses()
)

## Default S3 method:
updateMetaData(
  x,
  version = NULL,
  consistencyGroup = NULL,
  properties = NULL,
  aspectClasses = getAspectClasses()
)

```

### Arguments

<code>x</code>	<a href="#">RCX</a> object or an aspect of a RCX; its class must be one of the standard RCX aspect classes
<code>version</code>	named character (optional); version of the aspect (default:"1.0")
<code>consistencyGroup</code>	named numerical (optional); consistency group of the aspect (default:1)
<code>properties</code>	named list (optional); properties that need to be fetched or updated independently of aspect data
<code>aspectClasses</code>	named character; accession names and aspect classes <a href="#">aspectClasses</a>

### Details

If *version*, *consistencyGroup* or *properties* should have a different value, they can be set using a named vector (or named list for *properties*), where the name must be an accession name of that aspect in the [RCX-object](#) (e.g. `nodes` or `cyVisualProperties`).

Besides being a named list by aspect accession name, *properties* must also contain the single key-value pairs as a further named list. To remove all key-value pairs for one aspect, an empty list can be provided instead of a list with key-value pairs. To simplify adding of properties to a single aspect, there is the [updateMetaDataProperties](#) function available.

### Value

MetaDataAspect object or [RCX](#) object

### Note

The meta-data will always be updated automatically, when an aspect is added to or changed in the [RCX](#) object.

### See Also

[updateMetaDataProperties](#)

### Examples

```

## prepare RCX object:
nodes = createNodes(name = c("a", "b", "c", "d", "e", "f"))
edges = createEdges(source=c(1,2,0,0,0,2),
                    target=c(2,3,1,2,5,4))

```

```

rcx = createRCX(nodes, edges)
cySubNetworks = createCySubNetworks(
  id = c(1,2),
  nodes = list("all", c(1,2,3)),
  edges = list("all", c(0,2))
)
rcx = updateCySubNetworks(rcx, cySubNetworks)

## update meta-data manually
rcx = updateMetaData(rcx)

## update meta-data with some values
rcx = updateMetaData(rcx,
  version=c(edges="2.0"),
  consistencyGroup=c(nodes=3),
  properties=list(cySubNetworks=list(some="value",
    another="VALUE"),
    edges=list(some="edge",
    another="EDGE")))

## remove all properties for edges
rcx = updateMetaData(rcx, properties=list(edges=list()))

```

---

NetworkAttributes      *Network attributes*

---

## Description

This function creates an aspect for attributes of a network.

## Usage

```

createNetworkAttributes(
  name,
  value,
  dataType = NULL,
  isList = NULL,
  subnetworkId = NULL
)

```

## Arguments

name	character; key of the attribute
value	character; value of the attribute
dataType	character (optional); data type of the attribute
isList	logical (optional); a value should be considered as list
subnetworkId	integer (optional); reference to <a href="#">subnetwork id</a>

## Details

Networks may have describing attributes, that are defined in a key-value like manner, with the name of the attribute as key. The same attribute can also be defined for different [subnetworks](#) with different values. The values itself may differ in their data types, therefore it is necessary to provide the values as a list of the single values instead of a vector.

With *isList* it can be set, if a value should be considered as a list. This is of minor significance while working solely with [RCX](#) objects, unless it will be transformed to JSON. For some attributes it might be necessary that the values are encoded as lists, even if they contain only one element (or even zero elements). To force an element to be encoded correctly, this parameter can be used, for example: `name="A", value=a, isList=T` will be encoded in JSON as `A=["a"]`.

## Value

NetworkAttributesAspect object

## See Also

[updateNetworkAttributes](#); [NodeAttributes](#), [EdgeAttributes](#)

## Examples

```
## a minimal example
networkAttributes = createNetworkAttributes(
  name="A",
  value="a"
)

## defining several properties at once
networkAttributes = createNetworkAttributes(
  name=c("A", "B"),
  value=c("a", "b")
)

## with characters and numbers mixed
networkAttributes = createNetworkAttributes(
  name=c("A", "B"),
  value=list("a", 3.14)
)

## force the number to be characters
networkAttributes = createNetworkAttributes(
  name=c("A", "B"),
  value=list("a", 3.14),
  dataType=c("character", "character")
)

## with a list as input for one value
networkAttributes = createNetworkAttributes(
  name=c("A", "B"),
  value=list(c("a1", "a2"),
            "b")
)

## force "B" to be a list as well
networkAttributes = createNetworkAttributes(
```

```

    name=c("A", "B"),
    value=list(c("a1", "a2"),
              "b"),
    isList=c(TRUE, TRUE)
  )

## with a subnetwork
networkAttributes = createNetworkAttributes(
  name=c("A", "A"),
  value=c("a", "a with subnetwork"),
  subnetworkId=c(NA, 1)
)

## with all parameters
networkAttributes = createNetworkAttributes(
  name=c("A", "A", "B", "B"),
  value=list(c("a1", "a2"),
            "a with subnetwork",
            "b",
            "b with subnetwork"),
  isList=c(TRUE, FALSE, TRUE, FALSE),
  subnetworkId=c(NA, 1, NA, 1)
)

```

---

NodeAttributes

*Node attributes*


---

## Description

This function creates an aspect for additional attributes of nodes.

## Usage

```

createNodeAttributes(
  propertyOf,
  name,
  value,
  dataType = NULL,
  isList = NULL,
  subnetworkId = NULL
)

```

## Arguments

propertyOf	integer; reference to <a href="#">node ids</a>
name	character; key of the attribute
value	character; value of the attribute
dataType	character (optional); data type of the attribute
isList	logical (optional); a value should be considered as list
subnetworkId	integer (optional); reference to <a href="#">subnetwork id</a>

## Details

Nodes may have additional attributes besides a name and a representation. Those additional attributes reference a node by its id and are defined in a key-value like manner, with the name of the attribute as key. The same attribute can also be defined for different [subnetworks](#) with different values. The values itself may also differ in their data types, therefore it is necessary to provide the values as a list of the single values instead of a vector.

With *isList* it can be set, if a value should be considered as a list. This is of minor significance while working solely with [RCX](#) objects, unless it will be transformed to JSON. For some attributes it might be necessary that the values are encoded as lists, even if they contain only one element (or even zero elements). To force an element to be encoded correctly, this parameter can be used, for example: `name="A", value=a, isList=T` will be encoded in JSON as `A=["a"]`.

## Value

*NodeAttributesAspect* object

## Note

The *propertyOf* parameter references the node ids to which the attributes belong to. When adding an *NodeAttributesAspect* object to an [RCX](#) object, those ids must be present in the [Nodes](#) aspect, otherwise an error is raised.

## See Also

[updateNodeAttributes](#), [EdgeAttributes](#), [NetworkAttributes](#)

## Examples

```
## a minimal example
nodeAttributes = createNodeAttributes(
  propertyOf=1,
  name="A",
  value="a"
)

## defining several properties at once
nodeAttributes = createNodeAttributes(
  propertyOf=c(1,1),
  name=c("A", "B"),
  value=c("a", "b")
)

## with characters and numbers mixed
nodeAttributes = createNodeAttributes(
  propertyOf=c(1,1),
  name=c("A", "B"),
  value=list("a", 3.14)
)

## force the number to be characters
nodeAttributes = createNodeAttributes(
  propertyOf=c(1,1),
  name=c("A", "B"),
  value=list("a", 3.14),
  dataType=c("string", "string")
)
```

```

)

## with a list as input for one value
nodeAttributes = createNodeAttributes(
  propertyOf=c(1,1),
  name=c("A", "B"),
  value=list(c("a1", "a2"),
            "b")
)

## force "B" to be a list as well
nodeAttributes = createNodeAttributes(
  propertyOf=c(1,1),
  name=c("A", "B"),
  value=list(c("a1", "a2"),
            "b"),
  isList=c(TRUE, TRUE)
)

## with a subnetwork
nodeAttributes = createNodeAttributes(
  propertyOf=c(1,1),
  name=c("A", "A"),
  value=c("a", "a with subnetwork"),
  subnetworkId=c(NA, 1)
)

## with all parameters
nodeAttributes = createNodeAttributes(
  propertyOf=c(1,1,1,1,1,1),
  name=c("A", "A", "b", "d", "i", "l"),
  value=list(c("a1", "a2"),
            "a with subnetwork",
            TRUE,
            3.14,
            314,
            314),
  dataType=c("string", "string", "boolean", "double", "integer", "long"),
  isList=c(TRUE, FALSE, FALSE, FALSE, FALSE, FALSE),
  subnetworkId=c(NA, 1, NA, NA, NA, NA)
)

```

---

Nodes

*Nodes*


---

## Description

This function creates nodes for networks.

## Usage

```
createNodes(id = NULL, name = NULL, represents = NULL)
```

**Arguments**

<code>id</code>	integer (optional); node IDs
<code>name</code>	character (optional); names of the nodes
<code>represents</code>	character (optional); representation, e.g. a link to another database

**Details**

Nodes are represented by *NodesAspect* objects. A single node is defined by its unique *id*, which must be an (positive) integer, which serves as reference to other aspects. Optionally, nodes can have a name and a *represents* attribute. If no IDs are provided, but either names or representations (or both) IDs are assigned automatically. To be valid, a nodes aspect must contain at least one node. However, if no parameters are set (i.e. *id*, *name* and *represents* = NULL) there is still one node created with neither name nor representation, just an ID. The *NodesAspect* is the only mandatory aspect for an [RCX-object](#).

**Value**

*NodesAspect* object

**See Also**

[updateNodes](#), [RCX-object](#)

**Examples**

```
## a minimal example
nodes = createNodes()

## ids will be generated
nodes = createNodes(name = c("a", "b", "c"))

## with all parameters
nodes = createNodes(id=c(1, 2, 3),
                    name=c("CDK1", "CDK2", "CDK3"),
                    represents=c("HGNC:CDK1",
                                "Uniprot:P24941",
                                "Ensembl:ENSG00000250506"))
```

**Description**

Create, handle, validate, visualize and convert networks in the Cytoscape exchange (CX) format to standard data types and objects.

**Details**

The CX format is also used by the NDEx platform, a online commons for biological networks, and the network visualization software Cytoscape.

```
browseVignettes("RCy3")
```

**Author(s)**

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**See Also**

Useful links:

- <https://github.com/frankkramer-lab/RCX>
- Report bugs at <https://github.com/frankkramer-lab/RCX/issues>

---

RCX-object

*Create an RCX object from aspects*

---

**Description**

An RCX object consists of several aspects, but at least one node in the [nodes](#) aspect. The network can either be created by creating every single aspect first and then creating the network with all aspects present, or by creating the aspect only with the nodes and adding the remaining aspects one by one.

**Usage**

```
createRCX(  
  nodes,  
  edges,  
  nodeAttributes,  
  edgeAttributes,  
  networkAttributes,  
  cartesianLayout,  
  cyGroups,  
  cyVisualProperties,  
  cyHiddenAttributes,  
  cyNetworkRelations,  
  cySubNetworks,  
  cyTableColumn,  
  checkReferences = TRUE  
)
```

**Arguments**

nodes            [Nodes](#) aspect;  
edges            [Edges](#) aspect (optional);  
nodeAttributes [NodeAttributes](#) aspect (optional);  
edgeAttributes [EdgeAttributes](#) aspect (optional);  
networkAttributes            [NetworkAttributes](#) aspect (optional);  
cartesianLayout            [CartesianLayout](#) aspect (optional);  
cyGroups        [CyGroups](#) aspect (optional);

```

cyVisualProperties      CyVisualProperties aspect (optional);
cyHiddenAttributes     CyHiddenAttributes aspect (optional);
cyNetworkRelations    CyNetworkRelations aspect (optional);
cySubNetworks         CySubNetworks aspect (optional);
cyTableColumn         CyTableColumn aspect (optional);
checkReferences        logical; whether to check if references to other aspects are present in the RCX
                        object

```

### Details

vignette("01. RCX - an R package implementing the Cytoscape Exchange (CX) format", package = "RCX") vignette("02. Creating RCX from scratch", package = "RCX") vignette("Appendix: The RCX and CX Data Model", package = "RCX")

### Value

RCX object

### Examples

```

## minimal example
rcx = createRCX(createNodes())

## create by aspect
nodes = createNodes(name = c("a", "b", "c"))
edges = createEdges(source=c(0,0), target=c(1,2))

nodeAttributes = createNodeAttributes(
  propertyOf=c(1,1),
  name=c("A", "B"),
  value=c("a", "b")
)

edgeAttributes = createEdgeAttributes(
  propertyOf=c(0,0),
  name=c("A", "B"),
  value=c("a", "b")
)

networkAttributes = createNetworkAttributes(
  name=c("A", "B"),
  value=list("a", 3.14)
)

cartesianLayout = createCartesianLayout(
  node=c(0, 1),
  x=c(5.5, 110.1),
  y=c(200.3, 210.2)
)

cyGroups = createCyGroups(

```

```

    name = c("Group One", "Group Two"),
    nodes = list(c(0,1), 0)
)

vpPropertyP = createCyVisualPropertyProperties(c(NODE_BORDER_STROKE="SOLID"))
vpPropertyD = createCyVisualPropertyDependencies(c(nodeSizeLocked="false"))
vpPropertyM = createCyVisualPropertyMappings(c(NODE_FILL_COLOR="CONTINUOUS"),
                                              "COL=directed,T=boolean,K=0=true,V=0=ARROW")
vpProperty = createCyVisualProperty(properties=vpPropertyP,
                                    dependencies=vpPropertyD,
                                    mappings=vpPropertyM)

cyVisualProperties = createCyVisualProperties(nodes=vpProperty)

cyHiddenAttributes = createCyHiddenAttributes(
  name=c("A", "B"),
  value=list(c("a1", "a2"), "b")
)

cyNetworkRelations = createCyNetworkRelations(
  child = c(0,1),
  name = c("Network A", NA)
)

cySubNetworks = createCySubNetworks(
  nodes = list("all", c(0,1,2)),
  edges = list("all", c(0,1))
)

cyTableColumn = createCyTableColumn(
  appliesTo=c("nodes", "edges", "networks"),
  name=c("weight", "weight", "collapsed"),
  dataType=c("double", "double", "boolean")
)

rcx = createRCX(nodes, edges,
               nodeAttributes, edgeAttributes,
               networkAttributes,
               cartesianLayout,
               cyGroups,
               cyVisualProperties,
               cyHiddenAttributes,
               cyNetworkRelations,
               cySubNetworks,
               cyTableColumn)

## create all at once
rcx = createRCX(
  createNodes(name = c("a", "b", "c")),
  createEdges(source=c(0,0), target=c(1,2)),
  createNodeAttributes(
    propertyOf=c(1,1),
    name=c("A", "B"),
    value=c("a", "b")
  ),
  createEdgeAttributes(
    propertyOf=c(0,0),

```

```

    name=c("A", "B"),
    value=c("a","b")
  ),
  networkAttributes = createNetworkAttributes(
    name=c("A","B"),
    value=list("a",3.14)
  ),
  cartesianLayout = createCartesianLayout(
    node=c(0, 1),
    x=c(5.5, 110.1),
    y=c(200.3, 210.2)
  ),
  createCyGroups(
    name = c("Group One", "Group Two"),
    nodes = list(c(0,1), 0)
  ),
  createCyVisualProperties(
    nodes=createCyVisualProperty(
      properties=createCyVisualPropertyProperties(
        c(NODE_BORDER_STROKE="SOLID")
      ),
      dependencies=createCyVisualPropertyDependencies(
        c(nodeSizeLocked="false")
      ),
      mappings=createCyVisualPropertyMappings(
        c(NODE_FILL_COLOR="CONTINUOUS"),
        "COL=directed,T=boolean,K=0=true,V=0=ARROW")
    )
  ),
  createCyHiddenAttributes(
    name=c("A","B"),
    value=list(c("a1","a2"), "b")
  ),
  createCyNetworkRelations(
    child = c(0,1),
    name = c("Network A", NA)
  ),
  createCySubNetworks(
    nodes = list("all", c(0,1,2)),
    edges = list("all", c(0,1))
  ),
  createCyTableColumn(
    appliesTo=c("nodes","edges","networks"),
    name=c("weight","weight","collapsed"),
    dataType=c("double","double","boolean")
  )
)
)

```

**Description**

Functions for converting the different aspects to JSON following the CX data structure definition (see NDEx documentation: <https://home.ndexbio.org/data-model/>).

**Usage**

```
rcxToJson(aspect, verbose = FALSE, ...)  
  
## Default S3 method:  
rcxToJson(aspect, verbose = FALSE, ...)  
  
## S3 method for class 'MetaDataAspect'  
rcxToJson(aspect, verbose = FALSE, ...)  
  
## S3 method for class 'NodesAspect'  
rcxToJson(aspect, verbose = FALSE, ...)  
  
## S3 method for class 'EdgesAspect'  
rcxToJson(aspect, verbose = FALSE, ...)  
  
## S3 method for class 'NodeAttributesAspect'  
rcxToJson(aspect, verbose = FALSE, ...)  
  
## S3 method for class 'EdgeAttributesAspect'  
rcxToJson(aspect, verbose = FALSE, ...)  
  
## S3 method for class 'NetworkAttributesAspect'  
rcxToJson(aspect, verbose = FALSE, ...)  
  
## S3 method for class 'CartesianLayoutAspect'  
rcxToJson(aspect, verbose = FALSE, ...)  
  
## S3 method for class 'CyGroupsAspect'  
rcxToJson(aspect, verbose = FALSE, ...)  
  
## S3 method for class 'CyHiddenAttributesAspect'  
rcxToJson(aspect, verbose = FALSE, ...)  
  
## S3 method for class 'CyNetworkRelationsAspect'  
rcxToJson(aspect, verbose = FALSE, ...)  
  
## S3 method for class 'CySubNetworksAspect'  
rcxToJson(aspect, verbose = FALSE, ...)  
  
## S3 method for class 'CyTableColumnAspect'  
rcxToJson(aspect, verbose = FALSE, ...)  
  
## S3 method for class 'CyVisualPropertiesAspect'  
rcxToJson(aspect, verbose = FALSE, ...)  
  
## S3 method for class 'CyVisualProperty'  
rcxToJson(aspect, verbose = FALSE, propertyOf = "", ...)  
  
## S3 method for class 'CyVisualPropertyProperties'  
rcxToJson(aspect, verbose = FALSE, ...)  
  
## S3 method for class 'CyVisualPropertyDependencies'
```

```
rcxToJson(aspect, verbose = FALSE, ...)

## S3 method for class 'CyVisualPropertyMappings'
rcxToJson(aspect, verbose = FALSE, ...)
```

### Arguments

aspect	aspects of an <a href="#">RCX</a> object
verbose	logical; whether to print what is happening
...	additional parameters, that might needed for extending
propertyOf	character; provide propertyOf (only necessary for <a href="#">CyVisualProperty</a> )

### Details

For converting [RCX](#) objects to JSON, each aspect is processed by a generic function for its aspect class. Those functions return a character only containing the JSON of this aspect, which is then combined by [toCX](#) to be a valid CX data structure.

To support the conversion for non-standard or own-defined aspects, generic functions for those aspect classes have to be implemented.

### Value

character; JSON of an aspect

### See Also

[toCX](#), [writeCX](#), [jsonToRCX](#), [readCX](#)

### Examples

```
nodes = createNodes(name = c("a", "b", "c", "d", "e", "f"))
rcxToJson(nodes)
```

---

readCX	<i>Read CX from file, parse the JSON and convert it to an <a href="#">RCX</a> object</i>
--------	--

---

### Description

The readCX function combines three sub-task:

- read the JSON from file
- parse the JSON
- process the contained aspects to create an [RCX](#) object

### Usage

```
readCX(file, verbose = FALSE, aspectClasses = getAspectClasses())

readJSON(file, verbose = FALSE)

parseJSON(json, verbose = FALSE)

processCX(aspectList, verbose = FALSE, aspectClasses = getAspectClasses())
```

## Arguments

file	character; the name of the file which the data are to be read from
verbose	logical; whether to print what is happening
aspectClasses	named character; accession names and aspect classes <a href="#">aspectClasses</a>
json	character; raw JSON data
aspectList	list; list containing the aspect data (parsed JSON)

## Details

If any errors occur during this process, the single steps can be performed individually. This also allows to skip certain steps, for example if the JSON data is already available as text, there is no need to save it as file and read it again.

### Read the JSON from file:

The readJSON function only read the content of a text file and returns it as a simple character vector.

### Parse the JSON:

The parseJSON function uses the [jsonlite](#) package, to parse JSON text:

```
jsonlite::fromJSON(cx, simplifyVector = FALSE)
```

The result is a list containing the aspect data as elements. If, for some reason, the JSON is not valid, the [jsonlite](#) package raises an error.

### Process the contained aspects to create an RCX object:

With the processCX function, the single elements from the previous list will be processed with the [jsonToRCX](#) functions, which creating objects for the single aspects. The standard CX aspects are processed by generic functions named by the aspect names of the CX data structure, e.g. `jsonToRCX.nodeAttributes` for the samely named CX aspect the corresponding `NodeAttributesAspect` in [RCX](#) (see also vignette("02. The RCX and CX Data Model") or NDEx documentation: <https://home.ndexbio.org/data-model/>).

The CX network may contain additional aspects besides the officially defined ones. This includes self defined or deprecated aspects, that sill can be found in the networks at the NDEx platform. By default, those aspects are simply omitted. In those cases, the setting *verbose* to TRUE is a good idea to see, which aspects cannot be processed this package.

Those not processable aspects can be handled individually, but it is advisable to extend the [jsonToRCX](#) functions by implementing own versions for those aspects. Additionally, the **update** functions have to be implemented to add the newly generated aspect objects to [RCX](#) object (see e.g. [updateNodes](#) or [updateEdges](#)). Therefore, the function also have to be named "update<aspect-name>", where aspect-name is the capitalized version of the name used in the CX. (see also vignette("03. Extending the RCX Data Model"))

## Value

[RCX](#) object

## Functions

- readJSON(): Reads the CX/JSON from file and returns the content as text
- parseJSON(): Parses the JSON text and returns a list with the aspect data
- processCX(): Processes the list of aspect data and creates an [RCX](#)

**See Also**

[jsonToRCX](#), [writeCX](#)

**Examples**

```
cxFile = system.file(
  "extdata",
  "Imatinib-Inhibition-of-BCR-ABL-66a902f5-2022-11e9-bb6a-0ac135e8bacf.cx",
  package = "RCX"
)

rcx = readCX(cxFile)

## OR:

json = readJSON(cxFile)
aspectList = parseJSON(json)
rcx = processCX(aspectList)
```

---

referredBy

*List the aspects that are referred by an other aspect*

---

**Description**

This function returns a list of all aspects with all present aspects, that refer to it. As example, the aspect *NodesAspect* is referred by the property *source* and *target* of the *EdgesAspect* aspect.

**Usage**

```
referredBy(rcx, aspectClasses = getAspectClasses())
```

**Arguments**

`rcx` an object of one of the aspect classes (e.g. *NodesAspect*, *EdgesAspect*, etc.)  
`aspectClasses` named character; accession names and aspect classes [aspectClasses](#)

**Value**

named list; Aspect class names with names of aspect classes, that refer to them.

**Note**

Uses [hasIds\(\)](#) and [refersTo\(\)](#) to determine the referring aspects.

**See Also**

[hasIds\(\)](#), [idProperty\(\)](#), [refersTo\(\)](#), [maxId\(\)](#)

**Examples**

```

nodes = createNodes(name = c("CDK1", "CDK2", "CDK3"))
edges = createEdges(source = c(0,0), target = c(1,2))
rcx = createRCX(nodes = nodes, edges = edges)

referredBy(rcx)

```

---

refersTo

*Name of the property of an aspect that is an ID*


---

**Description**

This function returns the name of the property and the aspect class it refers to. As example, the aspect *EdgesAspect* has the property *source* that refers to the *ids* of the *NodesAspect* aspect.

**Usage**

```

refersTo(aspect)

## Default S3 method:
refersTo(aspect)

## S3 method for class 'EdgesAspect'
refersTo(aspect)

## S3 method for class 'NodeAttributesAspect'
refersTo(aspect)

## S3 method for class 'EdgeAttributesAspect'
refersTo(aspect)

## S3 method for class 'CartesianLayoutAspect'
refersTo(aspect)

## S3 method for class 'CyGroupsAspect'
refersTo(aspect)

## S3 method for class 'CyVisualPropertiesAspect'
refersTo(aspect)

## S3 method for class 'CySubNetworksAspect'
refersTo(aspect)

```

**Arguments**

aspect            an object of one of the aspect classes (e.g. *NodesAspect*, *EdgesAspect*, etc.)

**Details**

Uses method dispatch, so the default return is *NULL* and only aspect classes that refer to other aspects are implemented. This way it is easier to extend the data model.

**Value**

named list; Name of the referring property and aspect class name.

**Methods (by class)**

- `refersTo(default)`: of default returns *NULL*
- `refersTo(EdgesAspect)`: of `EdgesAspect` refers to `id` by *source* and *target*
- `refersTo(NodeAttributesAspect)`: of `NodeAttributesAspect` refers to `id` by *propertyOf* and to `id` by *subnetworkId*
- `refersTo(EdgeAttributesAspect)`: of `EdgeAttributesAspect` refers to `id` by *propertyOf* and to `id` by *subnetworkId*
- `refersTo(CartesianLayoutAspect)`: of `CartesianLayoutAspect` refers to `id` by *node* and to `id` by *view*
- `refersTo(CyGroupsAspect)`: of `CyGroupsAspect` refers to `id` by *nodes* and to `id` by *externalEdges* and *internalEdges*
- `refersTo(CyVisualPropertiesAspect)`: of `CyVisualPropertiesAspect` refers to `id` by *appliesTo* of the sub-aspects
- `refersTo(CySubNetworksAspect)`: of refers to `id` by *nodes* and to `id` by *edges*

**See Also**

[hasIds\(\)](#), [idProperty\(\)](#), [referredBy\(\)](#), [maxId\(\)](#)

**Examples**

```
edges = createEdges(source = c(0,0), target = c(1,2))
refersTo(edges)
```

---

setExtension

*Set or register an RCX extension*

---

**Description**

To simplify the usage of extension of the [RCX](#) data model new extensions can easily registered on load with this function. Registered extension then automatically are used for the conversion of [CX](#) data containing aspects of these extensions. The accession names and classes then are also added to [getAspectClasses](#).

**Usage**

```
setExtension(package, accession, className)
```

**Arguments**

package	character; name of the extension package
accession	character; accession name used in <a href="#">RCX</a> (e.g. <code>rcx\$accessionName</code> )
className	character; class name of the aspect (e.g. <code>is(rcx\$accessionName, "AccessionNameAspect")</code> )

**Value**

```
options()$RCX.options$extensions
```

**See Also**

[aspectClasses](#)

**Examples**

```
setExtension("RCXMyRcxExtension", "myRcxExtension", "MyRcxExtensionAspect")
```

---

summary

*RCX and aspect summary*

---

**Description**

summary is a generic function used to produce result summaries of the [RCX](#) object. The function invokes particular methods which depend on the class of the first argument.

**Usage**

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

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

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

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

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

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

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

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

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

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

```

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

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

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

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

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

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

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

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

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

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

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

```

### Arguments

object	an object; <a href="#">RCX</a> object or aspect (or column of data.frame)
...	additional arguments affecting the summary produced.

### Details

The form of the returned summary depends on the class of its argument, therefore it is possible to summarize [RCX](#) objects and their single aspects.

To enhance readability of the summary, some additional classes have summary functions, that are used to show for example ids of an aspect, required and optional references to ids of aspects, or the number of elements in lists.

### Value

object summary as list

**Methods (by class)**

- `summary(AspectIdColumn)`: Summarize an id property
- `summary(AspectRefColumn)`: Summarize an optional property, that references the ids of an other aspect
- `summary(AspectReqRefColumn)`: Summarize a required property, that references the ids of an other aspect
- `summary(AspectValueColumn)`: Summarize the occurrences of the different elements in the property
- `summary(AspectAttributeColumn)`: Summarize the different attributes in the property
- `summary(AspectListLengthColumn)`: The property is a list of vectors, so summarize the length of the vectors

**Examples**

```
rcx = createRCX(
  nodes = createNodes(name = c("a", "b", "c")),
  edges = createEdges(source=1, target=2)
)

summary(rcx)
```

toCX

*Convert an **RCX** object to CX (JSON)***Description**

This function converts an **RCX** object to JSON in a valid CX data structure (see NDEx documentation: <https://home.ndexbio.org/data-model/>).

**Usage**

```
toCX(rcx, verbose = FALSE, pretty = FALSE)
```

**Arguments**

<code>rcx</code>	<b>RCX</b> object
<code>verbose</code>	logical; whether to print what is happening
<code>pretty</code>	logical; adds indentation whitespace to JSON output. Can be TRUE/FALSE or a number specifying the number of spaces to indent. See <code>jsonlite::prettyfy()</code>

**Details**

The single aspects of the **RCX** object are processed by generic functions of `rcxToJson` for each aspect class. Therefore, not only the single aspects are converted to JSON, but also necessary additional aspects are added, so the resulting CX is accepted by the NDEx platform (<https://ndexbio.org/>):

- `numberVerification` shows the supported maximal number
- `status` is needed at the end to show, that no errors have occurred while creation

If the **RCX** object contains additional aspects besides the officially defined ones, the corresponding `rcxToJson` functions for those aspect classes have to be implemented in order to include them in the resulting CX.

**Value**

CX (JSON) text

**See Also**

[toCX](#), [rcxToJson](#), [readCX](#), [writeCX](#)

**Examples**

```
rcx = createRCX(
  nodes = createNodes(
    name = LETTERS[seq_len(10)]
  ),
  edges = createEdges(
    source=c(1,2),
    target = c(2,3)
  )
)

json = toCX(rcx, pretty=TRUE)
```

---

updateCartesianLayout *Update Cartesian Layouts*

---

**Description**

This functions add a cartesian layout in the form of a [CartesianLayout](#) object to an other [CartesianLayout](#) or an [RCX](#) object.

**Usage**

```
updateCartesianLayout(
  x,
  cartesianLayout,
  replace = TRUE,
  stopOnDuplicates = FALSE,
  ...
)

## S3 method for class 'CartesianLayoutAspect'
updateCartesianLayout(
  x,
  cartesianLayout,
  replace = TRUE,
  stopOnDuplicates = FALSE,
  ...
)

## S3 method for class 'RCX'
updateCartesianLayout(
  x,
  cartesianLayout,
```

```

    replace = TRUE,
    stopOnDuplicates = FALSE,
    checkReferences = TRUE,
    ...
)

```

### Arguments

x	<a href="#">RCX</a> or <a href="#">CartesianLayout</a> object; (to which the new layout will be added)
cartesianLayout	<a href="#">CartesianLayout</a> object; (the layout, that will be added)
replace	logical; if existing values are updated (or ignored)
stopOnDuplicates	logical; whether to stop, if duplicates in nodes (and view if present) column are found
...	additional parameters
checkReferences	logical; whether to check if references to other aspects are present in the <a href="#">RCX</a> object

### Details

Networks, or more precisely its nodes may have a cartesian layout, that is represented as [CartesianLayout](#) object. [CartesianLayout](#) objects can be added to an [RCX](#) or an other [CartesianLayout](#) object.

In the case, that a [CartesianLayout](#) object is added to an other, or the [RCX](#) object already contains a [CartesianLayout](#) object, some attributes might be present in both. By default, the properties are updated with the values of the latest one. This can be prevented by setting the *replace* parameter to FALSE, in that case only new properties are added and the existing properties remain untouched.

Furthermore, if duplicated properties are considered as a preventable mistake, an error can be raised by setting *stopOnDuplicates* to TRUE. This forces the function to stop and raise an error, if duplicated properties are present.

### Value

[CartesianLayoutAspect](#) or [RCX](#) object with added layout

### Examples

```

## For CartesianLayoutAspects:
## prepare some aspects:
cartesianLayout = createCartesianLayout(
  node=c(0, 1),
  x=c(5.5, 110.1),
  y=c(200.3, 210.2),
  z=c(-1, 3.1),
)

## node 0 is updated, new view is added
cartesianLayout2 = createCartesianLayout(
  node=c(0, 0),
  x=c(5.7, 7.2),
  y=c(98, 13.9),
  view=c(NA, 1476)
)

```

```

)

## Simply update with new values
cartesianLayout3 = updateCartesianLayout(cartesianLayout, cartesianLayout2)

## Ignore already present keys
cartesianLayout3 = updateCartesianLayout(cartesianLayout, cartesianLayout2,
                                         replace=FALSE)

## Raise an error if duplicate keys are present
try(updateCartesianLayout(cartesianLayout, cartesianLayout2,
                          stopOnDuplications=TRUE))

## =>ERROR:
## Provided IDs (node, view) contain duplicates!

## For RCX:
## prepare RCX object:
nodes = createNodes(name = c("a","b"))
edges = createEdges(source = 0, target = 1)
cySubNetworks = createCySubNetworks(
  id = 1476,
  nodes = "all",
  edges = "all"
)
rcx = createRCX(nodes,
               edges = edges,
               cySubNetworks=cySubNetworks)

## add the network attributes
rcx = updateCartesianLayout(rcx, cartesianLayout)

## add additional network attributes and update existing
rcx = updateCartesianLayout(rcx, cartesianLayout2)

```

---

updateCyGroups

*Update Cytoscape Groups*


---

## Description

This functions add Cytoscape groups in the form of a [CyGroups](#) object to an [RCX](#) or an other [CyGroups](#) object.

## Usage

```
updateCyGroups(x, cyGroups, stopOnDuplications = FALSE, keepOldIds = TRUE, ...)
```

```
## S3 method for class 'CyGroupsAspect'
```

```
updateCyGroups(x, cyGroups, stopOnDuplications = FALSE, keepOldIds = TRUE, ...)
```

```
## S3 method for class 'RCX'
```

```
updateCyGroups(
  x,
  cyGroups,
  stopOnDuplications = FALSE,
```

```

    keepOldIds = TRUE,
    checkReferences = TRUE,
    ...
)

```

### Arguments

**x** [RCX](#) or [CyGroups](#) object; (to which the new Cytoscape groups will be added)

**cyGroups** [CyGroups](#) object; (the new aspect, that will be added)

**stopOnDuplications** logical; whether to stop, if duplicates in `id` column are found, or re-assign ids instead.

**keepOldIds** logical; if ids are re-assigned, the original ids are kept in the column `oldId`

**...** additional parameters

**checkReferences** logical; whether to check if references to other aspects are present in the [RCX](#) object

### Details

Cytoscape groups allow to group a set of nodes and corresponding internal and external edges together, and represent a group as a single node in the visualization. [CyGroups](#) objects can be added to an [RCX](#) or an other [CyGroups](#) object. The `nodes`, `internalEdges` and `externalEdges` parameters reference the node or edge IDs that belong to a group. When adding an [CyGroups](#) object to an [RCX](#) object, those IDs must be present in the [Nodes](#) or [Edges](#) aspect respectively, otherwise an error is raised.

When two groups should be added to each other some conflicts may rise, since the aspects might use the same IDs. If the aspects do not share any IDs, the two aspects are simply combined. Otherwise, the IDs of the new groups are re-assigned continuing with the next available ID (i.e. `maxId(cyGroupsAspect) + 1` and `maxId(rcx$cyGroups) + 1`, respectively). When adding the [CyGroups](#) aspect to an [RCX](#) object, its ids **must** be present as [Nodes](#) ids, in the [RCX](#) object, otherwise an error is raised (i.e. a [CyGroup](#) is represented as an additional [Node](#) in the [Nodes](#) aspect).

To keep track of the changes, it is possible to keep the old IDs of the newly added nodes in the automatically added column `oldId`. This can be omitted by setting `keepOldIds` to `FALSE`. Otherwise, if a re-assignment of the IDs is not desired, this can be prevented by setting `stopOnDuplications` to `TRUE`. This forces the function to stop and raise an error, if duplicated IDs are present.

### Value

[CyGroups](#) or [RCX](#) object with added Cytoscape groups

### See Also

[CyGroups](#);

### Examples

```

## For CyGroupsAspects:
## prepare some aspects:
cyGroups1 = createCyGroups(
  name = c("Group One", "Group Two"),
  nodes = list(c(1,2,3), 0),

```

```

    internalEdges = list(c(0,1),NA),
    externalEdges = list(NA,c(2,3)),
    collapsed = c(TRUE,NA)
  )

  cyGroups2 = createCyGroups(
    name = "Group Three",
    nodes = list(c(4,5)),
    externalEdges = list(c(4,5))
  )

  ## group ids will be kept
  cyGroups3 = updateCyGroups(cyGroups1, cyGroups2)

  ## old group ids will be omitted
  cyGroups3 = updateCyGroups(cyGroups1, cyGroups2,
                             keepOldIds=FALSE)

  ## Raise an error if duplicate keys are present
  try(updateCyGroups(cyGroups1, cyGroups2,
                    stopOnDuplications=TRUE))

  ## =>ERROR:
  ## Elements of "id" (in updateCyGroups) must not contain duplicates!

  ## For RCX
  ## prepare RCX object:
  nodes = createNodes(name = c("a","b","c","d","e","f"))
  edges = createEdges(source=c(1,2,0,0,0,2),
                      target=c(2,3,1,2,5,4))
  rcx = createRCX(nodes, edges)

  ## add the group
  rcx = updateCyGroups(rcx, cyGroups1)

  ## add an additional group
  rcx = updateCyGroups(rcx, cyGroups2)

  ## create a group with a not existing node...
  cyGroups3 = createCyGroups(
    name = "Group Three",
    nodes = list(9)
  )

  ## ...and try to add them
  try(updateCyGroups(rcx, cyGroups3))
  ## =>ERROR:
  ## Provided IDs of "additionalGroups$nodes" (in updateCyGroups)
  ## don't exist in "rcx$nodes$id"

  ## create a group with a not existing edge...
  cyGroups4 = createCyGroups(
    name = "Group Four",
    nodes = list(c(1,2)),
    internalEdges = list(c(9))
  )

  ## ...and try to add them

```

```
try(updateCyGroups(rcx, cyGroups4))
## =>ERROR:
## Provided IDs of "additionalGroups$internalEdges" (in updateCyGroups)
## don't exist in "rcx$edges$id"
```

---

```
updateCyHiddenAttributes
```

```
Update Cytoscape hidden attributes
```

---

## Description

This functions add hidden attributes in the form of a [CyHiddenAttributes](#) object to an other [CyHiddenAttributes](#) or an [RCX](#) object.

## Usage

```
updateCyHiddenAttributes(
  x,
  hiddenAttributes,
  replace = TRUE,
  stopOnDuplicates = FALSE,
  ...
)

## S3 method for class 'CyHiddenAttributesAspect'
updateCyHiddenAttributes(
  x,
  hiddenAttributes,
  replace = TRUE,
  stopOnDuplicates = FALSE,
  ...
)

## S3 method for class 'RCX'
updateCyHiddenAttributes(
  x,
  hiddenAttributes,
  replace = TRUE,
  stopOnDuplicates = FALSE,
  checkReferences = TRUE,
  ...
)
```

## Arguments

x	<a href="#">RCX</a> or <a href="#">CyHiddenAttributes</a> object; (to which the new hidden attributes will be added)
hiddenAttributes	<a href="#">CyHiddenAttributes</a> object; (the new aspect, that will be added)
replace	logical; if existing values are updated (or ignored)

```

stopOnDuplications
    logical; whether to stop, if duplicates in name (and subnetworkId if present)
    column are found
...
additional parameters
checkReferences
    logical; whether to check if references to other aspects are present in the RCX
    object

```

## Details

Cytoscape subnetworks allow to group a set of nodes and corresponding edges together, and network relations define the relations between those networks. [CyHiddenAttributes](#) objects can be added to an [RCX](#) or an other [CyHiddenAttributes](#) object.

In the case, that a [CyHiddenAttributes](#) object is added to an other, or the [RCX](#) object already contains a [CyHiddenAttributes](#) object, some attributes might be present in both. By default, the attributes are updated with the values of the latest one. This can be prevented by setting the *replace* parameter to FALSE, in that case only new attributes are added and the existing attributes remain untouched.

Furthermore, if duplicated attributes are considered as a preventable mistake, an error can be raised by setting *stopOnDuplications* to TRUE. This forces the function to stop and raise an error, if duplicated attributes are present.

## Value

[CyHiddenAttributes](#) or [RCX](#) object with added hidden attributes

## Examples

```

## For CyHiddenAttributesAspects:
## prepare some aspects:
hiddenAttributes1 = createCyHiddenAttributes(
  name=c("A", "A", "B", "B"),
  value=list(c("a1", "a2"),
            "a with subnetwork",
            "b",
            "b with subnetwork"),
  isList=c(TRUE, FALSE, TRUE, FALSE),
  subnetworkId=c(NA, 1, NA, 1)
)

## A is updated, C is new
hiddenAttributes2 = createCyHiddenAttributes(
  name=c("A", "A", "C"),
  value=list("new a",
            "new a with subnetwork",
            c(1,2)),
  subnetworkId=c(NA, 1, NA)
)

## Simply update with new values
hiddenAttributes3 = updateCyHiddenAttributes(hiddenAttributes1,
                                             hiddenAttributes2)

## Ignore already present keys

```

```

hiddenAttributes3 = updateCyHiddenAttributes(hiddenAttributes1,
                                             hiddenAttributes2,
                                             replace=FALSE)

## Raise an error if duplicate keys are present
try(updateCyHiddenAttributes(hiddenAttributes1, hiddenAttributes2,
                             stopOnDuplicates=TRUE))

## =>ERROR:
## Elements of "name" and "subnetworkId" (in updateCyHiddenAttributes)
## must not contain duplicates!

## For RCX
## prepare RCX object:
nodes = createNodes(name = c("a","b","c","d","e","f"))
edges = createEdges(source=c(1,2,0,0,0,2),
                    target=c(2,3,1,2,5,4))
rcx = createRCX(nodes, edges)
cySubNetworks = createCySubNetworks(
  id = c(1,2),
  nodes = list("all", c(1,2,3)),
  edges = list("all", c(0,2))
)
rcx = updateCySubNetworks(rcx, cySubNetworks)

## add a network relation
rcx = updateCyHiddenAttributes(rcx, hiddenAttributes1)

## add an additional relation (update with new values)
rcx = updateCyHiddenAttributes(rcx, hiddenAttributes2)

## create a relation with a not existing subnetwork...
hiddenAttributes3 = createCyHiddenAttributes(
  name="X",
  value="new x",
  subnetworkId=9
)

## ...and try to add them
try(updateCyHiddenAttributes(rcx, hiddenAttributes3))
## =>ERROR:
## Provided IDs of "additionalAttributes$subnetworkId" (in updateCyHiddenAttributes)
## don't exist in "rcx$cySubNetworks$id"

```

---

updateCyNetworkRelations

*Update Cytoscape network relations*

---

## Description

This functions add network relations in the form of a [CyNetworkRelations](#) object to an other [CyNetworkRelations](#) or an [RCX](#) object.

**Usage**

```

updateCyNetworkRelations(
  x,
  cyNetworkRelations,
  replace = TRUE,
  stopOnDuplications = FALSE,
  ...
)

## S3 method for class 'CyNetworkRelationsAspect'
updateCyNetworkRelations(
  x,
  cyNetworkRelations,
  replace = TRUE,
  stopOnDuplications = FALSE,
  ...
)

## S3 method for class 'RCX'
updateCyNetworkRelations(
  x,
  cyNetworkRelations,
  replace = TRUE,
  stopOnDuplications = FALSE,
  checkReferences = TRUE,
  ...
)

```

**Arguments**

<code>x</code>	<a href="#">RCX</a> or <a href="#">CySubNetworks</a> object; (to which the new network relations will be added)
<code>cyNetworkRelations</code>	<a href="#">CySubNetworks</a> object; (the network relations, that will be added)
<code>replace</code>	logical; if existing values are updated (or ignored)
<code>stopOnDuplications</code>	logical; whether to stop, if duplicates in the <i>child</i> column are found
<code>...</code>	additional parameters
<code>checkReferences</code>	logical; whether to check if references to other aspects are present in the <a href="#">RCX</a> object

**Details**

Cytoscape subnetworks allow to group a set of nodes and corresponding edges together, and network relations define the relations between those networks. [CyNetworkRelations](#) objects can be added to an [RCX](#) or an other [CyNetworkRelations](#) object.

When network relations are added to a [CyNetworkRelations](#) or a [RCX](#) object some conflicts may rise, since the aspects might use the same child IDs. If the aspects do not share any child IDs, the two aspects are simply combined, otherwise, the properties of the child are updated. If that is not wanted, the updating can be prevented by setting *replace* to `FALSE`. Furthermore, if duplicated properties are

considered as a preventable mistake, an error can be raised by setting *stopOnDuplicates* to TRUE. This forces the function to stop and raise an error, if duplicated child IDs are present.

### Value

`CyNetworkRelations` or `RCX` object with added network relations

### Examples

```
## For CyNetworkRelationsAspects:
## prepare some aspects:
cyNetworkRelations1 = createCyNetworkRelations(
  child = c(1,2),
  parent = c(NA,1),
  name = c("Network A",
           "View A"),
  isView = c(FALSE, TRUE)
)

cyNetworkRelations2 = createCyNetworkRelations(
  child = 2,
  name = "View B",
  isView = TRUE
)

## update the duplicated child
cyNetworkRelations3 = updateCyNetworkRelations(cyNetworkRelations1,
                                              cyNetworkRelations2)

## keep old child values
cyNetworkRelations3 = updateCyNetworkRelations(cyNetworkRelations1,
                                              cyNetworkRelations2,
                                              replace=FALSE)

## Raise an error if duplicate keys are present
try(updateCyNetworkRelations(cyNetworkRelations1,
                             cyNetworkRelations2,
                             stopOnDuplicates=TRUE))

## =>ERROR:
## Elements of "child" (in updateCyNetworkRelations)
## must not contain duplicates!

## For RCX
## prepare RCX object:
nodes = createNodes(name = c("a","b","c","d","e","f"))
edges = createEdges(source=c(1,2,0,0,0,2),
                    target=c(2,3,1,2,5,4))
rcx = createRCX(nodes, edges)
cySubNetworks = createCySubNetworks(
  id = c(1,2),
  nodes = list("all", c(1,2,3)),
  edges = list("all", c(0,2))
)
rcx = updateCySubNetworks(rcx, cySubNetworks)

## add a network relation
rcx = updateCyNetworkRelations(rcx, cyNetworkRelations1)
```

```

## add an additional relation (View A is replaced by B)
rcx = updateCyNetworkRelations(rcx, cyNetworkRelations2)

## create a relation with a not existing subnetwork...
cyNetworkRelations3 = createCyNetworkRelations(
  child = 9
)

## ...and try to add them
try(updateCyNetworkRelations(rcx, cyNetworkRelations3))
## =>ERROR:
## Provided IDs of "additionalNetworkRelations$child" (in addCyNetworkRelations)
## don't exist in "rcx$cySubNetworks$id"

## create a relation with a not existing parent subnetwork...
cyNetworkRelations4 = createCyNetworkRelations(
  child = 1,
  parent = 9
)

## ...and try to add them
try(updateCyNetworkRelations(rcx, cyNetworkRelations4))
## =>ERROR:
## Provided IDs of "additionalNetworkRelations$parent" (in addCyNetworkRelations)
## don't exist in "rcx$cySubNetworks$id"

```

---

updateCySubNetworks     *Update Cytoscape subnetworks*

---

## Description

This functions add subnetworks in the form of a [CySubNetworks](#) object to an other [CySubNetworks](#) or an [RCX](#) object.

## Usage

```

updateCySubNetworks(
  x,
  cySubNetworks,
  stopOnDuplicats = FALSE,
  keepOldIds = TRUE,
  ...
)

## S3 method for class 'CySubNetworksAspect'
updateCySubNetworks(
  x,
  cySubNetworks,
  stopOnDuplicats = FALSE,
  keepOldIds = TRUE,
  ...
)

```

```
## S3 method for class 'RCX'
updateCySubNetworks(
  x,
  cySubNetworks,
  stopOnDuplicates = FALSE,
  keepOldIds = TRUE,
  checkReferences = TRUE,
  ...
)
```

### Arguments

**x** [RCX](#) or [CySubNetworks](#) object; (to which the new subnetworks will be added)

**cySubNetworks** [CySubNetworks](#) object; (the subnetwork, that will be added)

**stopOnDuplicates** logical; whether to stop, if duplicates in *id* column are found, or re-assign ids instead.

**keepOldIds** logical; if ids are re-assigned, the original ids are kept in the column *oldId*

**...** additional parameters

**checkReferences** logical; whether to check if references to other aspects are present in the [RCX](#) object

### Details

Cytoscape subnetworks allow to group a set of nodes and corresponding edges together. [CySubNetworks](#) objects can be added to an [RCX](#) or an other [CySubNetworks](#) object. The *nodes* and *edges* parameters reference the node or edge IDs that belong to a subnetwork. When adding an [CySubNetworks](#) object to an [RCX](#) object, those IDs must be present in the [Nodes](#) or [Edges](#) aspect respectively, otherwise an error is raised. Unlike other aspects referring those IDs, the Cytoscape subnetwork aspect allows to refer to all nodes and edges using the keyword `all`.

When subnetworks should be added to a [CySubNetworks](#) or a [RCX](#) object some conflicts may rise, since the aspects might use the same IDs. If the aspects do not share any IDs, the two aspects are simply combined. Otherwise, the IDs of the new subnetworks are re-assinged continuing with the next available ID (i.e. `maxId(cySubNetworks) + 1` and `maxId(rcx$cySubNetworks) + 1`, respectively).

To keep track of the changes, it is possible to keep the old IDs of the newly added nodes in the automatically added column *oldId*. This can be omitted by setting *keepOldIds* to `FALSE`. Otherwise, if a re-assignment of the IDs is not desired, this can be prevented by setting *stopOnDuplicates* to `TRUE`. This forces the function to stop and raise an error, if duplicated IDs are present.

### Value

[CySubNetworks](#) or [RCX](#) object with added subnetworks

### See Also

[CyNetworkRelations](#);

**Examples**

```

## For CySubNetworksAspects:
## prepare some aspects:
cySubNetworks1 = createCySubNetworks(
  id = c(0,1),
  nodes = list("all",
               c(1,2,3)),
  edges = list("all",
               c(0,2))
)

cySubNetworks2 = createCySubNetworks(
  nodes = c(0,3),
  edges = c(1)
)

## subnetwork ids will be kept
cySubNetworks3 = updateCySubNetworks(cySubNetworks1, cySubNetworks2)

## old subnetwork ids will be omitted
cySubNetworks3 = updateCySubNetworks(cySubNetworks1, cySubNetworks2,
                                     keepOldIds=FALSE)

## Raise an error if duplicate keys are present
try(updateCySubNetworks(cySubNetworks1, cySubNetworks2,
                       stopOnDuplications=TRUE))

## =>ERROR:
## Elements of "id" (in updateCySubNetworks) must not contain duplicates!

## For RCX
## prepare RCX object:
nodes = createNodes(name = c("a","b","c","d","e","f"))
edges = createEdges(source=c(1,2,0,0,0,2),
                    target=c(2,3,1,2,5,4))
rcx = createRCX(nodes, edges)

## add the subnetwork
rcx = updateCySubNetworks(rcx, cySubNetworks1)

## add additional subnetwork
rcx = updateCySubNetworks(rcx, cySubNetworks2)

## create a subnetwork with a not existing node...
cySubNetworks3 = createCySubNetworks(
  nodes = list(9)
)

## ...and try to add them
try(updateCySubNetworks(rcx, cySubNetworks3))
## =>ERROR:
## Provided IDs of "additionalSubNetworks$nodes" (in addCySubNetworks)
## don't exist in "rcx$nodes$id"

## create a group with a not existing edge...
cySubNetworks4 = createCySubNetworks(
  nodes = c(0,1),

```

```

    edges = 9
  )

  ## ...and try to add them
  try(updateCySubNetworks(rcx, cySubNetworks4))
  ## =>ERROR:
  ## Provided IDs of "additionalSubNetworks$edges" (in addCySubNetworks)
  ## don't exist in "rcx$edges$id"

```

---

updateCyTableColumn    *Update Cytoscape table column properties*

---

### Description

This functions add hidden attributes in the form of a [CyTableColumn](#) object to an other [CyTableColumn](#) or an [RCX](#) object.

### Usage

```

updateCyTableColumn(
  x,
  cyTableColumns,
  replace = TRUE,
  stopOnDuplicates = FALSE,
  ...
)

## S3 method for class 'CyTableColumnAspect'
updateCyTableColumn(
  x,
  cyTableColumns,
  replace = TRUE,
  stopOnDuplicates = FALSE,
  ...
)

## S3 method for class 'RCX'
updateCyTableColumn(
  x,
  cyTableColumns,
  replace = TRUE,
  stopOnDuplicates = FALSE,
  checkReferences = TRUE,
  ...
)

```

### Arguments

x                    [RCX](#) or [CyTableColumn](#) object; (to which the new table column properties will be added)

cyTableColumns    [CyTableColumn](#) object; (the new aspect, that will be added)

replace	logical; if existing values are updated (or ignored)
stopOnDuplicates	logical; whether to stop, if duplicates in <i>appliesTo</i> and <i>name</i> (and <i>subnetworkId</i> if present) column are found
...	additional parameters
checkReferences	logical; whether to check if references to other aspects are present in the <a href="#">RCX</a> object

### Details

In the case, that a [CyTableColumn](#) object is added to an other, or the [RCX](#) object already contains a [CyTableColumn](#) object, some properties might be present in both. By default, the properties are updated with the values of the latest one. This can be prevented by setting the *replace* parameter to FALSE, in that case only new attributes are added and the existing attributes remain untouched.

Furthermore, if duplicated properties are considered as a preventable mistake, an error can be raised by setting *stopOnDuplicates* to TRUE. This forces the function to stop and raise an error, if duplicated properties are present.

Cytoscape does not currently support table columns for the root network, but this option is included here for consistency.

### Value

[CyTableColumn](#) or [RCX](#) object with added hidden attributes

### See Also

[CySubNetworks](#)

### Examples

```
## For CyTableColumnssAspects:
## prepare some aspects:
tableColumn1 = createCyTableColumn(
  appliesTo=c("nodes", "edges", "networks"),
  name=c("weight", "weight", "collapsed"),
  dataType=c("numeric", "double", "logical"),
  isList=c(FALSE, FALSE, TRUE),
  subnetworkId=c(NA, NA, 1)
)

## nodes is updated, networks is new
tableColumn2 = createCyTableColumn(
  appliesTo=c("nodes", "networks"),
  name=c("weight", "collapsed"),
  dataType=c("double", "character")
)

## Simply update with new values
tableColumn3 = updateCyTableColumn(tableColumn1, tableColumn2)

## Ignore already present keys
tableColumn3 = updateCyTableColumn(tableColumn1, tableColumn2,
                                   replace=FALSE)
```

```

## Raise an error if duplicate keys are present
try(updateCyTableColumn(tableColumn1, tableColumn2,
                        stopOnDuplicates=TRUE))
## =>ERROR:
## Elements of "appliesTo", "name" and "subnetworkId" (in updateCyTableColumn)
## must not contain duplicates!

## For RCX
## prepare RCX object:
nodes = createNodes(name = c("a","b","c","d","e","f"))
edges = createEdges(source=c(1,2,0,0,0,2),
                    target=c(2,3,1,2,5,4))
rcx = createRCX(nodes, edges)
cySubNetworks = createCySubNetworks(
  id = c(1,2),
  nodes = list("all", c(1,2,3)),
  edges = list("all", c(0,2))
)
rcx = updateCySubNetworks(rcx, cySubNetworks)

## add a table column property
rcx = updateCyTableColumn(rcx, tableColumn1)

## add an additional property (update with new values)
rcx = updateCyTableColumn(rcx, tableColumn2)

## create a prpperty with a not existing subnetwork...
tableColumn3 = createCyTableColumn(
  appliesTo="nodes",
  name="weight",
  subnetworkId=9
)

## ...and try to add them
try(updateCyTableColumn(rcx, tableColumn3))
## =>ERROR:
## Provided IDs of "additionalColumns$subnetworkId" (in addCyTableColumn)
## don't exist in "rcx$cySubNetworks$id"

```

---

```
updateCyVisualProperties
```

*Update Cytoscape Visual Properties (aspect)*

---

## Description

This function is used to add [Cytoscape visual properties](#) aspects to each other or to an [RCX](#) object. In a [CyVisualProperties](#) aspect, [CyVisualProperty](#) objects define networks, nodes, edges, and default nodes and edges.

## Usage

```
updateCyVisualProperties(
  x,
```

```

    cyVisualProperties,
    replace = TRUE,
    stopOnDuplications = FALSE,
    ...
)

## S3 method for class 'CyVisualPropertiesAspect'
updateCyVisualProperties(
  x,
  cyVisualProperties,
  replace = TRUE,
  stopOnDuplications = FALSE,
  ...
)

## S3 method for class 'RCX'
updateCyVisualProperties(
  x,
  cyVisualProperties,
  replace = TRUE,
  stopOnDuplications = FALSE,
  checkReferences = TRUE,
  ...
)

```

### Arguments

**x** [RCX](#) or [CyVisualProperties](#) object; (to which it will be added)  
**cyVisualProperties** [CyVisualProperties](#) object; (that will be added)  
**replace** logical; if existing values are updated (or ignored)  
**stopOnDuplications** logical; whether to stop, if duplicates in name (and subnetworkId if present) column are found  
**...** additional parameters  
**checkReferences** logical; whether to check if references to other aspects are present in the [RCX](#) object

### Details

#### Structure of Cytoscape Visual Property:

```

CyVisualProperty
|---properties = CyVisualPropertyProperties
|   |--name
|   |--value
|---dependencies = CyVisualPropertyDependencies
|   |--name
|   |--value
|---mappings = CyVisualPropertyMappings
|   |--name

```



```

        appliesTo = c(NA,
                      1),
        view = c(NA,
                 1))
vpProperty2 = createCyVisualProperty(properties=vpPropertyP2,
                                     dependencies=vpPropertyD2,
                                     mappings=vpPropertyM2)
vpProperty3 = createCyVisualProperty(properties=vpPropertyP3,
                                     dependencies=vpPropertyD3,
                                     mappings=vpPropertyM3)

## Create a visual properties aspect
## (using the same visual property object for simplicity)
visProp1 = createCyVisualProperties(network=vpProperty1,
                                   nodes=vpProperty1,
                                   edges=vpProperty1,
                                   defaultNodes=vpProperty1,
                                   defaultEdges=vpProperty1)

visProp2 = createCyVisualProperties(network=vpProperty2,
                                   nodes=vpProperty2,
                                   edges=vpProperty2,
                                   defaultNodes=vpProperty2,
                                   defaultEdges=vpProperty2)

visProp3 = createCyVisualProperties(network=vpProperty3,
                                   nodes=vpProperty3,
                                   edges=vpProperty3,
                                   defaultNodes=vpProperty3,
                                   defaultEdges=vpProperty3)

## Adding a different visual property (Properties, Dependencies, Mappings)
## (e.g. "NODE_BORDER_WIDTH", which is not present before)
visProp4 = updateCyVisualProperties(visProp1, visProp2)

## Update a existing visual property
visProp5 = updateCyVisualProperties(visProp4, visProp3)

## Raise an error if duplicate keys are present
try(updateCyVisualProperties(visProp4, visProp3,
                           stopOnDuplicates=TRUE))

## =>ERROR:
## Elements of name (in VisualProperties$network$properties<appliesTo=NA,view=NA>)
## must not contain duplicates!

## For RCX
## prepare RCX object:
nodes = createNodes(name = c("a", "b", "c", "d", "e", "f"))
edges = createEdges(source=c(1,2,0,0,0,2),
                    target=c(2,3,1,2,5,4))
rcx = createRCX(nodes, edges)
cySubNetworks = createCySubNetworks(
  id = c(1,2),
  nodes = list("all", c(1,2,3)),
  edges = list("all", c(0,2))
)
rcx = updateCySubNetworks(rcx, cySubNetworks)

```

```

## Adding visual properties to an RCX object
rcx = updateCyVisualProperties(rcx, visProp1)

## Adding a different visual property (Properties, Dependencies, Mappings)
## (e.g. "NODE_BORDER_WIDTH", which is not present before)
rcx = updateCyVisualProperties(rcx, visProp2)

## Update a existing visual property
rcx = updateCyVisualProperties(rcx, visProp3)

## Raise an error if duplicate keys are present
try(updateCyVisualProperties(rcx, visProp3,
                           stopOnDuplications=TRUE))

## =>ERROR:
## Elements of "name" (in VisualProperties$network$properties<appliesTo=NA,view=NA>)
## must not contain duplicates!

```

---

```
updateCyVisualProperty
```

*Update Cytoscape Visual Property objects and sub-objects (used in CyVisualProperties aspect)*

---

## Description

This function is used to add Cytoscape visual property objects ([CyVisualProperty](#)) and its sub-objects ([CyVisualPropertyProperties](#), [CyVisualPropertyDependencies](#) and [CyVisualPropertyMappings](#)) to each other. Cytoscape visual property objects define networks, nodes, edges, and default nodes and edges in a [CyVisualProperties](#) aspect.

## Usage

```

updateCyVisualProperty(
  cyVisualProperty,
  additionalProperty,
  replace = TRUE,
  stopOnDuplications = FALSE,
  .log = c()
)

## S3 method for class 'CyVisualPropertyProperties'
updateCyVisualProperty(
  cyVisualProperty,
  additionalProperty,
  replace = TRUE,
  stopOnDuplications = FALSE,
  .log = c()
)

## S3 method for class 'CyVisualPropertyDependencies'
updateCyVisualProperty(
  cyVisualProperty,

```

```

    additionalProperty,
    replace = TRUE,
    stopOnDuplicates = FALSE,
    .log = c()
  )

## S3 method for class 'CyVisualPropertyMappings'
updateCyVisualProperty(
  cyVisualProperty,
  additionalProperty,
  replace = TRUE,
  stopOnDuplicates = FALSE,
  .log = c()
)

## S3 method for class 'CyVisualProperty'
updateCyVisualProperty(
  cyVisualProperty,
  additionalProperty,
  replace = TRUE,
  stopOnDuplicates = FALSE,
  .log = c()
)

```

### Arguments

**cyVisualProperty** object; (to which it will be added)  
**additionalProperty** object; (that will be added)  
**replace** logical; if existing values are updated (or ignored)  
**stopOnDuplicates** logical; whether to stop, if duplicates in name (and subnetworkId if present) column are found  
**.log** character (optional); name of the calling function used in error logging

### Details

#### Structure of Cytoscape Visual Property:

```

CyVisualProperty
|---properties = CyVisualPropertyProperties
|  |--name
|  |--value
|---dependencies = CyVisualPropertyDependencies
|  |--name
|  |--value
|---mappings = CyVisualPropertyMappings
|  |--name
|  |--type
|  |--definition
|---appliesTo = <reference to subnetwork id>
|---view = <reference to subnetwork id>

```



```

                                vpPropertyP1),
dependencies=list(vpPropertyD1,
                 vpPropertyD1,
                 NA),
mappings=list(vpPropertyM1,
              NA,
              vpPropertyM1),
appliesTo = c(NA,
              NA,
              1),
view = c(NA,
         1,
         NA))
vpProperty2 = createCyVisualProperty(properties=vpPropertyP2,
                                   dependencies=vpPropertyD2,
                                   mappings=vpPropertyM2)
vpProperty3 = createCyVisualProperty(properties=vpPropertyP3,
                                   dependencies=vpPropertyD3,
                                   mappings=vpPropertyM3)

## add two visual property objects
vpProperty4 = updateCyVisualProperty(vpProperty1, vpProperty2)

## update values
updateCyVisualProperty(vpProperty4, vpProperty3)

## keep old values
updateCyVisualProperty(vpProperty4, vpProperty3,
                       replace = FALSE)

## keep old values
try(updateCyVisualProperty(vpProperty4, vpProperty3,
                          stopOnDuplications = TRUE))

## =>ERROR:
## Elements of name (in properties<appliesTo=NA,view=NA>) must not contain duplicates!

```

---

updateEdgeAttributes    *Update edge attributes*

---

### Description

This functions add edge attributes in the form of a [EdgeAttributes](#) object to an [RCX](#) or an other [EdgeAttributes](#) object.

### Usage

```

updateEdgeAttributes(
  x,
  edgeAttributes,
  replace = TRUE,
  stopOnDuplications = FALSE,
  ...
)

```

```

## S3 method for class 'EdgeAttributesAspect'
updateEdgeAttributes(
  x,
  edgeAttributes,
  replace = TRUE,
  stopOnDuplications = FALSE,
  ...
)

## S3 method for class 'RCX'
updateEdgeAttributes(
  x,
  edgeAttributes,
  replace = TRUE,
  stopOnDuplications = FALSE,
  checkReferences = TRUE,
  ...
)

```

### Arguments

x [RCX](#) or [EdgeAttributes](#) object; (to which the new edge attributes will be added)

edgeAttributes [EdgeAttributes](#) object; (the new aspect, that will be added)

replace logical; if existing values are updated (or ignored)

stopOnDuplications logical; whether to stop, if duplicates in *propertyOf* and *name* (and *subnetworkId* if present) column are found

... additional parameters

checkReferences logical; whether to check if references to other aspects are present in the [RCX](#) object

### Details

Edges may have additional attributes besides a name and a representation, and are represented as [EdgeAttributes](#) objects. [EdgeAttributes](#) objects can be added to an [RCX](#) or an other [EdgeAttributes](#) object. The *propertyOf* parameter references the [Edges](#) ids to which the attributes belong to. When adding an [EdgeAttributes](#) object to an [RCX](#) object, those ids must be present in the [Edges](#) aspect, otherwise an error is raised.

In the case, that a [EdgeAttributes](#) object is added to an other, or the [RCX](#) object already contains a [EdgeAttributes](#) object, some attributes might be present in both. By default, the attributes are updated with the values of the latest one. This can be prevented by setting the *replace* parameter to *FALSE*, in that case only new attributes are added and the existing attributes remain untouched.

Furthermore, if duplicated attributes are considered as a preventable mistake, an error can be raised by setting *stopOnDuplications* to *TRUE*. This forces the function to stop and raise an error, if duplicated attributes are present.

### Value

[EdgeAttributes](#) or [RCX](#) object with added node attributes

**See Also**

[NodeAttributes](#), [NetworkAttributes](#)

**Examples**

```

## For EdgeAttributesAspects:
## prepare some aspects:
edgeAttributes = createEdgeAttributes(
  propertyOf=c(0,0,0,0),
  name=c("A", "A", "B", "B"),
  value=list(c("a1", "a2"),
            "a with subnetwork",
            "b",
            "b with subnetwork"),
  isList=c(TRUE, FALSE, TRUE, FALSE),
  subnetworkId=c(NA, 1, NA, 1)
)

## A is updated, C is new
edgeAttributes2 = createEdgeAttributes(
  propertyOf=c(0,0,0),
  name=c("A", "A", "C"),
  value=list("new a",
            "new a with subnetwork",
            c(1,2)),
  subnetworkId=c(NA, 1, NA)
)

## Simply update with new values
edgeAttributes3 = updateEdgeAttributes(edgeAttributes, edgeAttributes2)

## Ignore already present keys
edgeAttributes3 = updateEdgeAttributes(edgeAttributes, edgeAttributes2,
                                       replace=FALSE)

## Raise an error if duplicate keys are present
try(updateEdgeAttributes(edgeAttributes, edgeAttributes2,
                        stopOnDuplicates=TRUE))

## =>ERROR:
## Elements of "propertyOf", "name" and "subnetworkId" (in updateEdgeAttributes)
## must not contain duplicates!

## For RCX
## prepare RCX object:
nodes = createNodes(name = c("a", "b", "c", "d", "e", "f"))
edges = createEdges(source=c(1,2,0,0,0,2),
                    target=c(2,3,1,2,5,4))
rcx = createRCX(nodes, edges)
cySubNetworks = createCySubNetworks(
  id = c(1,2),
  nodes = list("all", c(1,2,3)),
  edges = list("all", c(0,2))
)
rcx = updateCySubNetworks(rcx, cySubNetworks)

## add the edge attributes

```

```

rcx = updateEdgeAttributes(rcx, edgeAttributes)

## add additional edge attributes and update existing
rcx = updateEdgeAttributes(rcx, edgeAttributes2)

## create edge attributes for a not existing edge...
edgeAttributes3 = createEdgeAttributes(propertyOf=9,
                                       name="A",
                                       value="a")

## ...and try to add them
try(updateEdgeAttributes(rcx, edgeAttributes3))
## =>ERROR:
## Provided IDs of "additionalAttributes$propertyOf" (in updateEdgeAttributes)
## don't exist in "rcx$edges$id"

```

---

updateEdges

*Update edges*


---

### Description

This functions add edges in the form of a [Edges](#) object to an other [Edges](#) or an *RCX* object.

### Usage

```

updateEdges(x, edges, stopOnDuplicats = FALSE, keepOldIds = TRUE, ...)

## S3 method for class 'EdgesAspect'
updateEdges(x, edges, stopOnDuplicats = FALSE, keepOldIds = TRUE, ...)

## S3 method for class 'RCX'
updateEdges(
  x,
  edges,
  stopOnDuplicats = FALSE,
  keepOldIds = TRUE,
  checkReferences = TRUE,
  ...
)

```

### Arguments

x	<a href="#">RCX-object</a> or <a href="#">Edges</a> object; (to which the new <a href="#">Edges</a> will be added)
edges	<a href="#">Edges</a> object; (the <a href="#">Edges</a> , that will be added)
stopOnDuplicats	logical (optional); whether to stop, if duplicates in <i>id</i> column are found, or re-assign ids instead.
keepOldIds	logical (optional); if ids are re-assigned, the original ids are kept in the column <i>oldId</i>
...	additional parameters
checkReferences	logical; whether to check if references to other aspects are present in the <a href="#">RCX</a> object

## Details

When edges should be added to a [Edges](#) or a [RCX-object](#) some conflicts may rise, since the aspects might use the same IDs. If the aspects do not share any IDs, the two aspects are simply combined. Otherwise, the IDs of the new edges are re-assinged continuing with the next available ID (i.e. `maxId(edgesAspect) + 1` and `maxId(rcx$edges) + 1`, respectively).

To keep track of the changes, it is possible to keep the old IDs of the newly added edges in the automatically added column `oldId`. This can be omitted by setting `keepOldIds` to `FALSE`. Otherwise, if a re-assignment of the IDs is not desired, this can be prevented by setting `stopOnDuplicatas` to `TRUE`. This forces the function to stop and raise an error, if duplicated IDs are present.

## Value

[Edges](#) or [RCX](#) with added edges

## Examples

```
## create some edges
edges1 = createEdges(source=c(1,1,0), target=c(2,0,1))
edges2 = createEdges(id=c(3,2,4),
                     source=c(0,0,1),
                     target=c(1,2,2),
                     interaction=c("activates","inhibits", NA))

## simply add the edges and keep old ids
edges3 = updateEdges(edges1, edges2)

## add the edges
edges4 = updateEdges(edges1, edges2, keepOldIds=FALSE)

## force an error because of duplicated ids
try(updateEdges(edges1, edges2, stopOnDuplicatas=TRUE))
## =>Error:
## Elements of "id" (in updateEdges) must not contain duplicates!

## Prepare an RCX object
rcx = createRCX(createNodes(name = c("EGFR", "AKT1", "WNT")))

## add edges to the RCX object
rcx = updateEdges(rcx, edges1)

## add new edges and don't keep old ids
rcx = updateEdges(rcx, edges2, keepOldIds=FALSE)

## force an error because of duplicated ids
try(updateEdges(rcx, edges2, stopOnDuplicatas=TRUE))
## =>Error:
## Elements of "id" (in updateEdges) must not contain duplicates!
```

---

updateMetaDataProperties

*Update meta-data properties*

---

**Description**

The **Meta-data** aspect contains meta-data about the aspects in the **RCX-object**. Properties that need to be fetched or updated independently of aspect data are added with this function.

**Usage**

```
updateMetaDataProperties(rcx, aspectName, property)
```

**Arguments**

rcx	<b>RCX</b> object;
aspectName	character; name of the aspect as displayed in <b>Meta-data</b> (e.g. "nodes")
property	named list; property as key-value pairs (empty list to remove all)

**Value**

**RCX** object with updated **Meta-data** aspect

**Examples**

```
## prepare RCX object:
nodes = createNodes(name = c("a","b","c","d","e","f"))
edges = createEdges(source=c(1,2,0,0,0,2),
                    target=c(2,3,1,2,5,4))
rcx = createRCX(nodes, edges)
cySubNetworks = createCySubNetworks(
  id = c(1,2),
  nodes = list("all", c(1,2,3)),
  edges = list("all", c(0,2))
)
rcx = updateCySubNetworks(rcx, cySubNetworks)

## add properties for edges
updateMetaDataProperties(rcx,
                        "edges",
                        list(some="value",
                            another="VALUE"))

## remove properties for edges
updateMetaDataProperties(rcx,
                        "edges",
                        list())
```

---

updateNetworkAttributes

*Update network attributes*

---

**Description**

This functions add network attributes in the form of a **NetworkAttributes** object to an **RCX** or an other **NetworkAttributes** object.

**Usage**

```

updateNetworkAttributes(
  x,
  networkAttributes,
  replace = TRUE,
  stopOnDuplicates = FALSE,
  ...
)

## S3 method for class 'NetworkAttributesAspect'
updateNetworkAttributes(
  x,
  networkAttributes,
  replace = TRUE,
  stopOnDuplicates = FALSE,
  ...
)

## S3 method for class 'RCX'
updateNetworkAttributes(
  x,
  networkAttributes,
  replace = TRUE,
  stopOnDuplicates = FALSE,
  checkReferences = TRUE,
  ...
)

```

**Arguments**

<code>x</code>	<a href="#">RCX</a> object; (to which the new network attributes will be added)
<code>networkAttributes</code>	<a href="#">NetworkAttributes</a> object; (the new aspect, that will be added)
<code>replace</code>	logical; if existing values are updated (or ignored)
<code>stopOnDuplicates</code>	logical; whether to stop, if duplicates in <i>name</i> (and <i>subnetworkId</i> if present) column are found
<code>...</code>	additional parameters
<code>checkReferences</code>	logical; whether to check if references to other aspects are present in the <a href="#">RCX</a> object

**Details**

Networks may have attributes, that are represented as [NetworkAttributes](#) objects. [NetworkAttributes](#) objects can be added to an [RCX](#) or an other [NetworkAttributes](#) object.

In the case, that a [NetworkAttributes](#) object is added to an other, or the [RCX](#) object already contains a [NetworkAttributes](#) object, some attributes might be present in both. By default, the attributes are updated with the values of the latest one. This can prevented by setting the *replace* parameter to FALSE, in that case only new attributes are added and the existing attributes remain untouched.

Furthermore, if duplicated attributes are considered as a preventable mistake, an error can be raised by setting *stopOnDuplicates* to TRUE. This forces the function to stop and raise an error, if duplicated attributes are present.

### Value

[NetworkAttributes](#) or [RCX](#) object with added network attributes

### See Also

[NetworkAttributes](#); [NodeAttributes](#), [EdgeAttributes](#)

### Examples

```
## For NetworkAttributesAspects:
## prepare some aspects:
networkAttributes1 = createNetworkAttributes(
  name=c("A", "A", "B", "B"),
  value=list(c("a1", "a2"),
            "a with subnetwork",
            "b",
            "b with subnetwork"),
  isList=c(TRUE, FALSE, TRUE, FALSE),
  subnetworkId=c(NA, 1, NA, 1)
)

## A is updated, C is new
networkAttributes2 = createNetworkAttributes(
  name=c("A", "A", "C"),
  value=list("new a",
            "new a with subnetwork",
            c(1, 2)),
  subnetworkId=c(NA, 1, NA)
)

## Simply update with new values
networkAttributes3 = updateNetworkAttributes(networkAttributes1, networkAttributes2)

## Ignore already present keys
networkAttributes3 = updateNetworkAttributes(networkAttributes1, networkAttributes2,
                                           replace=FALSE)

## Raise an error if duplicate keys are present
try(updateNetworkAttributes(networkAttributes1, networkAttributes2,
                           stopOnDuplicates=TRUE))

## =>ERROR:
## Provided IDs (name, subnetworkId) contain duplicates!

## For RCX
## prepare RCX object:
nodes = createNodes(name = c("a", "b", "c", "d", "e", "f"))
edges = createEdges(source=c(1, 2, 0, 0, 0, 2),
                   target=c(2, 3, 1, 2, 5, 4))
rcx = createRCX(nodes, edges)
cySubNetworks = createCySubNetworks(
  id = c(1, 2),
  nodes = list("all", c(1, 2, 3)),
```

```

    edges = list("all", c(0,2))
  )
  rcx = updateCySubNetworks(rcx, cySubNetworks)

  ## add the network attributes
  rcx = updateNetworkAttributes(rcx, networkAttributes1)

  ## add additional network attributes and update existing
  rcx = updateNetworkAttributes(rcx, networkAttributes2)

  ## create a relation with a not existing subnetwork...
  networkAttributes3 = createNetworkAttributes(
    name="X",
    value="new x",
    subnetworkId=9
  )

  ## ...and try to add them
  try(updateNetworkAttributes(rcx, networkAttributes3))
  ## =>ERROR:
  ## NetworkAttributesAspect$subnetworkId IDs don't exist in CySubNetworksAspect

```

---

updateNodeAttributes *Update node attributes*

---

### Description

This functions add node attributes in the form of a [NodeAttributes](#) object to an [RCX](#) or an other [NodeAttributes](#) object.

### Usage

```

updateNodeAttributes(
  x,
  nodeAttributes,
  replace = TRUE,
  stopOnDuplicates = FALSE,
  ...
)

## S3 method for class 'NodeAttributesAspect'
updateNodeAttributes(
  x,
  nodeAttributes,
  replace = TRUE,
  stopOnDuplicates = FALSE,
  ...
)

## S3 method for class 'RCX'
updateNodeAttributes(
  x,
  nodeAttributes,

```

```

    replace = TRUE,
    stopOnDuplicates = FALSE,
    checkReferences = TRUE,
    ...
)

```

### Arguments

x [RCX](#) or [NodeAttributes](#) object; (to which the new node attributes will be added)

nodeAttributes [NodeAttributes](#) object; (the new aspect, that will be added)

replace logical; if existing values are updated (or ignored)

stopOnDuplicates logical; whether to stop, if duplicates in *propertyOf* and *name* (and *subnetworkId* if present) columns are found

... additional parameters

checkReferences logical; whether to check if references to other aspects are present in the [RCX](#) object

### Details

Nodes may have additional attributes besides a name and a representation, and are represented as [NodeAttributes](#) objects. [NodeAttributes](#) objects can be added to an [RCX](#) object or an other [NodeAttributes](#) object. The *propertyOf* parameter references the node IDs to which the attributes belong to. When adding an [NodeAttributes](#) object to an [RCX](#) object, those IDs must be present in the [Nodes](#) aspect, otherwise an error is raised.

In the case, that a [NodeAttributes](#) object is added to an other, or the [RCX](#) object already contains a [NodeAttributes](#) object, some attributes might be present in both. By default, the attributes are updated with the values of the latest one. This can be prevented setting the *replace* parameter to FALSE, in that case only new attributes are added and the existing attributes remain untouched.

Furthermore, if duplicated attributes are considered as a preventable mistake, an error can be raised by setting *stopOnDuplicates* to TRUE. This forces the function to stop and raise an error, if duplicated attributes are present.

### Value

[NodeAttributes](#) or [RCX](#) object with added node attributes

### See Also

[EdgeAttributes](#), [NetworkAttributes](#)

### Examples

```

## For NodeAttributesAspects:
## prepare some aspects:
nodeAttributes1 = createNodeAttributes(
  propertyOf=c(1,1,1,1),
  name=c("A", "A", "B", "B"),
  value=list(c("a1", "a2"),
            "a with subnetwork",

```

```

        "b",
        "b with subnetwork"),
    isList=c(TRUE,FALSE,TRUE,FALSE),
    subnetworkId=c(NA,1,NA,1)
)

## A is updated, C is new
nodeAttributes2 = createNodeAttributes(
  propertyOf=c(1,1,1),
  name=c("A","A","C"),
  value=list("new a",
            "new a with subnetwork",
            c(1,2)),
  subnetworkId=c(NA,1,NA)
)

## Simply update with new values
nodeAttributes3 = updateNodeAttributes(nodeAttributes1, nodeAttributes2)

## Ignore already present keys
nodeAttributes4 = updateNodeAttributes(nodeAttributes1, nodeAttributes2,
                                       replace=FALSE)

## Raise an error if duplicate keys are present
try(updateNodeAttributes(nodeAttributes1, nodeAttributes2,
                        stopOnDuplications=TRUE))

## =>ERROR:
## Elements of "propertyOf", "name" and "subnetworkId" (in addNodeAttributes)
## must not contain duplicates!

## For RCX
## prepare RCX object:
nodes = createNodes(name = c("a","b","c","d","e","f"))
edges = createEdges(source=c(1,2,0,0,0,2),
                    target=c(2,3,1,2,5,4))
rcx = createRCX(nodes, edges)
cySubNetworks = createCySubNetworks(
  id = c(1,2),
  nodes = list("all", c(1,2,3)),
  edges = list("all", c(0,2))
)
rcx = updateCySubNetworks(rcx, cySubNetworks)

## add the node attributes, even if no subnetworks are present
rcx = updateNodeAttributes(rcx, nodeAttributes1, checkReferences=FALSE)

## add the node attributes
rcx = updateNodeAttributes(rcx, nodeAttributes1)

## add additional node attributes and update existing
rcx = updateNodeAttributes(rcx, nodeAttributes2)

## create node attributes for a not existing node...
nodeAttributes3 = createNodeAttributes(propertyOf=9,
                                       name="A",
                                       value="a")

## ...and try to add them

```

```
try(updateNodeAttributes(rcx, nodeAttributes3))
## =>ERROR:
## Provided IDs of "additionalAttributes$propertyOf" (in addNodeAttributes)
## don't exist in "rcx$nodes$id"
```

---

updateNodes	<i>Update nodes</i>
-------------	---------------------

---

## Description

This functions add nodes in the form of a [Nodes](#) object to an other [Nodes](#) or an [RCX-object](#).

## Usage

```
updateNodes(x, nodes, stopOnDuplications = FALSE, keepOldIds = TRUE)

## S3 method for class 'NodesAspect'
updateNodes(x, nodes, stopOnDuplications = FALSE, keepOldIds = TRUE)

## S3 method for class 'RCX'
updateNodes(x, nodes, stopOnDuplications = FALSE, keepOldIds = TRUE)
```

## Arguments

x	<a href="#">RCX-object</a> or <a href="#">Nodes</a> object; (to which the new <a href="#">Nodes</a> will be added)
nodes	<a href="#">Nodes</a> object; (the <a href="#">Nodes</a> , that will be added)
stopOnDuplications	logical (optional); whether to stop, if duplicates in id column are found, or re-assign ids instead.
keepOldIds	logical (optional); if ids are re-assigned, the original ids are kept in the column <code>oldId</code>

## Details

When nodes should be added to a [Nodes](#) or a [RCX-object](#) object some conflicts may rise, since the aspects might use the same IDs. If the aspects do not share any IDs, the two aspects are simply combined. Otherwise, the IDs of the new nodes are re-assinged continuing with the next available ID (i.e. `maxId(nodesAspect) + 1` and `maxId(rcx$nodes) + 1`, respectively).

To keep track of the changes, it is possible to keep the old IDs of the newly added nodes in the automatically added column `oldId`. This can be omitted by setting `keepOldIds` to `FALSE`. Otherwise, if a re-assignment of the IDs is not desired, this can be prevented by setting `stopOnDuplications` to `TRUE`. This forces the function to stop and raise an error, if duplicated IDs are present.

## Value

[Nodes](#) or [RCX](#) object with added nodes

**Examples**

```

## create some nodes
nodes1 = createNodes(name = c("EGFR", "AKT1", "WNT"))
nodes2 = createNodes(name=c("CDK1", "CDK2", "CDK3"),
                      represents=c("HGNC:CDK1",
                                   "Uniprot:P24941",
                                   "Ensembl:ENSG00000250506"))

## simply add the nodes and keep old ids
nodes3 = updateNodes(nodes1, nodes2)

## add the nodes
nodes4 = updateNodes(nodes1, nodes2, keepOldIds=FALSE)

## force an error because of duplicated ids
try(updateNodes(nodes1, nodes2, stopOnDuplications=TRUE))
## =>Error:
## Elements of "id" (in updateNodes) must not contain duplicates!

## create an RCX object with nodes
rcx = createRCX(nodes1)

## add additional nodes
rcx = updateNodes(rcx, nodes2, keepOldIds=FALSE)

## force an error because of duplicated ids
try(updateNodes(rcx, nodes2, stopOnDuplications=TRUE))
## =>Error:
## Elements of "id" (in updateNodes) must not contain duplicates!

```

---

 validate

*Validate RCX and its aspects*


---

**Description**

Validate RCX objects and its aspects.

**Usage**

```

validate(x, verbose = TRUE)

## Default S3 method:
validate(x, verbose = TRUE)

## S3 method for class 'NodesAspect'
validate(x, verbose = TRUE)

## S3 method for class 'EdgesAspect'
validate(x, verbose = TRUE)

## S3 method for class 'NodeAttributesAspect'
validate(x, verbose = TRUE)

```

```
## S3 method for class 'EdgeAttributesAspect'  
validate(x, verbose = TRUE)  
  
## S3 method for class 'NetworkAttributesAspect'  
validate(x, verbose = TRUE)  
  
## S3 method for class 'CartesianLayoutAspect'  
validate(x, verbose = TRUE)  
  
## S3 method for class 'CyGroupsAspect'  
validate(x, verbose = TRUE)  
  
## S3 method for class 'CyVisualPropertiesAspect'  
validate(x, verbose = TRUE)  
  
## S3 method for class 'CyVisualProperty'  
validate(x, verbose = TRUE)  
  
## S3 method for class 'CyVisualPropertyProperties'  
validate(x, verbose = TRUE)  
  
## S3 method for class 'CyVisualPropertyDependencies'  
validate(x, verbose = TRUE)  
  
## S3 method for class 'CyVisualPropertyMappings'  
validate(x, verbose = TRUE)  
  
## S3 method for class 'CyHiddenAttributesAspect'  
validate(x, verbose = TRUE)  
  
## S3 method for class 'CyNetworkRelationsAspect'  
validate(x, verbose = TRUE)  
  
## S3 method for class 'CySubNetworksAspect'  
validate(x, verbose = TRUE)  
  
## S3 method for class 'CyTableColumnAspect'  
validate(x, verbose = TRUE)  
  
## S3 method for class 'RCX'  
validate(x, verbose = TRUE)
```

### Arguments

x	object to validate; <a href="#">RCX</a> object or an aspect
verbose	logical; whether to print the test results.

### Details

Different tests are performed on aspects and the [RCX](#) network. This includes checks of the correct aspect structure, data types, uniqueness of IDs and attribute names, presence of NA values, and references between the aspects.

**Value**

logical; whether the object passed all tests.

**Methods (by class)**

- `validate(default)`: Default
- `validate(NodesAspect)`: Nodes
- `validate(EdgesAspect)`: Edges
- `validate(NodeAttributesAspect)`: Node attributes
- `validate(EdgeAttributesAspect)`: Edge attributes
- `validate(NetworkAttributesAspect)`: Network attributes
- `validate(CartesianLayoutAspect)`: Cartesian layout
- `validate(CyGroupsAspect)`: Cytoscape Groups
- `validate(CyVisualPropertiesAspect)`: Cytoscape Visual Properties
- `validate(CyVisualProperty)`: Cytoscape Visual Properties
- `validate(CyVisualPropertyProperties)`: Cytoscape visual property: Properties
- `validate(CyVisualPropertyDependencies)`: Cytoscape visual property: Dependencies
- `validate(CyVisualPropertyMappings)`: Cytoscape visual property: Mappings
- `validate(CyHiddenAttributesAspect)`: Cytoscape hidden attributes
- `validate(CyNetworkRelationsAspect)`: Cytoscape network relations
- `validate(CySubNetworksAspect)`: Cytoscape sub-networks
- `validate(CyTableColumnAspect)`: Cytoscape table column aspect
- `validate(RCX)`: The whole RCX object with all its aspects

**Examples**

```
## Read from a CX file
## reading the provided example network of the package
cxFile <- system.file(
  "extdata",
  "Imatinib-Inhibition-of-BCR-ABL-66a902f5-2022-11e9-bb6a-0ac135e8bacf.cx",
  package = "RCX"
)

rcx = readCX(cxFile)

## validate the network
validate(rcx)

## validate a single aspect
validate(rcx$nodes)
```

---

visualize	<i>Visualize a Network</i>
-----------	----------------------------

---

## Description

Visualize [RCX](#) and CX networks in RStudio or in an external browser.

## Usage

```
visualize(x, layout = NULL, openExternal = FALSE)

## S3 method for class 'RCX'
visualize(x, layout = NULL, openExternal = FALSE)

## S3 method for class 'CX'
visualize(x, layout = NULL, openExternal = FALSE)
```

## Arguments

x	network; <a href="#">RCX</a> or CX object
layout	named character or list; e.g. <code>c(name="random")</code>
openExternal	logical; whether to open in an external browser instead of the RStudio viewer

## Details

This function uses the Java Script library used by the NDEx platform (<https://ndexbio.org/>) to visualize the [RCX](#) or CX network from [toCX](#). In the first case, the [RCX](#) is converted to CX (JSON) using [toCX](#).

By default the visualization is opened in RStudio in the *Viewer* panel. If this function is not executed in RStudio, the visualization is opened in the standard web-browser. This also can be forced from within RStudio using *openExternal*.

If the network contains the necessary Cytoscape styles (see <http://manual.cytoscape.org/en/stable/Styles.html>) the network is visualized as seen on the NDEx platform.

To define the layout of the network the coordinate from [CartesianLayout](#) are used to determine the location of the nodes. If this aspect is missing, or the the coordinates should be ignored, the *layout* parameter can be used to set a different layout.

*layout* follows therefore the definition of Cytoscape.js (see <https://js.cytoscape.org/#layouts>). A simple definition can be setting only the *name* of the desired layout, e.g. `random`. Additional options can be passed as named list, where the values are passed without quoting. This allows for even passing Java Script functions to Cytoscape.js.

The visualization can also be saved as HTML file using the [writeHTML](#) function instead of this one.

## Value

NULL

## See Also

[rcxToJson](#), [readCX](#), [writeCX](#)

**Examples**

```

## prepare RCX
rcx = createRCX(
  createNodes(name = c("a","b","c")),
  createEdges(
    source=c(0,0,1),
    target=c(1,2,2)
  )
)

## visualize the network
visualize(rcx)

## force a different layout
visualize(rcx, c(name="cose"))

## force a different layout with Java Script parameters
visualize(rcx, layout = c(name="random",animate="true"))

## even pass a Java Script function
visualize(
  rcx,
  layout = c(
    name="random",
    animate="true",
    animateFilter="function ( node, i ){ return true; }"
  )
)

## open the visualization in an external browser
visualize(
  rcx,
  layout = c(name="cose"),
  openExternal = TRUE
)

```

---

writeCX

*Write RCX to file*


---

**Description**

These function write an [RCX](#) object or a [CX](#) object to a file.

**Usage**

```

writeCX(x, file, verbose = FALSE, pretty = FALSE)

## S3 method for class 'RCX'
writeCX(x, file, verbose = FALSE, pretty = FALSE)

## S3 method for class 'CX'
writeCX(x, file, verbose = FALSE, pretty = FALSE)

```

**Arguments**

x	<a href="#">RCX</a> or <a href="#">CX</a> object
file	character; the name of the file to which the data are written
verbose	logical; whether to print what is happening
pretty	logical; adds indentation whitespace to JSON output. Can be TRUE/FALSE or a number specifying the number of spaces to indent. See <a href="#">jsonlite::prettyfy()</a>

**Value**

file character; the name of the file to which the data were written

**See Also**

[toCX](#), [rcxToJson](#), [readCX](#)

**Examples**

NULL

---

writeHTML	<i>Save network visualization as HTML file</i>
-----------	--

---

**Description**

Save an interactive single page visualization of [RCX](#) and [CX](#) networks as an HTML file containing all necessary Java Script.

**Usage**

```
writeHTML(x, file, layout = NULL, verbose = FALSE)
```

```
## S3 method for class 'RCX'
writeHTML(x, file, layout = NULL, verbose = FALSE)
```

```
## S3 method for class 'CX'
writeHTML(x, file, layout = NULL, verbose = FALSE)
```

**Arguments**

x	network; <a href="#">RCX</a> or <a href="#">CX</a> object
file	character; path, where the html file should be saved
layout	named character or list; e.g. <code>c(name="random")</code>
verbose	logical; whether to print what is happening

## Details

This function uses the Java Script library used by the NDEx platform (<https://ndexbio.org/>) to visualize the **RCX** or **CX** network. The **RCX** is therefore converted to CX (JSON) using **toCX**.

If the network contains the necessary Cytoscape styles (see <http://manual.cytoscape.org/en/stable/Styles.html>) the network is visualized as seen on the NDEx platform.

To define the layout of the network the coordinate from **CartesianLayout** are used to determine the location of the nodes. If this aspect is missing, or the the coordinates should be ignored, the *layout* parameter can be used to set a different layout.

*layout* follows therefore the definition of Cytoscape.js (see <https://js.cytoscape.org/#layouts>). A simple definition can be setting only the *name* of the desired layout, e.g. random. Additional options can be passed as named list, where the values are passed without quoting. This allows for even passing Java Script functions to Cytoscape.js.

To visualize the network in RStudio the **visualize** function can be used instead.

## Value

file character; path, where the html file has been saved

## See Also

[rcxToJson](#), [readCX](#), [writeCX](#)

## Examples

```
## prepare RCX
rcx = createRCX(
  createNodes(name = c("a", "b", "c")),
  createEdges(
    source=c(0,0,1),
    target=c(1,2,2)
  )
)

cx = toCX(rcx)

htmlFile = tempfile(fileext = ".html")

## save the html
writeHTML(rcx, htmlFile)

## or
writeHTML(cx, htmlFile)

## force a different layout
writeHTML(rcx, htmlFile, c(name="cose"))

## force a different layout with Java Script parameters
writeHTML(rcx, htmlFile, layout = c(name="random", animate="true"))

## even pass a Java Script function
writeHTML(
  rcx,
  htmlFile,
  layout = c(
```

```
        name="random",
        animate="true",
        animateFilter="function ( node, i ){ return true; }"
    )
)
```

# Index

- \* **Only**
  - .aspectClass, 5
- \* **‘aspectClasses’**
  - .aspectClass, 5
- \* **are**
  - .aspectClass, 5
- \* **aspects**
  - .aspectClass, 5
- \* **class**
  - .aspectClass, 5
- \* **datasets**
  - aspectClasses, 26
- \* **defined**
  - .aspectClass, 5
- \* **get**
  - .aspectClass, 5
- \* **internal**
  - .addAspectNameToJson, 3
  - .addAttributeData, 4
  - .aspectClass, 5
  - .convertRawList, 6
  - .createAttributeAspect, 6
  - .createCyVpPorD, 7
  - .errorCodes, 8
  - .filterBy, 10
  - .format, 11
  - .infer, 12
  - .json2RDataType, 13
  - .jsonL, 14
  - .jsonV, 15
  - .log, 15
  - .mergeAttributesAspect, 16
  - .mergeIdAspect, 17
  - .modClass, 18
  - .pasteC, 19
  - .renameDF, 20
  - .stop, 20
  - .summaryAspect, 23
  - .transformListLength<-, 23
  - .transformVLD, 24
  - .validateAttributesAspect, 25
  - .validateCyVisualPropertyPandD, 25
  - checks, 28
    - convert-data-types-and-values, 32
    - convert2json, 34
    - dot\_test, 55
    - markAttributeColumn, 71
    - markRefColumn, 72
    - RCX, 80
- \* **in**
  - .aspectClass, 5
- \* **of**
  - .aspectClass, 5
- \* **that**
  - .aspectClass, 5
- \* **the**
  - .aspectClass, 5
  - .addAspectNameToJson, 3
  - .addAttributeData, 4
  - .addClass (.modClass), 18
  - .addClass<- (.modClass), 18
  - .aspectClass, 5
  - .checkAllClass (checks), 28
  - .checkAllNumeric (checks), 28
  - .checkAllNumericOrInDict (checks), 28
  - .checkAnyNotNull (checks), 28
  - .checkBContainsAllA (checks), 28
  - .checkCharacter (checks), 28
  - .checkClass (checks), 28
  - .checkClassOneOf (checks), 28
  - .checkIsId (checks), 28
  - .checkIsUniqueId (checks), 28
  - .checkList (checks), 28
  - .checkLogical (checks), 28
  - .checkNamed (checks), 28
  - .checkNamedCharacter (checks), 28
  - .checkNamedList (checks), 28
  - .checkNamedLogical (checks), 28
  - .checkNamedNumeric (checks), 28
  - .checkNoNa (checks), 28
  - .checkNonNeg (checks), 28
  - .checkNumeric (checks), 28
  - .checkRefPresent (checks), 28
  - .checkRefs (checks), 28
  - .checkSameLength (checks), 28
  - .checkUnique (checks), 28

- .checkUniqueDF (checks), 28
- .convert2json (convert2json), 34
- .convertDataTypes
  - (convert-data-types-and-values), 32
- .convertRawList, 6
- .convertValues
  - (convert-data-types-and-values), 32
- .createAttributeAspect, 6, 17, 18
- .createCyVpPorD, 7
- .elementsBContainsAllA (checks), 28
- .elementsInDict (checks), 28
- .elementsUnique (checks), 28
- .elementsUniqueDF (checks), 28
- .errorCodes, 8
- .filterBy, 10
- .format, 11
- .formatComma (.format), 11
- .formatData (.format), 11
- .formatLog (.format), 11
- .formatO (.format), 11
- .formatParams (.format), 11
- .formatQuote (.format), 11
- .infer, 12
- .inferDataType (.infer), 12
- .inferIsList (.infer), 12
- .json2RDataType, 13
- .jsonL, 14
- .jsonV, 15
- .listAllNumeric (checks), 28
- .listAllNumericOrInDict (checks), 28
- .log, 15
- .markAttributeColumn<-
  - (markAttributeColumn), 71
- .markRefColumn<- (markRefColumn), 72
- .markReqRefColumn<- (markRefColumn), 72
- .mergeAttributesAspect, 7, 16, 18
- .mergeIdAspect, 7, 17, 17
- .modClass, 18
- .paramAnyNotNull (checks), 28
- .paramClass (checks), 28
- .paramIsOptionalId (checks), 28
- .paramNamed (checks), 28
- .paramNoNa (checks), 28
- .paramNonNeg (checks), 28
- .pasteC, 19
- .removeClass (.modClass), 18
- .removeClass<- (.modClass), 18
- .renameDF, 20
- .stop, 20
- .summaryAspect, 23
- .test\_AllowedColumnsPresent (dot\_test), 55
- .test\_AspectExist (dot\_test), 55
- .test\_AtLeastOneColumnPresent (dot\_test), 55
- .test\_AtLeastOneElementPresent (dot\_test), 55
- .test\_ContainsNA (dot\_test), 55
- .test\_DataTypeColumn (dot\_test), 55
- .test\_ElementIsList (dot\_test), 55
- .test\_ElementIsNumeric (dot\_test), 55
- .test\_IdsInAspect (dot\_test), 55
- .test\_IsCVPclass (dot\_test), 55
- .test\_IsCharacter (dot\_test), 55
- .test\_IsClass (dot\_test), 55
- .test\_IsList (dot\_test), 55
- .test\_IsLogical (dot\_test), 55
- .test\_IsNamedList (dot\_test), 55
- .test\_IsNumeric (dot\_test), 55
- .test\_IsPos (dot\_test), 55
- .test\_IsUnique (dot\_test), 55
- .test\_IsUniqueInLists (dot\_test), 55
- .test\_ListAllCharacter (dot\_test), 55
- .test\_ListAllContainsNA (dot\_test), 55
- .test\_ListAllNumeric (dot\_test), 55
- .test\_ListAllNumericOrInDict (dot\_test), 55
- .test\_ListAllOfClass (dot\_test), 55
- .test\_ListAllUnique (dot\_test), 55
- .test\_ListAllUniqueInLists (dot\_test), 55
- .test\_ListAllowedColumnsPresent (dot\_test), 55
- .test\_ListOfCVPclass (dot\_test), 55
- .test\_ListRequiredColumnsPresent (dot\_test), 55
- .test\_NoMergeColumn (dot\_test), 55
- .test\_OneNodePresent (dot\_test), 55
- .test\_RequiredColumnsPresent (dot\_test), 55
- .test\_ValuesInSet (dot\_test), 55
- .transformListLength<-, 23
- .transformVLD, 24
- .validateAttributesAspect, 25
- .validateCyVisualPropertyPandD, 25
- .validateListOfCyVisualPropertyPandD (.validateCyVisualPropertyPandD), 25
- aspectClass2Name
  - (Convert-Names-and-Classes), 32
- aspectClasses, 26, 74, 87, 88, 91

- aspectName2Class  
(Convert-Names-and-Classes), 32
- base::print(), 37
- cartesian layout, 64, 68
- CartesianLayout, 27, 81, 94, 95, 131, 134
- checks, 28
- convert-data-types-and-values, 32
- Convert-Names-and-Classes, 32
- convert2json, 34
- countElements, 35, 73
- createCartesianLayout  
(CartesianLayout), 27
- createCyGroups (CyGroups), 37
- createCyHiddenAttributes  
(CyHiddenAttributes), 39
- createCyNetworkRelations  
(CyNetworkRelations), 41
- createCySubNetworks (CySubNetworks), 42
- createCyTableColumn (CyTableColumn), 43
- createCyVisualProperties  
(CyVisualProperties), 45
- createCyVisualProperty  
(CyVisualProperty), 47
- createCyVisualPropertyDependencies  
(CyVisualPropertyDependencies), 49
- createCyVisualPropertyMappings  
(CyVisualPropertyMappings), 51
- createCyVisualPropertyProperties  
(CyVisualPropertyProperties), 53
- createEdgeAttributes (EdgeAttributes), 58
- createEdges (Edges), 60
- createNetworkAttributes  
(NetworkAttributes), 75
- createNodeAttributes (NodeAttributes), 77
- createNodes (Nodes), 79
- createRCX (RCX-object), 81
- custom-print, 36
- CX, 132–134
- CyGroups, 37, 81, 96, 97
- CyHiddenAttributes, 39, 82, 99, 100
- CyNetworkRelations, 27, 41, 42, 44, 82, 101–103, 105
- CySubNetworks, 7, 27, 42, 82, 102, 104, 105, 108, 111, 115
- CyTableColumn, 43, 82, 107, 108
- Cytoscape visual properties, 49, 51, 53, 109
- CyVisualProperties, 35, 45, 45, 47, 50, 51, 53, 61, 82, 109–111, 113
- CyVisualProperty, 45, 47, 47, 48–51, 53, 61, 62, 86, 109, 111, 113, 115
- CyVisualPropertyDependencies, 8, 25, 45, 47, 48, 49, 50, 51, 53, 61, 111, 113, 115
- CyVisualPropertyMappings, 8, 46–50, 51, 52–54, 62, 111, 113, 115
- CyVisualPropertyProperties, 8, 25, 45, 47–51, 53, 53, 61, 111, 113, 115
- dot\_test, 55
- edge, 64, 68
- edge id, 42
- edge ids, 38, 58
- EdgeAttributes, 58, 76, 78, 81, 116, 117, 123, 125
- edgeAttributes, 64, 68
- Edges, 38, 59, 60, 81, 97, 105, 117, 119, 120
- edges, 64, 68
- fromGraphNEL (graphNEL), 63
- fromIgraph (Igraph), 67
- getAspectClasses, 90
- getAspectClasses (aspectClasses), 26
- getCyVisualProperty, 46, 61, 111, 115
- graph vertex attributes, 64
- graphNEL, 63, 63, 64, 69
- hasIds, 65, 73
- hasIds(), 35, 67, 73, 88, 90
- idProperty, 66
- idProperty(), 35, 66, 73, 88, 90
- Igraph, 64, 67
- igraph, 67, 68
- igraph graph attributes, 68
- igraph vertex attributes, 68
- igraph::as\_graphnel(), 64
- jsonlite, 70, 87
- jsonlite::prettify(), 93, 133
- jsonToRCX, 69, 86–88
- markAttributeColumn, 71
- markRefColumn, 72
- maxId, 72, 73, 97, 105, 120, 127
- maxId(), 35, 66, 67, 73, 88, 90
- Meta-data, 73
- NetworkAttributes, 75, 78, 81, 118, 121–123, 125

- node, [27](#), [63](#), [64](#), [68](#)
- node id, [42](#), [60](#)
- node ids, [27](#), [38](#), [77](#)
- NodeAttributes, [70](#), [76](#), [77](#), [81](#), [118](#), [123–125](#)
- nodeAttributes, [64](#), [68](#)
- Nodes, [35](#), [38](#), [60](#), [64](#), [68](#), [78](#), [79](#), [81](#), [97](#), [105](#), [125](#), [127](#)
- nodes, [64](#), [68](#), [81](#)
- parseJSON (readCX), [86](#)
- print.CartesianLayoutAspect (custom-print), [36](#)
- print.CyGroupsAspect (custom-print), [36](#)
- print.CyHiddenAttributesAspect (custom-print), [36](#)
- print.CyNetworkRelationsAspect (custom-print), [36](#)
- print.CySubNetworksAspect (custom-print), [36](#)
- print.CyTableColumnAspect (custom-print), [36](#)
- print.CyVisualPropertiesAspect (custom-print), [36](#)
- print.CyVisualProperty (custom-print), [36](#)
- print.CyVisualPropertyDependencies (custom-print), [36](#)
- print.CyVisualPropertyMappings (custom-print), [36](#)
- print.CyVisualPropertyProperties (custom-print), [36](#)
- print.EdgeAttributesAspect (custom-print), [36](#)
- print.EdgesAspect (custom-print), [36](#)
- print.MetaDataAspect (custom-print), [36](#)
- print.NetworkAttributesAspect (custom-print), [36](#)
- print.NodeAttributesAspect (custom-print), [36](#)
- print.NodesAspect (custom-print), [36](#)
- print.RCX (custom-print), [36](#)
- processCX, [70](#)
- processCX (readCX), [86](#)
- RCX, [26](#), [35–38](#), [40](#), [44](#), [58](#), [59](#), [63](#), [64](#), [67](#), [68](#), [70](#), [73](#), [74](#), [76](#), [78](#), [80](#), [82](#), [86](#), [87](#), [90–97](#), [99–105](#), [107–111](#), [116](#), [117](#), [119–125](#), [127](#), [129](#), [131–134](#)
- RCX-object, [81](#)
- RCX-package (RCX), [80](#)
- rcxToJson, [71](#), [84](#), [93](#), [94](#), [131](#), [133](#), [134](#)
- readCX, [71](#), [86](#), [86](#), [94](#), [131](#), [133](#), [134](#)
- readJSON (readCX), [86](#)
- referredBy, [88](#)
- referredBy(), [35](#), [66](#), [67](#), [73](#), [90](#)
- refersTo, [89](#)
- refersTo(), [35](#), [66](#), [67](#), [73](#), [88](#)
- setExtension, [26](#), [90](#)
- subAspectClasses (aspectClasses), [26](#)
- subnetwork, [47](#), [64](#), [68](#)
- subnetwork id, [27](#), [41](#), [44](#), [58](#), [64](#), [68](#), [75](#), [77](#)
- subnetworks, [39](#), [41](#), [44](#), [58](#), [76](#), [78](#)
- summary, [37](#), [91](#)
- toCX, [71](#), [86](#), [93](#), [94](#), [131](#), [133](#), [134](#)
- toGraphNEL (graphNEL), [63](#)
- toIgraph (Igraph), [67](#)
- updateAspectClasses (aspectClasses), [26](#)
- updateCartesianLayout, [28](#), [94](#)
- updateCyGroups, [38](#), [96](#)
- updateCyHiddenAttributes, [40](#), [99](#)
- updateCyNetworkRelations, [42](#), [101](#)
- updateCySubNetworks, [43](#), [104](#)
- updateCyTableColumn, [44](#), [107](#)
- updateCyVisualProperties, [46](#), [48](#), [50](#), [52](#), [54](#), [62](#), [109](#), [115](#)
- updateCyVisualProperty, [46](#), [48](#), [50](#), [52](#), [54](#), [62](#), [111](#), [113](#)
- updateEdgeAttributes, [59](#), [116](#)
- updateEdges, [61](#), [87](#), [119](#)
- updateMetaData (Meta-data), [73](#)
- updateMetaDataProperties, [74](#), [120](#)
- updateNetworkAttributes, [76](#), [121](#)
- updateNodeAttributes, [78](#), [124](#)
- updateNodes, [80](#), [87](#), [127](#)
- validate, [128](#)
- vertex, [64](#), [68](#)
- visualize, [131](#), [134](#)
- writeCX, [71](#), [86](#), [88](#), [94](#), [131](#), [132](#), [134](#)
- writeHTML, [131](#), [133](#)