Package ‘nonmemica’

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Title Create and Evaluate NONMEM Models in a Project Context
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Author Tim Bergsma
Maintainer Tim Bergsma <bergsmat@gmail.com>
Description Systematically creates and modifies NONMEM(R) control streams. Harvests NONMEM output, builds run logs, creates derivative data, generates diagnostics. NONMEM (ICON Development Solutions <http://www.iconplc.com/>) is software for nonlinear mixed effects modeling. See 'package?nonmemica'.
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<td>tad1</td>
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<td>tod</td>
</tr>
</tbody>
</table>
### absolute

**Description**

Checks if file path is absolute.

**Usage**

```r
absolute(x)
```

**Arguments**

- `x` character (a file path)

**Value**

logical; TRUE if x starts with / or .: (e.g. C:)

---

### as.halfmatrix.default

**Coerce to Half Matrix by Default**

**Description**

Coerces to half matrix. Treats x as halfmatrix, coerces to matrix and takes half.

**Usage**

```r
## Default S3 method:
as.halfmatrix(x, ...)
```

**Arguments**

- `x` object
- `...` passed arguments
See Also

Other halfmatrix: `as.data.frame.halfmatrix()`, `as.halfmatrix.default()`, `as.halfmatrix.halfmatrix()`, `as.matrix.halfmatrix()`, `half()`, `is.square.matrix()`, `is.square()`, `offdiag.halfmatrix()`, `offdiag()`, `ord.halfmatrix()`, `ord.matrix()`, `ord()`, `print.halfmatrix()`

---

as.matrix.halfmatrix  Coerce Half Matrix to Matrix

Description

Coerces half matrix to matrix.

Usage

```r
## S3 method for class 'halfmatrix'
as.matrix(x, ...)
```

Arguments

- `x`: object
- `...`: passed arguments

See Also

Other halfmatrix: `as.data.frame.halfmatrix()`, `as.halfmatrix.default()`, `as.halfmatrix.halfmatrix()`, `as.halfmatrix()`, `half.matrix()`, `half()`, `is.square.matrix()`, `is.square()`, `offdiag.halfmatrix()`, `offdiag()`, `ord.halfmatrix()`, `ord.matrix()`, `ord()`, `print.halfmatrix()`

---

as.xml_document  Create an xml_document in a Project Context

Description

Creates an xml_document in a project context.

Usage

```r
as.xml_document(x, ...)
```

```
## S3 method for class 'xml_document'
as.xml_document(x, ...)
```

```
## S3 method for class 'character'
as.xml_document(x, strip.namespace = TRUE, ...)
```
contains

Arguments

  x  object of dispatch
  ... arguments to methods
  strip.namespace whether to strip e.g. nm: from xml elements

Value

xml_document
xml_document
xml_document

Methods (by class)

  • xml_document: xml_document method
  • character: filepath method

See Also

xpath

Other xpath: as.xml_document.numeric(), xpath()
  Other xpath: as.xml_document.numeric(), xpath()
  Other xpath: as.xml_document.numeric(), xpath()

Examples

library(magrittr)
options(project = system.file('project/model', package='nonmemica'))
1001 %>% as.xml_document

contains  Check Whether Text Contains Pattern

Description

Checks whether text contains pattern.

Usage

contains(pattern, text, ...)

Arguments

  pattern regular expression
  text character vector to check
  ... arguments to methods
Value

logical

See Also

%contains%

datafile.character Identify the Datafile for a Model

Description

Identifies the datafile used by a model. Expresses it relative to current working directory.

Usage

## S3 method for class 'character'
datafile(x, ...)

Arguments

x the model name or path to a control stream

... ext can be passed to modelfile, etc.

Value

character

See Also

Other path: datafile.numeric(), datafile(), modeldir(), modelfile(), modelpath.character(), modelpath.numeric(), modelpath(), psn_options(), specfile.character(), specfile.numeric(), specfile()

Examples

library(spec)
source <- system.file(package = 'nonmemica', 'project')
target <- tempdir()
target <- gsub('\\\\', '/', target) # for windows
file.copy(source, target, recursive = TRUE)
project <- file.path(target, 'project', 'model')
options(project = project)
library(magrittr)
1001 %>% datafile
datafile(1001) %matches% specfile(1001)
1001 %>% specfile
1001 %>% specfile %>% read.spec
**Harvest Model Item Definitions**

**Description**
Harvests model item definitions.

Creates a model item definitions from a definitions object.

Create Item Definitions from Model Name

**Usage**
definitions(x, ...)

```r
## S3 method for class 'definitions'
definitions(x, ...)

## S3 method for class 'character'
definitions(
x,
verbose = FALSE,
ctlfile = modelfile(x, ...),
metafile = modelpath(x, "def", ...),
fields =getOption("fields", default = c("symbol", "label", "unit")),
read = length(metafile) == 1,
write = FALSE,
...
)
```

**Arguments**
- `x` object of dispatch
- `...` arguments to methods
- `verbose` set FALSE to suppress messages
- `ctlfile` path to control stream (pass length-zero argument to ignore)
- `metafile` path to definitions file (pass length-zero argument to ignore)
- `fields` metadata fields to read from control stream if no metafile
- `read` whether to read the definitions file
- `write` whether to write the definitions file

**Details**
x can be numeric or character model name, assuming project is identified by argument or option.
Just returns the object unmodified.

Creates item definitions from a model name. Scavenges definitions optionally from the control stream and optionally from the definitions file. Optionally writes the result to the definitions file. Always returns a data.frame with at least the column ’item’ but possibly no rows.
depends.default

Value

object of class definitions, or path to metafile if write = TRUE.

Methods (by class)

- definitions: definitions method
- character: character method

See Also

definitions.character
as.xml_document.character
as.bootstrap.character
as.model.character

Other definitions: definitions.numeric()

Examples

library(magrittr)
options(project = system.file('project/model',package='nonmemica'))
1001 %>% definitions

--------

depsends.default Identify Model Dependencies

Description

Identify those models in the lineage of models in x.

Usage

## Default S3 method:
depends(x, ...)

Arguments

x object
...

passed arguments

Value

character
errors.character

See Also

Other depends: depends()

 errors.character Get Errors for Character

Description

Gets model asymptotic standard errors in canonical order, treating character as model names. See parameters for a less formal interface.

Usage

## S3 method for class 'character'
errors(
  x,
  xmlfile = modelpath(x, ext = "xml", ...),
  stripnamespace = TRUE,
  digits = 3,
  ...
)

Arguments

  x            character (modelname)
  xmlfile      path to xml file
  strip.namespace whether to strip e.g. nm: from xml elements for easier xpath syntax
  digits       passed to signif
  ...          dots

Value

numeric

See Also

nms_canonical errors

Other errors: errors.numeric(), errors()

Examples

library(magrittr)
options(project = system.file('project/model',package='nonmemica'))
1001 %>% errors
estimates.character  

Get Estimates for Character

Description

Gets model parameter estimates in canonical order, treating character as model names. See parameters for a less formal interface.

Usage

## S3 method for class 'character'
estimates(
  x,
  xmlfile = modelpath(x, ext = "xml", ...),
  strip.namespace = TRUE,
  digits = 3,
  ...
)

Arguments

- **x** character (modelname)
- **xmlfile** path to xml file
- **strip.namespace** whether to strip e.g. nm: from xml elements for easier xpath syntax
- **digits** passed to signif
- **...** dots

Value

numeric

See Also

nms_canonical errors
Other estimates: estimates.numeric(), estimates()

Examples

library(magrittr)
options(project = system.file('project/model',package='nonmemica'))
1001 %>% estimates
## Check If Model is Fixed

### Description

Checks if model is fixed. Returns a logical vector with element for each init, in canonical order.

### Usage

```r
## S3 method for class 'model'
fixed(x, ...)
```

### Arguments

- `x`: object
- `...`: dots

### Value

Logical

### See Also

Other fixed: `fixed<-.inits()`, `fixed<-.init()`, `fixed<-.model()`, `fixed<-()`, `fixed()`

### Examples

```r
library(magrittr)
options(project = system.file('project/model', package='nonmemica'))
1001 %>% as.model %>% fixed
```

## Generalize a Nonmissing Value

### Description

# Generalize a nonmissing value. If there is only one such among zero or more NA, impute that value for all NA.

### Usage

```r
generalize(x, ...)
```

### Arguments

- `x`: vector
- `...`: ignored
See Also

Other superset: meta.character(), meta.numeric(), metaplot.character(), metaplot.numeric(),
metaplot_character(), metasuperset(), meta(), ninput.character(), ninput.numeric(),
ninput(), shuffle(), superset.character(), superset.numeric(), superset(), superspec.character(),
superspec.numeric(), superspec()

---

initial.model

*Get Model Initial Estimates*

**Description**

Gets model initial estimates.

**Usage**

```r
## S3 method for class 'model'
initial(x, ...)
```

**Arguments**

- `x`: model
- `...`: dots

**See Also**

Other initial: initial<-.model(), initial<-, initial()

**Examples**

```r
library(magrittr)
options(project = system.file('project/model',package='nonmemica'))
1001 %>% as.model %>% initial
```

---

initial<-.model

*Set Upper Bounds for Model Initial Estimates*

**Description**

Sets upper bounds for model initial estimates.

**Usage**

```r
## S3 replacement method for class 'model'
initial(x) <- value
```
likebut

Arguments

<table>
<thead>
<tr>
<th>x</th>
<th>model name, presumably interpretable as numeric</th>
</tr>
</thead>
<tbody>
<tr>
<td>but</td>
<td>a short description of the characteristic difference from x</td>
</tr>
<tr>
<td>y</td>
<td>optional name for model to be created, auto-incremented by default</td>
</tr>
<tr>
<td>project</td>
<td>project directory</td>
</tr>
<tr>
<td>nested</td>
<td>model files nested in run-specific directories</td>
</tr>
<tr>
<td>overwrite</td>
<td>whether to overwrite if it exists</td>
</tr>
<tr>
<td>ext</td>
<td>extension for the model file</td>
</tr>
<tr>
<td>include</td>
<td>regular expressions for files to copy to new directory</td>
</tr>
<tr>
<td>update</td>
<td>use final estimates of x as initial estimates of y</td>
</tr>
<tr>
<td>...</td>
<td>passed arguments, including PsN runrecord elements (experimental)</td>
</tr>
</tbody>
</table>

See Also

Other initial: initial.model(), initial<-(), initial()
lower.model

Value

the value of y

See Also

runlog.character

Examples

# Create a working project.
source <- system.file(package = 'nonmemica', 'project')
target <- tempdir()
target <- gsub('\\','/',target) # for windows
source
target
file.copy(source,target,recursive = TRUE)
project <- file.path(target,'project','model')

# Point project option at working project
options(project = project)
library(magrittr)

# Derive models.
1001 %>% likebut('revised',y = 1002, overwrite=TRUE )

# At this point, edit 1002.ctl to match whatever 'revised' means.
# Then run it with NONMEM.
**lower<-.model**

### Examples

```r
library(magrittr)
options(project = system.file('project/model', package='nonmemica'))
1001 %>% as.model %>% lower
```

---

**lower<- .model**  
*Set Lower Bounds for Model Initial Estimates*

### Description

Sets lower bounds for model initial estimates.

### Usage

```r
## S3 replacement method for class 'model'
lower(x) <- value
```

### Arguments

- `x`: model
- `value`: numeric

### See Also

Other lower: `lower.model()`, `lower<-()`, `lower()`

---

**meta.character**  
*Get Metadata for Character*

### Description

Gets metadata for character, treating it as a model name. Blends metadata from specfile with metadata from control stream, removing both exact duplicates as well as redefined values (with warning).

### Usage

```r
## S3 method for class 'character'
meta(x, simplify = TRUE, ...)
```

### Arguments

- `x`: object
- `simplify`: logical: remove range information from guide text
- `...`: passed arguments
### metaplot.character

**Value**

data.frame

**See Also**

Other superset: `generalize()`, `meta.numeric()`, `metaplot.character()`, `metaplot.numeric()`, `metaplot_character()`, `metasuperset()`, `meta()`, `ninput.character()`, `ninput.numeric()`, `ninput()`, `shuffle()`, `superset.character()`, `superset.numeric()`, `superset()`, `superspec.character()`, `superspec.numeric()`, `superspec()`

### Examples

```r
library(magrittr)
options(project = system.file('project/model',package='nonmemica'))
1001 %>% meta
```

---

#### metaplot.character

**Metaplot Character**

**Description**

Plots character by treating as model name. A dataset is constructed by combining the meta version of the model input with a meta version of the model output and calling metaplot with the result.

**Usage**

```r
## S3 method for class 'character'
metaplot(x, ..., groups, meta = match.fun("meta")(x), subset)
```

**Arguments**

- `x` object
- `...` unquoted names of variables to plot, or other named arguments (passed)
- `groups` columns by which to group the dataset
- `meta` metadata; `meta(x)` by default
- `subset` a condition for filtering data

**See Also**

Other superset: `generalize()`, `meta.character()`, `meta.numeric()`, `metaplot.numeric()`, `metaplot_character()`, `metasuperset()`, `meta()`, `ninput.character()`, `ninput.numeric()`, `ninput()`, `shuffle()`, `superset.character()`, `superset.numeric()`, `superset()`, `superspec.character()`, `superspec.numeric()`, `superspec()`
Examples

```r
library(magrittr)
library(metaplot)
options(project = system.file('project/model', package = 'nonmemica'))

## Not run:
1001 %>% metaplot(CWRESI, TAD, SEX, groups = c('ID', 'TIME'),
                   subset = 'MDV == 0', yref = 0, ysmooth = TRUE)

## End(Not run)
```

Description

Plots character by treating as model name. A dataset is constructed by combining the model input with a the model output and calling metaplot with the result.

Usage

```r
metaplot_character(x, groups, meta = NULL, subset, var, ...)
```

Arguments

- `x` object
- `groups` columns by which to group the dataset
- `meta` metadata; meta(x) by default
- `subset` a condition for filtering data
- `var` variables to plot
- `...` passed arguments

See Also

Other superset: `generalize()`, `meta.character()`, `meta.numeric()`, `metaplot.character()`, `metaplot.numeric()`, `metasuperset()`, `meta()`, `ninput.character()`, `ninput.numeric()`, `ninput()`, `shuffle()`, `superset.character()`, `superset.numeric()`, `superset()`, `superspec.character()`, `superspec.numeric()`, `superspec()`
### metasuperset

#### Retrieve Model Outputs with Metadata

**Description**

Retrieves model outputs with metadata.

**Usage**

```r
metasuperset(
  x,
  groups,
  meta = match.fun("meta")(...),
  subset =getOption("metasuperset_subset", NULL),
  ...
)
```

**Arguments**

- `x`  
  model name
- `groups`  
  vector of key column names in superset, e.g. USUBJID, TIME
- `meta`  
  metadata with column 'item' and possibly attributes such as 'label' and 'guide'
- `subset`  
  length-one character: a condition for filtering results, e.g. 'EVID == 0'
- `...`  
  passed arguments

**Value**

data.frame

**See Also**

Other superset: `generalize()`, `meta.character()`, `meta.numeric()`, `metaplot.character()`, `metaplot.numeric()`, `ninput.character()`, `ninput.numeric()`, `shuffle()`, `superset.character()`, `superset.numeric()`, `superspec.character()`, `superspec.numeric()`, `superspec()`

**Examples**

```r
library(magrittr)
options(project = system.file('project/model',package='nonmemica'))
1001 %>% metasuperset(c('ID','TIME')) %>% head
```
modeldir

Identify the Directory for a Model

Description
Identifies the directory used by a model.

Usage
modeldir(x, ext, ...)

Arguments
- x: the model name
- ext: model file extension
- ...: passed arguments

Value
character

See Also
Other path: datafile.character(), datafile.numeric(), datafile(), modelfile(), modelpath.character(),
modelpath.numeric(), modelpath(), psn_options(), specfile.character(), specfile.numeric(),
specfile()

Examples
library(magrittr)
options(project = system.file('project/model', package='nonmemica'))
1001 %>% modeldir

modelfile

Identify the Modelfile for a Model

Description
Identifies the modelfile used by a model.

Usage
modelfile(x, ext = getOption("modex", "ctl"), ...)

modelpath

Resolve A Path to a Model-related File

Description
Resolves a path to a model-related file.

Usage
modelpath(x, ...)

Arguments
x object
... passed arguments

Value
character

See Also
Other path: datafile.character(), datafile.numeric(), datafile(), modeldir(), modelpath.character(), modelpath.numeric(), modelpath(), psn_options(), specfile.character(), specfile.numeric(), specfile()
Examples

```r
library(magrittr)
options(project = system.file('project/model', package='nonmemica'))
1001 %>% modelpath
```

---

`modelpath.character`  
**Resolve A Path to a Model-related File for Character**

Description

Resolves a path to a model-related file, treating `x` as a model name. By default (`ext` is `NULL`) the run directory is returned. As of version 0.9.2, `nested` can be a function of `ext` and ... That returns logical.

Usage

```r
## S3 method for class 'character'
modelpath(
  x,
  ext = NULL,
  project =getOption("project", getwd()),
  nested =getOption("nested", TRUE),
  ... 
)
```

Arguments

- `x` object
- `ext` file extension, no leading dot
- `project` project directory
- `nested` whether model files are nested in eponymous directories
- `...` passed arguments

Value

character

See Also

Other path: `datafile.character()`, `datafile.numeric()`, `datafile()`, `modeldir()`, `modelfile()`, `modelpath.numeric()`, `modelpath()`, `psn_options()`, `specfile.character()`, `specfile.numeric()`, `specfile()`
Calculate Number of Inputs

Description

Calculates number of inputs.

Usage

```r
ninput(x, ...)
```

Arguments

- `x`: object
- `...`: passed arguments

See Also

Other superset: `generalize()`, `meta.character()`, `meta.numeric()`, `metaplot.character()`, `metaplot.numeric()`, `metasuperset()`, `meta()`, `ninput.character()`, `ninput.numeric()`, `shuffle()`, `superset.character()`, `superset.numeric()`, `superset()`, `superspec.character()`, `superspec.numeric()`, `superspec()`

Calculate Number of Inputs for Character

Description

Calculates number of inputs for character by treating as a model name.

Usage

```r
## S3 method for class 'character'
ninput(x, ...)
```

Arguments

- `x`: character
- `...`: passed arguments

Value

integer
nininput.numeric

See Also

Other superset: generalize(), meta.character(), meta.numeric(), metaplot.character(), metaplot.numeric(), metaplot_character(), metasuperset(), meta(), nininput.numeric(), nininput(), shuffle(), superset.character(), superset.numeric(), superset(), superspec.character(), superspec.numeric(), superspec()

---

nininput.numeric

Calculate Number of Inputs for Numeric

Description

Calculates number of inputs for numeric by coercing to character.

Usage

```r
## S3 method for class 'numeric'
ininput(x, ...)
```

Arguments

- `x`: numeric
- `...`: passed arguments

See Also

Other superset: generalize(), meta.character(), meta.numeric(), metaplot.character(), metaplot.numeric(), metaplot_character(), metasuperset(), meta(), nininput.character(), nininput(), shuffle(), superset.character(), superset.numeric(), superset(), superspec.character(), superspec.numeric(), superspec()

---

nms_canonical.character

Generate Canonical Names for Character

Description

Generates canonical names for character by converting to parsed model.

Usage

```r
## S3 method for class 'character'
nms_canonical(x, ...)
```
nms_canonical.model

Arguments

x  object of dispatch

... passed arguments

Examples

library(magrittr)
options(project = system.file('project/model',package='nonmemica'))
1001 %>% nms_canonical

Description

Generates canonical names for a NONMEM control stream object. Canonical names indicate all and only the declared model parameters in lower-case conventional order (theta, omega row-major, sigma) with underscores and two-digit (or more) indices. E.g. theta_01, theta_02, omega_01_01, omega_02_01, omega_02_02, omega_01_01.

Usage

## S3 method for class 'model'
nms_canonical(x, ...)

Arguments

x  a model designator

... passed arguments

Value

canonical (character)

See Also

as.model
nms_nonmem.character  Generate NONMEM-style Names for Character

Description
Generates NONMEM-style names for numeric by converting to parsed model.

Usage
## S3 method for class 'character'
nms_nonmem(x, ...)

Arguments
x object of dispatch
...

passed arguments

See Also
Other nms_nonmem: nms_nonmem.model(), nms_nonmem.numeric(), nms_nonmem()

Examples
library(magrittr)
options(project = system.file('project/model',package='nonmemica'))
1001 %>% nms_nonmem

nms_nonmem.model  Generate NONMEM-style Names for Model

Description
Generates NONMEM-style names for parameters declared in a NONMEM control stream object. PsN uses NONMEM-style names, substituting a comment, if any: everything after the first semicolon, up to the second semicolon if present, without leading/trailing spaces/tabs.

Usage
## S3 method for class 'model'
nms_nonmem(x, ...)

Arguments
x a model designator
...

passed arguments
Value

nonmem (character)

See Also

as.model

Other nms_nonmem: nms_nonmem.character(), nms_nonmem.numeric(), nms_nonmem()

---

nms_psn.character  Generate PsN-style Names for Character

Description

Generates PsN-style names for numeric by converting to parsed model.

Usage

```r
## S3 method for class 'character'
nms_psn(x, ...)
```

Arguments

x  
object of dispatch

...  
passed arguments

Examples

```r
library(magrittr)
options(project = system.file('project/model', package='nonmemica'))
1001 %>% nms_psn
```

---

nms_psn.model  Generate PsN-style Names for Model

Description

Generates PsN-style names for parameters declared in a NONMEM control stream object. PsN uses NONMEM-style names, substituting a comment, if any: everything after the first semicolon, up to the second semicolon if present, without leading/trailing spaces/tabs.

Usage

```r
## S3 method for class 'model'
nms_psn(x, ...)
```
Arguments

- x: a model designator
- ... passed arguments

Value

psn (character)

See Also

as.model

Nonmemica (emphasis like 'America') creates and evaluates NONMEM models in a project context.

Details

NONMEM (ICON Development Solutions) is software for nonlinear mixed effects modeling. The fundamental interface is a text file (control stream, typ. *.mod or *.ctl) that specifies model input, structure, and output. There are many add-on interfaces for NONMEM (see references for a few examples). However, much day-to-day modeling, even for R users, involves substantial manual interventions.

Nonmemica streamlines interactions with NONMEM. It adopts some established conventions and techniques (e.g. from PsN and metrumrg), but introduces others that may be useful. Principally, it parses existing control streams for systematic analysis and alteration. Relatively simple, single-problem control streams are supported; see the example.

Of course, NONMEM itself is licensed software that must be installed independently. Nonmemica is largely indifferent to how NONMEM is installed or invoked. However, several features depend on the *.xml output that NONMEM creates; make sure it is available. Also, the best-supported directory structure is that which has numbers for model names, with all model-specific files in eponymous subdirectories of a "project" directory. An example is given below.

Nonmemica adopts three control stream encoding conventions that merit special mention. First, the problem statement is encoded in the form //like/x//but/y// where x is a reference model name and y is a feature difference from the reference model (see likebut() ). This allows any given model to be described by chaining together its legacy of features (use runlog(depenencies = TRUE, ... ) ), which generally works better than trying to describe it exhaustively in the model name. As of version 0.9.2, experimental support is available for natural-language problem statements of the form "like run1001 but fixed additive error".

Second, Nonmemica only needs a single output table ($TABLE record). Be sure to use ONE-HEADER but avoid FIRSTONLY. Nonmemica will integrate model inputs and outputs, regardless of table counts, into one data.frame (see superset() ).
Third, Nonmemica supports integrated metadata. With respect to model inputs, use package spec to store column metadata in a companion file (a data specification, e.g. *.spec). Keep the data file and data specification in a central location, not copied to the model directory. For model outputs (tabled items) supply column metadata directly in the control stream (or a *.def file; see example and help).

Nonmemica supports three global options: 'project' (default getwd() ) is the parent directory of model-specific files or directories; 'nested' (default TRUE) tells whether model-specific files are nested within eponymous directories; 'modex' (default 'ctl') gives the file extension for control streams. In many cases you can pass these options to the relevant functions; but since they likely won’t change for the scope of a given project, it saves effort to set them as global options (if they differ from the defaults) using e.g. options(project=).

Numbers make good names for models because it is never hard for you or the software to think of a new one. That said, model names are typically processed as character in Nonmemica. There are many generic functions with both numeric and character methods that simply assume the (length-one) argument you supply is a model name.

References

NONMEM
Icon
PsN
Xpose
Wings for NONMEM
R speaks NONMEM
metrumrg

Examples

# Create a working project.
source <- system.file(package = 'nonmemica','project')
target <- tempdir()
target <- gsub('\\','/',target) # for windows
source
target
file.copy(source,target,recursive = TRUE)
project <- file.path(target,'project','model')

# Point project option at working project
options(project = project)

# Load some packages
library(magrittr)
library(metaplot)
library(wrangle)
library(spec)
library(dplyr,warn.conflicts = FALSE)
# Identify features of a model.
1001 %>% modelpath
1001 %>% modeldir
1001 %>% modelfile
1001 %>% modelpath('xml')
1001 %>% datafile
datafile(1001) %matches% specfile(1001)
1001 %>% specfile
1001 %>% specfile %>% read.spec
1001 %>% as.model
1001 %>% as.model %>% comments
1001 %>% definitions
1001 %>% runlog(TRUE)
1001 %>% runlog
1001 %>% partab
1001 %>% num_parameters
1001 %>% mms_canonical
1001 %>% mms_psn
1001 %>% mms_nonmem
1001 %>% parameters
1001 %>% errors
1001 %>% as.model %>% initial
1001 %>% as.model %>% lower
1001 %>% as.model %>% upper
1001 %>% as.model %>% fixed
1001 %>% meta %>% class
1001 %>% meta

# Derive datasets.
1001 %>% superset %>% head
1001 %>% superset %>% filter(VISIBLE == 1) %>% group_by(ID,TIME) %>% status
1001 %>% metasuperset(c('ID','TIME')) %>% head
1001 %>% metasuperset(c('ID','TIME')) %>% sapply(attr,'label')

# Make diagnostic plots.
1001 %>% metaplot(
    CWRESI, TAD, SEX,
    groups = c('ID','TIME'),
    subset = 'MDV == 0',
    yref = 0,
    ysmooth = TRUE
)
1001 %>% metaplot(
    ETA1, SEX,
    ref = 0,
    groups = c('ID','TIME'),
    subset = 'MDV == 0'
)
1001 %>% metaplot(
    SEX, ETA1,
    ref = 0,
    groups = c('ID','TIME'),
    subset = 'MDV == 0'
Isolate Off-diagonal of Half Matrix

Description

Isolates off-diagonal of halfmatrix.

Usage

```r
## S3 method for class 'halfmatrix'
offdiag(x, ...)
```

Arguments

- `x` object
- `...` passed arguments

See Also

Other halfmatrix: `as.data.frame.halfmatrix()`, `as.halfmatrix.default()`, `as.halfmatrix.halfmatrix()`, `as.halfmatrix()`, `as.matrix.halfmatrix()`, `half.matrix()`, `half()`, `is.square.matrix()`, `is.square()`, `offdiag()`, `ord.halfmatrix()`, `ord.matrix()`, `ord()`, `print.halfmatrix()`
parameters.character

Get Parameters for Character

Description

Gets parameters, treating character as model names. If x is length one, slightly more details are returned such as datafile, reference model, and feature. Otherwise results are bound together, one model per column. See estimates and errors for a more formal interface to model estimates and asymptotic standard errors.

Usage

## S3 method for class 'character'
parameters(x, simplify = FALSE, ...)

Arguments

x object
simplify if x is length one and simplify is TRUE, return a named vector
... passed arguments

Value
data.frame

See Also

Other parameters: parameters.numeric(), parameters()

Examples

library(magrittr)
options(project = system.file('project/model',package='nonmemica'))
1001 %>% parameters

partab

Create Parameter Table

Description

Creates a parameter table.

Creates a model parameter table from a partab object.
partab.character

Create a Parameter Table from Model Name

Description

Creates a parameter table from a model name. Pass the project argument or set the project option.

Usage

```r
## S3 method for class 'character'
partab(
  x,
  verbose = FALSE,
  lo = "5",
  hi = "95",
  metafile = modelpath(x, "def", ...),
  xmlfile = modelpath(x, "xml", ...),
  ctlfile = modelfile(x, ...),
  bootcsv,
  strip.namespace = TRUE,
)```
skip = 28,
check.names = FALSE,
digits = 3,
ci = TRUE,
open = "(",
close = ")",
sep = ",",
format = TRUE,
fields = getOption("fields", default = c("symbol", "label", "unit")),
relative = TRUE,
percent = relative,
going = TRUE,
nonzero = TRUE,
shrinkage = FALSE,
correlation = FALSE,
...  
)

Arguments

x # a model name (numeric or character)
verbose # set FALSE to suppress messages
lo # the PsN bootstrap lower confidence limit (%)
hi # the PsN bootstrap upper confidence limit (%)
metafile # optional metadata for parameter table (see also: fields)
xmlfile # path to xml file
ctrlfile # path to control stream
bootscsv # path to PsN bootstrap_results.csv
strip.namespace # whether to strip e.g. nm: from xml elements for easierxpath syntax
skip # number of lines to skip in bootstrap_results.csv
check.names # passed to bootstrap reader
digits # limits numerics to significant digits (use NULL to suppress)
ci # combine bootstrap lo and hi into an enclosed interval
open # first character for bootstrap interval
close # last character for bootstrap interval
sep # separator for bootstrap interval
format # format numerics as character
fields # metadata fields to read from control stream. See details.
relative # transform standard errors to relative standard errors: rse replaces se
percent # if relative is true, express as percent (else ignore): prse replaces se
nonzero # limit random effects to those with nonzero estimates
shrinkage # whether to include percent shrinkage on random effects
correlation # whether to include correlation of random effects (as percent if percent is true)
... # passed to other functions
problem.character

Details

Normally you can just call the generic. Suitable defaults are supplied, but much customization is supported by means of arguments documented here and in called functions.

Metadata can be added to the parameter table two ways: as markup in the control stream, and as a *.def file in the model directory. See vignette('parameter-table') for details.

Value

object of class partab, data.frame

See Also

as.xml_document.character
as.bootstrap.character
as.model.character
as.csv

Other partab: partab.numeric(), partab()

Examples

library(magrittr)
options(project = system.file('project/model',package='nonmemica'))
1001 %>% partab
1001 %>% partab(shrinkage = TRUE, correlation = TRUE)

problem.character Identify the Model Problem Statement for Character

Description

Identifies the model problem statement for character (model name).

Usage

## S3 method for class 'character'
problem(x, ...)

Arguments

x object
...

passed arguments

Value

character
## psn_nested

**See Also**

Other problem: `as.problem()`, `problem.numeric()`, `problem()`

---

**Description**

PsN Model File is Nested Check whether a particular file extension corresponds to a file that is nested within a subdirectory using default PsN conventions.

**Usage**

```r
psn_nested(x, ...)
```

**Arguments**

- `x` character, a file extension, without dot.
- `...` ignored

**Value**

logical

**Examples**

```r
psn_nested('mod')
```

---

## psn_options

**Description**

Set PsN Options Sets PsN-style directory and control stream options. Supports control streams with semicolon-delimited metadata including symbol, unit, transform, and label. Expects model files to be found in nested directory, except for *.mod and *.lst.

```r
psn_options
```

**Value**

Set PsN Options Sets PsN-style directory and control stream options. Supports control streams with semicolon-delimited metadata including symbol, unit, transform, and label. Expects model files to be found in nested directory, except for *.mod and *.lst.
Usage

psn_options(
    project = "NONMEM",
    modex = "mod",
    fields = c("symbol", "unit", "transform", "label"),
    nested = psn_nested,
    ...
)

Arguments

project character, path to project directory
modex character, extension for model control stream (no dot)
fields character
nested logical, or function of file extension returning logical
... ignored

Value

used for side-effects (sets options 'fields' and 'nested')

See Also

Other path: datafile.character(), datafile.numeric(), datafile(), modeldir(), modelfile(), modelpath.character(), modelpath.numeric(), modelpath(), specfile.character(), specfile.numeric(), specfile()

Examples

## Not run:
psn_options()

## End(Not run)

---

relativizePath Relativize a Path

Description

Relativizes a path.

Usage

relativizePath(x, dir = getwd(), sep = "/", ...)

relativizePath
Relativize a Path

Description

Relativizes a path.

Usage

relativizePath(x, dir = getwd(), sep = "/", ...)

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Usage

relativizePath(x, dir = getwd(), sep = "/", ...)

relativizePath
Relativize a Path

Description

Relativizes a path.

Usage

relativizePath(x, dir = getwd(), sep = "/", ...)

relativizePath
Relativize a Path

Description

Relativizes a path.
Arguments

- `x` a file path
- `dir` a reference directory
- `sep` path separator
- `...` ignored arguments

Details

`x` and `dir` are first normalized, then `x` is expressed relative to `dir`. If `x` and `dir` are on different drives (i.e. C:/ D:/) `x` is returned as an absolute path.

---

### resolve

**Resolve File Path**

**Description**

Resolves a file path. Returns the path if absolute. If relative, concatenates the directory and file.

**Usage**

```r
resolve(file, dir)
```

**Arguments**

- `file` path to a file
- `dir` reference directory for a relative file path

**Value**

character

---

### runlog.character

**Create a Runlog for Character**

**Description**

Creates a Runlog for character by treating `x` as `modelname(s)`.

**Usage**

```r
## S3 method for class 'character'
runlog(x, dependencies = FALSE, digits = 3, places = 0, ...)
```
safe_join

Arguments

- **x**: object
- **dependencies**: whether to log runs in lineage(s) as well
- **digits**: significance for parameters
- **places**: rounding for objective function
- **...**: passed arguments

Value

data.frame

See Also

- **likebut**
- Other runlog: `runlog.numeric()`, `runlog()`

Examples

```r
library(magrittr)
options(project = system.file('project/model', package='nonmemica'))
# likebut(2001,'2 cmt', 2002) # edit manually, then ...
# likebut(2002,'add. err.', 2003) # edit manually, then ...
# likebut(2003,'allo. WT on CL',2004) # edit manually, then ...
# likebut(2004,'estimate allometry', 2005) # edit manually, then ...
# likebut(2005,'SEX on CL', 2006) # edit manually, then ...
# likebut(2006,'full block omega', 2007) # edit manually, then run all
2007 %>% runlog(dependencies = TRUE)
```

Description

Joins data safely. Generic, with method for data.frame.

Usage

```r
safe_join(x, ...)
```

Arguments

- **x**: object of dispatch
- **...**: arguments to methods

See Also

- **safe_join.data.frame**
- Other safe_join: `safe_join.data.frame()`
safe_join.data.frame  Join Data Frames Safely

Description

Joins data frames safely. I.e., a left join that cannot alter row order or number. Supports the case where you only intend to augment existing rows with additional columns and are expecting singular matches. Gives an error if row order or number would have been altered by a left join.

Usage

## S3 method for class 'data.frame'
safe_join(x, y, ...)

Arguments

x  data.frame
y  data.frame
... passed to dplyr::left_join

See Also

Other safe_join: safe_join()

Examples

library(magrittr)
x <- data.frame(code = c('a','b','c'), value = c(1:3))
y <- data.frame(code = c('a','b','c'), roman = c('I','II','III'))
x %>% safe_join(y)
try(
x %>% safe_join(rbind(y,y))
)

shuffle  Move the Columns of a Data Frame Relative to Each Other

Description

Move the columns of a data frame relative to each other.

Usage

shuffle(x, who, after = NA, ...)

shuffle
Move the Columns of a Data Frame Relative to Each Other
specfile.character

Identify the Data Specification File for a Model

Description

Identifies the data specification file associated with the datafile used by a model. Locates the datafile specified in the control stream, and substitutes a different extension.

Usage

```r
## S3 method for class 'character'
specfile(x, find = "\.csv\$", use = ".spec", ...)
```

Arguments

- `x` the model name
- `find` file extension to replace
- `use` file extension to use
- `...` pass ext over-ride default file extension in datafile()

Value

character

Arguments

- `x` data.frame
- `who` a character vector of column names to move, or a logical vector of length names(x), or a vector of indices
- `after` column after which to put who: may be character, integer, NA, or NULL
- `...` ignored

Value

data.frame

See Also

Other superset: `generalize()`, `meta.character()`, `meta.numeric()`, `metaplot.character()`, `metaplot.numeric()`, `metaplot_character()`, `metasuperset()`, `meta()`, `ninput.character()`, `ninput.numeric()`, `ninput()`, `superset.character()`, `superset.numeric()`, `superset()`, `superspec.character()`, `superspec.numeric()`, `superspec()`
superset.character

See Also
datafile
Other path: datafile.character(), datafile.numeric(), datafile(), modeldir(), modelfile(), modelpath.character(), modelpath.numeric(), modelpath(), psn_options(), specfile.numeric(), specfile()

Examples

library(spec)
source <- system.file(package = 'nonmemica', 'project')
target <- tempdir()
target <- gsub('\', '/', target) # for windows
file.copy(source, target, recursive = TRUE)
project <- file.path(target, 'project', 'model')
options(project = project)
library(magrittr)
1001 %>% datafile
datafile(1001) %matches% specfile(1001)
1001 %>% specfile
1001 %>% specfile %>% read.spec

superset.character Coerce to Superset from Character

Description

Coerces to superset from character, treating x as a model name.

Usage

## S3 method for class 'character'
superset(
  x, 
  read.input = list(read.csv, header = TRUE, as.is = TRUE),
  read.output = list(read.table, header = TRUE, as.is = TRUE, skip = 1, comment.char = "", check.names = FALSE, na.strings = c("", "\\s", ",", "NA")),
  include = character(0),
  exclude = character(0),
  rename = NULL,
  digits = 5,
  visible = "VISIBLE",
  after = NULL,
  groups = character(0),
  imputation = generalize,
  ...
)
Arguments

- **x**
  - object

- **read.input**
  - a methodology for acquiring the input

- **read.output**
  - a methodology for acquiring the output

- **include**
  - column names in output to consider adding

- **exclude**
  - column names in output to reject

- **rename**
  - logical: whether to keep and rename columns with re-used names

- **digits**
  - significant digits for assessing informativeness when exclusive=NULL

- **visible**
  - a name for the flag column indicating visibility

- **after**
  - place new columns after this column; at end by default (NULL); TRUE places them after last model-visible column (see input statement)

- **groups**
  - character vector of groupings within which any imputations will be performed

- **imputation**
  - a list of functions (or arguments to match.fun()) to perform imputations within cells defined by groups: e.g. generalize, forbak, etc (to be tried in succession for new columns only).

Details

Given a model name, (project passed or set as global option) superset() figures out the run directory and location of a NONMEM control stream. It reads the control stream to identify the run-time location of input and output files, as well as the "ignore" (and/or "accept") criteria that relate extent of input records to extent of output records. 'read.input' and 'read.output' are lists consisting of functions and arguments appropriate for reading input and output file formats, respectively. The ignore criteria will be reconstructed per row so that output can be mapped unambiguously to input. A column named VISIBLE is bound to the input data, showing 1 where a record was visible to NONMEM, and 0 otherwise. During integration, naming convention of the input is retained, and output column names are mapped by position, using the control stream input criteria. Output tables are restored to input dimensions using the "ignore" criteria, then checked for length: currently, superset ignores output tables having fewer rows than the input, as well as output tables whose row count is not a multiple of input row count. Output tables may contain versions of input columns. Disposition depends on the values of include, exclude, and rename. If include has length, other columns are excluded. Then, if exclude has length, these columns are excluded. Then, if rename is FALSE all remaining columns with re-used names will be dropped. If TRUE, such columns will be renamed (*.n, where n is table number). If NULL, only informative columns will be retained and renamed. A column is informative if any element is informative. An element is informative if it is newly generated (not NA and not zero, but original is NA) or if it is an alteration (non-NA, and different from non-NA original). If the column pair can be interpreted as numeric, "different" is determined using only the first digits digits. Only the first instance of any column among successive output tables is retained. In the control stream, avoid use of FIRSTONLY, as this alters the number of rows.

Value

superset: a data.frame where row count is a multiple of (typically equal to) input row count.
See Also

Other superset: `generalize()`, `meta.character()`, `meta.numeric()`, `metaplot.character()`, `metaplot.numeric()`, `metasuperset()`, `meta()`, `ninput.character()`, `ninput.numeric()`, `ninput()`, `shuffle()`, `superset.numeric()`, `superset()`, `superspec.character()`, `superspec.numeric()`, `superspec()`

Examples

```r
library(magrittr)
library(dplyr)
library(wrangle)
options(project = system.file('project/model', package = 'nonmemica'))
1001 %>% superset %>% head
1001 %>% superset %>% filter(VISIBLE == 1) %>% group_by(ID, TIME) %>% status
```

---

superspec Create Specification for Model Inputs and Outputs

Description

Create a specification for the result of superset().

Usage

```r
superspec(x, ...)
```

Arguments

- `x` object
- `...` passed arguments

See Also

`superspec.character`

Other superset: `generalize()`, `meta.character()`, `meta.numeric()`, `metaplot.character()`, `metaplot.numeric()`, `metasuperset()`, `meta()`, `ninput.character()`, `ninput.numeric()`, `ninput()`, `shuffle()`, `superset.character()`, `superset.numeric()`, `superset()`, `superspec.character()`, `superspec.numeric()`
Create Specification for Model Inputs and Outputs From Character

Description

Create a specification for the result of superset() from character by treating as a model name. By default, gives a spec template for superset(x). Tries to supplement with labels and units from parent specification, if it exists. Tries to supplement with any additional labels and units in definitions(x). Defers to actual data if provided. Specify exclusive, visible, and after as for superset.

Usage

```r
## S3 method for class 'character'
superspec(x,
    include = character(0),
    exclude = character(0),
    rename = NULL,
    visible = "VISIBLE",
    after = NULL,
    data = NULL,
    ...
)
```

Arguments

- `x` character
- `include` column names in output to consider adding
- `exclude` column names in output to reject
- `rename` logical: whether to keep and rename columns with re-used names
- `visible` a name for the flag column indicating visibility
- `after` place new columns after this column; at end by default (NULL); TRUE places them after
- `data` an alternative dataset on which to model the specification
- `...` passed arguments

See Also

Other superset: generalize(), meta.character(), meta.numeric(), metaplot.character(), metaplot.numeric(), metasuperset(), meta(), ninput.character(), ninput.numeric(), shuffle(), superset.character(), superset.numeric(), superset(), superspec.numeric(), superspec()
**superspec.numeric**

Create Specification for Model Inputs and Outputs From Numeric

---

**Description**

Create a specification for the result of superset() from numeric by coercing to character.

**Usage**

```r
## S3 method for class 'numeric'
superspec(x, ...)
```

**Arguments**

- `x`: numeric
- `...`: passed arguments

**See Also**

Other superset: `generalize()`, `meta.character()`, `meta.numeric()`, `metaplot.character()`, `metaplot.numeric()`, `metaplot_character()`, `metasuperset()`, `meta()`, `ninput.character()`, `ninput.numeric()`, `ninput()`, `shuffle()`, `superset.character()`, `superset.numeric()`, `superset()`, `superspec.character()`, `superspec()`

---

**tad**

Calculate Time Since Most Recent Dose

---

**Description**

Calculate time since most recent dose. Considers ADDL, but may not work with simultaneous dose records.

**Usage**

```r
tad(
  x,
  dose = rep(FALSE, length(x)),
  addl = rep(0, length(x)),
  ii = rep(0, length(x)),
  index = rep(1, length(x)),
  pre = TRUE,
  ...
)
```
Arguments

- x: a numeric vector of event times
- dose: length x logical indicating which of x are dose times
- addl: length x integer: number of additional doses
- ii: length x numeric: interdose interval for addl
- index: length x factor (optional) indicating subgroups to evaluate
- pre: assume that simultaneous sample precedes implied dose
- ... passed to tod()

Value

numeric

See Also

tod

Other tad: tod()

Examples

data(tad1)
x <- tad1
head(x)
x$tad <- tad(
x = x$TIME,
dose = x$EVID %in% c(1,4) & is.na(x$C),
addl = x$ADDL,
ii = x$II,
index = x$ID
)
head(x)

tad1 A NONMEM-like Dataset

Description

A dataset showing dose and observation records for several subjects. Doses are duplicated across compartments 1 and 2 as for mixed absorption modeling.

Usage

data(tad1)
### Details

- **C.** An exclusion flag, NA by default, or ‘C’.
- **ID.** Integer subject identifier.
- **TIME.** Numeric event time (h).
- **EVID.** Event type identifier: observation (0) or dose (1).
- **CMT.** Event compartment: dose (1), central (2) or peripheral (4).
- **AMT.** Amount of dose (mg).
- **RATE.** NONMEM RATE item.
- **ADDL.** Number of additional doses, or NA for observations.
- **II.** Interdose interval for additional doses, or NA for observations.
- **DV.** Observation placeholder.

### tod

**Calculate Time of Most Recent Dose**

### Description

Calculates time of most recent dose.

### Usage

```r
tod(x, ref, addl, ii, pre = T, ...)
```

### Arguments

- **x**
  - a numeric vector of event times
- **ref**
  - length x vector of reference dose times
- **addl**
  - length x integer: number of additional doses
- **ii**
  - length x numeric: interdose interval for addl
- **pre**
  - assume that simultaneous sample precedes implied dose
- **...**
  - ignored

### Value

numeric

### See Also

- `tad`
  Other tad: `tad()`
tweak.default  
Tweak a Model by Default

Description

Tweaks a model by jittering initial estimates. Creates a new model directory in project context and places the model there. Copies helper files as well. Expects that x is a number. Assumes nested directory structure (run-specific directories).

Usage

```r
## Default S3 method:
tweak(
x,
  project = getOption("project", getwd()),
  ext = getOption("modex", "ctl"),
  start = NULL,
  n = 10,
  include = ".def$",
  ...
)
```

Arguments

- `x`: object
- `project`: project directory
- `ext`: file extension for control streams
- `start`: a number to use as the first modelname
- `n`: the number of variants to generate (named `start:n`)
- `include`: regular expressions for files to copy to new directory
- `...`: pass `ext` to over-ride default model file extension

Value

character: vector of names for models created

See Also

Other tweak: `tweak.init()`, `tweak.init()`, `tweak.model()`, `tweak()`
## Description

Tweaks model.

## Usage

```r
## S3 method for class 'model'
tweak(x, sd = 0.13, digits = 3, ...)
```

## Arguments

- `x` object
- `sd` numeric
- `digits` integer
- `...` dots

## Value

model

## See Also

Other tweak: `tweak.default()`, `tweak.inits()`, `tweak.init()`, `tweak()`

## Examples

```r
# Create a working project.
source <- system.file(package = 'nonmemica', 'project')
target <- tempdir()
target <- gsub('\\', '/', target) # for windows
source
target
target.copy(source, target, recursive = TRUE)
project <- file.path(target, 'project', 'model')

# Point project option at working project
options(project = project)
library(magrittr)

# Make ten new models with slightly different initial estimates.
1001 %>% tweak
```
updated.character  
*Create the Updated Version of Character*

**Description**

Creates the updated version of character by treating as a modelname. Parses the associated control stream and ammends the initial estimates to reflect model results (as per xml file).

**Usage**

```r
## S3 method for class 'character'
updated(x, initial = estimates(x, ...), parse = TRUE, verbose = FALSE, ...)
```

**Arguments**

- `x`: character
- `initial`: values to use for initial estimates (numeric)
- `parse`: whether to parse the initial estimates, etc.
- `verbose`: extended messaging
- `...`: dots

**Value**

model

**See Also**

Other updated: `updated.numeric()`, `updated()`

---

upper.model  
*Get Upper Bounds for Model Initial Estimates*

**Description**

Gets upper bounds for model initial estimates.

**Usage**

```r
## S3 method for class 'model'
upper(x, ...)
```

**Arguments**

- `x`: model
- `...`: dots
upper<-.model

See Also

Other upper: upper<-.model(), upper<-, upper()

Examples

library(magrittr)
options(project = system.file('project/model', package='nonmemica'))
1001 %>% as.model %>% upper

upper<-.model  Set Upper Bounds for Model Initial Estimates

Description

Sets upper bounds for model initial estimates.

Usage

## S3 replacement method for class 'model'
upper(x) <- value

Arguments

x  model
value  numeric

See Also

Other upper: upper.model(), upper<-, upper()

xpath  Evaluate Xpath Expression

Description

Evaluates an xpath expression.

Coerces x to xml_document and evaluates.

Evaluates an xpath expression for a given document.
Usage

xpath(x, ...)

## Default S3 method:
xpath(x, ...)

## S3 method for class 'xml_document'
xpath(x, xpath, ...)

Arguments

x xml_document

... passed arguments

xpath xpath expression to evaluate

Details

The resulting nodeset is scavenged for text, and coerced to best of numeric or character.
The resulting nodeset is scavenged for text, and coerced to best of numeric or character.

Value

vector

vector

Methods (by class)

- default: default method
- xml_document: xml_document method

See Also

Other xpath: `as.xml_document.numeric()`, `as.xml_document()`

Examples

library(magrittr)
options(project = system.file('project/model', package = 'nonmemica'))
1001 %>% xpath('//etashrink/row/col')
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