# Package ‘RDML’

**September 25, 2017**

<table>
<thead>
<tr>
<th>Type</th>
<th>Package</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Title</strong></td>
<td>Importing Real-Time Thermo Cycler (qPCR) Data from RDML Format Files</td>
</tr>
<tr>
<td><strong>Version</strong></td>
<td>0.9-9</td>
</tr>
<tr>
<td><strong>LazyData</strong></td>
<td>true</td>
</tr>
<tr>
<td><strong>Date</strong></td>
<td>2017-09-25</td>
</tr>
<tr>
<td><strong>Description</strong></td>
<td>Imports real-time thermo cycler (qPCR) data from Real-time PCR Data Markup Language (RDML) and transforms to the appropriate formats of the 'qpcR' and 'chipPCR' packages. Contains a dendrogram visualization for the structure of RDML object and GUI for RDML editing.</td>
</tr>
<tr>
<td><strong>License</strong></td>
<td>MIT + file LICENSE</td>
</tr>
<tr>
<td><strong>URL</strong></td>
<td><a href="https://github.com/kablag/RDML">https://github.com/kablag/RDML</a></td>
</tr>
<tr>
<td><strong>Depends</strong></td>
<td>R (&gt;= 3.2.0)</td>
</tr>
<tr>
<td><strong>Imports</strong></td>
<td>checkmate (&gt;= 1.6.2), data.table, pipeR, readxl, rlist (&gt;= 0.4), R6 (&gt;= 2.0.1), stringr, tools (&gt;= 3.2), xml2 (&gt;= 1.0), lubridate (&gt;= 1.6.0)</td>
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<tr>
<td><strong>Collate</strong></td>
<td>'RDML.types.R' 'RDML.R' 'RDML.AsDendrogram.R' 'RDML.AsTable.R' 'RDML.GetFData.R' 'RDML.Merge.R' 'RDML.SetFData.R' 'RDML.init.R' 'functional_wrappers.R' 'rdmlEdit.R'</td>
</tr>
<tr>
<td><strong>Suggests</strong></td>
<td>chipPCR, magrittr, reshape2, qpcR, dplyr, ggplot2, knitr, kfigr, MBmca, shiny, shinyjs, shinythemes, V8, testthat</td>
</tr>
<tr>
<td><strong>VignetteBuilder</strong></td>
<td>knitr</td>
</tr>
<tr>
<td><strong>RoxygenNote</strong></td>
<td>6.0.1</td>
</tr>
<tr>
<td><strong>NeedsCompilation</strong></td>
<td>no</td>
</tr>
<tr>
<td><strong>Author</strong></td>
<td>Konstantin A. Blagodatskikh [cre, aut], Stefan Roediger [aut], Michal Burdukiwicz [aut], Andrej-Nikolai Spiess [aut]</td>
</tr>
<tr>
<td><strong>Maintainer</strong></td>
<td>Konstantin A. Blagodatskikh <a href="mailto:k.blag@yandex.ru">k.blag@yandex.ru</a></td>
</tr>
<tr>
<td><strong>Repository</strong></td>
<td>CRAN</td>
</tr>
<tr>
<td><strong>Date/Publication</strong></td>
<td>2017-09-25 12:07:17 UTC</td>
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R topics documented:

- adpsType
- annotationType
- as.character.idType
- as.character.reactIdType
- AsDendrogram
- AsTable
- baseTemperatureType
- cdnaSynthesisMethodType
- commercialAssayType
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- dataCollectionSoftwareType
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- rdmIlBaseType
- rdmIlEdit
- rdmIlIdType
- reactIdType
- reactType
- runType
adpsType R6 class.

Description
adpsType R6 class.

Usage
adpsType

Format
An R6Class generator object.

Details
Contains matrix of amplification data. Must have three columns:
cyc  PCR cycle at which data point was collected (every cycle must have unique number).
tmp  temperature in degrees Celsius at the time of measurement (optional).
fluor raw fluorescence intensity measured.

Inherits: rdmlBaseType.

Initialization
adpsType$new(fpoints)

Fields
fpoints assertMatrix. Matrix with amplification data points.
Examples

```r
#cycles
cyc <- c(1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40)

#fluorescence

data <- data.frame(cyc = cyc, tmp = temp, fluo = fluo)

#data <- data[, -2]
```

---

**annotationType R6 class.**

**Description**

Annotate samples by setting a property and its value. For example, sex could be a property with the possible values M or F. Inherits: `rdmlBaseType`.

**Usage**

annotationType

**Format**

An `R6Class` generator object.

**Fields**

- `property` `checkString`. Property name
- `value` `checkString`. Value
Examples

```r
#set sex property
annotationType$new(property = "sex", value = "M")
```

---

as.character.idType  
*Convert idType object to character*

---

Description

Function to convert idType object to character.

Usage

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

Arguments

- `x`  
idType object.
- `...`  
Further arguments to be passed.

---

as.character.reactIdType  
*Convert reactIdType object to character*

---

Description

Function to convert reactIdType object to character.

Usage

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

Arguments

- `x`  
reactIdType object.
- `...`  
Further arguments to be passed.
AsDendrogram  

RDML$AsDendrogram() wrapper

Description

Read more at RDML.AsDendrogram

Usage

AsDendrogram(obj, ...)

Arguments

obj  RDML object.
...
AsDendrogram params.

AsTable  

RDML$AsTable() wrapper

Description

Read more at RDML.AsTable

Usage

AsTable(obj, ...)

Arguments

obj  RDML object.
...
AsTable params.
baseTemperatureType

Description
Parent class for inner usage. Inherits: rdmlBaseType.

Usage
baseTemperatureType

Format
An R6Class generator object.

Initialization
baseTemperatureType$new(duration,
  temperatureChange = NULL, durationChange = NULL, measure = NULL, ramp =
  NULL)

Fields
duration checkCount. Duration of this step in seconds.
temperatureChange checkNumber. Change of the temperature between two consecutive cycles:
  actual temperature = temperature + (temperatureChange * cycle counter)
durationChange checkCount. Change of the duration between two consecutive cycles: actual
  duration = duration + (durationChange * cycle counter)
measure measureType. Indicates to make a measurement and store it as meltcurve or real-time
  data.
ramp checkNumber. Allowed temperature change between two consecutive cycles in degrees Cel-
  sius per second. If unstated, the maximal change rate is assumed.

cdnasynthesismethodType

Description
Description of the cDNA synthesis method. Inherits: rdmlBaseType.

Usage
cdnasynthesismethodType
commercialAssayType

Format

An \texttt{R6Class} generator object.

Initialization

\begin{verbatim}
commercialAssayType$new(enzyme = NULL, 
  primingMethod = NULL, dnaseTreatment = NULL, thermalCyclingConditions = NULL)
\end{verbatim}

@section Fields:

enzyme \texttt{checkString}. Name of the enzyme used for reverse transcription.
primingMethod \texttt{primingMethodType}.
dnaseTreatment \texttt{checkFlag} if TRUE if RNA was DNASE treated prior cDNA synthesis.
thermalCyclingConditions \texttt{idReferencesType}.

Description

For some commercial assays, the primer sequences may be unknown. This element allows to describe commercial assays. Inherits: \texttt{rdmlBaseType}.

Usage

commercialAssayType

Format

An \texttt{R6Class} generator object.

Initialization

\begin{verbatim}
commercialAssayType$new(company, orderNumber)
\end{verbatim}

@section Fields:

company \texttt{checkString}.
orderNumber \texttt{checkString}. 
cqDetectionMethodType

cqDetectionMethodType  cqDetectionMethodType R6 class.

Description

The method used to determine the Cq value. Can take values:

"automated threshold and baseline settings"
"manual threshold and baseline settings"
"second derivative maximum"
"other"

Inherits: enumType.

Usage

cqDetectionMethodType

Format

An R6Class generator object.

Initialization

cqDetectionMethodType$new(value)

@section Fields:

value  checkString.

dataCollectionSoftwareType

dataCollectionSoftwareType R6 class.

Description

Software name and version used to collect and analyze the data. Inherits: rdmlBaseType.

Usage

dataCollectionSoftwareType

Format

An R6Class generator object.
**Initialization**

dataCollectionSoftwareType$new(name, version)

@section Fields:

name checkString.

version checkString.

**Examples**

dataCollectionSoftwareType$new(name = "ExampleSoft",
version = "1.0")

dataType dataType R6 class.

**Description**

Inherits: rdmlBaseType.

**Usage**

dataType
dataType

**Format**

An R6Class generator object.

**Initialization**

dataType$new(tar, cq = NULL, excl = NULL,
adp = NULL, mdp = NULL, endPt = NULL, bgFluor = NULL, bgFluorSlp = NULL,
quantFluor = NULL)

**Fields**

tar  idReferencesType. TargetID - A reference to a target.
cq  checkNumber. Calculated fractional PCR cycle used for downstream quantification. Negative values express following condition: Not Available: -1.0
excl  checkString. Excluded. If excl is present, this entry should not be evaluated. Do not set this element to FALSE if the entry is valid. Instead, leave the entire excl element out instead. It may contain a string with a reason for the exclusion. Several reasons for exclusion should be seperated by semicolons ";".

adp  adpsType.

mdp  mdpsType.

dlp  checkNumber. Value of the endpoint measurement.
documentationType

bgFluor checkNumber. Background fluorescence (the y-intercept of the baseline trend based on the estimated background fluorescence).

bgFluorSlp checkNumber. Background fluorescence slope - The slope of the baseline trend based on the estimated background fluorescence. The element should be absent to indicate a slope of 0.0; If this element is present without the bgFluor element it should be ignored.

quantFluor checkNumber. Quantification fluorescence - The fluorescence value corresponding to the threshold line.

Methods

AsDataFrame(dp.type = "adp") Represents amplification (dp.type = "adp") or melting (dp.type = "mdp") data points as data.frame

---

documentationType documentationType R6 class.

Description

These elements should be used if the same description applies to many samples, targets or experiments. Inherits: rdmlBaseType.

Usage

documentationType

Format

An R6Class generator object.

Initialization

documentationType$new(id, text = NULL)

@section Fields:

id idType. Identificator.

text checkString. Text.
**dyeType**

---

**dyeType R6 class.**

**Description**

Detailed information about the dye. Inherits: rdmlBaseType.

**Usage**

dyeType

**Format**

An r6Class generator object.

**Initialization**

dyeType$new(id, description = NULL)

@section Fields:

- id  idType. Identificator.
- description  checkString. Description.

---

**enumType**

---

**enumType R6 class.**

**Description**

Generic class for creating objects that can take limited list of values.

Inherits: rdmlBaseType.

**Usage**

enumType

**Format**

An r6Class generator object.

**Initialization**

enumType$new(value)

@section Fields:

- value  checkString. Value.
Description

Contact details of the experimenter. Inherits: rdmlBaseType.

Usage

experimentertype

Format

An R6Class generator object.

Initialization

experimentertype$new(id, firstName, lastName, 
email = NULL, labName = NULL, labAddress = NULL)

Fields:

id idType. Identifier.
firstName checkString. First name.
lastName checkString. Last name.
email checkString. Email.
labName checkString. Lab name.
labAddress checkString. Lab address.
Initialization

```r
eperimentType$new(id, description = NULL, documentation = NULL, run = NULL)
```

@section Fields:

- `id` `idType`
- `description` `checkString`
- `documentation` list of `idReferencesType`
- `run` list of `runType`

Methods

```r
AsDataFrame(dp.type = "adp", long.table = FALSE) Represents amplification (dp.type = "adp")
or melting (dp.type = "mdp") data points as `data.frame`. 
long.table = TRUE means that fluorescence data for all runs and reacts will be at one column.
```

---

**GetFData**

RDML$GetFData() *wrapper*

---

**Description**

Read more at **RDML.GetFData**

**Usage**

`GetFData(obj, ...)`

**Arguments**

- `obj` RDML object.
- `...` GetFData params.

---

**gradientType**

*gradientType R6 class.*

---

**Description**

Details of the temperature gradient across the PCR block. Inherits: **baseTemperatureType**.

**Usage**

`gradientType`
**idReferencesType**

**Format**

An *R6Class* generator object.

**Initialization**

```plaintext
gradientType$new(highTemperature,
lowTemperature, ...)
```

**Fields**

- `highTemperature checkNumber`: The highest temperature of the gradient in degrees Celsius.
- `lowTemperature checkNumber`: The lowest temperature of the gradient in degrees Celsius.
- `...`: Params of parent class `baseTemperatureType`.

---

**Description**

Contains id of another RDML object. Inherits: `idType`.

**Usage**

`idReferencesType`

**Format**

An *R6Class* generator object.

**Initialization**

```plaintext
idReferencesType$new(id)
```

**Fields**

- `id checkString`: Identifier.
idType

**idType R6 class.**

**Description**
Contains identifier for various RDML types. Inherits: `rdmlBaseType`.

**Usage**
idType

**Format**
An `R6Class` generator object.

**Initialization**

```r
idType$new(id)
@section Fields:
id checkString. Identificator.
```

---

labelFormatType

**labelFormatType R6 class.**

**Description**
Label used for `pcrFormatType`. Can take values:

- ABC
- 123
- A1a1

Inherits: `enumType`.

**Usage**

```r
labelFormatType
```

**Format**
An `R6Class` generator object.

**Initialization**

```r
labelFormatType$new(value)
@section Fields:
value checkString.
```
**lidOpenType**

| lidOpenType | lidOpenType R6 class. |

**Description**

This step waits for the user to open the lid and continues afterwards. It allows to stop the program and to wait for the user to add for example enzymes and continue the program afterwards. The temperature of the previous step is maintained. Inherits: rdmlBaseType.

**Usage**

```
lidOpenType
```

**Format**

An `R6Class` generator object.

**Initialization**

```
lidOpenType$new()
```

---

**loopType**

| loopType | loopType R6 class. |

**Description**

This step allows to form a loop or to exclude some steps. It allows to jump to a certain "goto" step for "repeat" times. If the "goto" step is outside of the loop range, it must have "repeat" value "0". Inherits: rdmlBaseType.

**Usage**

```
loopType
```

**Format**

An `R6Class` generator object.

**Initialization**

```
loopType$new(goto, repeat.n)
```

**Fields**

- `goto` `assertCount`. The step to go to to form the loop.
- `repeat.n` `assertCount`. Determines how many times the loop is repeated. The first run through the loop is counted as 0, the last loop is "repeat" - 1.
**measureType**

---

**mdpsType** *mdpsType R6 class.*

**Description**

Contains matrix of melting data points (single data points measured during amplification).

**Usage**

mdpsType

**Format**

An R6Class generator object.

**Details**

Columns:

- **tmp** (temperature in degrees Celsius at the time of measurement. Every point must have unique value.
- **fluor** fluorescence intensity measured without any correction (including baselining).

Inherits: rdmlBaseType.

**Initialization**

    mdpsType$new(fpoints)

@section Fields:

- **fpoints** assertMatrix. Matrix with amplification data points.

---

**measureType** *measureType R6 class.*

**Description**

Can take values:

- **real time**
- **meltcurve**

Inherits: enumType.

**Usage**

measureType
Format

An `R6Class` generator object.

Initialization

\[\text{measureType}\$\text{new}(\text{value})\]

@section Fields:

\text{value \ checkString}.

---

<table>
<thead>
<tr>
<th>MergeRDMLs</th>
<th>Merges RDML objects</th>
</tr>
</thead>
</table>

Description

Merges list of RDML objects. The first object in the list becomes base object.

Usage

\[\text{MergeRDMLs}(\text{to.merge})\]

Arguments

\[\text{to.merge} \quad \text{RDML objects that should be merged.}\]

Examples

```r
## Not run:
PATH <- path.package("RDML")
filename <- paste(PATH, "/extdata/", "lc96_bACTXY.rdml", sep ="")
lc96 <- RDML$\text{new}(filename)
filename <- paste(PATH, "/extdata/", "stepone_std.rdml", sep ="")
stepone <- RDML$\text{new}(filename)
merged <- MergeRDMLs(list(lc96, stepone))
merged$\text{AsDendrogram}()

## End(Not run)
```
Description

This function has been designed to import data from RDML v1.1 and v1.2 format files or from xls file generated by Applied Biosystems 7500. To import from xls this file have to contain Sample Setup and Multicomponent Data sheets!

Arguments

- filename: string – path to file
- show.progress: logical – show loading progress bar if TRUE
- conditions.sep: separator for condition defined at sample name
- format: string – input file format. Possible values auto, rdml, abi, excel, csv. See Details.

Details

File format options:

- auto: Tries to detect format by extension. .xlsx – excel, .xls – abi, .csv – csv, other – rdml
- abi: Reads .xls files generated by ABI 7500 v.2. To create such files use File>Export; check 'Sample Setup' and 'Multicomponent Data'; select 'One File'
- excel: .xls or .xlsx file with sheets 'description', 'adp', 'mdp'. See example file table.xlsx
- csv: .csv file with first column 'cyc' or 'tmp' and fluorescence data in other columns
- rdml: .rdml or .lc96p files

Warning

Although the format RDML claimed as data exchange format, the specific implementation of the format at devices from real manufacturers differ significantly. Currently this function is checked against RDML data from devices: Bio-Rad CFX96, Roche LightCycler 96 and Applied Biosystems StepOne.

Author(s)

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Examples

```r
## Not run:
## Import from RDML file
PATH <- path.package("RDML")
filename <- paste(PATH, "/extdata/", "lc96_bACTXY.rdml", sep ="")
lc96 <- RDML$new(filename)

## Some kind of overview for lc96
lc96$asTable(name.pattern = sample[[react$sample$id]]$description)
lc96$asDendrogram()

## End(Not run)
```

---

**nucleotideType**

*nucleotideType R6 class.*

---

**Description**

Type of nucleic acid used as a template in the experiment. May have following values:

- DNA
- genomic DNA
- cDNA
- RNA

**Usage**

`nucleotideType`

**Format**

An `R6Class` generator object.

**Details**

Inherits: `enumType`.

**Initialization**

`nucleotideType$new(value)`

@section Fields:

value `checkString`. Value.
oligoType

**Description**
Inherits: rdmlBaseType.

**Usage**
oligoType

**Format**
An R6Class generator object.

**Initialization**
oligoType$new(threePrimeTag = NULL, fivePrimeTag = NULL, sequence)

@section Fields:
threePrimeTag checkString. Description of three prime modification (if present).
fivePrimeTag checkString. Description of five prime modification (if present).
sequence checkString.

pauseType

**Description**
This step allows to pause at a certain temperature. It is typically the last step in an amplification protocol. Inherits: rdmlBaseType.

**Usage**
pauseType

**Format**
An R6Class generator object.

**Initialization**
pauseType$new(temperature)

**Fields**
temperature checkNumber. The temperature in degrees Celsius maintained during the pause.
pcrFormatType R6 class.

Description
The display format of the PCR, analogous to the qPCR instrument run format. Inherits: rdmlBaseType.

Usage
pcrFormatType

Format
An R6Class generator object.

Details
Rotor formats always have 1 column; rows correspond to the number of places in the rotor. Values for common formats are:

<table>
<thead>
<tr>
<th>Format</th>
<th>rows</th>
<th>columns</th>
<th>rowLabel</th>
<th>columnLabel</th>
</tr>
</thead>
<tbody>
<tr>
<td>single-well</td>
<td>1</td>
<td>1</td>
<td>123</td>
<td>123</td>
</tr>
<tr>
<td>48-well plate</td>
<td>6</td>
<td>8</td>
<td>ABC</td>
<td>123</td>
</tr>
<tr>
<td>96-well plate</td>
<td>8</td>
<td>12</td>
<td>ABC</td>
<td>123</td>
</tr>
<tr>
<td>384-well plate</td>
<td>16</td>
<td>24</td>
<td>ABC</td>
<td>123</td>
</tr>
<tr>
<td>1536-well plate</td>
<td>32</td>
<td>48</td>
<td>ABC</td>
<td>123</td>
</tr>
<tr>
<td>3072-well array</td>
<td>32</td>
<td>96</td>
<td>1a1</td>
<td>1a1</td>
</tr>
<tr>
<td>5184-well chip</td>
<td>72</td>
<td>72</td>
<td>ABC</td>
<td>123</td>
</tr>
<tr>
<td>32-well rotor</td>
<td>32</td>
<td>1</td>
<td>123</td>
<td>123</td>
</tr>
<tr>
<td>72-well rotor</td>
<td>72</td>
<td>1</td>
<td>123</td>
<td>123</td>
</tr>
<tr>
<td>100-well rotor</td>
<td>100</td>
<td>1</td>
<td>123</td>
<td>123</td>
</tr>
<tr>
<td>free format</td>
<td>-1</td>
<td>1</td>
<td>123</td>
<td>123</td>
</tr>
</tbody>
</table>

If rows field has value -1, the function will not try to reconstruct a plate and just display all run data in a single column. If the columns field has value 1 then the function will not display a column label.

Initialization

pcrFormatType$new(rows, columns, rowLabel, columnLabel)

@section Fields:
rows checkCount.
columns checkCount.
rowLabel labelFormatType.
**Description**

The primers used in the reverse transcription. Can take values:

- oligo-dt
- random
- target-specific
- oligo-dt and random
- other

**Usage**

```
primingMethodType
```

**Format**

An `R6Class` generator object.

**Details**

Inherits: `enumType`.

**Initialization**

```
primingMethodType$new(value)
```

@section Fields:

```
value checkString. Value.
```
**quantityType**

*quantityType* R6 class.

**Description**

A quantity is always defined by its value and its unit. Inherits: rdmlBaseType.

**Usage**

quantityType

**Format**

An R6Class generator object.

**Initialization**

quantityType$new(value, unit)

@section Fields:

- **value**: checkNumber. Value.
- **unit**: quantityUnitType. Unit.

---

**quantityUnitType**

*quantityUnitType* R6 class.

**Description**

The unit the quantity. Can take values:

- **cop**: copies per microliter
- **fold**: fold change
- **dil**: dilution (10 would mean 1:10 dilution)
- **nMol**: nanomol per microliter
- **ng**: nanogram per microliter
- **other**: other unit (must be linear, no exponents or logarithms allowed)

**Usage**

quantityUnitType

**Format**

An R6Class generator object.
Details

Inherits: `enumType`.

Initialization

```r
quantityUnitType$new(value)
```

@section Fields:

- `value`: `checkString`. Value.

---

**RDML**

*R6 class RDML – contains methods to read and overview fluorescence data from RDML v1.1 and v1.2 format files*

Description

This class is a container for RDML format data (Lefever et al. 2009). The data may be further transformed to the appropriate format of the *qpcR* (Ritz et al. 2008, Spiess et al. 2008) and *chipPCR* (Roediger et al. 2015) packages (see `RDML.new` for import details). Real-time PCR Data Markup Language (RDML) is the recommended file format element in the Minimum Information for Publication of Quantitative Real-Time PCR Experiments (MIQE) guidelines (Bustin et al. 2009). The inner structure of imported data faithfully reflects the structure of RDML file v1.2. All data with the exception for fluorescence values can be represented as `data.frame` by method `AsTable`. Such possibility of data representation streamlines sample filtering (by targets, types, etc.) and serves as request for `GetFData` method, which extracts fluorescence data for specified samples.

Usage

```r
RDML
```

Format

An *R6Class* generator object.

Fields

Type, structure of data and description of fields can be viewed at RDML v1.2 file description. Names of fields are first level of XML tree.

Methods

- `new` creates a new instance of *RDML* class object (see `RDML.new`)
- `AsTable` represent RDML data as `data.frame` (see `RDML.AsTable`)
- `GetFData` gets fluorescence data (see `RDML.GetFData`)
- `SetFData` sets fluorescence data (see `RDML.SetFData`)
- `Merge` merges two RDML to one (see `MergeRDMLs`)
- `AsDendrogram` represents structure of RDML object as dendrogram (see `RDML.AsDendrogram`)
Author(s)
Konstantin A. Blagodatskikh <k.blag@yandex.ru>, Stefan Roediger <stefan.roediger@b-tu.de>, Michal Burdukiewicz <michalburdukiewicz@gmail.com>

References

Examples
```r
## EXAMPLE 1:
## internal dataset lc96_bACTXY.rdml (in 'data' directory)
## generated by Roche LightCycler 96. Contains qPCR data
## with four targets and two types.
## Import with default settings.
PATH <- path.package("RDML")
filename <- paste(PATH, "/extdata/", "lc96_bACTXY.rdml", sep ="")
lc96 <- RDML$new(filename)

# Show dyes names
unique(tab$target$dyeId)
# Show types of the samples for dye 'FAM'
library(dplyr)
unique(filter(tab, target$dyeId == "FAM")$sample.type)

# Show template quantities for dye 'FAM' type 'std'#
# Not run:
COPIES <- filter(tab, target$dyeId == "FAM", sample.type == "std")$quantity
# Define calibration curves (type of the samples - 'std').
# No replicates.
```
library(qpcR)
CAL <- modlist(lc96$GetFData(filter(tab,
    target.dyeId == "FAM",
    sample.type == "std"),
    baseline="lin", basecyc=8:15))
## Define samples to predict (first two samples with the type - 'unkn').
PRED <- modlist(lc96$GetFData(filter(tab,
    target.dyeId == "FAM",
    sample.type == "unkn"),
    baseline="lin", basecyc=8:15))
## Conduct quantification.
calib(refcurve = CAL, predcurve = PRED, thresh = "cpD2",
    dil = COPIES)
## End(Not run)
## Not run:
## EXAMPLE 2:
## internal dataset lc96_bACTXY.rdml (in 'data' directory)
## generated by Roche LightCycler 96. Contains qPCR data
## with four targets and two types.
## Import with default settings.
library(chipPCR)
PATH <- path.package("RDML")
filename <- paste(PATH, "/extdata/", "lc96_bACTXY.rdml", sep="")
lc96 <- RDML$new(filename)
tab <- lc96$AsTable(name.pattern = paste(sample[[react$sample$id]]$description,
    react$id$id),
    quantity = sample[[react$sample$id]]$quantity$value)
## Show targets names
unique(tab$target)
## Fetch cycle dependent fluorescence for HEX chanel
tmp <- lc96$GetFData(filter(tab, target == "bACT", sample.type == "std"))
## Fetch vector of dillutions
dilution <- filter(tab, target.dyeId == "FAM", sample.type == "std"$quantity

## Use plotCurves function from the chipPCR package to
## get an overview of the amplification curves
plotCurves(tmp[,1], tmp[,1],
par(mfrow = c(1,1))
## Use inder function from the chipPCR package to
## calculate the Cq (second derivative maximum, SDM)
SDMout <- sapply(2L:n(c(tmp), function(i) {
    SDM <- summary(inder(tmp[1,], tmp[1,], print = FALSE)[2]
})
## Use the effcalc function from the chipPCR package and
## plot the results for the calculation of the amplification
## efficiency analysis.
plot(effcalc(dilution, SDMout), CI = TRUE)
## End(Not run)
## Not run:
RDML.AsDendrogram

## EXAMPLE 3:
### internal dataset BioRad_qPCR_melt.rdml (in 'data' directory)
### generated by Bio-Rad CFX96. Contains qPCR and melting data.
### Import with custom name pattern.
PATH <- path.package("RDML")
filename <- paste(PATH, "/extdata/", "BioRad_qPCR_melt.rdml", sep ="")
cfx96 <- RDML$new(filename)
### Use plotCurves function from the chipPCR package to
### get an overview of the amplification curves
library(chipPCR)
### Extract all qPCR data
tab <- cfx96$AsTable()
cfx96.qPCR <- cfx96$GetFData(tab)
plotCurves(cfx96.qPCR[,1], cfx96.qPCR[-1], type = "l")

### Extract all melting data
cfx96.melt <- cfx96$GetFData(tab, dp.type = "mdp")
### Show some generated names for samples.
colnames(cfx96.melt)[2L:5]
### Select columns that contain
### samples with dye 'Evagreen' and have type 'pos'
### using filtering by names.
cols <- cfx96$GetFData(filter(tab, grepl("pos_Evagreen\$", fdata.name)),
              dp.type = "mdp")
### Conduct melting curve analysis.
library(qpcR)
invisible(meltcurve(cols, fluos = 2:ncol(cols),
          temps = rep(1, ncol(cols) - 1)))

## End(Not run)

---

RDML.AsDendrogram Represents structure of RDML file as dendrogram

### Description
Plots and/or returns the structure of RDML file as dendrogram (tree-like structure.)

### Arguments
- **plot.dendrogram**
  plots dendrogram if TRUE

### Value
dendrogram object

### Author(s)
Konstantin A. Blagodatskikh <k.blag@yandex.ru>, Stefan Roediger <stefan.roediger@b-tu.de>, Michal Burdukiewicz <michalburdukiewicz@gmail.com>
Examples

```r
## Not run:
PATH <- path.package("RDML")
filename <- paste(PATH, "/extdata/", "BioRad_qPCR_melt.rdml", sep ="")
cfx96 <- RDML$new(filename)
#plot dendrogram

cfx96$AsDendrogram()
#assign dendrogram to the object
dendr <- cfx96$AsDendrogram(plot.dendrogram = FALSE)

## End(Not run)
```

**RDML.AsTable**  
*Represents fields of RDML object as data.frame*

**Description**

Formats particular fields of RDML object as data.frames, filters or passes them to **RDML.GetFData** and **RDML.SetFData** functions.

**Arguments**

- `.default`  
  list of default columns

- `name.pattern`  
  expression to form `fdata.name` (see Examples)

- `add.columns`  
  list of additional columns

- `treat.null.as`  
  if value is NULL then convert it to NA. Helps to deal with incomplete records.

  - `na`  
    additional columns

**Details**

By default input this function forms data.frame with following columns:

- `exp.id`  
  experiment$id

- `run.id`  
  run$id

- `react.id`  
  react$id

- `position`  
  react$position

- `sample`  
  react$sample

- `target`  
  dataStar$id

- `target.dyeId`  
  target[[dataSid]]$dyeId

- `sample.type`  
  sample[[react$sample]]$type

You can overload default columns list by parameter `.default` but note that columns

- `exp.id`, `run.id`, `react.id`, `target`
are necessary for usage AsTable output as input for GetFData and SetFData. Additional columns can be introduced by specifying them at input parameter ... (see Examples). All default and additional columns accession expressions must be named.

Experiment, run, react and data to which belongs each fluorescence data vector can be accessed by experiment, run, react, data (see Examples).

Result table does not contain data from experiments with ids starting with "."!

Author(s)

Konstantin A. Blagodatskikh <k.blag@yandex.ru>, Stefan Roediger <stefan.roediger@b-tu.de>, Michal Burdukiewicz <michalburdukiewicz@gmail.com>

Examples

```r
## Not run:
## internal dataset stepone_std.rdlm (in 'data' directory)
## generated by Applied Biosystems Step-One. Contains qPCR data.
library(chipPCR)
PATH <- path.package("RDML")
filename <- paste(PATH, "/extdata/", "stepone_std.rdlm", sep ="")
stepone <- RDML$new(filename)
## Mark fluorescence data which Cq > 30 and add quantities to
## AsTable output.
## Names for fluorescence data will contain sample name and react
## positions
tab <- stepone$AsTable(  
  name.pattern = paste(react$sample$id, react$position),
  add.columns = list(cq30 = if(data$cq >= 30) ">=30" else "<30",
    quantity = as.factor(sample[[react$sample$id]]$quantity$value))
)
## Show cq30 and quantities
tab[,c("cq30", "quantity")]
## Get fluorescence values for 'std' type samples
## in format ready for ggplot function
library(dplyr)
fdata <- stepone$GetFData(  
  filter(tab, sample.type == "std"),
  long.table = TRUE)
## Plot fdata with colour by cq30 and shape by quantity
library(ggplot2)
ggplot(fdata, aes(x = cyc, y = fluor,
  group = fdata.name,
  colour = cq30,
  shape = quantity)) +
  geom_line() + geom_point()
## End(Not run)
```
**Description**

Gets fluorescence data vectors from RDML object for specified method of experiment.

**Arguments**

- **request**: Output from AsTable method (*RDML.AsTable*)
- **dp.type**: Type of fluorescence data (i.e. 'adp' for qPCR or 'mdp' for melting)
- **long.table**: Output table is ready for ggplot (See *RDML.AsTable* for example)

**Value**

matrix which contains selected fluorescence data and additional information fromm request if long.table = TRUE.

**Author(s)**

Konstantin A. Blagodatskikh <k.blag@yandex.ru>, Stefan Roediger <stefan.roediger@b-tu.de>, Michal Burdukiewicz <michalburdukiewicz@gmail.com>

**Examples**

```r
## Not run:
## internal dataset BioRad_qPCR_melt.rdml (in 'data' directory)
## generated by Bio-Rad CFX96. Contains qPCR and melting data.
## Import without splitting by targets/types and with custom name pattern.
PATH <- path.package("RDML")
filename <- paste(PATH, "/extdata/", "BioRad_qPCR_melt.rdml", sep="")
cfx96 <- RDML$new(filename)
## Select melting fluorescence data with sample.type 'unkn'.
library(dplyr)
tab <- cfx96$AsTable()
fdata <- cfx96$GetFData(filter(tab, sample.type == "unkn"),
                       dp.type = "adp")
## Show names for obtained fdata
colnames(fdata)
## End(Not run)
```
RDML.SetFData

Sets fluorescence data vectors to RDML object for specified method of experiment.

Arguments

data: matrix containing in the first column data corresponding to all fluorescence values in the following columns. The name of the first column is the name of variable and names of other column are fdata.names (links to rows at description).
description: output from AsTable function that describes fluorescence data.
fdata.type: 'adp' for qPCR, 'mdp' for melting data.

Examples

```r
## Not run:
PATH <- path.package("RDML")
filename <- paste0(PATH, "/extdata/", "stepone_std.rdml")
cfx96 <- RDML$new(filename)
## Use plotCurves function from the chipPCR package to
## get an overview of the amplification curves
library(chipPCR)
## Extract all qPCR data
tab <- cfx96$AsTable()
tab2 <- tab
tab2$run.id <- "cpp"
cfx96.qPCR <- cfx96$qPCRGetData(tab)
cpp <- cbind(cyc = cfx96.qPCR[, 1],
               apply(cfx96.qPCR[, -1], 2,
               function(y) CFP(x = cfx96.qPCR[, 1], y = y)$y.norm))
cfx96$qSetFData(cpp, tab2)
library(ggplot2)
library(gridExtra)
cfx96.gg <- cfx96$qSetFData(tab, long.table = TRUE)
cpp.gg <- cfx96$qSetFData(tab2,
                           long.table = TRUE)
plot1 <- ggplot(cfx96.gg, aes(x = cyc, y = fluo,
                          group=fdata.name)) +
          geom_line() +
          ggtitle("Raw data")
plot2 <- ggplot(cpp.gg, aes(x = cyc, y = fluo,
                          group=fdata.name)) +
          geom_line() +
          ggtitle("CPP processed data")
grid.arrange(plot1, plot2, nrow=2)

## End(Not run)
```
**rdmlBaseType**  
*Base R6 class for RDML package.*

**Description**
Most classes from RDML package inherit this class. It is designed for internal usage and should not be directly accessed.

**Usage**
```
rdmlBaseType()
```

**Format**
An `R6Class` generator object.

**Initialization**
```
rdmlBaseType$new()
```

**Methods**
- `.asXMLNodes(node.name)` Represents object as XML nodes. Should not be called directly. node.name – name of the root node for the generated XML tree.
- `print(...)` prints object

**rdmlEdit**  
*RDML Editor Graphical User Interface*

**Description**
Launches graphical user interface that can edit RDML metadata and show qPCR or melting curves.

**Usage**
```
rdmlEdit()
```
**rdmlIdType**

**rdmlIdType R6 class.**

**Description**

This element can be used to assign a publisher and id to the RDML file. Inherits: *rdmlBaseType*.

**Usage**

```
rdmlIdType
```

**Format**

An *R6Class* generator object.

**Initialization**

```
rdmlIdType$new(publisher, serialNumber, MD5Hash = NULL)
```

**Fields**

publisher *checkString*. RDML file publisher.

serialNumber *checkString*. Serial number.

MD5Hash *checkString*. An MD5Hash calculated over the complete file after removing all rdmlID-Types and all whitespaces between elements.

---

**reactIdType**

**reactIdType R6 class.**

**Description**

Contains identifier for reactType. Inherits: *rdmlBaseType*.

**Usage**

```
reactIdType
```

**Format**

An *R6Class* generator object.
Initialization

`reactIdType$new(id)`

@section Fields:

- **id** `checkCount`: Identificator.

---

**reactType** `reactType R6 class.`

---

**Description**

A reaction is an independent chemical reaction corresponding for example to a well in a 96 well plate, a capillary in a rotor, a through-hole on an array, etc. Inherits: `rdmlBaseType`.

**Usage**

`reactType`

**Format**

An `R6Class` generator object.

**Details**

The ID of this reaction

Schemas:

- **rotor**: assign IDs according to the position of the sample on the rotor (1 for the 1st sample, 2 for the 2nd, ...)
- **plate** (96/384/1536 well): the IDs are assigned in a row-first/column-second manner. For each row, the samples are numbered according to the increasing column number. At the end of a row, the numbering starts at the first column of the next row. An example for this type of plate can be found below:

```
1 2 3 ...
A 1 2 3
B 13 14
...
```

or

```
1 2 3 ...
1 1 2 3
2 13 14
...
```
- multi-array plate (BioTrove): the IDs are assigned in a row-first/column-second manner, ignoring the organisation of sub-arrays. For each row, the samples are numbered according to the increasing column number. At the end of a row, the next row. An example for this type of plate can be found below: todo...

**Initialization**

```r
reactType$new(id, sample, data = NULL, pcrFormat = pcrFormatType$new(8, 12, labelFormatType$new("123"))
```

@section Fields:

- **id**: `reactIdType`. See ‘Details’.
- **sample**: `idReferencesType`. SampleID - A reference to a sample.
- **data**: list of `dataType`.
- **position**: Human readable form of the `react id` (i.e. ’13’ -> ’B1’).

**Methods**

- `AsDataFrame(dp.type = "adp")` Represents amplification (`dp.type = "adp"`) or melting (`dp.type = "mdp"`) data points of all targets as one `data.frame`.
- `.recalcPosition(pcrformat)` Converts react id to the human readable form (i.e. ’13’ -> ’B1’). This converted value can be accessed by position field. `pcrFormat` is `pcrFormatType`. Currently, only ’ABC’ and ’123’ are supported as labels. For ’123’ ’123’ the position will look like ’r01c01’, for ’ABC’ ’123’ it will be ’A01’ and for ’123’ ’ABC’ it will be 01A. ’ABC’ ’ABC’ is not currently supported. Note that ’ABC’ will result in loss of information if the experiment contains more than 26 rows!

---

**runType**

**runType R6 class.**

**Description**

A run is a set of reactions performed in one "run", for example one plate, one rotor, one array, one chip. Inherits: `rdmlBaseType`.

**Usage**

`runType`

**Format**

An `R6Class` generator object.
Initialization

```
runType$new(id, description = NULL, documentation = NULL, experimenter = NULL, instrument = NULL, dataCollectionSoftware = NULL, backgroundDeterminationMethod = NULL, cqDetectionMethod = NULL, thermalCyclingConditions = NULL, pcrFormat, runDate = NULL, react = NULL)
```

Fields

- **id** `idType`.
- **description** `checkString`.
- **documentation** `list of idReferencesType`.
- **experimenter** `list of idReferencesType`.
- **instrument** `checkString`. Description of the instrument used to acquire the data.
- **dataCollectionSoftware** `dataCollectionSoftwareType`. Description of the software used to analyze/collect the data.
- **backgroundDeterminationMethod** `checkString`. Description of method used to determine the background.
- **cqDetectionMethod** `cqDetectionMethodType`. Description of method used to calculate the quantification cycle.
- **thermalCyclingConditions** `idReferencesType`. The program used to acquire the data.
- **pcrFormat** `adpsType`.
- **runDate** `adpsType`. Time stamp of data acquisition.
- **react** `list of adpsType`.

Methods

```
AsDataFrame(dp.type = "adp") Represents amplification (dp.type = "adp") or melting (dp.type = "mdp")
data points as data.frame
```

---

**sampleType**

**sampleType R6 class.**

---

**Description**

A sample is a template solution with defined concentration. Since dilutions of the same material differ in concentration, they are considered different samples. A technical replicate samples should contain the same name (reactions are performed on the same material), and biological replicates should contain different names (the template derived from the different biological replicates is are divergent). Serial dilutions in a standard curve must have different names (preferably stating their dilution). Inherits: `rdmlBaseType`. 

---
Usage

sampleType

Format

An **R6Class** generator object.

Initialization

```r
sampleType$new(id, description = NULL, 
documentation = NULL, xRef = NULL, annotation = NULL, type = 
sampleType$new("unkn"), interRunCalibrator = FALSE, quantity = NULL, 
calibratorSample = FALSE, cdnaSynthesisMethod = NULL, templateQuantity = 
NULL)
```

@section Fields:

- **id**  idType. Concentration of the template in nanogram per microliter in the final reaction mix.
- **description**  checkString.
- **documentation**  list of **idReferencesType**.
- **xRef**  list of **xRefType**.
- **annotation**  list of **annotationType**.
- **type**  sampleTypeType.
- **interRunCalibrator**  checkFlag. TRUE if this sample is used as inter run calibrator.
- **quantity**  quantityType. Quantity - The reference quantity of this sample. It should be only used if the
sample is part of a standard curve. The provided value will be used to quantify unknown
samples in absolute quantification assays. Only the use of positive integers (like 1, 10, 100, 1000) and fractions (e.g. 1, 0.1, 0.01, 0.001) is acceptable. The use of exponents (1, 2, 3, 4 or -1, -2, -3, -4) if forbidden, because it will not be interpreted as 10E1, 10E2, 10E3, 10E4 or 10E-1, 10E-2, 10E-3, 10E-4.
- **calibratorSample**  checkFlag. TRUE if this sample is used as calibrator sample.
- **cdnaSynthesisMethod**  cdnaSynthesisMethodType.
- **templateQuantity**  templateQuantityType.

---

**sampleTypeType**  **sampleTypeType R6 class.**

Description

Can take values:

- **unkn**  unknown sample
- **ntc**  non template control
- **nac**  no amplification control
sequencesType

- **std** standard sample
- **ntp** no target present
- **nrt** minusRT
- **pos** positive control
- **opt** optical calibrator sample

**Usage**

```r
sampleType
```

**Format**

An **R6Class** generator object.

**Details**

Inherits: **enumType**.

**Initialization**

```r
sampleType$new(value)
```

@section Fields:

- **value** checkString. Value.
Initialization

@section Fields:

forwardPrimer oligoType.
reversePrimer oligoType.
probe1 oligoType.
probe2 oligoType.
amplicon oligoType.

---

**SetFData**

@rdoc

RDSL$SetFData() wrapper

---

**Description**

Read more at RDML.SetFData

**Usage**

SetFData(obj, ...)

**Arguments**

<table>
<thead>
<tr>
<th>var</th>
<th>type</th>
</tr>
</thead>
<tbody>
<tr>
<td>obj</td>
<td>RDM object.</td>
</tr>
<tr>
<td>...</td>
<td>SetFData params.</td>
</tr>
</tbody>
</table>

---

**stepType**

`stepType R6 class.`

---

**Description**

Inherits: rdmlBaseType.

**Usage**

stepType

**Format**

An `R6Class` generator object.
Initialization

```r
stepType$new(nr, description = NULL,
温度 = NULL, gradient = NULL, loop = NULL, pause = NULL, lidOpen =
NULL)
```

Fields

- `nr` checkCount. The incremental number of the step. First step should have value 1. The increment
  between steps should be constant and equivalent to 1.
- `description` checkString.
- `temperature` temperatureType.
- `gradient` gradientType.
- `loop` loopType.
- `pause` pauseType.
- `lidOpen` lidOpenType.

---

targetType targetType R6 class.

---

Description

A target is a PCR reaction with defined set of primers. PCR reactions for the same gene with distinct
primer sequences are considered different targets. Inherits: rdmlBaseType.

Usage

targetType

Format

An `R6Class` generator object.

Initialization

```r
targetType$new(id, description = NULL,
documentation = NULL, xRef = NULL, type, amplificationEfficiencyMethod =
NULL, amplificationEfficiency = NULL, amplificationEfficiencySE = NULL,
detectionLimit = NULL, dyeId, sequences = NULL, commercialAssay = NULL)
```
**Fields**

- **id** `idType`.
- **description** `checkString`.
- **documentation** list of `idReferencesType`.
- **xRef** list of `xRefType`.
- **type** `targetTypeType`.
- **amplificationEfficiencyMethod** `checkString`.
- **amplificationEfficiency** `checkNumber`.
- **amplificationEfficiencySE** `checkNumber`.
- **detectionLimit** `checkNumber`.
- **dyeId** `idReferencesType`.
- **sequences** `sequencesType`.
- **commercialAssay** `commercialAssayType`.

---

**Description**

Can take values:

- **ref** reference target
- **toi** target of interest

Inherits: `enumType`.

**Usage**

`targetTypeType`

**Format**

An `R6Class` generator object.

**Initialization**

`targetTypeType$new(value)`

@section Fields:

- **value** `checkString`.
templateQuantityType

**Description**

This step keeps a constant temperature on the heat block. Inherits: baseTemperatureType.

**Usage**

temperatureType

**Format**

An R6Class generator object.

**Initialization**

temperatureType$new(temperature, ...)

**Fields**

- temperature checkNumber. The temperature of the step in degrees Celsius.
- ... Params of parent class baseTemperatureType.

---

templateQuantityType  templateQuantityType R6 class.

**Description**

Inherits: rdmlBaseType.

**Usage**

templateQuantityType

**Format**

An R6Class generator object.

**Initialization**

templateQuantityType$new(conc, nucleotide)
@section Fields:

- conc checkNumber. Concentration of the template in nanogram per microliter in the final reaction mix.
- nucleotide nucleotideType.
**Description**

A cycling program for PCR or to amplify cDNA. Inherits: `rdmlBaseType`.

**Usage**

```
thermalCyclingConditionsType
```

**Format**

An `R6Class` generator object.

**Initialization**

```
thermalCyclingConditionsType$new(id, 
  description = NULL, documentation = NULL, lidTemperature = NULL, 
  experimenter = NULL, step)
```

**Fields**

- `id` `idType`
- `description` `checkString`
- `documentation` list of `idReferencesType`
- `lidTemperature` `checkNumber`. The temperature in degrees Celsius of the lid during cycling.
- `experimenter` list of `idReferencesType`. Reference to the person who made or uses this protocol.
- `step` list of `stepType`. The steps a protocol runs through to amplify DNA.

---

**Description**

Inherits: `rdmlBaseType`.

**Usage**

```
xRefType
```

**Format**

An `R6Class` generator object.
Initialization

```r
xRefType$new(name = NULL, id = NULL)
```

@section Fields:

- **name**: `checkString`. Reference to an external database, for example "GenBank".
- **id**: `checkString`. The ID of the entry within the external database, for example "AJ832138".

[.GetFData

*Extract data points from RDML object*

Description

Extract data points from RDML object as.data.frame.

Usage

```r
## S3 method for class 'RDML'
x[i, j, dp.type = "adp"]
```

Arguments

- **x**: RDML object.
- **i, j**: indices.
- **dp.type**: Type of fluorescence data (i.e. 'adp' for qPCR or 'mdp' for melting).
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