> devtools::document()

i Updating RJobTissueArea documentation

i Loading RJobTissueArea

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Start loading helper functions - RJob\_execution, Version 080322

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functions:

- check\_if\_chip\_data\_exist()

- check\_if\_gatefile\_exist()

- check.if.valid()

- check\_imported\_file\_lists()

- check\_input\_files()

- collect\_segments\_metadata()

- connect\_mongoDB()

- copy\_file\_positionCSV()

- create\_cellsCSV\_filepath()

- create\_flvalues\_allGate\_filename()

- create\_gatecsv\_filepath()

- create\_valuesCSV\_filepath()

- create\_MethodHistory\_from\_EDL()

- create\_XML\_filename()

- create\_working\_directory()

- determine\_scan\_position()

- execute\_mainscript\_FDR()

- export\_full\_input()

- extract\_files\_to\_process()

- extract\_gates\_to\_process()

- extract\_jobtype()

- extract\_chip\_IDs()

- extract\_gate\_names()

- extract\_gate\_metadata()

- extract\_information\_from\_RService\_XML()

- extract\_paths\_of\_fl\_files()

- extract\_paths\_of\_gates()

- find\_server\_path()

- find\_chip\_path()

- get\_channelID\_from\_EDL()

- get\_EDL\_from\_query\_result()

- get\_gate\_ID\_of\_AllGate()

- get\_sampleType\_from\_MethodHistory()

- get\_segment\_ID\_of\_chipID()

- get\_valid\_chip\_IDs()

- import\_customer\_form()

- import\_R\_Service\_XML\_file()

- import\_single\_fl\_file()

- import\_all\_fl\_files()

- import\_single\_gate\_file()

- import\_all\_gate\_files()

- import\_ZKW\_rawdata\_to\_flvalues()

- load\_mainscript\_output()

- merge\_fl\_and\_gate\_files()

- merge\_all\_input\_files\_to\_one\_list\_and\_export()

- remove\_comp()

- return\_segment\_metadata()

- select\_segment\_ID()

- set\_attrs\_full\_input()

- stop\_if\_fatal()

- tidy\_up\_XML\_file\_content()

- query\_mongoDB()

- query\_segment\_ID()

- query\_channel\_limslager()

- write\_lines\_task()

- find\_RService\_XML\_on\_imageserver()

- handle\_trycache\_error()

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Start loading function - FDR, Version 150222

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Writing NAMESPACE

Writing NAMESPACE

> devtools::check()

i Updating RJobTissueArea documentation

i Loading RJobTissueArea

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Start loading helper functions - RJob\_execution, Version 080322

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Start loading function - FDR, Version 150222

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Writing NAMESPACE

Writing NAMESPACE

-- Building --------------------------------------------------------------------------------------------------------------------------------------- RJobTissueArea --

Setting env vars:

\* CFLAGS : -Wall -pedantic

\* CXXFLAGS : -Wall -pedantic

\* CXX11FLAGS: -Wall -pedantic

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√ checking for file 'C:\Users\Ortmann\Documents\Zellkraftwerk\packages\RJobTissueArea/DESCRIPTION' ...

- preparing 'RJobTissueArea':

√ checking DESCRIPTION meta-information ...

- installing the package to build vignettes

√ creating vignettes (5.1s)

- checking for LF line-endings in source and make files and shell scripts

- checking for empty or unneeded directories

- building 'RJobTissueArea\_0.0.0.0.tar.gz'

-- Checking --------------------------------------------------------------------------------------------------------------------------------------- RJobTissueArea --

Setting env vars:

\* \_R\_CHECK\_CRAN\_INCOMING\_REMOTE\_: FALSE

\* \_R\_CHECK\_CRAN\_INCOMING\_ : FALSE

\* \_R\_CHECK\_FORCE\_SUGGESTS\_ : FALSE

\* NOT\_CRAN : true

-- R CMD check ------------------------------------------------------------------------------------------------------------------------------------------------------

- using log directory 'C:/Users/Ortmann/AppData/Local/Temp/RtmpsDXRKh/RJobTissueArea.Rcheck'

- using R version 3.6.3 (2020-02-29)

- using platform: x86\_64-w64-mingw32 (64-bit)

- using session charset: ISO8859-1

- using options '--no-manual --as-cran'

√ checking for file 'RJobTissueArea/DESCRIPTION' ...

- this is package 'RJobTissueArea' version '0.0.0.0'

- package encoding: UTF-8

√ checking package namespace information ...

√ checking package dependencies (1.1s)

√ checking if this is a source package ...

√ checking if there is a namespace

√ checking for executable files (927ms)

√ checking for hidden files and directories ...

√ checking for portable file names ...

√ checking serialization versions ...

√ checking whether package 'RJobTissueArea' can be installed (3s)

√ checking installed package size ...

√ checking package directory

√ checking for future file timestamps (696ms)

√ checking 'build' directory

√ checking DESCRIPTION meta-information ...

√ checking top-level files

√ checking for left-over files ...

√ checking index information ...

√ checking package subdirectories ...

√ checking R files for non-ASCII characters ...

√ checking R files for syntax errors ...

√ checking whether the package can be loaded ...

√ checking whether the package can be loaded with stated dependencies ...

√ checking whether the package can be unloaded cleanly ...

√ checking whether the namespace can be loaded with stated dependencies ...

√ checking whether the namespace can be unloaded cleanly ...

√ checking loading without being on the library search path ...

√ checking dependencies in R code (1.3s)

√ checking S3 generic/method consistency (518ms)

√ checking replacement functions ...

√ checking foreign function calls ...

N checking R code for possible problems (3.1s)

collect\_segments\_metadata: no visible binding for global variable

'segment\_ID'

determine\_scan\_position: no visible binding for global variable 'Tag'

determine\_scan\_position: no visible binding for global variable 'Type'

determine\_scan\_position: no visible binding for global variable

'ScanPosition'

execute\_mainscript\_FDR: no visible binding for global variable

'output\_dir'

extract\_gate\_metadata: no visible binding for global variable

'ObjRef\_Gate'

find\_RService\_XML\_on\_imageserver: no visible global function definition

for 'filling\_rule'

find\_RService\_XML\_on\_imageserver : <anonymous>: no visible binding for

global variable 'enable.quit'

find\_RService\_XML\_on\_imageserver : <anonymous>: no visible binding for

global variable 'subtask'

find\_server\_path: no visible binding for global variable '.data'

handle\_trycache\_error: no visible binding for global variable

'output.dir'

return\_segment\_metadata: no visible binding for global variable

'chip\_path'

return\_segment\_metadata: no visible binding for global variable 'data'

return\_segment\_metadata: no visible binding for global variable

'segments'

select\_segment\_ID: no visible binding for global variable 'status'

select\_segment\_ID: no visible binding for global variable 'chip\_ID'

select\_segment\_ID: no visible binding for global variable 'lastchange'

write\_lines\_task: no visible global function definition for

'filling\_rule'

Undefined global functions or variables:

.data ObjRef\_Gate ScanPosition Tag Type chip\_ID chip\_path data

enable.quit filling\_rule lastchange output.dir output\_dir segment\_ID

segments status subtask

Consider adding

importFrom("graphics", "segments")

importFrom("utils", "data")

to your NAMESPACE file.

√ checking Rd files ...

√ checking Rd metadata ...

√ checking Rd line widths ...

√ checking Rd cross-references ...

√ checking for missing documentation entries ...

√ checking for code/documentation mismatches (727ms)

W checking Rd \usage sections ...

Documented arguments not in \usage in documentation object 'check\_imported\_file\_lists':

'filesToProcess' 'gatesToProcess'

Undocumented arguments in documentation object 'query\_channel\_limslager'

'chip\_IDs'

Documented arguments not in \usage in documentation object 'query\_channel\_limslager':

'chip\_path'

Functions with \usage entries need to have the appropriate \alias

entries, and all their arguments documented.

The \usage entries must correspond to syntactically valid R code.

See chapter 'Writing R documentation files' in the 'Writing R

Extensions' manual.

W checking Rd contents (713ms)

Argument items with no description in Rd object 'query\_channel\_limslager':

'chip\_path'

Argument items with no description in Rd object 'query\_segment\_ID':

'segment\_IDs'

√ checking for unstated dependencies in examples ...

√ checking installed files from 'inst/doc' ...

√ checking files in 'vignettes' ...

√ checking examples (2.4s)

- found \donttest examples: check also with --run-donttest

√ checking for unstated dependencies in vignettes ...

√ checking package vignettes in 'inst/doc' ...

√ checking re-building of vignette outputs (3.7s)

√ checking for detritus in the temp directory

See

'C:/Users/Ortmann/AppData/Local/Temp/RtmpsDXRKh/RJobTissueArea.Rcheck/00check.log'

for details.

-- R CMD check results ------------------------------------------------------------------------------------------------------------------ RJobTissueArea 0.0.0.0 ----

Duration: 24.7s

> checking Rd \usage sections ... WARNING

Documented arguments not in \usage in documentation object 'check\_imported\_file\_lists':

'filesToProcess' 'gatesToProcess'

Undocumented arguments in documentation object 'query\_channel\_limslager'

'chip\_IDs'

Documented arguments not in \usage in documentation object 'query\_channel\_limslager':

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entries, and all their arguments documented.

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See chapter 'Writing R documentation files' in the 'Writing R

Extensions' manual.

> checking Rd contents ... WARNING

Argument items with no description in Rd object 'query\_channel\_limslager':

'chip\_path'

Argument items with no description in Rd object 'query\_segment\_ID':

'segment\_IDs'

> checking R code for possible problems ... NOTE

collect\_segments\_metadata: no visible binding for global variable

'segment\_ID'

determine\_scan\_position: no visible binding for global variable 'Tag'

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segments status subtask

Consider adding

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to your NAMESPACE file.

0 errors √ | 2 warnings x | 1 note x