

# Package ‘OhdsiRTools’

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**Type** Package

**Title** Tools Used by Observational Health Data Science and Informatics (OHDSI)

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**Description**

Includes functions to format and check syntax of R code and packages following the 'OHDSI' R style guidelines. Generate renv lock files for OHDSI study packages.

**License** Apache License 2.0

**Depends** R (>= 3.1.0),

**Imports** remotes,  
codetools,  
formatR,  
RJSONIO,  
httr (>= 1.3.1),  
openxlsx (>= 4.0.17),  
methods,  
utils

**Suggests** testthat

**URL** <http://ohdsi.github.io/OhdsiRTools/>, <https://github.com/OHDSI/OhdsiRTools>

**BugReports** <https://github.com/OHDSI/OhdsiRTools/issues>

**NeedsCompilation** no

**RoxygenNote** 7.1.1

**Encoding** UTF-8

## R topics documented:

checkUsagePackage . . . . .	2
createConceptSetWorkbook . . . . .	3
createRenvLockFile . . . . .	4
findNonAsciiStringsInFolder . . . . .	4
fixHadesLogo . . . . .	5
formatRFile . . . . .	5
formatRFolder . . . . .	6

formatRText . . . . .	6
getCohortDefinitionExpression . . . . .	7
getCohortDefinitionName . . . . .	7
getCohortDefinitionSql . . . . .	8
getCohortGenerationStatuses . . . . .	9
getConceptSetConceptIds . . . . .	9
getConceptSetExpression . . . . .	10
getConceptSetName . . . . .	10
getConceptSetsAndConceptsFromCohort . . . . .	11
getCorePackages . . . . .	12
getOhdsiGitHubPackages . . . . .	12
getPriorityVocabKey . . . . .	13
getSetExpressionConceptIds . . . . .	13
insertCohortDefinitionInPackage . . . . .	14
insertCohortDefinitionSetInPackage . . . . .	15
insertConceptSetConceptIdsInPackage . . . . .	16
insertEnvironmentSnapshotInPackage . . . . .	16
invokeCohortSetGeneration . . . . .	17
restoreEnvironment . . . . .	17
restoreEnvironmentFromPackage . . . . .	18
restoreEnvironmentFromPackageOnGithub . . . . .	19
takeEnvironmentSnapshot . . . . .	20
updateCopyrightYearFile . . . . .	21
updateCopyrightYearFolder . . . . .	21
updatePackageName . . . . .	21
updatePackageNameFolder . . . . .	22

## Index 23

---

checkUsagePackage	<i>Check all code in a package</i>
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---

### Description

Check all code in a package

### Usage

```
checkUsagePackage(
  package,
  ignoreHiddenFunctions = TRUE,
  suppressBindingKeywords = c("ggplot2", "ffwhich", "subset.ffdf", "glm")
)
```

### Arguments

package	The name of the package to check.
ignoreHiddenFunctions	Ignore functions for which the definition cannot be retrieved?
suppressBindingKeywords	A set of keywords that are indicative of non-standard evaluation.

## Details

This function uses the `codetools` package to check the code from problems. Heuristics are used to eliminate false positives due to non-standard evaluation.

## Examples

```
checkUsagePackage("OhdsiRTools")
```

---

```
createConceptSetWorkbook
```

*Save a set of concept sets expressions, included concepts, and mapped concepts into a workbook*

---

## Description

Save a set of concept sets expressions, included concepts, and mapped concepts into a workbook

## Usage

```
createConceptSetWorkbook(  
  conceptSetIds,  
  workFolder = NULL,  
  baseUrl,  
  included = FALSE,  
  mapped = FALSE  
)
```

## Arguments

<code>conceptSetIds</code>	A vector of concept set IDs.
<code>workFolder</code>	Directory location where the workbook will be saved, defaults to working directory.
<code>baseUrl</code>	The base URL for the WebApi instance, for example: "http://server.org:80/WebAPI".
<code>included</code>	Should included concepts be included in the workbook?
<code>mapped</code>	Should mapped concepts be included in the workbook?

## Value

A `xlsx` workbook (`conceptSetExpressions.xlsx`) that includes a list of all concept set IDs and names and a worksheet for the concepts in each set. Options to include an included concepts and mapped concepts worksheet for each concept set are available.

---

createRenvLockFile	<i>Create a renv lock file</i>
--------------------	--------------------------------

---

### Description

Create a renv lock file

### Usage

```
createRenvLockFile(
  rootPackage,
  ohdsiGitHubPackages = getOhdsiGitHubPackages(),
  ohdsiStudiesGitHubPackages = rootPackage,
  fileName = "renv.lock"
)
```

### Arguments

rootPackage	The name of the root package, the package that we'd like to be able to run in the end.
ohdsiGitHubPackages	Names of R packages that need to be installed from the OHDSI GitHub.
ohdsiStudiesGitHubPackages	Names of R packages that need to be installed from the OHDSI-Studies GitHub.
fileName	Name of the lock file to be generated.

### Details

Create a lock file that allows reconstruction of the R environment using the renv package. This function will include the root file and all of its dependencies in the lock file, requiring the same package versions as currently installed on this computer.

### Value

Does not return a value. Is executed for the side-effect of creating the lock file.

---

findNonAsciiStringsInFolder	<i>Find non-ASCII strings in R files</i>
-----------------------------	--

---

### Description

Find non-ASCII string in R files.

### Usage

```
findNonAsciiStringsInFolder(path = ".", recursive = TRUE)
```

**Arguments**

path                      Path to the folder containing the R files.  
recursive                If TRUE, subfolders will also be searched for R files.

**Value**

A table listing the lines per R file containing non-ASCII characters.

---

fixHadesLogo	<i>Fix HADES logo in pkgdown output</i>
--------------	---

---

**Description**

In all HTML files in the docs folder, each occurrence of 'hadesLogo' is replaced with an HTML image tag referring to the HADES logo.

**Usage**

```
fixHadesLogo(path = ".")
```

**Arguments**

path                      Path to the root of the package for which the pkgdown output needs to be fixed.

**Value**

This function returns nothing.

---

formatRFile	<i>Format an R file</i>
-------------	-------------------------

---

**Description**

Format an R file

**Usage**

```
formatRFile(file, width.cutoff = 100)
```

**Arguments**

file                      The path to the file.  
width.cutoff            Number of characters that each line should be limited to.

---

formatRFolder	<i>Format all R files in a folder</i>
---------------	---------------------------------------

---

**Description**

Format all R files in a folder

**Usage**

```
formatRFolder(path = ".", recursive = TRUE, skipAutogenerated = TRUE, ...)
```

**Arguments**

path	Path to the folder containing the files to format. Only files with the .R extension will be formatted.
recursive	Include all subfolders?
skipAutogenerated	Skip auto-generated files such as RcppExports.R?
...	Parameters to be passed on the the formatRFile function

---

formatRText	<i>Format R code</i>
-------------	----------------------

---

**Description**

Format R code

**Usage**

```
formatRText(text, width.cutoff = 100)
```

**Arguments**

text	A character vector with the R code to be formatted.
width.cutoff	Number of characters that each line should be limited to.

**Value**

A character vector with formatted R code.

**Examples**

```
code <- "example <- function(x,foobar){paste(x,foobar)}"
formatted <- formatRText(code)
writeLines(formatted)
```

---

```
getCohortDefinitionExpression
```

*Get a cohort definition expression*

---

**Description**

Get a cohort definition expression

**Usage**

```
getCohortDefinitionExpression(definitionId, baseUrl)
```

**Arguments**

definitionId	The number indicating which cohort definition to fetch.
baseUrl	The base URL for the WebApi instance, for example: "http://server.org:80/WebAPI".

**Details**

Obtain the JSON expression from WebAPI for a given cohort id

**Value**

A JSON list object representing the cohort definition

**Examples**

```
## Not run:  
# This will obtain a cohort definition's JSON expression:  
  
getCohortDefinitionExpression(definitionId = 282, baseUrl = "http://server.org:80/WebAPI")  
  
## End(Not run)
```

---

```
getCohortDefinitionName
```

*Get a cohort definition's name from WebAPI*

---

**Description**

Get a cohort definition's name from WebAPI

**Usage**

```
getCohortDefinitionName(baseUrl, definitionId, formatName = FALSE)
```

**Arguments**

baseUrl	The base URL for the WebApi instance, for example: "http://server.org:80/WebAPI".
definitionId	The cohort definition id in Atlas.
formatName	Should the name be formatted to remove prefixes and underscores?

**Details**

Obtains the name of a cohort.

**Value**

The name of the cohort.

---

`getCohortDefinitionSql`

*Get a cohort definition's SQL from WebAPI*

---

**Description**

Get a cohort definition's SQL from WebAPI

**Usage**

```
getCohortDefinitionSql(baseUrl, definitionId)
```

**Arguments**

baseUrl	The base URL for the WebApi instance, for example: "http://server.org:80/WebAPI".
definitionId	The cohort definition id in Atlas.

**Details**

Obtains the template SQL of a cohort.

**Value**

The templated SQL to generate the cohort



---

`getCohortGenerationStatuses`*Get Cohort Generation Statuses*

---

**Description**

Get Cohort Generation Statuses

**Usage**

```
getCohortGenerationStatuses(baseUrl, definitionIds, sourceKeys)
```

**Arguments**

<code>baseUrl</code>	The base URL for the WebApi instance, for example: "http://server.org:80/WebAPI".
<code>definitionIds</code>	A list of cohort definition Ids
<code>sourceKeys</code>	A list of CDM source keys. These can be found in Atlas -> Configure.

**Details**

Obtains cohort generation statuses for a collection of cohort definition Ids and CDM sources. Useful if running multiple cohort generation jobs that are long-running.

**Value**

A data frame of cohort generation statuses, start times, and execution durations per definition id and source key.

---

`getConceptSetConceptIds`*Get Concept Set Concept Ids*

---

**Description**

Get Concept Set Concept Ids

**Usage**

```
getConceptSetConceptIds(baseUrl, setId, vocabSourceKey = NULL)
```

**Arguments**

<code>baseUrl</code>	The base URL for the WebApi instance, for example: "http://server.org:80/WebAPI".
<code>setId</code>	The concept set id in Atlas.
<code>vocabSourceKey</code>	The source key of the Vocabulary. By default, the priority Vocabulary is used.

**Details**

Obtains the full list of concept Ids in a concept set.

**Value**

A list of concept Ids.

---

`getConceptSetExpression`*Get a concept set expression*

---

**Description**

Get a concept set expression

**Usage**

```
getConceptSetExpression(baseUrl, setId)
```

**Arguments**

<code>baseUrl</code>	The base URL for the WebApi instance, for example: "http://server.org:80/WebAPI".
<code>setId</code>	The concept set id in Atlas.

**Details**

Obtain the JSON expression from WebAPI for a given concept set

**Value**

A JSON list object representing the concept set

**Examples**

```
## Not run:  
# This will obtain a concept set's JSON expression:  
  
getConceptSetExpression(setId = 282, baseUrl = "http://server.org:80/WebAPI")  
  
## End(Not run)
```

---

`getConceptSetName`*Get a concept set's name from WebAPI*

---

**Description**

Get a concept set's name from WebAPI

**Usage**

```
getConceptSetName(baseUrl, setId, formatName = FALSE)
```

**Arguments**

baseUrl	The base URL for the WebApi instance, for example: "http://server.org:80/WebAPI".
setId	The concept set id in Atlas.
formatName	Should the name be formatted to remove prefixes and underscores?

**Details**

Obtains the name of a concept set.

**Value**

The name of the concept set.

---

getConceptSetsAndConceptsFromCohort

*Get a list of concept sets and concepts from a cohort definition*

---

**Description**

Get a list of concept sets and concepts from a cohort definition

**Usage**

```
getConceptSetsAndConceptsFromCohort(
    baseUrl,
    definitionId,
    vocabSourceKey = NULL
)
```

**Arguments**

baseUrl	The base URL for the WebApi instance, for example: "http://server.org:80/WebAPI".
definitionId	The cohort id to fetch concept sets and concepts from
vocabSourceKey	A mysterious parameter.

**Details**

For a given cohort definition id, get all concept sets and resolve all concepts from each

**Value**

A list of concept sets, set names, and concepts

**Examples**

```
## Not run:
# This will obtain a list of concept sets and concepts from a cohort id:

getConceptsFromCohortId(baseUrl = "http://server.org:80/WebAPI", definitionId = 123)

## End(Not run)
```

---

getCorePackages	<i>Get a list of R core packages</i>
-----------------	--------------------------------------

---

**Description**

Get a list of R core packages

**Usage**

```
getCorePackages()
```

**Details**

Returns names of packages that are part of the R code, and can therefore not be installed.

**Value**

A character vector.

---

getOhdsiGitHubPackages	<i>Get a list of packages in the OHDSI GitHub.</i>
------------------------	--

---

**Description**

Get a list of packages in the OHDSI GitHub.

**Usage**

```
getOhdsiGitHubPackages()
```

**Details**

Returns names of packages that need to be installed from <https://github.com/ohdsi>.

**Value**

A character vector.

---

getPriorityVocabKey	<i>Get Priority Vocab Source Key</i>
---------------------	--------------------------------------

---

**Description**

Get Priority Vocab Source Key

**Usage**

```
getPriorityVocabKey(baseUrl)
```

**Arguments**

baseUrl	The base URL for the WebApi instance, for example: "http://server.org:80/WebAPI".
---------	---

**Details**

Obtains the source key of the default OMOP Vocab in Atlas.

**Value**

A string with the source key of the default OMOP Vocab in Atlas.

---

getSetExpressionConceptIds	<i>Get Concepts from a Concept Set Expression</i>
----------------------------	---

---

**Description**

Get Concepts from a Concept Set Expression

**Usage**

```
getSetExpressionConceptIds(baseUrl, expression, vocabSourceKey = NULL)
```

**Arguments**

baseUrl	The base URL for the WebApi instance, for example: "http://server.org:80/WebAPI".
expression	A JSON string that represents the concept set expression
vocabSourceKey	The source key of the Vocabulary. By default, the priority Vocabulary is used.

**Value**

A list of concept ids

**Examples**

```
## Not run:
# This will obtain the concept ids from a concept set expression:

getSetExpressionConceptIds(baseUrl = "http://server.org:80/WebAPI",
                           expression = someJsonExpression)

## End(Not run)
```

---

```
insertCohortDefinitionInPackage
```

*Load a cohort definition and insert it into this package*

---

**Description**

Load a cohort definition and insert it into this package

**Usage**

```
insertCohortDefinitionInPackage(
  definitionId,
  name = NULL,
  baseUrl,
  generateStats = FALSE
)
```

**Arguments**

definitionId	The number indicating which cohort definition to fetch.
name	The name that will be used for the json and SQL files. If not provided, the name in cohort will be used, but this may not lead to valid file names.
baseUrl	The base URL for the WebApi instance, for example: "http://server.org:80/WebAPI".
generateStats	Should the SQL include the code for generating inclusion rule statistics? Note that if TRUE, several additional tables are expected to exist as described in the details.

**Details**

Load a cohort definition from a WebApi instance and insert it into this package. This will fetch the json object and store it in the 'inst/cohorts' folder, and fetch the template SQL and store it in the 'inst/sql/sql\_server' folder. Both folders will be created if they don't exist. When using generateStats = TRUE, the following tables are required to exist when executing the SQL: cohort\_inclusion, cohort\_inclusion\_result, cohort\_inclusion\_stats, and cohort\_summary\_stats. Also note that the cohort\_inclusion table should be populated with the names of the rules prior to executing the cohort definition SQL.

## Examples

```
## Not run:
# This will create 'inst/cohorts/Angioedema.json' and 'inst/sql/sql_server/Angioedema.sql':

insertCohortDefinitionInPackage(definitionId = 282,
                                name = "Angioedema",
                                baseUrl = "http://server.org:80/WebAPI")

## End(Not run)
```

---

```
insertCohortDefinitionSetInPackage
```

*Insert a set of cohort definitions into package*

---

## Description

Insert a set of cohort definitions into package

## Usage

```
insertCohortDefinitionSetInPackage(
  fileName,
  baseUrl,
  insertTableSql = TRUE,
  insertCohortCreationR = TRUE,
  generateStats = FALSE,
  packageName
)
```

## Arguments

<code>fileName</code>	Name of a CSV file in the inst/settings folder of the package specifying the cohorts to insert. See details for the expected file format.
<code>baseUrl</code>	The base URL for the WebApi instance, for example: "http://server.org:80/WebAPI".
<code>insertTableSql</code>	Should the SQL for creating the cohort table be inserted into the package as well? This file will be called CreateCohortTable.sql.
<code>insertCohortCreationR</code>	Insert R code that will create the cohort table and instantiate the cohorts? This will create a file called R/CreateCohorts.R containing a function called <code>.createCohorts</code> .
<code>generateStats</code>	Should cohort inclusion rule statistics be created?
<code>packageName</code>	The name of the package (only needed when inserting the R code as well).

## Details

The CSV file should have at least the following fields:

**atlasId** The cohort ID in ATLAS.

**cohortId** The cohort ID that will be used when instantiating the cohort (can be different from atlasId).

**name** The name to be used for the cohort. This name will be used to generate file names, so please use letters and numbers only (no spaces).

---

```
insertConceptSetConceptIdsInPackage
```

*Insert a set of concept sets' concept ids into package*

---

### Description

Insert a set of concept sets' concept ids into package

### Usage

```
insertConceptSetConceptIdsInPackage(fileName, baseUrl)
```

### Arguments

fileName	Name of a CSV file in the inst/settings folder of the package specifying the concept sets to insert. See details for the expected file format.
baseUrl	The base URL for the WebApi instance, for example: "http://server.org:80/WebAPI".

### Details

The CSV file should have:

**atlasId** The concept set Id in ATLAS.

---

```
insertEnvironmentSnapshotInPackage
```

*Store snapshot of the R environment in the package*

---

### Description

Store snapshot of the R environment in the package

### Usage

```
insertEnvironmentSnapshotInPackage(
  rootPackage,
  pathToCsv = "inst/settings/rEnvironmentSnapshot.csv"
)
```

### Arguments

rootPackage	The name of the root package
pathToCsv	The path for saving the snapshot (as CSV file).

### Details

This function records all versions used in the R environment that are used by one root package, and stores them in a CSV file in the R package that is currently being developed. The default location is `inst/settings/rEnvironmentSnapshot.csv`. This can be used for example to restore the environment to the state it was when a particular study package was run using the [restoreEnvironment](#) function.



**Examples**

```
## Not run:
insertEnvironmentSnapshotInPackage("OhdsiRTools")

## End(Not run)
```

---

invokeCohortSetGeneration

*Invoke the generation of a set of cohort definitions*

---

**Description**

Invoke the generation of a set of cohort definitions

**Usage**

```
invokeCohortSetGeneration(baseUrl, sourceKeys, definitionIds)
```

**Arguments**

baseUrl	The base URL for the WebApi instance, for example: "http://server.org:80/WebAPI".
sourceKeys	A list of CDM source keys. These can be found in Atlas -> Configure.
definitionIds	A list of cohort definition Ids

**Details**

Invokes the generation of a set of cohort definitions across a set of CDMs set up in WebAPI. Use getCohortGenerationStatuses to check the progress of the set.

---

restoreEnvironment

*Restore the R environment to a snapshot*

---

**Description**

Restore the R environment to a snapshot

**Usage**

```
restoreEnvironment(
  snapshot,
  stopOnWrongRVersion = FALSE,
  strict = FALSE,
  skipLast = TRUE
)
```

**Arguments**

snapshot	The snapshot data frame as generated using the <a href="#">takeEnvironmentSnapshot</a> function.
stopOnWrongRVersion	Should the function stop when the wrong version of R is installed? Else just a warning will be thrown when the version doesn't match.
strict	If TRUE, the exact version of each package will installed. If FALSE, a package will only be installed if (a) a newer version is required than currently installed, or (b) the major version number is different.
skipLast	Skip last entry in snapshot? This is usually the study package that needs to be installed manually.

**Details**

This function restores the R environment to a previous snapshot, meaning all the packages will be restored to the versions they were at at the time of the snapshot. Note: on Windows you will very likely need to have RTools installed to build the various packages.

**Examples**

```
## Not run:
snapshot <- takeEnvironmentSnapshot("OhdsiRTools")
write.csv(snapshot, "snapshot.csv")

# 5 years later

snapshot <- read.csv("snapshot.csv")
restoreEnvironment(snapshot)

## End(Not run)
```

---

```
restoreEnvironmentFromPackage
```

*Restore environment stored in package*

---

**Description**

Restore environment stored in package

**Usage**

```
restoreEnvironmentFromPackage(
  pathToCsv = "inst/settings/rEnvironmentSnapshot.csv",
  stopOnWrongRVersion = FALSE,
  strict = FALSE,
  skipLast = TRUE
)
```

**Arguments**

pathToCsv	The path for saving the snapshot (as CSV file).
stopOnWrongRVersion	Should the function stop when the wrong version of R is installed? Else just a warning will be thrown when the version doesn't match.
strict	If TRUE, the exact version of each package will installed. If FALSE, a package will only be installed if (a) a newer version is required than currently installed, or (b) the major version number is different.
skipLast	Skip last entry in snapshot? This is usually the study package that needs to be installed manually.

**Details**

This function restores all packages (and package versions) described in the environment snapshot stored in the package currently being developed. The default location is `inst/settings/rEnvironmentSnapshot.csv`.

**Examples**

```
## Not run:
restoreEnvironmentFromPackage()

## End(Not run)
```

---

```
restoreEnvironmentFromPackageOnGithub
      Restore environment stored in package
```

---

**Description**

Restore environment stored in package

**Usage**

```
restoreEnvironmentFromPackageOnGithub(
  githubPath,
  pathToCsv = "inst/settings/rEnvironmentSnapshot.csv",
  stopOnWrongRVersion = FALSE,
  strict = FALSE,
  skipLast = TRUE
)
```

**Arguments**

githubPath	The path for the GitHub repo containing the package (e.g. 'OHDSI/StudyProtocols/AlendronateVsRa
pathToCsv	The path for the snapshot inside the package.
stopOnWrongRVersion	Should the function stop when the wrong version of R is installed? Else just a warning will be thrown when the version doesn't match.

strict	If TRUE, the exact version of each package will be installed. If FALSE, a package will only be installed if (a) a newer version is required than currently installed, or (b) the major version number is different.
skipLast	Skip last entry in snapshot? This is usually the study package that needs to be installed manually.

### Details

This function restores all packages (and package versions) described in the environment snapshot stored in the package currently being developed. The default location is `inst/settings/rEnvironmentSnapshot.csv`.

### Examples

```
## Not run:
restoreEnvironmentFromPackageOnGithub("OHDSI/StudyProtocols/AlendronateVsRaloxifene")

## End(Not run)
```

---

```
takeEnvironmentSnapshot
```

*Take a snapshot of the R environment*

---

### Description

Take a snapshot of the R environment

### Usage

```
takeEnvironmentSnapshot(rootPackage)
```

### Arguments

rootPackage      The name of the root package

### Details

This function records all versions used in the R environment that are used by one root package. This can be used for example to restore the environment to the state it was when a particular study package was run using the [restoreEnvironment](#) function.

### Value

A data frame listing all the dependencies of the root package and their version numbers, in the order in which they should be installed.

### Examples

```
snapshot <- takeEnvironmentSnapshot("OhdsiRTools")
snapshot
```

---

`updateCopyrightYearFile`*Update the copyright year in a R or SQL file*

---

**Description**

Update the copyright year in a R or SQL file

**Usage**

```
updateCopyrightYearFile(file)
```

**Arguments**

file	The path to the file.
------	-----------------------

---

`updateCopyrightYearFolder`*Update the copyright year in all R and SQL files in a folder*

---

**Description**

Update the copyright year in all R and SQL files in a folder

**Usage**

```
updateCopyrightYearFolder(path = ".", recursive = TRUE)
```

**Arguments**

path	Path to the folder containing the files to update. Only files with the .R and .SQL extension will be updated.
recursive	Include all subfolders?

---

`updatePackageName`*Update the package name in a R or SQL file*

---

**Description**

Update the package name in a R or SQL file

**Usage**

```
updatePackageName(file, packageName)
```

**Arguments**

file	The path to the file.
packageName	The replacement package name

---

`updatePackageNameFolder`*Update the package name in all R and SQL files in a folder*

---

**Description**

Update the package name in all R and SQL files in a folder

**Usage**

```
updatePackageNameFolder(path = ".", packageName, recursive = TRUE)
```

**Arguments**

<code>path</code>	Path to the folder containing the files to update. Only files with the .R and .SQL extension will be updated.
<code>packageName</code>	The replacement package name
<code>recursive</code>	Include all subfolders?

# Index

checkUsagePackage, [2](#)  
createConceptSetWorkbook, [3](#)  
createRenvLockFile, [4](#)  
  
findNonAsciiStringsInFolder, [4](#)  
fixHadesLogo, [5](#)  
formatRFile, [5](#)  
formatRFolder, [6](#)  
formatRText, [6](#)  
  
getCohortDefinitionExpression, [7](#)  
getCohortDefinitionName, [7](#)  
getCohortDefinitionSql, [8](#)  
getCohortGenerationStatuses, [9](#)  
getConceptSetConceptIds, [9](#)  
getConceptSetExpression, [10](#)  
getConceptSetName, [10](#)  
getConceptSetsAndConceptsFromCohort,  
[11](#)  
getCorePackages, [12](#)  
getOhdsiGitHubPackages, [12](#)  
getPriorityVocabKey, [13](#)  
getSetExpressionConceptIds, [13](#)  
  
insertCohortDefinitionInPackage, [14](#)  
insertCohortDefinitionSetInPackage, [15](#)  
insertConceptSetConceptIdsInPackage,  
[16](#)  
insertEnvironmentSnapshotInPackage, [16](#)  
invokeCohortSetGeneration, [17](#)  
  
restoreEnvironment, [16](#), [17](#), [20](#)  
restoreEnvironmentFromPackage, [18](#)  
restoreEnvironmentFromPackageOnGithub,  
[19](#)  
  
takeEnvironmentSnapshot, [18](#), [20](#)  
  
updateCopyrightYearFile, [21](#)  
updateCopyrightYearFolder, [21](#)  
updatePackageName, [21](#)  
updatePackageNameFolder, [22](#)