Package 'Herper'

July 26, 2025

Type Package

Title The Herper package is a simple toolset to install and manage
conda packages and environments from R

Version 1.19.3

Description Many tools for data analysis are not available in R, but are present in public reposito-
ries like conda. The Herper package provides a comprehensive set of functions to inter-
act with the conda package managament system. With Herper users can install, man-
age and run conda packages from the comfort of their R session. Herper also provides an ad-
hoc approach to handling external system requirements for R packages. For people develop-
ing packages with python conda dependencies we recommend us-
ing basilisk (https://bioconductor.org/packages/release/bioc/html/basilisk.html) to internally sup-
port these system requirments pre-hoc.

URL https://github.com/RockefellerUniversity/Herper

Depends R (>= 4.0), reticulate

Imports utils, rjson, withr, stats

Suggests BiocStyle, testthat, knitr, rmarkdown

License GPL-3

Encoding UTF-8

LazyData false

RoxygenNote 7.3.1

VignetteBuilder knitr

biocViews Infrastructure, Software

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Contents

Index **10**

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conda_search   *Search package availability*

Description

Search package availability

Usage

```
conda_search(package, channel = NULL, print_out = TRUE, pathToMiniConda = NULL)
```

Arguments

package   Package to search for. If an exact match is found, the funtion will return true
                    (assuming 'package_version' is left NULL or is a valid entry). If there is not an
                    exact match and other packages contain this text, the function will return FALSE
                    but the alternative options will be printed if print_out = TRUE.

channel   Channels for to search in (bioconda and conda-forge are defaults).

print_out   Either True or FALSE indicating whether to print out information about avail-
                    able builds and channels for the search entry.

pathToMiniConda
                    Path to miniconda installation. If this is set to NULL (default), then the output
                    of 'reticulate::miniconda_path()' is used.

Details

This function will search to see if a package is available from the conda repository For a more
detailed walkthrough check our webpage: https://rockefelleruniversity.github.io/Herper_Page/

Value

TRUE/FALSE

Author(s)

Doug Barrows and Matt Paul

---

export_CondaEnv   *Export Conda environment.*

Description

Export Conda environment

Import Conda environment

Usage

```
export_CondaEnv(
  env_name,
  yml_export = NULL,
  pathToMiniConda = NULL,
  depends = TRUE
)

import_CondaEnv(
  yml_import,
  name = NULL,
  pathToMiniConda = NULL,
  install = TRUE,
  channels = NULL,
  mamba = FALSE
)
```

Arguments

env_name	Name of environment you want to save
yml_export	Destination for exported environment yml file
pathToMiniConda	
	NULL Path to miniconda installation
depends	if FALSE will only include packages explicitly installed and not dependencies
yml_import	conda environment yml file
name	Name of the environment to create.
install	TRUE/FALSE whether to install miniconda at path if it doesn't exist.
channels	Channels for miniconda (bioconda and conda-forge are defaults).
mamba	A logical about whether to use the mamba solver to speed up the resolution of environment dependencies (Default is FALSE).

Details

This function will export a yml config file corresponding to the provided conda environment. For a more detailed walkthrough check our webpage: https://rockefelleruniversity.github.io/Herper_Page/

This function will recreate a conda environment from a provided yml config file.

Value

Nothing returned. Output written to file.

Nothing returned. Output written to file.

Author(s)

Matt Paul

---

install_CondaSysReqs	*Install Conda requirements listed in the System Requirement field of description*

Description

Install Conda requirements

Usage

```
install_CondaSysReqs(
  pkg,
  channels = NULL,
  env = NULL,
  pathToMiniConda = NULL,
  updateEnv = FALSE,
  SysReqsAsJSON = FALSE,
  SysReqsSep = ",",
  verbose = FALSE,
  mamba = FALSE
)
```

Arguments

pkg	Package to install Conda System Requirements from.
channels	Channels for miniconda (bioconda and conda-forge are defaults).
env pathToMiniConda	Name of Conda environment to install tools into.
	NULL Path to miniconda installation
updateEnv	Update existing package's conda environment if already installed.
SysReqsAsJSON	Parse the SystemRequirements in JSON format (see Details). Default is TRUE.
SysReqsSep	Separator used in SystemRequirement field.
verbose	Print system messages from conda on progress (Default is FALSE). There is a third option "silent" which suppresses Herper and Conda messaging.
mamba	A logical about whether to use the mamba solver to speed up the resolution of environment dependencies (Default is FALSE).

Details

This function will install any software listed as a System Requirement in the provided R package. For a more detailed walkthrough check our webpage: https://rockefelleruniversity.github.io/Herper_Page/

Value

Nothing returned. Output written to file.

Author(s)

Thomas Carroll and Matt Paul

---

install_CondaTools   *Install Conda requirements.*

Description

Install Conda requirements

Usage

```
install_CondaTools(
  tools,
  env,
  channels = NULL,
  pathToMiniConda = NULL,
  updateEnv = FALSE,
  search = FALSE,
  verbose = FALSE,
  mamba = FALSE
)
```

Arguments

tools	Vector of software to install using conda.
env	Name of Conda environment to install tools into.
channels	Channels for miniconda (bioconda and conda-forge are defaults).
pathToMiniConda	
	NULL Path to miniconda installation
updateEnv	Update existing package's conda environment if already installed.
search	Whether to search for the package name and version before installing. It is highly recommended this be set to TRUE as information about available versions or similar packages will be included in the output if the exact match is not found.
verbose	Print system messages from conda on progress (Default is FALSE). There is a third option "silent" which suppresses Herper and Conda messaging.
mamba	A logical about whether to use the mamba solver to speed up the resolution of environment dependencies (Default is FALSE).

Details

This function will install conda software. For a more detailed walkthrough check our webpage:
https://rockefelleruniversity.github.io/Herper_Page/

Value

Nothing returned. Output written to file.

Author(s)

Thomas Carroll and Matt Paul

---

list_CondaEnv *List Conda environments.*

Description

List Conda environments

Usage

```
list_CondaEnv(pathToMiniConda = NULL, allCondas = FALSE, env = NULL)
```

Arguments

pathToMiniConda
        NULL Path to miniconda installation

allCondas   Logical. Whether to return conda environments, for all discoverable conda installs, or just the conda specified in pathToMiniConda.

env   Environment name. If this is supplied to list_CondaEnv, it will query whether that environment is present in the given conda.

Details

This function will list all environments available from a specific conda installation (or across all conda installations). For a more detailed walkthrough check our webpage: https://rockefelleruniversity.github.io/Herper_

Value

Conda environment names and the file paths to their conda installation are printed to the screen. If environment name is supplied a TRUE/FALSE will be returned depending on whether that environment is present or not.

Author(s)

Matt Paul

---

list_CondaPkgs   *List Conda packages.*

Description

List Conda packages

Usage

```
list_CondaPkgs(env, pathToMiniConda = NULL, pkg = NULL)
```

Arguments

env   environment to look in

pathToMiniConda
                   NULL Path to miniconda installation

pkg   Package name. If this is supplied to list_CondaPkg, it will query whether that
                   package is present in the given environment.

Details

This function will list all packages from a specific conda environment. For a more detailed walk-
through check our webpage: https://rockefelleruniversity.github.io/Herper_Page/

Value

Conda package information is printed to the screen. If package name is supplied a TRUE/FALSE
will be returned depending on whether that package is present or not.

Author(s)

Matt Paul

---

with_CondaEnv   *Use Conda environments.*

Description

Use Conda environments

Use Conda environments

Usage

```
with_CondaEnv(
  new,
  code,
  pathToMiniConda = NULL,
  path_action = "prefix",
  pythonpath_action = "replace",
  perl5lib_action = "replace",
  path_additional = NULL,
  pythonpath_additional = NULL,
  perl5lib_additional = NULL
)

local_CondaEnv(
  new = list(),
  pathToMiniConda = NULL,
  path_action = "prefix",
  pythonpath_action = "replace",
  perl5lib_action = "replace",
  path_additional = NULL,
  pythonpath_additional = NULL,
  perl5lib_additional = NULL,
  .local_envir = parent.frame()
)
```

Arguments

`new`	The name of conda environment to include in the temporary R environment.
`code`	Code to execute in the temporary R environment
`pathToMiniConda`	
	Path to miniconda.
`path_action`	Should new values "replace", "prefix" or "suffix" existing PATH variable.
`pythonpath_action`	
	Should new values "replace", "prefix" or "suffix" existing PYTHONPATH variable.
`perl5lib_action`	
	Should new values "replace", "prefix" or "suffix" existing PERL5LIB variable.
`path_additional`	
	Additional paths to suffix to existing PATH variable.
`pythonpath_additional`	
	Additional paths to suffix to existing PYTHONPATH variable.
`perl5lib_additional`	
	Additional paths to suffix to existing PERL5LIB variable.
`.local_envir`	The environment to use for scoping.

Details

This function will execute the provided code while using a the specific conda environment provided. For a more detailed walkthrough check our webpage: https://rockefelleruniversity.github.io/Herper_Page/

This function will update the local environment to use a specific conda environment provided. For a more detailed walkthrough check our webpage: https://rockefelleruniversity.github.io/Herper_Page/

Value

Nothing returned.

Author(s)

Thomas Carroll

Examples

```
local_CondaEnv(new = "herper_env")
```

Index