Package ‘Herper’

December 3, 2025

Type Package

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

Version 1.21.0

Description Many tools for data analysis are not available in R, but are present in public repositories like conda. The Herper package provides a comprehensive set of functions to interact with the conda package managament system. With Herper users can install, manage 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 developing packages with python conda dependencies we recommend using basilisk (https://bioconductor.org/packages/release/bioc/html/basilisk.html) to internally support 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

git_url https://git.bioconductor.org/packages/Herper

git_branch devel

git_last_commit 2c2b888

git_last_commit_date 2025-10-29

Repository Bioconductor 3.23

Date/Publication 2025-12-02

Author Matt Paul [aut] (ORCID: <`https://orcid.org/0000-0002-3020-7729`>),
Thomas Carroll [aut, cre] (ORCID:
<`https://orcid.org/0000-0002-0073-1714`>),
Doug Barrows [aut],
Kathryn Rozen-Gagnon [ctb]

Maintainer Thomas Carroll <`tc.infomatics@gmail.com`>

Contents

`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 available 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`	Name of Conda environment to install tools into.
`pathToMiniConda`	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_Page

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 walkthrough 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