Package 'basilisk.utils'

May 8, 2026

Version 1.25.0

Date 2025-11-09

Title Centralized Conda Installation for Bioconductor Packages

Imports utils, methods, tools, dir.expiry

Suggests knitr, rmarkdown, BiocStyle, testthat

biocViews Infrastructure

Description Provides a centralized conda installation for use by other Bioconductor packages.
If conda is not already available on the system, it is downloaded and installed from the Miniforge project; otherwise, no action is performed.
Historically, this package was used to provide a Python installation for basilisk, hence the name.

License GPL-3

RoxygenNote 7.3.2

VignetteBuilder knitr

Encoding UTF-8

git_url https://git.bioconductor.org/packages/basilisk.utils

git_branch devel

git_last_commit 1c8ebe2

git_last_commit_date 2026-04-28

Repository Bioconductor 3.24

Date/Publication 2026-05-08

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Contents

binaryPath *Get binary paths*

Description

Get binary paths

Usage

```
condaBinary(loc)

pythonBinary(loc)
```

Arguments

loc	String containing the path to the root of a conda instance or environment.

Details

This code is largely copied from **reticulate**, and is only present here as they do not export these utilities for general consumption.

Value

String containing the path to the conda or Python executable inside `loc`. If `loc` is not supplied, the relative path from the root of a conda instance or environment is returned.

Author(s)

Aaron Lun

Examples

```
condaBinary()
pythonBinary()
```

configureEnvironments *Create environments with system installs*

Description

Create conda environments during installation of the R package, typically by calling this function in a package's `configure` file.

Usage

```
configureEnvironments(src)
```

Arguments

src	String containing the local path to an R source file that defines the environments to be created.

Details

Sometimes, the lazy creation of new environments is not desirable. For example, administrators of multi-user R instances would not want to create a separate environment in each user's cache. Similarly, users of Docker images would not want to recreate the environment inside every new container.

In these cases, an alternative is to use a "system install", where the environments are created during R package installation. Each environment is directly created in the package's installation directory and is immediately available when `createEnvironment` is called. Administrators can enable this mode by setting the `BIOCCMAKE_USE_SYSTEM_INSTALL` environment variable to 1. Note that this setting takes effect during R package installation so should be set before (re-)installation of **basilisk.utils** and its dependencies.

Developers can support system installs by adding `configure(.win)` scripts to the root of their package. These scripts should call `configureEnvironments` to trigger creation of the conda environments during R package installation. Details of the environments to be created are taken from the `src` file, which should be executable as a standalone R file (i.e., it can be `source`d). Each conda environment is defined as a list with a name ending in `_args`, where the list contains arguments to `createEnvironment`.

Packages that support system installs should also set `StagedInstall: no` in their `DESCRIPTION` files. This ensures that the conda environments are created with the correct hard-coded paths in the package installation directory.

Value

`NULL` is invisibly returned. Conda environments are created in the R package installation directory if system installs are enabled. Otherwise, no action is performed.

Author(s)

Aaron Lun

Examples

```
# If we have a package with an 'R/environments.R' file,
# we could put the following in our 'configure' file.
## Not run: configureEnvironments('R/environments.R')
```

`createEnvironment` *Create a new conda environment*

Description

Create a new conda environment if it does not already exist in the cache/system.

Usage

```
createEnvironment(
  pkg,
  name,
  version,
  packages,
  cache.dir = NULL,
  ignore.cache = FALSE,
  conda = NULL,
  channels = "conda-forge",
  override.channels = TRUE,
  extra = "--quiet"
)
```

Arguments

pkg	String containing the name of the R package that owns this conda environment.
name	String containing the name of the environment.
version	String containing the version of the environment. Ignored for system installs.
packages	Character vector of conda packages (possibly with version specifications) to be installed in this environment.
cache.dir	String containing the location of the cache for lazily instantiated environments. If NULL, this defaults to a location returned by R_user_dir with package. Ignored for system installs.
ignore.cache	Logical scalar indicating whether to ignore cached environments if they already exist. Ignored for system installs.
conda	String containing the path to the conda command or executable. If NULL, a suitable value is obtained from find.
channels	Character vector of channels to use for conda environment creation.
override.channels	Logical scalar indicating whether to set the --override-channels option during conda environment creation.
extra	Character vector of additional arguments to pass to conda create.

Details

In general, createEnvironment should be called inside any function of a downstream package that relies on the conda environment. On its first call, it will then lazily instantiate the environment based on the specified arguments. All subsequent calls in the same or new R sessions will use the cached environments.

The version string is used to distinguish between different versions of the same name environments. This allows package developers to safely update their environments without affecting other R installations that are re-using the same cache. Older unused versions of the environment will be automatically removed over time via **dir.expiry**.

Note that the version string does not necessarily have to be the same as the version of the pkg package. Any version-like string is fine as long as they are compatible with package_version. In fact, having independent versions for the environments and their parent package is often more convenient, as it means that the environments don't always need to be recreated when the package is updated.

To avoid lazy evaluation, administrators of an R installation can enable system installs, see configureEnvironments for details.

Value

String containing the path to the conda environment.

Author(s)

Aaron Lun

Examples

```
createEnvironment(
   pkg="basilisk.utils.test",
   name="test_env",
   version="1.0.0",
   packages="hdf5"
)

# Repeated calls will just get the same environment back.
createEnvironment(
   pkg="basilisk.utils.test",
   name="test_env",
   version="1.0.0",
   packages="hdf5"
)
```

---

defaults *Defaults for* **biocconda**

Description

Defaults for **biocconda**

Usage

```
defaultCommand()

defaultDownloadVersion()

defaultMinimumVersion()

defaultCacheDirectory()
```

Details

The BIOCCONDA_CONDA_COMMAND environment variable will override the default setting of defaultCommand.

The BIOCCONDA_CONDA_DOWNLOAD_VERSION environment variable will override the default setting of defaultDownloadVersion.

The BIOCCONDA_CONDA_MINIMUM_VERSION environment variable will override the default setting of defaultMinimumVersion.

The BIOCCONDA_CONDA_CACHE_DIRECTORY environment variable will override the default setting of defaultCacheDirectory.

Value

For defaultCommand, a string specifying the expected command-line invocation of an existing conda installation.

For defaultDownloadVersion, a string specifying the version of conda to download if no existing installation can be found.

For defaultMinimumVersion, a string specifying the minimum version of an existing conda installation.

For defaultCacheDirectory, a string containing the path to the cache directory for **biocconda**-managed conda installations.

Author(s)

Aaron Lun

Examples

```
defaultCommand()
defaultDownloadVersion()
defaultMinimumVersion()
defaultCacheDirectory()
```

---

download *Install conda*

Description

Install conda via the Miniforge project to an appropriate destination path, skipping the installation if said path already exists.

Usage

```
download(
  download.version = defaultDownloadVersion(),
  cache.dir = defaultCacheDirectory(),
  ignore.cache = FALSE
)
```

Arguments

download.version	String specifying the Miniforge version to download.
cache.dir	String specifying the location of the directory in which to cache Miniforge installations.
ignore.cache	Logical scalar specifying whether to ignore any existing cached version of Miniforge, in which case the binaries will be downloaded again.

Details

This function was originally created from code in https://github.com/hafen/rminiconda, also borrowing code from **reticulate**'s `install_miniconda` for correct Windows installation. It downloads and runs a Miniforge installer to create a Bioconductor-managed Conda instance.

Whenever `download` is re-run, any old conda instances and their associated **basilisk** environments are deleted from the external installation directory. This avoids duplication of large conda instances after their obselescence.

Value

A conda instance is created at the cache location. Nothing is performed if a complete instance already exists at that location. A string is returned containing the path to the conda installation.

Author(s)

Aaron Lun

Examples

```
download()
```

`find` *Find conda*

Description

Find an existing conda installation or, if none can be found, install a **biocconda**-managed conda instance.

Usage

```
find(
  command = defaultCommand(),
  minimum.version = defaultMinimumVersion(),
  can.download = TRUE,
  forget = FALSE,
  ...
)
```

Arguments

`command`	String containing the command to check for an existing installation.
`minimum.version`	String specifying the minimum acceptable version of an existing installation.
`can.download`	Logical scalar indicating whether to download conda if no acceptable existing installation can be found.
`forget`	Logical scalar indicating whether to forget the results of the last call.
`...`	Further arguments to pass to `download`.

Details

If the BIOCCONDA_FIND_OVERRIDE environment variable is set to a command or path to a conda executable, it is returned directly and all other options are ignored.

By default, find will remember the result of its last call in the current R session, to avoid re-checking the versions, cache, etc. This can be disabled by setting forget=TRUE to force a re-check, e.g., to detect a new version of conda that was installed while the R session is active.

Value

String containing the command to use to run conda.

Author(s)

Aaron Lun

Examples

```
cmd <- find()
system2(cmd, "--version")
```

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