# Package 'basilisk.utils'

March 29, 2021

Version 1.2.2

Date 2021-01-27

Title Basilisk Installation Utilities

Imports utils, methods, rappdirs, filelock

Suggests knitr, rmarkdown, BiocStyle, testthat, BiocFileCache

biocViews Infrastructure

**Description** Implements utilities for installation of the basilisk package, primarily for creation of the underlying Conda instance. This allows us to avoid re-writing the same R code in both the configure script (for centrally administered R installations) and in the lazy installation mechanism (for distributed package binaries). It is highly unlikely that developers - or, heaven forbid, end-users! - will need to interact with this package directly; they should be using the basilisk package instead.

License GPL-3

RoxygenNote 7.1.1

VignetteBuilder knitr

git\_url https://git.bioconductor.org/packages/basilisk.utils

git\_branch RELEASE\_3\_12

git\_last\_commit d4795d1

git\_last\_commit\_date 2021-01-27

Date/Publication 2021-03-29

Author Aaron Lun [aut, cre, cph]

Maintainer Aaron Lun <infinite.monkeys.with.keyboards@gmail.com>

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#### clearExternalDir

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clearExternalDir Clear the external installation directory

#### Description

Clear the external installation directory by removing old Conda instances installed for different versions of **basilisk** with the same middle version number (i.e., same Bioconductor release).

# Usage

clearExternalDir()

clearObsoleteDir(path = getExternalDir())

### Arguments

path

String containing the path to the latest version of the directory of interest.

#### Details

clearObsoleteDir can also be applied to the directories for the individual Conda environments, as the package version is also suffixed onto those directory paths. This is useful for clearing out obsolete versions of package environments.

#### Value

For clearExternalDir, all conda instances (and associated environments) of the same Bioconductor release as the current **basilisk** installation are destroyed.

The same applies for clearObsoleteDir except that the conda instance generated by the latest **basilisk** installation is retained.

#### Author(s)

Aaron Lun

### See Also

getExternalDir, which determines the location of the external directory.
installConda, for the motivation behind this function.

#### Examples

```
# We can't actually run clearExternalDir() here, as it
# relies on basilisk already being installed.
print("dummy test to pass BiocCheck")
```

destroyOldVersions Destroy old versions?

# Description

Should we destroy old installations of Conda from previous versions of **basilisk** (or old environment installations, for **basilisk** client packages)?

#### Usage

```
destroyOldVersions()
```

#### Details

The default value is TRUE, in order to save some hard drive space. This can be changed by setting BASILISK\_NO\_DESTROY environment variable to "1".

#### Value

Logical scalar providing an answer to the above.

#### Author(s)

Aaron Lun

# See Also

installConda, where this function is used.

clearObsoleteDir, which may be triggered by this function.

dir.create2 Safe directory construction

# Description

Create a directory with an error message if it does not succeed.

#### Usage

```
dir.create2(path, recursive = TRUE, ...)
```

# Arguments

path, recursive, ...

Further arguments to pass to dir.create.

#### Details

This is primarily necessary to avoid incomprehensible errors when a directory cannot be created, usually due to insufficient permissions. We set recursive=TRUE by default for convenience.

Note that the presence of an existing directory at path will cause this function to fail. This is usually desirable in the context of **basilisk.utils** as stale directories should be unlink2ed beforehand.

#### Value

Either path is created or an error is raised. NULL is invisibly returned.

#### See Also

unlink2, for a similarly safe deletion function.

#### Examples

```
out <- tempfile()
dir.create2(out)</pre>
```

getBinaries

Get binary paths

#### Description

Get binary paths

#### Usage

```
getCondaBinary(loc)
```

```
getPythonBinary(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 the environment is returned.

# Author(s)

Aaron Lun

#### getCondaDir

#### Examples

getCondaBinary()

getPythonBinary()

getCondaDir

# Get the basilisk Conda directory

#### Description

Find the installation directory for the basilisk-managed Conda instance.

#### Usage

getCondaDir(installed = TRUE)

#### Arguments

installed Logical scalar indicating whether **basilisk** is already installed.

# Details

By default, conda is installed to a location specified by getExternalDir. This ensures that R package build systems do not attempt to generate binaries that include the conda instance; such binaries are not relocatable due to the presence of hard-coded paths, resulting in run-time failures.

If the BASILISK\_EXTERNAL\_CONDA environment variable is set to a path to an existing conda instance, the function will return it directly without modification. This allows users to use their own conda instances with **basilisk** but, in turn, they are responsible for managing it.

If the BASILISK\_USE\_SYSTEM\_DIR environment variable is set to "1", the function will return a path to a location inside the basilisk system installation directory. This is the ideal approach when installing from source as any conda and **basilisk** re-installations are synchronized. It also ensures that any R process that can load **basilisk** will also have permissions to access the conda instance, which makes life easier for sysadmins of clusters or other shared resources.

We suggest always calling this function after an installConda call, which guarantees the presence of the conda installation directory (or dies trying). Setting installed=FALSE should only happen inside the **basilisk** configure script.

### Value

String containing the path to the conda instance.

# Author(s)

Aaron Lun

#### Examples

```
# Setting the environment variable to run this example:
# all other modes rely on installation of basilisk.
old <- Sys.getenv("BASILISK_USE_SYSTEM_DIR")
Sys.setenv(BASILISK_USE_SYSTEM_DIR=1)
```

getCondaDir(installed=FALSE)

Sys.setenv(BASILISK\_USE\_SYSTEM\_DIR=old)

getExternalDir Get an external conda directory

#### Description

Define an external location for installing the conda instance and **basilisk** environments.

#### Usage

getExternalDir()

#### Details

The default path contains the version number so that re-installation of **basilisk** will install a new instance of Conda. (This assumes that **basilisk** and **basilisk.utils** have synchronized version bumps.) See installConda for more details on how old versions of Conda are managed in this external directory.

If the BASILISK\_EXTERNAL\_DIR environment variable is set to some location, this will be used instead as the installation directory. Setting this variable is occasionally necessary if the default path returned by user\_cache\_dir has spaces; or on Windows, if the 260 character limit is exceeded after combining the default path with deeply nested conda paths.

We assume that the user has read-write access to the external directory. Write access is necessary to generate new environments and to handle locking in lockExternalDir.

# Value

String containing a path to an appropriate external folder. The last component of the path will always be the **basilisk** version number.

#### Author(s)

Aaron Lun

#### See Also

getCondaDir, to obtain the Conda installation directory.

#### Examples

```
# We can't actually run getExternalDir() here, as it
# either relies on basilisk already being installed.
print("dummy test to pass BiocCheck")
```

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getSystemDir

#### Description

Get the system installation directory for a package. This is not entirely trivial as it may be called before the package is installed.

# Usage

```
getSystemDir(pkgname, installed)
```

# Arguments

| pkgname   | String containing the package name.  |
|-----------|--|
| installed | Logical scalar specifying whether the package is likely to be installed yet. |

# Value

String containing the path to the (likely, if installed=FALSE) installation directory for pkgname.

#### Author(s)

Aaron Lun

# Examples

getSystemDir("basilisk", installed=FALSE)

installConda

Install (Mini)conda

# Description

Install conda - usually Miniconda, sometimes Anaconda - to an appropriate destination path, skipping the installation if said path already exists.

#### Usage

```
installConda(installed = TRUE)
```

# Arguments

installed Logical scalar indicating whether **basilisk** is already installed. Should only be set to FALSE in **basilisk** configure scripts.

#### 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 an appropriate conda installer to create a conda instance for use by **basilisk**. We use **BiocFileCache** if available to avoid redownloading the installer upon **basilisk** re-installation.

Currently, we use version 4.8.3 of the Miniconda3 installer. On MacOS, this is followed by installation of **nomkl** package to avoid issues with notarization, see https://github.com/rstudio/ reticulate/issues/758.

#### Value

A conda instance is created at the location specified by getCondaDir. Nothing is performed if a complete instance already exists at that location. A logical scalar is returned indicating whether a new instance was created.

#### **Destruction of old instances**

Whenever installConda is re-run (and BASILISK\_USE\_SYSTEM\_DIR is not set, see ?getCondaDir), any previous conda instances and their associated **basilisk** environments are destroyed. This avoids duplication of large conda instances after their obselescence. Client packages are expected to recreate their environments in the latest conda instance.

Users can disable this destruction by setting the BASILISK\_NO\_DESTROY environment variable to "1". This may be necessary on rare occasions when running multiple R instances on the same Bioconductor release. Note that setting this variable is not required for R instances using different Bioconductor releases; the destruction is smart enough to only remove conda instances generated from the same release.

#### Author(s)

Aaron Lun

#### Examples

# We can't actually run installConda() here, as it # either relies on basilisk already being installed or # it has a hard-coded path to the basilisk system dir. print("dummy test to pass BiocCheck")

isWindows

Find the operating system

#### Description

Indicate whether we are on Windows or MacOSX.

#### Usage

isWindows()

isMacOSX()

#### lockExternalDir

#### Value

Logical scalar indicating whether we are on the specified OS.

#### Author(s)

Aaron Lun

# Examples

isWindows()
isMacOSX()

lockExternalDir Lock external directory

#### Description

Lock the external Conda installation directory so that multiple processes cannot try to install at the same time.

#### Usage

```
lockExternalDir(...)
```

unlockExternalDir(lock)

#### Arguments

|      | Further arguments to pass to lock, such as exclusive. |
|------|---|
| lock | An existing filelock_lock object.                     |

#### Details

This will apply a lock to the (possibly user-specified) external Conda installation directory, so that a user trying to run parallel **basilisk** processes will not have race conditions during lazy Conda installation. We use **filelock** to manage the locking process for us, with the following strategy:

- If a system installation is being performed, we do not perform any locking. Rather, the R package manager will lock the entire R installation directory for us.
- If the external directory is not yet present, we establish an exclusive lock. We then proceed to the creation of said directory and installation of Conda.
- If an external installation directory is already present, we establish a shared lock. This will wait for any exclusive lock to expire (and thus any currently running installation to finish). No waiting is required if there are no existing exclusive locks.

Note that locking is only required during installation of Conda (or its environments), not during actual use. Once an installation/environment is created, we assume that it is read-only for all processes. Technically, this might not be true if one were to install a new version of **basilisk** halfway through an R session, which would prompt installConda to wipe out the old Conda installations; but one cannot in general guarantee the behavior of running R sessions when package versions change anyway, so we won't bother to protect against that.

#### setVariable

# Value

lockExternalDir will return a filelock\_lock object from lock.

unlockExternalDir will unlock the file and return NULL invisibly.

# Author(s)

Aaron Lun

# See Also

installConda, for an example of how to implement this locking approach.

# Examples

```
loc <- lockExternalDir()
unlockExternalDir(loc)</pre>
```

setVariable

Set an environment variable

# Description

Set an environment variable safely, unsetting it if the supplied value is NA.

# Usage

```
setVariable(name, value)
```

# Arguments

| name  | String containing the name of an environment variable.  |
|-------|---|
| value | String containing the value of an environment variable. This can be NA to unset the variable. |

# Value

String containing the value of the variable before running this function; or NA, if the variable was not set.

# Author(s)

Aaron Lun

unlink2

#### Description

Delete files or directories with an error message if it does not succeed.

#### Usage

```
unlink2(x, recursive = TRUE, force = TRUE, ...)
```

#### Arguments

x, recursive, force, ... Further arguments to pass to unlink.

# Details

This is primarily necessary to avoid incomprehensible errors when a directory containing a stale environment or installation is not successfully deleted. We set recursive=TRUE by default for convenience; we also set force=TRUE by default to avoid difficulties due to rogue permissions.

#### Value

Either all x are successfully deleted or an error is raised. NULL is invisibly returned.

#### See Also

dir.create2, for a similarly safe directory creation function.

#### Examples

```
out <- tempfile()
unlink2(out) # no error from deleting non-existent file.
write(file=out, "whee")
unlink2(out)</pre>
```

useSystemDir Use the R system directory?

#### Description

Should we use the R system directory for installing **basilisk**'s Conda instance (or client environments)?

## Usage

useSystemDir()

# Details

The default value is FALSE to avoid problems with position-dependent code in packaged binaries. This can be changed by setting BASILISK\_USE\_SYSTEM\_DIR environment variable to "1".

# Value

Logical scalar providing an answer to the above.

# Author(s)

Aaron Lun

# See Also

getCondaDir, where this function is used.

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