Package: biocmake (via r-universe)

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Title CMake for Bioconductor

Description Manages the installation of CMake for building Bioconductor packages. This avoids the need for end-users to manually install CMake on their system. No action is performed if a suitable version of CMake is already available.

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Encoding UTF-8

VignetteBuilder knitr

Imports utils, tools, dir.expiry

Suggests knitr, rmarkdown, BiocStyle, testthat

biocViews Infrastructure

URL https://github.com/LTLA/biocmake

BugReports https://github.com/LTLA/biocmake/issues

RoxygenNote 7.3.2

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configure *Configure Cmake*

Description

Propagate R's configuration variables into the Cmake options, where possible.

Usage

```
configure(
  c.compiler = TRUE,
  c.flags = c.compiler,
  cxx.compiler = TRUE,
  cxx.flags = cxx.compiler,
  fortran.compiler = TRUE,
  fortran.flags = fortran.compiler,
  cpp.flags = c.compiler || cxx.compiler,
  pic.flags = TRUE,
  ld.flags = c("exe", "module", "shared"),
  make = TRUE,
  ar = TRUE,
  ranlib = TRUE,
  release.build = TRUE
)

formatArguments(options)
```

Arguments

c.compiler	Logical scalar indicating whether to propagate R's choice of C compiler.
c.flags	Logical scalar indicating whether to propagate R's choice of C flags.
cxx.compiler	Logical scalar indicating whether to propagate R's choice of C++ compiler.
cxx.flags	Logical scalar indicating whether to propagate R's choice of C++ flags.
fortran.compiler	Logical scalar indicating whether to propagate R's choice of Fortran compiler.
fortran.flags	Logical scalar indicating whether to propagate R's choice of Fortran flags.
cpp.flags	Logical scalar indicating whether to propagate R's choice of C/C++ preprocessing flags.
pic.flags	Logical scalar indicating whether to propagate R's choice of each language's position-independent flags. This also sets the CMAKE_POSITION_INDEPENDENT_CODE variable.
ld.flags	Logical scalar indicating whether to add R's choice of linker flags to the CMake variables for each target type.
make	Logical scalar indicating whether to propagate R's choice of make command.

ar	Logical scalar indicating whether to propagate R's choice of command to make static libraries.
ranlib	Logical scalar indicating whether to propagate R's choice of command to index static libraries.
release.build	Logical scalar indicating whether to configure Cmake for a release build.
options	Character vector of optional arguments from configure.

Value

For configure, a named character vector containing the name and value of each option.

For formatArguments, a character vector with Cmake arguments on the command line. NA values are ignored, and values with spaces or empty strings are quoted.

Author(s)

Aaron Lun

Examples

```
options <- configure()
options
formatArguments(options)
```

---

defaults *Defaults for* **biocmake**

Description

Defaults for **biocmake**

Usage

```
defaultCommand()

defaultDownloadVersion()

defaultMinimumVersion()

defaultCacheDirectory()
```

Details

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

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

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

The BIOCMAKE_CMAKE_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 Cmake installation.

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

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

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

Author(s)

Aaron Lun

Examples

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

---

download *Download Cmake*

Description

Download Cmake binaries for the current architecture. This uses **dir.expiry** to remove unused versions of the **biocmake**-managed Cmake.

Usage

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

Arguments

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

Value

String containing the path to the Cmake executable.

Author(s)

Aaron Lun

Examples

```
download()
```

---

find *Find Cmake*

Description

Find an existing Cmake installation or, if none can be found, install a **biocmake**-managed Cmake 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 Cmake 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 BIOCMAKE_FIND_OVERRIDE environment variable is set to a command or path to a Cmake executable, it is returned directly and all other options are ignored.

On Windows, it is strongly recommended to download Rtools (see https://cran.r-project.org/bin/windows/Rtools/rtools44/rtools.html). This provides a pre-configured Cmake that is guaranteed to work.

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 Cmake that was installed while the R session is active.

Value

String containing the command to use to run Cmake.

Author(s)

Aaron Lun

Examples

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

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