

# Package ‘reproducible’

March 18, 2019

**Type** Package

**Title** A Set of Tools that Enhance Reproducibility Beyond Package Management

**Description** Collection of high-level, robust, machine- and OS-independent tools for making deeply reproducible and reusable content in R. This includes light weight package management (similar to 'packrat' and 'checkpoint', but more flexible, lightweight and simpler than both), tools for caching, downloading and verifying or writing checksums, post-processing of common spatial datasets, and accessing GitHub repositories. Some features are still under active development.

**SystemRequirements** 'unrar' (Linux/macOS) or '7-Zip' (Windows) to work with '.rar' files.

**URL** <http://reproducible.predictiveecology.org>,  
<https://github.com/PredictiveEcology/reproducible>

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**Depends** R (>= 3.3)

**Imports** `archivist` (>= 2.1.2), `backports`, `crayon`, `data.table` (>= 1.10.4), `digest`, `dplyr`, `fastdigest`, `fasterize`, `fpCompare`, `gdalUtils`, `git2r` (>= 0.18), `googledrive`, `httr`, `magrittr`, `memoise`, `methods`, `parallel`, `quickPlot`, `R.utils`, `raster`, `Rcpp` (>= 0.12.13), `RCurl` (>= 1.95-4.8), `remotes`, `rgdal`, `rgeos`, `rlang`, `sf`, `sp`, `testthat`, `tools`, `utils`, `versions`

**Suggests** `covr`, `future`, `knitr`, `rmarkdown`, `TimeWarp`

**Encoding** UTF-8

**Language** en-CA

**LinkingTo** `Rcpp`

**License** GPL-3

**VignetteBuilder** `knitr`, `rmarkdown`

**BugReports** <https://github.com/PredictiveEcology/reproducible/issues>

**ByteCompile** yes

**RoxygenNote** 6.1.1

**Collate** 'RcppExports.R' 'cache-helpers.R' 'cache-internals.R'  
'cache-tools.R' 'robustDigest.R' 'cache.R' 'checksums.R'  
'cloud.R' 'consistentPaths.R' 'convertPaths.R' 'download.R'  
'gis.R' 'git.R' 'helpers.R' 'objectSize.R' 'options.R'  
'packages.R' 'pipe.R' 'postProcess.R' 'preProcess.R'  
'prepInputs.R' 'reproducible-package.R' 'search.R' 'zzz.R'

**NeedsCompilation** yes

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---

reproducible-package *The reproducible package*

---

## Description

Built on top of **git2r** and **archivist**, this package aims at making high-level, robust, machine and OS independent tools for making deeply reproducible and reusable content in R. This extends beyond the package management utilities of **packrat** and **checkpoint** by including tools for caching, and accessing GitHub repositories.

## Main Tools

There are many elements within the reproducible package. However, there are currently 3 main ones that are critical for reproducible research. The key element for reproducible research is that the code must always return the same content every time it is run, but it must be vastly faster the 2nd, 3rd, 4th etc, time it is run. That way, the entire code sequence for a project of arbitrary size can be run from the start every time.

### Function

Cache

A robust wrapper for any function, including those with environment

prepInputs A function to download, or load objects, and possible post process them. The main advantage to using this over

Require

## Package options

See [reproducibleOptions](#) for a complete description of package [options](#) to configure behaviour.

## Author(s)

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- Her Majesty the Queen in Right of Canada, as represented by the Minister of Natural Resources Canada [copyright holder]

## See Also

Useful links:

- <http://reproducible.predictiveecology.org>

- <https://github.com/PredictiveEcology/reproducible>
- Report bugs at <https://github.com/PredictiveEcology/reproducible/issues>

---

`.addChangedAttr`      *Add an attribute to an object indicating which named elements change*

---

### Description

This is a generic definition that can be extended according to class.

### Usage

```
.addChangedAttr(object, preDigest, origArguments, ...)  
  
## S4 method for signature 'ANY'  
.addChangedAttr(object, preDigest, origArguments, ...)
```

### Arguments

<code>object</code>	Any R object returned from a function
<code>preDigest</code>	The full, element by element hash of the input arguments to that same function, e.g., from <code>.robustDigest</code>
<code>origArguments</code>	These are the actual arguments (i.e., the values, not the names) that were the source for <code>preDigest</code>
<code>...</code>	Anything passed to methods.

### Value

The object, modified

### Author(s)

Eliot McIntire

### Examples

```
a <- 1  
.addChangedAttr(a) # does nothing because default method is just a pass through
```

---

`.addTagsToOutput`      *Add tags to object*

---

### **Description**

This is a generic definition that can be extended according to class. This function and methods should do "deep" copy for archiving purposes.

### **Usage**

```
.addTagsToOutput(object, outputObjects, FUN, preDigestByClass)
```

```
## S4 method for signature 'ANY'
```

```
.addTagsToOutput(object, outputObjects, FUN,  
  preDigestByClass)
```

### **Arguments**

<code>object</code>	Any R object.
<code>outputObjects</code>	Optional character vector indicating which objects to return. This is only relevant for list, environment (or similar) objects
<code>FUN</code>	A function
<code>preDigestByClass</code>	A list, usually from <code>.preDigestByClass</code>

### **Value**

New object with tags attached.

### **Author(s)**

Eliot McIntire

---

`.cacheMessage`      *Create a custom cache message by class*

---

### **Description**

This is a generic definition that can be extended according to class.

### Usage

```
.cacheMessage(object, functionName,  
  fromMemoise = getOption("reproducible.useMemoise", TRUE))  
  
## S4 method for signature 'ANY'  
.cacheMessage(object, functionName,  
  fromMemoise = getOption("reproducible.useMemoise", TRUE))
```

### Arguments

object	Any R object.
functionName	A character string indicating the function name
fromMemoise	Logical. If TRUE, the message will be about recovery from memoised copy

### Value

Nothing; called for its messaging side effect.

### Author(s)

Eliot McIntire

### Examples

```
a <- 1  
.cacheMessage(a, "mean")
```

---

.checkCacheRepo	<i>Check for cache repository info in ...</i>
-----------------	---

---

### Description

This is a generic definition that can be extended according to class. Normally, checkPath can be called directly, but does not have class-specific methods.

### Usage

```
.checkCacheRepo(object, create = FALSE)  
  
## S4 method for signature 'ANY'  
.checkCacheRepo(object, create = FALSE)
```

### Arguments

object	An R object
create	Logical. If TRUE, then it will create the path for cache.

**Value**

A character string with a path to a cache repository.

**Author(s)**

Eliot McIntire

**Examples**

```
a <- "test"
.checkCacheRepo(a) # no cache repository supplied
```

---

.debugCache

*Attach debug info to return for Cache*

---

**Description**

Internal use only. Attaches an attribute to the output, usable for debugging the Cache.

**Usage**

```
.debugCache(obj, preDigest, ...)
```

**Arguments**

obj	An arbitrary R object.
preDigest	A list of hashes.
...	Dots passed from Cache

**Value**

The same object as obj, but with 2 attributes set.

**Author(s)**

Eliot McIntire



---

.installPackages      *Internal function to install packages*

---

### Description

Internal function to install packages

### Usage

```
.installPackages(packages, repos = getOption("repos"),  
  githubPkgs = character(0), githubPkgNames,  
  nonLibPathPkgs = character(0), install_githubArgs,  
  install.packagesArgs = list(), libPath = .libPaths()[1],  
  standAlone = standAlone, forget = FALSE)
```

### Arguments

- |                      |  |
|----------------------|--|
| packages             | Character vector of packages to install via <code>install.packages</code> , then load (i.e., with <code>library</code> ). If it is one package, it can be unquoted (as in <code>require</code> )   |
| repos                | The remote repository (e.g., a CRAN mirror), passed to <code>install.packages</code> ,   |
| githubPkgs           | Character vector of github repositories and packages, in the form <code>repository/package@branch</code> , with <code>branch</code> being optional.  |
| githubPkgNames       | Character vector of the package names, i.e., just the R package name.  |
| nonLibPathPkgs       | Character vector of all installed packages that are in <code>.libPaths</code> , but not in <code>libPath</code> . This would normally include a listing of base packages, but may also include other library paths if <code>standAlone</code> if <code>FALSE</code>  |
| install_githubArgs   | List of optional named arguments, passed to <code>install_github</code> .  |
| install.packagesArgs | List of optional named arguments, passed to <code>install.packages</code> .  |
| libPath              | The library path where all packages should be installed, and looked for to load (i.e., call <code>library</code> )   |
| standAlone           | Logical. If <code>TRUE</code> , all packages will be installed and loaded strictly from the <code>libPaths</code> only. If <code>FALSE</code> , all <code>.libPaths</code> will be used to find the correct versions. This can be create dramatically faster installs if the user has a substantial number of the packages already in their personal library. In the case of <code>TRUE</code> , there will be a hidden file place in the <code>libPath</code> directory that lists all the packages that were needed during the <code>Require</code> call. Default <code>FALSE</code> to minimize package installing. |
| forget               | Internally, this function identifies package dependencies using a memoised function for speed on reuse. But, it may be inaccurate in some cases, if packages were installed manually by a user. Set this to <code>TRUE</code> to refresh that dependency calculation.  |

**Examples**

```
## Not run:
  .installPackages("crayon")

## End(Not run)
```

---

*.objSizeInclEnviros*     *Determine object size of all objects inside environments*

---

**Description**

This is a generic definition that can be extended according to class.

**Usage**

```
.objSizeInclEnviros(object)

## S4 method for signature 'ANY'
.objSizeInclEnviros(object)

## S4 method for signature 'environment'
.objSizeInclEnviros(object)
```

**Arguments**

object            Any R object.

**Value**

A numeric, the result of `object.size` for all objects in environments.

**Author(s)**

Eliot McIntire

**Examples**

```
a <- new.env()
a$b <- 1:10
object.size(a)
.objSizeInclEnviros(a) # much larger
```

---

.preDigestByClass      *Any miscellaneous things to do before .robustDigest and after FUN call*

---

### Description

The default method for preDigestByClass and simply returns NULL. There may be methods in other packages.

### Usage

```
.preDigestByClass(object)

## S4 method for signature 'ANY'
.preDigestByClass(object)
```

### Arguments

object                  Any R object.

### Value

A list with elements that will likely be used in .postProcessing

### Author(s)

Eliot McIntire

### Examples

```
a <- 1
.preDigestByClass(a) # returns NULL in the simple case here.
```

---

.prefix                  *Add a prefix or suffix to the basename part of a file path*

---

### Description

Prepend (or postpend) a filename with a prefix (or suffix). If the directory name of the file cannot be ascertained from its path, it is assumed to be in the current working directory.

### Usage

```
.prefix(f, prefix = "")

.suffix(f, suffix = "")
```

**Arguments**

<code>f</code>	A character string giving the name/path of a file.
<code>prefix</code>	A character string to prepend to the filename.
<code>suffix</code>	A character string to postpend to the filename.

**Author(s)**

Jean Marchal and Alex Chubaty

**Examples**

```
# file's full path is specified (i.e., dirname is known)
myFile <- file.path("~/data", "file.tif")
.prefix(myFile, "small_") ## "/home/username/data/small_file.tif"
.suffix(myFile, "_cropped") ## "/home/username/data/myFile_cropped.shp"

# file's full path is not specified
.prefix("myFile.shp", "small") ## "./small_myFile.shp"
.suffix("myFile.shp", "_cropped") ## "./myFile_cropped.shp"
```

---

```
.prepareFileBackedRaster
```

*Copy the file-backing of a file-backed Raster\* object*

---

**Description**

Rasters are sometimes file-based, so the normal save and copy and assign mechanisms in R don't work for saving, copying and assigning. This function creates an explicit file copy of the file that is backing the raster, and changes the pointer (i.e., `filename(object)`) so that it is pointing to the new file.

**Usage**

```
.prepareFileBackedRaster(obj, repoDir = NULL, overwrite = FALSE, ...)
```

**Arguments**

<code>obj</code>	The raster object to save to the repository.
<code>repoDir</code>	Character denoting an existing directory in which an artifact will be saved.
<code>overwrite</code>	Logical. Should the raster be saved to disk, overwriting existing file.
<code>...</code>	passed to <code>archivist::saveToRepo</code>

**Value**

A raster object and its newly located file backing. Note that if this is a legitimate archivist repository, the new location will be a subdirectory called 'rasters/' of 'repoDir/'. If this is not a repository, the new location will be within `repoDir`.

**Author(s)**

Eliot McIntire

**Examples**

```
library(raster)
archivist::createLocalRepo(tempdir())

r <- raster(extent(0,10,0,10), vals = 1:100)

# write to disk manually -- will be in tempdir()
r <- writeRaster(r, file = tempfile())

# copy it to the cache repository
r <- .prepareFileBackedRaster(r, tempdir())

r # now in "rasters" subfolder of tempdir()
```

---

.prepareOutput	<i>Make any modifications to object recovered from cacheRepo</i>
----------------	--

---

**Description**

This is a generic definition that can be extended according to class.

**Usage**

```
.prepareOutput(object, cacheRepo, ...)
```

```
## S4 method for signature 'RasterLayer'
.prepareOutput(object, cacheRepo, ...)
```

```
## S4 method for signature 'ANY'
.prepareOutput(object, cacheRepo, ...)
```

**Arguments**

- object            Any R object
- cacheRepo        A repository used for storing cached objects. This is optional if Cache is used inside a SpADES module.
- ...               Arguments of FUN function .

**Value**

The object, modified

**Author(s)**

Eliot McIntire

**Examples**

```
a <- 1
.prepareOutput(a) # does nothing

b <- "Null"
.prepareOutput(b) # converts to NULL

# For rasters, it is same as .prepareFileBackedRaster
try(archivist::createLocalRepo(tempdir()))

library(raster)
r <- raster(extent(0,10,0,10), vals = 1:100)

# write to disk manually -- will be in tempdir()
r <- writeRaster(r, file = tempfile())

# copy it to the cache repository
r <- .prepareOutput(r, tempdir())
```

---

.setSubAttrInList      *Set subattributes within a list by reference*

---

**Description**

This uses `data.table::setattr`, but in the case where there is only a single element within a list attribute.

**Usage**

```
.setSubAttrInList(object, attr, subAttr, value)
```

**Arguments**

object	An arbitrary object
attr	The attribute name (that is a list object) to change
subAttr	The list element name to change
value	The new value

---

.sortDotsUnderscoreFirst

*Sort or order any named object with dotted names and underscores first*

---

## Description

Internal use only. This exists so Windows, Linux, and Mac machines can have the same order after a sort. It will put dots and underscores first (with the sort key based on their second character, see examples. It also sorts lower case before upper case.

## Usage

```
.sortDotsUnderscoreFirst(obj)
.orderDotsUnderscoreFirst(obj)
```

## Arguments

obj                    An arbitrary R object for which a names function returns a character vector.

## Value

The same object as obj, but sorted with .objects first.

## Author(s)

Eliot McIntire

## Examples

```
items <- c(A = "a", Z = "z", \.D` = ".d", \_C` = "_C")
.sortDotsUnderscoreFirst(items)

# dots & underscore (using 2nd character), then all lower then all upper
items <- c(B = "Upper", b = "lower", A = "a", \.D` = ".d", \_C` = "_C")
.sortDotsUnderscoreFirst(items)

# with a vector
.sortDotsUnderscoreFirst(c(".C", "_B", "A")) # _B is first
```

`.tagsByClass`      *Add extra tags to an archive based on class*

---

**Description**

This is a generic definition that can be extended according to class.

**Usage**

```
.tagsByClass(object)

## S4 method for signature 'ANY'
.tagsByClass(object)
```

**Arguments**

`object`      Any R object.

**Value**

A character vector of new tags.

**Author(s)**

Eliot McIntire

**Examples**

```
.tagsByClass(character()) # Nothing interesting. Other packages will make methods
```

---

`assessDataType`      *Assess the appropriate raster layer data type*

---

**Description**

Can be used to write prepared inputs on disk.



**Usage**

```
assessDataType(ras, type = "writeRaster")

## S3 method for class 'Raster'
assessDataType(ras, type = "writeRaster")

## S3 method for class 'RasterStack'
assessDataType(ras, type = "writeRaster")

## Default S3 method:
assessDataType(ras, type = "writeRaster")
```

**Arguments**

ras	The RasterLayer or RasterStack for which data type will be assessed.
type	Character. 'writeRaster' or 'GDAL' to return the recommended data type for writing from the raster and gdalUtils packages, respectively, or 'projectRaster' to return recommended resampling type. Default is 'writeRaster'.

**Value**

The appropriate data type for the range of values in ras. See [dataType](#) for details.

**Author(s)**

Eliot McIntire  
Ceres Barros  
Ian Eddy

**Examples**

```
## LOG1S
library(raster)
ras <- raster(ncol = 10, nrow = 10)
ras[] <- rep(c(0,1),50)
assessDataType(ras)

ras[] <- rep(c(TRUE,FALSE),50)
assessDataType(ras)

ras[] <- c(NA, NA, rep(c(0,1),49))
assessDataType(ras)

ras <- raster(ncol = 10, nrow = 10)
ras[] <- c(0, NaN, rep(c(0,1),49))
assessDataType(ras)

## INT1S
```

```
ras[] <- -1:98
assessDataType(ras)

ras[] <- c(NA, -1:97)
assessDataType(ras)

## INT1U
ras <- raster(ncol = 10, nrow = 10)
ras[] <- 1:100
assessDataType(ras)

ras[] <- c(NA, 2:100)
assessDataType(ras)

## INT2U
ras <- raster(ncol = 10, nrow = 10)
ras[] <- round(runif(100, min = 64000, max = 65000))
assessDataType(ras)

## INT2S
ras <- raster(ncol = 10, nrow = 10)
ras[] <- round(runif(100, min = -32767, max = 32767))
assessDataType(ras)

ras[54] <- NA
assessDataType(ras)

## INT4U
ras <- raster(ncol = 10, nrow = 10)
ras[] <- round(runif(100, min = 0, max = 500000000))
assessDataType(ras)

ras[14] <- NA
assessDataType(ras)

## INT4S
ras <- raster(ncol = 10, nrow = 10)
ras[] <- round(runif(100, min = -200000000, max = 200000000))
assessDataType(ras)

ras[14] <- NA
assessDataType(ras)

## FLT4S
ras <- raster(ncol = 10, nrow = 10)
ras[] <- runif(100, min = -10, max = 87)
assessDataType(ras)

ras <- raster(ncol = 10, nrow = 10)
ras[] <- round(runif(100, min = -3.4e+26, max = 3.4e+28))
assessDataType(ras)

ras <- raster(ncol = 10, nrow = 10)
```

```

ras[] <- round(runif(100, min = 3.4e+26, max = 3.4e+28))
assessDataType(ras)

ras <- raster(ncol = 10, nrow = 10)
ras[] <- round(runif(100, min = -3.4e+26, max = -1))
assessDataType(ras)

## FLT8S
ras <- raster(ncol = 10, nrow = 10)
ras[] <- c(-Inf, 1, rep(c(0,1),49))
assessDataType(ras)

ras <- raster(ncol = 10, nrow = 10)
ras[] <- c(Inf, 1, rep(c(0,1),49))
assessDataType(ras)

ras <- raster(ncol = 10, nrow = 10)
ras[] <- round(runif(100, min = -1.7e+30, max = 1.7e+308))
assessDataType(ras)

ras <- raster(ncol = 10, nrow = 10)
ras[] <- round(runif(100, min = 1.7e+30, max = 1.7e+308))
assessDataType(ras)

ras <- raster(ncol = 10, nrow = 10)
ras[] <- round(runif(100, min = -1.7e+308, max = -1))
assessDataType(ras)

# stack
ras <- raster(ncol = 10, nrow = 10)
ras[] <- rep(c(0,1),50)
ras1 <- raster(ncol = 10, nrow = 10)
ras1[] <- round(runif(100, min = -1.7e+308, max = -1))
sta <- stack(ras, ras1)
assessDataType(sta)

```

---

assessDataTypeGDAL      *Assess the appropriate raster layer data type for GDAL*

---

**Description**

Can be used to write prepared inputs on disk.

**Usage**

```
assessDataTypeGDAL(ras)
```

**Arguments**

ras                      The RasterLayer or RasterStack for which data type will be assessed.

**Value**

The appropriate data type for the range of values in `ras` for using GDAL. See [dataType](#) for details.

**Author(s)**

Eliot McIntire, Ceres Barros, Ian Eddy, and Tati Micheletti

**Examples**

```
library(raster)

## Byte
ras <- raster(ncol = 10, nrow = 10)

ras[] <- 1:100
assessDataTypeGDAL(ras)

ras[] <- c(NA, 2:100)
assessDataTypeGDAL(ras)

##Int16
ras <- raster(ncol = 10, nrow = 10)

ras <- setValues(ras, -1:98)
assessDataTypeGDAL(ras)

ras[] <- c(NA, -1:97)
assessDataTypeGDAL(ras)

ras[] <- round(runif(100, min = -32767, max = 32767))
assessDataTypeGDAL(ras)

## UInt16
ras <- raster(ncol = 10, nrow = 10)
ras[] <- round(runif(100, min = 64000, max = 65000))
assessDataTypeGDAL(ras)

## UInt32
ras <- raster(ncol = 10, nrow = 10)
ras[] <- round(runif(100, min = 0, max = 500000000))
assessDataTypeGDAL(ras)

ras[14] <- NA
assessDataTypeGDAL(ras)

## Int32
ras <- raster(ncol = 10, nrow = 10)
ras[] <- round(runif(100, min = -200000000, max = 200000000))
assessDataTypeGDAL(ras)

ras[14] <- NA
```

```

assessDataTypeGDAL(ras)

## Float32
ras <- raster(ncol = 10, nrow = 10)
ras[] <- runif(100, min = -10, max = 87)
assessDataTypeGDAL(ras)

ras <- raster(ncol = 10, nrow = 10)
ras[] <- round(runif(100, min = -3.4e+26, max = 3.4e+28))
assessDataTypeGDAL(ras)

ras <- raster(ncol = 10, nrow = 10)
ras[] <- round(runif(100, min = 3.4e+26, max = 3.4e+28))
assessDataTypeGDAL(ras)

ras <- raster(ncol = 10, nrow = 10)
ras[] <- round(runif(100, min = -3.4e+26, max = -1))
assessDataTypeGDAL(ras)

```

---

basename2	<i>A version of base::basename that is NULL resistant</i>
-----------	---

---

**Description**

Returns NULL if x is NULL, otherwise, as `basename`.

**Usage**

```
basename2(x)
```

**Arguments**

x                      A character vector of paths

**Value**

Same as [basename](#)

---

Cache	<i>Cache method that accommodates environments, S4 methods, Rasters, &amp; nested caching</i>
-------	---

---

**Description**

Still experimental and may change. This form cannot pass any arguments to `jcodeCache`, such as `cacheRepo`, thus it is of limited utility. However, it is a clean alternative for simple cases.

**Usage**

```
Cache(FUN, ..., notOlderThan = NULL, .objects = NULL,
      outputObjects = NULL, algo = "xxhash64", cacheRepo = NULL,
      length = getOption("reproducible.length", Inf),
      compareRasterFileLength, userTags = c(), digestPathContent,
      omitArgs = NULL, classOptions = list(), debugCache = character(),
      sideEffect = FALSE, makeCopy = FALSE,
      quick = getOption("reproducible.quick", FALSE),
      verbose = getOption("reproducible.verbose", 0), cacheId = NULL,
      useCache = getOption("reproducible.useCache", TRUE),
      showSimilar = getOption("reproducible.showSimilar", FALSE))
```

```
## S4 method for signature 'ANY'
```

```
Cache(FUN, ..., notOlderThan = NULL, .objects = NULL,
      outputObjects = NULL, algo = "xxhash64", cacheRepo = NULL,
      length = getOption("reproducible.length", Inf),
      compareRasterFileLength, userTags = c(), digestPathContent,
      omitArgs = NULL, classOptions = list(), debugCache = character(),
      sideEffect = FALSE, makeCopy = FALSE,
      quick = getOption("reproducible.quick", FALSE),
      verbose = getOption("reproducible.verbose", 0), cacheId = NULL,
      useCache = getOption("reproducible.useCache", TRUE),
      showSimilar = getOption("reproducible.showSimilar", FALSE))
```

```
lhs %<% rhs
```

**Arguments**

FUN	Either a function or an unevaluated function call (e.g., using quote).
...	Arguments of FUN function .
notOlderThan	load an artifact from the database only if it was created after notOlderThan.
.objects	Character vector of objects to be digested. This is only applicable if there is a list, environment (or similar) named objects within it. Only this/these objects will be considered for caching, i.e., only use a subset of the list, environment or similar objects.
outputObjects	Optional character vector indicating which objects to return. This is only relevant for list, environment (or similar) objects
algo	The algorithms to be used; currently available choices are md5, which is also the default, sha1, crc32, sha256, sha512, xxhash32, xxhash64 and murmur32.
cacheRepo	A repository used for storing cached objects. This is optional if Cache is used inside a SpaDES module.
length	Numeric. If the element passed to Cache is a Path class object (from e.g., asPath(filename)) or it is a Raster with file-backing, then this will be passed to digest::digest, essentially limiting the number of bytes to digest (for speed). This will only be used if quick = FALSE. Default is getOption("reproducible.length"), which is set to Inf.

compareRasterFileLength	Being deprecated; use length.
userTags	A character vector with Tags. These Tags will be added to the repository along with the artifact.
digestPathContent	Being deprecated. Use quick.
omitArgs	Optional character string of arguments in the FUN to omit from the digest.
classOptions	Optional list. This will pass into <code>.robustDigest</code> for specific classes. Should be options that the <code>.robustDigest</code> knows what to do with.
debugCache	Character or Logical. Either "complete" or "quick" (uses partial matching, so "c" or "q" work). TRUE is equivalent to "complete". If "complete", then the returned object from the Cache function will have two attributes, <code>debugCache1</code> and <code>debugCache2</code> , which are the entire <code>list(...)</code> and that same object, but after all <code>.robustDigest</code> calls, at the moment that it is digested using <code>digest</code> , respectively. This <code>attr(mySimOut, "debugCache2")</code> can then be compared to a subsequent call and individual items within the object <code>attr(mySimOut, "debugCache1")</code> can be compared. If "quick", then it will return the same two objects directly, without evaluating the <code>FUN(...)</code> .
sideEffect	Logical or path. Determines where the function will look for new files following function completion. See Details. <i>NOTE: this argument is experimental and may change in future releases.</i>
makeCopy	Logical. If <code>sideEffect = TRUE</code> , and <code>makeCopy = TRUE</code> , a copy of the downloaded files will be made and stored in the <code>cacheRepo</code> to speed up subsequent file recovery in the case where the original copy of the downloaded files are corrupted or missing. Currently only works when set to TRUE during the first run of Cache. Default is FALSE. <i>NOTE: this argument is experimental and may change in future releases.</i>
quick	Logical. If TRUE, little or no disk-based information will be assessed, i.e., mostly its memory content. This is relevant for objects of class <code>character</code> , <code>Path</code> and <code>Raster</code> currently. For class <code>character</code> , it is ambiguous whether this represents a character string or a vector of file paths. The function will assess if it is a path to a file or directory first. If not, it will treat the object as a character string. If it is known that character strings should not be treated as paths, then <code>quick = TRUE</code> will be much faster, with no loss of information. If it is file or directory, then it will digest the file content, or <code>basename(object)</code> . For class <code>Path</code> objects, the file's metadata (i.e., filename and file size) will be hashed instead of the file contents if <code>quick = TRUE</code> . If set to FALSE (default), the contents of the file(s) are hashed. If <code>quick = TRUE</code> , length is ignored. <code>Raster</code> objects are treated as paths, if they are file-backed.
verbose	Numeric, with 0 being off, 1 being a little, 2 being more verbose etc. Above 1 will output much more information about the internals of Caching, which may help diagnose Caching challenges.
cacheId	Character string. If passed, this will override the calculated hash of the inputs, and return the result from this <code>cacheId</code> in the <code>cacheRepo</code> . Setting this is equivalent to manually saving the output of this function, i.e., the object will be on disk, and will be recovered in subsequent This may help in some particularly

	finicky situations where Cache is not correctly detecting unchanged inputs. This will guarantee the object will be identical each time; this may be useful in operational code.
useCache	Logical or "overwrite" or "devMode". See details.
showSimilar	A logical or numeric. Useful for debugging. If TRUE or 1, then if the Cache does not find an identical archive in the cacheRepo, it will report (via message) the next most similar archive, and indicate which argument(s) is/are different. If a number larger than 1, then it will report the N most similar archived objects.
lhs	A name to assign to.
rhs	A function call

### Details

Caching R objects using [cache](#) has five important limitations:

1. the `archivist` package detects different environments as different;
2. it also does not detect S4 methods correctly due to method inheritance;
3. it does not detect objects that have file-base storage of information (specifically `RasterLayer-class` objects);
4. the default hashing algorithm is relatively slow.
5. heavily nested function calls may want Cache arguments to propagate through

This version of the Cache function accommodates those four special, though quite common, cases by:

1. converting any environments into list equivalents;
2. identifying the dispatched S4 method (including those made through inheritance) before hashing so the correct method is being cached;
3. by hashing the linked file, rather than the Raster object. Currently, only file-backed `Raster*` objects are digested (e.g., not `ff` objects, or any other R object where the data are on disk instead of in RAM);
4. Uses `digest` (formerly `fastdigest`, which does not translate between operating systems). This is used for file-backed objects as well.
5. Cache will save arguments passed by user in a hidden environment. Any nested Cache functions will use arguments in this order 1) actual arguments passed at each Cache call, 2) any inherited arguments from an outer Cache call, 3) the default values of the Cache function. See section on *Nested Caching*.

If Cache is called within a SpADES module, then the cached entry will automatically get 3 extra `userTags`: `eventTime`, `eventType`, and `moduleName`. These can then be used in `clearCache` to selectively remove cached objects by `eventTime`, `eventType` or `moduleName`.

Cache will add a tag to the artifact in the database called `accessed`, which will assign the time that it was accessed, either read or write. That way, artifacts can be shown (using `showCache`) or removed (using `clearCache`) selectively, based on their access dates, rather than only by their creation dates. See example in [clearCache](#). Cache (uppercase C) is used here so that it is not confused with, and does not mask, the `archivist::cache` function.



## Value

As with `cache`, returns the value of the function call or the cached version (i.e., the result from a previous call to this same cached function with identical arguments).

## Nested Caching

Commonly, Caching is nested, i.e., an outer function is wrapped in a Cache function call, and one or more inner functions are also wrapped in a Cache function call. A user *can* always specify arguments in every Cache function call, but this can get tedious and can be prone to errors. The normal way that *R* handles arguments is it takes the user passed arguments if any, and default arguments for all those that have no user passed arguments. We have inserted a middle step. The order or precedence for any given Cache function call is 1. user arguments, 2. inherited arguments, 3. default arguments. At this time, the top level Cache arguments will propagate to all inner functions unless each individual Cache call has other arguments specified, i.e., "middle" nested Cache function calls don't propagate their arguments to further "inner" Cache function calls. See example.

`userTags` is unique of all arguments: its values will be appended to the inherited `userTags`.

## Caching Speed

Caching speed may become a critical aspect of a final product. For example, if the final product is a shiny app, rerunning the entire project may need to take less than a few seconds at most. There are 3 arguments that affect Cache speed: `quick`, `length`, and `algo`. `quick` is passed to `.robustDigest`, which currently only affects `Path` and `Raster*` class objects. In both cases, `quick` means that little or no disk-based information will be assessed.

## Filepaths

If a function has a path argument, there is some ambiguity about what should be done. Possibilities include:

1. hash the string as is (this will be very system specific, meaning a Cache call will not work if copied between systems or directories);
2. hash the `basename(path)`;
3. hash the contents of the file.

If paths are passed in as is (i.e., character string), the result will not be predictable. Instead, one should use the wrapper function `asPath(path)`, which sets the class of the string to a `Path`, and one should decide whether one wants to digest the content of the file (using `quick = FALSE`), or just the filename (`quick = TRUE`). See examples.

## Stochasticity

In general, it is expected that caching will only be used when stochasticity is not relevant, or if a user has achieved sufficient stochasticity (e.g., via sufficient number of calls to `experiment`) such that no new explorations of stochastic outcomes are required. It will also be very useful in a reproducible workflow.

### useCache

If FALSE, then the entire Caching mechanism is bypassed and the function is evaluated as if it was not being Cached. Default is `getOption("reproducible.useCache")`, which is TRUE by default, meaning use the Cache mechanism. This may be useful to turn all Caching on or off in very complex scripts and nested functions.

If "overwrite" (which can be set with `options("reproducible.useCache" = "overwrite")`), then the function invoke the caching mechanism but will purge any entry that is matched, and it will be replaced with the results of the current call.

If "devMode": The point of this mode is to facilitate using the Cache when functions and datasets are continually in flux, and old Cache entries are likely stale very often. In 'devMode', the cache mechanism will work as normal if the Cache call is the first time for a function OR if it successfully finds a copy in the cache based on the normal Cache mechanism. It *differs* from the normal Cache if the Cache call does *not* find a copy in the 'cacheRepo', but it does find an entry that matches based on 'userTags'. In this case, it will delete the old entry in the 'cacheRepo' (identified based on matching 'userTags'), then continue with normal 'Cache'. For this to work correctly, 'userTags' must be unique for each function call. This should be used with caution as it is still experimental. Currently, if userTags are not unique to a single entry in the cacheRepo, it will default to the behaviour of useCache = TRUE with a message. This means that "devMode" is most useful if used from the start of a project.

### sideEffect

If sideEffect is not FALSE, then metadata about any files that added to sideEffect will be added as an attribute to the cached copy. Subsequent calls to this function will assess for the presence of the new files in the sideEffect location. If the files are identical (`quick = FALSE`) or their file size is identical (`quick = TRUE`), then the cached copy of the function will be returned (and no files changed). If there are missing or incorrect files, then the function will re-run. This will accommodate the situation where the function call is identical, but somehow the side effect files were modified. If sideEffect is logical, then the function will check the cacheRepo; if it is a path, then it will check the path. The function will assess whether the files to be downloaded are found locally prior to download. If it fails the local test, then it will try to recover from a local copy if (`makeCopy` had been set to TRUE the first time the function was run. Currently, local recovery will only work if `makeCopy` was set to TRUE the first time Cache was run). Default is FALSE.

### Note

As indicated above, several objects require pre-treatment before caching will work as expected. The function `.robustDigest` accommodates this. It is an S4 generic, meaning that developers can produce their own methods for different classes of objects. Currently, there are methods for several types of classes. See [.robustDigest](#).

See [.robustDigest](#) for other specifics for other classes.

### Author(s)

Eliot McIntire

**See Also**

[cache](#), [.robustDigest](#)

**Examples**

```
tmpDir <- file.path(tempdir())

# Basic use
ranNumsA <- Cache(rnorm, 10, 16, cacheRepo = tmpDir)

# All same
ranNumsB <- Cache(rnorm, 10, 16, cacheRepo = tmpDir) # recovers cached copy
ranNumsC <- Cache(cacheRepo = tmpDir) %C% rnorm(10, 16) # recovers cached copy
ranNumsD <- Cache(quote(rnorm(n = 10, 16)), cacheRepo = tmpDir) # recovers cached copy

#####
# experimental devMode
#####
opt <- options("reproducible.useCache" = "devMode")
clearCache(tmpDir, ask = FALSE)
centralTendency <- function(x)
  mean(x)
funnyData <- c(1,1,1,1,10)
uniqueUserTags <- c("thisIsUnique", "reallyUnique")
ranNumsB <- Cache(centralTendency, funnyData, cacheRepo = tmpDir,
  userTags = uniqueUserTags) # sets new value to Cache
showCache(tmpDir) # 1 unique artifact -- cacheId is 8be9cf2a072bdbb0515c5f0b3578f474

# During development, we often redefine function internals
centralTendency <- function(x)
  median(x)
# When we rerun, we don't want to keep the "old" cache because the function will
# never again be defined that way. Here, because of userTags being the same,
# it will replace the entry in the Cache, effectively overwriting it, even though
# it has a different cacheId
ranNumsD <- Cache(centralTendency, funnyData, cacheRepo = tmpDir, userTags = uniqueUserTags)
showCache(tmpDir) # 1 unique artifact -- cacheId is bb1195b40c8d37a60fd6004e5d526e6b

# If it finds it by cacheID, doesn't matter what the userTags are
ranNumsD <- Cache(centralTendency, funnyData, cacheRepo = tmpDir, userTags = "thisIsUnique")

options(opt)

# For more in depth uses, see vignette
## Not run:
  browseVignettes(package = "reproducible")

## End(Not run)
# Equivalent
a <- Cache(rnorm, 1)
b %<% rnorm(1)
```

---

CacheDigest	<i>The exact digest function that Cache uses</i>
-------------	--

---

### Description

This can be used by a user to pre-test their arguments before running Cache, for example to determine whether there is a cached copy.

### Usage

```
CacheDigest(objsToDigest, algo = "xxhash64", calledFrom = "Cache", ...)
```

### Arguments

objsToDigest	A list of all the objects (e.g., arguments) to be digested
algo	The algorithms to be used; currently available choices are md5, which is also the default, sha1, crc32, sha256, sha512, xxhash32, xxhash64 and murmur32.
calledFrom	a Character string, length 1, with the function to compare with. Default is "Cache". All other values may not produce robust CacheDigest results.
...	passed to .robustDigest; this is generally empty except for advanced use.

### Value

A list of length 2 with the outputHash, which is the digest that Cache uses for cacheId and also preDigest, which is the digest of each sub-element in objsToDigest.

### Examples

```
## Not run:
a <- Cache(rnorm, 1)
CacheDigest(list(rnorm, 1))

## End(Not run)
```

---

checkGDALVersion	<i>Check whether the system has a minimum version of GDAL available</i>
------------------	---

---

### Description

Check whether the system has a minimum version of GDAL available

### Usage

```
checkGDALVersion(version)
```

**Arguments**

version            The minimum GDAL version to check for.

**Value**

Logical.

**Author(s)**

Eliot McIntire and Alex Chubaty

**Examples**

```
## Not run:
  checkGDALVersion(2.0)

## End(Not run)
```

---

checkoutVersion            *Clone, fetch, and checkout from GitHub.com repositories*

---

**Description**

In reproducible research, not only do packages and R version have to be consistent, but also specific versions of version controlled scripts. This function allows a simple way to create an exactly copy locally of a git repository. It can use ssh keys (including GitHub deploy keys) or GitHub Personal Access Tokens.

**Usage**

```
checkoutVersion(repo, localRepoPath = ".", cred = "", ...)
```

**Arguments**

repo            Repository address in the format username/repo[/subdir][@ref|#pull]. Alternatively, you can specify subdir and/or ref using the respective parameters (see below); if both is specified, the values in repo take precedence.

localRepoPath    Character string. The path into which the git repo should be cloned, fetched, and checked out from.

cred            Character string. Either the name of the environment variable that contains the GitHub PAT or filename of the GitHub private key file.

...            Additional arguments passed to git2r functions.

**Value**

Invisibly returns a git\_repository class object, defined in **git2r**.

**Author(s)**

Eliot McIntire and Alex Chubaty

**Examples**

```
## Not run:
tmpDir <- tempfile("")
dir.create(tmpDir)
repo <- "PredictiveEcology/reproducible"

## get latest from master branch
localRepo <- checkoutVersion("PredictiveEcology/reproducible",
                             localRepoPath = tmpDir)
git2r::summary(localRepo)
unlink(tmpDir, recursive = TRUE)

## get latest from development branch
localRepo <- checkoutVersion(paste0(repo, "@", "development"), localRepoPath = tmpDir)
git2r::summary(localRepo)
unlink(tmpDir, recursive = TRUE)

## get a particular commit by sha
sha <- "8179e1910e7c617fdeacad0f9d81323e6aad57c3"
localRepo <- checkoutVersion(paste0(repo, "@", sha), localRepoPath = tmpDir)
git2r::summary(localRepo)
unlink(tmpDir, recursive = TRUE)

rm(localRepo, repo)

## End(Not run)
```

---

checkPath

*Check directory path*

---

**Description**

Checks the specified path to a directory for formatting consistencies, such as trailing slashes, etc.

**Usage**

```
checkPath(path, create)
```

```
## S4 method for signature 'character,logical'
checkPath(path, create)
```

```
## S4 method for signature 'character,missing'
checkPath(path)
```

```
## S4 method for signature '`NULL`,ANY'
checkPath(path)
```

```
## S4 method for signature 'missing,ANY'
checkPath()
```

### Arguments

`path`            A character string corresponding to a directory path.

`create`           A logical indicating whether the path should be created if it doesn't exist. Default is FALSE.

### Value

Character string denoting the cleaned up filepath.

### Note

This will not work for paths to files. To check for existence of files, use [file.exists](#), or use [file\\_test](#) with `op = "-f"`. To normalize a path to a file, use [normPath](#) or [normalizePath](#).

### See Also

[file.exists](#), [dir.create](#).

### Examples

```
## normalize file paths
paths <- list("./aaa/zzz",
             "./aaa/zzz/",
             "../aaa/zzz",
             "../aaa/zzz/",
             ".\\aaa\\zzz",
             ".\\aaa\\zzz\\",
             file.path(".", "aaa", "zzz"))

checked <- normPath(paths)
length(unique(checked)) ## 1; all of the above are equivalent

## check to see if a path exists
tmpdir <- file.path(tempdir(), "example_checkPath")

dir.exists(tmpdir) ## FALSE
tryCatch(checkPath(tmpdir, create = FALSE), error = function(e) FALSE) ## FALSE

checkPath(tmpdir, create = TRUE)
dir.exists(tmpdir) ## TRUE

unlink(tmpdir, recursive = TRUE)
```

Checksums

*Calculate checksum***Description**

Verify (and optionally write) checksums. Checksums are computed using `.digest`, which is simply a wrapper around `digest::digest`.

**Usage**

```
Checksums(path, write, quickCheck = FALSE,
  checksumFile = file.path(path, "CHECKSUMS.txt"), files = NULL, ...)

## S4 method for signature 'character,logical'
Checksums(path, write, quickCheck = FALSE,
  checksumFile = file.path(path, "CHECKSUMS.txt"), files = NULL, ...)

## S4 method for signature 'character,missing'
Checksums(path, write, quickCheck = FALSE,
  checksumFile = file.path(path, "CHECKSUMS.txt"), files = NULL, ...)
```

**Arguments**

<code>path</code>	Character string giving the directory path containing <code>CHECKSUMS.txt</code> file, or where it will be written if <code>checksumFile = TRUE</code> .
<code>write</code>	Logical indicating whether to overwrite <code>CHECKSUMS.txt</code> . Default is <code>FALSE</code> , as users should not change this file. Module developers should write this file prior to distributing their module code, and update accordingly when the data change.
<code>quickCheck</code>	Logical. If <code>TRUE</code> , then this will only use file sizes, rather than a <code>digest::digest</code> hash. This is generally faster, but will be <i>much</i> less robust.
<code>checksumFile</code>	The filename of the checksums file to read or write to. The default is <code>'CHECKSUMS.txt'</code> located at <code>file.path(path, module, "data", checksumFile)</code> . It is likely not a good idea to change this, and should only be used in cases such as <code>Cache</code> , which can evaluate if the <code>checksumFile</code> has changed.
<code>files</code>	An optional character string or vector of specific files to checksum. This may be very important if there are many files listed in a <code>CHECKSUMS.txt</code> file, but only a few are to be checksummed.
<code>...</code>	Passed to <code>digest</code> and <code>write.table</code> . For <code>digest</code> , the notable argument is <code>algo</code> . For <code>write.table</code> , the notable argument is <code>append</code> .

**Value**

A `data.table` with columns: `result`, `expectedFile`, `actualFile`, `checksum.x`, `checksum.y`, `algorithm.x`, `algorithm.y`, `filesize.x`, `filesize.y` indicating the result of comparison between local file (`x`) and expectation based on the `CHECKSUMS.txt` file.



**Note**

In version 1.2.0 and earlier, two checksums per file were required because of differences in the checksum hash values on Windows and Unix-like platforms. Recent versions use a different (faster) algorithm and only require one checksum value per file. To update your 'CHECKSUMS.txt' files using the new algorithm, see <https://github.com/PredictiveEcology/SpaDES/issues/295#issuecomment-246513405>.

**Author(s)**

Alex Chubaty

**Examples**

```
## Not run:
moduleName <- "my_module"
modulePath <- file.path("path", "to", "modules")

## verify checksums of all data files
Checksums(moduleName, modulePath)

## write new CHECKSUMS.txt file

# 1. verify that all data files are present (and no extra files are present)
list.files(file.path(modulePath, moduleName, "data"))

# 2. calculate file checksums and write to file (this will overwrite CHECKSUMS.txt)
Checksums(moduleName, modulePath, write = TRUE)

## End(Not run)
```

---

clearCache

*Examining and modifying the cache*

---

**Description**

These are convenience wrappers around archivist package functions. They allow the user a bit of control over what is being cached.

**Usage**

```
clearCache(x, userTags = character(), after, before,
  ask = getOption("reproducible.ask"), ...)

## S4 method for signature 'ANY'
clearCache(x, userTags = character(), after, before,
  ask = getOption("reproducible.ask"), ...)
```

```

cc(secs, ...)

showCache(x, userTags = character(), after, before, ...)

## S4 method for signature 'ANY'
showCache(x, userTags = character(), after, before, ...)

keepCache(x, userTags = character(), after, before,
  ask = getOption("reproducible.ask"), ...)

## S4 method for signature 'ANY'
keepCache(x, userTags = character(), after, before,
  ask = getOption("reproducible.ask"), ...)

```

### Arguments

x	A simList or a directory containing a valid archivist repository. Note: For compatibility with Cache argument, cacheRepo can also be used instead of x, though x will take precedence.
userTags	Character vector. If used, this will be used in place of the after and before. Specifying one or more userTag here will clear all objects that match those tags. Matching is via regular expression, meaning partial matches will work unless strict beginning (^) and end (\$) of string characters are used. Matching will be against any of the 3 columns returned by showCache(), i.e., artifact, tagValue or tagName. Also, length userTags > 1, then matching is by 'and'. For 'or' matching, use   in a single character string. See examples.  If neither after or before are provided, nor userTags, then all objects will be removed. If both after and before are specified, then all objects between after and before will be deleted. If userTags is used, this will override after or before.
after	A time (POSIX, character understandable by data.table). Objects cached after this time will be shown or deleted.
before	A time (POSIX, character understandable by data.table). Objects cached before this time will be shown or deleted.
ask	Logical. If FALSE, then it will not ask to confirm deletions using clearCache or keepCache. Default is TRUE
...	Other arguments. Currently, regexp, a logical, can be provided. This must be TRUE if the use is passing a regular expression. Otherwise, userTags will need to be exact matches. Default is missing, which is the same as TRUE. If there are errors due to regular expression problem, try FALSE. For cc, it is passed to clearCache, e.g., ask, userTags
secs	Currently 3 options: the number of seconds to pass to clearCache(after = secs), a POSIXct time e.g., from Sys.time(), or missing. If missing, the default, then it will delete the most recent entry in the Cache.

**Details**

cc(secs) is just a shortcut for clearCache(repo = Paths\$cachePath, after = secs), i.e., to remove any cache entries touched in the last secs seconds.

clearCache remove items from the cache based on their userTag or times values.

keepCache remove all cached items *except* those based on certain userTags or times values.

showCache display the contents of the cache.

**Value**

Will clear all objects (or those that match userTags, or those between after or before) from the repository located at cachePath of the sim object, if sim is provided, or located in cacheRepo. Invisibly returns a data.table of the removed items.

**Note**

If the cache is larger than 10MB, and clearCache is used, there will be a message and a pause, if interactive, to prevent accidentally deleting of a large cache repository.

**See Also**

[mergeCache](#), [splitTagsLocal](#). Many more examples in [Cache](#)

**Examples**

```
library(raster)

tmpDir <- file.path(tempdir(), "reproducible_examples", "Cache")
try(clearCache(tmpDir, ask = FALSE), silent = TRUE) # just to make sure it is clear

# Basic use
ranNumsA <- Cache(rnorm, 10, 16, cacheRepo = tmpDir)

# All same
ranNumsB <- Cache(rnorm, 10, 16, cacheRepo = tmpDir) # recovers cached copy
ranNumsC <- Cache(cacheRepo = tmpDir) %C% rnorm(10, 16) # recovers cached copy
ranNumsD <- Cache(quote(rnorm(n = 10, 16)), cacheRepo = tmpDir) # recovers cached copy

# Any minor change makes it different
ranNumsE <- Cache(cacheRepo = tmpDir) %C% rnorm(10, 6) # different

## Example 1: basic cache use with tags
ranNumsA <- Cache(rnorm, 4, cacheRepo = tmpDir, userTags = "objectName:a")
ranNumsB <- Cache(runif, 4, cacheRepo = tmpDir, userTags = "objectName:b")
ranNumsC <- Cache(runif, 40, cacheRepo = tmpDir, userTags = "objectName:b")

showCache(tmpDir, userTags = c("objectName"))
showCache(tmpDir, userTags = c("^a$")) # regular expression ... "a" exactly

# Fine control of cache elements -- pick out only the large runif object, and remove it
cache1 <- showCache(tmpDir, userTags = c("runif")) # show only cached objects made during runif
```

```

toRemove <- cache1[tagKey=="object.size"][as.numeric(tagValue) > 700]$artifact
clearCache(tmpDir, userTags = toRemove, ask = FALSE)
cacheAfter <- showCache(tmpDir, userTags = c("runif")) # Only the small one is left

tmpDir <- file.path(tempdir(), "reproducible_examples", "Cache")
try(clearCache(tmpDir, ask = FALSE), silent = TRUE) # just to make sure it is clear

Cache(rnorm, 1, cacheRepo = tmpDir)
thisTime <- Sys.time()
Cache(rnorm, 2, cacheRepo = tmpDir)
Cache(rnorm, 3, cacheRepo = tmpDir)
Cache(rnorm, 4, cacheRepo = tmpDir)
showCache(x = tmpDir) # shows all 4 entries
cc(ask = FALSE, x = tmpDir)
showCache(x = tmpDir) # most recent is gone
cc(thisTime, ask = FALSE, x = tmpDir)
showCache(x = tmpDir) # all those after thisTime gone, i.e., only 1 left
cc(ask = FALSE, x = tmpDir) # Cache is
cc(ask = FALSE, x = tmpDir) # Cache is already empty

```

---

clearStubArtifacts      *Clear erroneous archivist artifacts*

---

## Description

Stub artifacts can result from several causes. The most common being erroneous removal of a file in the SQLite database. This can be caused sometimes if an archive object is being saved multiple times by multiple threads. This function will clear entries in the SQLite database which have no actual file with data.

## Usage

```

clearStubArtifacts(repoDir = NULL)

## S4 method for signature 'ANY'
clearStubArtifacts(repoDir = NULL)

```

## Arguments

repoDir	A character denoting an existing directory of the repository for which meta-data will be returned. If NULL (default), it will use the repoDir specified in <code>archivist::setLocalRepo</code> .
---------	---

## Value

Invoked for its side effect on the repoDir.

## Author(s)

Eliot McIntire

**Examples**

```

tmpDir <- file.path(tempdir(), "reproducible_examples", "clearStubArtifacts")

lapply(c(runif, rnorm), function(f) {
  reproducible::Cache(f, 10, cacheRepo = tmpDir)
})

# clear out any stub artifacts
showCache(tmpDir)

file2Remove <- dir(file.path(tmpDir, "gallery"), full.name = TRUE)[1]
file.remove(file2Remove)
showCache(tmpDir) # repository directory still thinks files are there

# run clearStubArtifacts
suppressWarnings(clearStubArtifacts(tmpDir))
showCache(tmpDir) # stubs are removed

# cleanup
clearCache(tmpDir, ask = FALSE)
unlink(tmpDir, recursive = TRUE)

```

cloudCache

*Experimental use of googledrive for Caching***Description**

This is still very experimental. See examples.

**Usage**

```

cloudCache(..., useCloud = getOption("reproducible.useCloud", TRUE),
  checksumsFileID = NULL, cloudFolderID = NULL)

```

**Arguments**

...	Passed to <a href="#">Cache</a>
useCloud	Logical. This allows this to be turned off; will send all arguments to Cache (including possibly useCache, where all caching can be turned off)
checksumsFileID	A google file ID where the checksums data.table is located, provided as a character string.
cloudFolderID	The google folder ID where a new checksums file should be written. This will only be used if checksumsFileID is not provided provided as a character string.

**Details**

This has Cache internally. The main goal of this function is to look at local Cache first, if the object is there locally, then use it & upload it to googledrive. If the object is not there locally, check on googledrive for the object. If it is there, download it, then add it to the local Cache. If it is not there, then run the function de novo, wrapped in Cache and upload the object to googledrive (i.e., it will be in local Cache and cloud location).

**Note**

This is essentially a wrapper around Cache, so it will still use the local Cache.

**See Also**

[cloudSyncCache](#), [Cache](#), [cloudWrite](#), [cloudCheck](#), [cloudExtras](#)

**Examples**

```
## Not run:
# Make a folder on googledrive -- share it with yourself and anybody else -- either use
# googledrive package or do this manually on drive.google.com
# Grab the share link -- pass it here to cloudFolderID

# first time -- looks in cloudFolderID for checksums -- none there, so it makes it
# then it runs the function, caching locally, and uploading to cloud -- copy exists in
# 2 places
library(googledrive)
newDir <- drive_mkdir("testFolder")
a1 <- cloudCache(rnorm, 1, cloudFolderID = newDir$id)
# second time -- sees that it is in both places, takes local
a2 <- cloudCache(rnorm, 1, cloudFolderID = newDir$id)

# clear local -- get from cloud copy, make a local copy in cacheRepo
clearCache(ask = FALSE)
a3 <- cloudCache(rnorm, 1, cloudFolderID = newDir$id)

# now both local and cloud exist
a4 <- cloudCache(rnorm, 1, cloudFolderID = newDir$id)

# more than one cacheRepo
opts <- options("reproducible.cachePath" = c(tempdir(), file.path(tempdir(), "test"),
                                             file.path(tempdir(), "test2")),
               "reproducible.ask" = FALSE)
cachePaths <- getOption("reproducible.cachePath")
Cache(rnorm, 4, cacheRepo = cachePaths[3]) # put it in 3rd cacheRepo

# gets it locally even though it is in the 3rd cacheRepo, uploads to cloudCache
cloudCache(rnorm, 4, cloudFolderID = newDir$id)

# Clean up -- also see cloudSyncCache
clearCache(ask = FALSE)
# lapply(cachePaths, clearCache, ask = FALSE)
```

```
cloudSyncCache(cloudFolderID = newDir$id)

## End(Not run)
```

---

cloudCheck                      *Basic tool for using cloud-based caching*

---

### Description

Very experimental

### Usage

```
cloudCheck(toDigest, checksumsFileID = NULL, cloudFolderID = NULL)
```

### Arguments

`toDigest`                      The R object to consider, e.g., all the arguments to a function.

`checksumsFileID`                A google file ID where the checksums data.table is located, provided as a character string.

`cloudFolderID`                The google folder ID where a new checksums file should be written. This will only be used if `checksumsFileID` is not provided provided as a character string.

### See Also

[cloudSyncCache](#), [Cache](#), [cloudWrite](#)

---

cloudDownloadChecksums  
*Cloud extras*

---

### Description

Mostly for internal use, but may be useful to a user.

### Usage

```
cloudDownloadChecksums(checksumsFileID = NULL, cloudFolderID = NULL)

cloudUpdateChecksums(checksums, checksumsFileID)
```

**Arguments**

checksumsFileID	A google file ID where the checksums data.table is located, provided as a character string.
cloudFolderID	The google folder ID where a new checksums file should be written. This will only be used if checksumsFileID is not provided provided as a character string.
checksums	A data.table that is outputted from cloudCheck that is the the checksums file

**Details**

cloudDownloadChecksums gets the checksums data.table directly.

cloudDownloadChecksums gets the checksums data.table directly.

**See Also**

[cloudSyncCache](#), [cloudCache](#), [cloudExtras](#)

---

cloudSyncCache	<i>Sync cloud with local Cache</i>
----------------	------------------------------------

---

**Description**

This is still experimental, see examples.

**Usage**

```
cloudSyncCache(cacheRepo = getOption("reproducible.cachePath"),
  checksumsFileID = NULL, cloudFolderID = NULL, delete = TRUE,
  upload = TRUE, download = !delete,
  ask = getOption("reproducible.ask"), cacheIds = NULL, ...)
```

**Arguments**

cacheRepo	See x in <a href="#">showCache</a>
checksumsFileID	A google file ID where the checksums data.table is located, provided as a character string.
cloudFolderID	The google folder ID where a new checksums file should be written. This will only be used if checksumsFileID is not provided provided as a character string.
delete	Logical. If TRUE, the default, it will delete any objects that are in cloudFolderID that are absent from local cacheRepo. If FALSE, it will not delete objects.
upload	Logical. If TRUE, the default, it will upload any objects identified by the internal showCache(...) call. See examples. If FALSE, then no files will be uploaded. Can be used in conjunction with delete to create behaviours similar to clearCache and keepCache.



download	Logical. If FALSE, the default, then the function will either delete the remote copy if delete = TRUE and there is no local copy, or upload the local copy if upload = TRUE and there is a local copy. If TRUE, then this will override delete, and download to local machine if it exists remotely.
ask	Logical. If FALSE, then it will not ask to confirm deletions using clearCache or keepCache. Default is TRUE
cacheIds	If supplied, then only this/these cacheId objects will be uploaded or deleted. Default is NULL, meaning do full sync (i.e., match cloudFolder with local cacheRepo, constrained by delete or upload)
...	Passed to showCache to get the artifacts to delete

### Details

cloudSyncCache will remove any entries in a cloudCache that are not in a

### See Also

[cloudCache](#), [Cache](#), [cloudWrite](#), [cloudCheck](#), [cloudExtras](#)

### Examples

```
## Not run:
#make a google drive folder
# Can use >1 cacheRepo
opts <- options("reproducible.cachePath" = c(tempdir()),
               "reproducible.ask" = FALSE)
cachePaths <- getOption("reproducible.cachePath")
library(googledrive)
newDir <- drive_mkdir("testFolder")
#a <- Cache(rnorm, 1, cacheRepo = getOption("reproducible.cachePath")[3])
a <- Cache(rnorm, 1)
b <- Cache(rnorm, 2)

# Will copy the 2 to the cloud
cloudSyncCache(cloudFolderID = newDir$id)

# remove a local one
clearCache(userTags = CacheDigest(list(rnorm, 2))$outputHash)

# Now will delete the object in the cloud that was just deleted locally
cloudSyncCache(cloudFolderID = newDir$id)

# clean up
lapply(cachePaths, clearCache, ask = FALSE)
# clearCache(ask = FALSE) # if there were only 1 cacheRepo
cloudSyncCache(cloudFolderID = newDir$id)

#####
# use showCache args to have control ... on upload & delete NOTE difference!
#####
# a <- Cache(rnorm, 1, cacheRepo = getOption("reproducible.cachePath")[3]) # multiple cacheRepos!
```

```

a <- Cache(rnorm, 1)
b <- Cache(rnorm, 2)
# only sync the one with rnorm, 2 as arguments
# This CacheDigest is the same algorithm used by Cache
tag <- CacheDigest(list(rnorm, 2))$outputHash
cloudSyncCache(cloudFolderID = newDir$id, userTags = tag) # only syncs the one
# that is identified
# with userTags

cloudSyncCache(cloudFolderID = newDir$id) # sync any other ones

# Now clear an object locally -- next how to propagate this deletion to cloud
clearCache(userTags = tag)

# Add one more to local, so now local has 2 (a and d), cloud has 2 (a and b)
d <- Cache(rnorm, 4)

# DELETING IS DIFFERENT
# Doesn't quite work same way for deleting -- this tag is not in local Cache,
# so can't find it this way.
# This next line DOES THE WRONG THING -- IT DELETES EVERYTHING because there is
# no entry in the local cache -- use cacheId arg instead -- see below
# showCache(userTags = tags) shows empty
# cloudSyncCache(cloudFolderID = newDir$id, userTags = tag)

# Only delete the one that was removed from local cache, set upload = FALSE,
# leaving only 1 in cloud: a -- this is still a sync, so, it will only
# delete 1 file because local has 1 few files -- see next for just deleting 1 artifact
cloudSyncCache(cloudFolderID = newDir$id, upload = FALSE)
# Upload the d, because it is the only one in the localCache not in the cloudCache
cloudSyncCache(cloudFolderID = newDir$id)

f <- Cache(rnorm, 5)
g <- Cache(rnorm, 6)
# upload both
cloudSyncCache(cloudFolderID = newDir$id) # only syncs the one
tag5 <- CacheDigest(list(rnorm, 5))$outputHash # this is the same algorithm used by Cache
tag6 <- CacheDigest(list(rnorm, 6))$outputHash
clearCache(userTags = tag5)
clearCache(userTags = tag6)
# delete only one by tag
cloudSyncCache(cloudFolderID = newDir$id, cacheIds = tag5) # will delete only this obj in cloud
# delete another one by tag
cloudSyncCache(cloudFolderID = newDir$id, cacheIds = tag6)

# clean up
# clearCache(ask = FALSE) # if only one cacheRepo
lapply(cachePaths, clearCache, ask = FALSE)
cloudSyncCache(cloudFolderID = newDir$id)

# To remove whole folder:
drive_rm(as_id(newDir$id))
options(opts)

```

```
## End(Not run)
```

---

cloudWrite	<i>Basic tool for using cloud-based caching</i>
------------	---

---

### Description

Very experimental

### Usage

```
cloudWrite(object, digest, cloudFolderID = NULL, checksums,
           checksumsFileID, futurePlan = getOption("reproducible.futurePlan"))
```

### Arguments

object	The R object to write to cloud
digest	The cacheId of the input arguments, outputted from cloudCheck
cloudFolderID	The google folder ID where a new object should be written
checksums	A data.table that is outputted from cloudCheck that is the the checksums file
checksumsFileID	A google file ID where the checksums data.table is located, provided as a character string.
futurePlan	Which future::plan to use. Default: getOption("reproducible.futurePlan")

### See Also

[cloudSyncCache](#), [cloudCheck](#), [cloudExtras](#)

---

compareNA	<i>NA-aware comparison of two vectors</i>
-----------	---

---

### Description

Copied from [http://www.cookbook-r.com/Manipulating\\_data/Comparing\\_vectors\\_or\\_factors\\_with\\_NA/](http://www.cookbook-r.com/Manipulating_data/Comparing_vectors_or_factors_with_NA/). This function returns TRUE wherever elements are the same, including NA's, and FALSE everywhere else.

### Usage

```
compareNA(v1, v2)
```

**Arguments**

v1                    A vector  
v2                    A vector

**Examples**

```
a <- c(NA, 1, 2, NA)
b <- c(1, NA, 2, NA)
compareNA(a, b)
```

---

convertPaths	<i>Change the absolute path of a file</i>
--------------	---

---

**Description**

convertPaths is simply a wrapper around gsub for changing the first part of a path. convertRasterPaths is useful for changing the path to a file-backed raster (e.g., after copying the file to a new location).

**Usage**

```
convertPaths(x, patterns, replacements)

convertRasterPaths(x, patterns, replacements)
```

**Arguments**

x                    For convertPaths, a character vector of file paths. For convertRasterPaths, a disk-backed RasterLayer object, or a list of such rasters.

patterns            Character vector containing a pattern to match (see ?gsub).

replacements       Character vector of the same length of patterns containing replacement text (see ?gsub).

**Author(s)**

Eliot McIntire and Alex Chubaty  
Eliot McIntire and Alex Chubaty

**Examples**

```
filenames <- c("/home/user1/Documents/file.txt", "/Users/user1/Documents/file.txt")
oldPaths <- dirname(filenames)
newPaths <- c("/home/user2/Desktop", "/Users/user2/Desktop")
convertPaths(filenames, oldPaths, newPaths)

r1 <- raster::raster(system.file("external/test.grd", package = "raster"))
r2 <- raster::raster(system.file("external/rlogo.grd", package = "raster"))
```

```
rasters <- list(r1, r2)
oldPaths <- system.file("external", package = "raster")
newPaths <- file.path("~/rasters")
rasters <- convertRasterPaths(rasters, oldPaths, newPaths)
lapply(rasters, raster::filename)
```

---

Copy	<i>Recursive copying of nested environments, and other "hard to copy" objects</i>
------	---

---

### Description

When copying environments and all the objects contained within them, there are no copies made: it is a pass-by-reference operation. Sometimes, a deep copy is needed, and sometimes, this must be recursive (i.e., environments inside environments).

### Usage

```
Copy(object, filebackedDir = tempdir(), ...)

## S4 method for signature 'ANY'
Copy(object, filebackedDir = tempdir(), ...)

## S4 method for signature 'data.table'
Copy(object, filebackedDir = tempdir(), ...)

## S4 method for signature 'environment'
Copy(object, filebackedDir = tempdir(), ...)

## S4 method for signature 'list'
Copy(object, filebackedDir = tempdir(), ...)

## S4 method for signature 'data.frame'
Copy(object, filebackedDir = tempdir(), ...)

## S4 method for signature 'Raster'
Copy(object, filebackedDir = tempdir(), ...)
```

### Arguments

object	An R object (likely containing environments) or an environment.
filebackedDir	A directory to copy any files that are backing R objects, currently only valid for Raster classes. Defaults to tempdir(), which is unlikely to be very useful.
...	Only used for custom Methods

**Author(s)**

Eliot McIntire

**See Also**[.robustDigest](#)**Examples**

```
e <- new.env()
e$abc <- letters
e$one <- 1L
e$lst <- list(W = 1:10, X = runif(10), Y = rnorm(10), Z = LETTERS[1:10])
ls(e)

# 'normal' copy
f <- e
ls(f)
f$one
f$one <- 2L
f$one
e$one ## uh oh, e has changed!

# deep copy
e$one <- 1L
g <- Copy(e)
ls(g)
g$one
g$one <- 3L
g$one
f$one
e$one
```

---

`copySingleFile`*Copy a file using robocopy on Windows and rsync on Linux/macOS*

---

**Description**

This is replacement for `file.copy`, but for one file at a time. The additional feature is that it will use `robocopy` (on Windows) or `rsync` on Linux or Mac, if they exist. It will default back to `file.copy` if none of these exists. If there is a possibility that the file already exists, then this function should be very fast as it will do "update only", i.e., nothing.

**Usage**

```
copySingleFile(from = NULL, to = NULL, useRobocopy = TRUE,
               overwrite = TRUE, delDestination = FALSE, create = TRUE,
               silent = FALSE)
```

```
copyFile(from = NULL, to = NULL, useRobocopy = TRUE,
         overwrite = TRUE, delDestination = FALSE, create = TRUE,
         silent = FALSE)
```

### Arguments

from	The source file.
to	The new file.
useRobocopy	For Windows, this will use a system call to robocopy which appears to be much faster than the internal file.copy function. Uses /MIR flag. Default TRUE.
overwrite	Passed to file.copy
delDestination	Logical, whether the destination should have any files deleted, if they don't exist in the source. This is /purge for robocopy and -delete for rsync.
create	Passed to checkPath.
silent	Should a progress be printed.

### Author(s)

Eliot McIntire and Alex Chubaty

### Examples

```
tmpDirFrom <- file.path(tempdir(), "example_fileCopy_from")
tmpDirTo <- file.path(tempdir(), "example_fileCopy_to")
tmpFile1 <- tempfile("file1", tmpDirFrom, ".csv")
tmpFile2 <- tempfile("file2", tmpDirFrom, ".csv")
dir.create(tmpDirFrom)
f1 <- normalizePath(tmpFile1, mustWork = FALSE)
f2 <- normalizePath(tmpFile2, mustWork = FALSE)
t1 <- normalizePath(file.path(tmpDirTo, basename(tmpFile1)), mustWork = FALSE)
t2 <- normalizePath(file.path(tmpDirTo, basename(tmpFile2)), mustWork = FALSE)

write.csv(data.frame(a = 1:10, b = runif(10), c = letters[1:10]), f1)
write.csv(data.frame(c = 11:20, d = runif(10), e = letters[11:20]), f2)
copyFile(c(f1, f2), c(t1, t2))
file.exists(t1) ## TRUE
file.exists(t2) ## TRUE
identical(read.csv(f1), read.csv(f2)) ## FALSE
identical(read.csv(f1), read.csv(t1)) ## TRUE
identical(read.csv(f2), read.csv(t2)) ## TRUE

unlink(tmpDirFrom, recursive = TRUE)
unlink(tmpDirTo, recursive = TRUE)
```

---

 cropInputs

*Crop a Spatial\* or Raster\* object*


---

### Description

This function can be used to crop or reproject module inputs from raw data.

### Usage

```
cropInputs(x, studyArea, rasterToMatch, ...)

## Default S3 method:
cropInputs(x, studyArea, rasterToMatch, ...)

## S3 method for class 'spatialObjects'
cropInputs(x, studyArea = NULL,
  rasterToMatch = NULL, extentToMatch = NULL, extentCRS = NULL, ...)

## S3 method for class 'sf'
cropInputs(x, studyArea = NULL, rasterToMatch = NULL,
  extentToMatch = NULL, extentCRS = NULL, ...)
```

### Arguments

x	A Spatial*, sf, or Raster* object.
studyArea	SpatialPolygons* object used for masking and possibly cropping if no rasterToMatch is provided. If not in same CRS, then it will be spTransformed to CRS of x before masking. Currently, this function will not reproject the x. Optional in postProcess.
rasterToMatch	Template Raster* object used for cropping (so extent should be the extent of desired outcome) and reprojecting (including changing the resolution and projection). See details in <a href="#">postProcess</a> .
...	Passed to raster::crop
extentToMatch	Optional. Can pass an extent here and a crs to extentCRS instead of rasterToMatch. These will override rasterToMatch, with a warning if both passed.
extentCRS	Optional. Can pass a crs here with an extent to extentTomatch instead of rasterToMatch

### Author(s)

Eliot McIntire, Jean Marchal, Ian Eddy, and Tati Micheletti



**Examples**

```

# Add a study area to Crop and Mask to
# Create a "study area"
library(sp)
library(raster)
ow <- setwd(tempdir())

# make a SpatialPolygon
coords1 <- structure(c(-123.98, -117.1, -80.2, -100, -123.98, 60.9, 67.73, 65.58, 51.79, 60.9),
                    .Dim = c(5L, 2L))
Sr1 <- Polygon(coords1)
Srs1 <- Polygons(list(Sr1), "s1")
shpEcozone <- SpatialPolygons(list(Srs1), 1L)
crs(shpEcozone) <- "+init=epsg:4326 +proj=longlat +datum=WGS84 +no_defs +ellps=WGS84 +towgs84=0,0,0"

# make a "study area" that is subset of larger dataset
coords <- structure(c(-118.98, -116.1, -99.2, -106, -118.98, 59.9, 65.73, 63.58, 54.79, 59.9),
                    .Dim = c(5L, 2L))
Sr1 <- Polygon(coords)
Srs1 <- Polygons(list(Sr1), "s1")
StudyArea <- SpatialPolygons(list(Srs1), 1L)
crs(StudyArea) <- "+init=epsg:4326 +proj=longlat +datum=WGS84 +no_defs +ellps=WGS84 +towgs84=0,0,0"
#'
#'
#####
shpEcozonePostProcessed <- postProcess(shpEcozone, studyArea = StudyArea)
#'
# Try manually, individual pieces
shpEcozoneReprojected <- projectInputs(shpEcozone, StudyArea)
shpEcozoneCropped <- cropInputs(shpEcozone, StudyArea)
shpEcozoneClean <- fixErrors(shpEcozone)
shpEcozoneMasked <- maskInputs(shpEcozone, StudyArea)

setwd(ow)

```

---

determineFilename	<i>Determine filename, either automatically or manually</i>
-------------------	---

---

**Description**

Determine the filename, given various combinations of inputs.

**Usage**

```

determineFilename(filename2 = TRUE, filename1 = NULL,
  destinationPath = getOption("reproducible.destinationPath"),
  prefix = "Small", ...)

```

**Arguments**

filename2	filename2 is optional, and is either NULL (no writing of outputs to disk), or several options for writing the object to disk. If TRUE (the default), it will give it a file name determined by <code>.prefix(basename(filename1), prefix)</code> . If a character string, it will use this as its file name. See <a href="#">determineFilename</a> .
filename1	Character strings giving the file paths of the <i>input</i> object (filename1) filename1 is only used for messaging (i.e., the object itself is passed in as <code>x</code> ) and possibly naming of output (see details and filename2).
destinationPath	Optional. If filename2 is a relative file path, then this will be the directory of the resulting absolute file path.
prefix	The character string to prepend to filename1, if filename2 not provided.
...	Additional arguments passed to methods. For spatialObjects, these are: <a href="#">cropInputs</a> , <a href="#">fixErrors</a> , <a href="#">projectInputs</a> , <a href="#">maskInputs</a> , <a href="#">determineFilename</a> , and <a href="#">writeOutputs</a> . Each of these may also pass ... into other functions, like <a href="#">writeRaster</a> , or <code>sf::st_write</code> . This might include potentially important arguments like <code>datatype</code> , <code>format</code> . Also passed to <code>projectRaster</code> , with likely important arguments such as <code>method = "bilinear"</code> . See details.

**... passed to::**

Function	Arguments
<code>cropInputs</code>	<code>crop</code>
<code>projectInputs</code>	<code>projectRaster</code>
<code>maskInputs</code>	<code>fastMask</code> or <code>intersect</code>
<code>fixErrors</code>	<code>buffer</code>
<code>writeOutputs</code>	<code>writeRaster</code> or <code>shapefile</code>
<code>determineFilename</code>	

\* Can be overridden with `useSACrs` \*\* Will mask with NAs from `rasterToMatch` if `maskWithRTM`

**Details**

The post processing workflow, which includes this function, addresses several scenarios, and depending on which scenario, there are several file names at play. For example, Raster objects may have file-backed data, and so *possess a file name*, whereas Spatial objects do not. Also, if post processing is part of a [prepInputs](#) workflow, there will always be a file downloaded. From the perspective of `postProcess`, these are the "inputs" or filename1. Similarly, there may or may not be a desire to write an object to disk after all post processing, filename2.

This subtlety means that there are two file names that may be at play: the "input" file name (filename1), and the "output" filename (filename2). When this is used within `postProcess`, it is straight forward.

However, when `postProcess` is used within a `prepInputs` call, the filename1 file is the file name of the downloaded file (usually automatically known following the downloading, and referred to as `targetFile`) and the filename2 is the file name of the of post-processed file.

If filename2 is TRUE, i.e., not an actual file name, then the cropped/masked raster will be written to disk with the original filename1/targetFile name, with prefix prefixed to the basename(targetFile).

If filename2 is a character string, it will be the path of the saved/written object e.g., passed to writeOutput. It will be tested whether it is an absolute or relative path and used as is if absolute or prepended with destinationPath if relative.

If filename2 is logical, then the output filename will be prefix prefixed to the basename(filename1). If a character string, it will be the path returned. It will be tested whether it is an absolute or relative path and used as is if absolute or prepended with destinationPath if provided, and if filename2 is relative.

## Examples

```
# Add a study area to Crop and Mask to
# Create a "study area"
library(sp)
library(raster)
ow <- setwd(tempdir())

# make a SpatialPolygon
coords1 <- structure(c(-123.98, -117.1, -80.2, -100, -123.98, 60.9, 67.73, 65.58, 51.79, 60.9),
                    .Dim = c(5L, 2L))
Sr1 <- Polygon(coords1)
Srs1 <- Polygons(list(Sr1), "s1")
shpEcozone <- SpatialPolygons(list(Srs1), 1L)
crs(shpEcozone) <- "+init=epsg:4326 +proj=longlat +datum=WGS84 +no_defs +ellps=WGS84 +towgs84=0,0,0"

# make a "study area" that is subset of larger dataset
coords <- structure(c(-118.98, -116.1, -99.2, -106, -118.98, 59.9, 65.73, 63.58, 54.79, 59.9),
                    .Dim = c(5L, 2L))
Sr1 <- Polygon(coords)
Srs1 <- Polygons(list(Sr1), "s1")
StudyArea <- SpatialPolygons(list(Srs1), 1L)
crs(StudyArea) <- "+init=epsg:4326 +proj=longlat +datum=WGS84 +no_defs +ellps=WGS84 +towgs84=0,0,0"
#'
#'
#####
shpEcozonePostProcessed <- postProcess(shpEcozone, studyArea = StudyArea)
#'
# Try manually, individual pieces
shpEcozoneReprojected <- projectInputs(shpEcozone, StudyArea)
shpEcozoneCropped <- cropInputs(shpEcozone, StudyArea)
shpEcozoneClean <- fixErrors(shpEcozone)
shpEcozoneMasked <- maskInputs(shpEcozone, StudyArea)

setwd(ow)
```

---

downloadFile	<i>A wrapper around a set of downloading functions</i>
--------------	--

---

### Description

Currently, this only deals with [drive\\_download](#), and [download.file](#).

### Usage

```
downloadFile(archive, targetFile, neededFiles,
  destinationPath = getOption("reproducible.destinationPath"), quick,
  checksumFile, dlFun = NULL, checkSums, url, needChecksums,
  overwrite = getOption("reproducible.overwrite", TRUE), purge = FALSE,
  ...)
```

### Arguments

archive	Optional character string giving the path of an archive containing targetFile, or a vector giving a set of nested archives (e.g., c("xxx.tar", "inner.zip", "inner.rar")). If there is/are (an) inner archive(s), but they are unknown, the function will try all until it finds the targetFile. See table in <a href="#">preProcess</a> .
targetFile	Character string giving the path to the eventual file (raster, shapefile, csv, etc.) after downloading and extracting from a zip or tar archive. This is the file <i>before</i> it is passed to postProcess. Currently, the internal checksumming does not checksum the file after it is postProcessed (e.g., cropped/reprojected/masked). Using Cache around prepInputs will do a sufficient job in these cases. See table in <a href="#">preProcess</a> .
neededFiles	Character string giving the name of the file(s) to be extracted.
destinationPath	Character string of a directory in which to download and save the file that comes from url and is also where the function will look for archive or targetFile. NOTE (still experimental): To prevent repeated downloads in different locations, the user can also set options("reproducible.inputPaths") to one or more local file paths to search for the file before attempting to download. Default for that option is NULL meaning do not search locally.
quick	Logical. This is passed internally to <a href="#">Checksums</a> (the quickCheck argument), and to <a href="#">Cache</a> (the quick argument). This results in faster, though less robust checking of inputs. See the respective functions.
checksumFile	A character string indicating the absolute path to the CHECKSUMS.txt file.
dlFun	Optional "download function" name, such as "raster::getData", which does custom downloading, in addition to loading into R. Still experimental.
checkSums	A checksums file, e.g., created by Checksums(..., write = TRUE)
url	Optional character string indicating the URL to download from. If not specified, then no download will be attempted. If not entry exists in the CHECKSUMS.txt (in

	destinationPath), an entry will be created or appended to. This CHECKSUMS.txt entry will be used in subsequent calls to prepInputs or preProcess, comparing the file on hand with the ad hoc CHECKSUMS.txt. See table in <a href="#">preProcess</a> .
needChecksums	A numeric, with 0 indicating do not write a new checksums, 1 write a new one, 2 append new information to existing one.
overwrite	Logical. Should downloading and all the other actions occur even if they pass the checksums or the files are all there.
purge	Logical or Integer. 0/FALSE (default) keeps existing CHECKSUMS.txt file and prepInputs will write or append to it. 1/TRUE will deleted the entire CHECKSUMS.txt file. Other options, see details.
...	Passed to dlFun. Still experimental.

**Author(s)**

Eliot McIntire

---

extractFromArchive	<i>Extract files from archive</i>
--------------------	-----------------------------------

---

**Description**

Extract zip or tar archive files, possibly nested in other zip or tar archives.

**Usage**

```
extractFromArchive(archive,
  destinationPath = getOption("reproducible.destinationPath",
    dirname(archive)), neededFiles = NULL, extractedArchives = NULL,
  checkSums = NULL, needChecksums = 0, filesExtracted = character(),
  checksumFilePath = character(), quick = FALSE)
```

**Arguments**

archive	Character string giving the path of the archive containing the file to be extracted. This path must exist or be NULL
destinationPath	Character string giving the path where neededFiles will be extracted. Defaults to the archive directory.
neededFiles	Character string giving the name of the file(s) to be extracted.
extractedArchives	Used internally to track archives that have been extracted from.
checkSums	A checksums file, e.g., created by Checksums(..., write = TRUE)
needChecksums	A numeric, with 0 indicating do not write a new checksums, 1 write a new one, 2 append new information to existing one.

filesExtracted Used internally to track files that have been extracted.  
 checksumFilePath The full path to the checksum.txt file  
 quick Passed to Checksums  
 ... Passed to unzip or untar, e.g., overwrite

**Value**

A character vector listing the paths of the extracted archives.

**Author(s)**

Jean Marchal and Eliot McIntire

---

fastMask *Faster operations on rasters*

---

**Description**

This alternative to raster::mask is included here.

**Usage**

```
fastMask(x, y, cores = NULL)
```

**Arguments**

x A Raster\* object.  
 y A SpatialPolygons object. If it is not in the same projection as x, it will be reprojected on the fly to that of x  
 cores An integer\* or 'AUTO'. This will be used if gdalwarp is triggered. 'AUTO'\* will calculate 90 number of cores in the system, while an integer or rounded float will be passed as the exact number of cores to be used.

**Value**

A Raster\* object, masked (i.e., smaller extent and/or several pixels converted to NA)

**Author(s)**

Eliot McIntire

**Examples**

```
library(raster)

Sr1 <- Polygon(cbind(c(2, 4, 4, 0.9, 2), c(2, 3, 5, 4, 2)))
Sr2 <- Polygon(cbind(c(5, 4, 2, 5), c(2, 3, 2, 2)))
Sr3 <- Polygon(cbind(c(4, 4, 5, 10, 4), c(5, 3, 2, 5, 5)))

Srs1 <- Polygons(list(Sr1), "s1")
Srs2 <- Polygons(list(Sr2), "s2")
Srs3 <- Polygons(list(Sr3), "s3")
shp <- SpatialPolygons(list(Srs1, Srs2, Srs3), 1:3)
d <- data.frame(vals = 1:3, other = letters[3:1], stringsAsFactors = FALSE)
row.names(d) <- names(shp)
shp <- SpatialPolygonsDataFrame(shp, data = d)
poly <- list()
poly[[1]] <- raster(raster::extent(shp), vals = 0, res = c(1, 1))
poly[[2]] <- raster(raster::extent(shp), vals = 1, res = c(1, 1))
origStack <- stack(poly)
# original mask function in raster
newStack1 <- mask(origStack, mask = shp)
newStack2 <- fastMask(x = origStack, y = shp)

# test all equal
all.equal(newStack1, newStack2)

newStack1 <- stack(newStack1)
newStack2 <- stack(newStack2)

if (interactive()) {
  plot(newStack2[[1]])
  plot(shp, add = TRUE)
}
```

---

`getGDALVersion`*Check the GDAL version in use*

---

**Description**

Check the GDAL version in use

**Usage**

```
getGDALVersion()
```

**Value**

numeric\_version

**Author(s)**

Alex Chubaty and Eliot McIntire

---

getUserTags

*Cache helpers*

---

**Description**

A few helpers to get specific things from the cache repository

**Usage**

```
getUserTags(cacheRepo, shownCache, cacheId, concatenated = TRUE)
```

```
getCacheId(cacheRepo, shownCache, artifact)
```

```
getArtifact(cacheRepo, shownCache, cacheId)
```

**Arguments**

cacheRepo	A repository used for storing cached objects. This is optional if Cache is used inside a SpaDES module.
shownCache	Primary way of supplying cacheRepo; the data.table obj resulting from showCache, i.e., it will override cacheRepo. If this and cacheRepo are missing, then it will default to getOption('reproducible.cachePath')
cacheId	A character vector of 0 cacheId values to use in the cache
concatenated	Logical. If TRUE, the returned userTags will be concatenated tagKey:tagValue
artifact	Character vector of artifact values in the artifact column of showCache

**Value**

getCacheId returns the cacheId values for 1 or more artifacts in the cache.

getArtifact returns the artifact value for 1 or more entries in the cache, by cacheId.



---

installedVersions	<i>Determine versions all installed packages</i>
-------------------	--

---

### Description

This code is adapted from `installed.versions`, but uses an Rcpp alternative to `readLines` for speed. It will be anywhere from 2x to 10x faster than the `installed.versions` function. This is also many times faster than `utils::installed.packages`, especially if only a subset of "all" packages in `libPath` are desired (1000x ? for the 1 package case).

### Usage

```
installedVersions/packages, libPath)
```

### Arguments

packages	Character vector of packages to determine which version is installed in the <code>libPath</code> .
libPath	The library path where all packages should be installed, and looked for to load (i.e., call <code>library</code> )

### Examples

```
installedVersions("reproducible", .libPaths()[1])
```

---

installVersions	<i>Install exact package versions from a package version text file &amp; GitHub</i>
-----------------	---

---

### Description

Install exact package versions from a package version text file & GitHub

### Usage

```
installVersions(gitHubPackages,
  packageVersionFile = ".packageVersions.txt",
  libPath = .libPaths()[1], standAlone = FALSE,
  repos = getOption("repos")["CRAN"])
```

**Arguments**

githubPackages	Character vectors indicating repository/packageName@branch
packageVersionFile	Path to the package version file, defaults to the <code>‘.packageVersions.txt’</code> . This uses CRAN, CRAN archives, or MRAN (accessed via <code>versions::install.versions</code> ) for remote repositories. This will attempt to install all packages in the <code>packageVersionFile</code> , with their exact version described in that file. For GitHub packages, it will use <code>install_github</code> . This will be called internally by <code>Require</code> , and so often doesn’t need to be used by a user. Because of potential conflicts with loaded packages, this function will run <code>install.packages</code> in a separate R process.
libPath	The library path where all packages should be installed, and looked for to load (i.e., call <code>library</code> )
standAlone	Logical. If <code>TRUE</code> , all packages will be installed and loaded strictly from the <code>libPaths</code> only. If <code>FALSE</code> , all <code>.libPaths</code> will be used to find the correct versions. This can be create dramatically faster installs if the user has a substantial number of the packages already in their personal library. In the case of <code>TRUE</code> , there will be a hidden file place in the <code>libPath</code> directory that lists all the packages that were needed during the <code>Require</code> call. Default <code>FALSE</code> to minimize package installing.
repos	The remote repository (e.g., a CRAN mirror), passed to either <code>install.packages</code> , <code>install_github</code> or <code>installVersions</code> .

**Examples**

```
## Not run:
# requires the packageVersionFile -- this doesn't work -- safer to use Require
installVersions("PredictiveEcology/reproducible@development")

# make a package version snapshot -- this will be empty because no packages in directory
tempPkgFolder <- file.path(tempdir(), "Packages")
dir.create(tempPkgFolder)
packageVersionFile <- file.path(tempPkgFolder, ".packageVersion.txt")
pkgSnapshot(libPath = tempPkgFolder, packageVersionFile)

Require("crayon", libPath = tempPkgFolder) # install.packages first, then library

# install a specific version
# make a package version snapshot
packageVersionFile <- file.path(tempPkgFolder, ".packageVersion.txt")
pkgSnapshot(libPath=tempPkgFolder, packageVersionFile, standAlone = FALSE)

installVersions("crayon", packageVersionFile = packageVersionFile)

## End(Not run)
```

---

linkOrCopy	<i>Hardlink, symlink, or copy a file</i>
------------	--

---

**Description**

Attempt first to make a hardlink. If that fails, try to make a symlink (on non-windows systems and `symlink = TRUE`). If that fails, copy the file.

**Usage**

```
linkOrCopy(from, to, symlink = TRUE)
```

**Arguments**

<code>from, to</code>	Character vectors, containing file names or paths. <code>to</code> can alternatively be the path to a single existing directory.
<code>symlink</code>	Logical indicating whether to use symlink (instead of hardlink). Default <code>FALSE</code> .

**Note**

Use caution with files-backed objects (e.g., rasters). See examples.

**Author(s)**

Alex Chubaty and Eliot McIntire

**See Also**

[file.link](#), [file.symlink](#), [file.copy](#).

**Examples**

```
library(datasets)
library(magrittr)
library(raster)

tmpDir <- file.path(tempdir(), "symlink-test") %>%
  normalizePath(winslash = '/', mustWork = FALSE)
dir.create(tmpDir)

f0 <- file.path(tmpDir, "file0.csv")
write.csv(iris, f0)

d1 <- file.path(tmpDir, "dir1")
dir.create(d1)
write.csv(iris, file.path(d1, "file1.csv"))

d2 <- file.path(tmpDir, "dir2")
dir.create(d2)
```

```

f2 <- file.path(tmpDir, "file2.csv")

## create link to a file
linkOrCopy(f0, f2)
file.exists(f2) ## TRUE
identical(read.table(f0), read.table(f2)) ## TRUE

## deleting the link shouldn't delete the original file
unlink(f0)
file.exists(f0) ## FALSE
file.exists(f2) ## TRUE

## using rasters and other file-backed objects
f3a <- system.file("external/test.grd", package = "raster")
f3b <- system.file("external/test.gri", package = "raster")
r3a <- raster(f3a)
f4a <- file.path(tmpDir, "raster4.grd")
f4b <- file.path(tmpDir, "raster4.gri")
linkOrCopy(f3a, f4a) ## hardlink
linkOrCopy(f3b, f4b) ## hardlink
r4a <- raster(f4a)

isTRUE(all.equal(r3a, r4a)) # TRUE

## cleanup
unlink(tmpDir, recursive = TRUE)

```

---

makeMemoisable

*Generic method to make or unmake objects memoisable*


---

## Description

This is just a pass through for all classes in **reproducible**. This generic is here so that downstream methods can be created.

## Usage

```

makeMemoisable(x)

## Default S3 method:
makeMemoisable(x)

unmakeMemoisable(x)

## Default S3 method:
unmakeMemoisable(x)

```

## Arguments

x                    An object to make memoisable. See individual methods in other packages.

**Value**

The same object, but with any modifications, especially dealing with saving of environments, which memoising doesn't handle correctly in some cases.

---

maskInputs	<i>Mask module inputs</i>
------------	---------------------------

---

**Description**

This function can be used to mask inputs from data. Masking here is equivalent to `raster::mask` (though `fastMask` is used here) or `raster::intersect`.

**Usage**

```
maskInputs(x, studyArea, ...)

## S3 method for class 'Raster'
maskInputs(x, studyArea, rasterToMatch,
           maskWithRTM = FALSE, ...)

## S3 method for class 'Spatial'
maskInputs(x, studyArea, ...)

## S3 method for class 'sf'
maskInputs(x, studyArea, ...)
```

**Arguments**

<code>x</code>	An object to do a geographic <code>raster::mask/raster::intersect</code> . See methods.
<code>studyArea</code>	<code>SpatialPolygons*</code> object used for masking and possibly cropping if no <code>rasterToMatch</code> is provided. If not in same CRS, then it will be <code>spTransformed</code> to CRS of <code>x</code> before masking. Currently, this function will not reproject the <code>x</code> . Optional in <code>postProcess</code> .
<code>...</code>	Passed to methods. None currently implemented.
<code>rasterToMatch</code>	Template <code>Raster*</code> object used for cropping (so extent should be the extent of desired outcome) and reprojecting (including changing the resolution and projection). See details in <code>postProcess</code> .
<code>maskWithRTM</code>	Logical. If TRUE, then the default,

**Author(s)**

Eliot McIntire and Jean Marchal

**Examples**

```

# Add a study area to Crop and Mask to
# Create a "study area"
library(sp)
library(raster)
ow <- setwd(tempdir())

# make a SpatialPolygon
coords1 <- structure(c(-123.98, -117.1, -80.2, -100, -123.98, 60.9, 67.73, 65.58, 51.79, 60.9),
                    .Dim = c(5L, 2L))
Sr1 <- Polygon(coords1)
Srs1 <- Polygons(list(Sr1), "s1")
shpEcozone <- SpatialPolygons(list(Srs1), 1L)
crs(shpEcozone) <- "+init=epsg:4326 +proj=longlat +datum=WGS84 +no_defs +ellps=WGS84 +towgs84=0,0,0"

# make a "study area" that is subset of larger dataset
coords <- structure(c(-118.98, -116.1, -99.2, -106, -118.98, 59.9, 65.73, 63.58, 54.79, 59.9),
                    .Dim = c(5L, 2L))
Sr1 <- Polygon(coords)
Srs1 <- Polygons(list(Sr1), "s1")
StudyArea <- SpatialPolygons(list(Srs1), 1L)
crs(StudyArea) <- "+init=epsg:4326 +proj=longlat +datum=WGS84 +no_defs +ellps=WGS84 +towgs84=0,0,0"
#'
#'
#####
shpEcozonePostProcessed <- postProcess(shpEcozone, studyArea = StudyArea)
#'
# Try manually, individual pieces
shpEcozoneReprojected <- projectInputs(shpEcozone, StudyArea)
shpEcozoneCropped <- cropInputs(shpEcozone, StudyArea)
shpEcozoneClean <- fixErrors(shpEcozone)
shpEcozoneMasked <- maskInputs(shpEcozone, StudyArea)

setwd(ow)

```

---

mergeCache

---

*Merge two cache repositories together*


---

**Description**

All the cacheFrom artifacts will be put into cacheTo repository. All userTags will be copied verbatim, including accessed, with 1 exception: date will be the current Sys.time() at the time of merging. The createdDate column will be similarly the current time of merging.

**Usage**

```

mergeCache(cacheTo, cacheFrom)

## S4 method for signature 'ANY'
mergeCache(cacheTo, cacheFrom)

```

**Arguments**

cacheTo	The cache repository (character string of the file path) that will become larger, i.e., merge into this
cacheFrom	The cache repository (character string of the file path) from which all objects will be taken and copied from

**Details**

This is still experimental

**Value**

The character string of the path of cacheTo, i.e., not the objects themselves.

---

newLibPaths	<i>A shortcut to create a .libPaths() with only two directories</i>
-------------	---

---

**Description**

This will remove all but the top level of .libPaths(), which should be the core packages installed with R, and adds a second directory, the libPath.

**Usage**

```
newLibPaths(libPath)
```

**Arguments**

libPath	A path that will be the new .libPaths()[1]
---------	--

**Value**

Invisibly, the new .libPaths().

**Examples**

```
## Not run:  
newLibPaths("testPackages")  
.libPaths() # new .libPaths  
  
## End(Not run)
```

---

normPath	<i>Normalize filepath</i>
----------	---------------------------

---

**Description**

Checks the specified filepath for formatting consistencies: 1) use slash instead of backslash; 2) do tilde etc. expansion; 3) remove trailing slash.

**Usage**

```
normPath(path)

## S4 method for signature 'character'
normPath(path)

## S4 method for signature 'list'
normPath(path)

## S4 method for signature '`NULL`'
normPath(path)

## S4 method for signature 'missing'
normPath()
```

**Arguments**

path                    A character vector of filepaths.

**Value**

Character vector of cleaned up filepaths.

**Examples**

```
## normalize file paths
paths <- list("./aaa/zzz",
             "./aaa/zzz/",
             "./aaa/zzz",
             "./aaa/zzz/",
             ".\\aaa\\zzz",
             ".\\aaa\\zzz\\",
             file.path(".", "aaa", "zzz"))

checked <- normPath(paths)
length(unique(checked)) ## 1; all of the above are equivalent

## check to see if a path exists
tmpdir <- file.path(tmpdir(), "example_checkPath")
```



```

dir.exists(tmpdir) ## FALSE
tryCatch(checkPath(tmpdir, create = FALSE), error = function(e) FALSE) ## FALSE

checkPath(tmpdir, create = TRUE)
dir.exists(tmpdir) ## TRUE

unlink(tmpdir, recursive = TRUE)

```

---

package\_dependenciesMem

*Memoised version of package\_dependencies*

---

### Description

This have a 6 minute memory time window.

### Usage

```

package_dependenciesMem/packages = NULL, db = NULL,
  which = c("Depends", "Imports", "LinkingTo"), recursive = FALSE,
  reverse = FALSE, verbose = getOption("verbose"))

```

### Arguments

packages	a character vector of package names.
db	character matrix as from <a href="#">available.packages()</a> (with the default NULL the results of this call) or data frame variants thereof. Alternatively, a package database like the one available from <a href="https://cran.r-project.org/web/packages/packages.rds">https://cran.r-project.org/web/packages/packages.rds</a> .
which	a character vector listing the types of dependencies, a subset of c("Depends", "Imports", "LinkingTo". Character string "all" is shorthand for that vector, character string "most" for the same vector without "Enhances".
recursive	logical: should (reverse) dependencies of (reverse) dependencies (and so on) be included?
reverse	logical: if FALSE (default), regular dependencies are calculated, otherwise reverse dependencies.
verbose	logical indicating if output should monitor the package search cycles.

---

Path-class

*Coerce a character string to a class "Path"*

---

### Description

Allows a user to specify that their character string is indeed a filepath. Thus, methods that require only a filepath can be dispatched correctly.

### Usage

```
asPath(obj, nParentDirs = 0)

## S3 method for class 'character'
asPath(obj, nParentDirs = 0)
```

### Arguments

<code>obj</code>	A character string to convert to a Path.
<code>nParentDirs</code>	A numeric indicating the number of parent directories starting from <code>basename(obj)</code> = 0 to keep for the digest

### Details

It is often difficult or impossible to know algorithmically whether a character string corresponds to a valid filepath. In the case where it is an existing file, `file.exists` can work. But if it does not yet exist, e.g., for a save, it is difficult to know whether it is a valid path before attempting to save to the path.

This function can be used to remove any ambiguity about whether a character string is a path. It is primarily useful for achieving repeatability with Caching. Essentially, when Caching, arguments that are character strings should generally be digested verbatim, i.e., it must be an exact copy for the Cache mechanism to detect a candidate for recovery from the cache. Paths, are different. While they are character strings, there are many ways to write the same path. Examples of identical meaning, but different character strings are: path expanding of `~` vs. not, double back slash vs. single forward slash, relative path vs. absolute path. All of these should be assessed for their actual file or directory location, NOT their character string. By converting all character string that are actual file or directory paths with this function, then Cache will correctly assess the location, NOT the character string representation.

### Examples

```
tmpf <- tempfile(fileext = ".csv")
file.exists(tmpf) ## FALSE
tmpfPath <- asPath(tmpf)
is(tmpf, "Path") ## FALSE
is(tmpfPath, "Path") ## TRUE
```

---

pipe	<i>A cache-aware pipe that does not mask with %&gt;%</i>
------	--

---

## Description

*STILL EXPERIMENTAL. THIS MAY NOT WORK AS ANTICIPATED.*

## Usage

```
lhs %C% rhs
```

## Arguments

lhs	A value or the magrittr placeholder.
rhs	A function call using the magrittr semantics.

## Details

This pipe can only be used at any point in a pipe chain, but must be preceded by `Cache(...)` (which allows other `Cache` arguments to be passed).

This will take the input arguments of the first function immediately following the `Cache()` and the pipe chain until the special `%C%`, evaluate them both against the `cacheRepo` argument in `Cache`. If they exist, then the entire pipe chain will be skipped, and only the previous final result will be given. If there is no previous cached copy of the initial function's arguments, then all chain elements will be evaluated. The final result will be cached for future use. Therefore, the entire chain must be identical. The required usage should be straight forward to insert into existing code that uses pipes (`Cache() %C% ... remaining pipes`).

## Note

*This is still experimental; use with care.*

## Examples

```
library(magrittr) # standard pipe
# dontrun{ # these can't be automatically run due to package conflicts with magrittr
tmpdir <- file.path(tempdir(), "testCache")
checkPath(tmpdir, create = TRUE)
a <- rnorm(10, 16) %>%
  mean() %>%
  prod(., 6)
b <- Cache(cacheRepo = tmpdir) %C% # use of the %C% pipe!
  rnorm(10, 16) %>% # everything after here is NOT cached!
  mean() %>%
  prod(., 6)
d <- Cache(cacheRepo = tmpdir) %C%
  rnorm(10, 16) %>%
  mean() %>%
```

```

    prod(., 6)
e <- Cache(cacheRepo = tmpdir) %C%
  rnorm(10, 16) %>%
  mean() %>%
  prod(., 5) # changed
all.equal(b,d) # TRUE
all.equal(a,d) # different because 'a' uses a unique rnorm, 'd' uses the Cached rnorm
  # because the arguments to rnorm, i.e., 10 and 16, and
  # the subsequent functions in the chain, are identical
all.equal(a,e) # different because the final function, prod, has a changed argument.

#####
# multiple random elements shows Cached sequence up to %C%
a1 <- Cache(cacheRepo = tmpdir) %>%
  seq(1, 10) %>%
  rnorm(2, mean = .) %>%
  mean() %C% # Cache pipe here --
  # means this pipe is the last one that is Cached
  rnorm(3, mean = .) %>%
  mean(.) %>%
  rnorm(4, mean = .) # Random 4 numbers, the mean is same each time
a2 <- Cache(cacheRepo = tmpdir) %>%
  seq(1, 10) %>%
  rnorm(2, mean = .) %>%
  mean() %C% # Cache pipe here --
  # means this pipe is the last one that is Cached
  rnorm(3, mean = .) %>%
  mean(.) %>%
  rnorm(4, mean = .) # Random 4 numbers, the mean is same each time
sum(a1 - a2) # not 0 # i.e., numbers are different

# NOW DO WITH CACHE AT END
b1 <- Cache(cacheRepo = tmpdir) %>%
  seq(1, 10) %>%
  rnorm(2, mean = .) %>%
  mean() %>%
  # means this pipe is the last one that is Cached
  rnorm(3, mean = .) %>%
  mean(.) %C% # Cache pipe here --
  rnorm(4, mean = .) # These are samethe mean is same each time
b2 <- Cache(cacheRepo = tmpdir) %>%
  seq(1, 10) %>%
  rnorm(2, mean = .) %>%
  mean() %>%
  # means this pipe is the last one that is Cached
  rnorm(3, mean = .) %>%
  mean(.) %C% # Cache pipe here --
  rnorm(4, mean = .) # These are samethe mean is same each time
sum(b1 - b2) # 0 # i.e., numbers are same

unlink(tmpdir, recursive = TRUE)
#}

```

---

pkgDep *Determine package dependencies, first looking at local filesystem*

---

### Description

This is intended to replace `package_dependencies` or `pkgDep` in the **miniCRAN** package, but with modifications for speed. It will first check local package directories in `libPath`, and if the function cannot find the packages there, then it will use `package_dependencies`.

### Usage

```
pkgDep(packages, libPath, recursive = TRUE, depends = TRUE,
       imports = TRUE, suggests = FALSE, linkingTo = TRUE,
       repos = getOption("repos"))
```

```
pkgDep2(packages, libPath, recursive = TRUE, depends = TRUE,
        imports = TRUE, suggests = FALSE, linkingTo = TRUE,
        repos = getOption("repos"))
```

### Arguments

<code>packages</code>	a character vector of package names.
<code>libPath</code>	The library path where all packages should be installed, and looked for to load (i.e., call <code>library</code> )
<code>recursive</code>	Logical. Should dependencies of dependencies be searched, recursively. NOTE: Dependencies of suggests will not be recursive. Default TRUE.
<code>depends</code>	Logical. Include packages listed in "Depends". Default TRUE.
<code>imports</code>	Logical. Include packages listed in "Imports". Default TRUE.
<code>suggests</code>	Logical. Include packages listed in "Suggests". Default FALSE.
<code>linkingTo</code>	Logical. Include packages listed in "LinkingTo". Default TRUE.
<code>repos</code>	The remote repository (e.g., a CRAN mirror), passed to either <code>install.packages</code> , <code>install_github</code> or <code>installVersions</code> .

### Note

`package_dependencies` and `pkgDep` will differ under the following circumstances:

1. GitHub packages are not detected using `tools::package_dependencies`;
2. `tools::package_dependencies` does not detect the dependencies of base packages among themselves, e.g., `methods` depends on `stats` and `graphics`.

### Examples

```
pkgDep("crayon")
```

---

pkgSnapshot	<i>Take a snapshot of all the packages and version numbers</i>
-------------	--

---

## Description

This can be used later by `installVersions` to install or re-install the correct versions.

## Usage

```
pkgSnapshot(packageVersionFile, libPath, standAlone = FALSE)
```

## Arguments

<code>packageVersionFile</code>	A filename to save the packages and their currently installed version numbers. Defaults to <code>".packageVersions.txt"</code> .
<code>libPath</code>	The path to the local library where packages are installed. Defaults to the <code>.libPaths()[1]</code>
<code>standAlone</code>	Logical. If <code>TRUE</code> , all packages will be installed and loaded strictly from the <code>libPaths</code> only. If <code>FALSE</code> , all <code>.libPaths</code> will be used to find the correct versions. This can be create dramatically faster installs if the user has a substantial number of the packages already in their personal library. In the case of <code>TRUE</code> , there will be a hidden file place in the <code>libPath</code> directory that lists all the packages that were needed during the <code>Require</code> call. Default <code>FALSE</code> to minimize package installing.

## Details

A file is written with the package names and versions of all packages within `libPath`. This can later be passed to `Require`.

## Examples

```
pkgSnapFile <- tempfile()
pkgSnapshot(pkgSnapFile, .libPaths()[1])
data.table::fread(pkgSnapFile)
```

---

postProcess	<i>Generic function to post process objects</i>
-------------	---

---

### Description

The method for spatialObjects (Raster\* and Spatial\*) will crop, reproject, and mask, in that order. This function is a wrapper for [cropInputs](#), [fixErrors](#), [projectInputs](#), [maskInputs](#) and [writeOutputs](#), with a decent amount of data manipulating between these calls so that the crs match.

### Usage

```
postProcess(x, ...)

## Default S3 method:
postProcess(x, ...)

## S3 method for class 'list'
postProcess(x, ...)

## S3 method for class 'spatialObjects'
postProcess(x, filename1 = NULL,
  filename2 = TRUE, studyArea = NULL, rasterToMatch = NULL,
  overwrite = getOption("reproducible.overwrite", TRUE),
  useSAcrs = FALSE, useCache = getOption("reproducible.useCache",
  FALSE), ...)

## S3 method for class 'sf'
postProcess(x, filename1 = NULL, filename2 = TRUE,
  studyArea = NULL, rasterToMatch = NULL,
  overwrite = getOption("reproducible.overwrite", TRUE),
  useSAcrs = FALSE, useCache = getOption("reproducible.useCache",
  FALSE), ...)
```

### Arguments

x	An object of postProcessing, e.g., spatialObjects. See individual methods.
...	Additional arguments passed to methods. For spatialObjects, these are: <a href="#">cropInputs</a> , <a href="#">fixErrors</a> , <a href="#">projectInputs</a> , <a href="#">maskInputs</a> , <a href="#">determineFilename</a> , and <a href="#">writeOutputs</a> . Each of these may also pass ... into other functions, like <a href="#">writeRaster</a> , or <code>sf::st_write</code> . This might include potentially important arguments like datatype, format. Also passed to <code>projectRaster</code> , with likely important arguments such as <code>method = "bilinear"</code> . See details.

#### ... passed to::

Function	Arguments
cropInputs	<a href="#">crop</a>

projectInputs	<a href="#">projectRaster</a>
maskInputs	<a href="#">fastMask</a> or <a href="#">intersect</a>
fixErrors	<a href="#">buffer</a>
writeOutputs	<a href="#">writeRaster</a> or <a href="#">shapefile</a>
determineFilename	

\* Can be overridden with useSAcrs \*\* Will mask with NAs from rasterToMatch if maskWithRTM

filename1	Character strings giving the file paths of the <i>input</i> object (filename1) filename1 is only used for messaging (i.e., the object itself is passed in as x) and possibly naming of output (see details and filename2).
filename2	filename2 is optional, and is either NULL (no writing of outputs to disk), or several options for writing the object to disk. If TRUE (the default), it will give it a file name determined by <code>.prefix(basename(filename1), prefix)</code> . If a character string, it will use this as its file name. See <a href="#">determineFilename</a> .
studyArea	SpatialPolygons* object used for masking and possibly cropping if no rasterToMatch is provided. If not in same CRS, then it will be spTransformed to CRS of x before masking. Currently, this function will not reproject the x. Optional in postProcess.
rasterToMatch	Template Raster* object used for cropping (so extent should be the extent of desired outcome) and reprojecting (including changing the resolution and projection). See details in <a href="#">postProcess</a> .
overwrite	Logical. Should downloading and all the other actions occur even if they pass the checksums or the files are all there.
useSAcrs	Logical. If FALSE, the default, then the desired projection will be taken from rasterToMatch or none at all. If TRUE, it will be taken from studyArea. See table in details below.
useCache	Passed to Cache in various places. Defaults to <code>getOption("reproducible.useCache")</code>

### Post processing sequence

If the rasterToMatch or studyArea are passed, then the following sequence will occur:

1. Fix errors [fixErrors](#). Currently only errors fixed are for SpatialPolygons using `buffer(..., width = 0)`.
2. Crop using [cropInputs](#)
3. Project using [projectInputs](#)
4. Mask using [maskInputs](#)
5. Determine file name [determineFilename](#)
6. Write that file name to disk, optionally [writeOutputs](#)

NOTE: checksumming does not occur during the post-processing stage, as there are no file downloads. To achieve fast results, wrap prepInputs with Cache

NOTE: sf objects are still very experimental.



**Passing rasterToMatch and/or studyArea**

Depending on which of these were passed, different things will happen to the targetFile located at filename1.

**If targetFile is a Raster\* object::**

	rasterToMatch	studyArea	Both
extent	Yes	Yes	rasterToMatch
resolution	Yes	No	rasterToMatch
projection	Yes	No*	rasterToMatch*
alignment	Yes	No	rasterToMatch
mask	No**	Yes	studyArea**

\* Can be overridden with useSAcrs \*\* Will mask with NAs from rasterToMatch if maskWithRTM

**If targetFile is a Spatial\* object::**

	rasterToMatch	studyArea	Both
extent	Yes	Yes	rasterToMatch
resolution	NA	NA	NA
projection	Yes	No*	rasterToMatch*
alignment	NA	NA	NA
mask	No	Yes	studyArea

\* Can be overridden with useSAcrs

**See Also**

prepInputs

**Examples**

```
# Add a study area to Crop and Mask to
# Create a "study area"
library(sp)
library(raster)
ow <- setwd(tempdir())

# make a SpatialPolygon
coords1 <- structure(c(-123.98, -117.1, -80.2, -100, -123.98, 60.9, 67.73, 65.58, 51.79, 60.9),
                    .Dim = c(5L, 2L))
Sr1 <- Polygon(coords1)
Srs1 <- Polygons(list(Sr1), "s1")
shpEcozone <- SpatialPolygons(list(Srs1), 1L)
crs(shpEcozone) <- "+init=epsg:4326 +proj=longlat +datum=WGS84 +no_defs +ellps=WGS84 +towgs84=0,0,0"

# make a "study area" that is subset of larger dataset
coords <- structure(c(-118.98, -116.1, -99.2, -106, -118.98, 59.9, 65.73, 63.58, 54.79, 59.9),
```

```

        .Dim = c(5L, 2L))
Sr1 <- Polygon(coords)
Srs1 <- Polygons(list(Sr1), "s1")
StudyArea <- SpatialPolygons(list(Srs1), 1L)
crs(StudyArea) <- "+init=epsg:4326 +proj=longlat +datum=WGS84 +no_defs +ellps=WGS84 +towgs84=0,0,0"
#'
#'
#####
shpEcozonePostProcessed <- postProcess(shpEcozone, studyArea = StudyArea)
#'
# Try manually, individual pieces
shpEcozoneReprojected <- projectInputs(shpEcozone, StudyArea)
shpEcozoneCropped <- cropInputs(shpEcozone, StudyArea)
shpEcozoneClean <- fixErrors(shpEcozone)
shpEcozoneMasked <- maskInputs(shpEcozone, StudyArea)

setwd(ow)
# Add a study area to Crop and Mask to
# Create a "study area"
library(sp)
library(raster)
ow <- setwd(tempdir())

# make a SpatialPolygon
coords1 <- structure(c(-123.98, -117.1, -80.2, -100, -123.98, 60.9, 67.73, 65.58, 51.79, 60.9),
                    .Dim = c(5L, 2L))
Sr1 <- Polygon(coords1)
Srs1 <- Polygons(list(Sr1), "s1")
shpEcozone <- SpatialPolygons(list(Srs1), 1L)
crs(shpEcozone) <- "+init=epsg:4326 +proj=longlat +datum=WGS84 +no_defs +ellps=WGS84 +towgs84=0,0,0"

# make a "study area" that is subset of larger dataset
coords <- structure(c(-118.98, -116.1, -99.2, -106, -118.98, 59.9, 65.73, 63.58, 54.79, 59.9),
                    .Dim = c(5L, 2L))
Sr1 <- Polygon(coords)
Srs1 <- Polygons(list(Sr1), "s1")
StudyArea <- SpatialPolygons(list(Srs1), 1L)
crs(StudyArea) <- "+init=epsg:4326 +proj=longlat +datum=WGS84 +no_defs +ellps=WGS84 +towgs84=0,0,0"
#'
#'
#####
shpEcozonePostProcessed <- postProcess(shpEcozone, studyArea = StudyArea)
#'
# Try manually, individual pieces
shpEcozoneReprojected <- projectInputs(shpEcozone, StudyArea)
shpEcozoneCropped <- cropInputs(shpEcozone, StudyArea)
shpEcozoneClean <- fixErrors(shpEcozone)
shpEcozoneMasked <- maskInputs(shpEcozone, StudyArea)

setwd(ow)

```

---

 prepInputs

*Download and optionally post process files*


---

### Description

This function can be used to prepare R objects from remote or local data sources. The object of this function is to provide a reproducible version of a series of commonly used steps for getting, loading, and processing data. This function has two stages: Getting data (download, extracting from archives, loading into R) and postProcessing (for Spatial\* and Raster\* objects, this is crop, reproject, mask/intersect). To trigger the first stage, provide url or archive. To trigger the second stage, provide studyArea or rasterToMatch. See examples.

### Usage

```
prepInputs(targetFile = NULL, url = NULL, archive = NULL,
  alsoExtract = NULL,
  destinationPath = getOption("reproducible.destinationPath", "."),
  fun = NULL, quick = getOption("reproducible.quick"),
  overwrite = getOption("reproducible.overwrite", FALSE),
  purge = FALSE, useCache = getOption("reproducible.useCache", FALSE),
  ...)
```

### Arguments

targetFile	Character string giving the path to the eventual file (raster, shapefile, csv, etc.) after downloading and extracting from a zip or tar archive. This is the file <i>before</i> it is passed to postProcess. Currently, the internal checksumming does not checksum the file after it is postProcessed (e.g., cropped/reprojected/masked). Using Cache around prepInputs will do a sufficient job in these cases. See table in <a href="#">preProcess</a> .
url	Optional character string indicating the URL to download from. If not specified, then no download will be attempted. If not entry exists in the CHECKSUMS.txt (in destinationPath), an entry will be created or appended to. This CHECKSUMS.txt entry will be used in subsequent calls to prepInputs or preProcess, comparing the file on hand with the ad hoc CHECKSUMS.txt. See table in <a href="#">preProcess</a> .
archive	Optional character string giving the path of an archive containing targetFile, or a vector giving a set of nested archives (e.g., c("xxx.tar", "inner.zip", "inner.rar")). If there is/are (an) inner archive(s), but they are unknown, the function will try all until it finds the targetFile. See table in <a href="#">preProcess</a> .
alsoExtract	Optional character string naming files other than targetFile that must be extracted from the archive. If NULL, the default, then it will extract all files. Other options: "similar" will extract all files with the same filename without file extension as targetFile. NA will extract nothing other than targetFile. A character string of specific file names will cause only those to be extracted. See table in <a href="#">preProcess</a> .

destinationPath	Character string of a directory in which to download and save the file that comes from url and is also where the function will look for archive or targetFile. NOTE (still experimental): To prevent repeated downloads in different locations, the user can also set options("reproducible.inputPaths") to one or more local file paths to search for the file before attempting to download. Default for that option is NULL meaning do not search locally.
fun	Function or character string indicating the function to use to load targetFile into an R object, e.g., in form with package name: "raster::raster".
quick	Logical. This is passed internally to <a href="#">Checksums</a> (the quickCheck argument), and to <a href="#">Cache</a> (the quick argument). This results in faster, though less robust checking of inputs. See the respective functions.
overwrite	Logical. Should downloading and all the other actions occur even if they pass the checksums or the files are all there.
purge	Logical or Integer. 0/FALSE (default) keeps existing CHECKSUMS.txt file and prepInputs will write or append to it. 1/TRUE will deleted the entire CHECKSUMS.txt file. Other options, see details.
useCache	Passed to Cache in various places. Defaults to getOption("reproducible.useCache")
...	Additional arguments passed to fun (i.e., user supplied), <a href="#">postProcess</a> and <a href="#">Cache</a> . Since ... is passed to <a href="#">postProcess</a> , these will ... will also be passed into the inner functions, e.g., <a href="#">cropInputs</a> . See details and examples.

### Stage 1 - Getting data

See [preProcess](#) for combinations of arguments.

1. Download from the web via either [drive\\_download](#), [download.file](#);
2. Extract from archive using [unzip](#) or [untar](#);
3. Load into R using [raster](#), [shapefile](#), or any other function passed in with fun;
4. Checksumming of all files during this process. This is put into a 'CHECKSUMS.txt' file in the destinationPath, appending if it is already there, overwriting the entries for same files if entries already exist.

### Stage 2 - Post processing

This will be triggered if either rasterToMatch or studyArea is supplied.

1. Fix errors. Currently only errors fixed are for SpatialPolygons using `buffer(..., width = 0)`;
2. Crop using [cropInputs](#);
3. Project using [projectInputs](#);
4. Mask using [maskInputs](#);
5. Determine file name [determineFilename](#) via filename2;
6. Optionally, write that file name to disk via [writeOutputs](#).

NOTE: checksumming does not occur during the post-processing stage, as there are no file downloads. To achieve fast results, wrap prepInputs with Cache.

NOTE: sf objects are still very experimental.

#### **postProcessing of Raster\* and Spatial\* objects::**

If rasterToMatch or studyArea are used, then this will trigger several subsequent functions, specifically the sequence, *Crop, reproject, mask*, which appears to be a common sequence in spatial simulation. See [postProcess.spatialObjects](#).

*Understanding various combinations of rasterToMatch and/or studyArea:* Please see [postProcess.spatialObjects](#).

#### purge

In options for control of purging the CHECKSUMS.txt file are:

- 0 keep file
- 1 delete file
- 2 delete entry for targetFile
- 4 delete entry for alsoExtract
- 3 delete entry for archive
- 5 delete entry for targetFile & alsoExtract
- 6 delete entry for targetFile, alsoExtract & archive
- 7 delete entry that is failing (i.e., for the file downloaded by the url)

will only remove entries in the CHECKSUMS.txt that are associated with targetFile, alsoExtract or archive When prepInputs is called, it will write or append to a (if already exists) CHECKSUMS.txt file. If the CHECKSUMS.txt is not correct, use this argument to remove it.

#### Note

This function is still experimental: use with caution.

#### Author(s)

Eliot McIntire, Jean Marchal, and Tati Micheletti

#### See Also

[downloadFile](#), [extractFromArchive](#), [downloadFile](#), [postProcess](#).

#### Examples

```
# This function works within a module; however, currently,
# \code{sourceURL} is not yet working as desired. Use \code{url}.
## Not run:
# download a zip file from internet, unzip all files, load as shapefile, Cache the call
# First time: don't know all files - prepInputs will guess, if download file is an archive,
# then extract all files, then if there is a .shp, it will load with raster::shapefile
dPath <- file.path(tempdir(), "ecozones")
```

```

shpEcozone <- prepInputs(destinationPath = dPath,
                          url = "http://sis.agr.gc.ca/cansis/nsdb/ecostrat/zone/ecozone_shp.zip")

# Robust to partial file deletions:
unlink(dir(dPath, full.names = TRUE)[1:3])
shpEcozone <- prepInputs(destinationPath = dPath,
                          url = "http://sis.agr.gc.ca/cansis/nsdb/ecostrat/zone/ecozone_shp.zip")
unlink(dPath, recursive = TRUE)

# Once this is done, can be more precise in operational code:
# specify targetFile, alsoExtract, and fun, wrap with Cache
ecozoneFilename <- file.path(dPath, "ecozones.shp")
ecozoneFiles <- c("ecozones.dbf", "ecozones.prj",
                 "ecozones.sbn", "ecozones.sbx", "ecozones.shp", "ecozones.shx")
shpEcozone <- prepInputs(targetFile = ecozoneFilename,
                          url = "http://sis.agr.gc.ca/cansis/nsdb/ecostrat/zone/ecozone_shp.zip",
                          alsoExtract = ecozoneFiles,
                          fun = "shapefile", destinationPath = dPath)
unlink(dPath, recursive = TRUE)

#' # Add a study area to Crop and Mask to
# Create a "study area"
library(sp)
library(raster)
coords <- structure(c(-122.98, -116.1, -99.2, -106, -122.98, 59.9, 65.73, 63.58, 54.79, 59.9),
                   .Dim = c(5L, 2L))
Sr1 <- Polygon(coords)
Srs1 <- Polygons(list(Sr1), "s1")
StudyArea <- SpatialPolygons(list(Srs1), 1L)
crs(StudyArea) <- "+init=epsg:4326 +proj=longlat +datum=WGS84 +no_defs +ellps=WGS84 +towgs84=0,0,0"

# specify targetFile, alsoExtract, and fun, wrap with Cache
ecozoneFilename <- file.path(dPath, "ecozones.shp")
# Note, you don't need to "alsoExtract" the archive... if the archive is not there, but the
# targetFile is there, it will not redownload the archive.
ecozoneFiles <- c("ecozones.dbf", "ecozones.prj",
                 "ecozones.sbn", "ecozones.sbx", "ecozones.shp", "ecozones.shx")
shpEcozoneSm <- Cache(prepareInputs,
                      url = "http://sis.agr.gc.ca/cansis/nsdb/ecostrat/zone/ecozone_shp.zip",
                      targetFile = reproducible::asPath(ecozoneFilename),
                      alsoExtract = reproducible::asPath(ecozoneFiles),
                      studyArea = StudyArea,
                      fun = "shapefile", destinationPath = dPath,
                      filename2 = "EcozoneFile.shp") # passed to determineFilename

plot(shpEcozone)
plot(shpEcozoneSm, add = TRUE, col = "red")
unlink(dPath)

# Big Raster, with crop and mask to Study Area - no reprojecting (lossy) of raster,
# but the StudyArea does get reprojected, need to use rasterToMatch
dPath <- file.path(tempdir(), "LCC")
lcc2005Filename <- file.path(dPath, "LCC2005_V1_4a.tif")

```

```

url <- file.path("ftp://ftp.ccrs.nrcan.gc.ca/ad/NLCCLandCover",
                "LandcoverCanada2005_250m/LandCoverOfCanada2005_V1_4.zip")

# messages received below may help for filling in more arguments in the subsequent call
LCC2005 <- prepInputs(url = url,
                    destinationPath = asPath(dPath),
                    studyArea = StudyArea)

plot(LCC2005)

# if wrapped with Cache, will be fast second time, very fast 3rd time (via memoised copy)
LCC2005 <- Cache(prepInputs, url = url,
                targetFile = lcc2005Filename,
                archive = asPath("LandCoverOfCanada2005_V1_4.zip"),
                destinationPath = asPath(dPath),
                studyArea = StudyArea)

# Using dlFun -- a custom download function -- passed to preProcess
test1 <- prepInputs(targetFile = "GADM_2.8_LUX_adm0.rds", # must specify currently
                    dlFun = "raster::getData", name = "GADM", country = "LUX", level = 0,
                    path = dPath)

## End(Not run)

```

---

preProcess

*Download, Checksum, Extract files*


---

## Description

This does downloading (via `downloadFile`), checksumming (Checksums), and extracting from archives (`extractFromArchive`), plus cleaning up of input arguments (e.g., paths, function names). This is the first stage of three used in `prepInputs`.

## Usage

```

preProcess(targetFile = NULL, url = NULL, archive = NULL,
           alsoExtract = NULL,
           destinationPath = getOption("reproducible.destinationPath", "."),
           fun = NULL, dlFun = NULL, quick = getOption("reproducible.quick"),
           overwrite = getOption("reproducible.overwrite", FALSE),
           purge = FALSE, useCache = getOption("reproducible.useCache", FALSE),
           ...)

```

## Arguments

<code>targetFile</code>	Character string giving the path to the eventual file (raster, shapefile, csv, etc.) after downloading and extracting from a zip or tar archive. This is the file <i>before</i> it is passed to <code>postProcess</code> . Currently, the internal checksumming does not
-------------------------	--

checksum the file after it is postProcessed (e.g., cropped/reprojected/masked). Using Cache around prepInputs will do a sufficient job in these cases. See table in [preProcess](#).

url	Optional character string indicating the URL to download from. If not specified, then no download will be attempted. If not entry exists in the CHECKSUMS.txt (in destinationPath), an entry will be created or appended to. This CHECKSUMS.txt entry will be used in subsequent calls to prepInputs or preProcess, comparing the file on hand with the ad hoc CHECKSUMS.txt. See table in <a href="#">preProcess</a> .
archive	Optional character string giving the path of an archive containing targetFile, or a vector giving a set of nested archives (e.g., c("xxx.tar", "inner.zip", "inner.rar")). If there is/are (an) inner archive(s), but they are unknown, the function will try all until it finds the targetFile. See table in <a href="#">preProcess</a> .
alsoExtract	Optional character string naming files other than targetFile that must be extracted from the archive. If NULL, the default, then it will extract all files. Other options: "similar" will extract all files with the same filename without file extension as targetFile. NA will extract nothing other than targetFile. A character string of specific file names will cause only those to be extracted. See table in <a href="#">preProcess</a> .
destinationPath	Character string of a directory in which to download and save the file that comes from url and is also where the function will look for archive or targetFile. NOTE (still experimental): To prevent repeated downloads in different locations, the user can also set options("reproducible.inputPaths") to one or more local file paths to search for the file before attempting to download. Default for that option is NULL meaning do not search locally.
fun	Function or character string indicating the function to use to load targetFile into an R object, e.g., in form with package name: "raster::raster".
dlFun	Optional "download function" name, such as "raster::getData", which does custom downloading, in addition to loading into R. Still experimental.
quick	Logical. This is passed internally to <a href="#">Checksums</a> (the quickCheck argument), and to <a href="#">Cache</a> (the quick argument). This results in faster, though less robust checking of inputs. See the respective functions.
overwrite	Logical. Should downloading and all the other actions occur even if they pass the checksums or the files are all there.
purge	Logical or Integer. 0/FALSE (default) keeps existing CHECKSUMS.txt file and prepInputs will write or append to it. 1/TRUE will deleted the entire CHECKSUMS.txt file. Other options, see details.
useCache	Passed to Cache in various places. Defaults to getOption("reproducible.useCache")
...	Additional arguments passed to fun (i.e., user supplied), <a href="#">postProcess</a> and <a href="#">Cache</a> . Since ... is passed to <a href="#">postProcess</a> , these will ... will also be passed into the inner functions, e.g., <a href="#">cropInputs</a> . See details and examples.

### Value

A list with 5 elements, checkSums (the result of a Checksums after downloading), dots (cleaned up ..., including deprecated argument checks), fun (the function to be used to load the preProcessed object from disk), and targetFilePath (the fully qualified path to the targetFile).



**Combinations of targetFile, url, archive, alsoExtract**

# Params	url	targetFile	archive	alsoExtract	Result
<b>1</b>	char	NULL	NULL	NULL	Download, extract all files if an archive, guess at targetFile
	NULL	char	NULL	NULL	load targetFile into R
	NULL	NULL	char	NULL	extract all files, guess at targetFile, load into R
	NULL	NULL	NULL	char	guess at targetFile from files in alsoExtract, load into R
<b>2</b>	char	char	NULL	NULL	Download, extract all files if an archive, load targetFile into R
	char	NULL	char	NULL	Download, extract all files, guess at targetFile, load into R
	char	NULL	NULL	char	Download, extract only named files in alsoExtract, guess at targetFile
	NULL	char	NULL	char	load targetFile into R
	NULL	char	char	NULL	Extract all files, load targetFile into R
	NULL	NULL	char	char	Extract only named files in alsoExtract, guess at targetFile
<b>3</b>	char	char	char	NULL	Download, extract all files, load targetFile into R
	char	NULL	char	char	Download, extract files named in alsoExtract, guess at targetFile
	char	NULL	char	"similar"	Download, extract all files (can't understand "similar"), guess at targetFile
	char	char	NULL	char	Download, if an archive, extract files named in targetFile and alsoExtract
	char	char	NULL	"similar"	Download, if an archive, extract files with same base as targetFile and alsoExtract
	char	char	char	NULL	Download, extract all files from archive, load targetFile into R
	NULL	char	char	char	Extract files named in alsoExtract from archive, load targetFile into R
<b>4</b>	char	char	char	char	Download, extract files named in targetFile and alsoExtract
	char	char	char	"similar"	Download, extract all files with same base as targetFile, load targetFile into R

\* If the url is a file on Google Drive, checksumming will work even without a targetFile specified because there is an initial attempt to get the remote file information (e.g., file name). With that, the connection between the url and the filename used in the CHECKSUMS.txt file can be made.

**Author(s)**

Eliot McIntire

---

projectInputs

*Project Raster\* or Spatial\* or sf objects*

---

**Description**

A simple wrapper around the various different tools for these GIS types.

**Usage**

```

projectInputs(x, targetCRS, ...)

## Default S3 method:
projectInputs(x, targetCRS, ...)

## S3 method for class 'Raster'
projectInputs(x, targetCRS = NULL,
  rasterToMatch = NULL, cores = NULL, ...)

## S3 method for class 'sf'
projectInputs(x, targetCRS, ...)

## S3 method for class 'Spatial'
projectInputs(x, targetCRS, ...)

```

**Arguments**

x	A Raster*, Spatial* or sf object
targetCRS	The CRS of x at the end of this function (i.e., the goal)
...	Passed to <a href="#">projectRaster</a> .
rasterToMatch	Template Raster* object passed to the to argument of <a href="#">projectRaster</a> , thus will changing the resolution and projection of x. See details in <a href="#">postProcess</a> .
cores	An integer* or 'AUTO'. This will be used if gdalwarp is triggered. 'AUTO'* will calculate 90 number of cores in the system, while an integer or rounded float will be passed as the exact number of cores to be used.

**Value**

A file of the same type as starting, but with projection (and possibly other characteristics, including resolution, origin, extent if changed).

**Examples**

```

# Add a study area to Crop and Mask to
# Create a "study area"
library(sp)
library(raster)
ow <- setwd(tempdir())

# make a SpatialPolygon
coords1 <- structure(c(-123.98, -117.1, -80.2, -100, -123.98, 60.9, 67.73, 65.58, 51.79, 60.9),
  .Dim = c(5L, 2L))
Sr1 <- Polygon(coords1)
Srs1 <- Polygons(list(Sr1), "s1")
shpEcozone <- SpatialPolygons(list(Srs1), 1L)
crs(shpEcozone) <- "+init=epsg:4326 +proj=longlat +datum=WGS84 +no_defs +ellps=WGS84 +towgs84=0,0,0"

# make a "study area" that is subset of larger dataset

```

```
coords <- structure(c(-118.98, -116.1, -99.2, -106, -118.98, 59.9, 65.73, 63.58, 54.79, 59.9),
                    .Dim = c(5L, 2L))
Sr1 <- Polygon(coords)
Srs1 <- Polygons(list(Sr1), "s1")
StudyArea <- SpatialPolygons(list(Srs1), 1L)
crs(StudyArea) <- "+init=epsg:4326 +proj=longlat +datum=WGS84 +no_defs +ellps=WGS84 +towgs84=0,0,0"
#'
#'
#####
shpEcozonePostProcessed <- postProcess(shpEcozone, studyArea = StudyArea)
#'
# Try manually, individual pieces
shpEcozoneReprojected <- projectInputs(shpEcozone, StudyArea)
shpEcozoneCropped <- cropInputs(shpEcozone, StudyArea)
shpEcozoneClean <- fixErrors(shpEcozone)
shpEcozoneMasked <- maskInputs(shpEcozone, StudyArea)

setwd(ow)
```

---

readLinesRcpp

*Alternative to readLines that is faster*

---

## Description

This alternative is from <https://gist.github.com/hadley/6353939>

## Usage

```
readLinesRcpp(path)
```

## Arguments

path            Path to text file to read.

## Value

Similar to readLines. It may not return identical results.

## Examples

```
readLinesRcpp(system.file(package = "reproducible", "DESCRIPTION"))
```

---

`readLinesRcppInternal` *Alternative to readLines that is faster*

---

### Description

This alternative is from <https://gist.github.com/hadley/6353939>

### Usage

```
readLinesRcppInternal(path)
```

### Arguments

`path` Path to text file to read.

### Value

Similar to `readLines`, except with explicit `\n` embedded.

### Examples

```
readLinesRcpp(system.file(package = "reproducible", "DESCRIPTION"))
```

---

`reproducibleOptions` *reproducible options*

---

### Description

These provide top-level, powerful settings for a comprehensive reproducible workflow. To see defaults, run `reproducibleOptions()`. See Details below.

### Usage

```
reproducibleOptions()
```

### Details

Below are options that can be set with `options("reproducible.xxx" = newValue)`, where `xxx` is one of the values below, and `newValue` is a new value to give the option. Sometimes these options can be placed in the user's `.Rprofile` file so they persist between sessions.

The following options are likely of interest to most users

<i>OPTION</i>	<i>DEFAULT VALUE</i>	<i>DESCRIPTION</i>
<code>ask</code>	TRUE	Used in <code>clearCache</code> and <code>keepCache</code>
<code>cachePath</code>	<code>.reproducibleTempCacheDir</code>	Used in <code>Cache</code> and many others. The default path for repository
<code>destinationPath</code>	NULL	Used in <code>prepInputs</code> , <code>preProcess</code> . Can be set globally here.

futurePlan	FALSE	On Linux OSs, Cache and cloudCache have some functional
inputPaths	NULL	Used in <code>prepInputs</code> , <code>preProcess</code> . If set to a path, this will c
inputPathsRecursive	FALSE	Used in <code>prepInputs</code> , <code>preProcess</code> . Should the reproducibl
overwrite	FALSE	Used in <code>prepInputs</code> , <code>preProcess</code> , <code>downloadFile</code> , and <code>post</code>
quick	FALSE	Used in <code>Cache</code> . This will cause Cache to use <code>file.size(fil</code>
showSimilar	Passed to Cache. Default FALSE.	
useCache	TRUE	Used in <code>Cache</code> . If FALSE, then the entire Cache machinery is s
useCloud	Passed to Cache. Default FALSE.	
useMemoise	TRUE	Used in <code>Cache</code> . If TRUE, recovery of cached elements from the
useNewDigestAlgorithm	TRUE	This will mean that previous cache repositories will be defund
verbose	FALSE	If set to TRUE then every Cache call will show a summary of t

### Advanced

The following options are likely not needed by a user.

cloudChecksumsFilename	<code>file.path(dirname(.reproducibleTempCacheDir), "checksums.rds")</code>	Used in <code>cloudC</code>
length	Inf	Used in <code>Cache</code> ,
useragent	"http://github.com/PredictiveEcology/reproducible"	User agent for d

---

Require	<i>Repeatability-safe install and load packages, optionally with specific versions</i>
---------	--

---

### Description

This is an "all in one" function that will run `install.packages` for CRAN packages, `remotes::install_github` for `GitHub.com` packages and will install specific versions of each package if there is a `packageVersionFile` supplied. Plus, when `packages` is provided as a character vector, or a `packageVersionFile` is supplied, all package dependencies will be first assessed for `unique(dependencies)` so the same package is not installed multiple times. Finally `library` is called on the packages. If packages are already installed (`packages` supplied), and their version numbers are exact (when `packageVersionFile` is supplied), then the "install" component will be skipped very quickly with a message.

### Usage

```
Require(packages, packageVersionFile, libPath = .libPaths()[1],
  install_githubArgs = list(), install.packagesArgs = list(),
  standAlone = FALSE, repos = getOption("repos"), forget = FALSE)
```

### Arguments

packages	Character vector of packages to install via <code>install.packages</code> , then load (i.e., with <code>library</code> ). If it is one package, it can be unquoted (as in <code>require</code> )
----------	--

<code>packageVersionFile</code>	If provided, then this will override all <code>install.package</code> calls with <code>versions::install.versions</code>
<code>libPath</code>	The library path where all packages should be installed, and looked for to load (i.e., call library)
<code>install_githubArgs</code>	List of optional named arguments, passed to <code>install_github</code> .
<code>install.packagesArgs</code>	List of optional named arguments, passed to <code>install.packages</code> .
<code>standAlone</code>	Logical. If TRUE, all packages will be installed and loaded strictly from the <code>libPaths</code> only. If FALSE, all <code>.libPaths</code> will be used to find the correct versions. This can be create dramatically faster installs if the user has a substantial number of the packages already in their personal library. In the case of TRUE, there will be a hidden file place in the <code>libPath</code> directory that lists all the packages that were needed during the Require call. Default FALSE to minimize package installing.
<code>repos</code>	The remote repository (e.g., a CRAN mirror), passed to either <code>install.packages</code> , <code>install_github</code> or <code>installVersions</code> .
<code>forget</code>	Internally, this function identifies package dependencies using a memoised function for speed on reuse. But, it may be inaccurate in some cases, if packages were installed manually by a user. Set this to TRUE to refresh that dependency calculation.

### Details

`standAlone` will either put the Required packages and their dependencies *all* within the `libPath` (if TRUE) or if FALSE will only install packages and their dependencies that are otherwise not installed in `.libPaths()`, i.e., the personal or base library paths. Any packages or dependencies that are not yet installed will be installed in `libPath`. Importantly, a small hidden file (named `._packageVersionsAuto.txt`) will be saved in `libPath` that will store the *information* about the packages and their dependencies, even if the version used is located in `.libPaths()`, i.e., not the `libPath` provided. This hidden file will be used if a user runs `pkgSnapshot`, enabling a new user to rebuild the entire dependency chain, without having to install all packages in an isolated directory (as does **packrat**). This will save potentially a lot of time and disk space, and yet maintain reproducibility. *NOTE*: since there is only one hidden file in a `libPath`, any call to `pkgSnapshot` will make a snapshot of the most recent call to Require.

To build a snapshot of the desired packages and their versions, first run Require with all packages, then `pkgSnapshot`. If a `libPath` is used, it must be used in both functions.

This function works best if all required packages are called within one Require call, as all dependencies can be identified together, and all package versions will be saved automatically (with `standAlone = TRUE` or `standAlone = FALSE`), allowing a call to `pkgSnapshot` when a more permanent record of versions can be made.

### Note

This function will use memoise internally to determine the dependencies of all packages. This will speed up subsequent calls to Require dramatically. However, it will not take into account version numbers for this memoised step. If package versions are updated manually by the user, then this cached element should be wiped, using `forget = TRUE`.

**Examples**

```
## Not run:
# simple usage, like conditional install.packages then library
Require("stats") # analogous to require(stats), but slower because it checks for
                  # pkg dependencies, and installs them, if missing
tempPkgFolder <- file.path(tempdir(), "Packages")

# use standAlone, means it will put it in libPath, even if it already exists
#   in another local library (e.g., personal library)
Require("crayon", libPath = tempPkgFolder, standAlone = TRUE)

# make a package version snapshot
packageVersionFile <- file.path(tempPkgFolder, ".packageVersion.txt")
pkgSnapshot(libPath=tempPkgFolder, packageVersionFile)

# confirms that correct version is installed
Require("crayon", packageVersionFile = packageVersionFile)

# Create mismatching versions -- desired version is older than current installed
# This will try to install the older version, overwriting the newer version
desiredVersion <- data.frame(instPkgs="crayon", instVers = "1.3.2", stringsAsFactors = FALSE)
write.table(file = packageVersionFile, desiredVersion, row.names = FALSE)
# won't work because newer crayon is loaded
Require("crayon", packageVersionFile = packageVersionFile)

# unload it first
detach("package:crayon", unload = TRUE)

# run again, this time, correct "older" version installs in place of newer one
Require("crayon", packageVersionFile = packageVersionFile)

# Mutual dependencies, only installs once -- e.g., httr
Require(c("cranlogs", "covr"), libPath = tempPkgFolder)

## End(Not run)
```

---

searchFull

*Search up the full scope for functions*


---

**Description**

This is like `base::search` but when used inside a function, it will show the full scope (see figure in the section *Binding environments* on <http://adv-r.had.co.nz/Environments.html>). This full search path will be potentially much longer than just `search()` (which always starts at `.GlobalEnv`).

`searchFullEx` shows an example function that is inside this package whose only function is to show the Scope of a package function.

**Usage**

```
searchFull(env = parent.frame(), simplify = TRUE)
```

```
searchFullEx()
```

**Arguments**

`env`            The environment to start searching at. Default is calling environment, i.e., `parent.frame()`

`simplify`       Logical. Should the output be simplified to character, if possible (usually it is not possible because environments don't always coerce correctly)

**Details**

`searchFullEx` can be used to show an example of the use of `searchFull`.

**Value**

A list of environments that is the actual search path, unlike `search()` which only prints from `.GlobalEnv` up to base through user attached packages.

**See Also**

[search](#)

**Examples**

```
seeScope <- function() {
  searchFull()
}
seeScope()
searchFull()
searchFullEx()
```

---

unrarPath

*The known path for unrar or 7z*

---

**Description**

The known path for unrar or 7z

**Usage**

```
.unrarPath
```

**Format**

An object of class `NULL` of length 0.



---

writeFuture	<i>Write to archivist repository, using future::future</i>
-------------	--

---

**Description**

This will be used internally if `options("reproducible.futurePlan" = TRUE)`. This is still experimental.

**Usage**

```
writeFuture(written, outputToSave, cacheRepo, userTags)
```

**Arguments**

written	Integer. If zero or positive then it needs to be written still. Should be 0 to start.
outputToSave	The R object to save to repository
cacheRepo	The file path of the repository
userTags	Character string of tags to attach to this outputToSave in the CacheRepo

---

writeOutputs	<i>Write module inputs on disk</i>
--------------	------------------------------------

---

**Description**

Can be used to write prepared inputs on disk.

**Usage**

```
writeOutputs(x, filename2,
  overwrite = getOption("reproducible.overwrite", NULL), ...)

## S3 method for class 'Raster'
writeOutputs(x, filename2 = NULL,
  overwrite = getOption("reproducible.overwrite", FALSE), ...)

## S3 method for class 'Spatial'
writeOutputs(x, filename2 = NULL,
  overwrite = getOption("reproducible.overwrite", TRUE), ...)

## S3 method for class 'sf'
writeOutputs(x, filename2 = NULL,
  overwrite = getOption("reproducible.overwrite", FALSE), ...)

## Default S3 method:
writeOutputs(x, filename2, ...)
```

**Arguments**

x	The object save to disk i.e., write outputs
filename2	File name passed to <code>writeRaster</code> , or <code>shapefile</code> or <code>st_write</code> (dsn argument).
overwrite	Logical. Should file being written overwrite an existing file if it exists.
...	Passed into <code>shapefile</code> or <code>writeRaster</code> or <code>st_write</code>

**Author(s)**

Eliot McIntire and Jean Marchal

**Examples**

```
# Add a study area to Crop and Mask to
# Create a "study area"
library(sp)
library(raster)
ow <- setwd(tempdir())

# make a SpatialPolygon
coords1 <- structure(c(-123.98, -117.1, -80.2, -100, -123.98, 60.9, 67.73, 65.58, 51.79, 60.9),
                    .Dim = c(5L, 2L))
Sr1 <- Polygon(coords1)
Srs1 <- Polygons(list(Sr1), "s1")
shpEcozone <- SpatialPolygons(list(Srs1), 1L)
crs(shpEcozone) <- "+init=epsg:4326 +proj=longlat +datum=WGS84 +no_defs +ellps=WGS84 +towgs84=0,0,0"

# make a "study area" that is subset of larger dataset
coords <- structure(c(-118.98, -116.1, -99.2, -106, -118.98, 59.9, 65.73, 63.58, 54.79, 59.9),
                    .Dim = c(5L, 2L))
Sr1 <- Polygon(coords)
Srs1 <- Polygons(list(Sr1), "s1")
StudyArea <- SpatialPolygons(list(Srs1), 1L)
crs(StudyArea) <- "+init=epsg:4326 +proj=longlat +datum=WGS84 +no_defs +ellps=WGS84 +towgs84=0,0,0"
#'
#'
#####
shpEcozonePostProcessed <- postProcess(shpEcozone, studyArea = StudyArea)
#'
# Try manually, individual pieces
shpEcozoneReprojected <- projectInputs(shpEcozone, StudyArea)
shpEcozoneCropped <- cropInputs(shpEcozone, StudyArea)
shpEcozoneClean <- fixErrors(shpEcozone)
shpEcozoneMasked <- maskInputs(shpEcozone, StudyArea)

setwd(ow)
```

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