

# Package ‘nat.utils’

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**Title** File System Utility Functions for 'NeuroAnatomy Toolbox'

**Description** Utility functions that may be of general interest but are specifically required by the 'NeuroAnatomy Toolbox' ('nat'). Includes functions to provide a basic make style system to update files based on timestamp information, file locking and 'touch' utility. Convenience functions for working with file paths include 'abs2rel', 'split\_path' and 'common\_path'. Finally there are utility functions for working with 'zip' and 'gzip' files including integrity tests.

**Suggests** testthat (>= 0.9), roxygen2

**NeedsCompilation** no

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abs2rel	<i>Remove common part of two paths, leaving relative path</i>
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**Description**

Remove common part of two paths, leaving relative path

**Usage**

```
abs2rel(path, stempath = getwd(), StopIfNoCommonPath = FALSE)
```

**Arguments**

path	Paths to make relative
stempath	Root to which path will be made relative
StopIfNoCommonPath	Error if no path in common

**Value**

Character vector containing relative path

**Author(s)**

jefferis

**See Also**

[path.expand](#), [normalizePath](#)

Other path\_utils: [common\\_path](#); [split\\_path](#)

**Examples**

```
path = "/Volumes/JData/JPeople/Sebastian/images"  
abs2rel(path, '/Volumes/JData')
```

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common_path	<i>Find common prefix of two or more (normalised) file paths</i>
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## Description

Find common prefix of two or more (normalised) file paths

## Usage

```
common_path(paths, normalise = FALSE, fsep = .Platform$file.sep)
```

## Arguments

paths	Character vector of file paths
normalise	Whether to normalise paths (with <a href="#">normalizePath</a> , default FALSE)
fsep	Optional path separator (defaults to <code>.Platform\$file.sep</code> )

## Details

Note that for absolute paths, the common prefix will be returned e.g. `common_path(c("/a", "/b"))` is `"/"`

Note that [normalizePath](#) 1) operates according to the conventions of the current runtime platform 2) is called with `winslash=.Platform$file.sep` which means that normalised paths will eventually end up separated by `"\"` by default on Windows rather than by `"/"`, which is `normalizePath`'s standard behaviour.

## Value

Character vector of common prefix, `""` when there is no common prefix, or the original value of paths when fewer than 2 paths were supplied.

## See Also

[normalizePath](#)

Other path\_utils: [abs2rel](#); [split\\_path](#)

## Examples

```
common_path(c("/a", "/b"))
common_path(c("/a/b/", "/a/b"))
common_path(c("/a/b/d", "/a/b/c/d"))
common_path(c("/a/b/d", "/b/c/d"))
common_path(c("a", "b"))
common_path(c("", "a"))
common_path(c("~/", "~/"))
common_path(c("~/a/b/d", "~/a/b/c/d"), normalise = FALSE)
common_path(c("~/", "~/"), normalise = FALSE)
```

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<code>file.swap</code>	<i>Swap names of two files (by renaming first to a temporary file)</i>
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**Description**

Swap names of two files (by renaming first to a temporary file)

**Usage**

```
file.swap(f1, f2)
```

**Arguments**

<code>f1, f2</code>	Paths to files
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**Value**

logical indicating success

**Author(s)**

jefferis

**See Also**

[file.rename](#)

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<code>gzip.crc</code>	<i>Extract the CRC (32 bit hash) of a gzip file</i>
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**Description**

Reads the crc from a gzip file, assuming it is the last 4 bytes of the file. First checks for a valid gzip magic number at the start of the file.

**Usage**

```
gzip.crc(f)
```

**Arguments**

<code>f</code>	Path to a gzip file
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**Details**

CRC32 is not a strong hash like SHA1 or even MD5, but it does provide a basic hash of the **un-compressed contents** of the gzip file. NB CRCs are stored in little endian byte order regardless of platform.

**Value**

hexadecimal formatted

**Examples**

```
rdsfile=system.file('help/aliases.rds')
gzip.crc(rdsfile)
```

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is.gzip	<i>Check if a file is a gzip file</i>
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**Description**

Check if a file is a gzip file

**Usage**

```
is.gzip(f)
```

**Arguments**

f                    Path to file to test

**Value**

logical indicating whether f is in gzip format (or NA if the file cannot be accessed)

**Examples**

```
notgzipfile=tempfile()
writeLines('not a gzip', notgzipfile)
is.gzip(notgzipfile)
con=gzipfile(gzipfile<-tempfile(),open='wt')
writeLines('This one is gzipped', con)
close(con)
is.gzip(gzipfile)
unlink(c(notgzipfile,gzipfile))
```

---

`makelock`*Make and remove (NFS safe) lock files*

---

### Description

Creates a lock file on disk containing a message that should identify the current R session. Will return FALSE if someone else has already made a lockfile. In order to avoid race conditions typical on NFS mounted drives `makelock` appends a unique message to the lock file and then reads the file back in. Only if the unique message is the first line in the file will `makelock` return TRUE.

`removelock` displays a warning and returns false if lockfile cannot be removed. No error message is given if the file does not exist.

### Usage

```
makelock(lockfile, lockmsg, CreateDirectories = TRUE)
```

```
removelock(lockfile)
```

### Arguments

<code>lockfile</code>	Path to lockfile
<code>lockmsg</code>	Character vector with message to be written to lockfile
<code>CreateDirectories</code>	Recursively create directories implied by lockfile path

### Value

logical indicating success

### Author(s)

jefferis

### Examples

```
makelock(lock<-tempfile())
stopifnot(!makelock(lock))
removelock(lock)
```

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nat.utils	<i>nat.utils: File System Utility Functions for NeuroAnatomy Toolbox</i>
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### Description

Utility functions to support the NeuroAnatomy Toolbox (nat). Includes functions to provide a basic make style system to update files based on timestamp information, file locking and other convenience functions for working with the filesystem

### See Also

nat

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nat.utils-defunct	<i>nat.utils: Defunct functions</i>
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### Description

These functions have been retired from nat.utils

### Usage

```
file.hardlink(from, to)
```

### Arguments

from	Source file
to	(New) target hardlink file to create

### See Also

[file.link](#)

ncpus *Return number of cpus (or a default on failure)*

---

**Description**

Return number of cpus (or a default on failure)

**Usage**

```
ncpus(default = 1L)
```

**Arguments**

default            Number of cores to assume if detectCores fails

**Value**

Integer number of cores  
integer number of cores always >=1 for default values

**Author(s)**

jefferis

**See Also**

[detectCores](#)

**Examples**

```
ncpus()
```

---

RunCmdForNewerInput *Run a command if input files are newer than outputs*

---

**Description**

Run a command if input files are newer than outputs

**Usage**

```
RunCmdForNewerInput(cmd, infiles, outfiles, Verbose = FALSE,  
  UseLock = FALSE, Force = FALSE, ReturnInputTimes = FALSE, ...)
```



**Arguments**

cmd	An <a href="#">expression</a> , a string or NA/NULL
infile	Character vector of path to one or more input files
outfile	Character vector of path to one or more output files
Verbose	Write information to console (Default FALSE)
UseLock	Stop other processes working on this task (Default FALSE)
Force	Ignore file modification times and always produce output if input files exist.
ReturnInputTimes	Return mtimes of input files (default FALSE)
...	additional parameters passed to <a href="#">system</a> call.

**Details**

cmd can be an R expression, which is [evaluated](#) if necessary in the environment calling RunCmdForNewerInput, a string to be passed to [system](#) or NULL/NA in which cases the files are checked and TRUE or FALSE is returned depending on whether action is required.

When UseLock=TRUE, the lock file created is called outfile[1].lock

When ReturnInputTimes=TRUE, the input mtimes are returned as an attribute of a logical value (if available).

**Value**

logical indicating if cmd was run or for an R expression, eval(cmd)

**See Also**

[makelock](#), [eval](#), [expression](#)

**Examples**

```
## Not run:
RunCmdForNewerInput(expression(myfunc("somefile")))

## End(Not run)
```

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split_path	<i>Split file path into individual components (optionally including separators)</i>
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**Description**

Split file path into individual components (optionally including separators)

**Usage**

```
split_path(path, include.fseps = FALSE, omit.duplicate.fseps = FALSE,
           fsep = .Platform$file.sep)
```

**Arguments**

`path`            A path with directories separated by `fseps`.

`include.fseps`   Whether to include the separators in the returned character vector (default FALSE)

`omit.duplicate.fseps`   Whether to omit duplicate file separators if `include.fseps=TRUE` (default FALSE).

`fsep`            The path separator (default to `.Platform$file.sep`)

**Value**

A character vector with one element for each component in the path (including path separators if `include.fseps=TRUE`).

**See Also**

[file.path](#)

Other `path_utils`: [abs2rel](#); [common\\_path](#)

**Examples**

```
split_path("/a/b/c")
split_path("a/b/c")
parts=split_path("/a/b/c", include.fseps=TRUE)
# join parts back up again
paste(parts, collapse = "")
split_path("a/b//c", include.fseps=TRUE, omit.duplicate.fseps=TRUE)
# Windows style
split_path("C:\\a\\b\\c", fsep="\\")
```

---

touch

*Use unix touch utility to change file's timestamp*

---

**Description**

If neither a time or a reference file is provided then the current time is used. If the file does not already exist, it is created unless `Create=FALSE`.

**Usage**

```
touch(file, time, reference, timestouupdate = c("access", "modification"),
      Create = TRUE)
```

**Arguments**

file	Path to file to modify
time	Absolute time in POSIXct format
reference	Path to a reference file
timestoupdate	"access" or "modification" (default both)
Create	Logical indicating whether to create file (default TRUE)

**Value**

TRUE or FALSE according to success

**Author(s)**

jefferis

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zipinfo	<i>Return information about a zip archive using system unzip command</i>
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**Description**

Return information about a zip archive using system unzip command

**Usage**

zipinfo(f)

**Arguments**

f	Path to one (or more) files
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**Details**

Uses system unzip command.

**Value**

dataframe of information

**Author(s)**

jefferis

**See Also**

[zip](#)

Other ziputils: [zipok](#)

---

`zipok`*Verify integrity of one or more zip files*

---

**Description**

Verify integrity of one or more zip files

**Usage**

```
zipok(f, Verbose = FALSE)
```

**Arguments**

<code>f</code>	Path to one (or more) files
<code>Verbose</code>	Whether to be Verbose (default FALSE)

**Details**

Uses system unzip command.

**Value**

TRUE when file OK, FALSE otherwise

**Author(s)**

jefferis

**See Also**

Other ziputils: [zipinfo](#)

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