

Package: visualTest (via r-universe)

August 2, 2024

Title Perform Fuzzy Image Matching

Version 1.0.0

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Description Extract and match fingerprints, characteristic signal in plot files. It can be used for testing packages or other R code with graphical output. It is possible to set the level of fuzzyness when comparing the target and the tested images.

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Imports graphics, grDevices, methods, stats, tools

Suggests png, jpeg, bmp, testthat

RoxygenNote 5.0.1

Repository <https://predictiveecology.r-universe.dev>

RemoteUrl <https://github.com/MangoTheCat/visualTest>

RemoteRef HEAD

RemoteSha 9b835a707479a9162ca50f108308a5d814bbc923

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compareWithFingerprint

Compare a test fingerprint with a known fingerprint

Description

Compare a test fingerprint with a known fingerprint

Usage

```
compareWithFingerprint(test, fingerprint, threshold = 0.001, exact = FALSE)
```

Arguments

test	fingerprint
fingerprint	fingerprint
threshold	single numeric similarity parameter, for the original algorithm it defaults to 1e-3. For the dct method it is the number bits allowed to be different in the fingerprint (i.e. Hamming distance).
exact	single logical should fingerprints match exactly (default FALSE)

Value

single logical

Examples

```
compareWithFingerprint(test = 1:3, fingerprint = 1:3)
compareWithFingerprint(test = 1:3, fingerprint = 1:4)
compareWithFingerprint(test = 1:3, fingerprint = 1:3 + 1e-3)
compareWithFingerprint(test = 1:3, fingerprint = c(1, 2, 3.1))
compareWithFingerprint(
  test = 1:3,
  fingerprint = c(1, 2, 3.1),
  exact = TRUE
)
```

getFingerprint

Get Image Fingerprint

Description

Get a fingerprint of an image, that does not depend on the fine details of the image. The fingerprint can be used to compare images generated on different machines, platforms, etc. It supports PNG, JPG and BMP images currently.

Usage

```
getFingerprint(file, algorithm = c("dct", "original"))
```

Arguments

file	single character naming PNG, JPG or BMP file from which to get fingerprint. It can also be a gzip compressed file with extension .gz.
algorithm	fingerprint algorithm. Possible values: original, dct. See details below.

Details

It implements two algorithms. The default algorithm uses a Discrete Cosine Transform (DCT). It first resizes both images into 64x64 size to speed up further calculations. Then it calculates the DCT of both images, takes the top-left 8x8 cells of the DCT, and calculate the difference to the median DCT for both. The result is a 64-bit string represented as a hexadecimal string. The algorithm is similar to and inspired by phash (<http://www.phash.org/>) and imagehash (<https://github.com/jenssegers/imagehash>).

The original algorithm calculates the Fast Discrete Fourier Transform of both images, column-wise. Then it takes the imaginary parts of the results, sums them up rowwise, and checks when the sums switch sign.

Examples

```
getFingerprint(  
  system.file(package = "visualTest", "compare", "stest-00.jpg.gz")  
)
```

isSimilar

Is this Graphic a Match to this Fingerprint?

Description

A function to check similarity between plots. By default, fingerprint comparison is very fuzzy, and the fuzziness can be controlled by argument threshold (see [compareWithFingerprint](#)). Fingerprint exact matching can be selected with argument exact. Note that similar looking images may have the same fingerprint (see [getFingerprint](#)).

Usage

```
isSimilar(file, fingerprint, threshold = 0.001, exact = FALSE, ...)
```

Arguments

file	single character naming PNG or JPG file from which to get fingerprint
fingerprint	fingerprint, or filename. Character scalars without a dot in them and numeric vectors are taken as fingerprints.
threshold	single numeric similarity parameter (default 1e-3)
exact	single logical should fingerprints match exactly (default FALSE). Note that for the original algorithm, this is not equivalent to using a zero threshold.
...	additional arguments

Examples

```

rdata <- matrix(rnorm(200), ncol = 2)

## To create the images in a temporary directory
tmp <- function(path) file.path(tempdir(), path)

png(tmp("test1.png"))
plot(rdata)
dev.off()

fing1 <- getFingerprint(file = tmp("test1.png"))
rdata[2, 2] <- 0.1
png(tmp("test2.png"))
plot(rdata)
dev.off()

isSimilar(file = tmp("test2.png"), fingerprint = fing1)
isSimilar(file = tmp("test2.png"), fingerprint = fing1, threshold = 0.05)

png(tmp("test3.png"))
plot(rdata, col = 3)
dev.off()

isSimilar(file = tmp("test3.png"), fingerprint = fing1)
isSimilar(file = tmp("test3.png"), fingerprint = fing1, threshold = 0.05)

rdata2 <- matrix(rnorm(200), ncol = 2)
png(tmp("test4.png"))
plot(rdata2)
dev.off()

isSimilar(file = tmp("test4.png"), fingerprint = fing1)
isSimilar(file = tmp("test4.png"), fingerprint = fing1, threshold = 5)

png(tmp("test5.png"))
hist(rdata2)
dev.off()

isSimilar(file = tmp("test5.png"), fingerprint = fing1)
isSimilar(file = tmp("test5.png"), fingerprint = fing1, threshold = 5e6)

```

showFingerprint	<i>Plot some fingerprints against each other This currently only works for fingerprints from the 'original' algorithm.</i>
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Description

Plot some fingerprints against each other This currently only works for fingerprints from the 'original' algorithm.

Usage

```
showFingerprint(..., algorithm = "original")
```

Arguments

...	files to test
algorithm	The algorithm to use, see getFingerprint . Currently only the 'original' algorithm works.

Value

list of fingerprint(s) invisibly.

Examples

```
sf <- system.file(package = "visualTest")
eg <- "VR-616_plot-lm00.jpg.gz"
showFingerprint(
  file.path(sf, "compare", "windows", eg),
  file.path(sf, "compare", "unix", eg)
)
```

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