

Package ‘ringscale’

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Description Implementation of the “Ringscale” method as proposed in the student research project “DETECTION OF FAINT COMPANIONS AROUND YOUNG STARS IN SPECKLE PATTERNS OF VLT/NACO CUBE MODE IMAGES BY MEANS OF POST-PROCESSING” at the Friedrich-Schiller-University of Jena.

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Description

Implementation of the “Ringscale” method as proposed in the student research project “DETECTION OF FAINT COMPANIONS AROUND YOUNG STARS IN SPECKLE PATTERNS OF VLT/NACO CUBE MODE IMAGES BY MEANS OF POST-PROCESSING” at the Friedrich-Schiller-University of Jena.

Usage

```
analyze(filenamees = character(0),
result.filename = paste(format(Sys.time(),
"%Y-%m-%d-%H%M%S"), ".RData", sep = ""),
evaluate = TRUE,
header.skip = FALSE)
evaluate(filename = character(0), support.min = 0.5)
```

Arguments

filenamees	Filenamees of the FITS files to be analyzed.
result.filename	Filename of the result of analyze().
evaluate	If TRUE, evaluate() is called for the appropriate file just after the analysis finished.
header.skip	If TRUE, the FITS-header will not be read out at the beginning of the analysis. You may try this if you encounter performance problems or if you know that your header contains no information which is needed by Ringscale (such as telescope diameter, wavelength et cetera). You will have to enter these by hand then.
filename	Filename of the result of analyze() to be evaluated.
support.min	Minimum support value for which candidates are listed and marked in evaluate().

Details

The **ringscale** package basically provides two “public” functions: analyze() and evaluate().

analyze() applies the “Ringscale” method as proposed in the paper of the student research project on FITS files. Note, that these FITS files do not necessarily have to be pre-processed, so raw VLT/NACO images are applicable as input. If analyze() is called without parameters, a **tcltk**-dialog will open and let the user select the input files. Otherwise, the filenamees of the processed FITS files have to be given as character vector, including the entire path (see examples). The results of the analysis are saved in the file result.filename. This allows to have a look at the results at a later time again very quickly, as the analysis itself may take some time. If evaluate = TRUE, evaluate() is called for the appropriate file just after the analysis finished.

The `evaluate()` function evaluates the results provided by `analyze()`. Therefore, the input consists of only one file, the result of `analyze()`. The filename can be given as parameter. If omitted, a `tcltk`-dialog will let the user select it just like for `analyze()`. `evaluate()` shows the found companions in a hypothesis-map, where the possible companions are marked with circles according to their rank and support value (the lower the rank, the bigger the radius and the bigger the support, the bigger the line width of the circles). Additionally, a list of all found candidates is returned. `evaluate()` only records hypotheses which at least have a support value of `support.min` to prevent false positive detections.

Author(s)

Daniel Haase

References

Haase, Daniel (2009): *Detection of Faint Companions around Young Stars in Speckle Patterns of VLT/NACO Cube Mode Images by Means of Post-Processing*. Student research project, Friedrich-Schiller-University of Jena.

<http://ringscale.haase-zm.de>

Examples

```
# if analyze() is called without parameters,
# a dialog will let you select the FITS files;
# the result is saved in the working directory
# with a filename composed of the current time,
# as for instance "2009-07-30-134037.RData":
## Not run: analyze()

# the filename of the result can be changed by:
## Not run: analyze(result.filename = "/home/daniel/results/myResult.dat")

# the filenames of the FITS files may also be
# given as character vector; in this case, no
# dialog will appear:
## Not run: fn <- list.files("/var/fits", pattern = "\.[fF][iI][tT][sS]$")
## Not run: analyze(filename = fn)

# this also applies for the evaluation; if called without
# parameters, a dialog will appear:
## Not run: evaluate()

# otherwise, use
## Not run: evaluate(filename = "/home/daniel/results/myResult.dat")

# the candidate list returned by evaluate() can be viewed by
## Not run: candidates <- evaluate()
## Not run: print(candidates)
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