Package ‘peakROTS’

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Type Package

Title ROTS procedure for optimized ChIP-seq peak detection.

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Suggests R (>= 2.5.1)

Description ROTS procedure for ChIP-seq peak detection allows user to optimize parameters of common peak detection applications (MACS, PeakSeq).

License GPL (>= 3)

URL `http://www.nic.funet.fi/pub/sci/molbio/peakROTS/`

R topics documented:

`peakROTS-package` *ROTS procedure for optimized ChIP-seq peak detection*

Description

ROTS procedure for ChIP-seq peak detection allows user to optimize parameters of common peak detection applications (MACS, PeakSeq). Large optimization tasks can require significant computational resources. Therefore the package supports parallel processing either in a single node or multiple nodes (batch processing).

Details

Package:	peakROTS
Type:	Package
Version:	1.0
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License:	GPL (>= 3)

The workflow required is computationally heavy, so it cannot be run by a single function call. Start by initialising the workflow with `initialise`, then call `run` to start the actual jobs. Depending on the size of the workflow and available computational resources running time can be substantial. After the workflow is finished results can be viewed from the working directory (set in `path.work` parameter of function `initialise`), from subdirectory `results`.

Author(s)

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References

Laura L Elo, Aleksi Kallio, Teemu D Laajala, R David Hawkins, Eija Korpelainen & Tero Aittokallio. Optimized detection of transcription factor binding sites in ChIP-seq experiments. Submitted manuscript.

peakROTS web site at: http://www.nic.funet.fi/pub/sci/molbio/peakROTS/

`do.run.local` *Implements local running of jobs*

Description

Implements support for running peakROTS jobs locally, as processes in a single host. Is given as an argument to function `run`. User never calls this function directly.

Arguments

`job.command`	Job command, passed by peakROTS workflow system
`job.name`	Job name, passed by peakROTS workflow system
`log.file`	Log file, passed by peakROTS workflow system

Author(s)

Aleksi Kallio

`do.run.lsf` *Implements batch execution of jobs (LSF)*

Description

Implements support for running peakROTS jobs in a LSF batch processing system. Is given as an argument to function `run`. User never calls this function directly.

Arguments

`job.command`	Job command, passed by peakROTS workflow system
`job.name`	Job name, passed by peakROTS workflow system
`log.file`	Log file, passed by peakROTS workflow system
`max.run.time`	Maximum running time. Default is `24:00`.

Author(s)

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`initialise` *Initialises peakROTS workflow*

Description

Initialises peakROTS workflow. Based on the given parameters, this function creates the runtime directory structure, workflow description and the settings file. Workflow description contains all jobs with their dependencies. The settings file contains all information needed to run the workflow.

Arguments

`detector`	Peak detection applications, currently supported values are `MACS` and `PeakSeq`. Default is `MACS`.
`data.path`	Path to input data files. Is required.
`treatment.file`	Name of the treatment input file. Is required.
`control.file`	Name of the control input file. Is required.
`path.work`	Path to working directory for storing all runtime information and results. Default is `work`.
`path.bootstrap`	Path to bootstrap sample directory. Default is `<path.work>/bootstrap`.
`do.bootstrap`	If true, bootstrap samples are generated, otherwise existing samples are used from `path.bootstrap`. Is required.
`r.command`	The R executable to use. The R environment must have this library installed. Default is `R`.
`environment.initialiser`	Shell command that is run before peak detection applications: place platform specific initialisation code here. Default is empty.

`bootstrap.count`
: Number of individual bootstrap samples. Default is 100.

`pvalue` P-value cutoff for peak detection (MACS).

`shiftsize` List of shiftsizes for peak detection (MACS).

`tsize` List of tsizes for peak detection (MACS)

`bw` List of bw's for peak detection (MACS)

`nolambda` List of values of nolambda parameter for peak detection (MACS)

`mfold` List of mfold values for peak detection (MACS)

`gsize` List of gsize values for peak detection (MACS)

`READLENGTH` List of readlengths for peak detection (PeakSeq)

`WSIZE` List of window sizes for peak detection (PeakSeq)

`WPERC` List of WPERC values for peak detection (PeakSeq)

`MAXGAP` List of MAXGAP values for peak detection (PeakSeq)

`map.file` Mappability file for peak detection (PeakSeq)

`MAXCHR.defined`
MAXCHR for peak detection (PeakSeq)

`preprocess.address`
PeakSeq preprocessing tool binary path (PeakSeq)

`peakseq.address`
PeakSeq binary path (PeakSeq)

Author(s)

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`run` *Runs a previously initialised peakROTS workflow*

Description

Runs (starts or resumes) a peakROTS workflow that has been initialised by a call to function `initialise`. Actual implementation depends on the `do.run` function that is passed. This function can be interrupted and it will continue when called for the next time.

Arguments

`path.work` Path to peakROTS workflow, i.e., working directory

`do.run` The function that is called for each job to actually run it

`polling.timeout.seconds`
How often this function polls running jobs for state changes

`jobs.running.max`
Maximum number of simultaneous jobs

`verbosity` Level of verbosity for this function. Possible values are 0, 1, 2 and 3.

Details

State of the workflow (i.e., states of the individual jobs) is kept on disk. This function can be interrupted and called again later, as it resumes the state from the disk. However there should be only one instance of this function running against the same workflow at the same time. `do.run` function can be changed between calls to this function.

Author(s)

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