

dCheckParallel

July 22, 2015

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| dCheckParallel | <i>Function to check whether parallel computing should be used and how</i> |
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Description

dCheckParallel is used to check whether parallel computing should be used and how

Usage

```
dCheckParallel(multicores = NULL, verbose = T)
```

Arguments

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| multicores | an integer to specify how many cores will be registered as the multicore parallel backend to the 'foreach' package. If NULL, it will use a half of cores available in a user's computer |
| verbose | logical to indicate whether the messages will be displayed in the screen. By default, it sets to true for display |

Value

TRUE for using parallel computing; FALSE otherwise

Note

Whether parallel computation with multicores is used is system-specific (now only Linux or Mac OS). Also, it will depend on whether these two packages "foreach" and "doMC" have been installed. It can be installed via: `source("http://bioconductor.org/biocLite.R"); biocLite(c("foreach", "doMC"))`.

See Also

[dRWR](#), [dRWRcontact](#), [dRWRpipeline](#), [dDAGtermSim](#), [dDAGgeneSim](#)

Examples

```
dCheckParallel(multicores=2)
```