# **dCheckParallel**

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

# **Description**

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

# Usage

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

# **Arguments**

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)