

# dCheckParallel

March 27, 2017

---

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

---

## 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. Also, it will depend on whether these two packages "foreach" and "doParallel" have been installed. It can be installed via:  
`source("http://bioconductor.org/biocLite.R"); biocLite(c("foreach","doParallel"))`.

## See Also

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

## Examples

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