

## Installing R/qtl-related packages

It would be useful to install Rstudio on top of R. This is an intuitive platform to run R. To learn more, visit <http://www.rstudio.com> .

Install R/qtl, a package to visualize and analyze QTL data in a variety of inbred experimental crosses. Learn more at <http://www.rqtl.org> .

```
install.packages("qtl")
```

Install R/qtlhot, a package to find and analyze hotspots for multiple traits, and to perform causal pairs (CMST) tests. View vignettes to learn more. [Full hotspot analysis with permutations is time-consuming, and best done using distributed computing, such as <http://research.cs.wisc.edu/htcondor/> . This is only partly explained in vignettes at this point, and in documents in the parallel folder of the package.] R/qtlhot depends on packages qtl,lattice,corpcor,mnormt.

```
install.packages("qtlhot")
vignette("qtlhot", "qtlhot")
vignette("cmst", "qtlhot")
```

Install R/qtlnet, a package to infer small causal networks. It depends on some CRAN and some Bioconductor packages (qtl,graph,RBGL,pcalg,sem,igraph). [Computations for networks larger than 5 nodes probably require distributed computing. See parallel folder or contact the author.]

```
source("http://bioconductor.org/biocLite.R")
biocLite("graph")
biocLite("RBGL")
biocLite("pcalg")
install.packages("qtlnet")
```

Another package of interest is R/qtlyeast, which is available at <http://github.org/byandell/qtlyeast> . This has the Brem and Kruglyak yeast data set, and includes examples running R/qtlhot analyses.

If on Windows, you will first need to install Rtools from <http://cran.r-project.org/bin/windows/Rtools>. This is an executable that will install some applications in `c:\Rtools`. You will also need pdflatex, which means you need a TeX distribution such as MikTeX or TeX Live.

```
install.packages(devtools)
library(devtools)
install_github("qtlyeast", "byandell")
vignette("yeast_cmst", "qtlyeast")
```