HTSCluster **package instructions**

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HTSCluster is a package to perform co-expression analyses of RNA-seq data. The package implements a novel statistical method based on a Poisson mixture model, performs parameter estimation using an expectation-maximization algorithm, and performs model selection using the slope heuristics approach.

The full User's Guide for *HTSCluster* may be found by installing the *HTSCluster* package and loading it into an R session via `library(HTSCluster)`. In R for Windows, the User's Guide is then available from the drop-down menu called "Vignettes". In other operating systems, type

```
> library(HTSCluster)
> HTSClusterUsersGuide()
```

at the R prompt to open the User's Guide in a pdf viewer.