# How to write a HowTo

One of the goals of the Bioconductor project is to produce (and encourage others to produce) documentation on how to perform various tasks. Our main interest is in tasks associated with computational biology. However, we hope to produce HowTo documents for a wide variety of tasks.

R has a very good mechanism for documenting individual functions, methods and classes. However, there are many situations where the task that we want to perform requires the use of many components. In other cases we would like to document the overall purpose of an R package rather than the individual functions. In this document we provide some advice on how to construct a document to describe how to perform a task.

In most cases HowTo's will be written using `Sweave` in the *tools* package. In this document we give some general advice on how to write a HowTo. Of courese there is no *right* way to do this but we feel that we can provide a few design principles that will help authors write better HowTo's.

These design principles are listed below:

- It should be short (2 pages at most) and explicit.

- It should be about a single topic.

- It should contain runnable code and rely on data that are available in R or the libraries needed to carry out the task being documented.

- HowTo's should not be about single functions. The function documentation is the right place to document that. HowTo's should document a process or task and will typically involve several functions.

- To paraphrase Paul Halmos, you should imagine that you are writing a document for a friend who is as smart and has the same general level of knowledge as you but who does not know how to do the specific task at hand.

- Make use of the indexing system. The title of the document should be included in the `% \VignetteIndexEntry`. It should contain the word `HowTo` to easily allow for programmatic manipulation and sorting of the HowTo's.

# 1 Session Information

The version number of R and packages loaded for generating the vignette were:

```
R version 2.3.0, 2005-11-06, x86_64-unknown-linux-gnu
```

```
attached base packages:
```

```
[1] "tools"     "methods"   "stats"     "graphics"  "grDevices" "utils"
[7] "datasets"  "base"

other attached packages:
Biobase
"1.9.2"
```