

# The **microman** package vignette

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## 1 Using **dplyr** and **stringr**

A major change in this version of this package is the use of generic data structures in R instead of creating new data types. This makes it possible to use the power of standard data manipulation tools and visualization that R-users are familiar with.

Compared to previous versions you will find that some functions have been moved to the **microseq** package, upon which this package depends.

You will also find fewer plotting functions and no `casestudy-document`. However, if you locate the GitHub site for this package, you find a tutorial with code for how to make similar plots using **ggplot**. This is an example of using generic R tools instead of making functions for each special case.

## 2 External software

Some functions in this package calls upons external software that must be available on the system. Some of these are 'installed' by simply downloading a binary executable that you put somewhere proper on your computer. To make such programs visible to R, you typically need to update your `PATH` environment variable, to specify where these executables are located. Try it out, and use google for help!

### 2.1 Software **blast+**

The function `blastpAllAll` uses the free software **blast+** (<ftp://ftp.ncbi.nlm.nih.gov/blast/executables/blast+/L>). Source code and installers makes it straightforward to install. In the R console the command

```
> system("blastp -h")
```

should produce some sensible output.

### 2.2 Software **hmmer**

The functions `hmmerScan()` uses the free software **hmmer** (<http://hmmer.org/>). This software is developed for UNIX systems (e.g. Mac or Linux), and Windows

users may find it a little difficult to install and run from R. In the R console the command

```
> system("hmmScan -h")
```

should produce some sensible output.