

# The microseq package vignette

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## 1 Introduction

This small package contains some basic functions for handling biological sequence data. We have some other packages that make use of these functions, and thus depend on this package.

## 2 External software

The functions `msalign()`, `muscle()` and `cmalign()` use external softwares to compute multiple sequence alignments.

To use `msalign()` and `muscle()` you need the software MUSCLE installed, see <http://www.drive5.com/muscle>. NOTE: The executable must be named `muscle`, no more and no less (no version numbers etc.).

To use `cmalign()` you need the software Infernal installed, see <http://rfam.xfam.org/>.

These external programs must be available to R, i.e. the `PATH` environment variable must specify their location on the system. If you use RStudio you may also need to include an `.Renvirom` file in you home-directory, but this will depend on the system (we have found it necessary for linux but not for windows).