Installation Instructions for "slimr: An R package for integrating data and tailor-made population genomic simulations over space and time"
Russell Dinnage et al

To install the version of `slimr` that was used to run all examples in the manuscript and the website vignette, you can install `slimr` with the following command:

```
# install.packages("devtools")

devtools::install_github("rdinnager/slimr", ref = "v0.2.1")
```

Development will likely continue on `slimr` in the mean-time, s to try out the latest version just use:

```
devtools::install_github("rdinnager/slimr")
```

Installing SLiM

In order to use `slimr` in anything other than a trivial way you need to install the SLiM simulation software (the engine of `slimr`) on your system, and then link it to `slimr`.
The first thing you may want to try is the `slimr::slim_setup()` function. This will attempt to install SLiM and link it to `slimr` automatically. Unfortunately, due to the vagaries of system setups and cross-platform complexity, it frequently fails to work properly. In this case, you will have to install SLiM yourself.

Luckily, SLiM has excellent documentation for installing it on all the major operating systems. Click on your operating system to be taken to the installation instruction for SLiM tailored to that OS.

1) Windows

2) Linux

3) MacOS

Once SLiM is installed on your computer, linking it up to `slimr` is fairly straightforward. The first thing to try is loading up `slimr` in R and seeing if it can automatically find the executable by running `slimr::slim_is_avail()`. If this returns `TRUE`, then you are good to go. In many cases, `slimr` will be able to find SLiM this way once it is installed.

If this fails, then the first thing you need to do next is locate where the slim executable is. On linux it would be called simply `slim`, on Windows, `slim.exe`. You need to find out which folder on your system it is in. Then, the easiest way to make sure `slimr` can find this executable that will work every time you use `slimr` subsequently, is to set the path to the SLiM executable as an environmental variable in your .Renviron file. If you have the `usethis` package installed you can open this file for editing by running `usethis::edit_r_environ()`. In the file write a line like this:

`SLIM_HOME='path/where/slim/executable/is'`

Make sure it points to the folder where the executable is, not the executable itself. Now save the file and restart your R session. `slimr::slim_is_avail()` should now return `TRUE`.

To temporarily tell `slimr` where SLiM is, you can set the environmental variable with `Sys.setenv(SLIM_HOME='path/where/slim/executable/is')`, which will last until the current session is over. Alternatively, `slim_run()` includes a `slim_path` argument you can use to pass in the path to the executable to an individual run (note in this case it should be the path

to the actual executable file, not the folder it is in). This could be one way to maintain multiple versions of SLiM for use with different scripts.

More information on `slimr` can be found on the extensive package website:

https://rdinnager.github.io/slimr/index.html