A guide to using PeakR

Introduction

PeakR is an R shiny app which is designed to help speed up the processing of electropherogram data from the Applied Biosystems programs PeakScanner and GeneMapper. PeakR is not a finished program yet so certain data files or using it in a certain way may cause the program to crash without warning. Hopefully I can eventually improve PeakR so that it is more robust and usable.

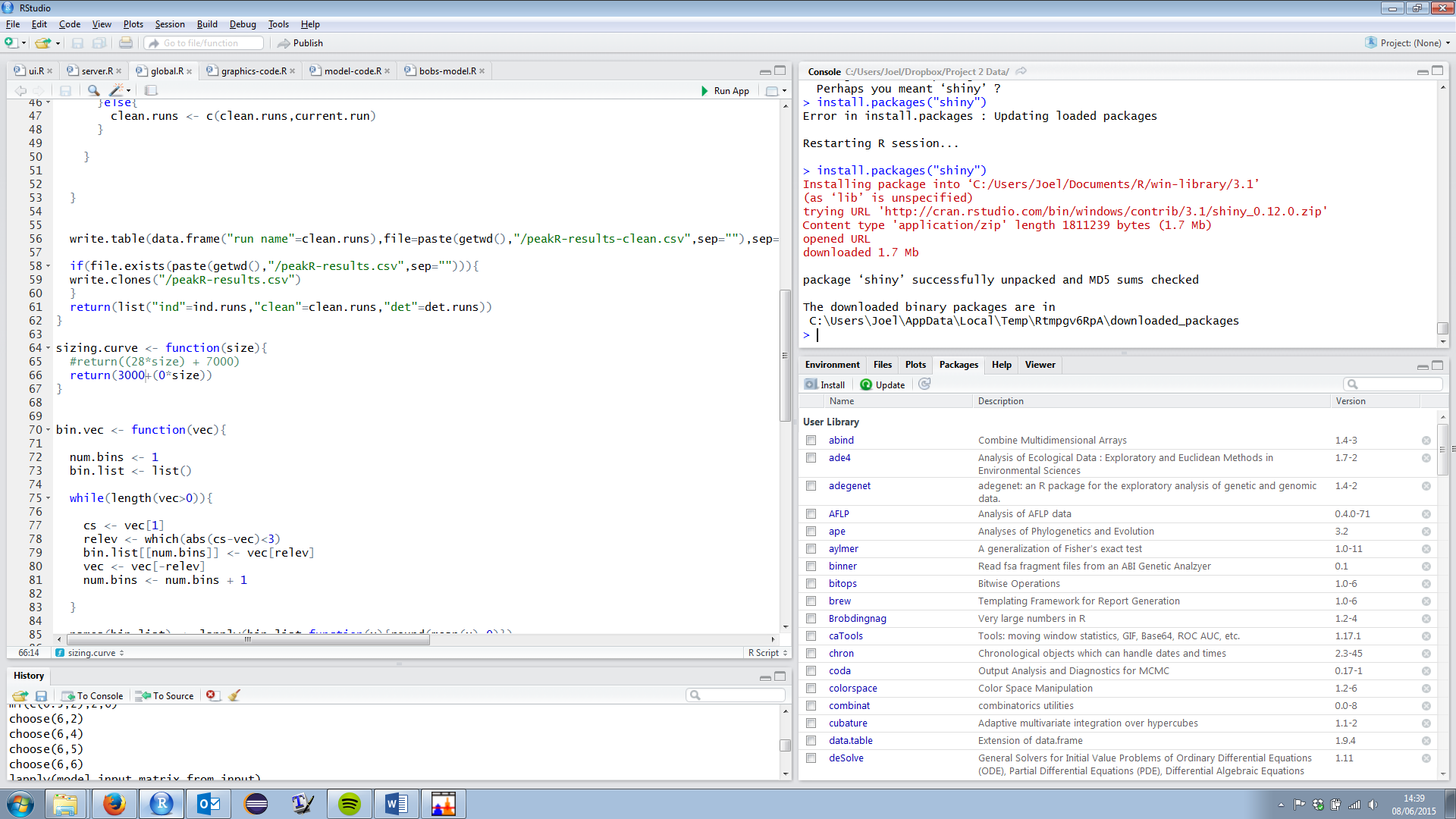
Downloading and installing PeakR

Firstly you will need to have the Applied Biosystems software Peak Scanner installed which is available from here (<http://www.appliedbiosystems.com/absite/us/en/home/support/software-community/free-ab-software.html>). This software will work the raw capillary electrophoresis data and turn it into a data format which PeakR can use.

Next you will need to install R Studio, an integrated development environment for the R statistical software (<http://www.rstudio.com/>). Once R Studio is installed, open it and type the following line into the box called *console*:

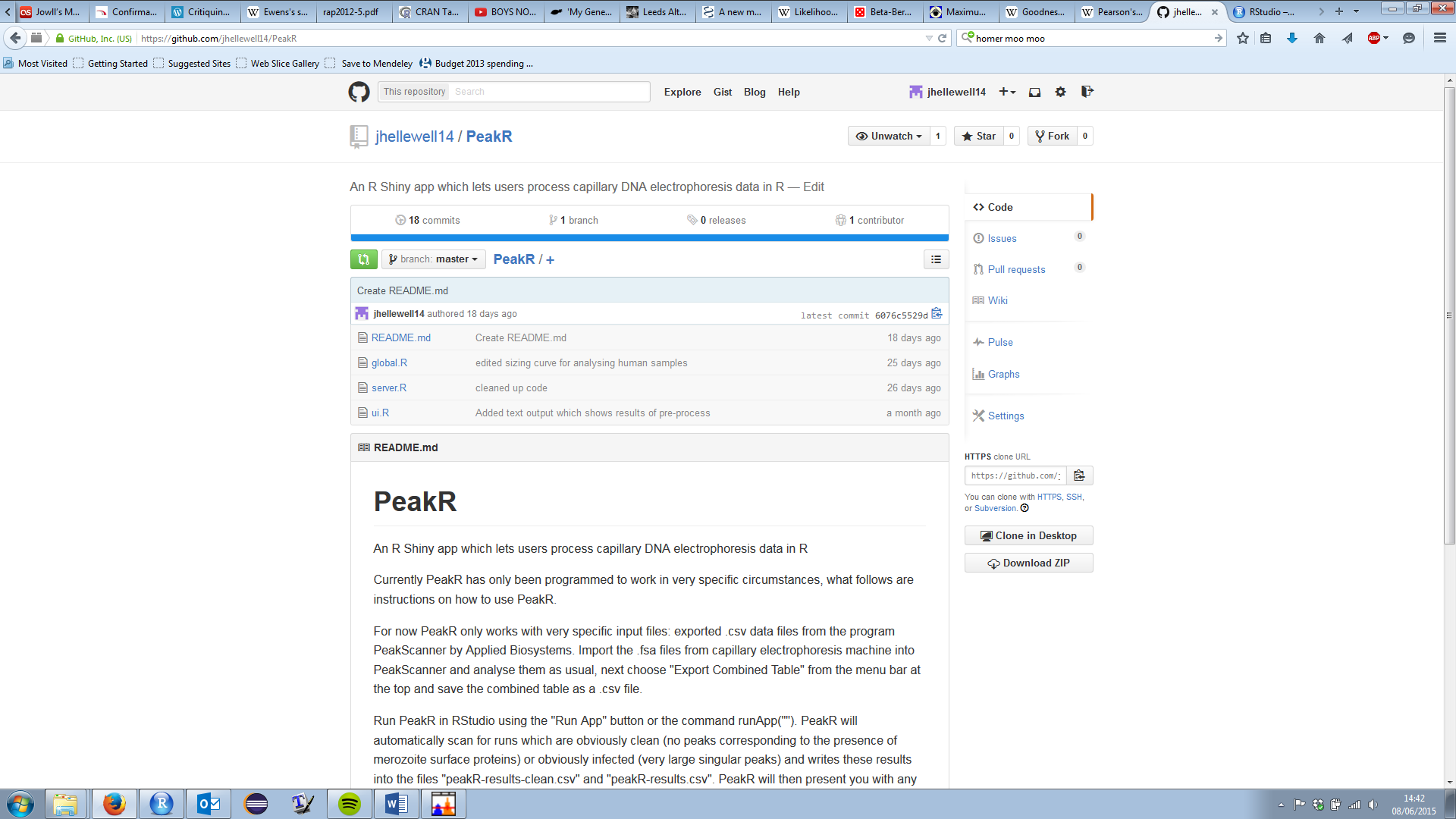
Install.packages(“shiny”)

Some output should appear which should look like this:



The next step before you can begin using PeakR is to download the application files from <https://github.com/jhellewell14/PeakR>

The easiest way to do this is to look for the Download ZIP button on the right hand side of the page. This is shown below in red. Unzip the zip file and put the contents wherever you want to keep them.



Hopefully now PeakR should be ready to use with your data.

Getting data for PeakR to use

In PeakScanner 2 start a new project and add all of the data files that you want to analyse to the project. Set the size standard and analysis method and run the analysis. Once the analysis is complete press the small down arrow next to the Export button at the top and select “Export Combined Table”. Make sure to change the save as type from “Tab Delimited” to “Comma Separated Variables” and save the file wherever you like.

Using PeakR

To run PeakR open R Studio and go to “File” and then “Open File…”, then open either “ui.R” or “server.R” which can be found wherever you saved the files from <https://github.com/jhellewell14/PeakR> earlier. To run PeakR press the “Run App” button which is located here:

