Ligand Optimisation using R

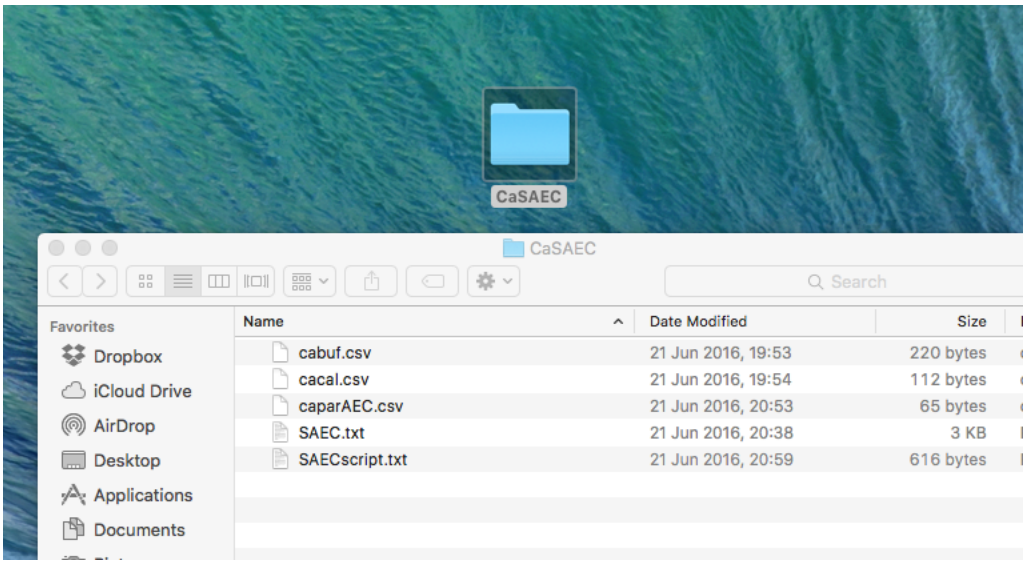
The purpose of these notes is to explain how to apply McGuigan's Ligand Optimisation Method (LOM) using software written in the package R. The software provides an automated version of the latest improved version of LOM which includes McGuigan's[1] modification of the Nicolsky-Eisenman equation.

The R package

The user is required to download and install the free package R from http://cran.r-project.org, if necessary.
Once the user has opened R, running the code involves copying and pasting some commands in a script file into the R window and pressing ENTER, as explained below. It is not necessary for the user to know anything about R itself.

The Data Files

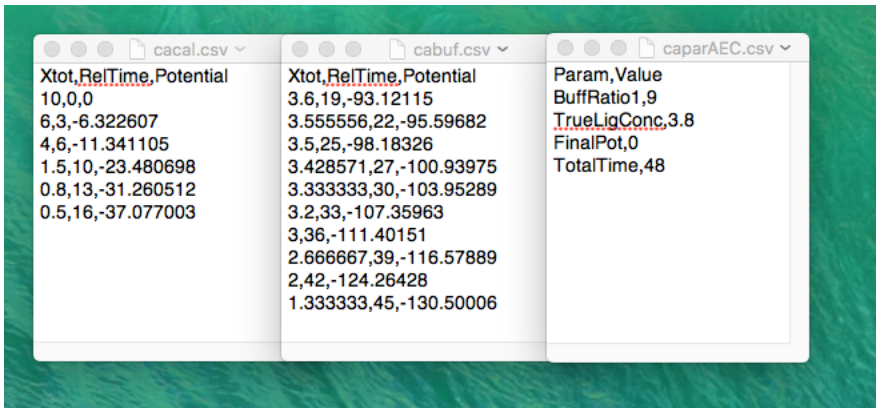
Let's assume that the folder CaSAEC (as sent by email) has been placed on the user's Desktop, as shown below.



The folder CaSAEC contains the five files that are necessary to run the program SAEC on the input data. The three files with .csv extensions contain the input data. The file cacal.csv contains the data obtained using the calibrating solutions. The file cabuf.csv has the data obtained from the buffer solutions. The file caparAEC.csv contains the values of the input parameters.

[1] McGuigan et al., Prog. Biophys. Mol. Biol., 116, 203-2011

Here is a screenshot of the contents of the files

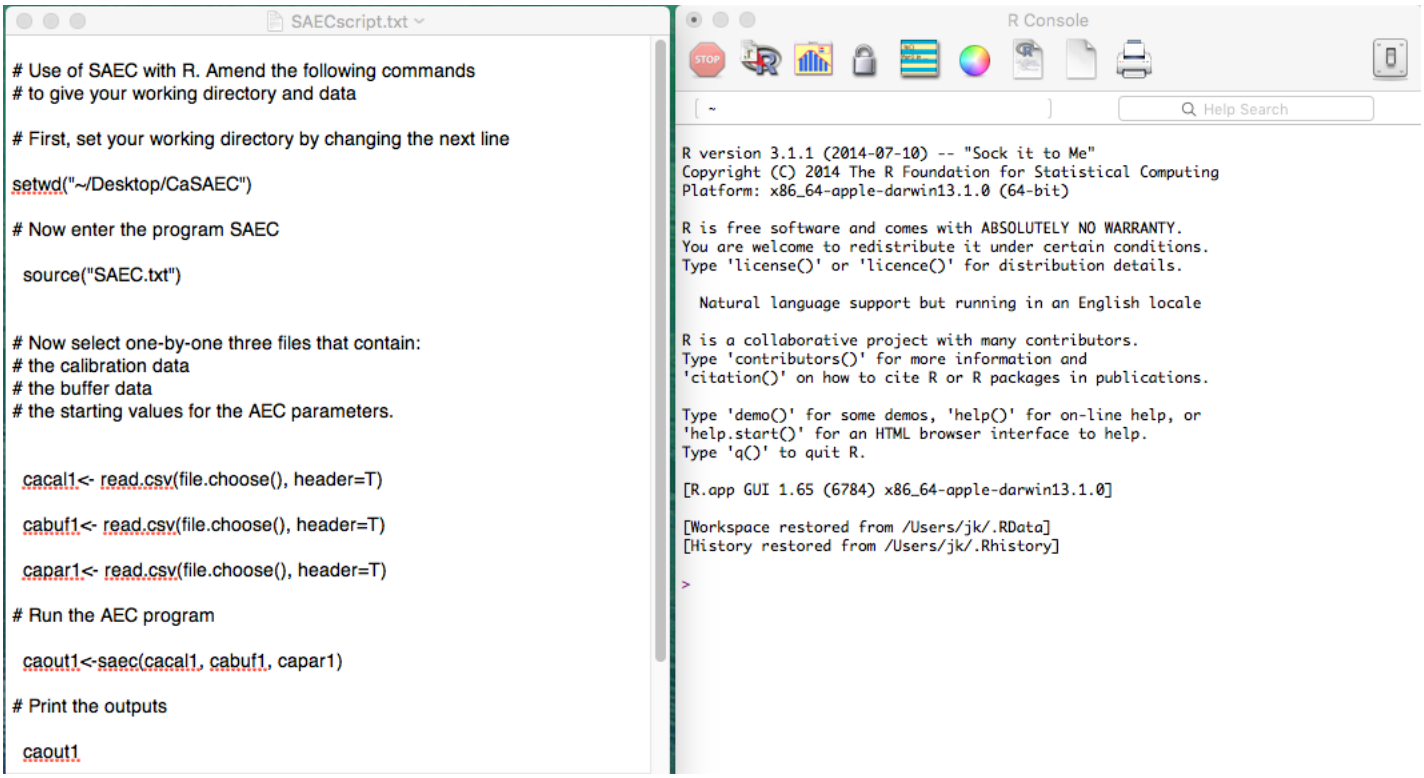


These files are in comma separated value (csv) format. A simple way to make data files in this format is to use Excel and then save the file in csv format. Alternatively, a text editor could be used to place the data in csv format; in each row the entries must be separated by commas rather than white space.

Note that the true ligand concentration is entered from the file caparAEC.csv.

Running the SAEC program

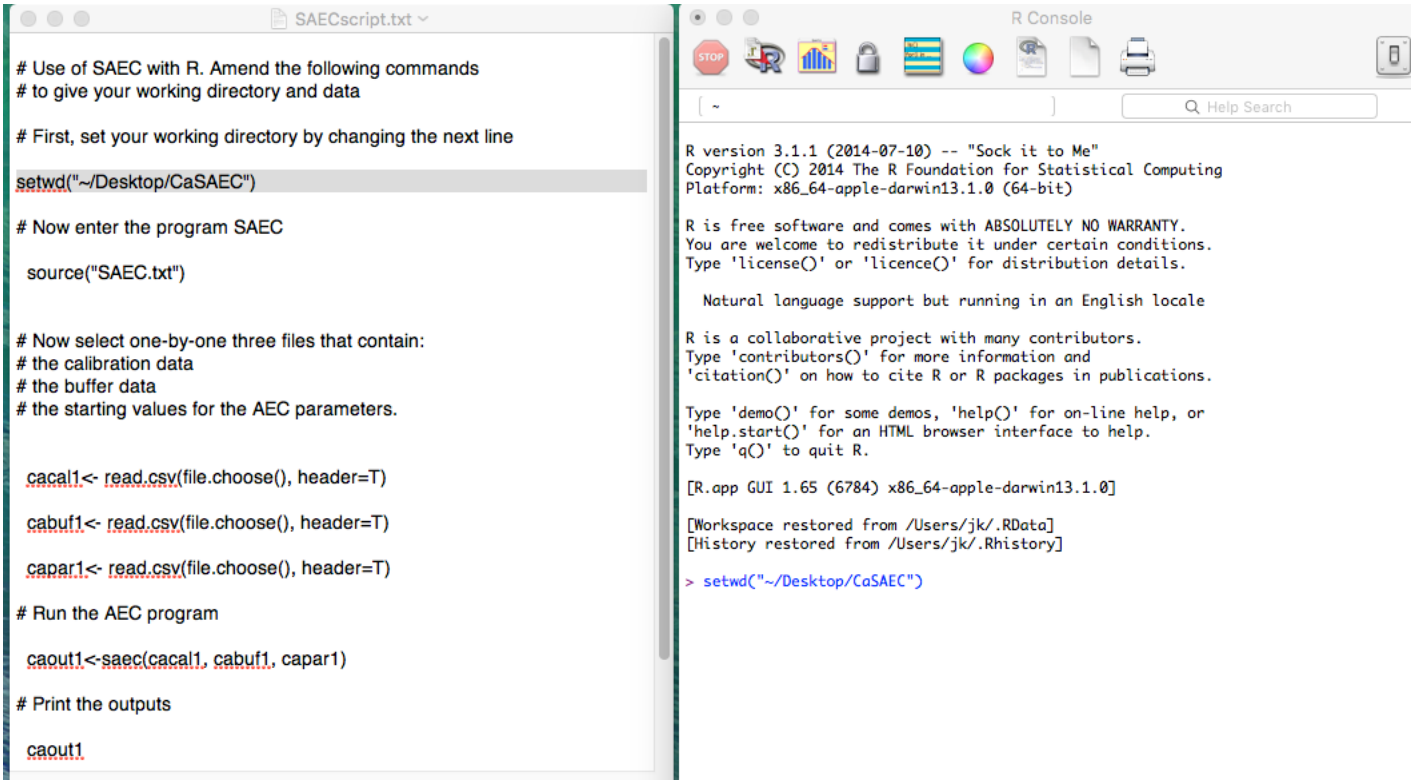
1. Run the application R. This will open a window into which R commands can be entered.
2. Open the file SAECscript.txt. This contains the the required R commands. The lines beginning with # are comment lines are are ignored by the R interpreter. Now, both windows will be open on the desktop, as shown below.



3. Set the working directory to tell R where the data files are; output will also be sent to this folder. For this illustration it has been assumed that the files are in a folder named CaSAEC and this is placed on the Desktop. The user can place the files in a folder with a name of their choosing and place the folder anywhere in their Documents folder; if so, the setwd( ) command needs editing.

   NB. The form of the folder name given here is suitable for a Mac, but in Windows the slashes would be different.

   Select setwd("~/Desktop/CaSAEC") and copy this to the R window at the command prompt >, and then press ENTER to run this command.

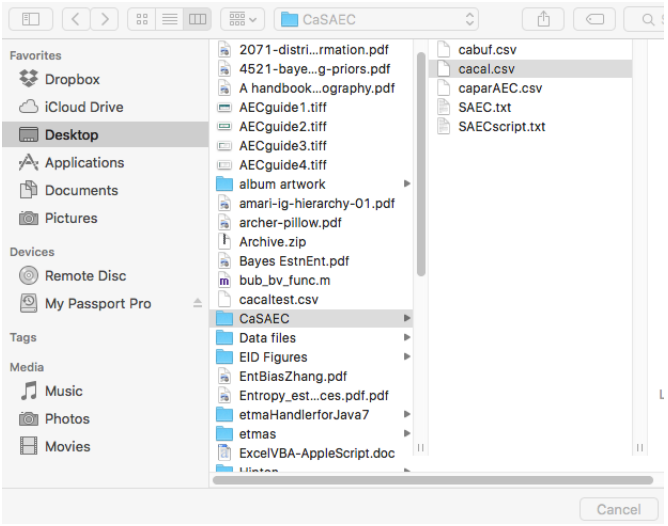


4. Select the line source("SAEC.txt") and copy and paste this into the R window at the command prompt, and then press ENTER to run this command. This loads the program SAEC into R, and this program will be run below once we have entered the data files.

5. Enter the data files one by one. Select the line

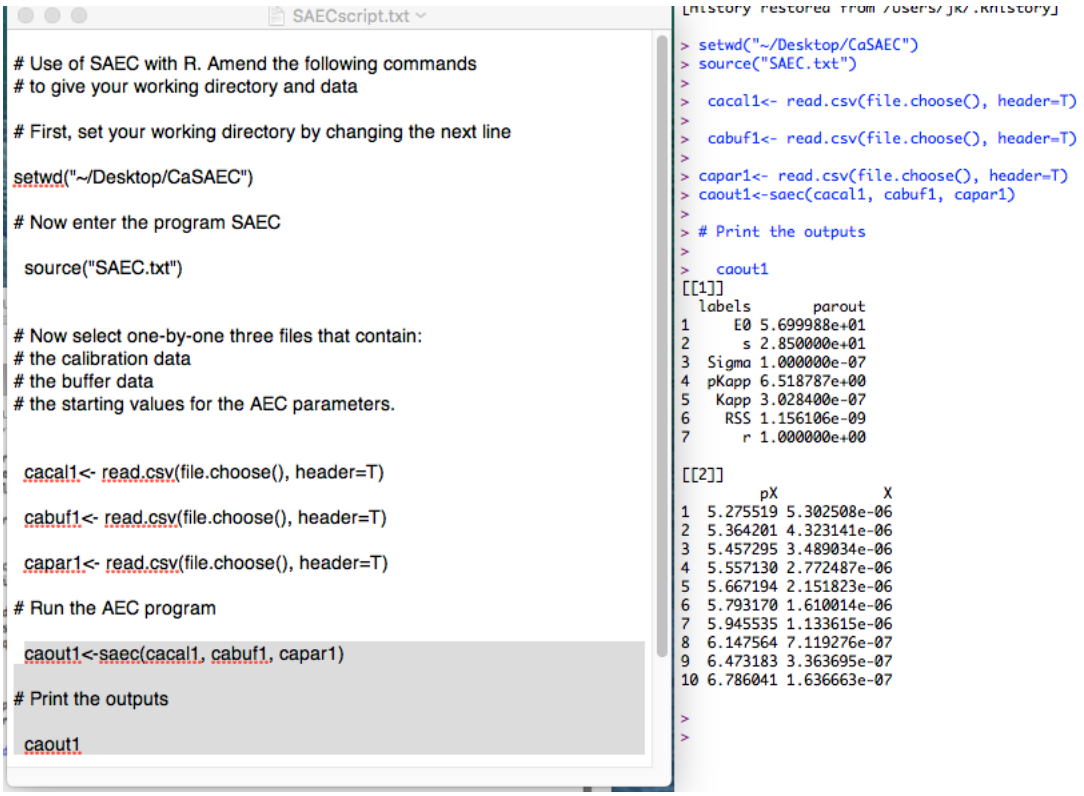
$$\text{cacal1} < - \text{ read.csv(file.choose(), header=T)}$$

   and copy and paste this into the R window at the command prompt; then press ENTER. This command opens a dialogue box and gives the user access to their filesystem. Select Desktop, then CaSAEC and then cacal.csv. Then Click Open. The calibration data will have been entered into R.



6. Repeat step 5 to enter the buffer data (cabuf.csv) and the input parameters (caparAEC.csv) into R.

7. Now the scene has been set and we can run the SAEC program. Select the lines containing caout1, as shown below, and copy and paste them into the R window, and press ENTER. The output will appear in the R window. Also a plot of the fitted model and data will appear in a separate window.



8. The program will have written the output data to the folder CaSAEC, in files with names starting with OUT, as shown below.