

Introduction to VA Analysis R Shiny App

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1 Introduction

2 Background

Check out the vignette for **openVA**.

3 Installing and Starting R Shiny App for Windows 10

3.1 Quick Version

Download the R Shiny zip file at

<https://github.com/jarathomas/openVA-Pipeline/tree/master/RShinyApp/shiny-openVA.zip>

and unzip it – the contents should include two files: (1) shiny-openVA.R (R Shiny script file) and (2) CrossVA_0.9.3.zip (an R package).

1. Install Java (<https://java.com/en/download/>)
2. Download the R executable (with same architecture as Java, e.g., 64-bit) from <https://cran.r-project.org/bin/windows/base/> and double-click the file to install R
3. Start R and install the necessary packages by typing the following in the R Console window at the prompt >

```
install.packages(c("openVA", "shiny", "shinyjs"), dependencies=TRUE)
```


A new window should appear asking the user to select a Secure CRAN mirror, and the installation will begin after clicking the Ok button.

4. Install the CrossVA package (included in the R Shiny zip file) by clicking, in the R menu bar, **Packages > Install package(s) from local files . . .** then select the CrossVA_0.9.3.zip file (you may need to navigate to the folder where the R Shiny zip file was downloaded) and click the open button at the bottom-right of the Select files window.

5. Open the shiny-openVA.R script (included in the R Shiny zip file) through the R menu bar **File > Open Script . . .** then select the shiny-openVA.R script file and click the open button at the bottom-right of the Open script window. This step should open a new R Editor window.
6. Make sure the focus is on the R Editor window (by clicking on it) and run the shiny-openVA.R script through the menu bar **Edit > Run all** which will execute the code (in the R Console) and open your web browser with the R Shiny app.

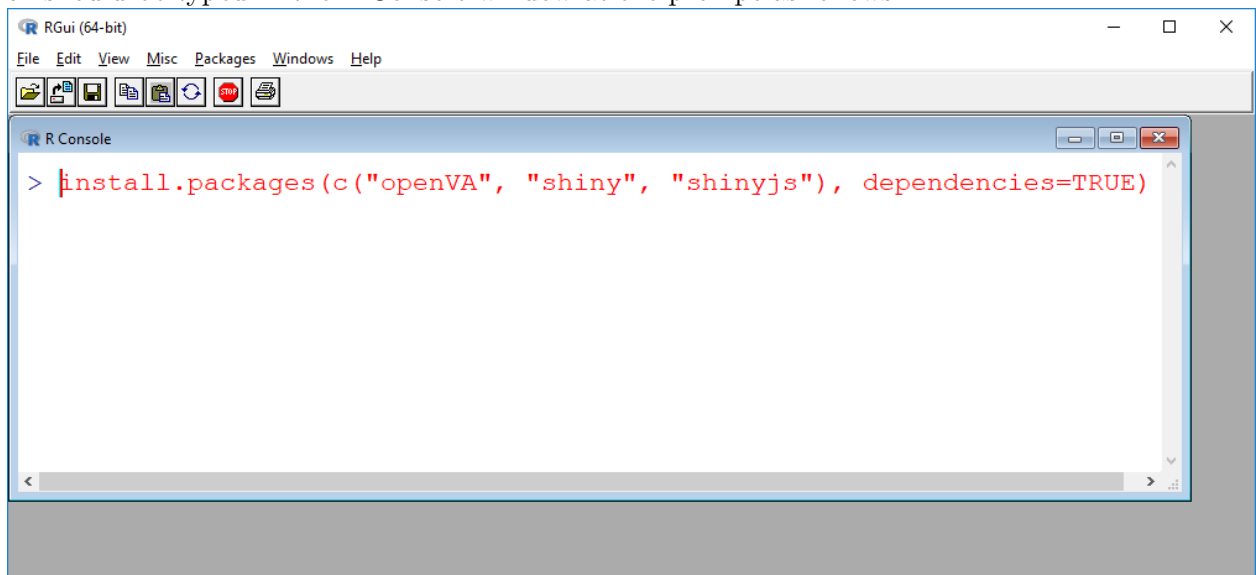
3.2 More Details

The R software is available for download from the Comprehensive R Archive Network (CRAN) <https://cran.r-project.org/bin/windows/base/>. Installation instructions are also available from CRAN, but the process should be familiar: download the executable file (ending in .exe and double-click the file. The R Shiny app uses several packages, one of which requires Java (version 6 or above) to be installed on your computer (<https://java.com/en/download/>). It is not unusual to experience difficulties while trying to configure R to work with Java. For more details about the configuration procedure, see the InSilicoVA manual (<https://github.com/richardli/InSilicoVA/blob/master/Documents/Insilico-manual.pdf>).

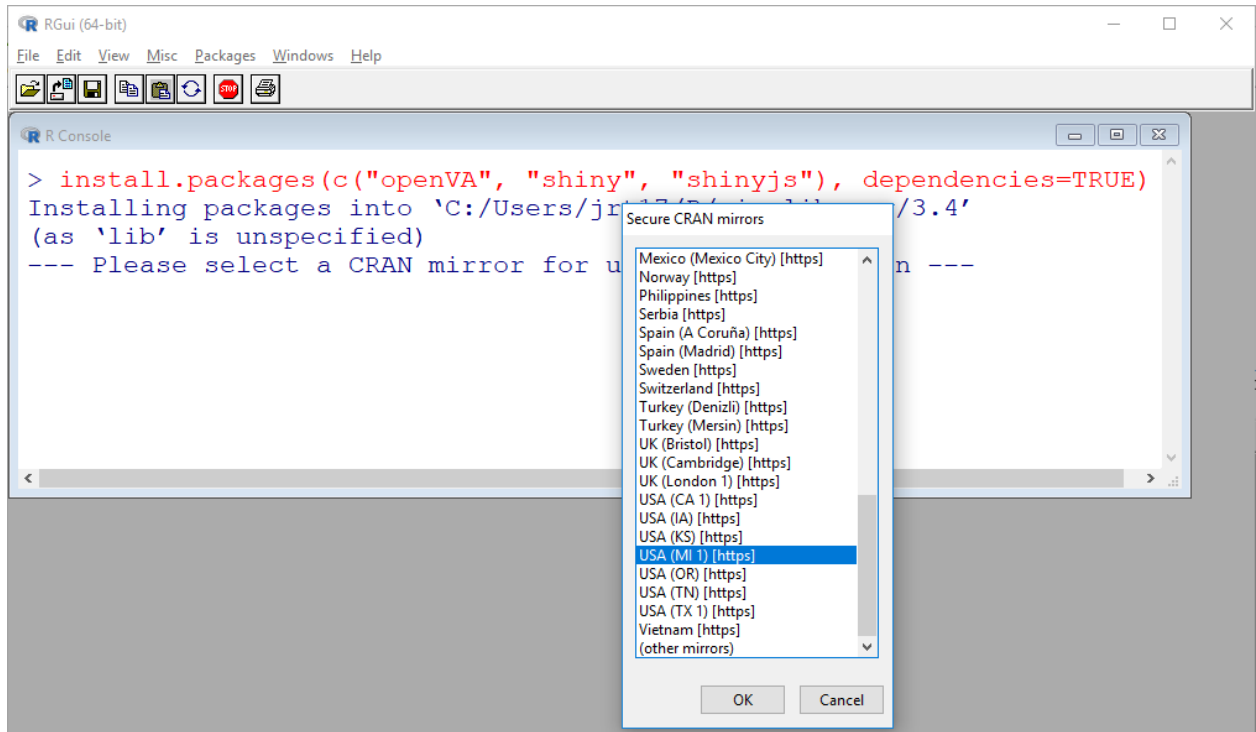
After Java and R have been installed, the next step is to install R packages that contain the tools needed for the Shiny app to run. Start the R Gui by double-clicking the icon  and install the necessary packages with the command

```
install.packages(c("openVA", "shiny", "shinyjs"), dependencies=TRUE)
```

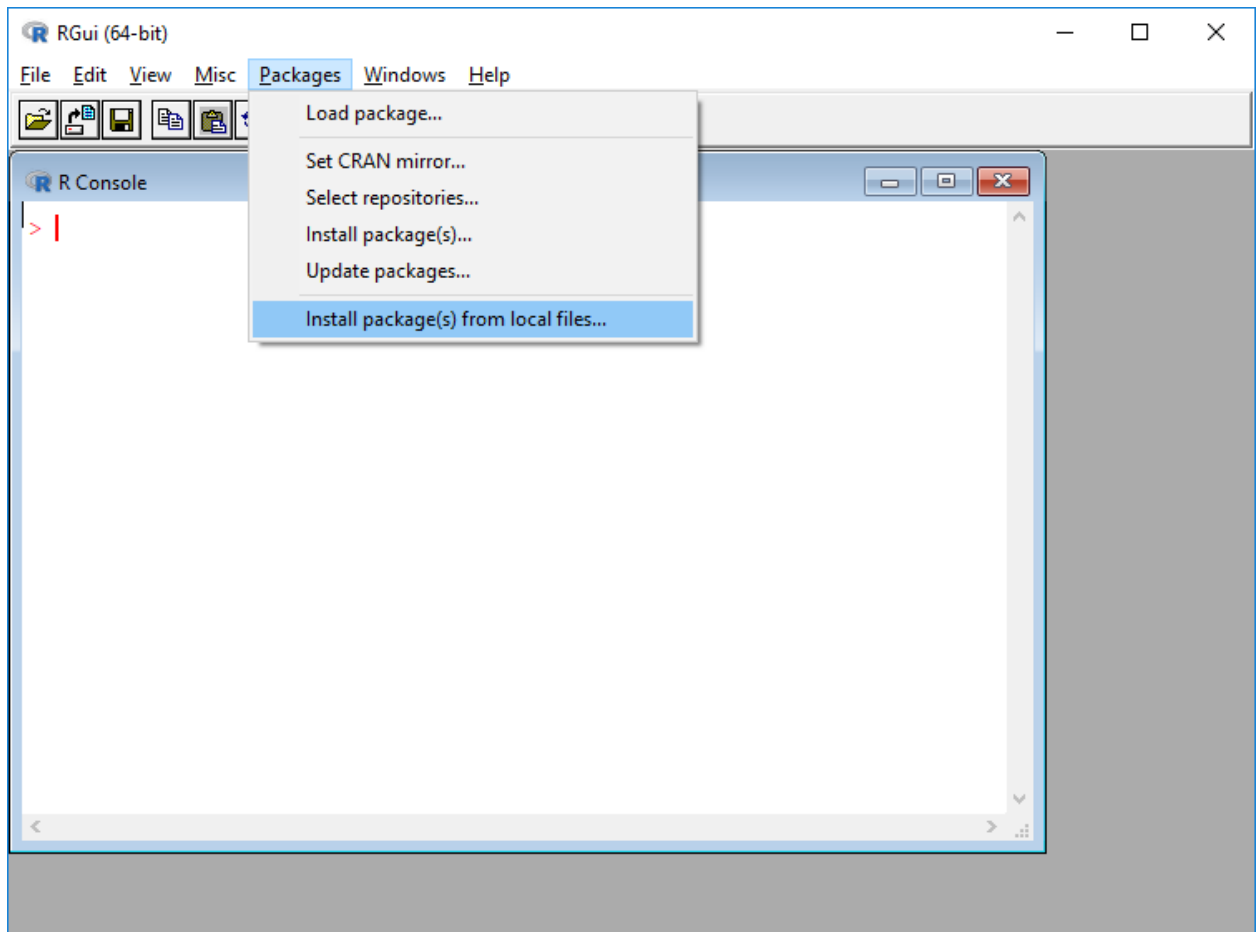
which should be typed in the R Console window at the prompt as follows:



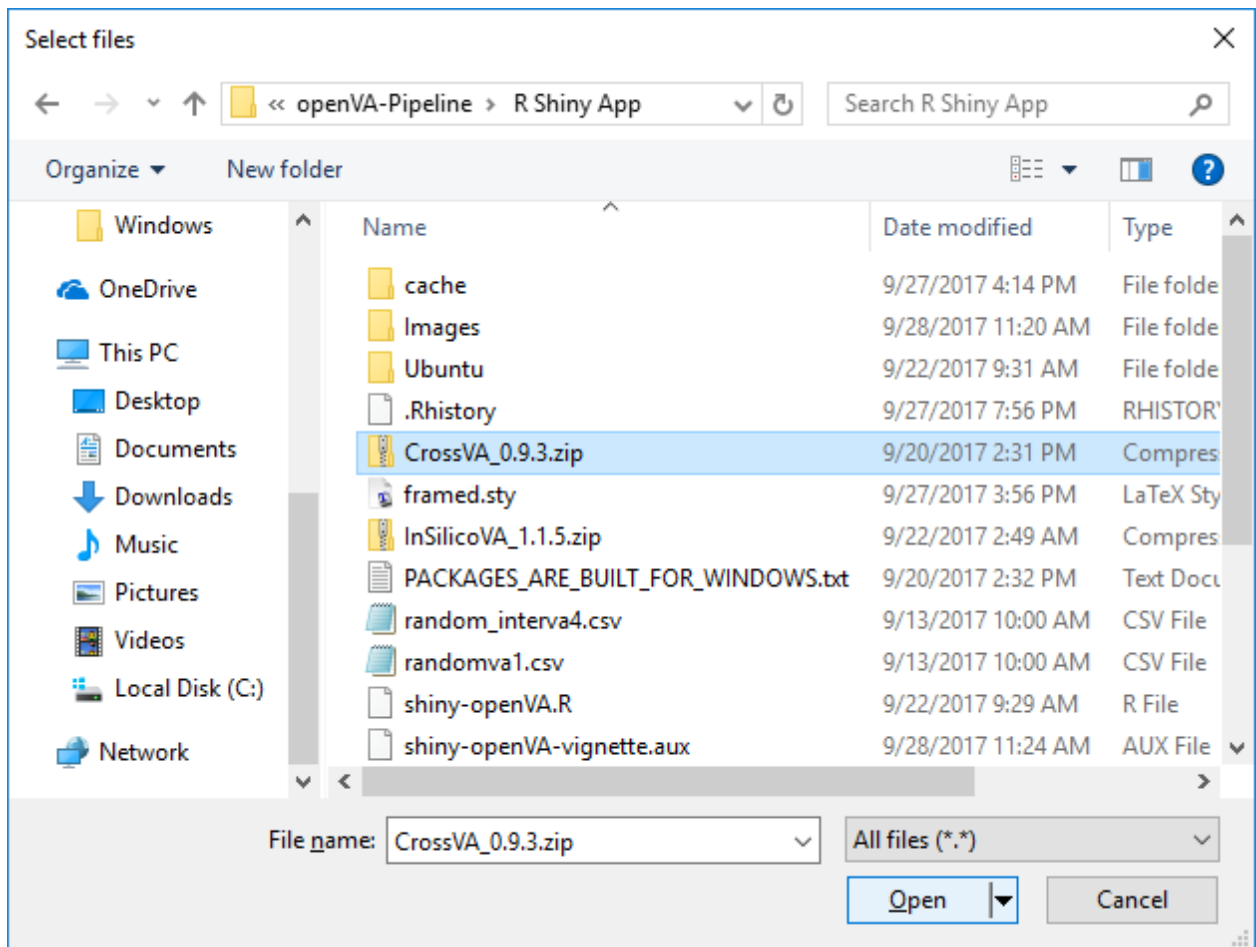
A new window should appear asking the user to select a Secure CRAN mirror (choose a CRAN mirror near your location), and the installation will begin after clicking the Ok button.



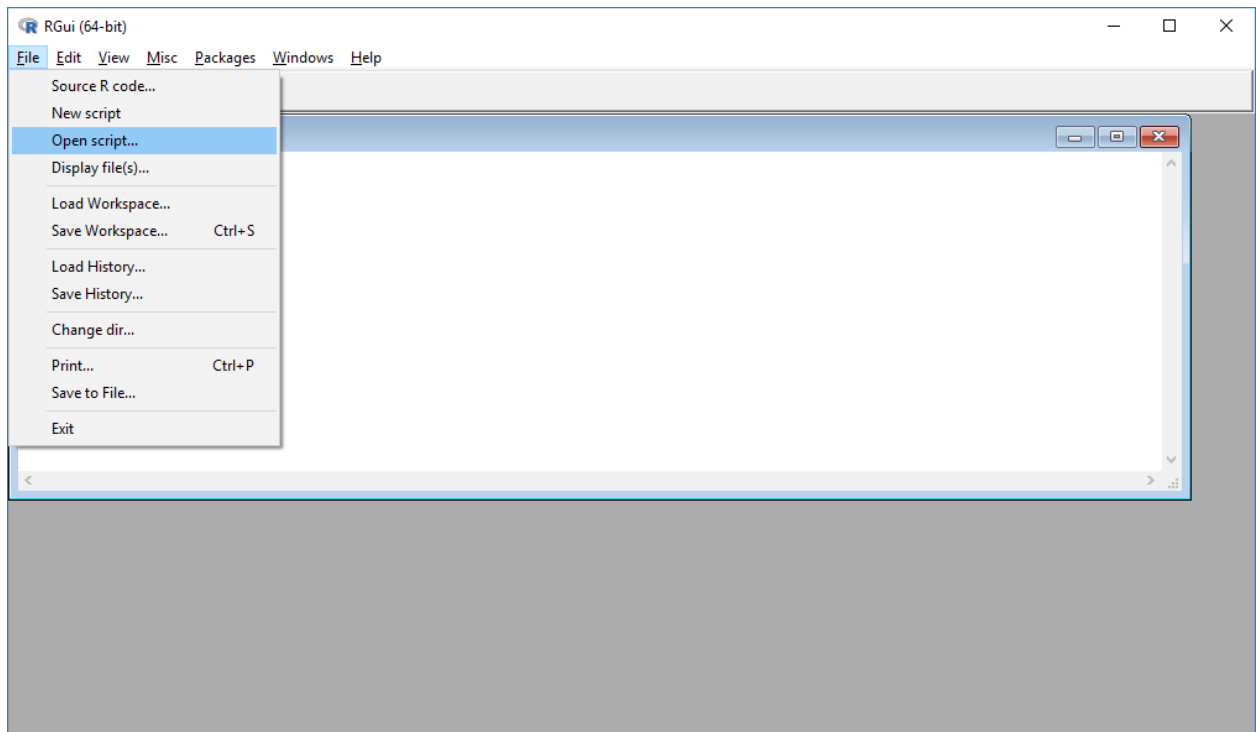
You will see A LOT of text scrolling in the R Console which describes the installation of the numerous packages the Shiny app needs. A modified version of the CrossVA package also needs to be installed with the following three steps: (1) select the R menu bar options **Packages > Install package(s) from local**



(2) select the CrossVA_0.9.3.zip file (you may need to navigate to the folder where the R Shiny zip file was downloaded); and (3) click the open button at the bottom-right of the Select files window.

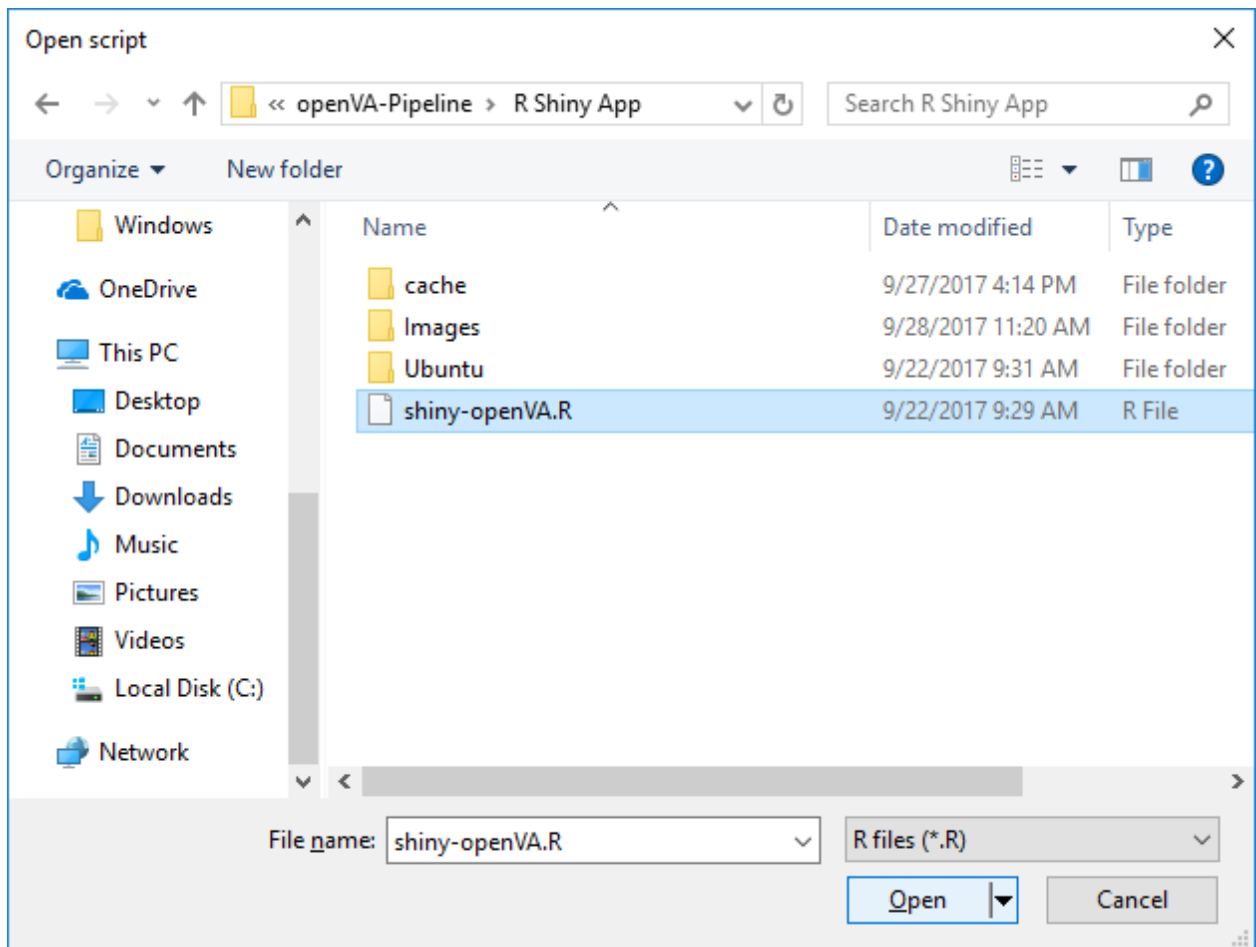


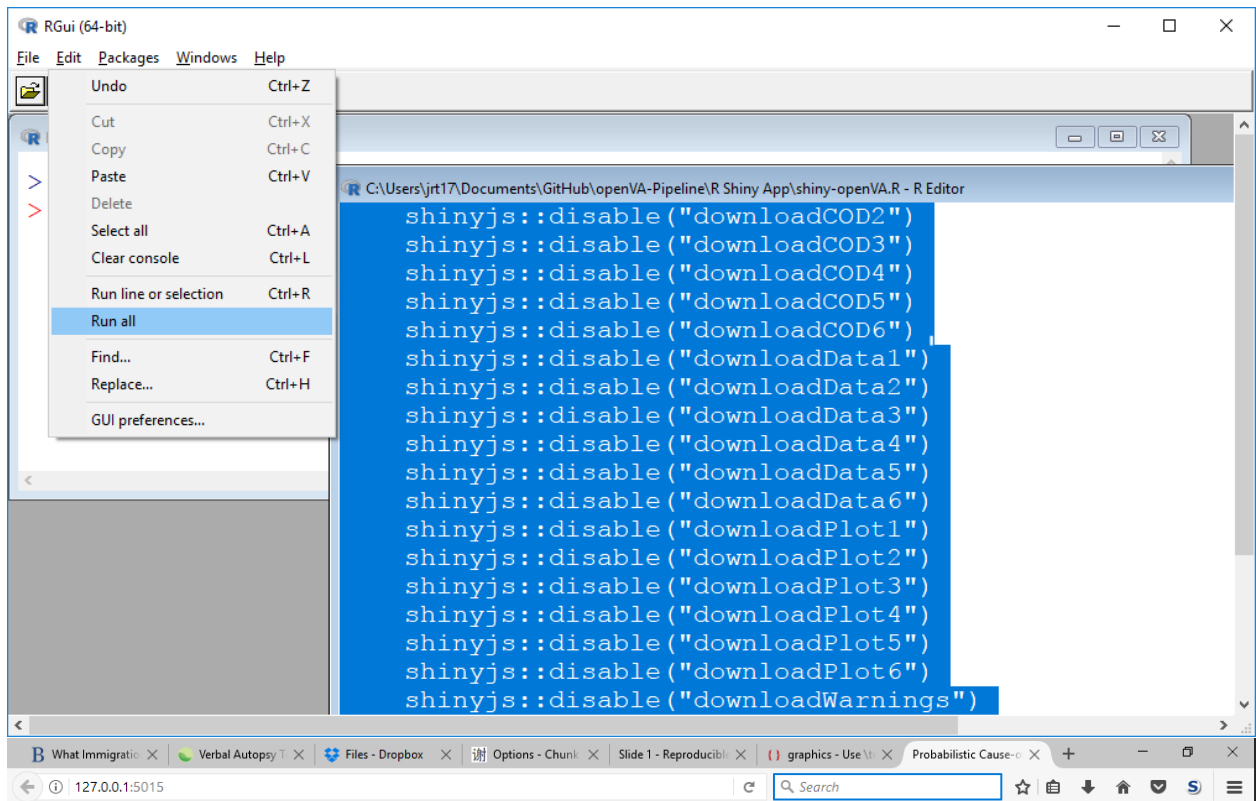
Next open the shiny-openVA.R script (included in the R Shiny zip file) through the R menu bar **File > Open Script...**



then select the shiny-openVA.R script file and click the open button at the bottom-right of the Open script window.

This step should open a new R Editor window. Make sure the focus is on the R Editor window (by clicking on it) and run the shiny-openVA.R script through the menu bar **Edit > Run all** which will execute the code (in the R Console) and open your web browser with the R Shiny app.





Probabilistic Cause-of-death Assignment using Verbal Autopsies

Developed by Tyler McCormick (tylerrmc@uw.edu) Zehang Richard Li (lizhang@uw.edu) and Samuel Clark (work@samclark.net)

The complete study can be viewed [here](#)

Upload your own data here

Browse... No file selected

Choose your preferences

☒ Include an analysis of all records?

☐ Include sex-specific results?

☐ Include age-specific results (infant, child, adult)?

Select Algorithm:

InSilico

Number of iterations in the simulation

300 5,000 7,000

300 970 1,640 2,310 2,980 3,650 4,320 4,990 5,660 6,330 7,000

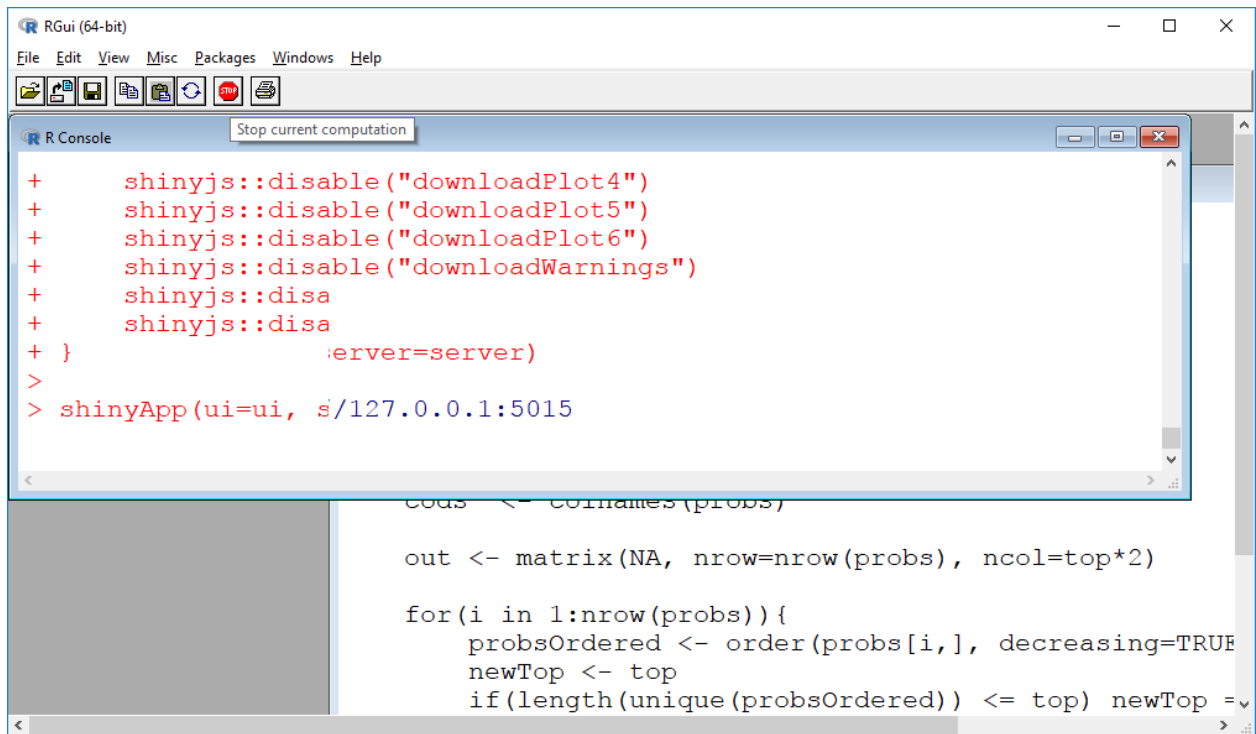
Data Checks

☒ Are the data from an ODKBriefcase export?

Counts of Deaths by Sex & Age
Summary of Results using All Records
CSMF Plot for Total Population

Summary of Results for Males
CSMF Plot for Males

Stop the Shiny app.



The screenshot shows the RGui (64-bit) window. The menu bar includes File, Edit, View, Misc, Packages, Windows, and Help. Below the menu bar is a toolbar with icons for opening, saving, running, and other functions. The R Console window is open, displaying the following R code:

```
+ shinyjs::disable("downloadPlot4")
+ shinyjs::disable("downloadPlot5")
+ shinyjs::disable("downloadPlot6")
+ shinyjs::disable("downloadWarnings")
+ shinyjs::disa
+ shinyjs::disa
+ }
+ }
>
> shinyApp(ui=ui, s/127.0.0.1:5015
```

The console also shows a "Stop current computation" button. Below the console, there is a preview area showing a snippet of R code:

```
cols <- colnames(probs)

out <- matrix(NA, nrow=nrow(probs), ncol=top*2)

for(i in 1:nrow(probs)){
  probsOrdered <- order(probs[i,], decreasing=TRUE
  newTop <- top
  if(length(unique(probsOrdered)) <= top) newTop =
```

4 Using the R Shiny App

4.1 InSilicoVA

4.2 InterVA