

PROAST as an R package QUICK START

First, install the required software (R), and then install the PROAST package in R (see Annex A). Once you have installed and loaded the PROAST package, you might consider mimicking the demo exercise below.

The two modes of PROAST (within R)

There are two modes by which PROAST operates:

- the (original) MENU version, where you can answer multiple choice questions to indicate what you want to do;
- the GUI (graphical user interface) version, which is driven by clicking in windows. Currently, the GUI supports the core of the PROAST software, which applies to most standard analyses (more specific options of the PROAST software will be implemented later in the GUI version).

You can start the GUI version by typing (if you get error messages go to the ANNEX)

```
g.proast()
```

The first time you do this, PROAST will automatically download and install some required R packages. This may take some time.

The MENU version is driven by

```
f.proast(filename)
```

where *filename* is the name of a datafile. For instance, when you type

```
data(das1)
```

then the example dataset *das1* is made available. After that you can type

```
f.proast(das1)
```

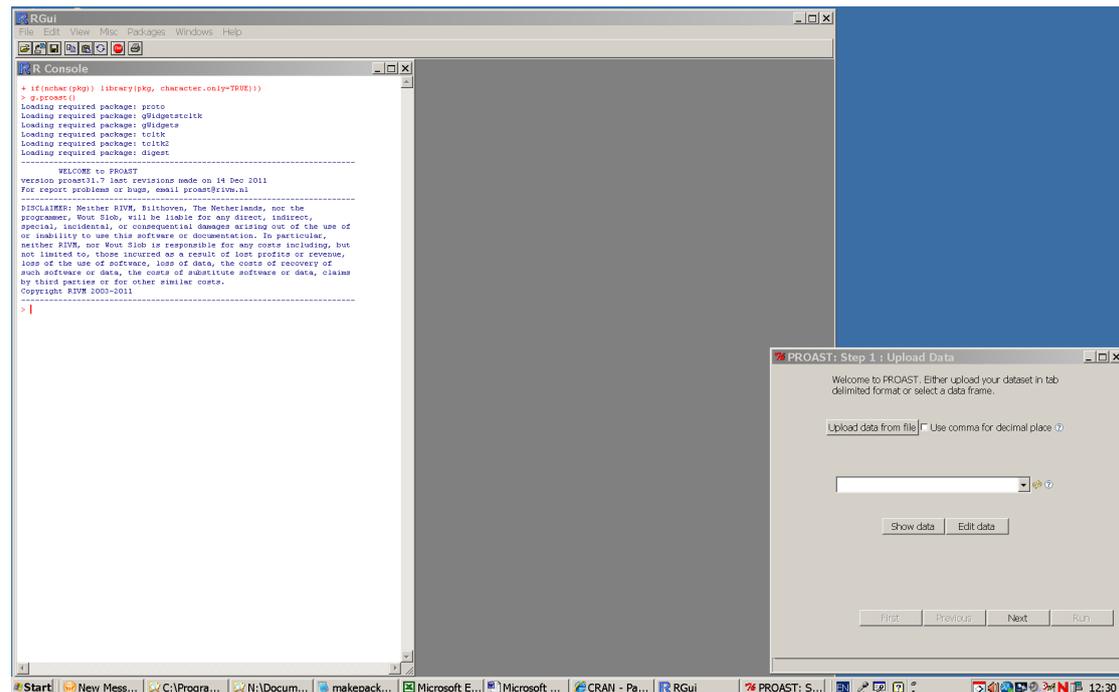
to start an analysis of the data in *das1*.

Demo exercise of the GUI version of PROAST

- make sure you have loaded the PROAST package
- type `g.proast()` in the R console window (if you have not already done that).

Before proceeding, make sure that the R window is not at full size, but covers about two-third of the width of your screen (and all of its height). Next, resize the Console window such that it covers the left 50% of the R window (to leave room for the plots). Move the PROAST GUI to the lower right corner of your screen. See illustration below.

Note that it might be necessary to re-scale the windows when the plots are made. The important thing is that the console window, the graphical window and the GUI window are visible all the time.



You will be guided through five consecutive PROAST windows, indicated as step 1 to step 5. You can find the data in the folder PROAST exercises (which can be downloaded from the web page).

PROAST: step 1: upload data

Click on “Upload data from file”

Browse to the folder PROASTxx.x, then go to the folder “exercises GUI version” and select the dataset “BBP.male.txt”.

Click on “Show data” to see the data.

Click on “next”

PROAST: step 2: specify dose column

In the scroll window select “dose” (already done in this case)

Click on next

PROAST: step 3: specify response columns

Tick on “data on groups of animals, continuous response”

After “Response:” select “foetal_w_mn”

Click on next

PROAST: Step 4: Specify response additional info

After “Dispersion measure:” select “SD”

Tick on “SD”

After “Group size” select “n”

Click on next

PROAST: step 5: Specify covariates

Click on next ('no covariate')

PROAST: step 6: specify BMR/CES and run

The default value for the BMR is 5% (for continuous data), but you might want to change it in specific cases.

Click on "run"

ATTENTION: The calculations do not immediately start: this is related to a technical problem in the R software, which we have reported to the R project team. As a temporary solution you need to answer the question in the Console window to press any key.

The calculations are now started; wait until you see the message that the analysis is finished. Note that R gives 'buffered' output, i.e. it waits until all calculations are finished before showing the output. It may be needed to click in the window before the output is shown. To avoid this, click on *Misc* in the main bar of the R GUI, and uncheck *buffered output*.

PROAST has now produced a graphical window, with the selected Exponential model in the left panel and the selected Hill model in the right panel.

Further, in the Console window you will see the message:

The lowest BMDL and highest BMDU from exponential and Hill models are:
477 and 572

where the two values 477 and 572 may be regarded as a confidence interval¹ for the BMD (at the specified BMR, in this case a 5% decrease in fetal weight).

Quick demo of the MENU version of PROAST

See the document "PROAST MANUAL menu version.docx" for some demos of example datasets.

How to proceed

If you are interested in learning more about the PROAST software, you may proceed as follows.

- Read all the preliminary sections in PROAST MANUAL GUI version.docx), for some basic information on R.
- For the GUI- version, you may continue with the PROAST MANUAL GUI version. For the MENU-version, see the PROAST MANUAL menu version.

¹ Strictly speaking, the confidence level of this confidence interval is higher than the nominal level, by taking the extremes of the two models. Further, it may be noted that in PROAST the default nominal confidence level for the BMD confidence interval is always 90% (two-sided).

ANNEX A. Installation of required software

- The R software needs to be installed on your computer (free download from www.cran.r-project.org).
 - Note 1: if you are asked to select a cran mirror, simply select one near to you. A cran mirror is a public server from where you can download files.
 - Note 2: when you do not have administrator rights on your computer, the installation may fail. In that case you may try installing again and, in the window "Select Installation Location", browse to a folder where you have writing rights (e.g., My Documents) on the hard disk of your computer. A memory stick is also possible, but it will make working in R slower.
- The PROAST package needs to be installed within R. *Make sure you are online*. After opening R, click on "packages", next on "Install package(s) from local zip files" (see Fig. 1). Browse to the folder where you have stored the PROAST package, and click on it. Note that the PROAST package comes as a zip file, and should **not** be unzipped. (Mac users should install `proastXX.X.tgz`).
- The GUI version of PROAST needs some auxiliary packages. These can be installed by copying the following line into the Console window of R:
> `install.packages(c('assertive', 'gWidgetstcltk', 'hwriter'))`
- Alternatively, you could install these packages one-by-one by clicking on Install package(s) in the R window (see Fig. 1)
- Note that installing these packages may take a couple of minutes, depending on your computer.
- Now, load the PROAST package, by clicking on "packages" and then "Load package".
- Finally, check if your installation was successful by typing
> `g.proast()`
in the Console window.

If you have problems with installing PROAST:

It might occur that you get error messages when trying to install or load PROAST, due to problems with the automatic installation of auxiliary packages, specifically related to your computer system. Read the error message, and determine the (first) package mentioned that could not be found. Then, click on "Install package(s)" (see Fig. 1), and you will get the list of all available R packages. Find the packages you are missing (e.g. "assertive"), and click on it. It will now be installed from the R website.

Note: If you get an error message related to `assertive`, you probably have an earlier version of `assertive` installed in your R library. You may solve this as follows. First type
> `remove.packages("assertive")`
and then re-install it:
> `install.packages("assertive")`

The PROAST package has a version number, so that you could reproduce results from earlier versions. It is recommended to always use the latest version, however, and only use earlier versions in specific circumstances (see Annex 2 for how to switch between versions).

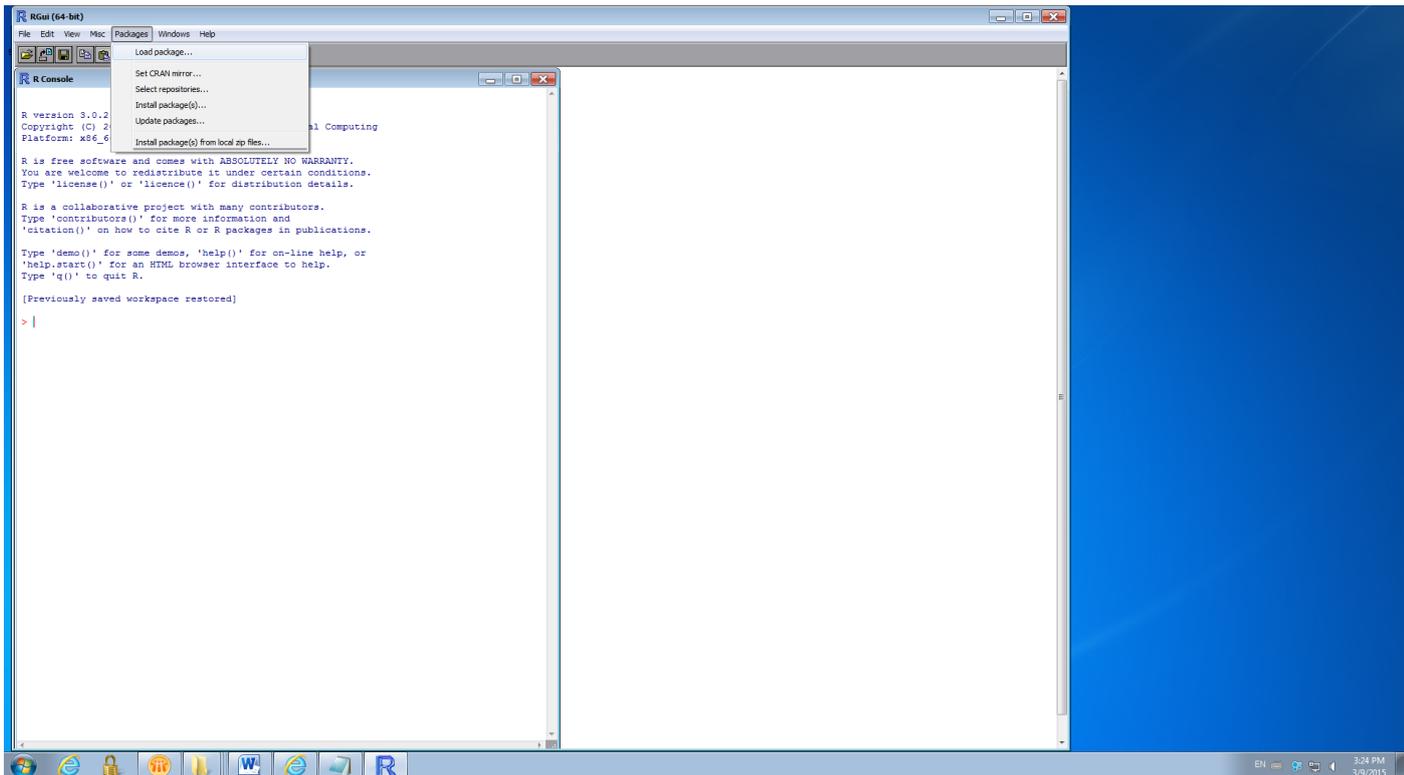


Fig. 1. The preferred setting of the R windows, and installing packages. The PROAST package can be installed by clicking on “Install package(s) from local zip files...” in the scroll down menu under “packages”. If necessary, auxiliary packages can be installed by clicking on “Install package(s)...”.

ANNEX B. Working in R

When working in R, you are working in an environment that can only be read by R. This is called the Workspace. The Workspace can be saved as a file that contains the data to be used and all the results created during an R session. Once you have save a Workspace, you can re-open it (double click on it) to continue the analyses starting from the point where you saved it. When you have various projects, you can create various Workspaces, to prevent confusion and keep oversight of your data and associated results. An R-Workspace has the extension .Rdata, actually the default name is just .Rdata.

An R-Workspace can be regarded as analogous to a Word document, which you first create, then you save it, and next you may re-open it to continue working on it. Just like the content of a Word document can only be read by opening it in Word, the content of an R-Workspace can only be read by opening it in R.

The following steps are recommended when you want to create a new R workspace:

1. *Define Working directory.* The Working directory is an existing or newly created folder that contains the relevant data (related to some defined problem or project). The use of different folders is just to make it easier for you to find back a specific dataset or analysis at a later point in time. The datasets need to have a specific format, as will be described below.

2. *Open R*. Open the R-GUI by double clicking on the R icon on your desktop (or in the start menu of your computer). In the upper left corner of the R-GUI click on “file”, and next on “Change dir ...”. Browse to the folder (the working directory) with the relevant data and click “OK”.

3. *Create Workspace*. In the R Console window type:

```
> getwd()
```

which means: get Working Directory. (Note that the first > is the prompt already present in the Console window). You should now see the path of the Working Directory that you selected in step 2. When you type

```
> dir()
```

you will see the files in your current Working Directory. When you type

```
> ls()
```

you will see the content of the current R Workspace (when you have not yet done anything it will be empty).

To illustrate how the R-Workspace stores new results, do the following simple exercise. In the Console window (see Fig. 1) type

```
> aa <- 5
```

which creates an object called aa, with content the number 5. Type

```
> ls()
```

and you will see aa as one of the objects in the list. Type

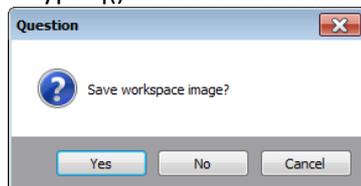
```
> aa
```

and you will see the content of aa.

Similarly, during an R session you can create all sorts of “objects” (usually more meaningful, like the results of an analysis), which will be kept in the Workspace.

If you save the Workspace during or at the end of the session (see next step), all objects will remain, and will be available when re-opening the Workspace.

4. *Save the Workspace*. Close the PROAST-GUI (click on the red cross in the upper right corner), and then close the R-GUI (click on the red cross in the upper right corner; or type `q()` in the Console window). You will now get the question:



Here, answer Yes. This will save the workspace in the current working directory with name `.Rdata`.

5. *Re-open the Workspace*. Browse to the folder where you saved the Workspace. When the Workspace is shown as a big blue R, this means the Windows recognizes it as an R application, and you can simply double click on it. This re-opens your last session. Type `ls()` to check if the object aa still exists.

- If Windows on your machine does not recognize the workspace as an R application, you may right click on saved Workspace (`.Rdata`) and select `Rgui.exe` (see folder `R/R-3.2.0/bin/i386`) as the associated program. If that does not work, repeat step 2, and then click File/Load workspace, to load your last saved workspace.
- When you re-open the workspace, it might happen that you get a welcome message from PROAST, without having loaded PROAST (this will happen if you closed R without having closed the PROAST GUI window first). To solve this type

```
> rm(.proast.wizard)
```

save the workspace and re-open it. Then the message should no longer appear. Further, it will take less time to open the workspace.

Names of Workspaces

When you save the Workspace at the end of the session, as in step 4 above, the Workspace will be saved under the name .Rdata (i.e., only the extension). During the session you can also save the Workspace by clicking File/Save Workspace. In that case, you could provide a name in front of the extension .Rdata. However, as long as you keep different projects organized in different folders, each with its own Workspace, different names for the Workspaces are not really needed. Actually, using various Workspaces in the same folder is somewhat risky, as they might be overwritten unintendedly (after step 4 above).

Regularly save your Workspace

When you are doing something unexpected, it might happen that the R session crashes. Therefore, it is recommendable to save your workspace during a session every now and then, in particular if you did a calculation taking a substantial amount of time.

When you want to re-open the session by double clicking .Rdata after an irregular ending of the session, it may happen that R opens very slowly, and then shows you the PROAST message, even though you did not yet load the package. This should be solved as soon as you have ended a session with the PROAST GUI in a regular fashion, i.e. first close the PROAST GUI, and next the R GUI, and save the workspace after that.