Q: How do I install nCal?

A: Please follow the following steps. Step 4 is necessary for running *nCal* GUI.

1. Install R. R can be downloaded from http://cran.r-project.org/
2. Run R. On Windows, this can be done by double-clicking on the R icon.
3. Install the *nCal* package. At the R console, type
   > install.packages ("nCal")
   and press enter.
4. Install the *gWidgetstcltk* package. At the R console, type
   > install.packages ("gWidgetstcltk")
   and press enter.

Q: How do I launch the nCal GUI?

A: The nCal GUI is launched from within R. Please follow the following steps.

1. Run R. On Windows, this can be done by by double-clicking on the R icon.
2. At the R console, load the nCal library by
   > library (nCal)
3. run nCal GUI by
   > ncalGUI()

Q: What other programs does nCal need to be able to import Luminex raw output?

A: To import data from raw Luminex files, PERL and the R package gdata are needed. PERL can be downloaded from http://www.activestate.com/activeperl/downloads

To install the gdata package, enter the following command in R.
> install.packages("gdata")

Q: What other programs does nCal need to be able to fit the robust Bayesian hierarchial model?

A: To fit Bayesian robust hierarchical model, JAGS and the R package rjags are needed. First, download and install JAGS from http://sourceforge.net/projects/mcmc-jags/files/JAGS/

Second, in R enter the following command to install the rjags package.
> install.packages("rjags")

Q: Help on GUI

A: The GUI (screenshot: http://research.fhcrc.org/content/dam/stripe/youyiFong/files/gui.pdf) is divided into four sections.

Input

- You can select a file containing the input data using the browse button. The nCal package comes with an example Luminex raw output xls file, 02-14A22-IgA-Biotin-tiny, and it is located at the R_installation_directory/library/nCal/misc folder. You can use this file to test the GUI.
- The input file can be in one of three different formats.
- The Response variable field allows users to enter the name of the response variable, and it defaults to log(fi).
- The Concentration/dose variable field allows users to enter the name of the concentration or dose variable, and it defaults to expected_conc.

Output

- The Estimated concentrations field allows users to enter the name of the file to save the estimated concentrations, and it defaults to estimated_concentrations.csv. The browse button next to it allows users to choose a folder to save the file in.
- The Calibration plots field allows users to enter the name of the file to save the calibration plots, and it defaults to Calibration_plots.pdf. The browse button next to it allows users to choose a folder to save the file in.

Curve fitting method

- Users can choose between two curve fitting methods.

The last section allows users to use the last fitted curve to estimate concentrations for any responses entered by users.

- More than one response can be separated by space or comma, e.g. 5.1, 6.3
- The *Apply* button becomes activated when there has been a fitted curve. When the *Apply* button is clicked, a new window pops up. In the window is a table, each row of which corresponds to one entered response.

Q: What is the relationship between nCal and Ruminex?

A: Ruminex is the precursor of nCal. To switch to nCal, the only necessary change is to replace Ruminex with nCal in the library() command because rumi is also provided in nCal and can be called in the same way as it was in Ruminex.