



It is important to make sure the labels are exactly the same (including white spaces and enter spaces), otherwise R will count them as separate categories. For example, each 'GAMT' above was entered without any extra white spaces at the end. It is also important to be consistent with upper- and lowercase letters. For example, each 'Mutant' above begins with an uppercase letter. Once all information has been entered, save the file as a .csv file and make sure file name doesn't have white spaces.

Although the file above specifies the image name, it does not direct R to the required information about each image. The user needs to create a script which will print into a file full pathways for all required information. The script must specify level of blur. We recommend either a 1.0 or 0.5 blur when looking at total brain structure and volume. This level of blur provides enough detail for the purposes of looking at total brain. However, when analyzing individual brain structures, we recommend a 0.1 blur instead. A smaller amount of blur is required because, otherwise, blurring would run over the boundaries of the individual brain structures. The MICe centre is happy to forward an example of such a script upon request.

Once the 'Glim' file is ready, it can be read into R and the user is ready to begin analysis. RMINC is a library which is necessary to read and write MINC data into R. R package can then be used to run linear models, plot data, etc. Numerous types of analyses are possible in R. The manuals mentioned above are a great place to start as they work through practical examples, employing a variety of analyses.<!-- @page

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