**How can I load RnBeads results into Galaxy?**

Most of the RnBeads output data are ready to be imported into Galaxy via standard “Upload File” tool. In case you have run RnBeads locally use the file selection control and browse the RnBeads output directory (the one supplied as an argument to *rnb.run.analysis* routine) to find necessary output files. The primary result files, i.e. a spreadsheet-like file with exported values and genome browser tracks, are located in the “export\_data” subdirectory. The data import is easier in case the RnBeads report is located on a web-server that is accessible to the Galaxy instance. In this case simply copy links to your output files from the analysis report via the context (right-click) menu and paste them into “URL/Text” text field of the “Upload File” tool.

**How do I load Galaxy-generated data into RnBeads?**

The standard way to import data into RnBeads is to download the files from Galaxy (or any other similar tool) and specify their location as arguments to RnBeads routines. However, RnBeads also provides a wrapper which integrates it with the Galaxy toolbox and allows running RnBeads as a Galaxy tool. The wrapper is available for installation from the official Galaxy toolshed under “Statistics” category (<http://toolshed.g2.bx.psu.edu/>). If your institution is running an own Galaxy instance, ask the local administrators to set up RnBeads for you.