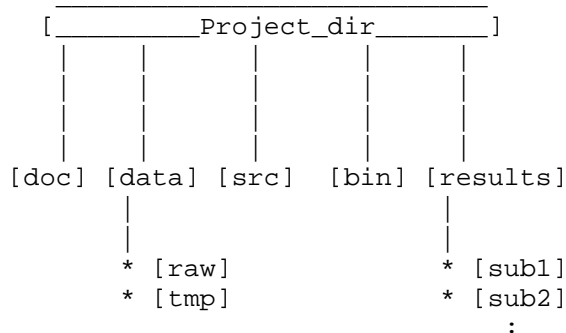


User manual for Project 'IamComparison'

The project structure should look like



No build process is necessary.

The R-scripts in this project (located in folder *src*) can be executed in the order they are listed in the driver file *main.R*.

The experimental datasets should be stored in folder *raw* as R list object.

All sub directories in the *results* folder are created automatically. If files/directories with the same name exist already, they are overwritten without notice!

The standalone software MALA should be placed in folder *bin*.

The execution of MALA on synthetic data is implemented in the file *MALA.R* and its dependency *runMALA.R*, and is fully integrated in the project workflow, however, it exclusively runs on Linux machines (tested on CentOS 6, 7).

The execution of MALA on experimental data is NOT integrated in the project workflow. Execution of MALA and insertion of result files into the project directory has to be performed manually for example with the script *MALA_linux.R* (see there for description).

The execution of the scripts can take extensive amounts of time. Especially, the application of methods to large biological datasets and to multiple synthetic datasets in order to get valid statistics for the performance measures can take several hours to days, depending on the parameter settings in *syntheticParameter.R* and *biologParameter.R* respectively.