

Python files organized as:

- **Main** – the script that needs to be Run. Edit to adapt functionality.
- **Plotting_script** – contains the figure generation algorithm. Edit the method `plot_info()` to add or remove figures.
- **Settings** – contains core settings for the script to be adapted to personal Clarius projects and figure size settings. Changes in the argument values will be used throughout all other scripts.
- **Utils** – holds commonly used methods for the main script
- **Plotting_utils** – defines figure generating methods. Adapt to personalize visualisation or add additional plotting methods.
- **Data_processing** – holds folder management, dump sorting and Excel files reading methods.

Folders are organized as:

- **Data** – contains folders sorted into chips-devices and organizes .xls, .pickle, and figure image files into Excel_files, Pickles, and Figures respectively. Additional folders are created automatically as new files are sorted from Dump.
- **Dump** – used to upload new .xls files to be automatically sorted when running main script (IMPORTANT: upload .xls files, not folders). If an identical file already exists it will be removed instead.

Clarius project organized by creating a subsite for each chip and copying new empty devices into subsites to perform tests for each device separately. This allows the entire project or a new part of it to be exported using `tools/export_data`. The Excel files can then be pasted into the Dump folder and sorted by the python script by names of the .xls files.

