**SOP: RAMPT start**

**SOP written by** Josua Carl   
**Initial Version created on:** 30.01.25

**Version Number:** 1

**Last modification date:** 30.01.25  
**Last modified by** Josua Carl

1. **Purpose**

Explaining the operation of the raw to annotation metabolomic pipeline tool (RAMPT).

1. **Procedure**
   1. **Introduction**

RAMPT is a tool for combining mass-spectrometry data analysis with mzmine and following annotation with SIRIUS and GNPS into one program. The program is accessible through the command line (albeit in separate steps) and through a graphical user interface (GUI).

* 1. **Material / Preparations**

To follow along, you need:

* + 1. RAMPT installed (See SOP\_rampt\_installation)
    2. msconvert, mzmine and Sirius installed and accessible in your PATH variable (normally happens automatically)
    3. Have a mzmine batch file (.mzbatch) prepared, which exports data for Sirius and feature-based molecular networking (FBMN) with GNPS

It is further recommended that:

* + 1. The folder structure of your mass-spec project keeps all raw / converted / annotated files in one respective folder (i.e.: “RawData”, “ConvertedData”,…)
  1. **Methods / Procedure**

After installing RAMPT and moving the shortcut / symbolic link to your desired location you may

* + 1. Start the application by opening the shortcut / symbolic link. This will cause a command-line window to be opened.
    2. The command-line window is your application! If you close this window, you will close the application. If you only close the tab in the browser, the application will remain unaffected.
    3. The application will automatically detect installed browsers and open a window at the address <http://127.0.0.1:5001/configuration>. If taipy is unable to detect a sufficient browser, you can access RAMPT by entering this address into a browser of your choosing.
    4. You may now select a point of entry to the workflow (for example at conversion)
    5. You have to select all given recommended settings, including an out path
       - The in file selection is the most complicated. You have to select a type of input “e.g. raw data files for conversion”, then upload a file/path by clicking on “Select in”. To add the uploaded data to the current run you are packaging, you have to select it in the tree selection that is next to select in.
       - Once selects, you will see, that the data type will be checked to indicate, that it was added. You can view your input files a bit further down at the data node viewer. You may also change your input there.
       - After you are contempt, click on “Add to run” to schedule one package for execution. You may always click “Clear package” to reset the entire input.
    6. After the selection, you have to lock the scenario (upper-right corner)
    7. The scenario execution button will be blue, if sufficient input was provided
    8. When you click on the blue “play” button, the computation will start
  1. **Results**

You should now have a workflow running.

* 1. **Troubleshooting**

If there is any trouble during these steps, please post an issue at <https://github.com/JosuaCarl/RAMPT/issues>.

1. **References**

<https://github.com/JosuaCarl/RAMPT>

<https://github.com/JosuaCarl/RAMPT/blob/main/Manual.md>