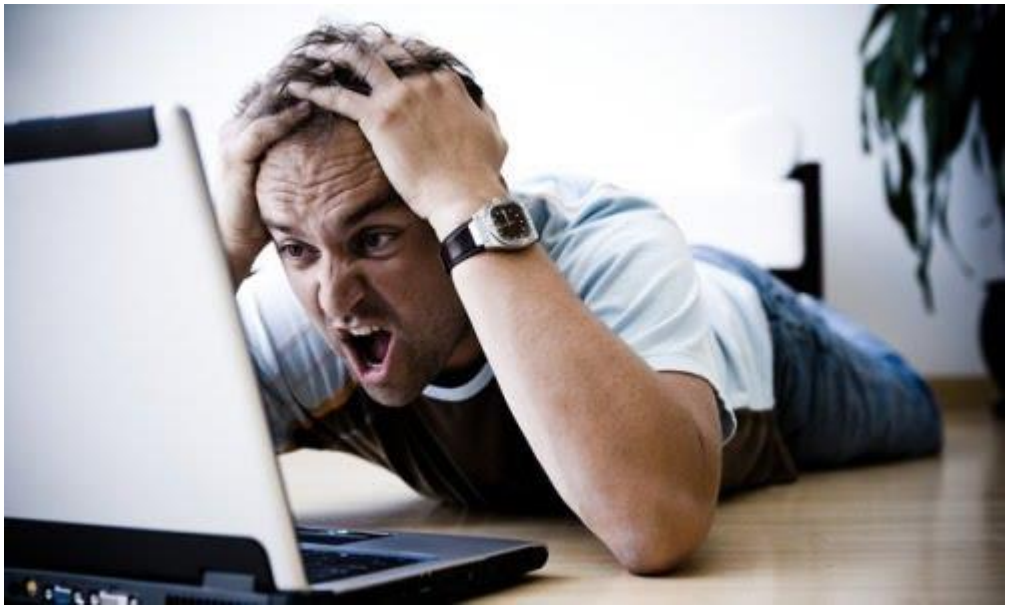
First steps in the expert mode



Version 1.1

Date 10/02/2020

Official MadAnalysis 5 website : https://launchpad.net/madanalysis5/

Goals of this tutorial

- Entering the expert mode
- Handling the structure of a job folder
- Configuring your environment for the expert mode
- Compiling and running your job
- Reading through the results of your analysis in the SAF files

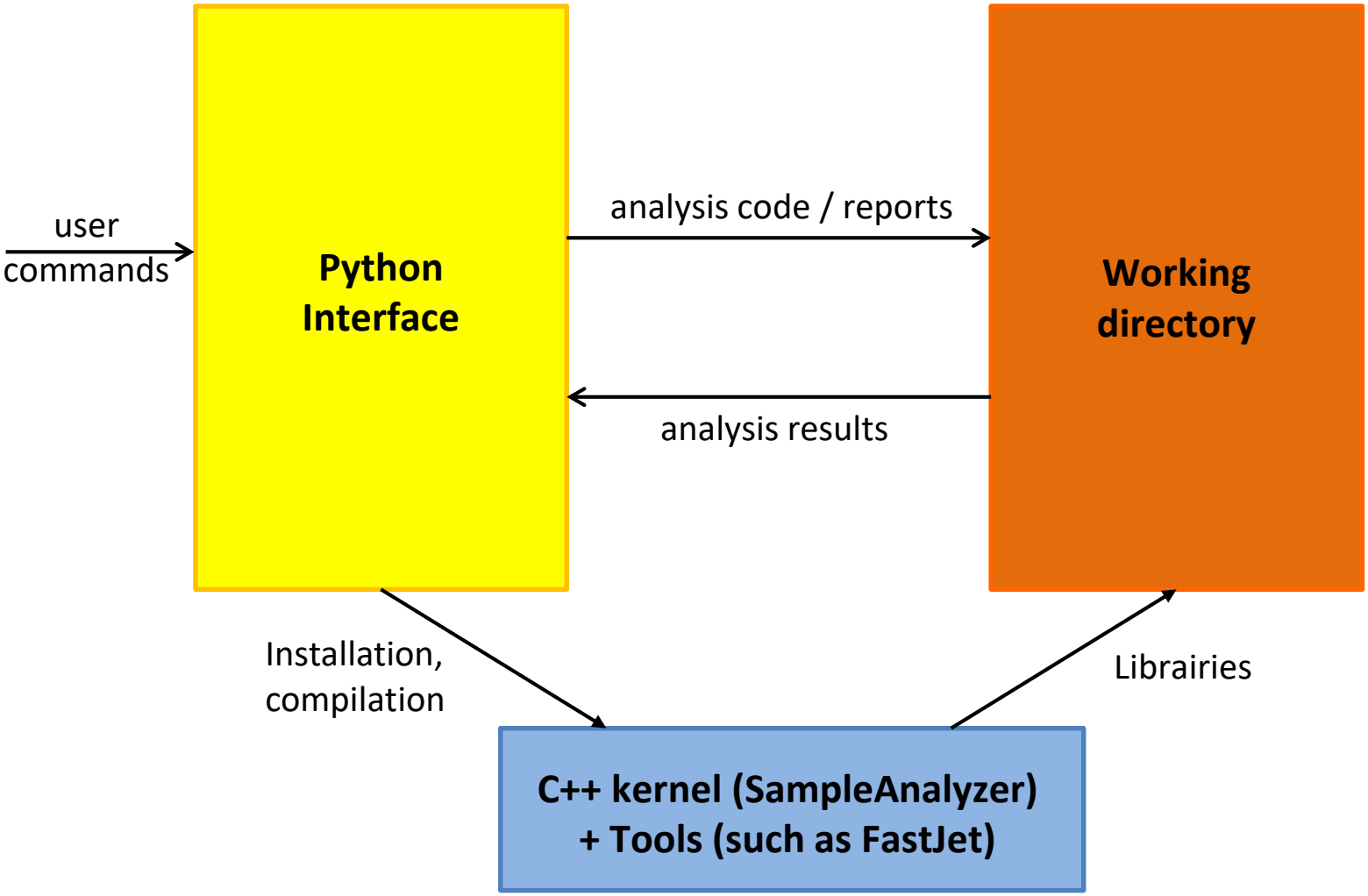
Requirements

- MadAnalysis 5 is installed on your system and has been launched successfully at least one time. The collection of example samples is installed too.
- Knowledge of the MadAnalysis 5 main concepts (see tutorials for beginners).
- For using the expert mode, basic skills in C++ programing are required. Nonetheless this introduction tutorial do not deal with any C++ code.
- You have chosen which text editor is your favorite ☺

Part 1

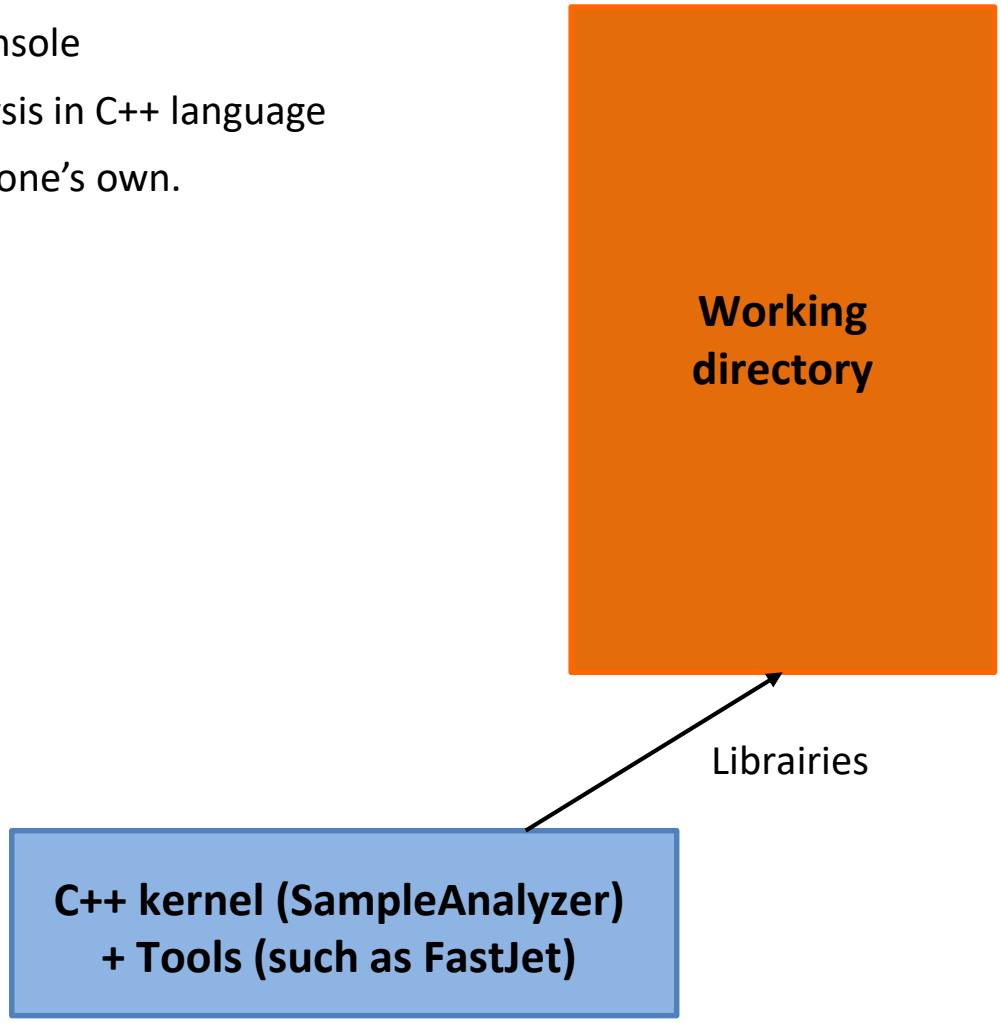
Introduction

Reminder: the “normal” mode



What is the expert mode ?

- Not using the Python console
- Coding directly the analysis in C++ language
- Analyzing the results on one's own.

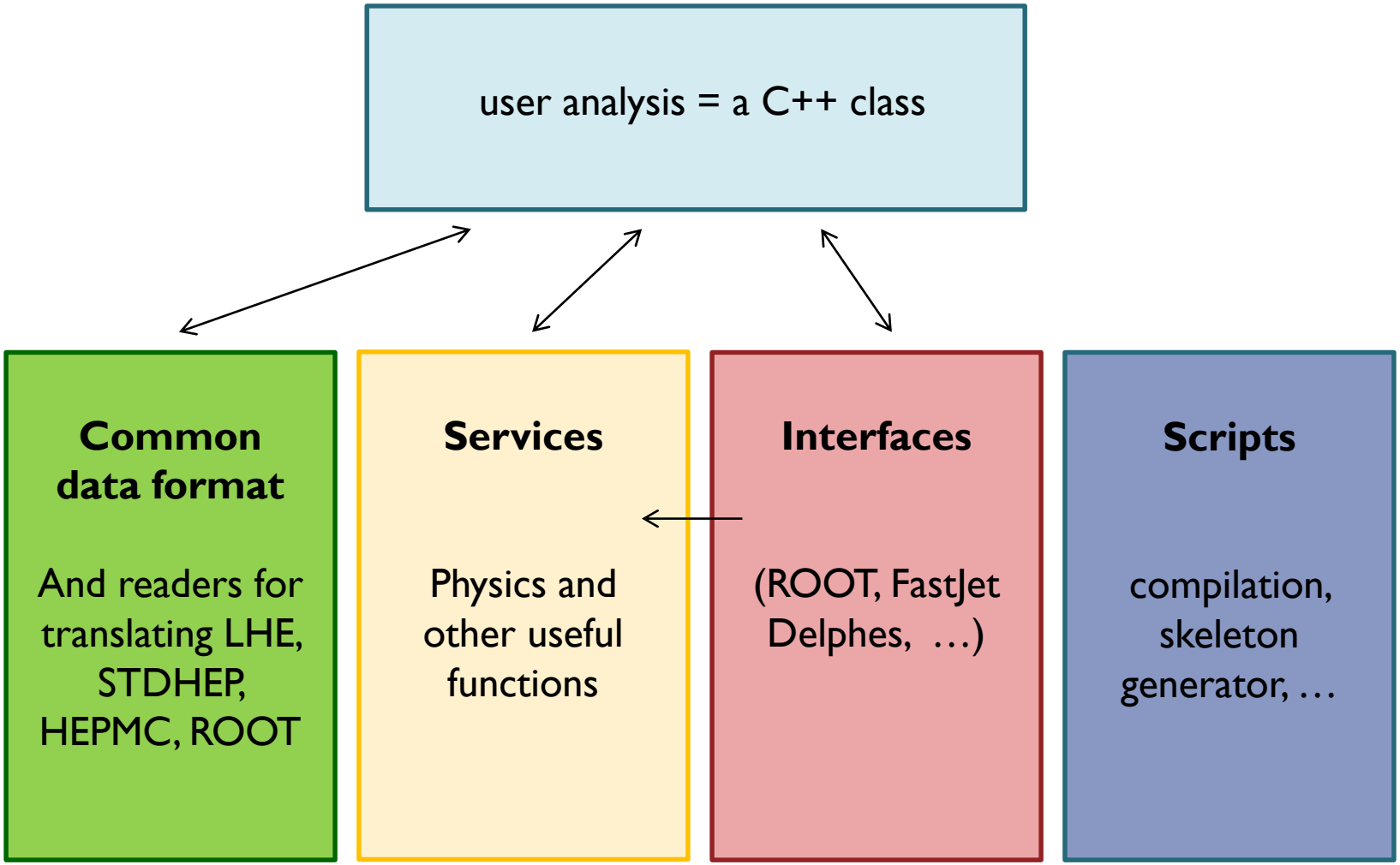


Motivations for the expert mode ?

The expert mode is motivated in several cases:

- Despite the potential of the Python console, the analysis planned is too sophisticated.
- The user would like to plug to MadAnalysis 5 an external package for which no interface is provided.
- The need to implement a specific output format for the analysis results (histograms, cuts, …) or for event data.
- The case where too many datasets must be analyzed. The user could use MadAnalysis 5 though standalone jobs and could take profit from computing resources such as a cluster or the Grid.
- Recasting an existed ATLAS/CMS experimental analyses.
- Linking SampleAnalyzer library to a software for generating plots. [AVAILABLE SOON]

Expert mode = developer-friendly



Part 2

Generating a template analysis

Prerequisites to this tutorial

1. MadAnalysis 5 has been downloaded.
   (see tutorial "Normal Mode - 2 - Installation & first launch")

2. MadAnalysis 5 has been launched at least one time and the building the SampleAnalyzer library has worked properly.
   (see tutorial "Normal Mode - 2 - Installation & first launch")

3. The collection of example samples has been installed through the MadAnalysis 5 console:

```
ma5> install samples
```

   (see tutorial "Normal Mode - 2 - Installation & first launch")

Entering the expert mode

To begin an analysis in the expert mode, the user must launch MadAnalysis 5 with the argument `-e` or equivalently `--expert`.

```
./bin/ma5 -e
```

MadAnalysis 5 will initialize itself normally but at the end, the `ma5>` prompt is replaced by a series of questions. You answer will help MadAnalysis 5 to generate the proper in order to know what you would like.

First question:

```
Welcome to the expert mode of MadAnalysis
Please enter a folder for creating an empty SampleAnalyzer job
```

Just specifying the name of the working directory you would like to create.

Second question:

```
Please enter a title for your analyzer :
```

At this step of the tutorial, this name is insignificant. Only for the display.

Entering the expert mode

Assuming you answer is 'MyAnalysis' to the questions 1 and 2, a working directory called `MyAnalysis` is created and contains an empty analysis called `MyAnalysis` and scripts (required in particular for compiling).

Some guidelines are displayed at the screen in order to survive in the expert mode. They can be considered as a reminder of the present tutorial.

```
Creating folder '/grid_mnt/home/econte/MA5/v1.4beta/MyAnalysis'...
  Copying required 'SampleAnalyzer' source files...
  Writing an empty analysis...
  Writing a Makefile...
```

Entering the expert mode

Alternative way to enter the expert mode: by console command-lines

The previous recipe can be done by one only command-line at the Linux shell.

```
./bin/ma5 -e -s MyAnalysis1 MyAnalysis2
```

The meaning of the different arguments is the following:

- **-e** entering the expert mode
- **-s** enabling the script mode (MA5 will not ask your permission to remove an existing folder)
- **MyAnalysis1** name of the folder
- **MyAnalysis2** name of the analysis

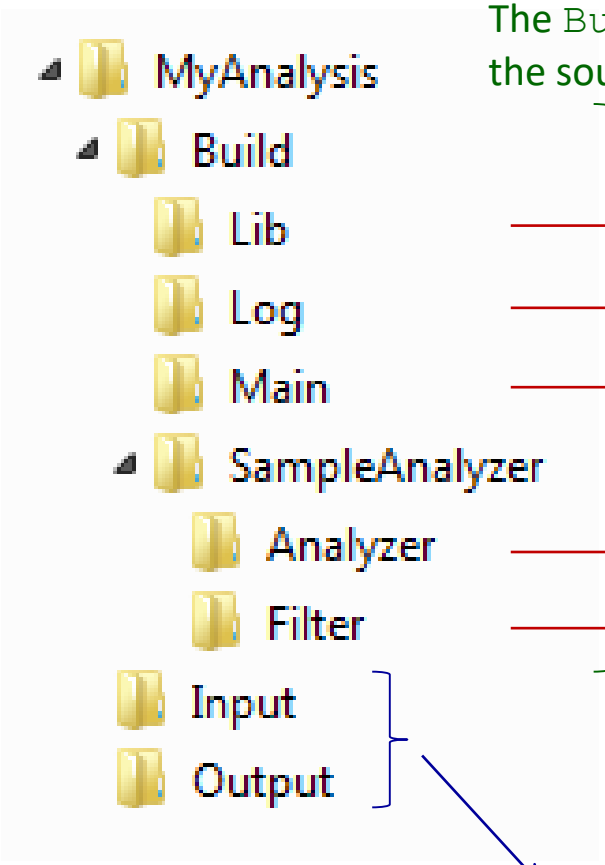
Alternative way to enter the expert mode: editing the source of an existing analysis

It is possible also to modify a working directory (and its files) generated by the Python interface in the «normal» mode.

Part 3

Launching the template analysis

Structure of the working directory



The `Build` folder contains the source code of the job.

Folder devoted to libraries generated during the compilation.

This empty folders can be used by the user to store log files during the compilation.

Folder containing the source of main program.

Folder containing the source of all analyses designed by the user.

Folder containing the source of all filters designed by the user.

These two empty folders can be used by the user to store the inputs and the outputs of the MadAnalysis 5 job.

Setting your environment

Before beginning to work, the environment variables required by MadAnalysis 5 must be set. To this end, entering the folder `Build` of `MyAnalysis`:

```
cd MyAnalysis/Build
```

and executing the script `setup.sh` if you use the shell BASH

```
source setup.sh
```

or the script `setup.csh` if you use the shell TCSH.

```
source setup.csh
```

If the script has been properly executed, the following message must appear:

```
------------------------------------------------------------
    Your environment is properly configured for MA5
------------------------------------------------------------
```

This first step must be carried out each time you start a new shell session.

Building your job

To build the job, you must type inside the `Build` folder

```
make
```

As all C++ programs, the building of the job is made up of two parts: compilation and linking. If the building is successful, an executable file called `MadAnalysis5Job` will be created.

When the executable is built, you can save disk space by removing the intermediate files produced during the compilation (object files). This purpose can be performed by issuing

```
make clean
```

You have also the option to remove all files produced during the building phase (the executable MadAnalysis5Job also) and to come back to the initial configuration.

```
make mrproper
```

Launching job

The executable file `MadAnlysis5job` built in the `Build` folder is fully independent from the place where it is. It can be moved in any folder of your choice.

Before launching the job, the list of samples you would like to process must be specified. It can be done by creating a text file containing the list of the files. The syntax is simple: one line by sample.

Be careful the wildcard characters * and ? are not allowed.

- Creating a such input file with the sample collection: `input.txt`

```
ls $MA5_BASE/samples/*.lhe > input.txt
```

- Reading through the file `input.txt` with your favourite editor.

- The job can be launched by issuing:

```
./MadAnalysis5job input.txt
```

What you should see at the screen

With the previous command, your empty job is executed on the samples registered in the file input.txt. Some information are dumped at the screen if everything works properly. This is an example of what you should get.

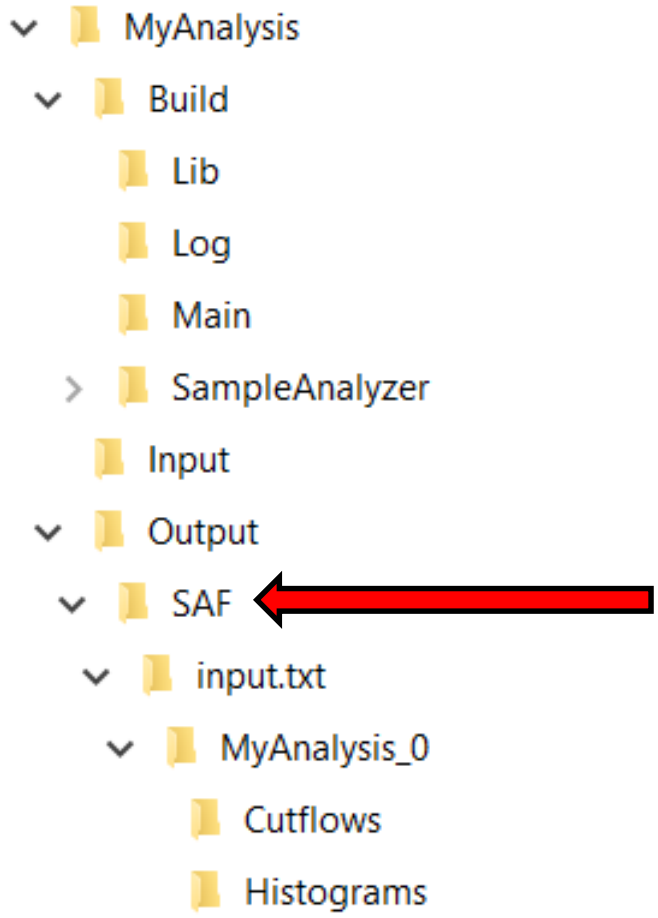
```
* SampleAnalyzer for MadAnalysis 5 - Welcome.
    * Initializing all components
      - version: 1.8.40 (2020/01/29)
      - general: everything is default.
      - extracting the list of event samples...
      - analyzer 'user'
BEGIN Initialization
END   Initialization
    * Running over files ...
    * 1/2  /home/bradpitt/MA5_v1.8/samples/ttbar_sl_1.lhe
        => file size: 1.67 Mo
        => sample format: LHE file produced by MadGraph5.
        => progress: [==================================]
        => total number of events: 1000 ( analyzed: 1000 ; skipped: 0 )
```

What you should see at the screen

```
* 2/2 /home/bradpitt/MA5_v1.8/samples/ ttbar_sl_2.lhe
        => file size: 1.67 Mo
        => sample format: LHE file produced by MadGraph5.
        => progress: [==================================]
        => total number of events: 1000 ( analyzed: 1000 ; skipped: 0 )
    * Finalizing all components ...
    * Total number of processed events: 2000.
BEGIN Finalization
END   Finalization
    * Goodbye.
```

Results of the analysis

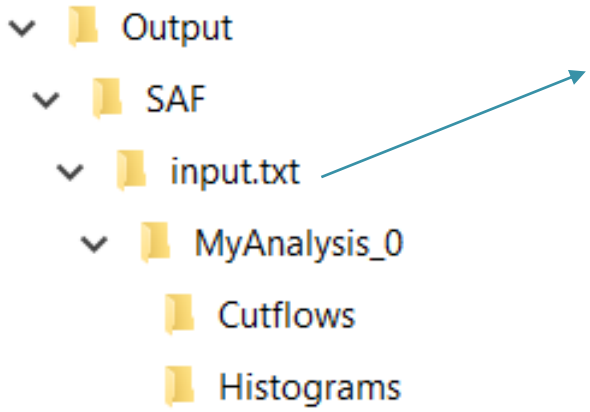
Some files are generated automatically by your job and contain the results of your empty analysis. To see these files, you should go to the folder `Output/SAF`.



Your results encoded in text-format called SAF (SampleAnalyzer Format).

Results of the analysis

Studying more the structure of the `SAF` folder.

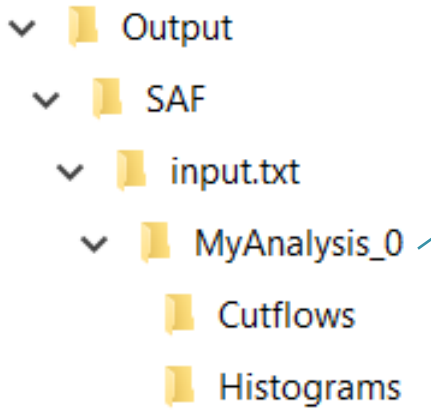


This folder has the same name than the text file containing the list of your samples.

If you use several input files in your job, each input file will have a specific folder.

Results of the analysis

Studying more the structure of the `SAF` folder.



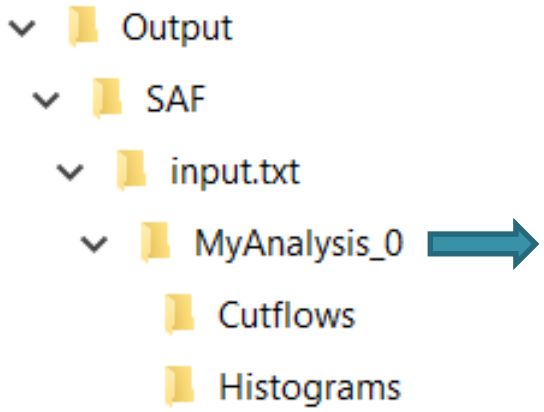
This folder has the same name than your analysis following by "_0".

If you would like to apply several analyses to samples in the same job, one specific folder will be created for each analysis with the name of analysis.

"_0" means that it is the first time that you have run the job. If you launch the job a second time, a folder "MyAnalysis_1" will be created. This feature allows you to save the results history of your previous jobs.

Results of the analysis

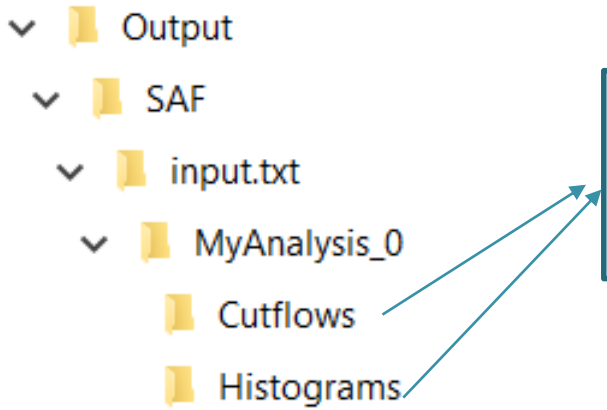
Studying more the structure of the `SAF` folder.



This folder contains a file called **input.txt.saf** with global informations related to the input samples.

Results of the analysis

Studying more the structure of the `SAF` folder.



Theses folders are empty because no cuts or histograms has been defined in your analysis.

Results of the analysis

You can edit with a text editor the `input.txt.saf` file in order to get global information on your samples.

```
<SampleGlobalInfo>
# xsection     xsection_error nevents        sum_weight+    sum_weight-
1.534058e+01   7.594284e-02   2000           0.000000e+00   0.000000e+00
</SampleGlobalInfo>

<FileInfo>
"/home/bradpitt/MA5_v1.8/samples/ttbar_sl_1.lhe" # file 1 / 2
"/home/bradpitt/MA5_v1.8/samples/ttbar_sl_2.lhe" # file 2 / 2
</FileInfo>

<SampleDetailedInfo>
# xsection    xsection_error nevents   sum_weight+    sum_weight-
1.544783e+01  1.139396e-01   1000      0.000000e+00   0.000000e+00    # file 1 / 2
1.523332e+01  1.004342e-01   1000      0.000000e+00   0.000000e+00    # file 2 / 2
</SampleDetailedInfo>
```

Results of the analysis

Each time you run the job, MadAnalysis 5 will not erased the previous results. It will create a new sub-folder called "`MyAnalysis_X`" where X is an incrementing number in the folder "`Output/SAF/input.txt/`".

If you do not care of this history, you can delete the folder "`Output/SAF`". MadAnalysis 5 will create a new one when a new job is launched.

GREAT!
JOB!

About this document

- The present document is a part of the tutorial collection of the package MadAnalysis 5 (MA5 in abbreviated form). It has to be conceived to explain in a practical and graphical way the functionalities and the various options available in the last public release of MA5.

- The up-to-date version of this document, also the complete collection of tutorials, can be found on the MadAnalysis 5 website :

  https://madanalysis.irmp.ucl.ac.be/wiki/tutorials

- Your feedback interests ourselves (bug reports, questions, comments, suggestions). You can contact the MadAnalysis 5 team by the email address : ma5team@iphc.cnrs.fr

Change log

Version	Date	Update
0.1	30/09/2013	Beta for MadAnalysis and Nsusy workshop @ Grenoble
1.0	29/10/2013	First public release
1.1	23/07/2016	Update related to vMA5 1.4
1.2	10/02/2020	Update related to vMA5 1.8