

**Tutorial category: Normal mode** 

## First analysis with MadAnalysis 5



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Official MadAnalysis 5 website : <u>https://launchpad.net/madanalysis5/</u>



## Goals of this tutorial

- Defining an elementary analysis in MadAnalysis 5 including plots and cut selection.
- Launching the analysis over the datasets and getting the results.
- To be able to use the Python console or a script for running an analysis.
- Changing the way to normalize or to stack the histograms.
- Selecting the figure of merit in a selection.



## 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.









## Part 1 A basic example



## A basic example

Type this example at the prompt of MadAnalysis 5.

```
ma5> define mu = mu+ mu-
```

```
ma5> import samples/ttbar_*.lhe.gz
```

- ma5> plot PT(mu)
- ma5> reject PT(mu) < 40</pre>
- ma5> plot PT(mu)
- ma5> submit
- ma5> open



## A basic example



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Note that this analysis could have been written in a text file ...

#### MyFirstExample.txt

```
define mu = mu+ mu-
import samples/ttbar_*.lhe.gz
plot PT(mu)
reject PT(mu) < 40
plot PT(mu)
submit
open
```

... and exectuted by the following command:

./bin/ma5 MyFirstExample.txt



# Part 2 Building your analysis step-by-step



In this section, we describe the different steps building a classical analysis with MadAnalysis 5 normal mode:

- 1. Defining your proper particle labels
- 2. Importing your samples
- 3. Defining your analysis by adding:
  - 3.1 some plots
  - 3.2 some cuts
- 4. Launching the analysis
- 5. Opening the report



- Particles are defined by labels which point to one PDG-id.
- A « multiparticle » correspond to a label pointing to several PDG-ids.
- SM and MSSM labels are automatically loaded at the starting of MadAnalysis.
- The command display\_particles & display\_multiparticles allow you to display all the labels predefined.

```
ma5>display_particles
```

```
MA5: a b b1 b1~ b2 b2~ b~ c cl cl~ cr cr~ c~ d dl dl~ dr dr~ d~ e+ e- el+ el- er+ er- g go h+ h- h1 h2 h3 met mht mu+ mu- mul+ mul- mur+ mur- n1 n2 n3 n4 s sl sl~ sr sr~ sve sve~ svm svm~ svt svt~ s~ t t1 t1~ t2 t2~ ta+ ta- ta1+ ta1- ta2+ ta2- t~ u ul ul~ ur ur~ u~ ve ve~ vm vm~ vt vt~ w+ w- x1+ x1- x2+ x2- z
```

```
ma5>display_multiparticles
MA5: hadronic invisible j l+ l- p vl vl~
```

- There are 2 special labels :
  - hadronic: contains all hadronic particles
  - invisible: contains all invisible partiles

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## 1. Defining (multi)particle labels

• To show to which PDG-id code a label refers:

```
ma5>display n1
The particle 'n1' is defined by the PDG-id 1000022.
```

• To create a new label for a PDG-id (useful for BSM particle):

```
ma5>define extrapart = 5000001
```

• To create a new label gathering several particles (useful in the analysis definition):

```
ma5>define extrapart = 5000001 -5000001
ma5>define mu = mu+ mu-
ma5>define b = b b~
```



## 2. Importing your samples

- For MadAnalysis, a dataset is a collection of samples which will be merged.
- All sample files are stored in a dataset.



• Possible to display all the datasets defined by the user with the command display\_datasets.

```
ma5>display_datasets
 ******** List of defined datasets *******
 defaultset (signal)
 Wjets (signal)
 ttbar (signal)
```



## 2. Importing your samples

Properties of a dataset could be changed by the command set. Some relevant properties:

• Possibility to tag datasets as signal or background (useful for selection and computation of the figure of merit).

```
ma5> set ttbar.type = signal
ma5> set Wjets.type = background
```

 Possibility to force the cross section value (normally this valeur is extracted from the sample). Unit = pb.

```
ma5> set ttbar.xsection = 1.0
```

• Possibility to multiply the cross section by a weight. For instance, this weight could be k-factor.

ma5> set defaultset.weight = 1.2



- Observable can be related to the event or the properties of a particle
- Plethora of observables: N, E, ET, M, MT, P, PT, PX, PY, PZ, THETA, ETA, ...,

ma5> plot NPID
ma5> plot MET
ma5> plot PT(mu)

• Combining particles is possible (vector sum of 4-vector momenta)

ma5> plot M(mu+ mu-)

• Number of bins and x-axis bounds are set by default. This value can be specified by the user if necessary.





#### • List of observables related to the events:

- multiplicity (N, NPID, NPID),
- Total energy (TET) or total hadronic energy (THT),
- Missing transverse energy (MET) or missing transverse hadronic energy (MHT)
- SUSY transverse observables (ALPHAT, MT2)
- Coupling/scales (ALPHA\_QCD, ALPHA\_QED, SQRTS, SCALE)

#### • List of observables related to one particle:

- energy (E and ET),
- mass (M,MT, MT MET),
- momentum magnitude and components (P, PT, PX, PY, PZ),
- angles (THETA, ETA, ABSETA and PHI),
- relativist factors (Y, BETA and GAMMA).

#### • List of observables related to tow particles:

• Manhattan distance in eta-phi plane (DELTAR),



Several options or syntaxes allow to extend the potential of MadAnalysis. 3 examples:

By default, a combination is interpreted as the vector sum of momenta.
 This interpretation can be changed by adding a prefix to the observable label.

For instance : vPT, sPT, dsPT, dvPT, rPT

• Selecting a particle according to its rank in energy (or to other observables)

ma5> plot PT(mu+[1])

• Selecting a particle according to its history (requirements on mother, grand-mother ...)

ma5> plot PT(mu+ < w+ < t $\sim$ )



• Options can be added to plots into square brackets []





## 3.2. Selection cuts

- Selection cuts can be performed by two commands: select and reject. These two commands are equivalent.
- Cuts : selecting / rejecting events

```
ma5> reject MHT < 50
ma5> select N(mu) >= 2
```

• Cuts : selecting / rejecting a particle or a combination

```
ma5> select (mu) PT > 50
ma5> select 80 < M (mu+ mu-) < 100
```

• The list of observables and syntax are identical to histograms ones.

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# 4. Launching the analysis over the samples

This can be done by the command submit

- Creating a working directory (with a default name if no name is specified)
- Compiling the C++ job
- Launching the analysis over the different samples contained in the datasets

```
ma5> submit
[...]
* SampleAnalyzer 2.0 for MadAnalysis 5 - Welcome.
* Option choices: selecting analysis = 'MadAnalysis5job'.
* Extracting the following sample files:
* 1/4 ~/samples/ttbar_sl_1.lhe.gz
=> file size : 107.09 Mo
=> sample produced by MadGraph.
=> progress [========> ]
```

If you modify, after the submission, the analysis or the layout of the plots, the results can be updated in an optimized way by the command resubmit.



## 5. Opening the analysis report

The command open displays the HTML report of the last job created. Reports in PDF and DVI format are also available.



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# Part 3 Some useful main options



## Options related to histogramming

• The histograms are by default normalized to the integrated luminosity. Integrated luminosity is by default 10 fb<sup>-1</sup>. This value can be set by the user:

ma5> set main.lumi = 100

• The histograms can be normalized to one by the following command:

ma5> set main.stacking method = normalize2one

• If you have several datasets, you can choose if you would like to stack the spectra (by default) or to superimpose them.

```
ma5> set main.stacking_method = stack
```

```
ma5> set main.stacking_method = superimpose
```



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## Figure of merit for the selection

- If you apply on datasets (with signal and background tags),
   MadAnalysis 5 will compute a cut-flow chart including a figure of merit.
- He must choose one formula among a predefined collection (by default option 4 is used).
  - 1: S/B
  - 2: S/sqrt(B)
  - 3: S/(S+B)
  - 4: S/sqrt(S+B)
  - 5: S/sqrt(S+B+(xB)\*\*2)
- Corresponding instruction in MadAnalyis 5.

ma5>set main.fom.formula = <formula number>

Special case: the x parameter in formula number 5

```
ma5>set main.fom.formula = 5
ma5>set main.fom.x = 0.2
```

with S and B mean respectively Signal and Background









## 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 : <u>ma5team@iphc.cnrs.fr</u>



## Change log

Versi	on	Date	Update
1.0		23/07/2016	First release

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