Using pyjetty

Reynier Cruz Torres

November 10, 2020

Contents

1 Processing

Example on running a local pp data job:

```
python process/user/rey/process_data_energy_drop.py \
-f /rstorage/alice/data/LHC17pq/448/20-06-2020/448_20200619-0610/unmerged/child_1/0001/AnalysisResults.root \
-c config/energy_drop/rey_pp.yaml
```

Example on running a local pp mc job:

```
python process/user/rey/process_mc_energy_drop.py \
-f /rstorage/alice/data/LHC18b8/449/child_1/TrainOutput/1/282008/0001/AnalysisResults.root \
-c config/energy_drop/rey_pp.yaml
```

Example on running a slurm data job:

```
cd slurm/sbatch/energy_drop/
sbatch slurm_LHC17pq.sh
```

2 Merging data root files

- `cd pyjetty/pyjetty/alice_analysis/slurm/utils/rey`
- open the file `merge_data.sh`

```
#! /bin/bash
#
# Script to merge output ROOT files
JOB_ID=209383
FILE_DIR="/rstorage/alice/AnalysisResults/rey/$JOB_ID"
FILES=$( find "$FILE_DIR" -name "*.root" )
OUTPUT_DIR=/rstorage/alice/AnalysisResults/rey/$JOB_ID
hadd -f -j 20 $OUTPUT_DIR/AnalysisResultsFinal.root $FILES
```

- edit this file and replace `rey` with your username and edit the number in `JOB_ID=209383` with the correct run number that you would like to merge
- `source merge_data.sh`

3 Scaling and merging MC root files

The MC files are produced separate in $\hat{p}_T$ bins. This is done to focus the generation in different bins and accrue similar amount of statistics even in the bins where the cross section is small. Consequently, these files need to be scaled by the cross section before combining them.

1. hadd all root files corresponding to the same $\hat{p}_T$ bin. See, for example: slurm_merge_LHC18b8.sh and merge_LHC18b8.sh. Edit both files and replace `rey` with the appropriate username. Also, modify the number in `JOB_ID=209384` in `merge_LHC18b8.sh` to reflect the right job number.

```
sbatch slurm_merge_LHC18b8.sh
```

2. cd into the directory containing the 1/, 2/, ... sub-directories and scale the combined files corresponding to a given $\hat{p}_T$ bin by the appropriate scale factor. To do so, run scaleHistograms.py (with the correct file path) and config file associated with the simulation, e.g. -c /rstorage/alice/data/LHC18b8/scaleFactors.yaml. Here's an example:

```
python /home/rey/pyjetty/pyjetty/alice_analysis/slurm/utils/rey/scaleHistograms.py \
-c /rstorage/alice/data/LHC18b8/scaleFactors.yaml
```

3. After the histograms have been scaled, you should merge the $\hat{p}_T$ bins. See for example merge_pthat.sh. The number in the line `JOB_ID=209384` and paths should be updated. Then do:

```
source merge_pthat.sh
```

4 Analysis

4.1 Writing analysis code

You need to begin by creating a code in: `pyjetty/pyjetty/alice_analysis/analysis/user/`. This code will inherit from /substructure/run_analysis.py. For an example analysis code see: run_analysis_energy_drop.py.

4.1.1 Functions the user needs to implement

There are three main functions the user needs to implement in the analysis code:

- `plot_single_result()`
- `plot_all_results()`
- `plot_performance()`

The function names are self-explanatory.

4.2 Running analysis code

```
python analysis/user/rey/run_analysis_energy_drop.py  -c config/energy_drop/rey_pp.yaml
```

4.3 What happens when you run the analysis code

Right away, what the code does is it runs the 'main' function run_analysis() defined in `run_analysis.py`. The first step in this function is to do unfolding (if the user requested it) through the function perform_unfolding(), also defined in `run_analysis.py`.

This function loops over the 'systematic' settings defined in the config file. For each setting, the code sets variables related to inputs and outputs:

```
output_dir = getattr(self, 'output_dir_{}'.format(systematic))
data = self.main_data
response = self.main_response
main_response_location = os.path.join(getattr(self, 'output_dir_main'), 'response.root')
rebin_response = self.check_rebin_response(output_dir)
```

It the initializes some variables:

```
prior_variation_parameter = 0.
truncation = False
binning = False
R_max =  self.R_max
prong_matching_response = False
```

And it finally sets these variables depending on the systematic setting to be unfolded:

```
if systematic == 'trkeff':
   response = self.trkeff_response
elif systematic == 'prior1':
   prior_variation_parameter = self.prior1_variation_parameter
elif systematic == 'prior2':
   prior_variation_parameter = self.prior2_variation_parameter
elif systematic == 'truncation':
   truncation = True
elif systematic == 'binning':
   binning = True
elif systematic == 'subtraction1':
   R_max = self.R_max1
elif systematic == 'subtraction2':
   R_max = self.R_max2
elif systematic == 'prong_matching':
   prong_matching_response = True
```

Once these variables have been properly set, the code creates an instance of the Roounfold_Obs class, and subsequently runs the function roounfold_obs().

4.3.1 Unfolding

The `Roounfold_Obs` class and the `roounfold_obs()` function are defined in roounfold_obs.py.

When the instance of the `Roounfold_Obs` class is created, the function `create_output_dirs()` is called. This function creates the following directories: 'RM', 'Data', 'KinematicEfficiency', 'Unfolded_obs', 'Unfolded_pt', 'Unfolded_ratio', 'Unfolded_stat_uncert', 'Test_StatisticalClosure', 'Test_Refolding', 'Correlation_Coefficients' and if the variable `thermal_model` is true, 'Test_ThermalClosure'. Also, two directories called 'Test_ShapeClosure{}' are created. Here, {} corresponds to the prior variation parameters defined at the bottom of the config file (with periods removed). For instance, if the config file has:

```
prior1_variation_parameter: 0.5
prior2_variation_parameter: -0.5
```

then you will get the directories 'Test_ShapeClosure-05' and 'Test_ShapeClosure05'.

During the unfolding procedure, three validation tests are carried out:

1. Refolding test: the Response Matrix (RM) is multiplied by the unfolded result, and compared to the original detector-level distribution.

2. Statistical closure test:

   - MC det-level is smeared by an amount equal to the measured statistical uncertainty
   - the smeared det-level MC is then unfolded
   - unfolded smeared MC is compared to MC truth-level

   This test checks whether the unfolding procedure is insensitive to statistical fluctuations of the measured spectra.

3. Shape closure test:

   - MC det-level and MC truth-level spectra are scaled
   - scaled MC det-level spectrum is unfolded
   - MC truth-level and unfolded scaled MC det-level spectra are compared

   This test checks whether the unfolding procedure is insensitive to the shape of the measured distribution.