

-- PabloMatorrasCuevas - 2021-03-05

This should really be completed but

Right now:

### 1. MC :

- ◆ python mkPostProc.py -p Fall17\_106X\_nAODv8\_Full2017v8 -s MCSusy2017v8 -T TTTto2L2Nu -b
- ◆ python mkPostProc.py -p Fall17\_106X\_nAODv8\_Full2017v8 -s MCSusyCorr2017v8 -i MCSusy2017v8 -T TTTto2L2Nu -b
- ◆ python mkPostProc.py -p Fall17\_106X\_nAODv8\_Full2017v8 -s MCSusyNomin2017v8 -i MCSusy2017v8\_\_MCSusyCorr2017v8 -T TTTto2L2Nu
- ◆ python mkPostProc.py -p Fall17\_106X\_nAODv8\_Full2017v8 -s susyMT2recoNomin -i MCSusy2017v8\_\_MCSusyCorr2017v8\_\_MCSusyNomin2017v8 -T TTTto2L2Nu

### 2. Data:

- ◆ python mkPostProc.py -p Run2016\_106X\_nAODv9\_HIPM\_Full2016v8 -s DATASusy2016v8 -T DoubleEG\_Run2016B-ver1\_HIPM\_UL2016-v1 -b
- ◆ python mkPostProc.py -p Run2017\_106X\_nAODv8\_Full2017v8 -s DATASusy2017v8 -T MuonEG\_Run2017C-UL2017\_MiniAODv1\_NanoAODv2-v1 -b
- ◆ python mkPostProc.py -p Run2017\_106X\_nAODv8\_Full2017v8 -s DATASusyCorr2017v8 -i DATASusy2017v8 -T MuonEG\_Run2017C-UL2017\_MiniAODv1\_NanoAODv2-v1 -b

Also, it needs to be ran on \$LATINOULRUN

(/afs/cern.ch/work/p/pmatorra/private/CMSSW\_10\_6\_19/src/LatinoAnalysis/NanoGardener/scripts)

And if want to see where each stuff is written go to

LatinoAnalysis/NanoGardener/python/framework/Sites\_cfg.py

Other typical options (from here):

- **-p** : Production, taken from LatinoAnalysis/NanoGardener/python/framework/Productions\_cfg.py
- **-s** : Step, taken from LatinoAnalysis/NanoGardener/python/framework/Steps\_cfg.py
- **-b** : submit to batch [default is interactive execution]
- **-c** : submit via crab=
- **-n** : dry-run just produce script in job directory but did not submit
- **-T <sample1>, ... ,< sampleN >** : run only on these samples
- **-E <sample1>, ... ,< sampleN >** : do not run on these samples
- **-R** : redo all jobs even if output file exist
- **-Q < queue name >** : specify queue like 8nh [default btw, see Site\_cfg.py ], Not needed by default
- **--sitescfg <File>** : alternative site cfg
- **--modcfg <File>** : alternative step/module cfg
- **--datacfg <File>** : alternative production cfg

There's this submitSusySteps.sh that can do stuff much quicker since it checks also old steps:

```
./submitSusySteps.sh 18 mc
```

```
=./mkPostProc.py -p Summer20UL16_106X_nAODv9_noHIPM_Full2016v8 -i MCSusy2016v8 -s MCSusyCorr2016v8noHIPM -b -Q cms_med=
```

This topic: Sandbox > LatinoAnalysis

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