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First tests on gbasf2 usage: physics analysis and MC production

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Test on gbasf2 usage



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- Gbasf2 tutorial at the last B2GM as starting point:

<https://kds.kek.jp/indico/event/23336/session/54/?slotId=0#20170208>

- Three types of test performed:

- Running simple analysis jobs on MC7 with release-00-07-02 *OK*

- Running production jobs with custom arguments *~OK*

- Running more complex analysis using Full Event Interpretation

not working



Run simple analysis example on MC7



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- **Reconstruction of $B^0 \rightarrow J/\psi K_s$** ($J/\psi \rightarrow \mu\mu$ and $K_s \rightarrow \pi\pi$)

- Perform kinematic cuts and save the info into ntuples

- Usage (example taken from tutorial):

```
gbasf2 ./ana_jmumuks.py -p analysis0 -i /belle/MC/release-00-07-02/DBxxxxxxxx/MC7/prod00000223/s00/e0000/4S/r00000/signal/sub00
```

- **gbasf2 creates n jobs, one for each mdst file.** For example

```
basf2 -i mdst_000044_prod00000223_task00000043.root ana_jmumuks-43.py
```

- Download jobs output with:

```
gb2_job_output -p analysis0
```

```
gb2_ds_get /belle/user/merola/analysis0
```

- **Everything works smoothly**



Run MC production jobs with custom arguments (1)



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- It might be **useful for tests before the official production** starts, or if **need signal samples with different BG configurations** and/or with old releases
- In my case, for example, I needed to produce $B \rightarrow \tau \nu$ without beam background (with an old release)
- I have to specify by hand the number of events and the seed for generation, through the option “--basf2opt”. Also, I have to submit one job for each generation, with a command like:

```
gbasf2 ./BtaunuGenReco.py --basf2opt="Btaunu_bkg_100_test.root 100 10000 -l  
ERROR" -p merola_taugen_test
```

output file

number of
events

seed



Run MC production jobs with custom arguments (2)



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- In this case the jobs submission and splitting is not handled automatically as for the first example, but it works.
- **N.B.** by default gbasf2 does not accept custom input arguments of the script you want to run, but only basf2 standard args (-n, -i, -l, etc.). If you want to use custom arguments (for example the seed) you need to modify the basf2helper module.



Run advanced analysis using Full Event Interpretation (1)



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- Reconstruction of $B \rightarrow \tau \nu$ using the Full Event Interpretation (FEI) for the Btag side reconstruction
- The script loads the weight files produced by the FEI training
~140MB
- There is a way to upload additional files needed by the script through the `gbasf2` option “`-f`”:

```
gbasf2 ./BtagBsig.py -f FEI.tar --basf2opt=" -n 10 -l ERROR" -p  
merola_tauanufei_test3 -s release-00-07-02
```

...but the **limit file size is 10MB** because they are temporary copied to the dirac server and then to the worker node of the site where the jobs will run.



Run advanced analysis using Full Event Interpretation (2)



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- The idea is to **bypass the tmp copy to the dirac server.**
- Copy **the file to a specific SE** (for example with `gb2_ds_generate` command) and then tell the worker node where the jobs run the logical path of the file.
- Different technical implementations under investigation