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MCWrapper and Monte Carlo production

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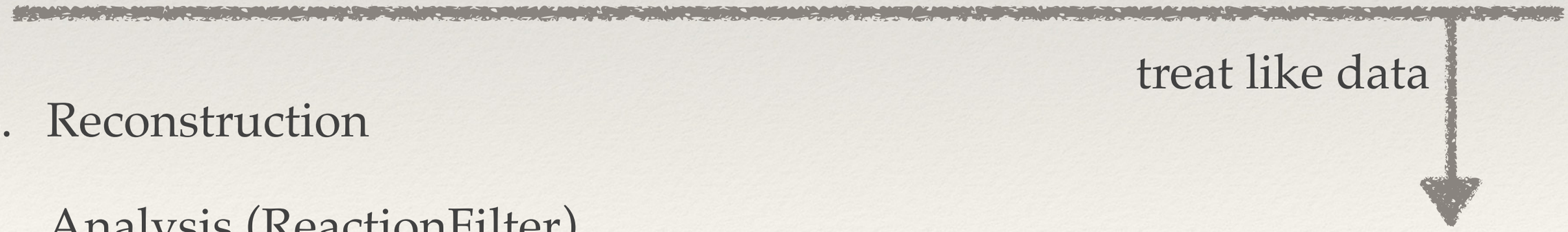
GlueX simulation chain

1. Event generation
   - Your favourite event generator (gen_amp, genr8, bggen, …)
2. Geant4 simulation
   - Use a Geant4 implementation of GlueX (hdgeant4) to simulate interactions inside the GlueX spectrometer
3. Smearing
   - Correct for deficiencies in simulation (“make it look more like data”)



4. Reconstruction
5. Analysis (ReactionFilter)

MCWrapper

- Most people doing simulations need to perform all these steps
  - Each step needs to be set up correctly
  - Environment variables, config files, …
  - Time consuming and prone to errors
- Solution: Write some code to do most of the work for you MCWrapper, a one-stop shop for MC production
- A few scripts that help to generate MC and are controlled by config files
- It is not almighty: garbage in - garbage out

MCWrapper

- Two ways to generate MC with MCWrapper:

  - Locally
    - Write a config file that controls MCWrapper
    - Run either in shell or submit to batch farm
  - OSG
    - Use a website to generate config file
    - Submit to the open science grid

- Software setup: It is already in your path when using gxenv!

```
setenv MCWRAPPER_CENTRAL /scigroup/mcwrapper/gluex_MCwrapper/
```

MCWrapper - locally

Usage: $MCWRAPPER_CENTRAL/gluex_MC.py

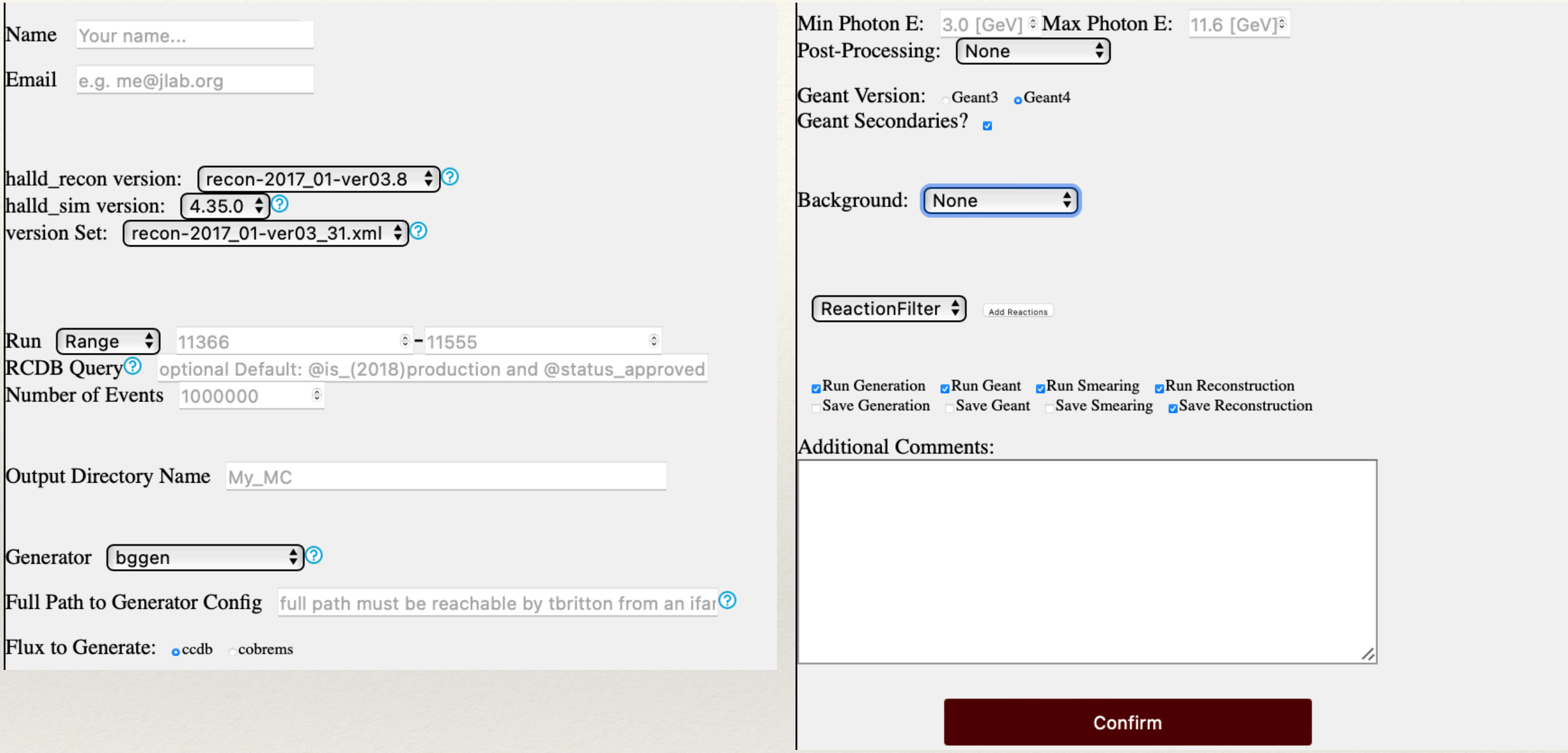
```
ifarm1901.jlab.org> $MCWRAPPER_CENTRAL/gluex_MC.py
Usage: gluex_MC.py config_file Run_Number/Range num_events [all other options]

 where [all other options] are:

 variation=%s where %s is a valid jana_calib_context variation string (default is "mc")
 per_file=%i where %i is the number of events you want per file/job (default is 10000)
 base_file_number=%i where %i is the starting number of the files/jobs (default is 0)
 numthreads=%i sets the number of threads to use to %i.  Note that this will overwrite the NCORES set in MC.config
 generate=[0/1] where 0 means that the generation step and any subsequent step will not run (default is 1)
 geant=[0/1] where 0 means that the geant step and any subsequent step will not run (default is 1)
 mcsmear=[0/1] where 0 means that the mcsmear step and any subsequent step will not run (default is 1)
 recon=[0/1] where 0 means that the reconstruction step will not run (default is 1)
 cleangenerate=[0/1] where 0 means that the generation step will not be cleaned up after use (default is 1)
 cleangeant=[0/1] where 0 means that the geant step will not be cleaned up after use (default is 1)
 cleanmcsmear=[0/1] where 0 means that the mcsmear step will not be cleaned up after use (default is 1)
 cleanrecon=[0/1]where 0 means that the reconstruction step will not be cleaned up after running (default is 0)
 batch=[0/1/2] where 1 means that jobs will be submitted, 2 will do the same as 1 but also run the workflow in the case
of swif(2) (default is 0 [interactive])
 logdir=[path] will direct the .out and .err files to the specified path for qsub


Options:
  -h, --help  show this help message and exit
```

- Need to provide config file

Example:
https://github.com/JeffersonLab/gluex_MCwrapper/blob/master/examples/MC.config

MCWrapper - OSG

https://halldweb.jlab.org/gluex_sim/SubmitSim.html



- Drop-downs and text boxes to set up MC submission
- Click ? to access documentation
- Automatically tested and submitted to Open Science Grid

MCWrapper - OSG

https://halldweb.jlab.org/gluex_sim/Dashboard.html

- Dashboard lets you monitor progress (new improved performance!)
- Status:
  - Red = test no successful (check your emails!)
  - Green = tested successful, project running
- Left click - more infos, right click - options (cancel, declare complete)

Projects

Show 10 entries

Progress %	ID	Email	Status	RunNumLow	RunNumHigh	NumEvents	Generator	BKG	R
2.7	2520	nwickjlb@jlab.org		50685	51768	250000000	gen_amp	Random:recon-2018_08-ver02.2	@is_ @s bean
0	2519	churaman@jlab.org		40856	42559	10000000	genEtaRegge	None	
30.79	2518	churaman@jlab.org		40856	42559	10000000	genEtaRegge	None	
29.41	2517	churaman@jlab.org		40856	42559	10000000	genEtaRegge	None	
0	2516	churaman@jlab.org		40856	42559	10000000	genEtaRegge	None	

MCWrapper - OSG

https://halldweb.jlab.org/gluex_sim/Records.html

- Records show all previously produced MC, worth checking before submitting new
- Contains all important information about projects

Projects

Refresh tables

Show 10 entries Search:

ID	Email	user_id	Exp	Submit_Time	Tested	Is_Dispatched	Dispatched_Time	Completed_Time	RunNumLow
2510	zbaldwin@andrew.cmu.edu	51	GlueX	2022-05-11 08:53:40	1	1.0	2022-05-13 10:53:42		30274
2509	zbaldwin@andrew.cmu.edu	51	GlueX	2022-05-11 08:14:37	1	1.0	2022-05-13 10:53:33		30274
2508	zbaldwin@andrew.cmu.edu	51	GlueX	2022-05-09 14:22:00	4	1.0	2022-05-09 21:57:48	2022-05-11 09:09:26	30274
2506	gabyrod7@gmail.com	29	GlueX	2022-05-06 15:44:55	1	1.0	2022-05-09 21:55:37		30274
2505	jzarling@jlab.org	20	GlueX	2022-05-05 17:43:51	1	1.0	2022-05-09 21:55:14		51384
2504	jzarling@jlab.org	20	GlueX	2022-05-05 17:42:26	1	1.0	2022-05-09 21:56:26		51384

Event generator

- Generic background samples:
  - bggen
- Simple phase space:
  - genr8
- Sophisticated amplitude models:
  - gen_amp
  - gen_vec_ps
- For studies:
  - particle gun
  - geantBEAM

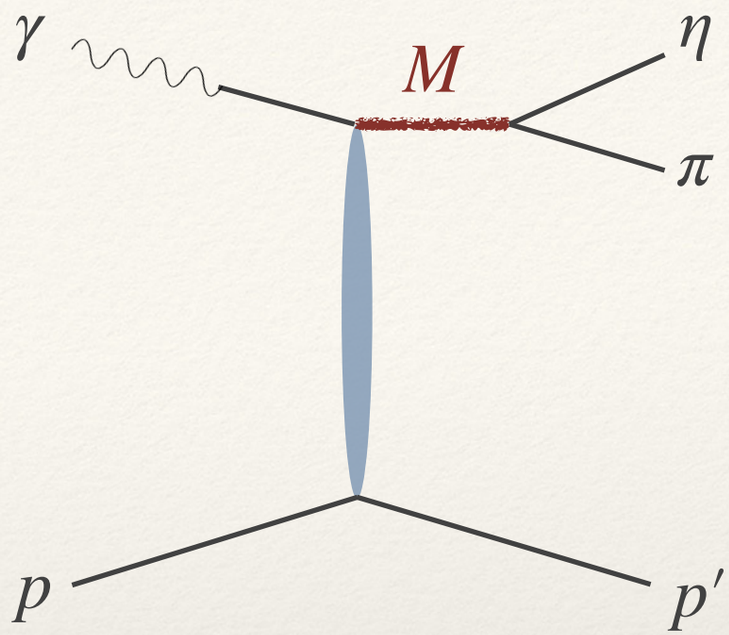
Decaying particles can either decay in hdgeant4 or you can specify the decay through generator post-processing, e.g. decay_evtgen

Choice of version set

- It is important to use the correct version set for the task at hand!
- In general, use the latest software version, linked to version.xml
  `gxenv $HALLD_VERSIONS/version.xml`
  - Latest versions of DSelector, amptools, etc…
- If you want to generate MC to use for acceptance correction you need to make sure that you **treat the simulations as data was treated**
  - Reconstruction code must be the same as during reconstruction
  - Analysis software must be the same as during analysis launch
  - There are special version sets for this
  - This might require to set up MCWrapper again, e.g.
    `setenv MCWRAPPER_CENTRAL /scigroup/mcwrapper/gluex_MCwrapper/`

Example: $\eta\pi$ simulations

- We need flat MC to perform fits for PWA
- Use gen_amp for both
  - First line in config file (commented out) contains switches for MCWrapper
    - Simple switch `-f` to generate flat MC
    - Choose appropriate t-slope, option `-t`
- Force $\eta \to \gamma\gamma$
- Generate for 2017-01 analysis ver52



session2b > EtaPi0Flat.cfg

```
1   # -f -u 3.0 -a 8.2 -b 8.8
2   reaction EtaPi0 Beam Proton Eta Pi0
3
```

session2b > EtaDecay.dec

```
1   Decay eta
2   1.000        gamma gamma          PHSP;
3   Enddecay
4
5   End
6
```

Example: $\eta\pi$ simulations (locally)

Make sure to source appropriate software versions!

session2b > MC.config

```
DATA_OUTPUT_BASE_DIR=/volatile/halld/home/ppauli/gluex_workshops/tutorial_2022/session2b/etapi_out/ #your desired output location
NCORES=1      # Number of CPU threads to use or nodes:node-id:ppn or nodes:ppn depending on your system

GENERATOR=gen_amp #or you may specifile file:/.../file-to-use.hddm
GENERATOR_CONFIG=/group/halld/Software/gluex_workshops/tutorial_2022/session2b/EtaPi0Flat.cfg
GENERATOR_POSTPROCESS=decay_evtgen:/group/halld/Software/gluex_workshops/tutorial_2022/session2b/EtaDecay.dec #:pathToEVT.PDL:pathToDECAY.DEC # last two are optional

#common parameters for generators
GEN_MIN_ENERGY=8.2
GEN_MAX_ENERGY=8.8

GEANT_VERSION=4
BKG=Random:recon-2017_01-ver03.2 #Use random trigger background for 2017-01
ANA_ENVIRONMENT_FILE=/group/halld/www/halldweb/html/halld_versions/analysis-2017_01-ver52.xml #optional either a .(c)sh file to be sourced or .xml before the below pl

#optional additional plugins that will be run along side danarest and hd_root.  This should be a comma separated list (e.g. plugin1,plugin2)
CUSTOM_PLUGINS=file:/group/halld/Software/gluex_workshops/tutorial_2022/session2b/jana_analysis.config #or file:/.../file-to-use which is a configuration file for jan
#============================================================================================
#EVERYTHING BELOW FOR BATCH ONLY

#VERBOSE=True
BATCH_SYSTEM=swif2 #can be swif or swif2 or condor or osg or qsub adding :[name] will pass -q [name] into PBS.

#environment file location
ENVIRONMENT_FILE=/group/halld/www/halldweb/html/halld_versions/recon-2017_01-ver03_32.xml     #change this to your own environment file

WORKFLOW_NAME=FlatEtaPi0Tut22 #SWIF WORKFLOW NAME

# for swif
PROJECT = gluex          # http://scicomp.jlab.org/scicomp/#/projects
TRACK= simulation        # https://scicomp.jlab.org/docs/batch_job_tracks
# for swif2
ACCOUNT = halld          # https://scicomp.jlab.org/scicomp/slurmJob/slurmAccount
PARTITION = production       # https://scicomp.jlab.org/scicomp/slurmJob/slurmInfo
EXPERIMENT = GlueX       # GlueX (default) or CPP

# RESOURCES for swif(2) jobs
DISK=5GB            # Max Disk usage
RAM=5GB            # Max RAM usage
TIMELIMIT=600minutes      # Max walltime.  This may be of the form xx:xx:xx depending on your system
OS=general        # Specify CentOS65 machines
```

`$MCWRAPPER_CENTRAL/gluex_MC.py MC.config 30274-31057 1000000 (batch=2)`

Example: $\eta\pi$ simulations (OSG)

Experiment

GlueX | CPP | JEF

Name Peter Pauli

Email ppauli@jlab.org

halld_recon version: recon-2017_01-ver03.8

halld_sim version: 4.35.0

version Set: recon-2017_01-ver03_31.xml

Run Range 30274 - 31057

RCDB Query optional Default: @is_(2018)production and @status_approved

Number of Events 1000000

Output Directory Name etapi0_gluex_workshop

Example: $\eta\pi$ simulations (OSG)

Generator gen_amp

Full Path to Generator Config /group/halld/Software/gluex_workshops/tutorial_2022/session

Flux to Generate: ccdb cobrems

Min Photon E: 8.2 Max Photon E: 8.80

Post-Processing: decay_evtgen

decay_evtgen Config: /group/halld/Software/gluex , (optional) pdl: Default ,

(optional) dec: Default

Geant Version: Geant3 Geant4

Geant Secondaries?

Background: Random recon-2017_01-ver03.2

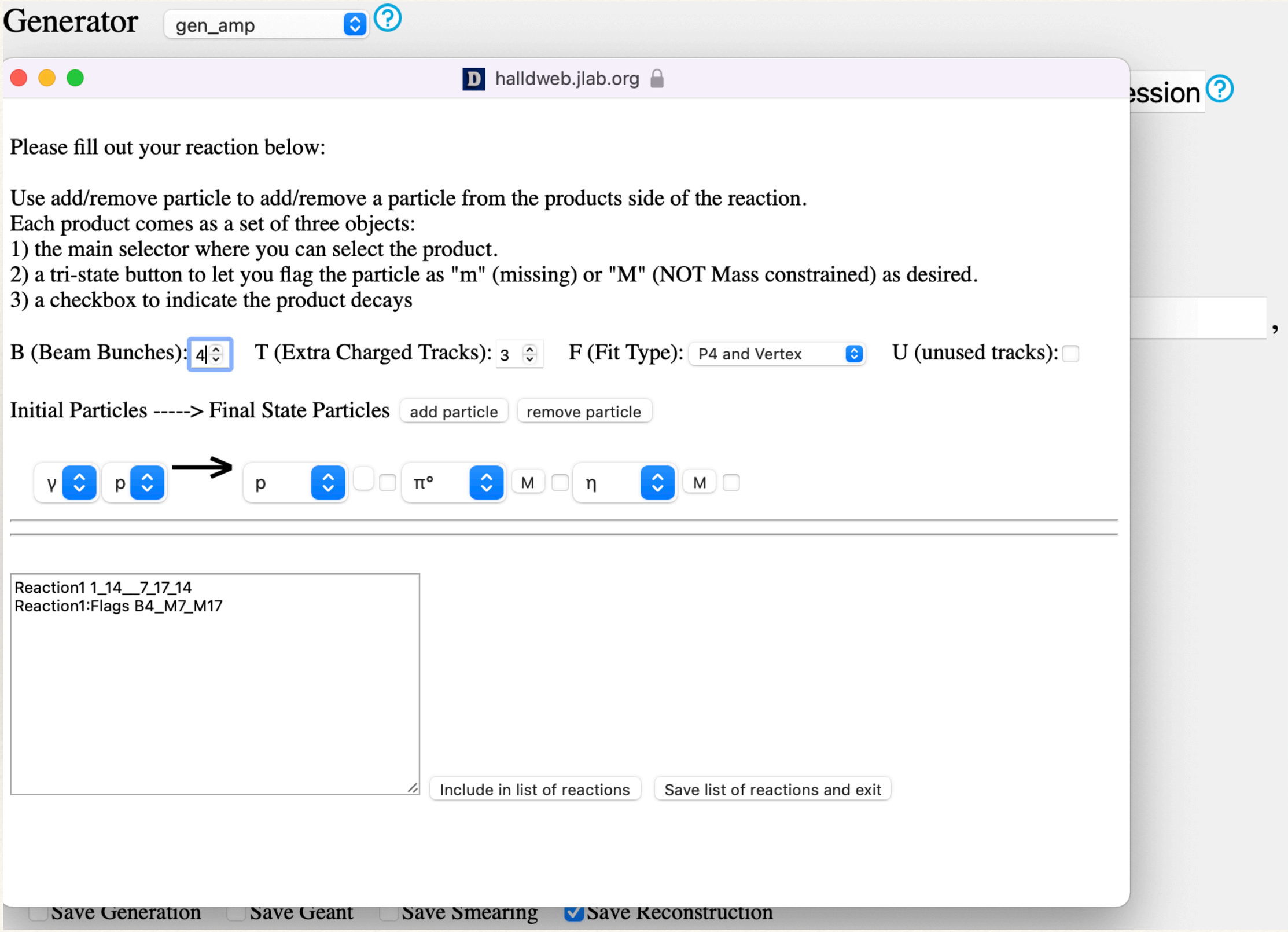
ReactionFilter Reactions Set Reaction1 1_14__7_17_14
Reaction1:Flags

analysis version Set: analysis-2017_01-ver52.xml

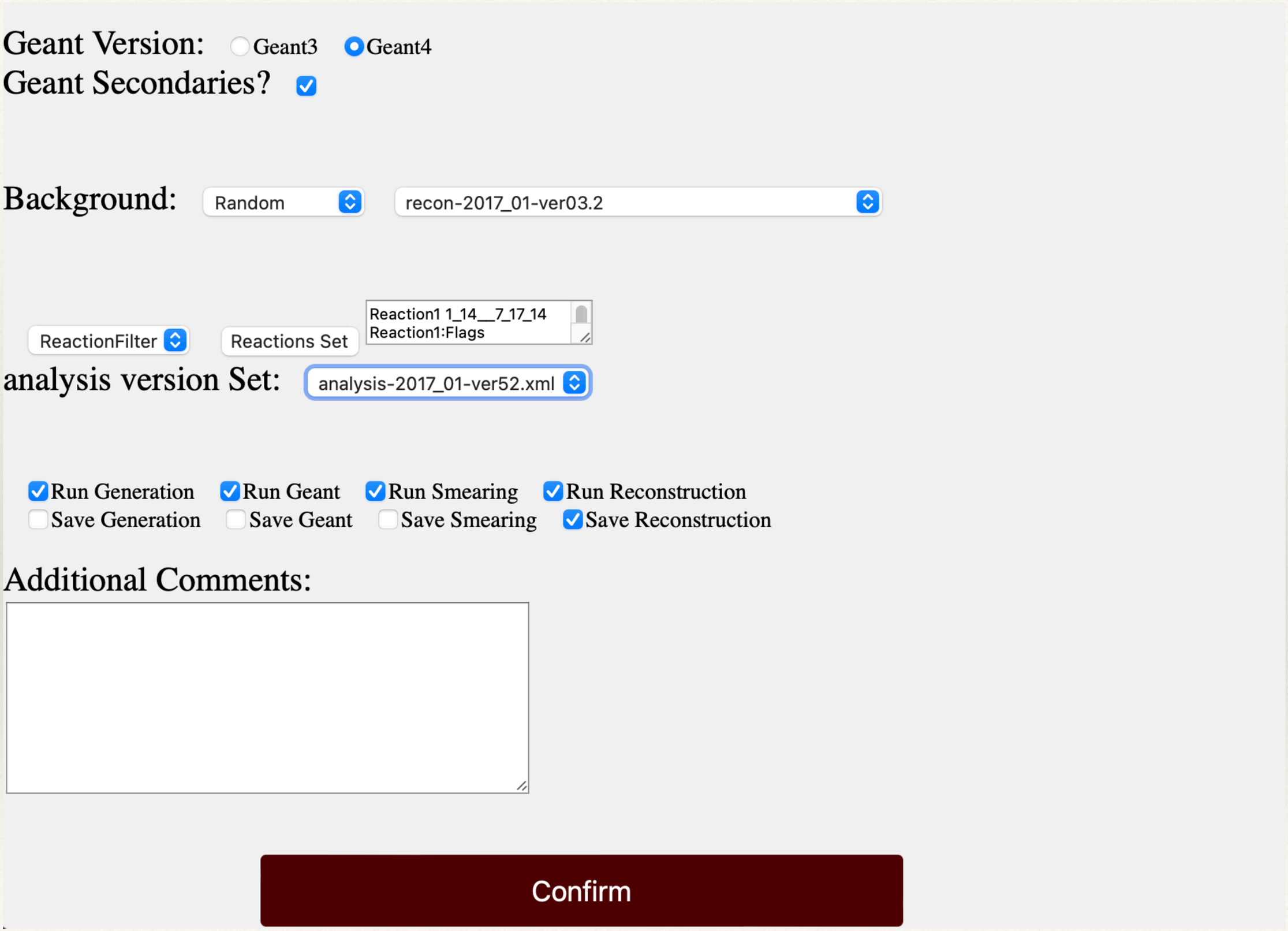
Run Generation Run Geant Run Smearing Run Reconstruction

Save Generation Save Geant Save Smearing Save Reconstruction

Example: $\eta\pi$ simulations (OSG)



Example: $\eta\pi$ simulations (OSG)



Summary and Resources

- MCWrapper is a collection of scripts (not compiled!) that aids in producing Monte Carlo samples
- Use it locally (with config file) or submit to OSG
- Documentation:
  - https://github.com/JeffersonLab/gluex_MCwrapper
  - DSelector: https://www.overleaf.com/read/bqynmnwstzfx
  - https://halldweb.jlab.org/wiki/index.php/Event_generators
  - https://halldweb.jlab.org/wiki/index.php/HOWTO_Use_EvtGen_to_simulate_particle_decays_in_GlueX
  - https://halldweb.jlab.org/wiki/index.php/How_to_choose_software_versions_on_the_MC_submission_form
- Need help? Email ppauli@jlab.org and tbritton@jlab.org