# Instructions for analysis shifts VCS E12-15-001 experiment

• Connect to cdaql1: ssh cdaql1 and go to /home/cdaq/vcs2019/hallc\_replay\_vcs

# Kinematic setting

- Each time the spectrometer move to a new kinematic setting, edit the file: DBASE/COIN/standard.kinematics
- On the last setting, enter the last run number of last setting instead of "9999"
- Using the same format than the last setting, enter the first run number of the new setting, followed by the generic "9999" as last run number for this new setting
- Enter new values (if relevant) for: beam energy (in principle it won't change), target mass (amu), HMS and SHMS central momentum and angle, particle mass detected in each arm (in principle, it won't change: proton in HMS, electron in SHMS). Note that the names of arm variable start with letter "h" for HMS and "p" for SHMS.

# • HMS and SHMS replay

- Run standard HMS and SHMS coincidence replay after 50000 events and after the run is done. Run:
- > ./run\_coin\_hms.sh > ./run\_coin\_shms.sh

It replays the most recent run and monitoring plots will automatically open.

- Check all the figures and compare them to the reference. If anything seems wrong, write it in the database and/or run sheet. If something needs to be fixed, do it or ask expert

## Analyzer coincidence and physics replay

- After 200,000 events and once the run is finished, run the analysis replay:
- > ./build\_singlecoinfile.csh (run number) 200000
- > ./build singlecoinfile.csh (run number) -1

Don't forget later to run the full replay at least once! It can take a long time to convert the data.

- This command will convert data to coincidence root files, build a database, run analysis monitoring plots and provide a reduced root file for this run.
- If needed for a second monitoring or after changing analysis cuts, run only the analyzer, without replaying the full run. It takes only a few minutes for a complete run. Do:
- > cd Ana

Then, change cuts in ANA\_CUTS.input if needed. Keep track of the cuts you set. Please don't change any source code in this directory. If you want to make modification, go the the github: jeffersonlab/hallc\_replay\_vcs and fork to your github directory. Then, you can make modification from your directory for testing cuts or monitoring other variables.

> ./HallCana "vcs" "ana" "LH2" "runnumber" -f "input file .root" (look at the README.txt for details)

#### • Things to check:

All the monitoring information will be open automatically at the end of the replay. Check additionnal information if needed.

#### 1) Timing cuts

- Open: Ana/files/timing\_(run).dat
- → the first line is information about the selected coincidence time peak in order:

peak position, charges – bkg, charges in peak, bkg (low), bkg (up), peak max

- check if the peak position is < 0.2, if not, change time shift in ANA\_CUTS.input and run again the analyzer

- check that charges in peak >> bkg (low, up)
- enter the value of charges bkg in the run database
- Look if there is a secondary or third peak: lines 2 and 3 correspond to potential physics peaks. If the value of charges background is significant, compare values of charges in peak and average background (up, low). If the number of charges in this peak is significantly higher, enter it in the run database and enter the peak position
- If no peak is found, try to figure out why:

Possibilities: open the range in the histogram to see if there is a peak somewhere, check the quality of the fit and of the peak finder (monitoring figures, see below), change cuts and replay the analyzer... It may also be that there is not enough events in this run: check the luminosity / running time if it is the case and if there is any reason for that. First check histograms, and make a log entry and/or write it is database and/or the run sheet if anything is wrong and/or write it in the database and the run sheet. Call the expert if needed to avoid loosing good data.

## 2) Luminosity

- Open: Ana/files/lumi\_(run).dat

The one line contains: run number, luminosity (HMS), luminosity (SHMS), actual running time (HMS), actual running time (SHMS), current (HMS), current (SHMS)

- check if the luminosity are the same in HMS and SHMS, and write them in the run database. If there are different, try to figure out why and call expert if needed.

## 3) Missing mass peaks position

- Open: Ana/files/missmass2\_(run).dat
- 3 lines correspond to possible 3 found peaks in the squared missing mass, with: M<sup>2</sup>, integral, index, max peak
- record the position of the 2 main peaks: VCS  $M^2 \sim 0$  GeV $^2$  and  $\pi^\circ$   $M^2 \sim 0.02$  GeV $^2$  and the ratio of the integrals int(VCS) / int ( $\pi^\circ$ )
- if the ratio doesn't make sense and is far from  $\sim 1/10$ , check the quality of the fit and/or try to understand. If something is wrong, write it in the database and/or run sheet.
- if less than one peak is found, or the 2 peaks (VCS and  $\pi^{\circ}$ ) are merged into one, it may be a problem with the calibration, resolution... Try to understand why. If the problem is very bad, write in database and run sheet.

## 4) Monitoring plots, to compare with reference plots

All the figures to look at will pop-up in a condensed replay "ana\_monitor\_(run).pdf. If additionnal check need to be done, open the extra pdf files as indicated.

Timing

Extra monitoring: Ana/Results/cointime (run).pdf

- → Look at the coincidence time distribution for ROC2: if no peak is found there is a problem, try to understand why. If no peak is found near 0 and/or no peak for the red curve, change the time shift in ANA\_CUTS.input and replay the analyzer.
- → Check the quality of the peak finder and the fitting
- $\rightarrow$  Compare  $\beta$  and missing mass distributions to reference
- · Kinematic distributions

Extra monitoring: Ana/Results/kinematics (run).pdf and Ana/Results/kinematics2D (run).pdf

- → Compare the figures with reference plots for each kinematic setting.
- → Check also Ana/Results/positions\_(run).pdf if something strange. If the HMS and SHMS positions don't match expectation from run plan, figure out why and/or call an expert.

· Exclusivity distributions

Extra monitoring: Ana/Results/exclusivity\_(run).pdf (multipage)

- → Compare selected data exclusivity distributions to the reference
- $\rightarrow$  Check if there are 2 missing mass peaks on the missing mass and squared missing mass distributions corresponding to 0 mass and  $\pi^{\circ}$  mass, compare to the reference
- · Analysis root data

Check if a root file has been created and contains data:

- > root -l Ana/files/HallCdata\_(run).root
- > (root) > HallCTree->GetEntries();
- > (root) > HallCTree->Show(0);

The number of entry depends on the number of events processed, but should be significant if cuts are properly set. The event 0 display contains reasonnable values (check other events in case). Write it down as run comment on the checklist if there is a problem.