Friendly guide for performing electron neutrino analysis with WatChMaL framework.

For running Charlie's analysis you need to have corresponding fitqun and softmax files, where softmax file is an output of evaluation with WatChMaL model on wesim data. Then you need to list files locations row-by-row in fitqun_files.txt and softmax_files.txt.

Usage of this files together required changes in **RecoInterface**. Also, Charlie's script *analysis_1ringe.cc*, was modified for next purposes:

- new_first_cut_analysis_1ringe_pmu, new_first_cut_analysis_1ringe_pe, new_first_cut_analysis_1ringe_pgamma for each class probability histos.
- log_first_cut_analysis_1ringe_pmu for log scale 1D probability histo.
- analysis_energy and analysis_momentum for energy and momentum 1D histos.
- logmomentum_pmu for reco momentum with log scale probability mu 2D histo.

For running the code you have to perform next steps:

module load StdEnv/2016 source Source_At_Start_nuPRISM.sh source \$DataTools/cedar_scripts/sourceme.sh

Then for single job run $run_single_job.sh$. Here you can change the scripts you need, e.g.:

./bin/logmomentum_pmu \$1 \$2 ./outputs/histo_\$3.root. Here arguments correspond to single fitqun_files_N.txt, softmax_files_N.txt and N respectively.

For multiple jobs in parallel just run run_all_jobs . It will produce multiple histos in root files, so you need split your softmax and fitqun files (as it was done in np_splited directory).

For converting softmax files to root format run $softmax_to_root.py$. Modify it for proper files locations which would be listed. If you need to split list of all files, use $files_split.py$.

Jupyter notebook contains plots for this analysis.