MINERvA Beginner User's Handbook

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MINERvA-doc-8772-v2

Contents

1 Getting Started

- The purpose of this Handbook is to help future graduate students to get involved with the physics analysis of the MINERvA Experiment.
- Any Comments & Suggestions welcomed!
  - oaltinok@fnal.gov
- For getting Fermilab ID and Computer Privileges, use the following reference:
  - https://cdcvs.fnal.gov/redmine/projects/minerva-sw/wiki/New_Users

2 Remote Connection

2.1 Remote Connection Addresses

- FNAL Minerva Machines
  - minervagpvm02.fnal.gov
  - minervagpvm03.fnal.gov
- FNAL Grid Settings Machine: Use this **ONLY** for setting your grid accounts.
  - gpsn01.fnal.gov

2.2 Installing MIT Kerberos on Windows

For a detailed procedure refer to the website:

- http://www.fnal.gov/docs/strongauth/winexceed7.html

For a short version[1]:

1. Log into an account with administrator privileges. Download the Kerberos client software from MIT. First browse to: http://web.mit.edu/network/kerberos-form.html.
2. This brings you to the MIT Kerberos Distribution Page. Scroll down to the latest MIT Kerberos for Windows and click. Next click on the file listed next to Installer. Save the file to disk. The default location it chooses is C:\Program Files\Accessories.
3. Once this file is copied on to your machine, execute it to install the Kerberos program. You will be asked a series of questions, but you can safely use the defaults, and just click through the screens. Checking the time synchronization when prompted is a good idea. The software gets installed under C:\Program Files\Kerberos by default.
4. After installing the files, it will ask if it's OK to restart your computer. Say yes.

2.3 Configuring Kerberos

1. Log back on to the same account with administrator privileges.
2. Create the configuration file krb5.ini same as the reference [2], and put it in your Kerberos folder. (If you accepted the default installation values, this folder is under C:\Program Files.) The krb5.ini file is comparable to the krb5.conf on UNIX.
3. Kerberos File Content:

- http://www.fnal.gov/docs/strongauth/winexceed7.html#57413

2.4 Software Solutions for Windows

- There are lots of different software to use for this purpose, my personal selection:

1. Remote connection terminal with kerberos privileges
   (a) Free Option: Putty.exe, good for short session connections
   (b) Commercial Solution: SecureCRT, very reliable and works with kerberos without any problem
2. For file transfer, I like to use FileZilla(Not working for Fermilab, at least I could not do the settings as in the reference: [2])
3. For XWindow, I like to use XMing

2.5 Remote Connection Procedure

1. Take a new kerberos ticket using Network Identity Manager(NetID)
2. Run XMing
3. Connect to a fermilab machine
4. If you are using “Putty.exe” you need to take a new kerberos ticket using: **kinit ’username’.** Apparently the SecureCRT does not need another kerberos ticket.

- The first ticket allows you to connect fermilab machine, the second ticket allows you to do stuff inside a fermilab machine.

3 MINERvA Software

3.1 Setup Files

Refer to website:

- https://cdcvs.fnal.gov/redmine/projects/minerva-sw/wiki/How_to_set_up_local_working_directory
- Every time you should run a setup file to let the system know which version to use.
- Everyone has their personal setup file for their needs but an example setup file looks like this:

```
export User_release_area=/minerva/app/users/USERNAME/cmtuser/
source /grid/fermiapp/minerva/software_releases/${MRELEASE}/setup.sh
export USER_DATA_AREA=/grid/data/minerva/USERNAME/
setenvMinerva
```

3.2 Software Packages in General

For a detailed explanation refer to website:

- https://cdcvs.fnal.gov/redmine/projects/minerva-sw/wiki/How_to_set_up_local_working_directory
- It is wise to consult an expert on that package before using it. Sometimes, latest versions may not be stable to use in your analysis.

Getting a Package Example

- For getting a new package always follow this example order:

```
>source setup.sh v10r6p2
>cd path/to/cmtuser
>setenvMinerva v10r6p2
> // While you are in cmtuser area, get the package you want
```

- to get the latest version of a package:

```
>cvs co ProductionScripts
```

- to get a specific version v10r4p4:

```
>cvs co -r v10r4p4 ProductionScripts
```

- Old Style: More stable,

```
>getpack -u Tools/SystemTests  //Choose 'h' (head) for latest version
```

- Some packages depend each other, if you have compilation problems, check for dependencies. (Consult an expert on that package)

Building a Package Example

- Only after getting a new package

```
>cd Tools/SystemTests/cmt
>cmt config //if you use "getpack -u" you do not need this line
>source setup.sh
>cmt make
```

- Every time you want to use a package

```
>cd Tools/SystemTests/cmt
>source setup.sh
```

- Every time after you change something in the package

```
>cd Tools/SystemTests/cmt
>source setup.sh
>cmt make
```

3.3 Tools/ProductionScripts

- Get & Compile the Package

```
>getpack -u Tools/ProductionScripts
>cd Tools/ProductionScripts/cmt
>source setup.sh
>cmt make
```

3.3.1 mc_scripts/ProcessMC.py

For a detailed information about ProcessMC.py, type:

```
>./ProcessMC.py --help
>./ProcessMC.py --help-pc
```

- To have different output with same files:

```
--outdir /path/to/different/dir
--outtag TestB
```

3.3.2 Particle Cannon with ProcessMC.py

Example for Particle Cannon: 100 events of

- μ^+: momentum = $4.0\,GeV$ & $\pm 10°$relative to beam direction
- π^- : momentum = $0.5\,GeV$

For this example, the **Output** DST file created in:

```
/minerva/data/users/‘‘user_name’’/mc_production/grid/central_value/
minerva/dst/v10r5p1/00/05/00/01/
SIM_minerva_00050001_0001_Reco_DST_v4_v10r5p1.root
```

Similarly the **Input** files for steps 2,3,4 are created in different folders(cal, reco, minos, etc.) in:

```
/minerva/data/users/‘‘user_name’’/mc_production/grid/central_value/
minerva/
```

3.3.3 ./ProcessMC.py –cal-pc

This is the first step to start, the code outline

-r	-s	-n
50001	1	100

Table 1: Event Specifications

	–name	–flux	–momentum	–thetamin	–thetamax	–phimin	–phimax	–vertex
μ^+	mu_plus	-13	4.0	-0.061	-0.057	1.545	1.57	primary
π^-	pi_minus	-211	0.5					primary

Table 2: Particle Specifications

	–name	–zCenter	–deltaZ
primary	primary	6950	1050

Table 3: Vertex Specifications

The code line: (all one line)

```
>./ProcessMC.py --cal-pc -r 50001 -s 1 -n 100
--particle "--name mu_plus
--flux -13
--momentum 4.0
--thetamin -0.061 --thetamax -0.057
--phimin 1.545 --phimax 1.57
--vertex primary"
--particle "--name pi_minus --flux -211 --momentum 0.5 --vertex primary"
--vertex "--name primary --zCenter 6950 --deltaZ 1050"
```

3.3.4 ./ProcessMC.py –minos

This is the step where MINOS information is added
Important Info: You may skip this step, if you do not have an energetic muon.
The code line:
>./ProcessMC.py –minos -r 50001 -s 1 -n 100

3.3.5 ./ProcessMC.py –reco

This is the step where RECO files created
Important Info: If you skipped minos step or there are no output file after minos step. Run with "–no_minos" option.
The code line:
>./ProcessMC.py –reco -r 50001 -s 1 -n 100 –inv v10r5p1
or
>./ProcessMC.py –reco -r 50001 -s 1 -n 100 –no_minos –inv v10r5p1

3.3.6 ./ProcessMC.py –dst

Last step creates the DST files

The code line:
>./ProcessMC.py –dst -r 50001 -s 1 -n 100 –inv v10r5p1

3.3.7 Another Example

Each ./ProcessMC.py line is one line:

```
========================================================================
Sample 6: mu_minus 4.0 GeV, K_plus 0.5 GeV
========================================================================
>./ProcessMC.py --cal-pc -r 50006 -f 1 -l 100 -n 1000
--particle "--name mu_minus --flux 13 --momentum 4.0
--thetamin -0.061 --thetamax -0.057 --phimin 1.545 --phimax 1.57
```

```
--vertex primary"
--particle "--name k_plus --flux 321 --momentum 0.5
--vertex primary"
--vertex "--name primary --zCenter 6950 --deltaZ 1050"
>./ProcessMC.py --minos -r 50006 -f 1 -l 100 -n 1000

>./ProcessMC.py --reco -r 50006 -f 1 -l 100 -n 1000 --inv v10r5p1

>./ProcessMC.py --dst -r 50006 -f 1 -l 100 -n 1000 --inv v10r5p1
```

3.4 Ana/CCPionInc

- Primary Contact: Brandon Eberly - eberly@FNAL.GOV
- "Ana/CCPionInc" depends on "Ana/AnaUtils"
- First Get & Compile "Ana/AnaUtils"

```
>getpack -u Ana/AnaUtils
>cd Ana/AnaUtils/cmt
>source setup.sh
>cmt make
```

- Second Get & Compile "Ana/CCPionInc"

```
>getpack -u Ana/CCPionInc
>cd Ana/CCPionInc/cmt
>source setup.sh
>cmt make
```

3.5 Options File

This information provided by

Brandon Eberly
Graduate Student
University of Pittsburgh
bme12@pitt.edu

To create an options file, it is easiest to use an existing one as a base.
Copy Tools/SystemTests/options/MCFullChain/MCReco_fCalDigits.opts to your disk space.
Open it, and look for a series of lines that look like this:

```
ApplicationMgr.TopAlg += { "MinosDataAlg" };
ApplicationMgr.TopAlg += { "XTalkScoreGraderAlg" };
ApplicationMgr.TopAlg += { "ClusterFormationAlg" };
ApplicationMgr.TopAlg += { "PrimaryVertexAndTrackBuilder" };
ApplicationMgr.TopAlg += { "AttenuationAlg" };
ApplicationMgr.TopAlg += { "PrimaryTrackProngAlg" };
ApplicationMgr.TopAlg += { "DSTWriterAlg" };
 ApplicationMgr.TopAlg += { "POTCounterAlg" };
```

This listing tells the Gaudi job which algorithms to run and specifies the order.
Notice that it is the typical reconstruction order:
Make clusters (ClusterFormationAlg) find tracks (PrimaryVertexAndTrackBuilder), etc...
You will want to add a new algorithm to this chain that finds short tracks.
The short track algorithm is VertexAnchoredShortTrackFinderAlg,
so you will want to insert a line like this into the algorithm chain:

```
ApplicationMgr.TopAlg += { "VertexAnchoredShortTrackFinderAlg" };
```

The best place to put this algorithm is between PrimaryVertexAndTrackBuilder and AttenuationAlg,
because you need vertices to anchor the short tracks and you will want attenuation to be applied to any short tracks that are found.

You can look at VertexAnchoredShortTrackFinderAlg here:

http://cdcvs.fnal.gov/cgi-bin/public-cvs/cvsweb-public.cgi/AnalysisFramework/Rec/EventReconstruction/src/VertexAnchoredShortTrackFinderAlg.cpp?cvsroot=mnvsoft

Notice that in the code, there are lines like these:

```
declareProperty( "PrioritizeStartPointVertices", m_prioritizeStartPointVertices = false );
declareProperty( "AddFoundTracksToVertex", m_addFoundTracksToVertex = true );
declareProperty( "RefitVertex", m_refitVertex = true );
 //refit the vertex if new tracks are added declareProperty
( "RunTrackAddClusters", m_runTrackAddClusters = false );
```

These are runtime options that you can specify in your options file.
For example, if you want to try to add additional clusters to a short track after it is found, simply put this line in your options file:

```
VertexAnchoredShortTrackFinderAlg.RunTrackAddClusters = true;
```

Otherwise, the default value (false) will be used.
I recommend that you initially run with all default values, but you can later try changing them
if you think that an alternative value would make better tracks.

Also notice that the code contains an initialize function that initializes Gaudi "Tools":

```
try { m_anchoredTracker = tool<IAnchoredTrackFormation>
( m_anchoredTrackerTool, m_anchoredTrackerAlias ); }
 catch( GaudiException& e ) { error() << "Could not obtain tool: "
<< m_anchoredTrackerTool << endmsg; return StatusCode::FAILURE; }
debug() << " Got tool " << m_anchoredTracker->name() << endmsg;
```

VertexAnchoredShortTrackFinderAlg is a Gaudi "Algorithm", and it can call Gaudi Tools to do its job.
You can also change the run time arguments for a Gaudi tool that is used by a Gaudi Algorithm.
You need to specify the tool in your options file with its alias; in the example above,
the alias is m_anchoredTrackerAlias, which is set at run time with a default value of "VertexAnchoredShortTracker".
So you can set a run time on the tool like this:

```
ToolSvc.VertexAnchoredShortTracker.MaxSearchDistance = 1000.0;
```

See here for other run time options in the AnchoredShortTracker tool:

http://cdcvs.fnal.gov/cgi-bin/public-cvs/cvsweb-public.cgi/AnalysisFramework/Rec/TrackShortPatRec/src/AnchoredShortTracker.cpp?cvsroot=mnvsoft

Finally, since you are interested in how this code works, you may want to turn up the output verbosity:

```
VertexAnchoredShortTrackFinderAlg.OutputLevel = 2;
 ToolSvc.VertexAnchoredShortTracker.OutputLevel = 2;
```

A level of "2" means that all messages labeled "debug()" in the code will be printed in your logfile.
The lower the number, the more messages you will receive.

3.6 NTupleAnalysis

This information provided by

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- NTupleAnalysis is used after you have run your analysis package. Generally it is a personal tool for people to present their results.
- This manual includes examples for Brandon Eberly's NTupleAnalysis Tool.

3.6.1 Getting Package & First Time Steps

- To Get the Package use:

```
>cvs checkout Personal/eberly/NTupleAnalysis
```

- Once you get the package NTupleAnalysis/ make a directory called 'playlists/v10r5p1' and copy the following files into it
- For Data:

```
/afs/fnal.gov/files/home/room1/mcgivern/minerva/NTupleAnalysis/playlists/
v10r5p1/pl_v10r5p1_minerva1.dat
```

- For Monte Carlo:

```
/afs/fnal.gov/files/home/room1/mcgivern/minerva/NTupleAnalysis/playlists/
v10r5p1/pl_v10r5p1_mc_overlay.dat
```

These .dat files are linked to Brandon's NuInt2012 datasets for data (9.43e19 pots) and MC (2.34e20 pots). See his analysis approval talk
(docDB 8063 - http://minerva-docdb.fnal.gov:8080/cgi-bin/ShowDocument?docid=8063)
for the details of the precuts/cuts.

3.6.2 Usage

The file 'CCNuPionIncNTuple.C' is used to create the output files for plotting, this code is where you add in new and/or construct variables (like E_nu, W, etc).

To run, use the commands

```
>root -l
>.L CCNuPionIncNTuple.C+
>CCNuPionIncNTuple t
>t.MakeComparisonPlots("playlists/v10r5p1/pl_v10r5p1_minerva1.dat","output_file_data.root",false);
>t.MakeComparisonPlots("playlists/v10r5p1/pl_v10r5p1_mc_overlay.dat","output_file_mc.root",true);
```

Argument	Purpose
playlists/v10r5p1/pl_v10r5p1_minerva1.dat	Input File Name
output_file_data.root	Output File Name
false	IsMC bool (false for data, true for MC)

Table 4: Arguments for *MakeComparisonPlots* Function

- If you run these codes as it is, it will loop over all data (297057 Events for Monte Carlo).
- It is highly suggested to run smaller playlists for test purposes.
  - For example, one can create a new playlist with lesser entries. (first 100 lines, first 500 lines etc...)

Once you have the output files, you can make plots using:

```
>root -l
>.L PlotterCompareDataMC.C
>PlotterCompareDataMC("output_file_mc.root", "output_file_data.root", false, false, "plots");
```

Argument	Purpose
output_file_mc.root	Input .root file for MC events
output_file_data.root	Input .root file for data events
false	POT_Normalize bool (false default)
false	sys_errors(false default)
plots	Output folder for the generated plots

Table 5: Arguments for *PlotterCompareDataMC* Function

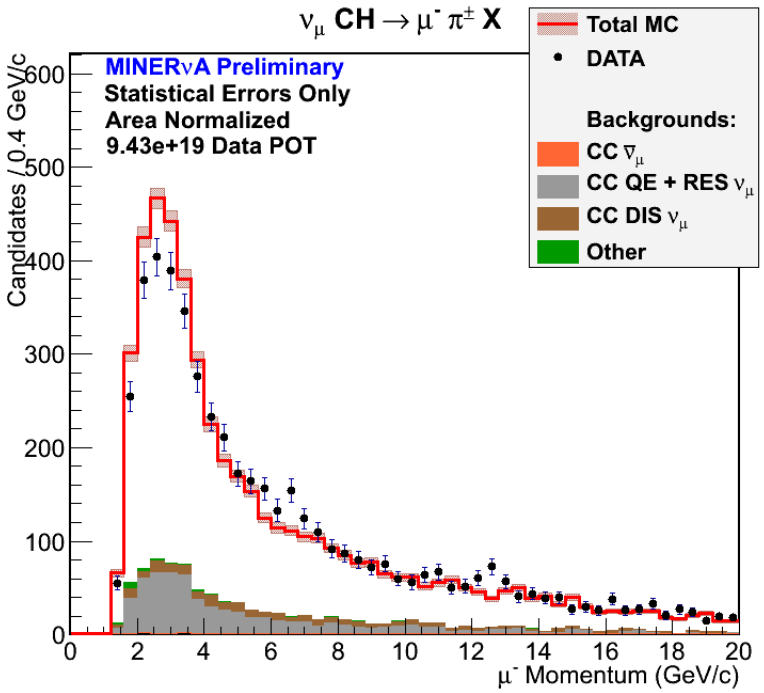
or make residual plots with

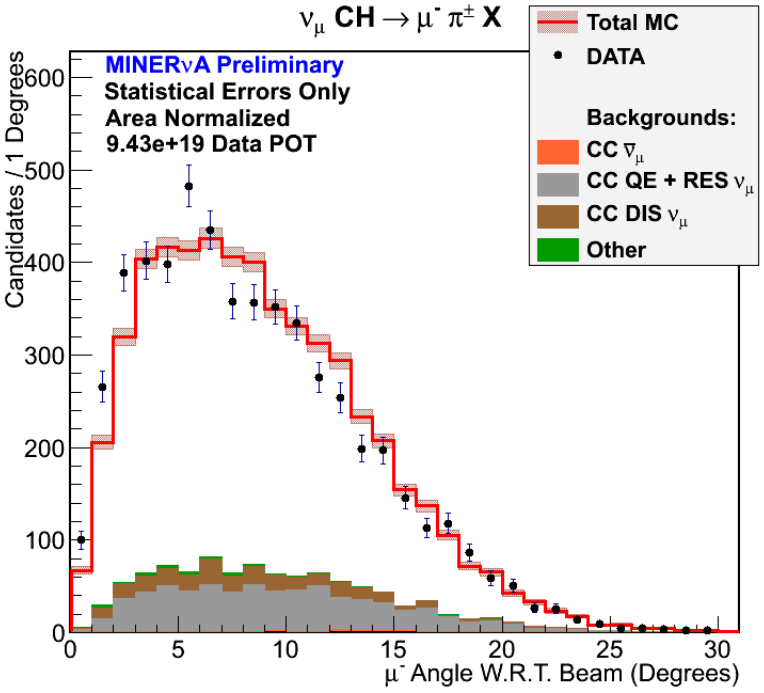
```
>root -l
>.L PlotterResiduals.C
>PlotterResiduals("output_file_mc.root","plots");
```

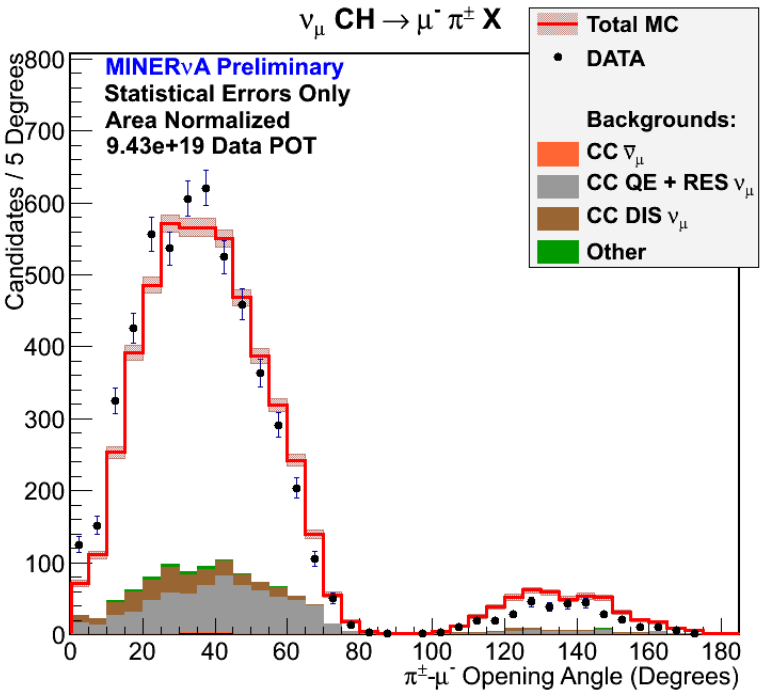
- Note 1: need to make a directory called 'plots' to store these figures. You can refer to the code to see what the inputs mean.
- Note 2: PlotterCompareDataMC.C is inside "NTupleAnalysis/Plotters/" & your output files generally in "NTupleAnalysis/", following code includes directory address as well.

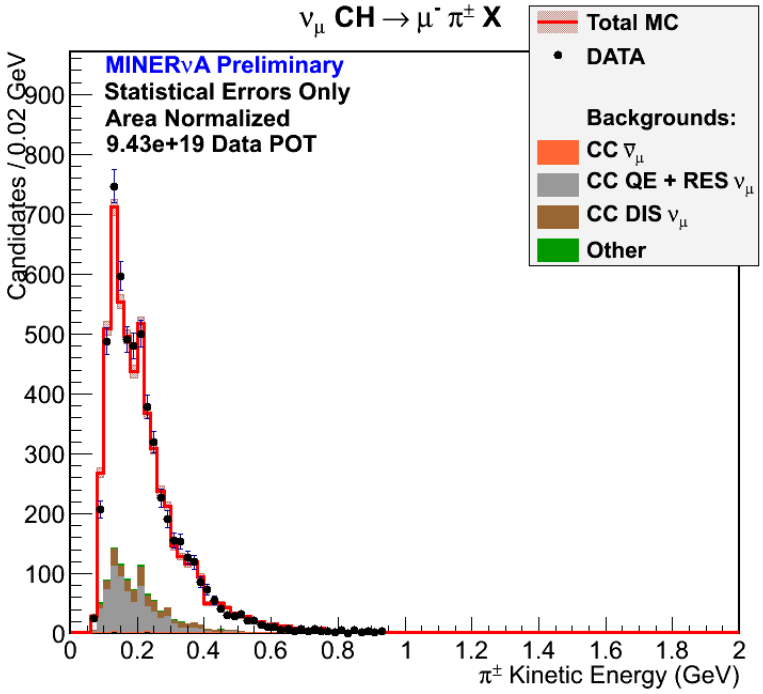
```
>root -l
>.L PlotterCompareDataMC.C
>PlotterCompareDataMC("../output_file_mc.root", "../output_file_data.root", false, false, "plots");
```

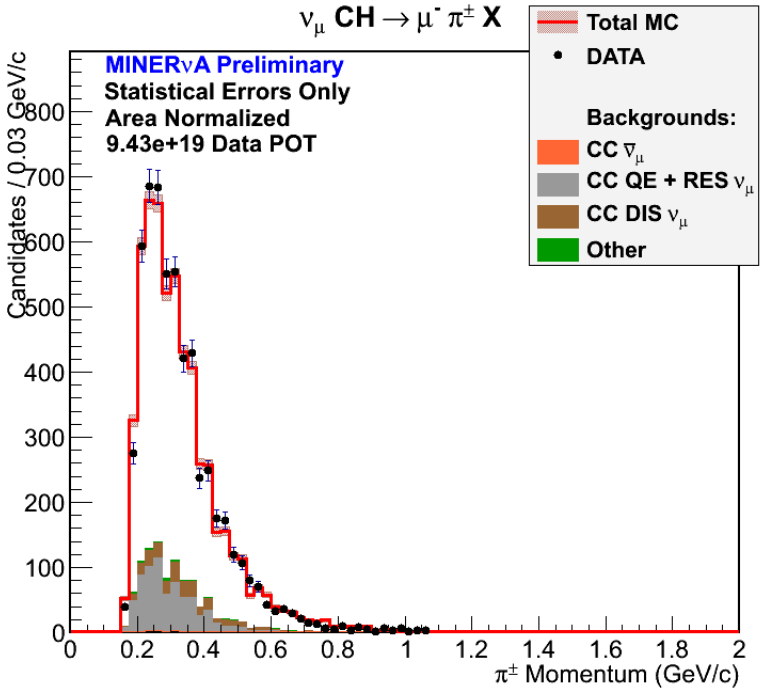
3.6.3 Example Plots for Default Commands

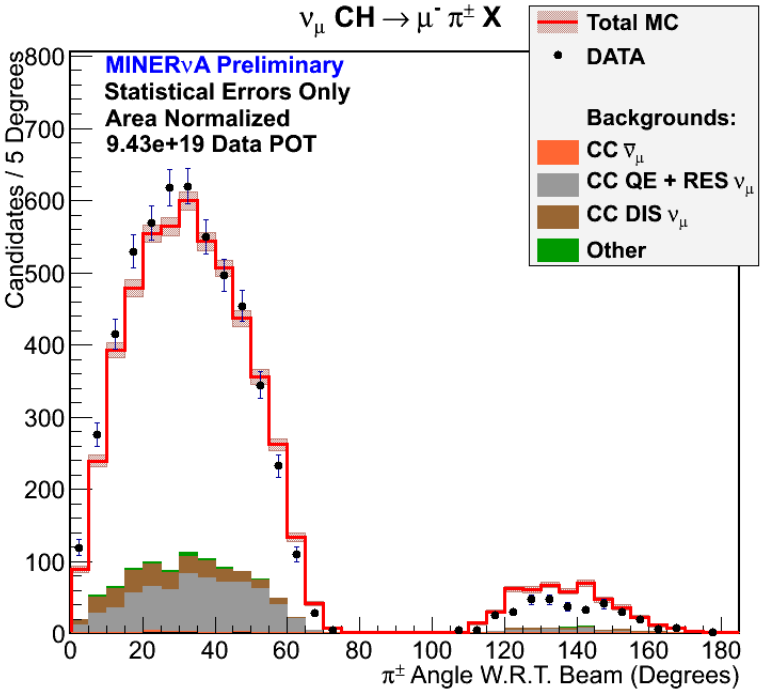





ν_μ CH $\rightarrow \mu^- \pi^\pm$ X
MINERνA Preliminary
Statistical Errors Only
Area Normalized
9.43e+19 Data POT
Total MC
DATA
Backgrounds:
CC $\bar{\nu}_\mu$
CC QE + RES ν_μ
CC DIS ν_μ
Other
Candidates / 5 Degrees
$\pi^\pm$-μ^- Opening Angle (Degrees)


ν_μ CH $\rightarrow \mu^- \pi^\pm$ X
MINERνA Preliminary
Statistical Errors Only
Area Normalized
9.43e+19 Data POT
Total MC
DATA
Backgrounds:
CC $\bar{\nu}_\mu$
CC QE + RES ν_μ
CC DIS ν_μ
Other
Candidates / 0.02 GeV
$\pi^\pm$ Kinetic Energy (GeV)





3.6.4 Creating Own Histograms

There are 2 files to be edited for creating your own histograms:

CCNuPionIncNTuple.C The general function that controls everything

Binning.C The function that holds binning information

Steps to create your own histogram

- Declaration of the Histogram: You can copy and edit the previous declarations to create your own. Example declaration for Vertex X histogram:

```
//Vertex X TH1F
*VertexX_reco = new TH1F("VertexX_reco","Reconstructed Vertex X",NBINS_X, MIN_X, MAX_X);
VertexX_reco->GetXaxis()->SetTitle("Vertex X (cm)");
VertexX_reco->GetYaxis()->SetTitle( Form("Candidates / %1.0f cm",WIDTH_X) );
TH1F* mcbkg_VertexX[N_MC_BKG];
for (int i=0; i != N_MC_BKG; i++) {
mcbkg_VertexX[i] = (TH1F*)VertexX_reco->Clone( Form("mcbkg_VertexX_%d",i) );
mcbkg_VertexX[i]->SetTitle( Form("Reconstructed Vertex X, %s",getMCBkgName(i).c_str()) );
}
TH1F* VertexX_resid = new TH1F("VertexX_resid","Vertex X Residuals",RES_NBINS_X,RES_MIN_X,RES_MAX_X);
VertexX_resid->GetXaxis()->SetTitle("Vertex X Residual (mm)");
VertexX_resid->GetYaxis()->SetTitle( Form("Counts / %1.0f mm",RES_WIDTH_X) );
```

Value	Correspondance	Notes:
Name of the Histogram	VertexX_reco	
Name of the Background Histogram (If exist)	mcbkg_VertexX[i]	It is an array
Name of the Residual Histogram (If exist)	VertexX_resid	
Name of the binning variables	NBINS_X, MIN_X, MAX_X	
Titles(Axis & Plot)	...->GetXaxis()->SetTitle(“....”)	

Table 6: Values to be edited in this sample

- After the histogram declaration, declare the binning variables inside Binning.C. You can copy and edit the previous declarations to create your own. Example declaration for Vertex X binning.

```
//VertexX
const int NBINS_X = 40;
const double MIN_X = -100.0;
const double MAX_X = 100.0;
const double WIDTH_X = getBinWidth(MIN_X, MAX_X, NBINS_X);
const int RES_NBINS_X = 200;
const double RES_MIN_X = -100.0;
const double RES_MAX_X = 100.0;
const double RES_WIDTH_X = getBinWidth(RES_MIN_X, RES_MAX_X, RES_NBINS_X);
```

- Fill your histograms with specific information you want.You can copy and edit the previous commands to create your own. Example command for filling VertexX_reco filling.

```
VertexX_reco->Fill(0.1*CCNuPionInc_vtx_x, tot_wt);
```

- Look for the Fill commands in the CCNuPionIncNTuple.C, and write your own command near them. (They are located below the cuts.)
- For background (if exist). This command is inside a loop.

```
mcbkg_Inertia_11[i]->Fill(0.000001*I_11, tot_wt);
```

4 Fermilab Grid

4.1 Setup for Grid

Here's the copy of the famous e-mail that explains everything:

> Hello,
>
> You are receiving this email because you have enabled grid submission from if01.fnal.gov but not (yet) from gpsn01.fnal.gov.
>
> If01, the minerva grid submission node, is an SL4 machine which must either be decommissioned or upgraded to SL5 by the end of February. This process may be disruptive, you are encouraged to test grid submission through gpsn01, an SL5 node prior to the upgrade, and move if feasible.
>
> The quick version of how to do this:
>
> 1) log on to gpsn01.fnal.gov
>
> 2) run /grid/fermiapp/common/tools/request_robot_cert as you did from if01 at some point, and follow the same steps you did last time, i.e. (press [p] to proceed).
>
> 3) kcroninit, follow the instructions
>
> 4) crontab -e and add the following line to your crontab:
>
> 27 1-23/2 * * * /usr/krb5/bin/kcron /scratch/grid/kproxy2 minerva
>
> Please use a random, different value than '27' (00 to 59) in the first column of this crontab entry, otherwise everyone will update their proxys at XX:27 which may cause random overloads.
>
> 5) minerva_jobsub checks for an environment variable MINERVA_SUBMIT_HOST which points to the grid submission node which defaults to if01.fnal.gov Export MINERVA_SUBMIT_HOST='gpsn01.fnal.gov' and test submission to gpsn01 after completing the above steps. Please send email to minerva-computing@fnal.gov if you encounter problems
>
> Further documentation is available at https://cdcvs.fnal.gov/redmine/
> projects/ifront/wiki/Getting_Started_on_GPCF
>
> Best Regards, Dennis

4.2 Sending jobs to Grid

Here's an example line to send a job to Grid: (It is one line)

```
> ./ProcessMC.py --ana -r 10201 -d minerva -f 1 -l 200 --pf 1 --opts
/path/to/options/file/v10r6/MCAna.opts --inv v10r6 --indir /minerva/data/mc_production/ --outdir
/minerva/data/users/your_user_name/output_dir/
```

4.3 Checking jobs on Grid

Data Location: /minerva/data/users/oaltinok/mc_production/grid/central_value/minerva/...

List:

```
>condor_q ‘‘username’’
```

Remove all jobs from that user:

```
>condor_rm ‘‘username’’
```

5 Additional Information

5.1 Basic Analysis Procedure

- Process Monte Carlo files with the analysis package you would like to use. Refer to section 3.5 to modify the options file that will be used with the analysis.
- Use ProcessMC: As an example, for run 10201, subrun range: 1-200 (Valid MC files: https://cdcvs.fnal.gov/redmine/projects/minerva-sw/wiki/Monte_Carlo_Production_Run_Numbers)

  ```
  > ./ProcessMC.py --ana -r 10201 -d minerva -f 1 -l 200 --pf 1 --opts
  /path/to/options/file/v10r6/MCAna.opts --inv v10r6 --indir /minerva/data/mc_production/
  --outdir
  /minerva/data/users/your_user_name/output_dir/
  ```

- Process Data files with the analysis package you would like to use. Refer to section 3.5 to modify the options file that will be used with the analysis.
- Use SubmitDataRuns: As an example, for run range: 2300 - 2360, (options file differs between MC and Data)

  ```
  > ./SubmitDataRuns.py -f 2300 -l 2360 --args "--ana --pf 1 --opts
  /path/to/options/file/v10r6/Ana.opts --inv v10r6 --outdir
  /minerva/data/users/your_user_name/output_dir/"
  ```

- Search for output files and create playlists (specific for CCPionInc output, your analysis package will use different output file name)

  ```
  > find /minerva/data/users/your_user_name/output_dir/
  -name "*Ana_Tuple*.root" -printf "%p\n" | sort > output_file.dat
  ```

- Use an NTupleAnalysis Tool to present your results from your analysis output.
  - Read the information from Data and MC playlists.
  - Apply additional cuts if necessary (most of the cuts done by the analysis package).
  - Calculate new variables related with your analysis topic(For example: Calculate moment of inertia of the hadronic system from the momentums of the hadrons in the event).
  - Compare your results for Data and Monte Carlo.

5.2 Useful Websites

- MINERvA Home Page:
  - http://minerva.fnal.gov/
- MINERvA Wiki:
  - https://cdcvs.fnal.gov/redmine/projects/minerva/wiki
- MINERvA Software Wiki:
  - https://cdcvs.fnal.gov/redmine/projects/minerva-sw/wiki
- MINERvA DocDB
  - http://minerva-docdb.fnal.gov:8080/cgi-bin/DocumentDatabase/
- Arachne
  - http://minerva05.fnal.gov:8080/Arachne/arachne.html
- Some Minerva websites have a private area which requires a general user name and password: You can learn it from your Professor.

References

[1] http://www.fnal.gov/docs/strongauth/winexceed7.html

[2] http://www.fnal.gov/docs/strongauth/winexceed7.html#57413

[3] https://cdcvs.fnal.gov/redmine/projects/minerva-sw/wiki/How_to_set_up_local_working_directory