Practical Session 3 Minimum bias at LHC

CTEQ/MCnet Summer School, Lauterbad, 2010-08-02

Exploring min bias at LHC

Today's practical is centered on writing a Rivet analysis which reproduces one of the LHC minimum bias measurements.

We will be reproducing the published **ATLAS 900 GeV min bias analysis** – sorry, CMS/ALICE people! (Although there is a lesson here...)

This looks at η , p_{\perp} , N_{ch} , and $\langle p_{\perp} \rangle$ vs. N_{ch} in min bias events.

As mentioned in the MC lectures, much of min bias physics is not perturbative \rightarrow pheno models in the MC codes have quite a few parameters! MPI parameters, diffractive parameters, ...

Once you have an analysis which you think does what is described in the paper, play with the params to see what effect they have.

Writing the Rivet analysis

Last time you used Rivet as a **black box**: you gave it a command with specified analyses, magic occured \rightarrow plots on a web page!

Today we open the box a bit more: you will be given a template analysis with the basic code structure in place, but the **details of particle selection, cuts, etc. are up to you.**

If this was just a pure MC analysis, you can do anything you like – but since we want to compare to data, you need to match the ATLAS paper's description.

As a template, we supply you with the source code of a similar analysis at CDF: everything in the ATLAS analysis has an equivalent bit of code in the CDF one.

Projections

The main unfamiliar element in Rivet is the *projection*. These are **calculator objects** which are applied to the event and "project" out observable properties: collections of stable (charged) particles, event shapes, jets...

Don't worry about the details: all you need to know is

- In the init () method, set them up and call addProjection(myproj, "MyObs");
- In the analyze (event) method, retrieve them to get the results with applyProjection<ProjType>(event, "MyObs");

Histogramming

Rivet tries to avoid hard-coding details of the analysis histograms: we have reference data whos binnings must be matched, so **booking the MC histogram is usually done automatically from the reference histo ID.**

The histo IDs are taken from HepData (http://hepdata.cedar.ac.uk) – they are a 3-tuple of IDs for the dataset (= table), *x*-axis, and *y*-axis.

To book the (1,1,1) histogram, you use this: _hist_pt = bookHistogram1D(1, 1, 1); // d01-x01-y01 Similar for profile histograms.

After that, use the <u>hist_pt</u> object for filling, scaling etc. in **analyze(event)** and **finalize()**.

Logistics

Today's session isn't done in your groups: please **go to the same room as you did on Friday.**

If you would rather work together, please do – but in pairs at most.

If (when) you have trouble, try first to work it out with help from the session instruction sheets, and the CDF example analysis. If it is still mysterious, of course, ask for help!