Subject: Re: Bear Smear and Cross Sections Posted by Ingo Fröhlich on Mon, 27 Aug 2012 20:59:06 GMT

View Forum Message <> Reply to Message

Michael Kunkel wrote on Mon, 27 August 2012 21:07ls \_f the density function? If so, wouldn't using Input : \_x s cos(theta), \_y is differential cross section

Output: cross section suffice?

No, it's a very simple implementation: there are 2 input variables, mapped on the 2 axis of TF2, and one output variable, named \_f, and this is the return value of the TF2. How you fill the \_f is up to you, but it must be defined.

Michael Kunkel wrote on Mon, 27 August 2012 21:07 I ask this, because I have 64 different models I want to use, each a segment of c.m. energy covering the range 1.68 - 2.84 GeV in the c.m. frame.

Than maybe the simplest method is that you use a 2-dimensional histogram, if the binning is the same for all the models, it should be no problem to merge them. Keep in mind that there is no linear interpolation implemented yet.

Michael Kunkel wrote on Mon, 27 August 2012 21:07

Would you please elaborate more on how to add more histograms into the model to ensure I get the right topology with the scaleing of the cross sections, the beam smearing, etc. I have having a hard time understanding everything so far.

You can concat the calculation:

```
\label{eq:model-AddHistogram} $$ model->AddHistogram(distribution1,"_f = Eval(_x. _y);"); $$ model->AddHistogram(distribution2,"_f = _f * Eval(_x. _y);"); $$ or $$ model->AddHistogram(distribution3,"_f = _f * Eval(_y);"); $$ $$
```

as indicated in the example, you can also make transformations:

```
model->AddEquation("t_lab = (_y*_y - g.mass*g.mass - p.mass*p.mass)/(2*p.mass*p.mass) - g.mass;");
model->AddHistogram(profile,"_f = <math>_f * Eval(t_lab);");
```

...just in case that your histogram profile is a function of t lab.

In the same way you can replace a beam profile by an analytical function.