Subject: [FIXED] Possible bug in scrut14 release?
Posted by Dmitry Morozov on Tue, 26 Aug 2014 10:50:24 GMT

Dear colleagues,

I faced the following strange behaviour which i don't understand.

I'm trying to reconstruct and analyse hc -> J/psi pi0 pi0 process, giving e+e- 4gamma in the final state.
I'm following the standard analysis strategy through ana_complete.C macro.
So the relative part of the analysis macro:

```
// *** Mass selector for the J/psi cands
 double m0_jpsi = TDatabasePDG::Instance()->GetParticle("J/psi")->Mass();
 RhoMassParticleSelector *jpsiMassSel=new RhoMassParticleSelector("jpsi",m0_jpsi,0.3);

// *** Mass selector for the pi0 cands
 double m0_pi0 = TDatabasePDG::Instance()->GetParticle("pi0")->Mass();
 RhoMassParticleSelector *pi0MassSel = new RhoMassParticleSelector("pi0", m0_pi0, 0.05);

// *** the lorentz vector of the initial hc
 TLorentzVector ini(0, 0, 5.5827, 6.598952222);

 theAnalysis->FillList(eplus,  "ElectronAllPlus");
 theAnalysis->FillList(eminus, "ElectronAllMinus");
 theAnalysis->FillList(gamma, "Neutral");

// *** combinatorics for J/psi -> e+ e-
 jpsi.Combine(eplus, eminus);

// *** combinatorics for pi0 -> gamma gamma
 pi0.Combine(gamma, gamma);

// *** jspi mass selection
     jpsi.Select(jpsiMassSel);
// *** pi0  mass selection
 pi0.Select(pi0MassSel);

// *** combinatorics for hc -> J/psi pi0 pi0
 hc.Combine(jpsi, pi0, pi0);


// ***
// *** do 4C FIT (initial hc system)
// ***
 for (j = 0; j < hc.GetLength(); ++j)
 {
  PndKinFitter fitter(hc[j]); // instantiate the kin fitter in hc
  fitter.Add4MomConstraint(ini); // set 4 constraint
  fitter.Fit();          // do fit
```

```
double chi2_4c = fitter.GetChi2(); // get chi2 of fit
double prob_4c = fitter.GetProb(); // access probability of fit
hhc_chi2_4c->Fill(chi2_4c);
hhc_prob_4c->Fill(prob_4c);
RhoCandidate *hc_4cf = hc[j]->GetFit(); //get fitted hc itself
hhc_mass_4cf_prob0->Fill(hc_4cf->M());
    }
```

I tried to analysed two sets of simulated data - from scrut14 and trunk (rev. 25710). Version of analysis macro does not matter - the results are the same.

I attached two png files - 3 histos in each: mass of fitted hc by 4c fit (by Add4MomConstraint), probability and chi^2 of the fit.

In trunk case - I have all hc masses in one bin (which is how it should be? Am i right? Correct me please if I am confused.), probabilities is mostly populated around 0 and chi^2 is more or less spread over the histogramm.
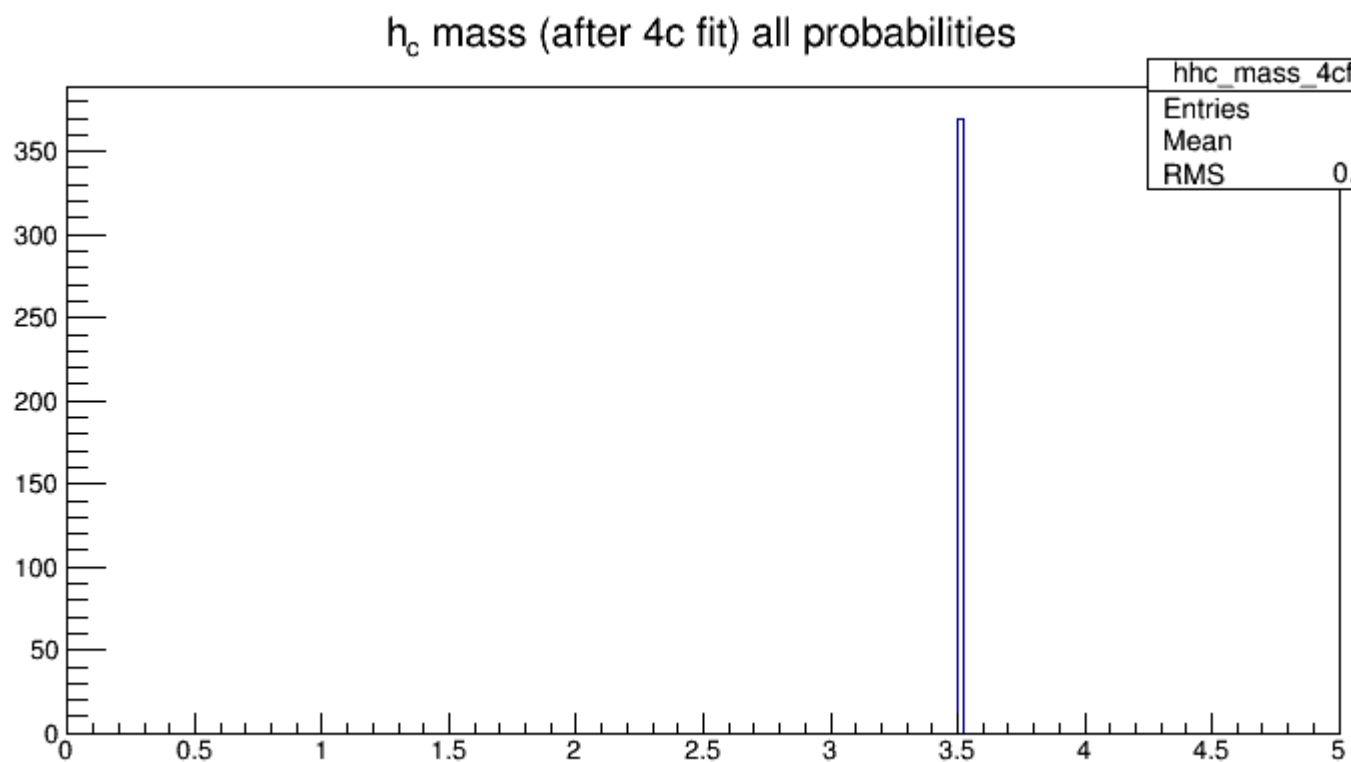
In scrut14 case - I have relatively wide hc mass distribution, probabilities are close to 1, and chi^2 are close to 0.

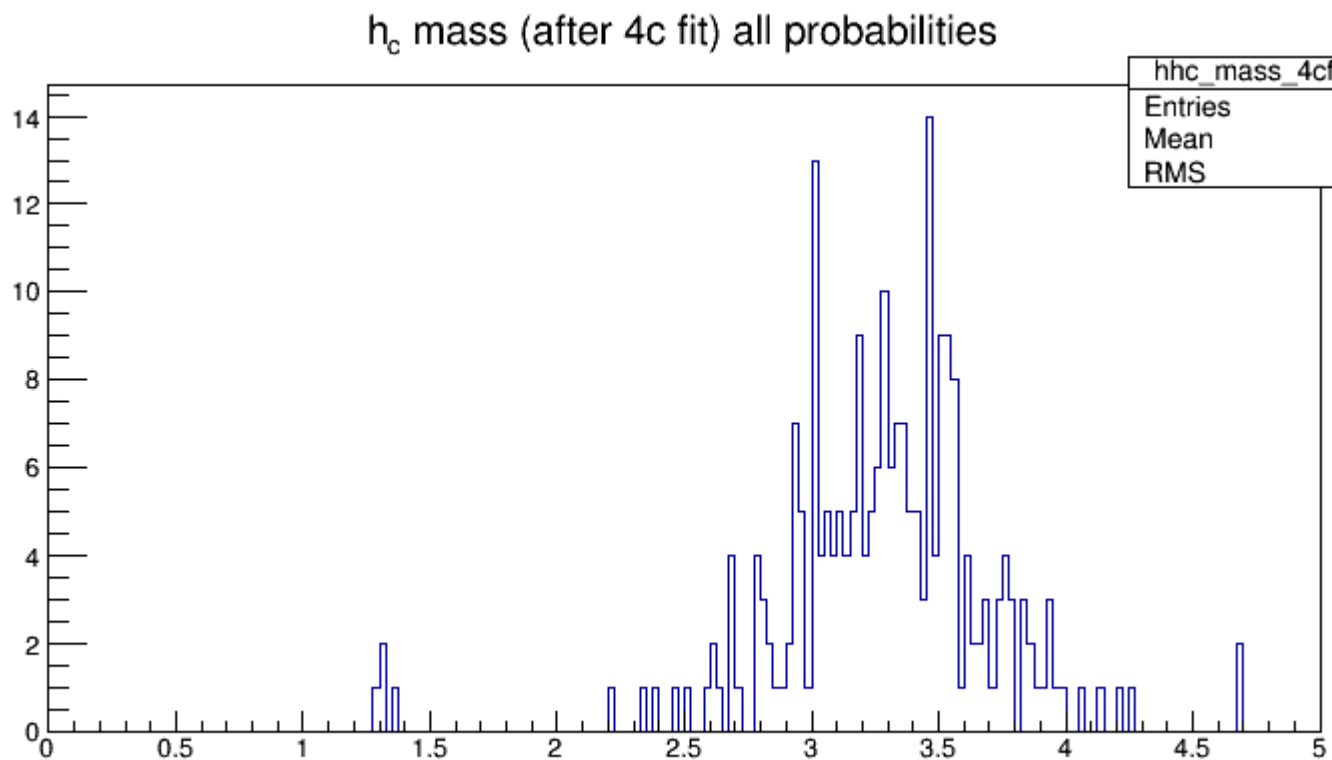Maybe somebody can comment on the source of this difference?

Thank you in advance.

File Attachments
1) hc_4c_fit_trunk_25710.png, downloaded 672 times

h_c mass (after 4c fit) all probabilities

hhc_mass_4c	
Entries	
Mean	
RMS	0.

h_c mass (after 4c fit) all probabilities

hhc_mass_4cf
Entries
Mean
RMS

Which version of scrut14 are you using? There was a bug fixing in 25577 for the neutral covariance matrix.

Subject: Re: Possible bug in scrut14 release?
Posted by Dmitry Morozov on Wed, 03 Sep 2014 07:18:56 GMT
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Stefano, thanks for the answer.

My scrut14 version is 24967, so maybe you are right.

I though release versions are frozen.
Is it true that for now scrut14 = trunk?

Subject: Re: Possible bug in scrut14 release?
Posted by StefanoSpataro on Wed, 03 Sep 2014 14:38:52 GMT
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The scrut14 is a particular release which is updated only when we fix analysis bugs. In this case, since the EMC covariance matrix was buggy, it was updated.