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

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

I'm trying to reconstruct and analyse $hc \rightarrow J/\psi \pi^0 \pi^0$ process, giving $e^+e^- 4\gamma$ 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 cand
double m0_jpsi = TDatabasePDG::Instance()->GetParticle("J/psi")->Mass();
RhoMassParticleSelector *jpsiMassSel=new RhoMassParticleSelector("jpsi",m0_jpsi,0.3);

// *** Mass selector for the pi0 cand
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 χ^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 χ^2 is more or less spread over the histogramm.

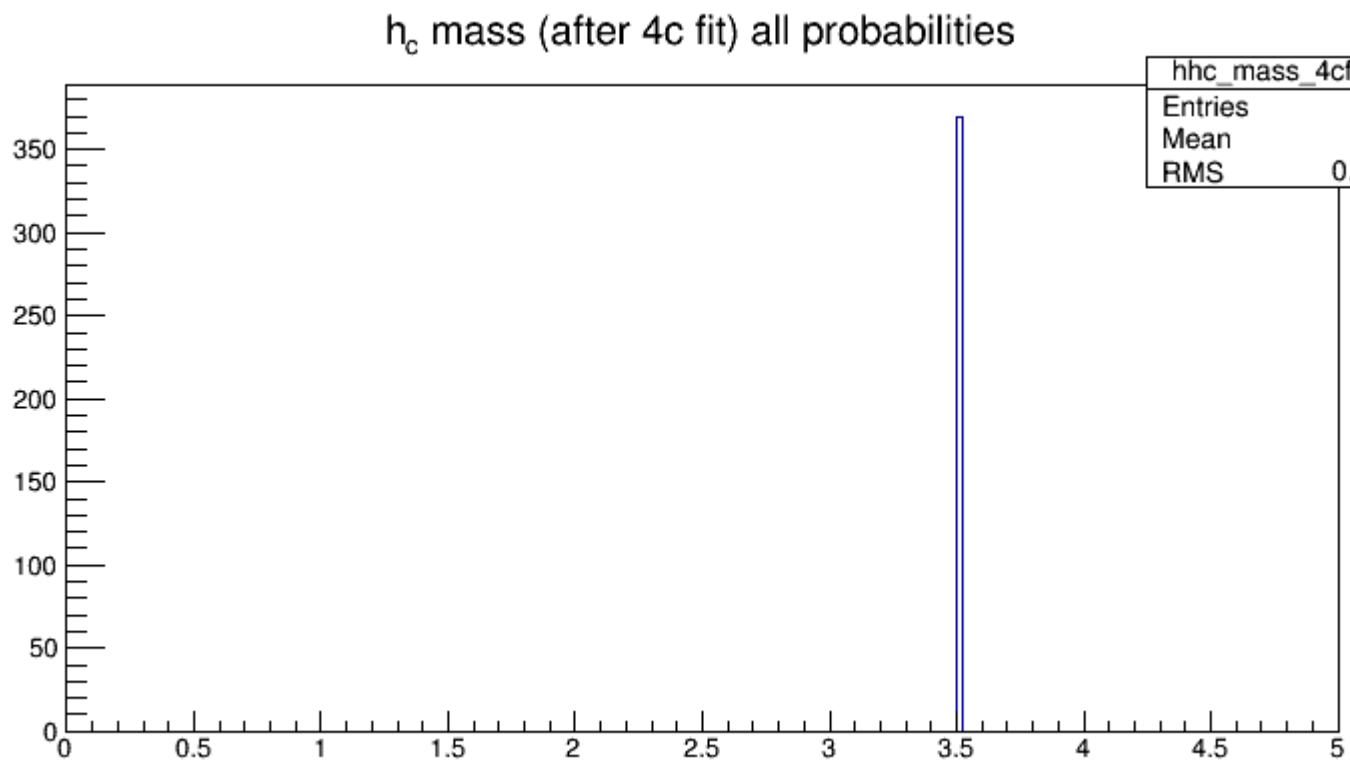
In scrut14 case - I have relatively wide hc mass distribution, probabilities are close to 1, and χ^2 are close to 0.

Maybe somebody can comment on the source of this difference?

Thank you in advance.

File Attachments

1) [hc_4c_fit_trunk_25710.png](#), downloaded 1086 times



2) [hc_4c_fit_scrut14.png](#), downloaded 1214 times

h_c mass (after 4c fit) all probabilities

