Subject: Psi3770 study with run981 tpc mode
Posted by donghee on Wed, 20 Jul 2011 13:01:52 GMT
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Hi,

I'm now testing latest production of psi3770 at Gridka.
The data corresponds to run981 with tpc mode and just look 84500 events from totally produced 0.1M evt. PndKinVtxFitter failed and cannot go through whole 500 events.

I require following cuts.

At least 3 positive particles and also 3 negative particles since psi3770 will decay with 6 final states.

E/p < 0.85 due to electron tracks (Energy from EMC info.)

Rejects bad reconstructed track with checking GetMicroCandidate().GetChiSquared() == -1 in the track lists.

In figure tracks.gif, total charged and reconstructed tracks from 84500 events for psi3770 data is shown.

In D_mass.gif, you can find D_mass distribution with three different categories.
First column is raw D+ and D- distribution, and second column shows D+ and D- mass distributions after applying a PndKinVtxFitter.
Third one is the plots matched with MC true information, if 6 reconstruced(candidate tracks) tracks are associated with MC true tracks IDs and without overlapping and double counting, then assigned as a MC true matched events.
The mean position of D+ and D- masses are slightly shifted from norminal position.

The resolution of D+ and D- vertex are shown in Resolution.gif.
In order to get precise vertex resolution, one need to apply sidebin subtraction for signal region, because bg+sig cannot be separated.
So, I took the data only region within 1.8693 +/-0.05 from fitted D+ and D- mass distribution, and then got the vertex position for that.
Subtraction of true with reco for vertex position X, Y, Z of D+ and D- are plotted in this plot.
I have still 0.13 cm resolution for x, y direction.
Even if I take only MC true matched events, the resolution doesn't change so much.

Psi_distribution.gif shows psi3770 reconstruction with using signal region of D+ and D- mass.
Here once again vertex fits for psi3770 have been applied in second, and in third coloumn psi3770 with MC true matched events are additionally plotted to get the feeling for estimation of Psi3770 efficiency.

When I required the MC true matching to reconstructed track, some events have double or even more counting at MC true matching, since sometimes two or three reconstructed tracks are induced essencially same origin of one MC track.
If I have those event, I throw away those events. I need still some tests to reduce those multi-counting problem in my analysis.

PID would be real solution.

So, efficiency of Psi3770 is extremely low with this approach.
If I try same analysis with 4CFitter, I couldn't achieve until finishing complete analysis with 500 events, simply run crash with 4Cfitter for psi3770.

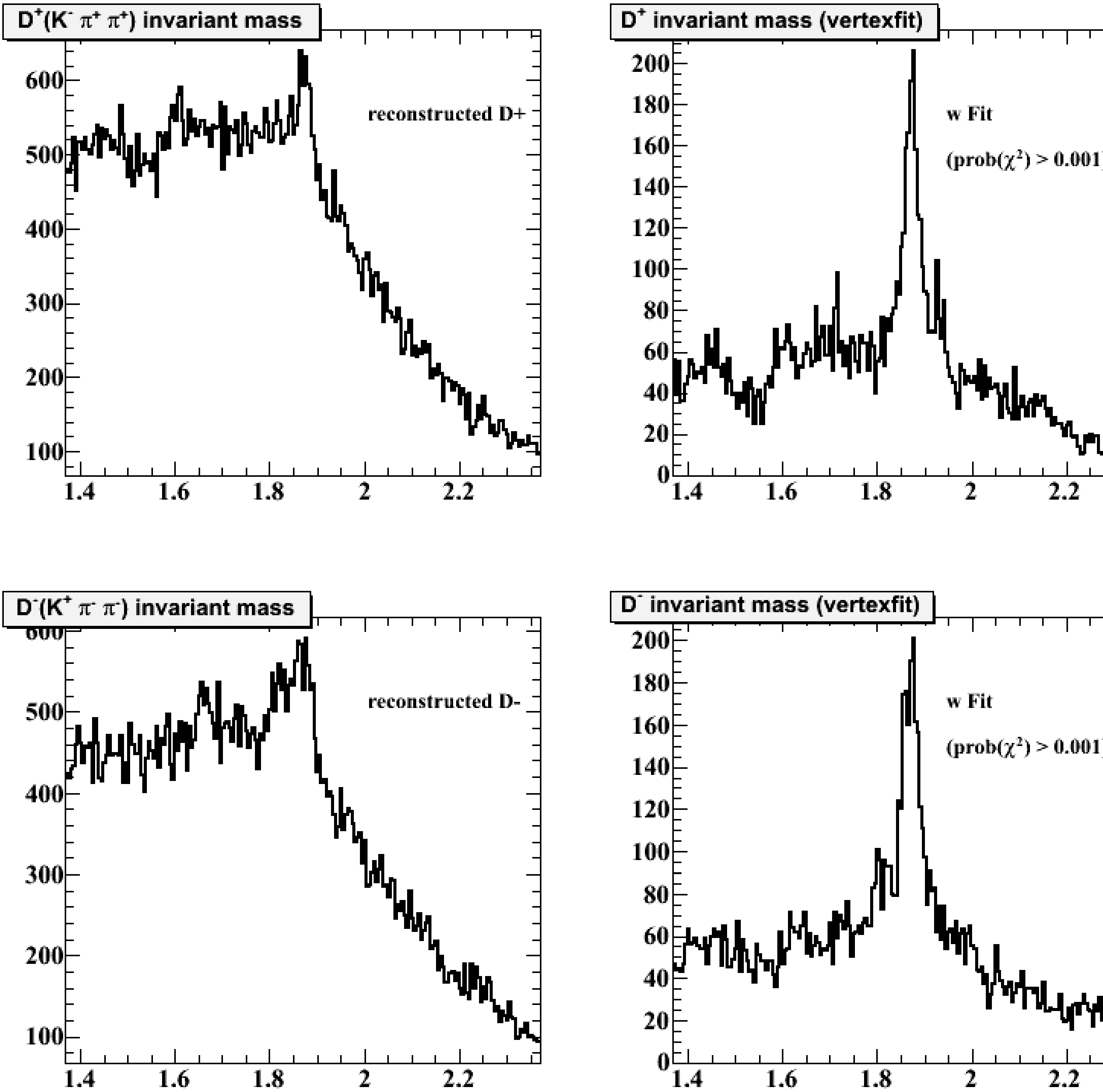
If you have some other suggestions and items, which we need to check in psi3770 data, please don't hesitate make an advice.

Best wishes,
Donghee

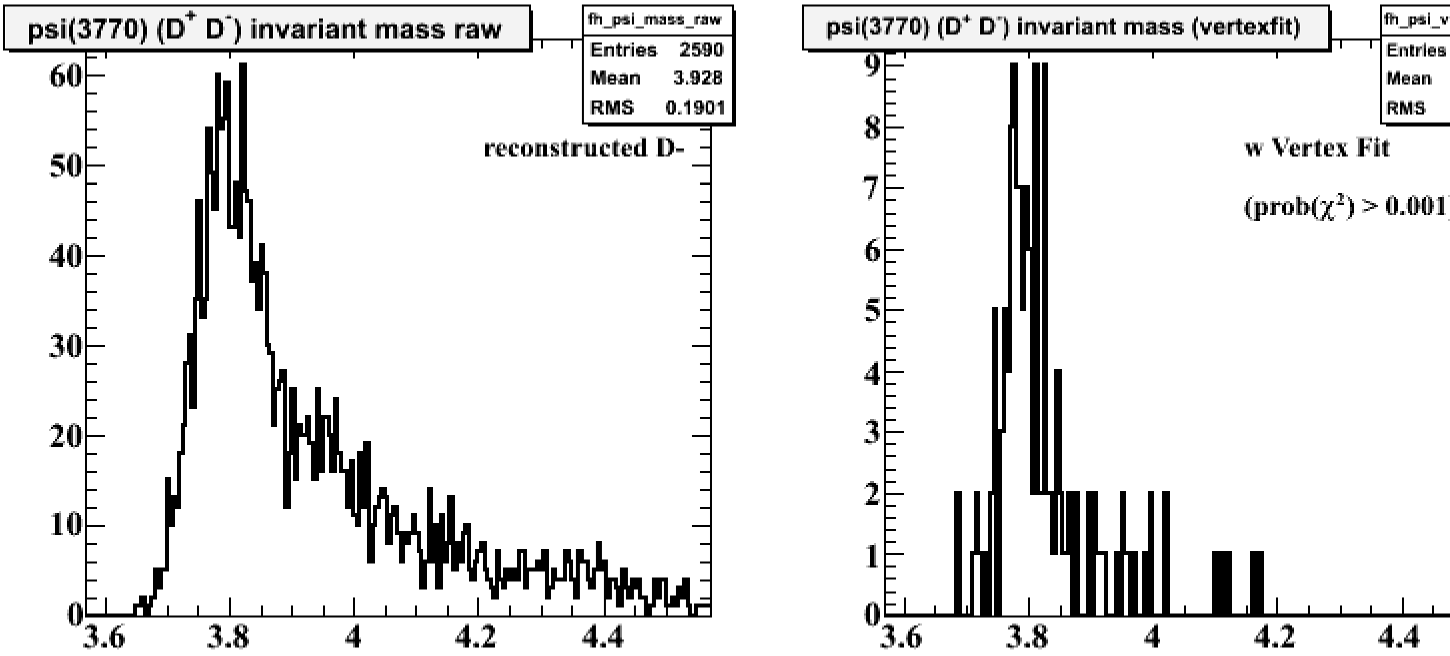
I found D_mass

File Attachments

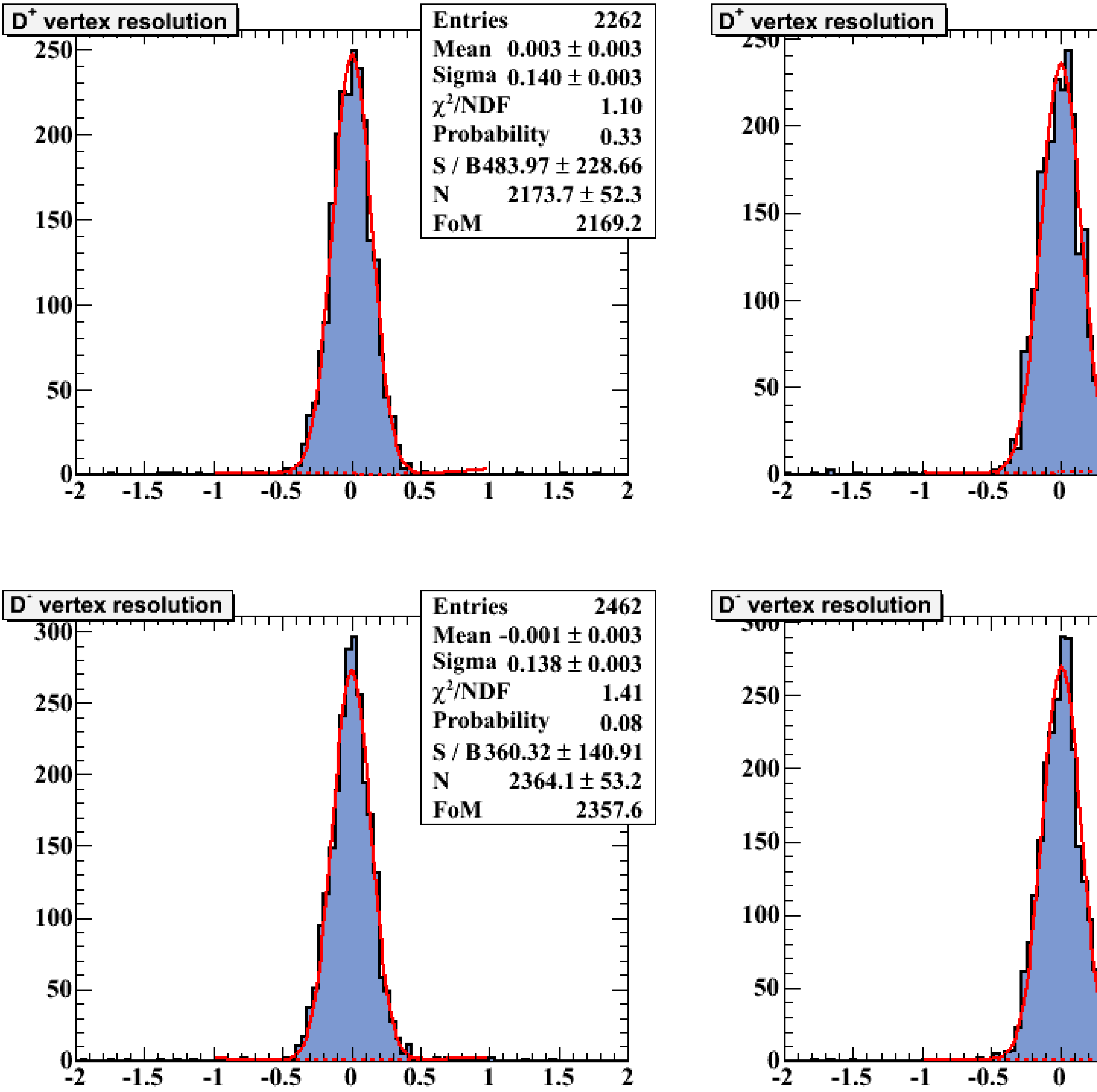
1) D_mass.gif, downloaded 781 times



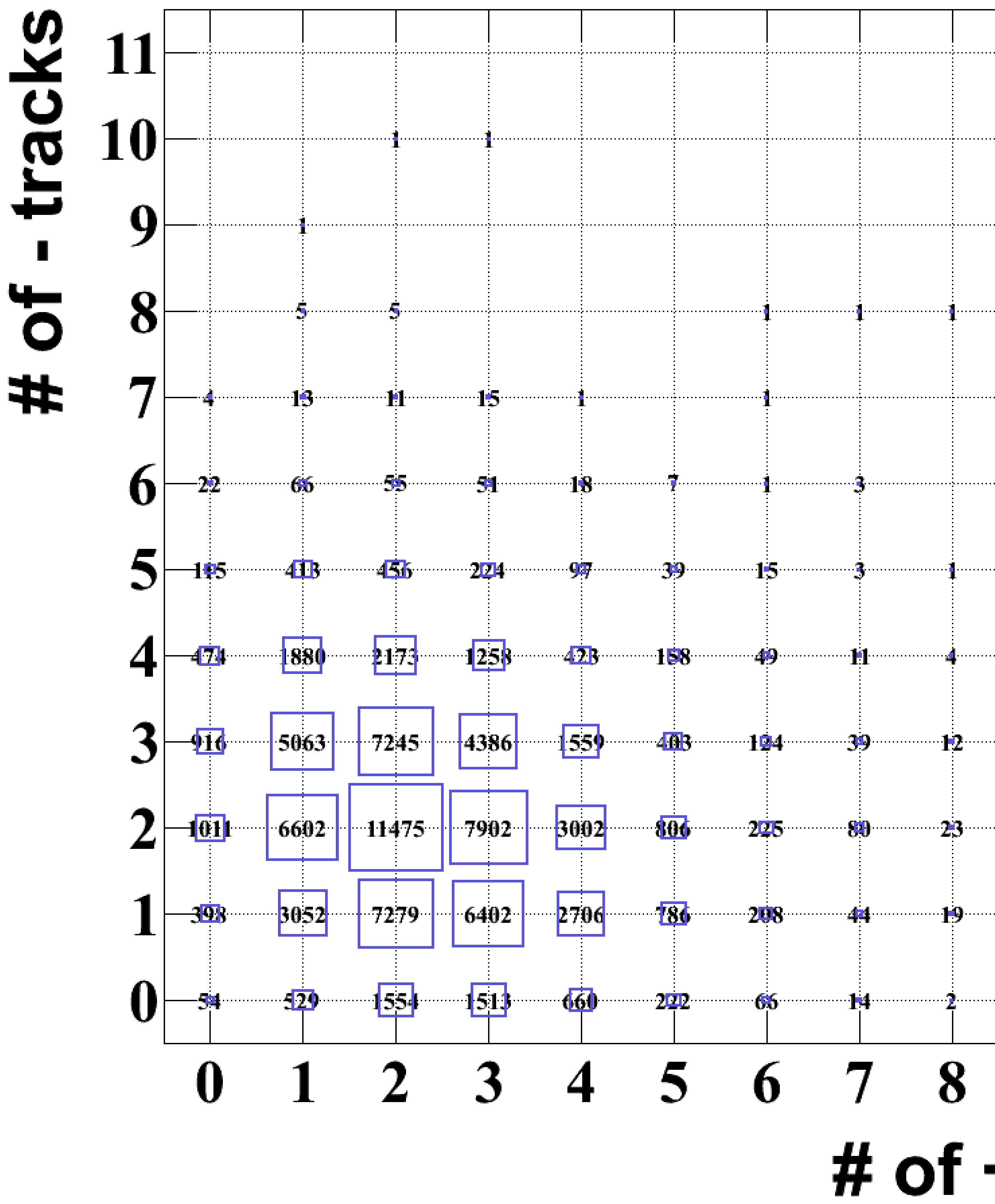
2) Psi_distribution.gif, downloaded 760 times



3) Resolution.gif, downloaded 712 times



4) tracks.gif, downloaded 723 times

# of - tracks
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4 13 11 15 1 1
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115 413 456 224 97 39 15 3 1
474 1880 2173 1258 423 158 49 11 4
916 5063 7245 4386 1559 403 124 39 12
1011 6602 11475 7902 3002 806 225 80 23
398 3052 7279 6402 2706 786 208 44 19
54 529 1554 1513 660 222 66 14 2
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