Light (Anti)Nucleus Absorption from Geant4

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We use GEANT3 to extract the reconstruction efficiencies in embedding simulations

GEANT3 treats light (anti)nuclei with `ITRTYP=8 (GTHION)`
Even if this is switched to `ITRTYP=4(GTHADR)`, there are still no cross-sections available! (so these `ITRTYP`s are effectively equivalent)

That is, GEANT3 basically treats light (anti)nuclei as generic hadrons (~p,pbar).
So, embedding efficiencies for light (anti)nuclei are too high!

Every STAR publication so far, all on antinuclei, typically treats this deficiency with an additional "Absorption correction"

How does one handle the light nucleus (Z>0) corrections?
A specific scaling from pbar to Abar has been used: is this reasonable?

These questions were studied using GEANT4
for which carefully validated light (anti)nucleus cross-sections exist!

Just to be clear though, we're talking about a ~10% correction...

The typical STAR approach: C. Struck's thesis w/ updated scale factors…

used in STAR's antiproton analysis [57], where the absorption was studied with Monte Carlo simulations. This is not possible for $\overline{d}$ and $^3\overline{\text{He}}$, as GEANT does not contain a model for antinuclei interactions in matter. Therefore, the correction relies on the assumption, how the antiproton/proton annihilation cross section $\sigma_{anni}(\overline{p}p)$ scales with the nucleon number.
The absorption loss, considered in the antiproton analysis, is parameterized as a function of momentum,

$$abs(p) = 1 - e^{-\sigma_{anni}\rho_t p/p_t}, \tag{6.4}$$

where ρ_t is the density of nucleons in the detector material perpendicular to the beam pipe. Furthermore, a simple parametrization of the annihilation cross section is used, similar to the parametrization in UrQMD [58], which relates the annihilation cross section to the well known total cross section,

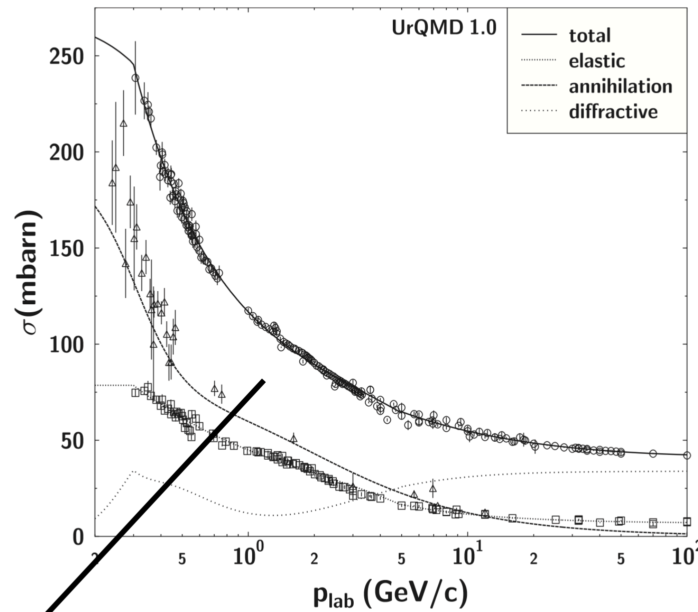
$$\sigma_{anni}(\overline{p}p) = 1.2\,\sigma_{total}(\overline{p}p)/\sqrt{s}. \tag{6.5}$$

Here, s is the center-of-mass energy given in GeV^2. Figure 6.14, taken from [58], illustrates the antiproton/proton total, elastic and annihilation cross sections as well as the parametrizations used in UrQMD (for the total cross section see also [59]). In the relevant momentum region, the total cross section can be described as a function of the antiproton laboratory momentum p by

$$\sigma_{total}(\overline{p}p) = 120\,p^{-0.65}\text{mb}. \tag{6.6}$$

The transverse nucleon density ρ_t is extracted from a fit to the simulation. From this, the antiproton absorption loss correction for the year 2001 data was calculated,

$$abs^{\overline{p}}_{corr}(p) = \exp\left(\frac{0.089}{\sqrt{1+\gamma}}\,p^{-0.65}\,\frac{p}{p_t}\right). \tag{6.7}$$



The scale factor 0.089 came from fitting the ratio eff(pbar)/eff(p) from embedding
(Geant3 does absorb pbars!)

Antialpha paper scaled 0.089 to account for the different STAR geometry in Run-10…

The **scaling assumption** for the light antinucleus cross-sections…

For the $\overline{d}$ and $^{3}\overline{\mathrm{He}}$ absorption correction only the annihilation cross section itself is in question, as the amount of detector material faced is the same. Here, a parametrization from reaction data [60] is used, which predicts a scaling of the inelastic cross sections from pA to AA collisions as

$$\sigma_{inel}(d,^{3}\mathrm{He}) \approx (\sqrt{2}, 2)\sigma_{inel}(p). \tag{6.8}$$

Assuming that the same relation holds for $\overline{d}$ as well as $^{3}\overline{\mathrm{He}}$, the exponential factor in Equation 6.7 is multiplied by a factor $\sqrt{2}$ (2) to define the $\overline{d}$ ($^{3}\overline{\mathrm{He}}$)

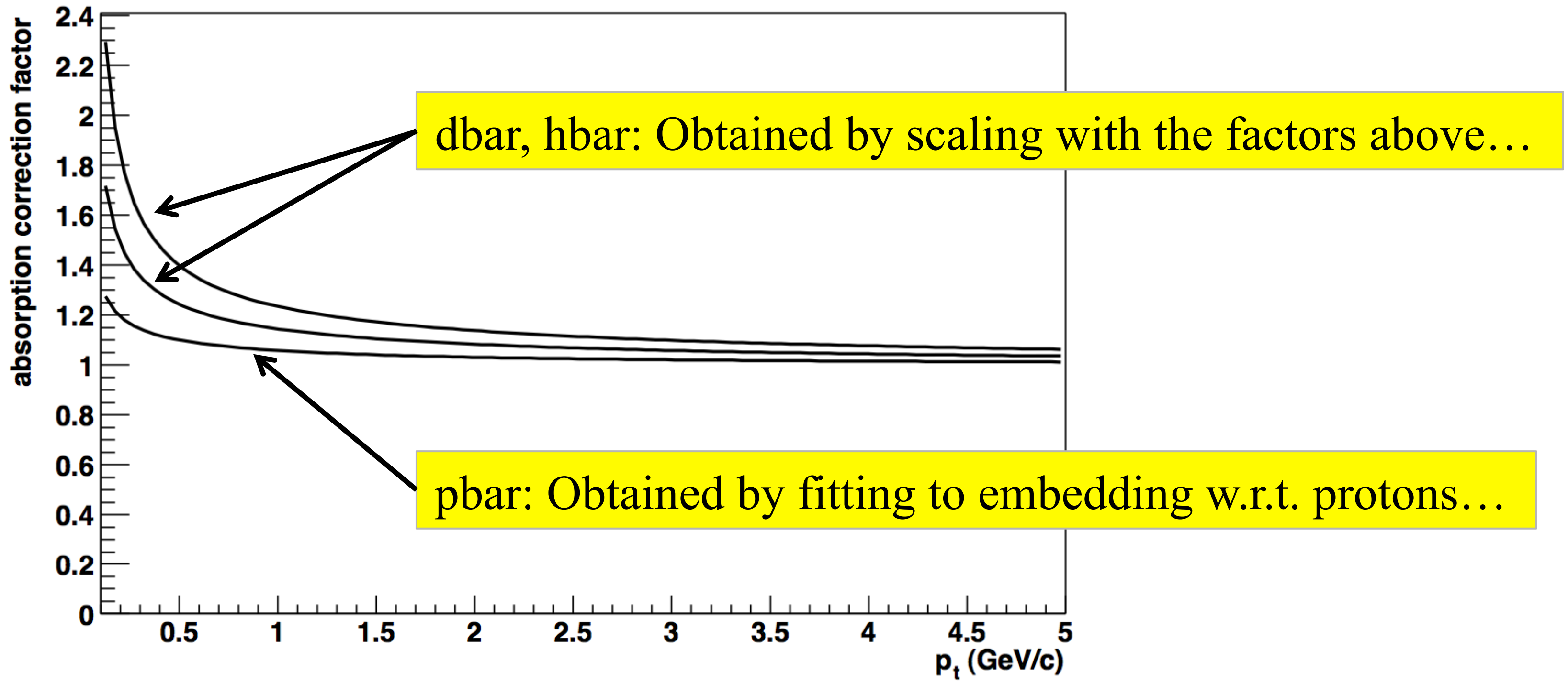
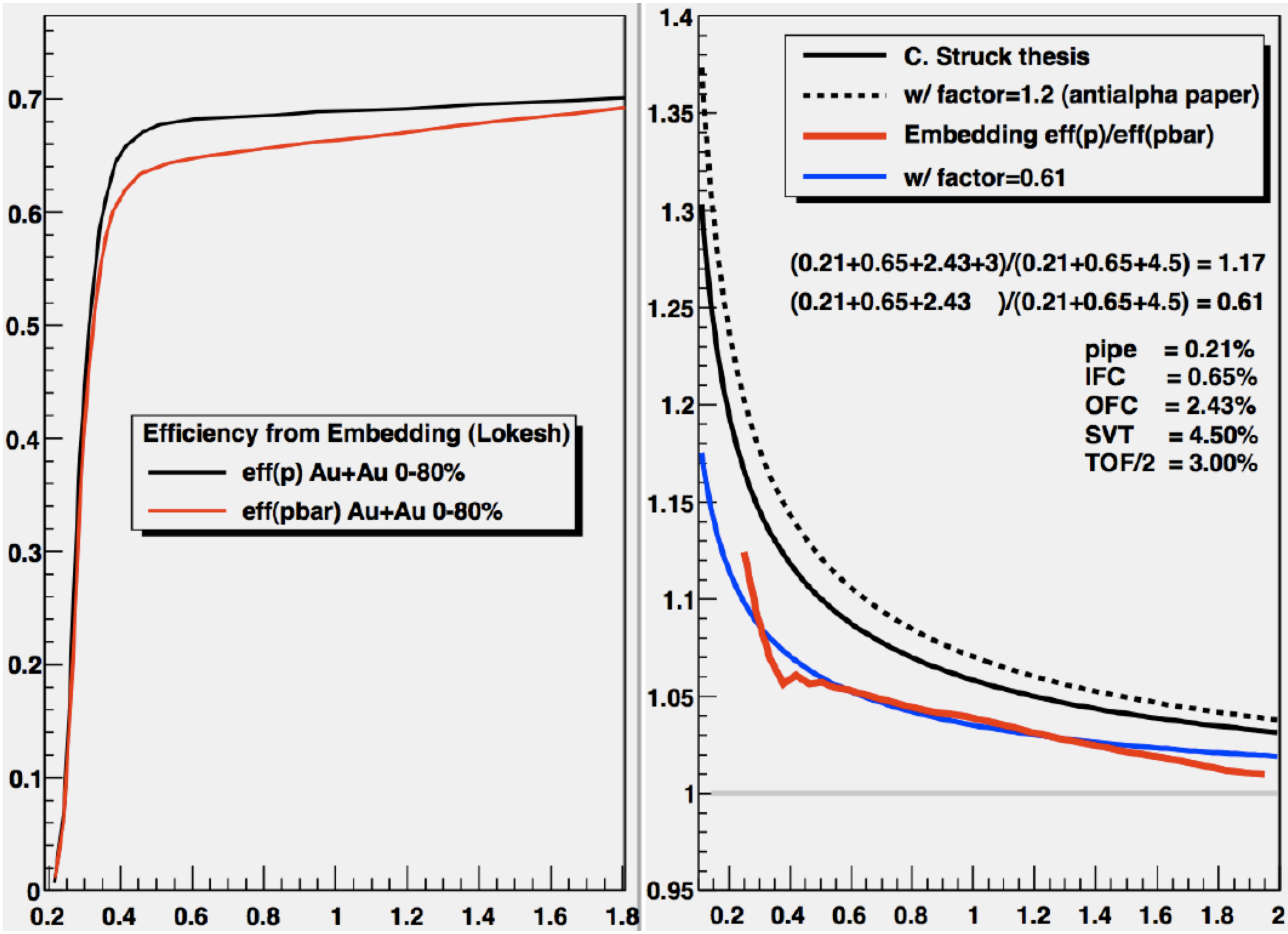


Figure 6.15: Absorption correction factor at mid-rapidity as a function of transverse momentum for $\overline{p}$ (lower curve), $\overline{d}$ (middle curve) and $^{3}\overline{\mathrm{He}}$ (upper curve).

An "old" test of mine on the best value of the scale factor for Run-10/11

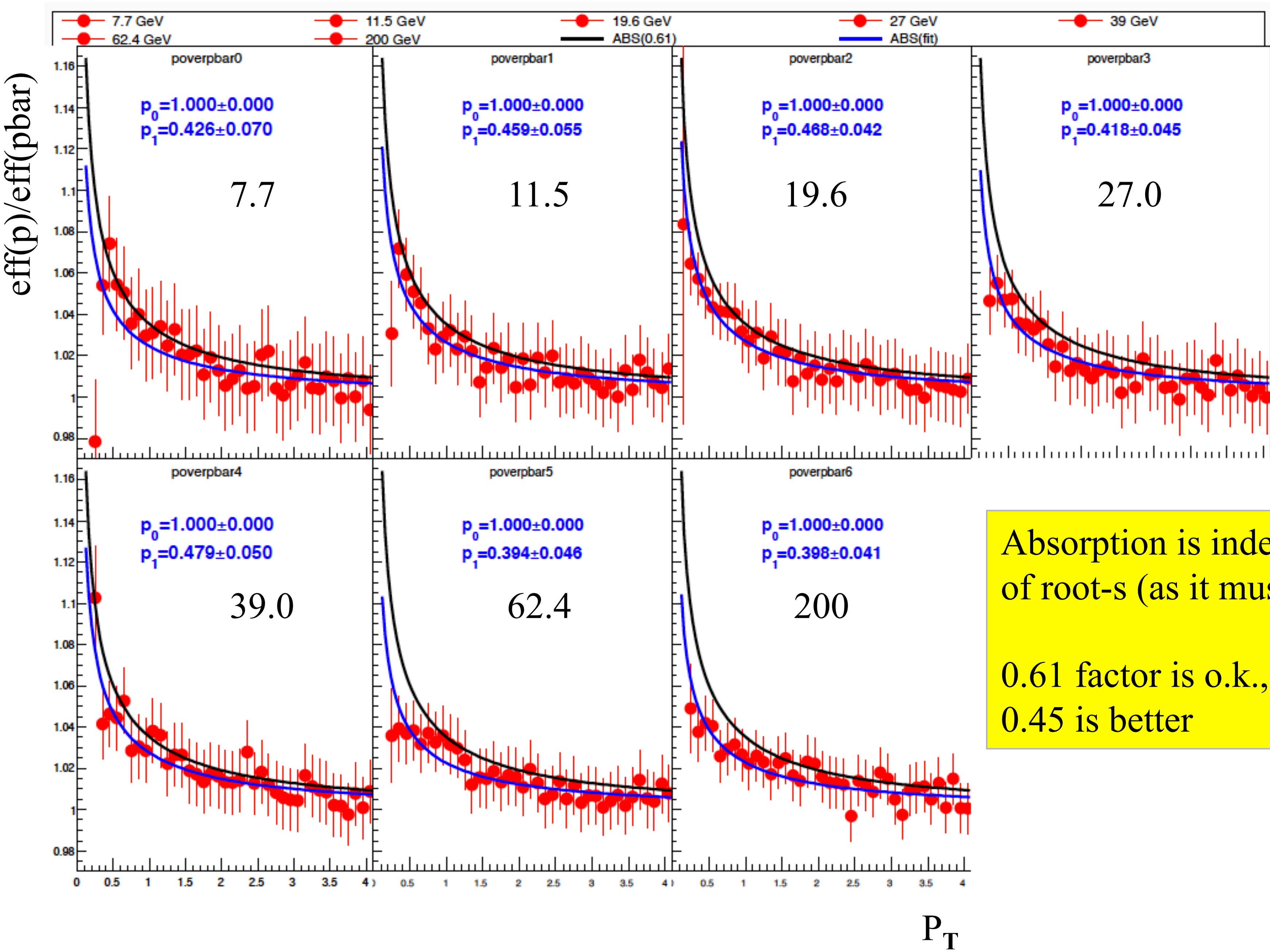
LFSpectra Parallel session at UC-Davis mtg: http://wjllope.rice.edu/d/protected/LFspectra_20110825.pdf

Take Lokesh's p and pbar embedding (now obsolete) and test the absorption correction…



The expected factor of 0.61 seemed to work o.k. for the Run-10/11 geometry…

Now with all brand new embedding for p and pbar at all root-s…



Absorption is independent of root-s (as it must be).

0.61 factor is o.k., but 0.45 is better

Testing the standard absorption correction recipe with GEANT4…

So, for the antinucleus half of my analyses, in principle all I'd have to do is the usual thing but use the scale factor of ~0.45 instead of 0.61.

But….

1. What am I supposed to do about the nucleus absorption?
2. is this pbar to Abar xsec-scaling the only approach?

These questions can be answered with GEANT4.

GEANT4 has extensively validated cross-sections for light (anti)nuclei based on experimental data…

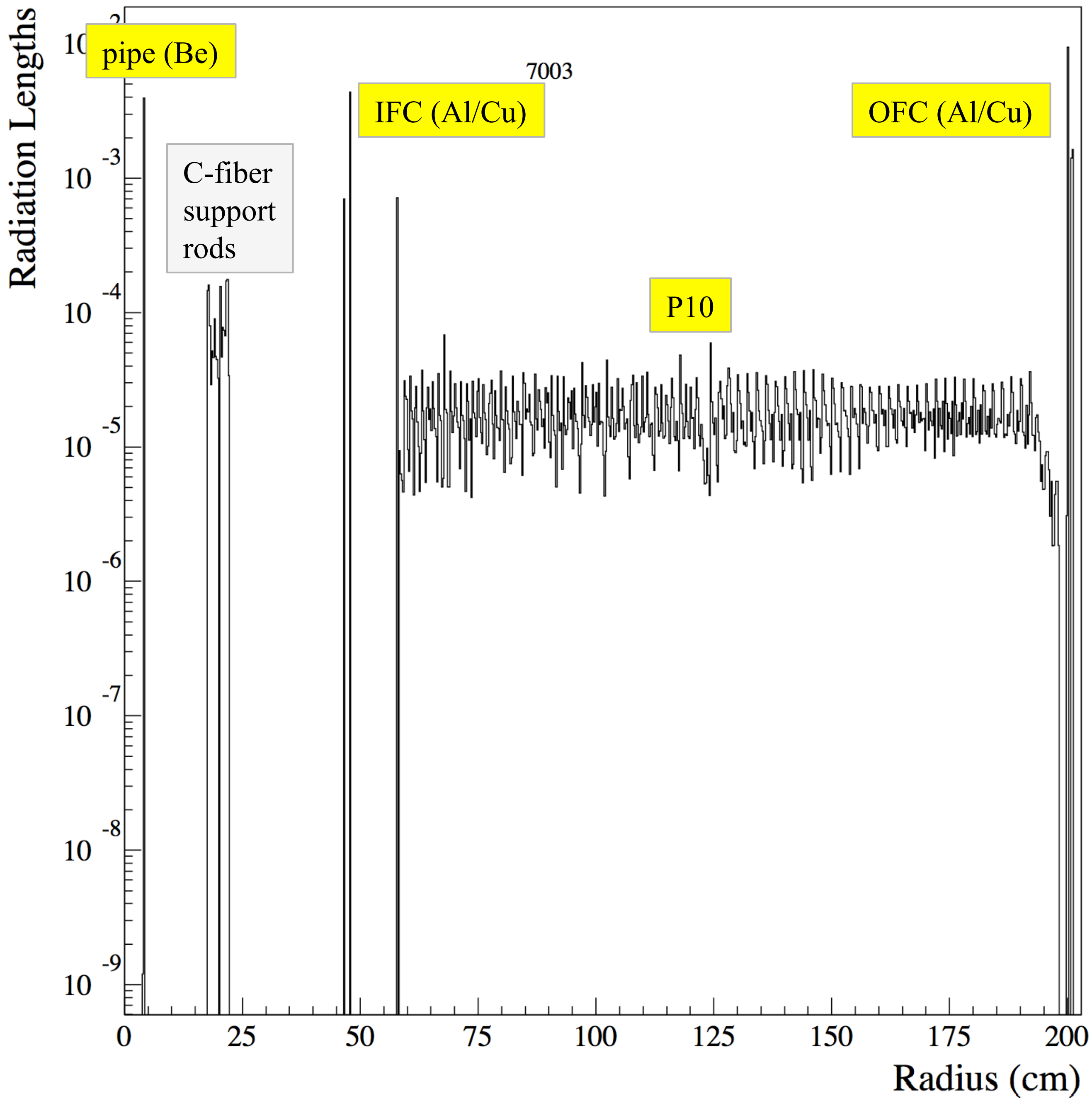
Google 'geant4 validation' *etc*…
See also *e.g.* http://arxiv.org/abs/1208.3614v1
http://arxiv.org/abs/1209.4455v1

Do a GEANT3 simulation with a STAR mock-up
Do a GEANT4 simulation with the same STAR mock-up. And then compare!

As I am only interested in the absorption itself, the STAR mock-up used in both only needs to be good, not perfect (STARSIM)... *This can be tested* (in two ways)!

Embedding still handles all the real-life reconstruction aspects (resn, merging, cuts *etc*)

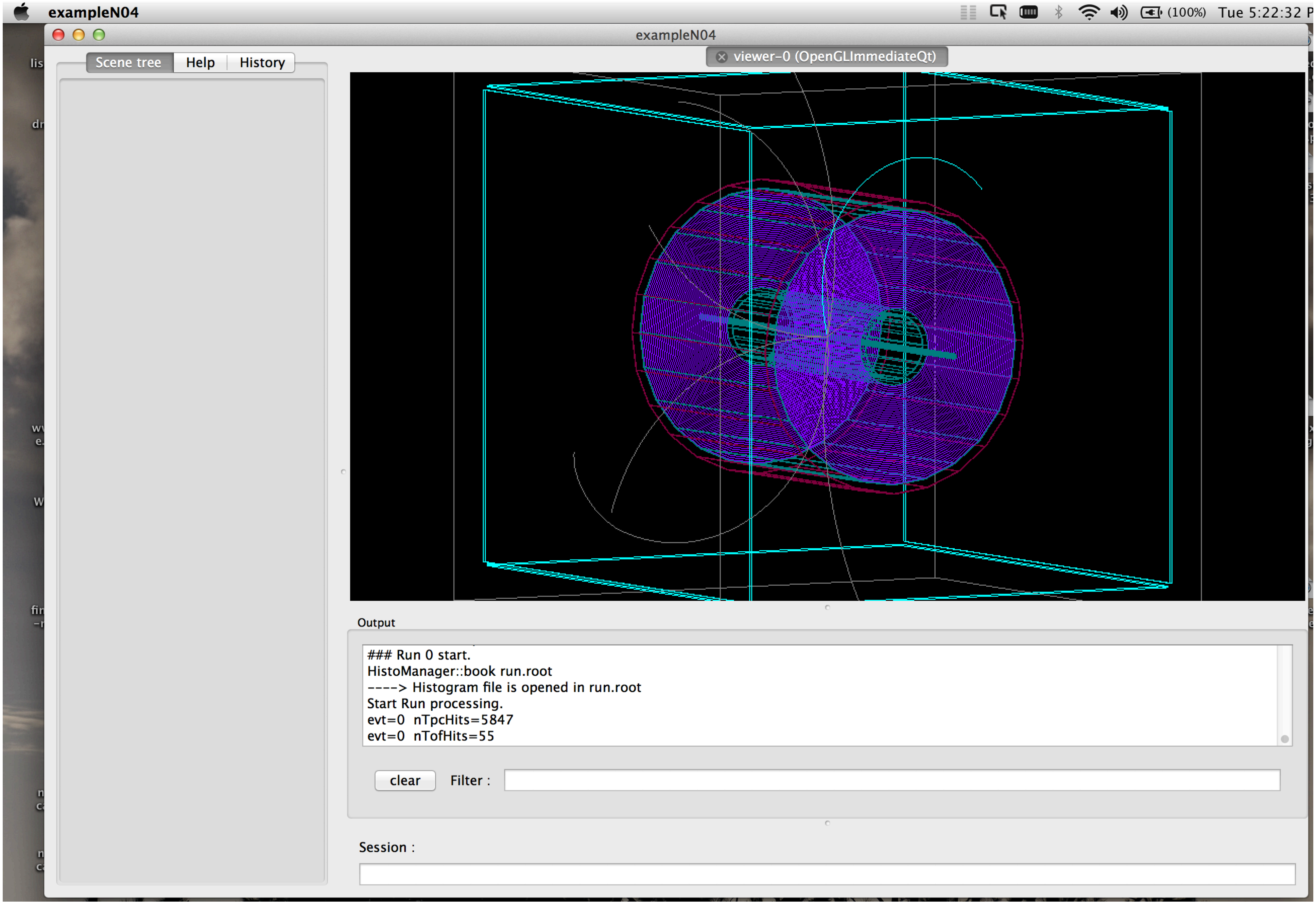
STAR Geometry from STARSIM, Y2010/11 "final"



STARSIM X_0 values used to define the G3 & G4 geometries…

First test is to use the "material" functions in G3 and G4 to show the expected X_0 values are reproduced.. ✔

GEANT4


exampleN04
Tue 5:22:32
exampleN04
Scene tree
Help
History
viewer-0 (OpenGLImmediateQt)
Output
Run 0 start.
HistoManager::book run.root
----> Histogram file is opened in run.root
Start Run processing.
evt=0 nTpcHits=5847
evt=0 nTofHits=55
clear
Filter :
Session :

Approach…

Throw 10 particles (p, pbar, d, dbar, t, tbar, h, hbar, a, abar)
flat P_T distribution
$|\eta|<0.5$, or, as in my analysis, $|y|<0.1$, $0.1<|y|<0.3$, $0.3<|y|<0.5$

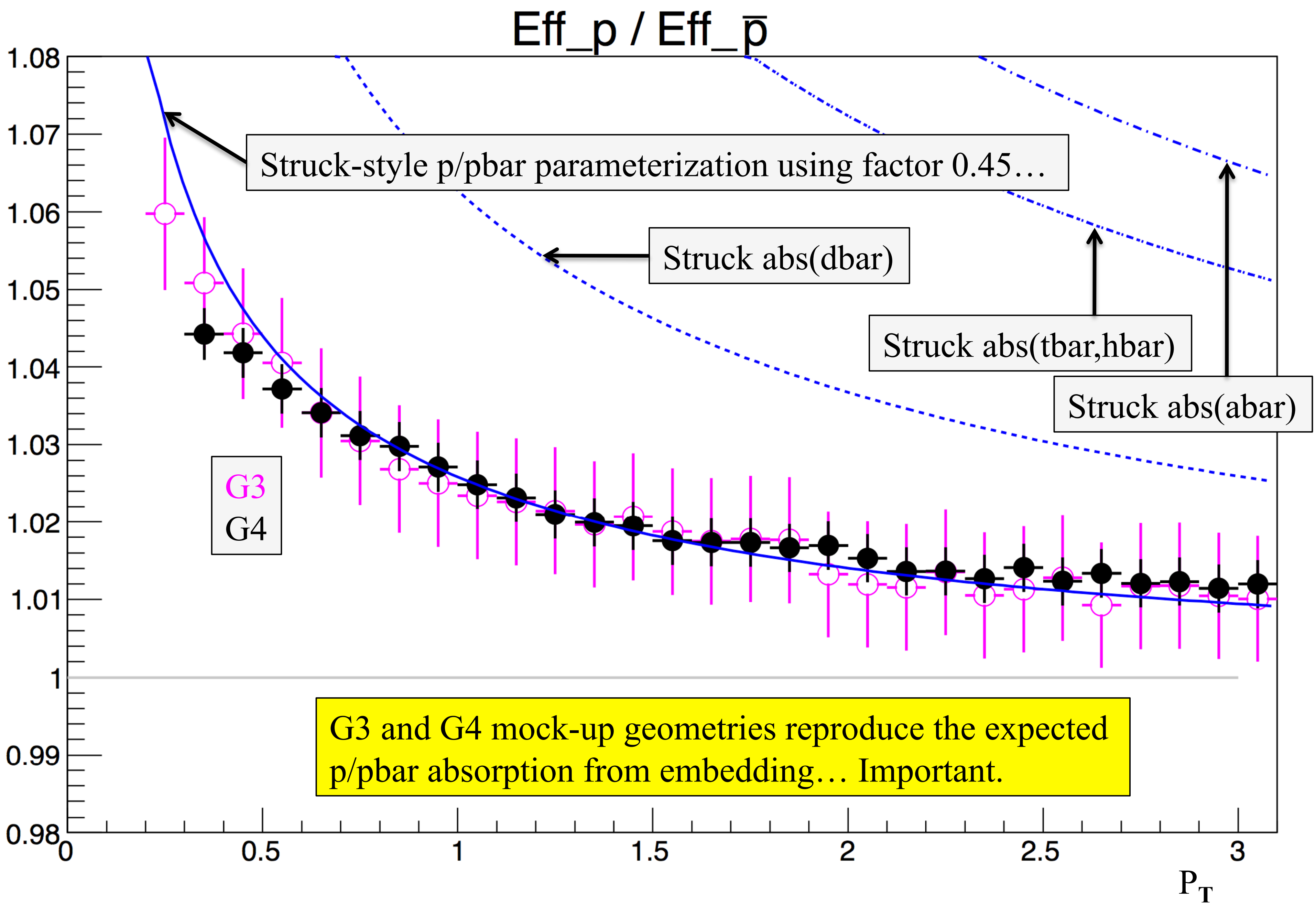
Wasted some time comparing different G4 physics lists. All but one were nonsensical.
Then I learned `FTFP_BERT` is recommended. And this is the one that made sense!
http://geant4.cern.ch/support/proc_mod_catalog/physics_lists/useCases.shtml

Let G3 and G4 swim these tracks, and deposit hits in a "TPC" and a "perfect TOF"
If the particle exits the TPC (or makes hits the "TOF" layer) this track is "not absorbed"

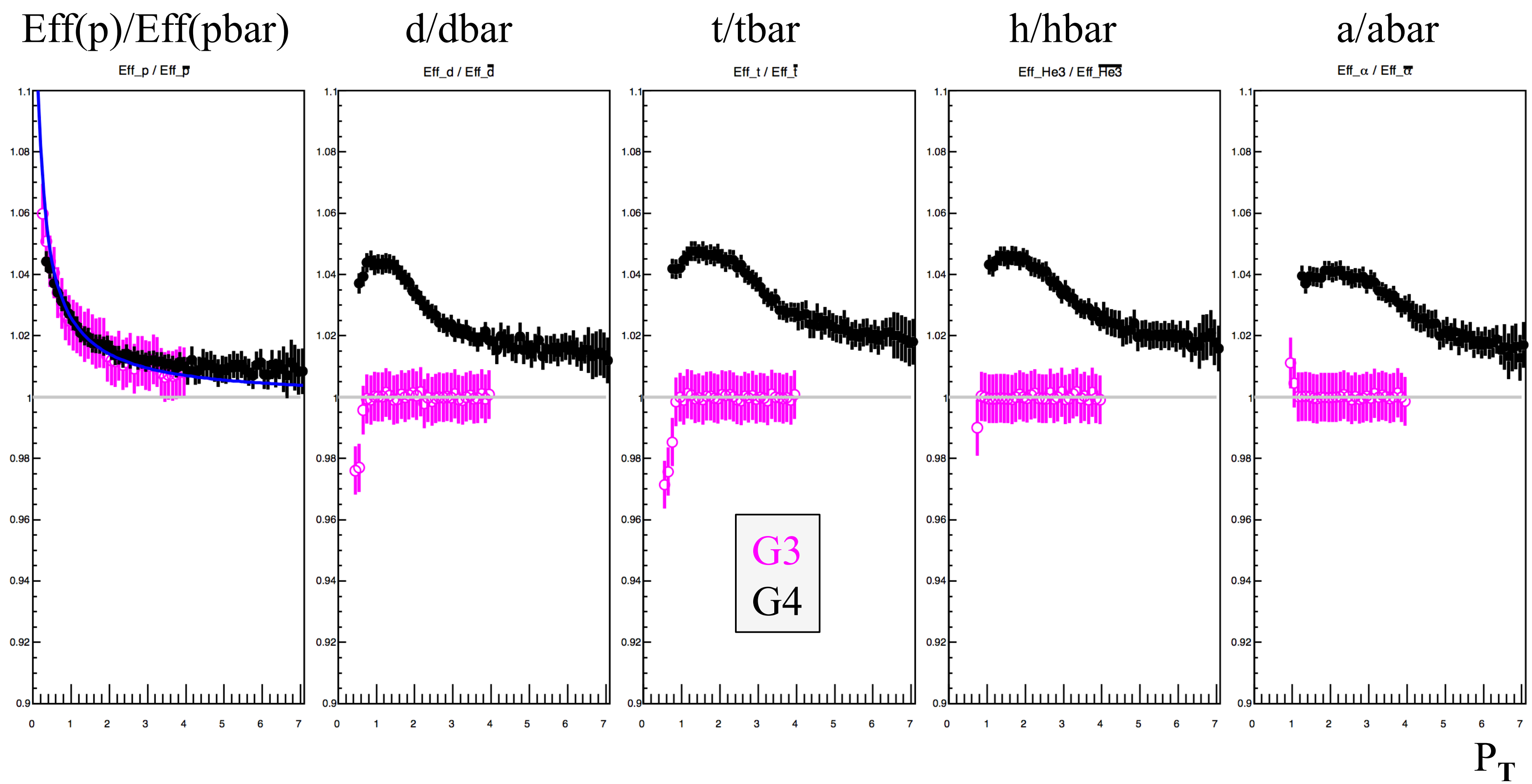
Form the ratios of "not absorbed"/"generated" *vs.* P_T for each particle thrown…
This defines an "not absorbed efficiency" -- This is precisely what I need.
Make ratios of these efficiencies to compare to the Struck approach…

G4 events were generated on the DAVINCI cluster at RICE.
…several 10's of millions of events last weekend…
G3 events were generated on my laptop (10M events in ~5 hours)

Second key test… pbar absorption w.r.t. protons from G3 and G4

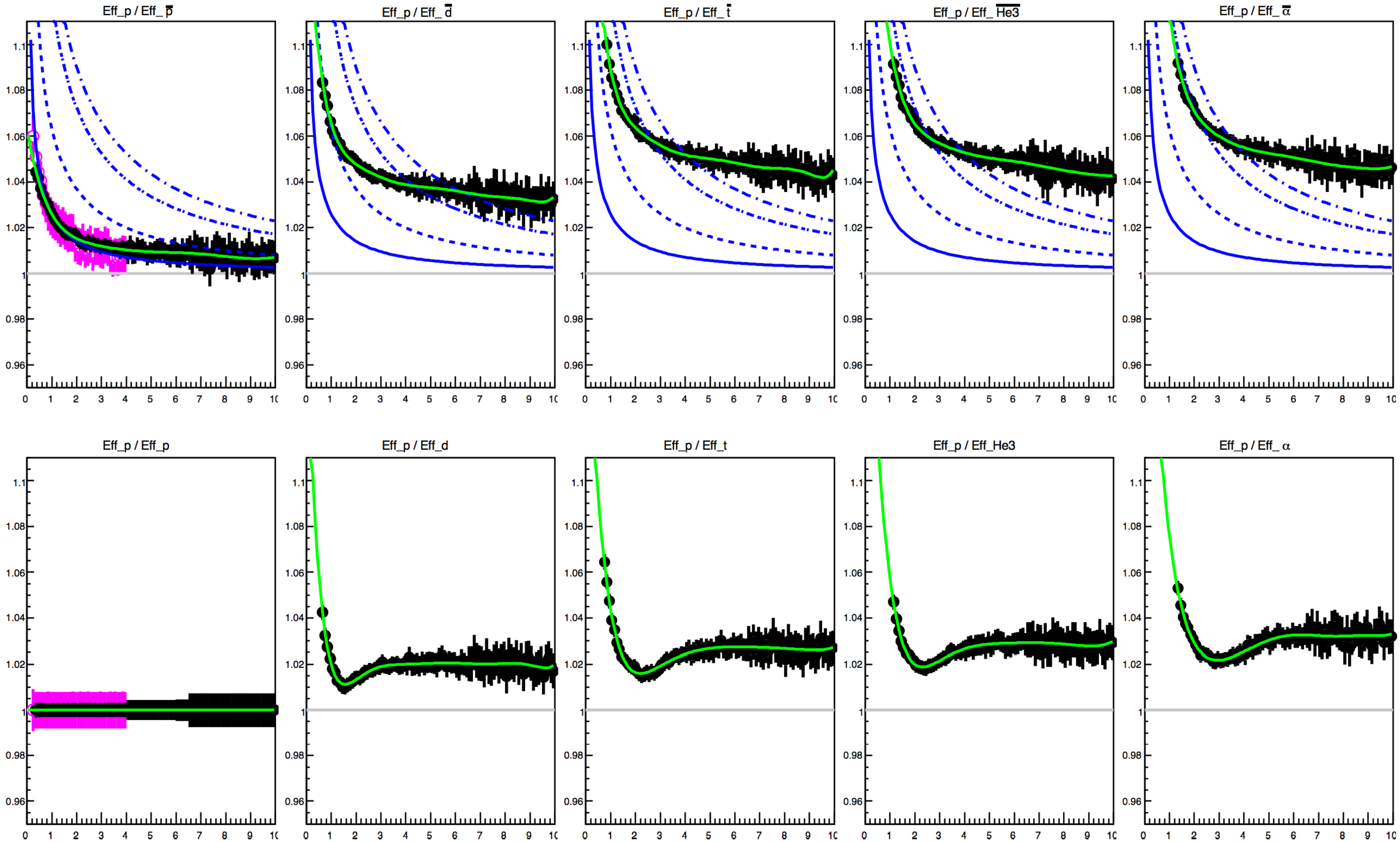


Eff(A)/Eff(Abar)



G3 reproduces the expected values of Eff(p)/Eff(pbar), as expected
G3 gives Eff(A)/Eff(Abar) = 1 independent of PT, which is nonsense, as expected
G4 shows that Eff(Abar) < Eff(A), as expected

Now forming the ratios that I need: Eff(p)/Eff(X)…



Green lines are a pol8 fit and define the absorption corrections I will use…

Summary

Embedding efficiencies for (anti)nuclei in STAR are too high
because Geant3 (STARSIM) effectively propagates them as protons…

C. Struck parameterization is typically used in STAR **anti**nucleus papers
with modified scale factors depending on the geometry assumed in the analysis

This provides no guidance on how to treat the absorption for nuclei...

It makes a scaling assumption for σ^{abs}(Abar) w.r.t. σ^{abs}(pbar)…

We're talking about ~5% corrections here, but still…

GEANT3 and GEANT4 were compared to test the approach…
GEANT4 was then used to provide improved absorption corrections…

Struck's approach is not bad at low P_T (where his data was, but I have TOF!)
The Struck scaling assumption seems to slightly overestimate A>>1 absorption…

Absorption corrections are now available for both nuclei and antinuclei.