

---+ fit for neutron multiplicity

Nate: I think what is done here is mostly fine, but could possibly be done in a better way.

Nate: You could use the Gaussian mixture model to calculate the probability of events belonging to different neutron multiplicity components and then use those as weights to propagate the alpha, mass, etc. histograms.

- We used this method at the very beginning. The weight method results in a fixed efficiency and purity (efficiency == purity) for selected neutron samples because one can only calculate probability, then classify events into different neutron categories according to probability or fill the same event into different different neutron categories by weighting probability. The purity and efficiency of selected 1n neutron sample of weight method are < 80%, which are worse than our current method.
  - Nate: I think whatever you do is fine as long as you account for the effect of the contamination which you do in section 6.3. Given the effect seems to have minimal impact on <alpha> or <M\_mumu>, I wouldn't worry about this further.

---+ dissociative pileup corrections

Nate: The first thing I would request is that this be presented a little more clearly. The matrix in equation 5 should just be factorized into one matrix for the minus side and one of the plus. There is \*no correlation\* between the sides so there's no need to use a single matrix. Also,

everything in lines 250-263 could be written more clearly (like in a matrix or table).

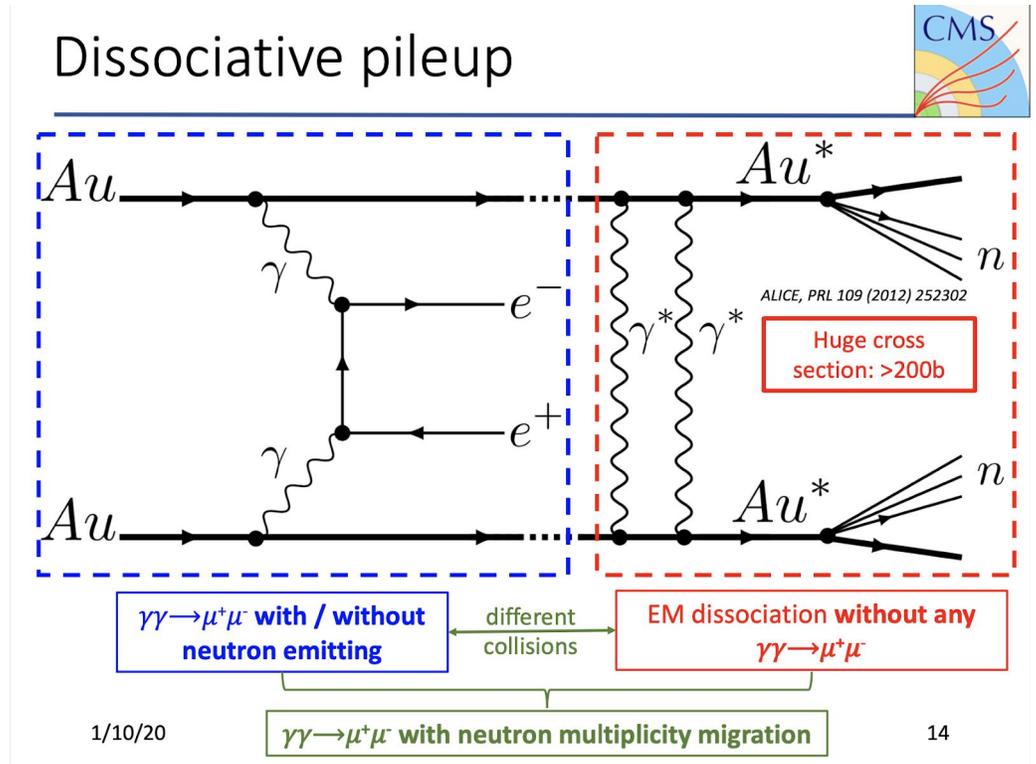
- We cannot factorize the matrix in eq. 5 into two pieces. We agree the neutrons detected in two sides have no correlation, but the impact parameter range of collisions is determined by the neutron multiplicity of both sides, e.g. the  $Xp1m$  in eq 5 means the distribution in neutron multiplicity bin with  $X(X \geq 2)$  neutrons detected (emitted) in plus side and 1 neutron detected (emitted) in minus side. From eq. 5, the measured distributions in  $XpXm$  bin could be from the true distribution in each analyzed neutron multiplicity bin due to the pileup effects.
- Thank you. We will try to make everything in lines 250-263 (AN v3) clear in the updated analysis note during ARC review.
  - Nate: What you say is correct with regards to how you want to mix events. I was thinking along the lines of the probability terms being factorizable, that is, the  $p(0p0m \rightarrow 1p1m)$  term can be written as  $p(0p \rightarrow 1p)p(0m \rightarrow 1m)$  and those would be the same terms that appear in the  $p(0p1m \rightarrow 1p1m) = p(0p \rightarrow 1p)$  and  $p(1p0m \rightarrow 1p1m) = p(0m \rightarrow 1m)$  terms.

- I see. We assume you have agreed with our current approach of treating  $XpXm$  as a whole.

Nate: The logic of the relations in 250-263 does not seem obvious. Could you explain the reasoning?

- The event interested in this analysis is the  $\gamma+\gamma \rightarrow \mu\mu$  which **could be** in conjunction with the excitation of one or both of the **same ions inducing gamma gamma interaction**. The emitted neutron multiplicity (from  $0n0n$  to  $XnXn$ ) is used to classify the events into different impact parameter ranges. If there exists pure EMD but no photon photon interaction **in the same bunch crossing but different ion pair**. Compared to the true emitted neutron multiplicity associated with  $\gamma+\gamma \rightarrow \mu\mu$ , the detected neutron multiplicity value migrates to a large number.
- Because the aforementioned two processes (EMD associated with  $\gamma+\gamma \rightarrow \mu\mu$  and pure EMD) are independent. If one can measure the probability of each analyzed neutron multiplicity from **pure EMD** (do not associated with photon photon interaction) using selected zero-bias data, the migration probability of **true** to **measured** neutron multiplicity associated with interested  $\gamma+\gamma \rightarrow \mu\mu$  can be easily derived, as shown in eq. 5. For instance, if one know the probability of  $0p1m$  from pure EMD is  $p_{\{0p1m\}^{ZB}}$ , the probabilities of true  $0p0m$  to detected  $0p1m$  associated with  $\gamma+\gamma \rightarrow \mu\mu$ , true  $0p1m$  to detected  $0pXm$ , true  $1p0m$  to detected  $1p1m$  are  $p_{\{0p1m\}^{ZB}}$ , and so on. The **detected  $0pXm$**  could be from **true  $0p0m$**  (+  $0pXm$  from pure EMD,  $p_{\{0pXm\}^{ZB}}$ ), **true  $0p1m$**  (+  $0p1m$  or  $0pXm$  from pure EMD,  $p_{\{0p1m\}^{ZB}} + p_{\{0pXm\}^{ZB}}$ ), **true  $0pXm$**  (+  $0p0m$  or  $0p1m$  or  $0pXm$  from pure EMD,  $p_{\{0p0m\}^{ZB}} + p_{\{0p1m\}^{ZB}} + p_{\{0pXm\}^{ZB}}$ )
  - **Nate: To be clear, you assume that the neutron multiplicity distribution is the same in all EMD processes? Is the zero-bias triggered data assumed to have no pileup?**
    - **No, we do not assume either of them.** The measured neutron multiplicity in selected zero-bias triggered data includes the contribution of “pure EMD” pileup. For instance, two ion pairs produce “pure EMD” processes in the same bunch crossing: one ion pair emits  $1p1m$  and the other ion pair emits  $1p0m$ . The measured neutron multiplicity in this zero-bias event is  $2p1m$  (pileup contribution). Here, the selected zero-bias events mean that no valid collision vertex and track is allowed to be present in the event. However, the same HF veto thresholds as the  $\gamma+\gamma \rightarrow \mu\mu$  events are applied.
    - We only assume the probability of each “pure EMD” process (even the “pure EMD” pileup probability) are the same in selected zero-bias triggered events and “ $\gamma+\gamma \rightarrow \mu\mu$ ” events. In other words, the measured neutron multiplicity distribution **from “pure EMD” process(es)** is the same in selected zero-bias and  $\gamma+\gamma \rightarrow \mu\mu$  events. This is because the probability of “pure EMD” process is only related to luminosity and nucleon-nucleon center-of-mass energy. In

this analysis, the zero-bias and single muon UPC triggered data are from the same run period. In the interested “gamma+gamma->mu+mu-” events, the measured neutron multiplicity includes emitted neutrons from the same ion pair producing mu+mu- (**true neutron multiplicity**) and emitted neutrons from different ion pair(s) producing “pure EMD” gprocess(es), as shown in the figure below. Therefore, if we know the probability of neutron multiplicity (not necessary from one ion-pair) from “pure EMD”, the migration probability from true to measured (true + neutron multiplicity from “pure EMD”) will be determined.



Nate: It's not clear how the corrections are applied: do you invert the matrix in eq. 5 to get a response matrix? It seems like you would want to use unfolding here.

- Yes, we multiplied the invert matrix in both sides of eq. 5 and convoluted measured distributions to true distributions (unfolding) in differential neutron multiplicity bins.
  - Nate: Okay. Thanks for the clarification.

Nate: In general, I think there are two pdfs at play here: the probability of the neutron multiplicity per EMD and the probability of the pileup. That is, you could have a single EMD interaction that produces two neutrons or you could have two EMD interactions that produce one each. The two effects are going to be combined in your ZDC spectrum, but you need to disentangle them to know what the purely pileup effect is in your ggmm events are.

- In this analysis, one event can only have one gamma+gamma->mumu pair ( $N_{\text{trk}}^{\text{HP}} == 2$  requirement) and the in-bunch pileup effect refers to **pure EMD process(s) associated with no gamma gamma interaction.**
- We do not need to disentangle different pure EMD scenarios. The probabilities of various pure EMD scenarios are independent with triggers, therefore, we only need the total probability of each analyzed neutron multiplicity from the pure EMD process(s) causing the migration of true neutron multiplicity associated with gamma+gamma -> mumu. The estimated probability of each analyzed neutron multiplicity from pure EMD using selected zero-bias data is the total probability of the various pure EMD scenarios.
  - Nate: Again I wonder about the assumptions of pileup in your zero-bias data. What you're saying seems to suggest that the "pure EMD" process is pileup free. Is that correct? Have you performed any closure tests to validate this procedure?
    - No, we do not assume the "pure EMD" process is pileup free and it is not pileup free. Please see our detailed response to your last question marked as red.

---+ fit of alpha spectrum

Nate: It's not clear to me why a fit is even necessary here. The quantity of interest is  $\langle \alpha \rangle$  which would only seem to require a fit if the model parameters were meaningful (perhaps I'm mistaken, but they don't seem to be) or the separation from the LO and HO was used to characterize LO and HO effects. You could do the average based on the raw (unbinned) events.

- We only report the  $\langle \alpha \rangle$  from leading order gamma gamma scattering (**core**) so we need to subtract the contribution from high order photon interactions (**tail**) to  $\langle \alpha \rangle$  distribution using fit
  - Nate: Okay, sounds good. I might have just overlooked this, but it did not seem to be stated explicitly.
    - We mentioned this in the abstract and result sections.

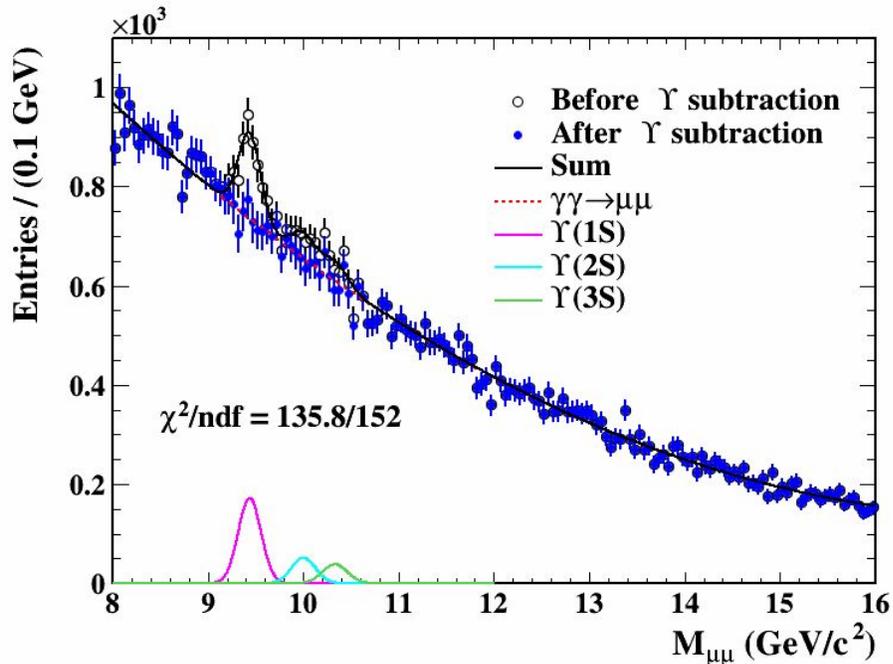
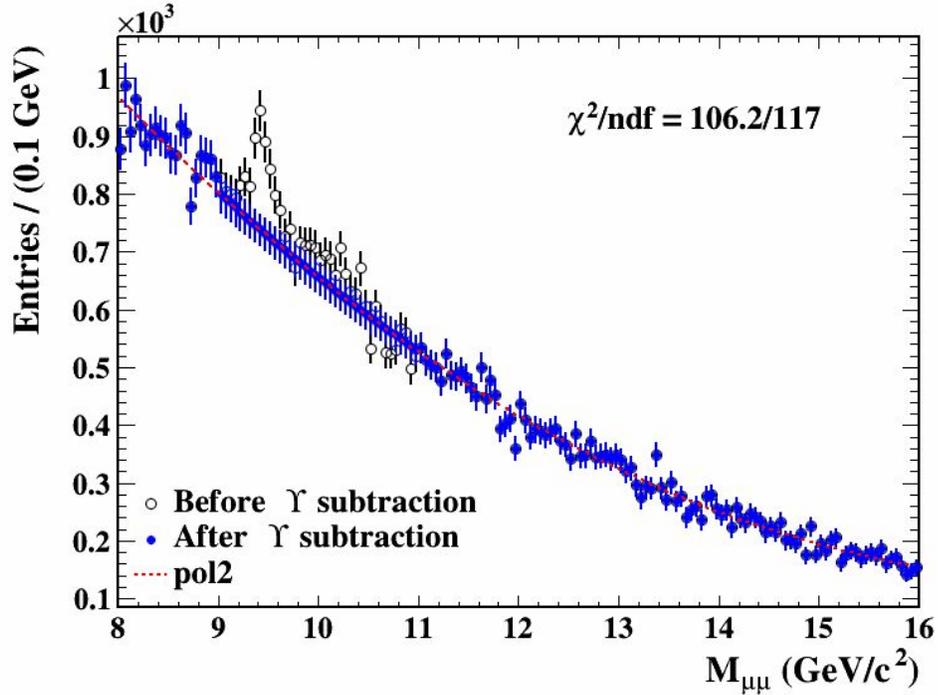
---+ epsilon subtraction

Nate: I think it would make more sense to fit using a mixture model (polynomial + gaussian with parameters constrained or fixed by Upsilon properties). This will also give you your uncertainty on the Upsilon yield which can be used for the systematic uncertainty.

- We agree that a more standard way is using continuum + peaks to fit the distributions. However, these two methods should give consistent continuum contribution underneath Upsilon peaks if both methods have good fit quality. In this analysis, the overall Upsilon significance is  $< 10 \sigma$  and the significance in differential neutron multiplicity bin is

worse. We cannot even observe epsilon peak in some neutron multiplicity bins, which makes continuum + peaks fit much harder.

- We compared these two methods using the inclusive mass spectrum (all neutron multiplicity bins combined) and found the difference on  $\langle M \rangle$  between these two method is  $<0.01\%$  (Extrapolation method:  $\langle M \rangle = 12.903 \pm 0.02$  vs. mixture model:  $\langle M \rangle = 12.904 \pm 0.02$ ), the fit details can be found below



- The systematic uncertainty on  $\langle M \rangle$  from this part is estimated by employing polynomial functions with different orders which should be equivalent to that from Upsilon yield
  - Nate: This sounds fine. It seems that the contamination is not significant.

---+ results

Nate: It would be a good idea to quantify the statement of the change in average quantities being correlated with the impact parameter (neutron flux). Instead of quoting the deviation of the first and last points (as in lines 406 and 415), it would be better to use a measure of how much better a linear model fits versus a constant. This should be possible with a likelihood ratio.

- We cannot perform a linear model fit, because the X-axis is an event category which is not a physics quantity like impact parameter. However, we can definitely perform a constant fit to check the  $\chi^2/\text{ndf}$  and p-value to estimate the significance of deviation from constant. Please let us know if you have additional suggestions or comments related to this quantification.
  - Nate: Carrying out the calculation of p values sounds like a good first step. I guess the exact mapping between the neutron multiplicity and the impact parameter is not known so I agree that a linear relation is not applicable.
    - Yes, there is no available mapping between neutron multiplicity and the impact parameter