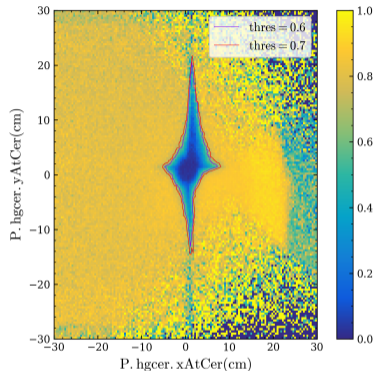
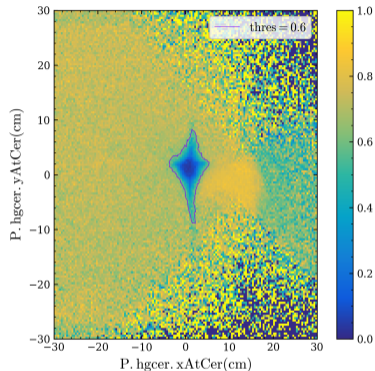


Kaon LT Meeting

April 09, 2026

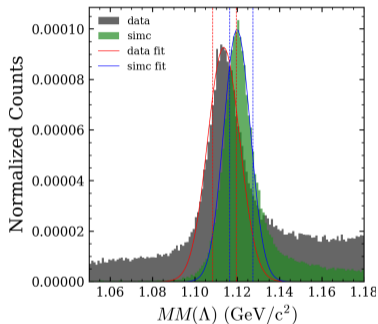
Chi-Kin Tam

Improved HGcer hole cut



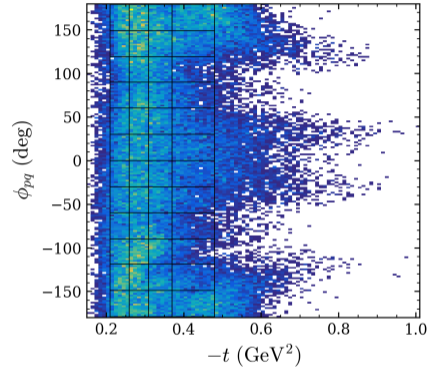
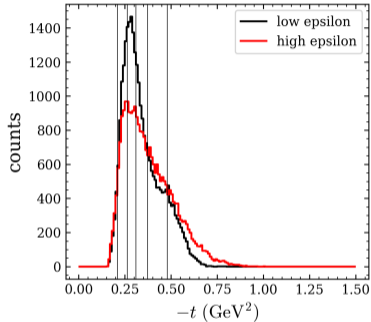
- ▷ z axis represents efficiency $N_{\text{did}}/N_{\text{should}}$.
- ▷ Start at (0, 0), radiates out and find the bin passing threshold efficiency.

MM shifts



- ▷ use the latest replay `Pass4a_Apr_2026`
- ▷ MM shifted as before even with improved HGcer hole cut. Other reasons?
- ▷ The 2018 matrix element instead of the NPS used.
- ▷ Difference in optics offset `hphi_offset` in BOTH hms and shms.

Binnings



- ▷ redefine the binnings due to t -shifts.
- ▷ increase lower limit ($0.19 \rightarrow 0.21$) and upper limit ($0.43 \rightarrow 0.47$).

Faster iteration

Before

- ▷ Loop ROOT events \rightarrow apply cuts \rightarrow recalculate weight \rightarrow fill histograms \rightarrow calculate yields $\rightarrow \dots$
- ▷ too slow

New

- ▷ preprocess SIMC events as a table of Q_i, t_i, \dots , bin indices and weight.

$\epsilon_{H,L}$	SHMS	$i^{\text{th}} t$ bin	$i^{\text{th}} \phi$ bin	W_i	t_i	ϵ_{cm}	Weight	σ_{cm}
0	10	15	20	0.5	1.2
1	12	18	25	0.6	1.3
1	8	14	22	0.4	1.1
\vdots					\vdots			

- ▷ All operations are now vectorized \rightarrow one-shot reweighting.
- ▷ Cut by slicing, i.e. `arr[Qi][(ieps == 0) & (ishms == 1)]` \leftarrow center low.
- ▷ `Yield = sum(arr["Weight"] / arr["sigcm"] * sig_new)`

Systematics studies

Goal

- ▷ Get sensitivity of $\sigma_{L,T,LT,TT}$ to different systematic changes.
- ▷ Old method was to redo LT iteration. Easier to perform Rosenbluth in a model-independent way.

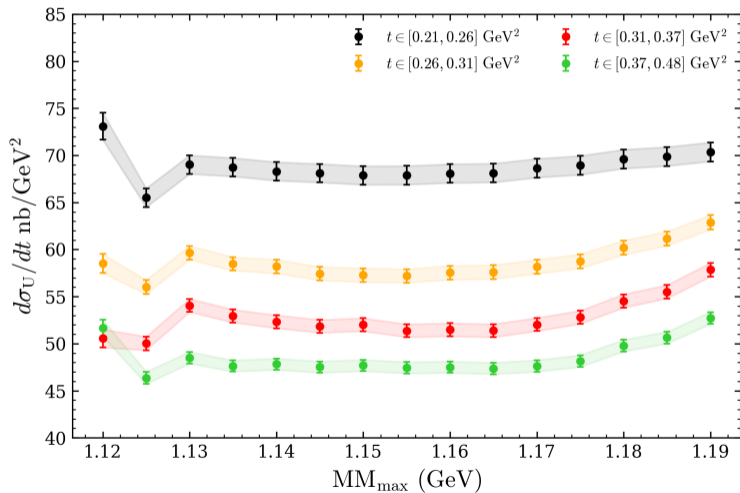
Procedures

- ▷ generate data missing mass distribution in all settings.
- ▷ preprocess SIMC events as a table of Q_i, t_i, \dots , bin indices and weight.
- ▷ for each systematic change, extract $\sigma_{L,T,LT,TT}$ by performing a χ^2 fit:
 - select data events in the missing mass range and calculate yields.
 - select SIMC events in the missing mass range.
 - reweight as $\text{Weight} \cdot \frac{\sigma_{\text{new}}}{\sigma_{\text{old}}}$, where σ_{old} is a branch in SIMC and σ_{new} is from Rosenbluth formula.
 - calculate the χ^2 between data and SIMC yields in ALL settings (not averaged over).
 - optimize for $\sigma_{L,T,LT,TT}$.
- ▷ redo for each $-t$ bin.

Systematics studies (MM range)

Missing mass range

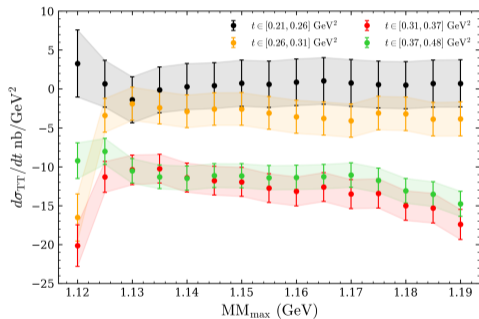
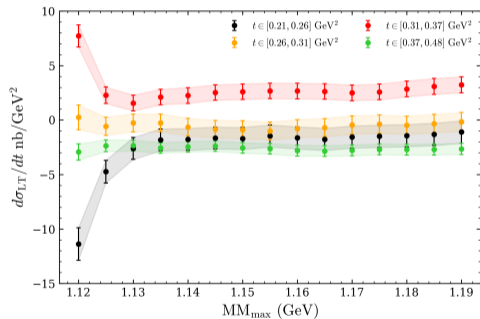
▷ fixed lower bound to 1.10 and vary upper bound from 1.12 to 1.19, $dM = 0.005$.



Systematics studies (MM range) - cont.

Missing mass range

- ▷ fixed lower bound to 1.10 and vary upper bound from 1.12 to 1.19, $dM = 0.005$.



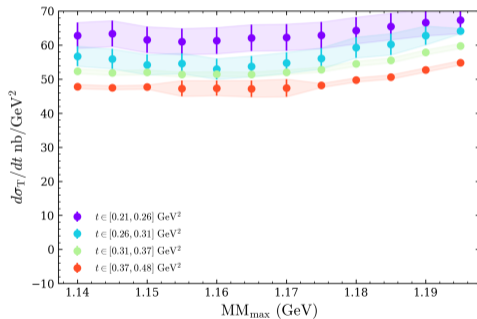
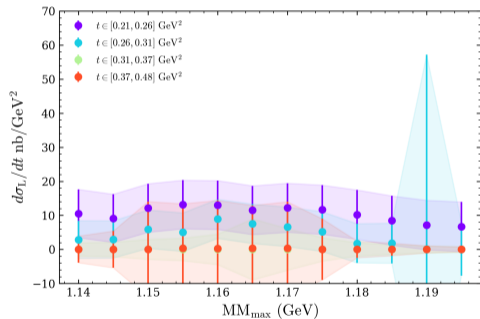
Next steps

- refine background subtraction
- add the distribution plot back

Systematics studies (MM range)

Missing mass range

- ▷ fixed lower bound to 1.10 and vary upper bound from 1.14 to 1.19, $dM = 0.005$.



Systematics studies (MM range) - cont.

Missing mass range

- ▷ fixed lower bound to 1.10 and vary upper bound from 1.14 to 1.19, $dM = 0.005$.

