

Typical Analysis Workflow

Justin Stevens

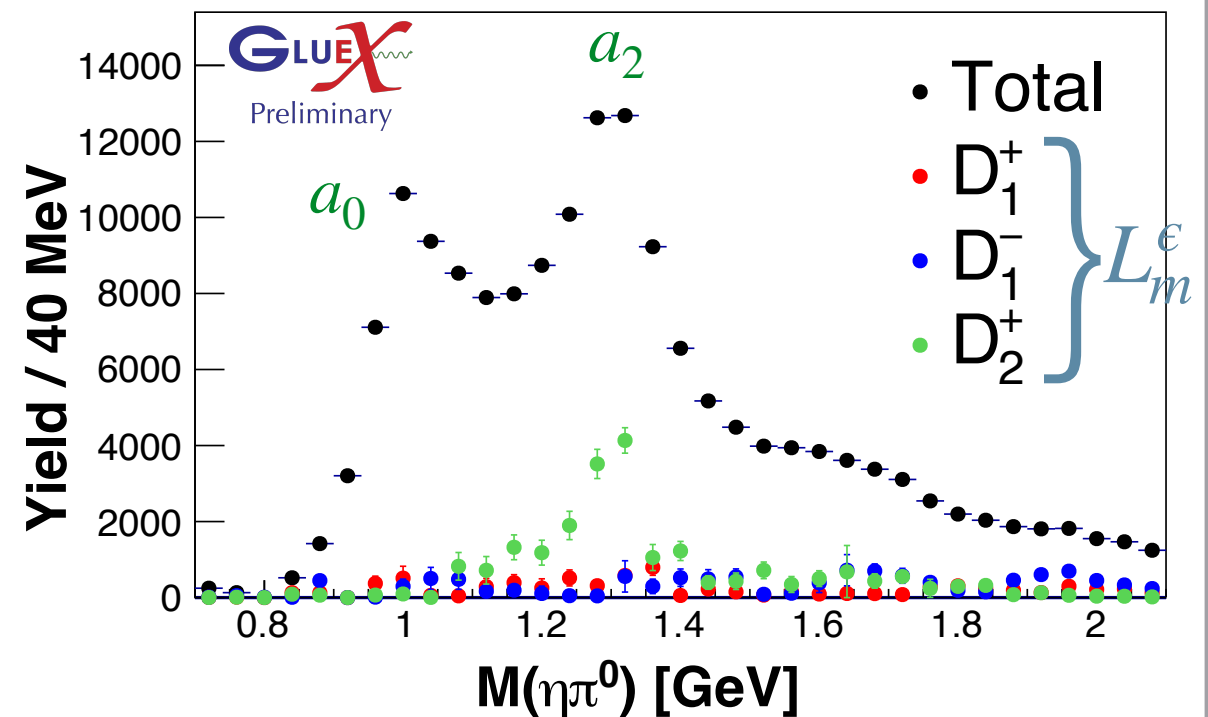
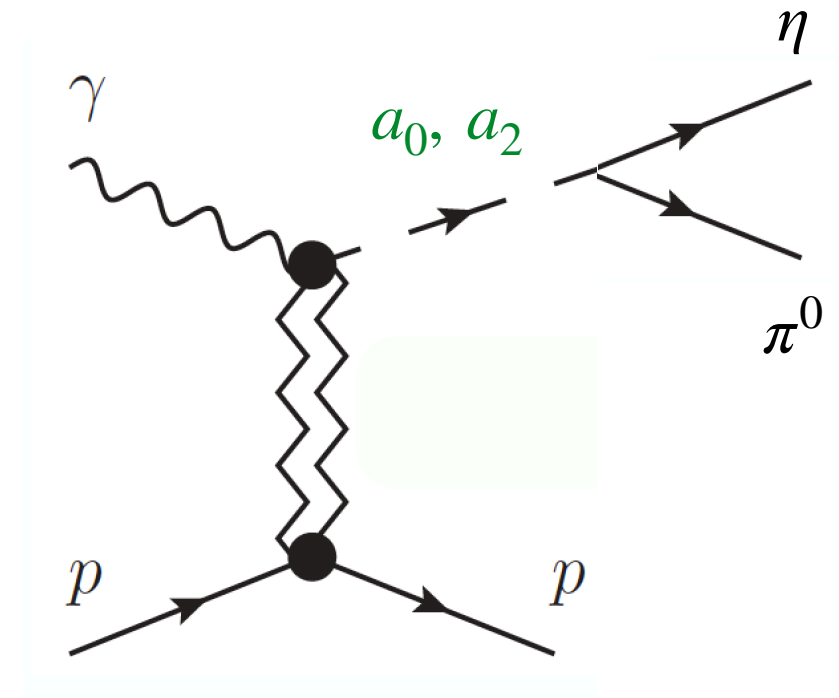


WILLIAM & MARY

CHARTERED 1693

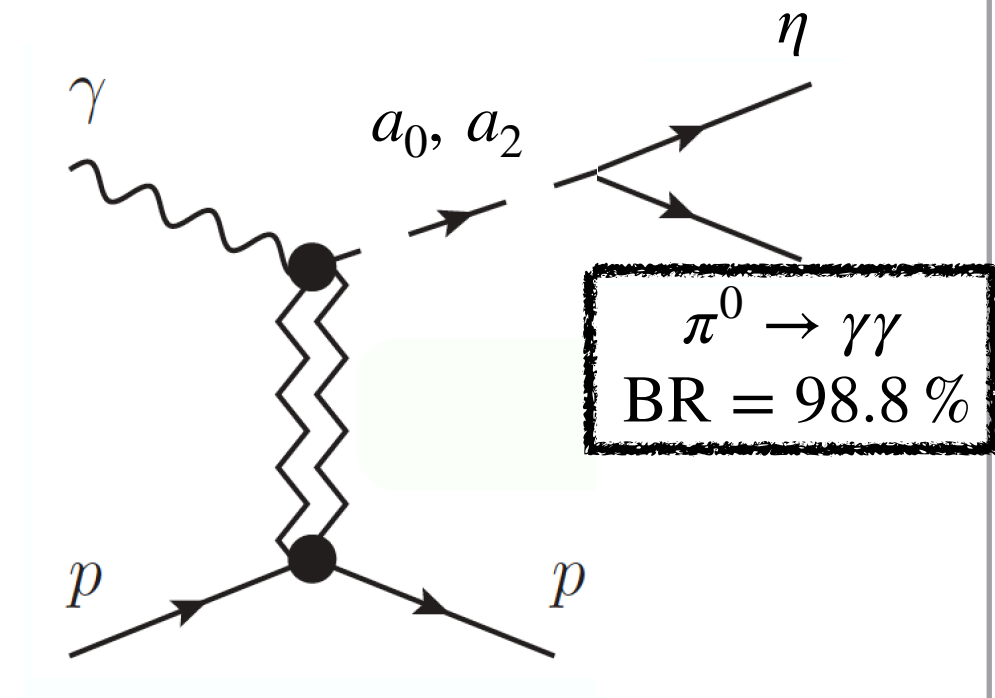
Big picture analysis strategy

- * **Goal:** obtain pure sample of $\gamma p \rightarrow \eta \pi^0 p$ to study contributing amplitudes
- * **Necessary steps:**
 - * Choose appropriate ReactionFilter and Kinematic Fit options
 - * Apply selection criteria (i.e. cuts) which efficiently reject background but keep signal of interest
 - * Statistically subtract remaining background, not removed by cuts
 - * Measure yield for cross section or fit angular distributions for beam asymmetry or amplitude analysis



How to reconstruct your final state?

	Mode	Fraction (Γ_i / Γ)
▼ Neutral modes		
Γ_1	neutral modes	$(72.12 \pm 0.34)\%$
Γ_2	2γ	$(39.41 \pm 0.20)\%$
Γ_3	$3 \pi^0$	$(32.68 \pm 0.23)\%$
▼ Charged modes		
Γ_8	charged modes	$(27.89 \pm 0.29)\%$
Γ_9	$\pi^+ \pi^- \pi^0$	$(22.92 \pm 0.28)\%$
Γ_{10}	$\pi^+ \pi^- \gamma$	$(4.22 \pm 0.08)\%$

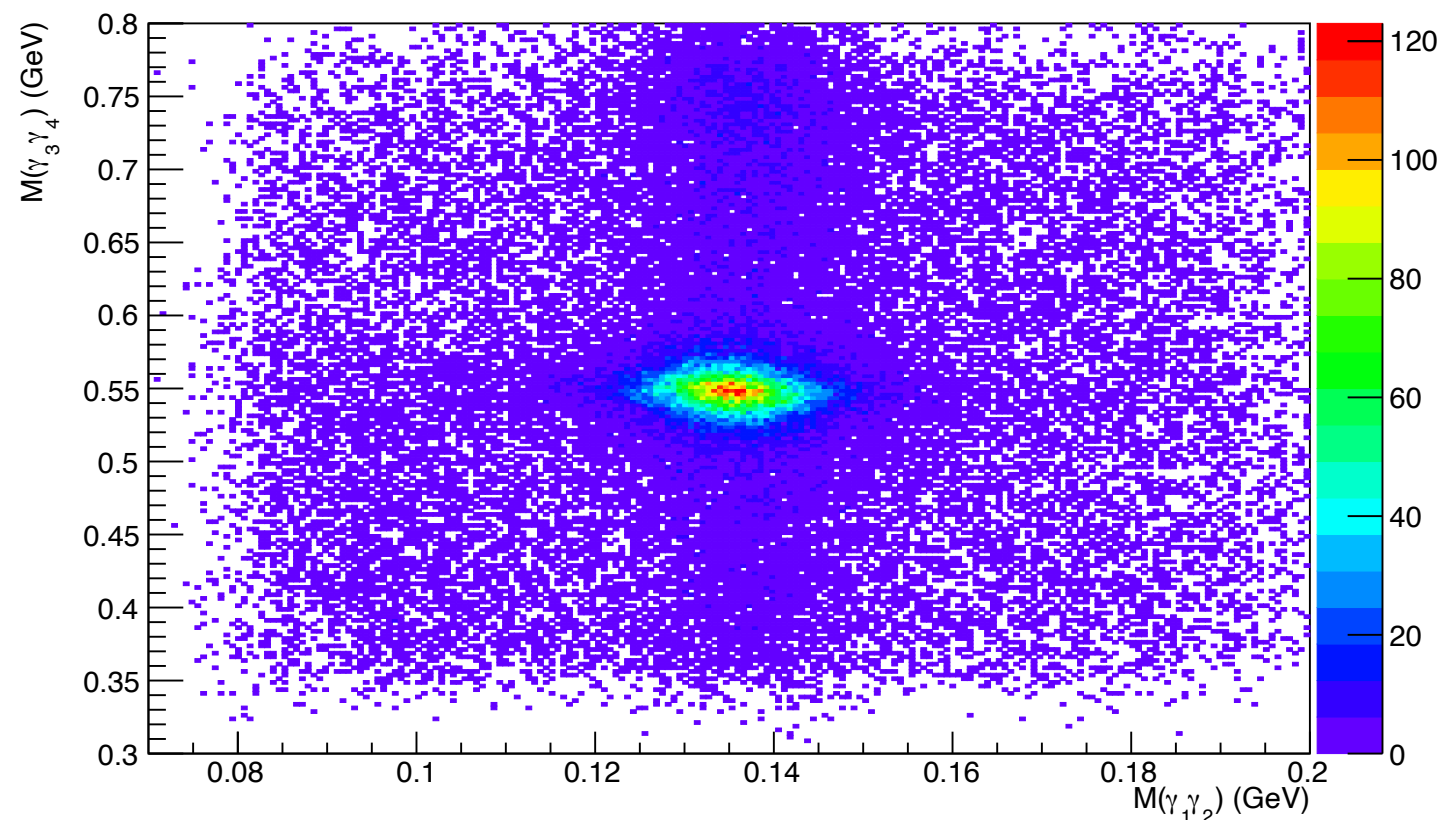


- ✱ **Exclusive:** if at all possible, reconstruct all final state particles!
- ✱ **Decay modes:** large branching ratio and simpler to reconstruct preferred
 - ✱ Comparison of multiple decay modes provides systematic cross check, which is a major strength of GlueX
- ✱ For this tutorial we'll use exclusive $\gamma p \rightarrow \eta \pi^0 p$ with $\eta \rightarrow \gamma\gamma$ and $\pi^0 \rightarrow \gamma\gamma$

ReactionFilter, Kinematic Fit and Mass Constraints

- * ReactionFilter is an analysis plugin to define the reaction you intend to study and write ROOT trees for analysis (see Beni's talk)
- * $\gamma p \rightarrow \eta \pi^0 p$ with decays $\eta \rightarrow \gamma\gamma$ and $\pi^0 \rightarrow \gamma\gamma$ specify the reaction with
 - * `Reaction1 1_14__7_17_14`

Signal Reaction: $\gamma p \rightarrow \eta \pi^0 p, 4\gamma p$

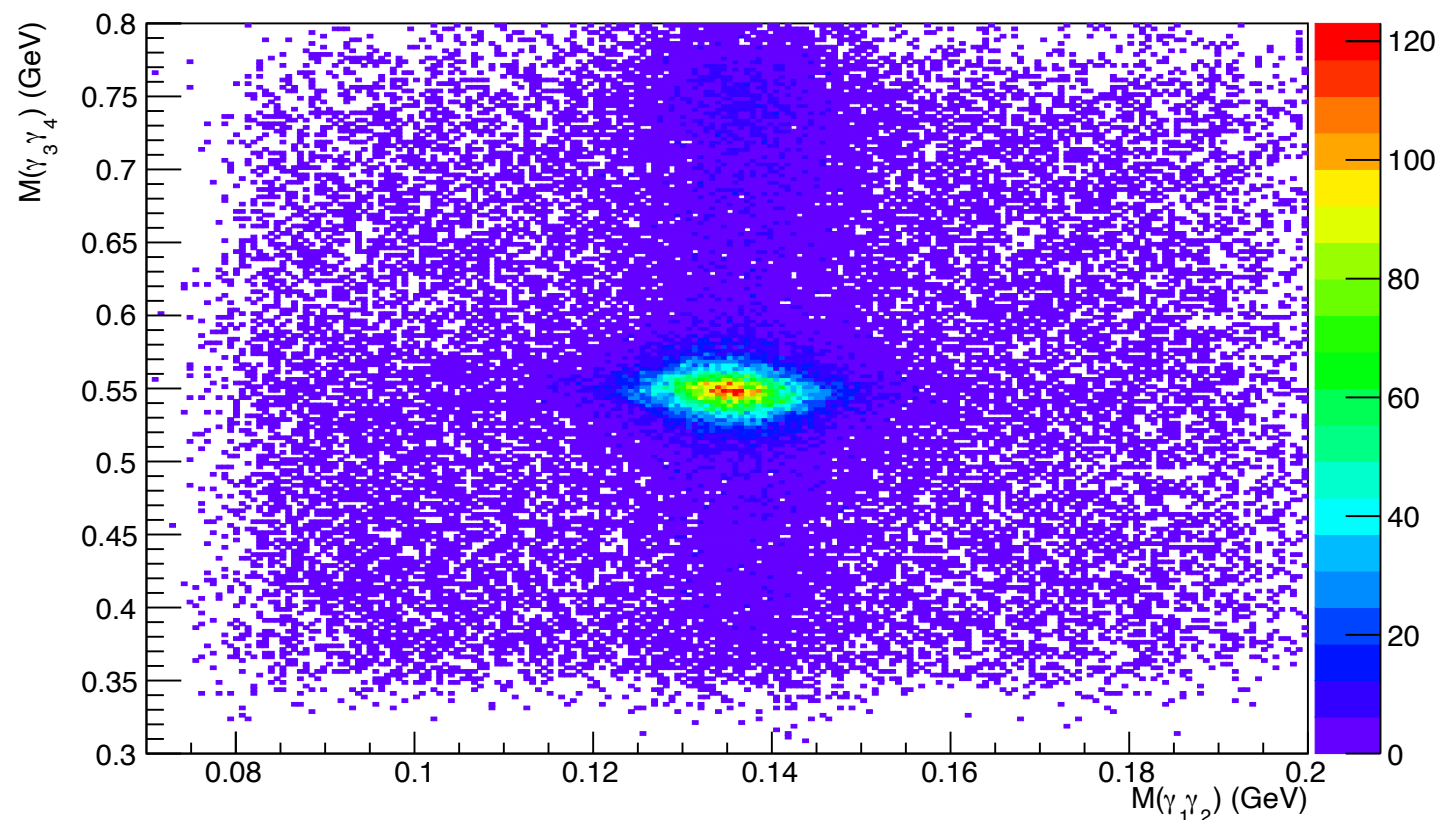


Neither π or η
constrained:
B4_M17_M7

ReactionFilter, Kinematic Fit and Mass Constraints

- * ReactionFilter is an analysis plugin to define the reaction you intend to study and write ROOT trees for analysis (see Beni's talk)
- * $\gamma p \rightarrow \eta \pi^0 p$ with $\eta \rightarrow \gamma\gamma$ and $\pi^0 \rightarrow \gamma\gamma$: `Reaction1 1_14__7_17_14`
- * What Kinematic Fit flags should we use?
 - * `Reaction1:Flags B4_M17_M7` or `B4_M7` or `B4_M17` or `B4`

Signal Reaction: $\gamma p \rightarrow \eta \pi^0 p, 4\gamma p$

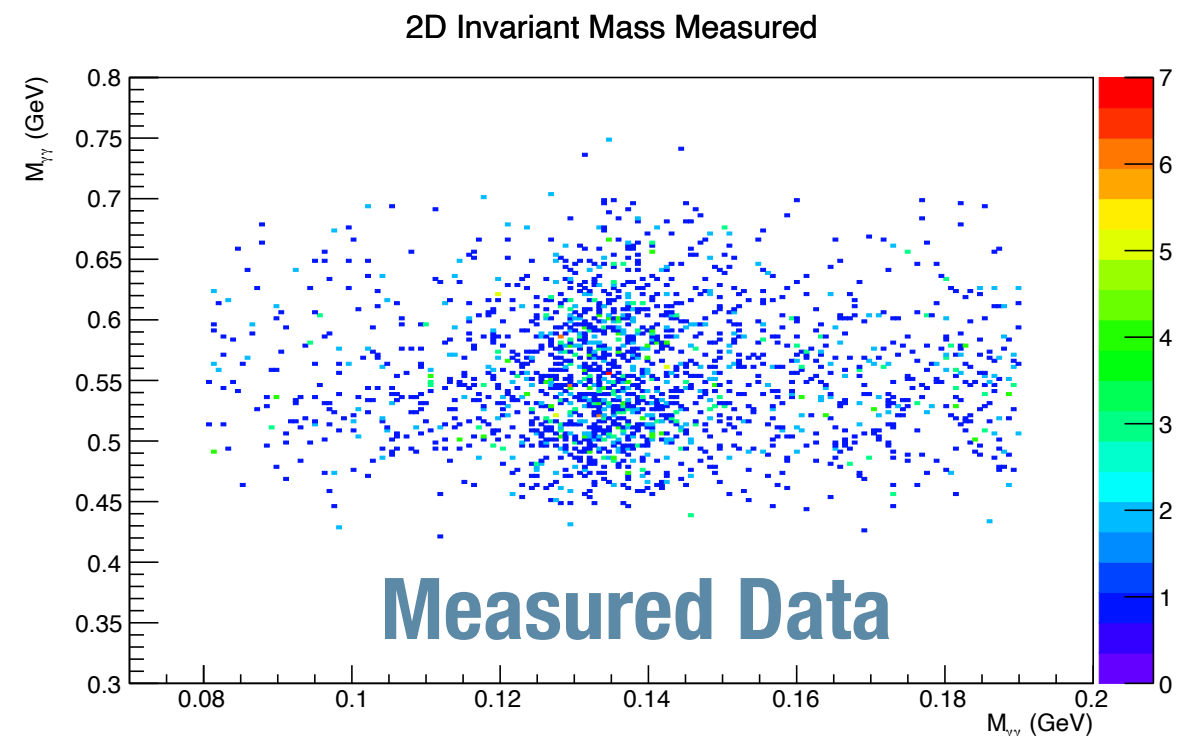
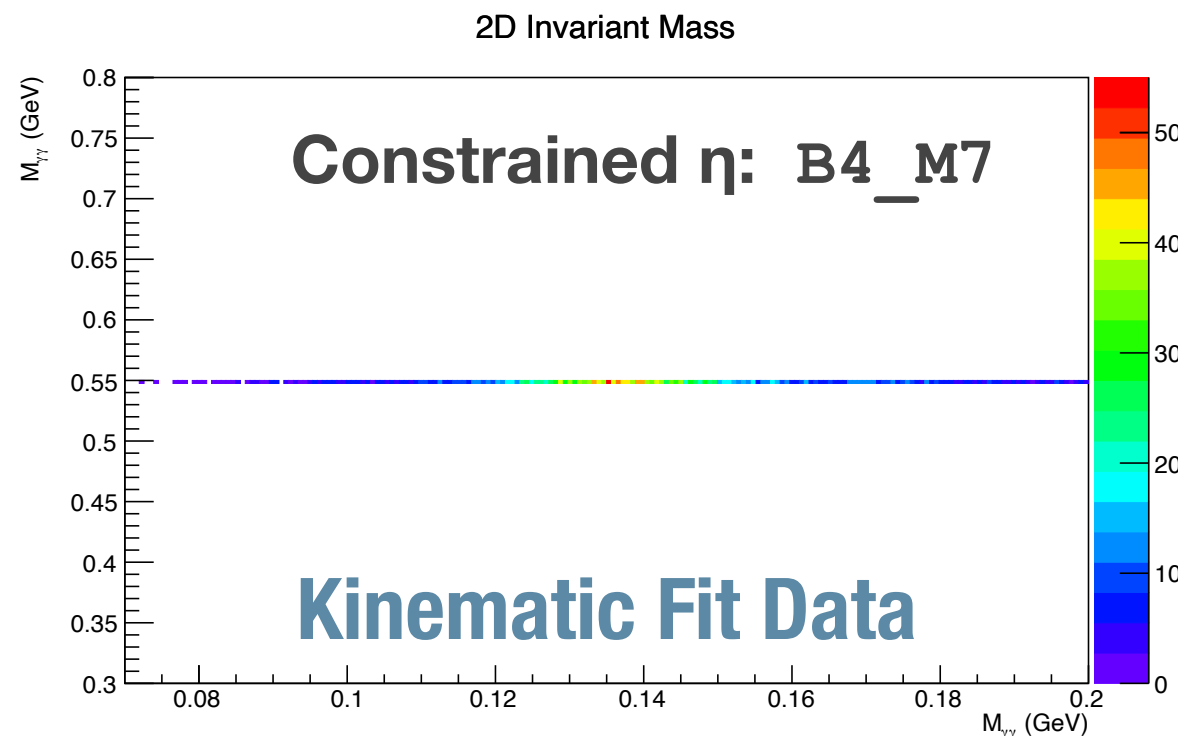


Neither π or η
constrained:
B4_M17_M7

ReactionFilter, Kinematic Fit and Mass Constraints

- * ReactionFilter is an analysis plugin to define the reaction you intend to study and write ROOT trees for analysis (see Beni's talk)
- * $\gamma p \rightarrow \eta \pi^0 p$ with $\eta \rightarrow \gamma\gamma$ and $\pi^0 \rightarrow \gamma\gamma$: `Reaction1 1_14__7_17_14`
- * What Kinematic Fit flags should we use?
 - * `Reaction1:Flags B4_M7_M17` or **`B4_M7`** or `B4_M17` or `B4`

Background Reaction: $\gamma p \rightarrow \omega \pi^0 p, 5\gamma p$

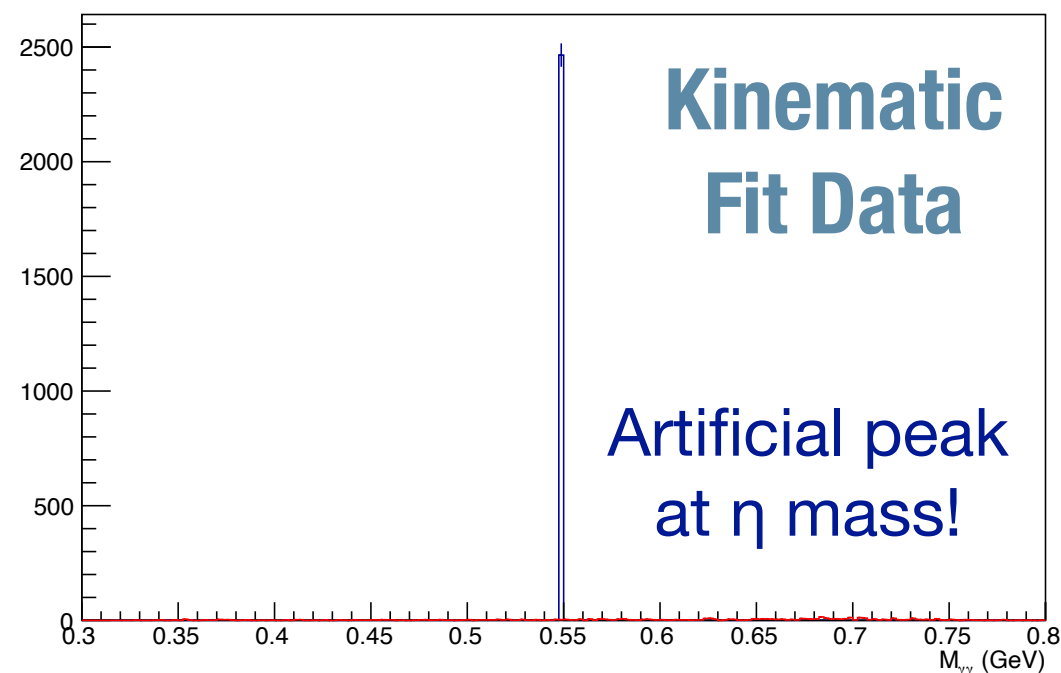


ReactionFilter, Kinematic Fit and Mass Constraints

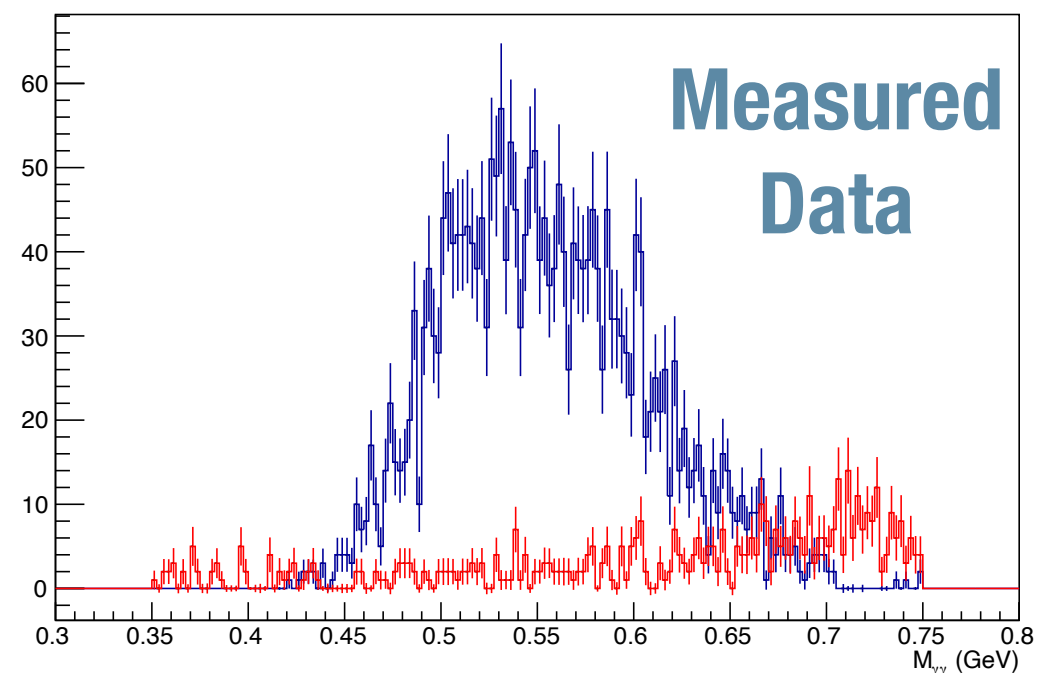
- * ReactionFilter is an analysis plugin to define the reaction you intend to study and write ROOT trees for analysis (see Beni's talk)
- * $\gamma p \rightarrow \eta \pi^0 p$ with $\eta \rightarrow \gamma\gamma$ and $\pi^0 \rightarrow \gamma\gamma$: `Reaction1 1_14__7_17_14`
- * What Kinematic Fit flags should we use?
 - * `Reaction1:Flags` **B4_M7_M17** or **B4_M7** or `B4_M17` or `B4`

Background Reaction: $\gamma p \rightarrow \omega \pi^0 p, 5\gamma p$

2D Invariant Mass



2D Invariant Mass Measured

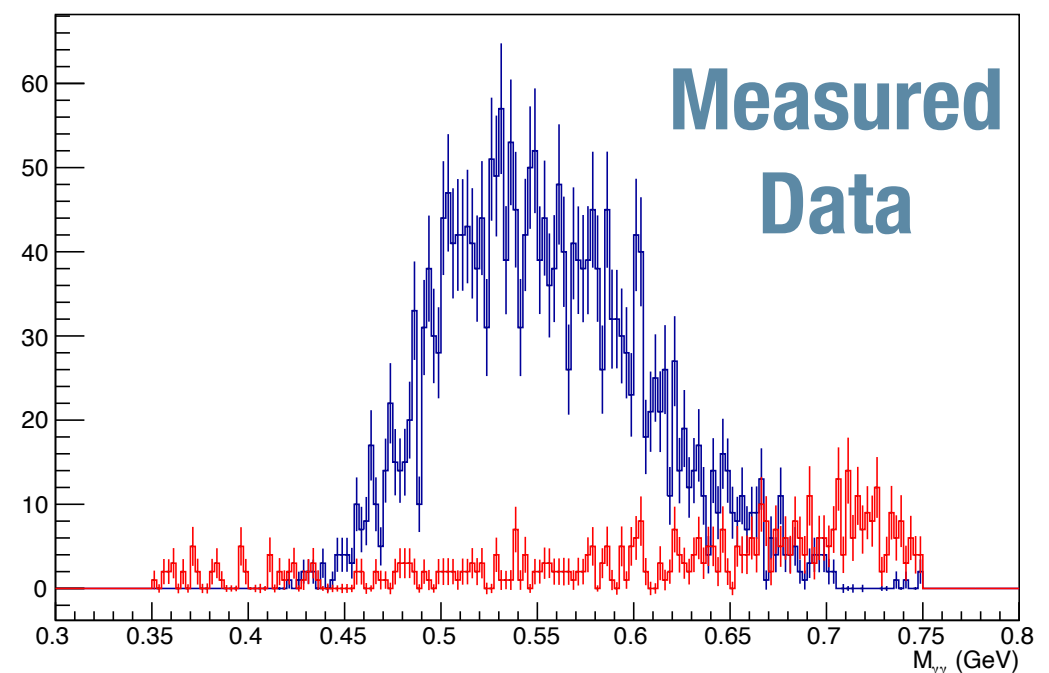
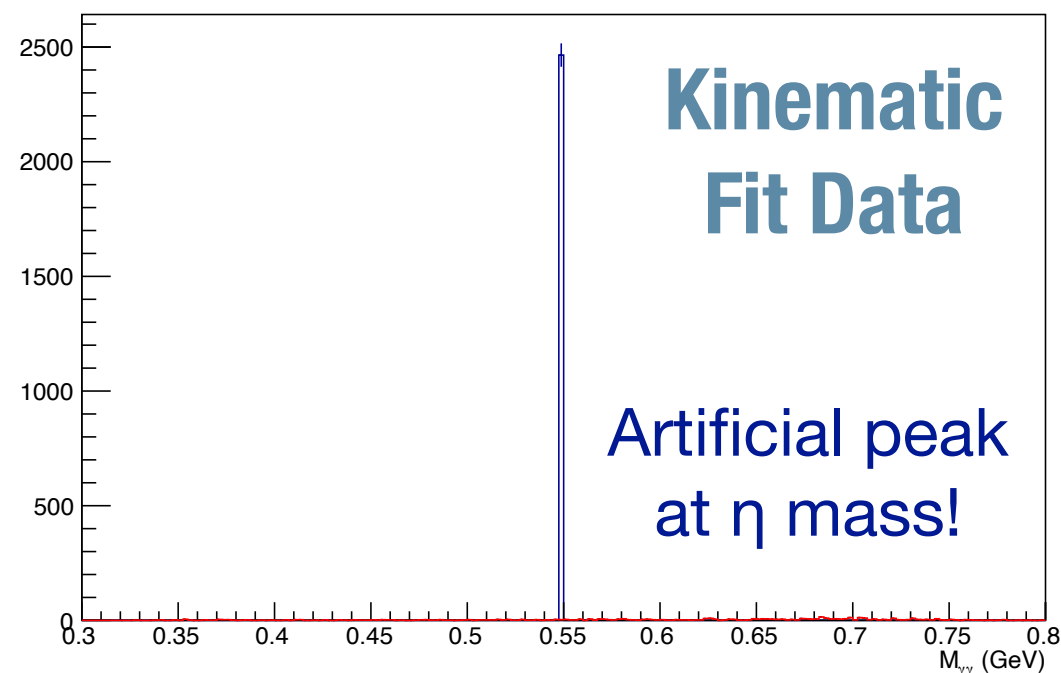


ReactionFilter, Kinematic Fit and Mass Constraints

- * ReactionFilter is an analysis plugin to define the reaction you intend to study and write ROOT trees for analysis (see Beni's talk)
- * $\gamma p \rightarrow \eta \pi^0 p$ with $\eta \rightarrow \gamma\gamma$ and $\pi^0 \rightarrow \gamma\gamma$: `Reaction1 1_14__7_17_14`
- * What Kinematic Fit flags should we use?
 - * `Reaction1:Flags` **B4_M7_M17** or **B4_M7** or `B4_M17` or `B4`

Background Reaction: $\gamma p \rightarrow \omega \pi^0 p, 5\gamma p$

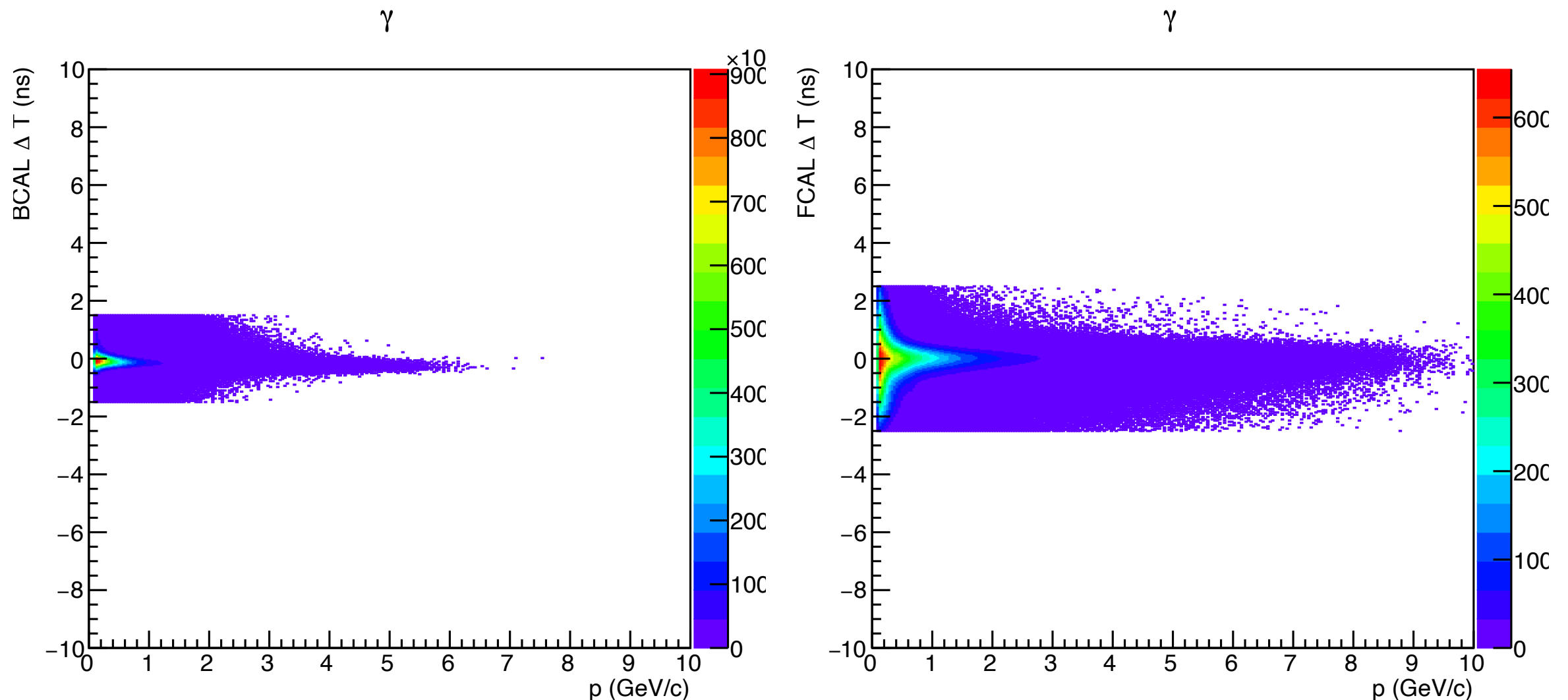
Take home message: leave at least one mass un-constrained!



Event selection 101

- * Analysis Launch Cuts: “loose” cuts that are already applied in ReactionFilter by default

PID	BCAL/RF Δt (ns)	TOF/RF Δt (ns)	FCAL/RF Δt (ns)	SC/RF Δt (ns)
γ	± 1.5	NA	± 2.5	NA
p	± 1.0	± 0.6	± 2.0	± 2.5

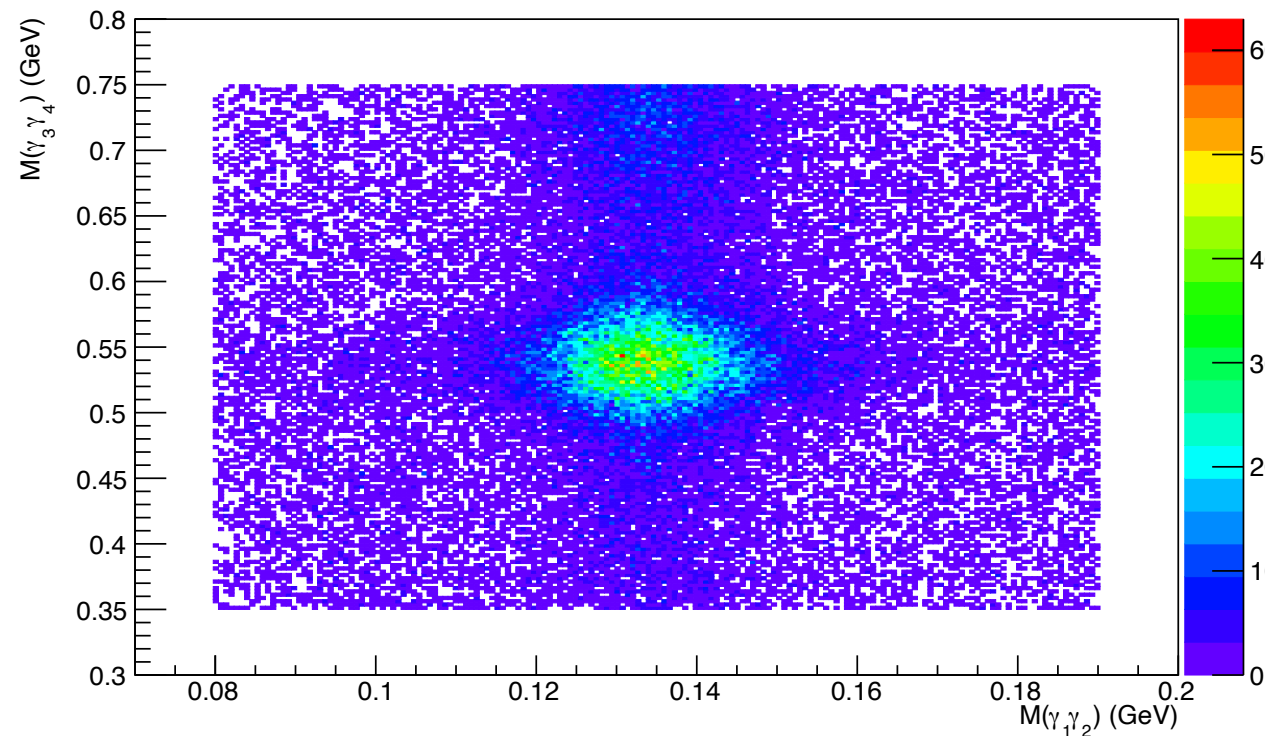


Event selection 101

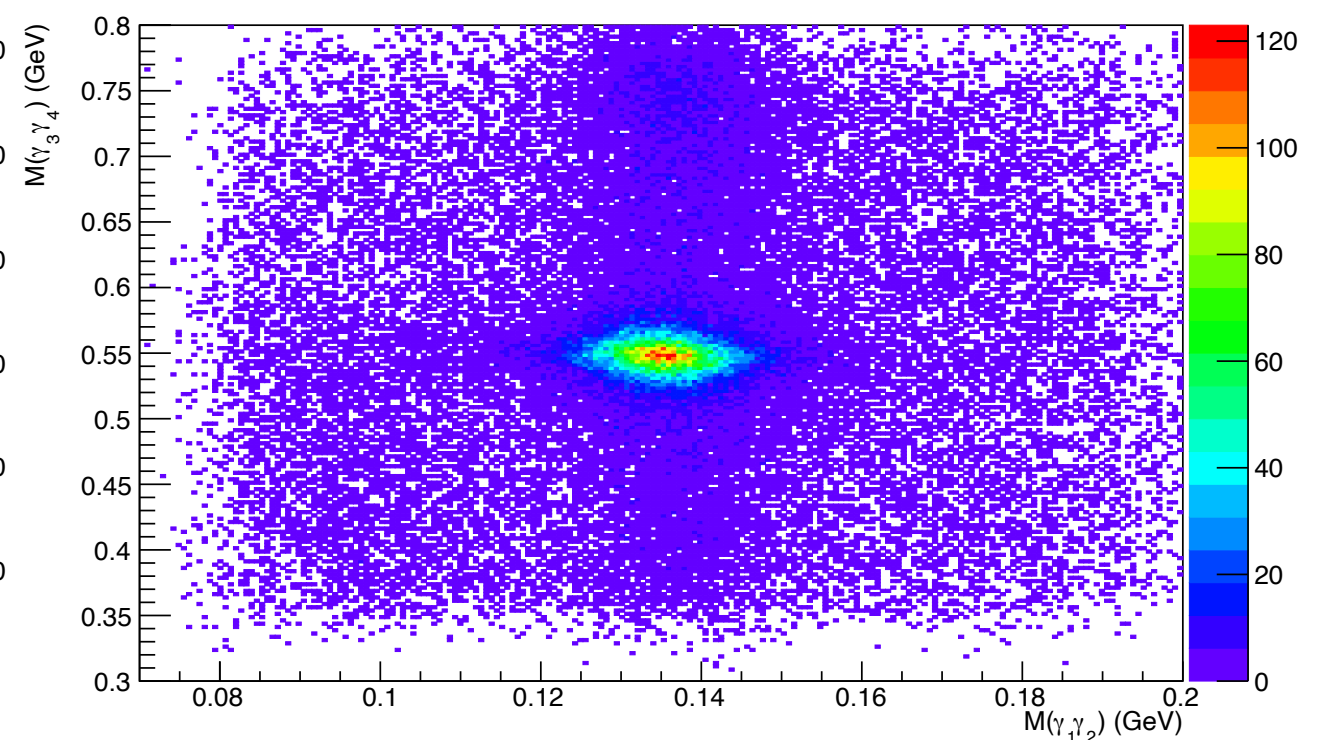
- ✱ Analysis Launch Cuts: “loose” cuts that are already applied in ReactionFilter by default

PID	Invariant Mass (GeV/c ²)
π^0	$0.08 < IM < 0.19$
K_S	$0.3 < IM < 0.7$
η	$0.35 < IM < 0.75$

Measured Data



Kinematic Fit Data

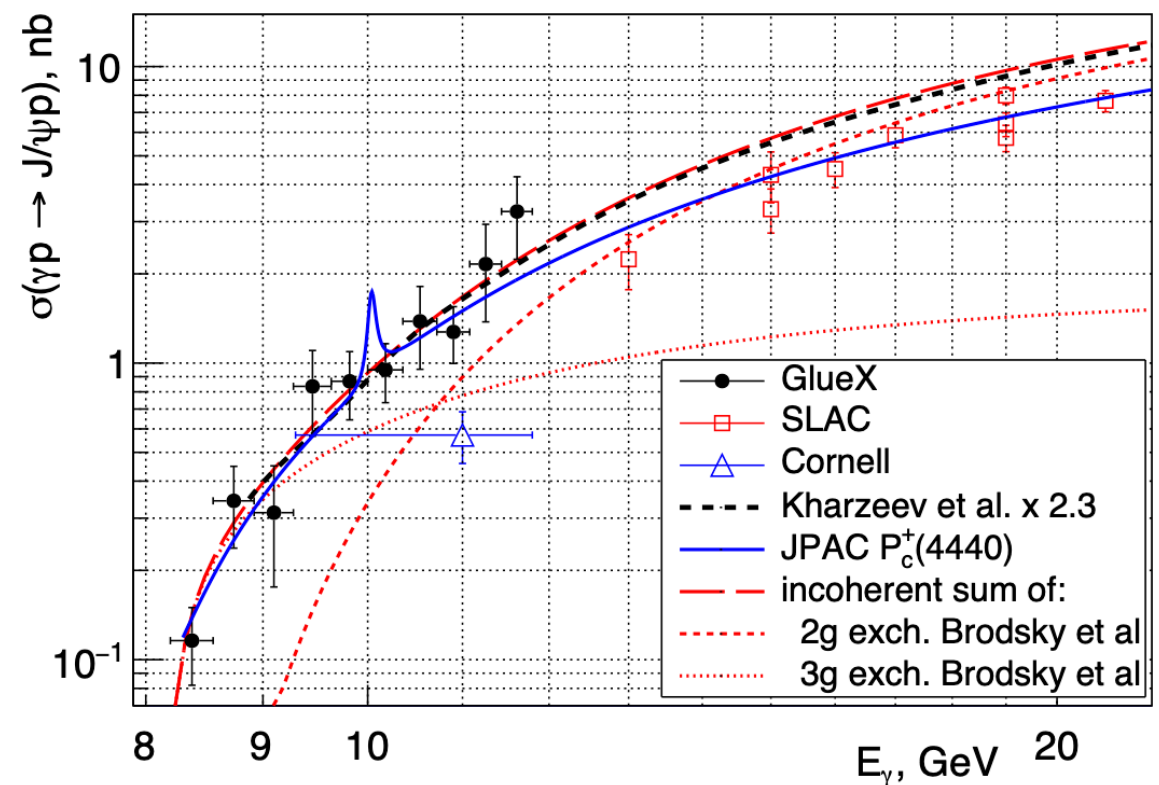
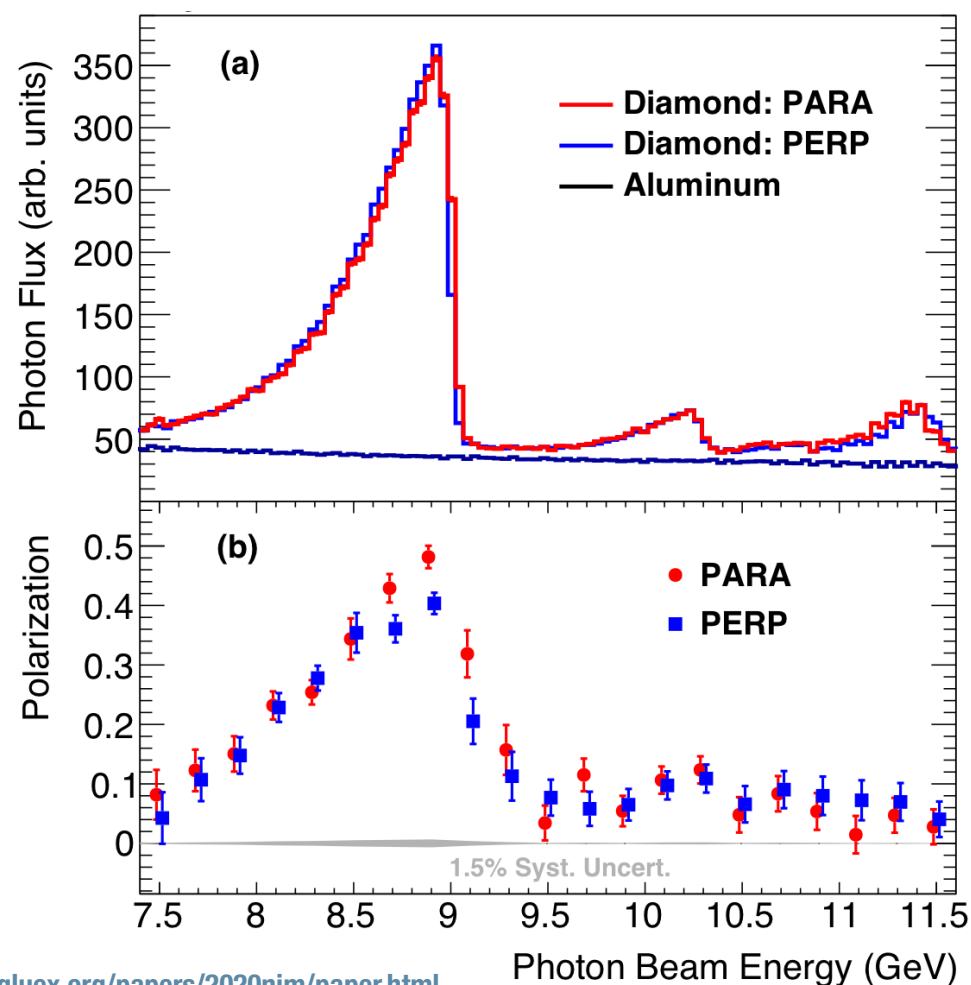


Event selection 101

- * [Analysis Launch Cuts](#): “loose” cuts that are already applied in ReactionFilter by default
- * Common event selections applied by individual analyzers
 - * Kinematic Fit χ^2 /NDF, Particle ID, Beam energy, Unused tracks or showers, etc.
- * Simulation is a powerful tool to choose your cuts
 - * Background MC with bggen or other dedicated generators for background processes
 - * Signal MC to study efficiency and resolutions

Beam energy selection

- * Linearly polarized photons: beam asymmetry or amplitude analysis (see Matt's talk)
- * Energy-dependence of production: cross section
- * Energy-dependence of detection: systematic comparisons (e.g. branching ratio) between different beam energy regions



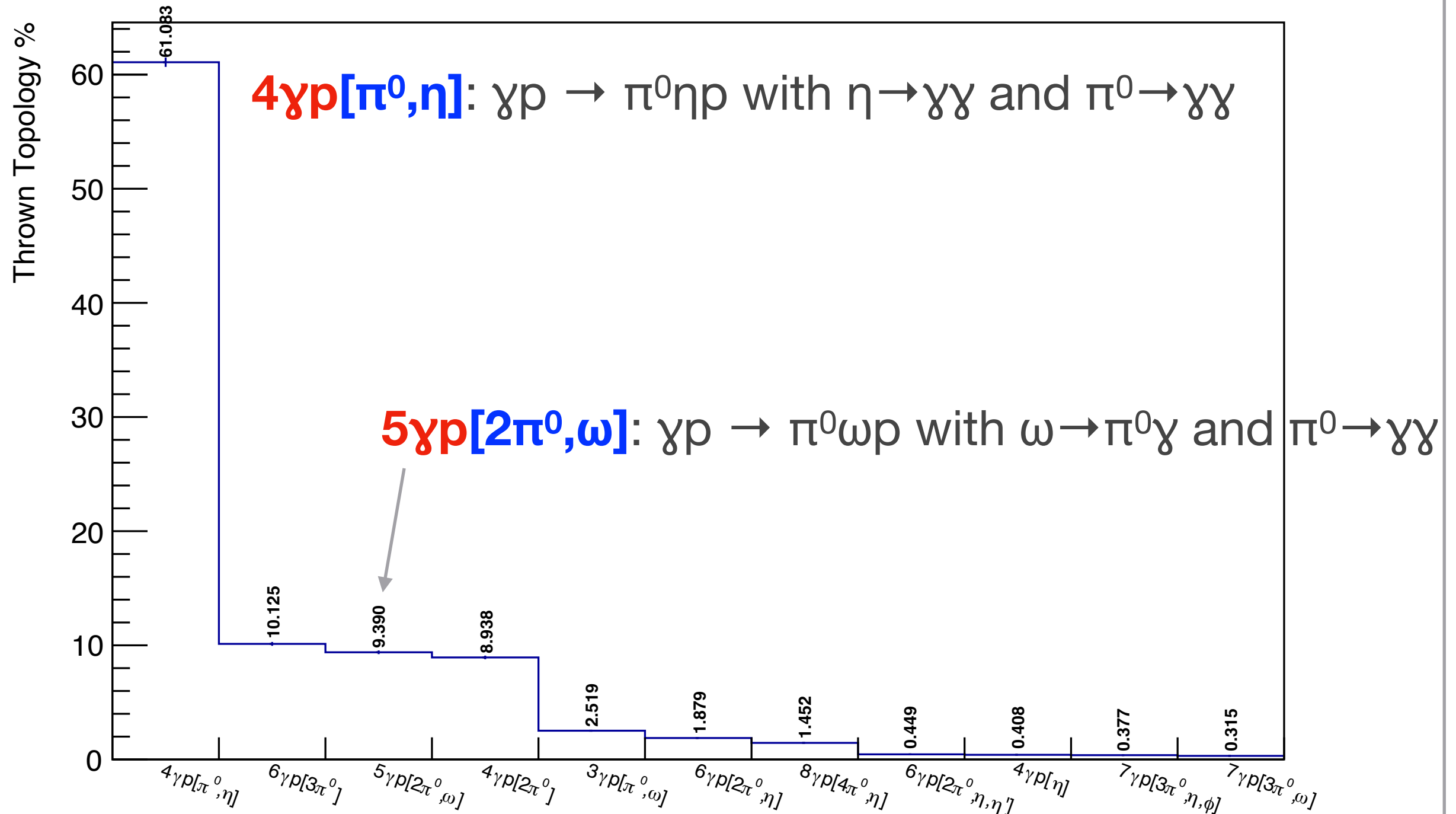
Studying backgrounds with bggen

- * **bggen**: an inclusive MC generator for “all” photoproduction processes based primarily on PYTHIA (some caveats)
- * In simulation we know the truth information, so we can cheat and sort events by their reaction or “topology”
- * DSelector library `Get_ThrownTopologyString()` unique TString for each topology: **NumFinalState****[Decaying]**
- * Signal topology $\gamma p \rightarrow \pi^0 \eta p$ with $\eta \rightarrow \gamma\gamma$ and $\pi^0 \rightarrow \gamma\gamma$ corresponds to: **4** γp **[π^0, η]**
- * Example background topology $\gamma p \rightarrow \pi^0 \omega p$ with $\omega \rightarrow \pi^0 \gamma$ and $\pi^0 \rightarrow \gamma\gamma$ corresponds to: **5** γp **[2 π^0, ω]**

https://github.com/JeffersonLab/hd_utilities/tree/master/AnalysisHowTo/ThrownTopology

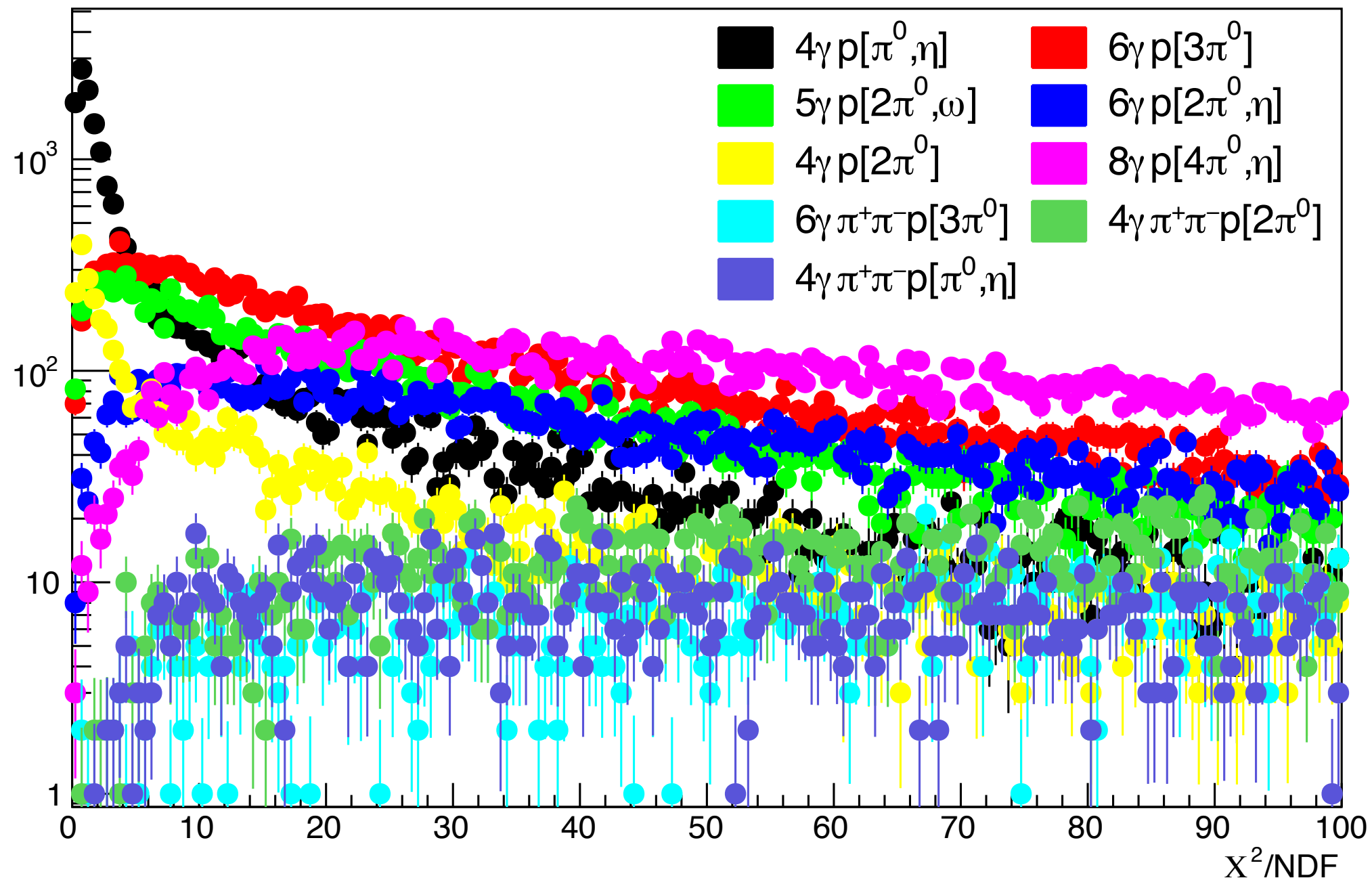
Identify leading backgrounds

- * DSelector library `Get_ThrownTopologyString()` unique TString for for each topology: **NumFinalState****[Decaying]**



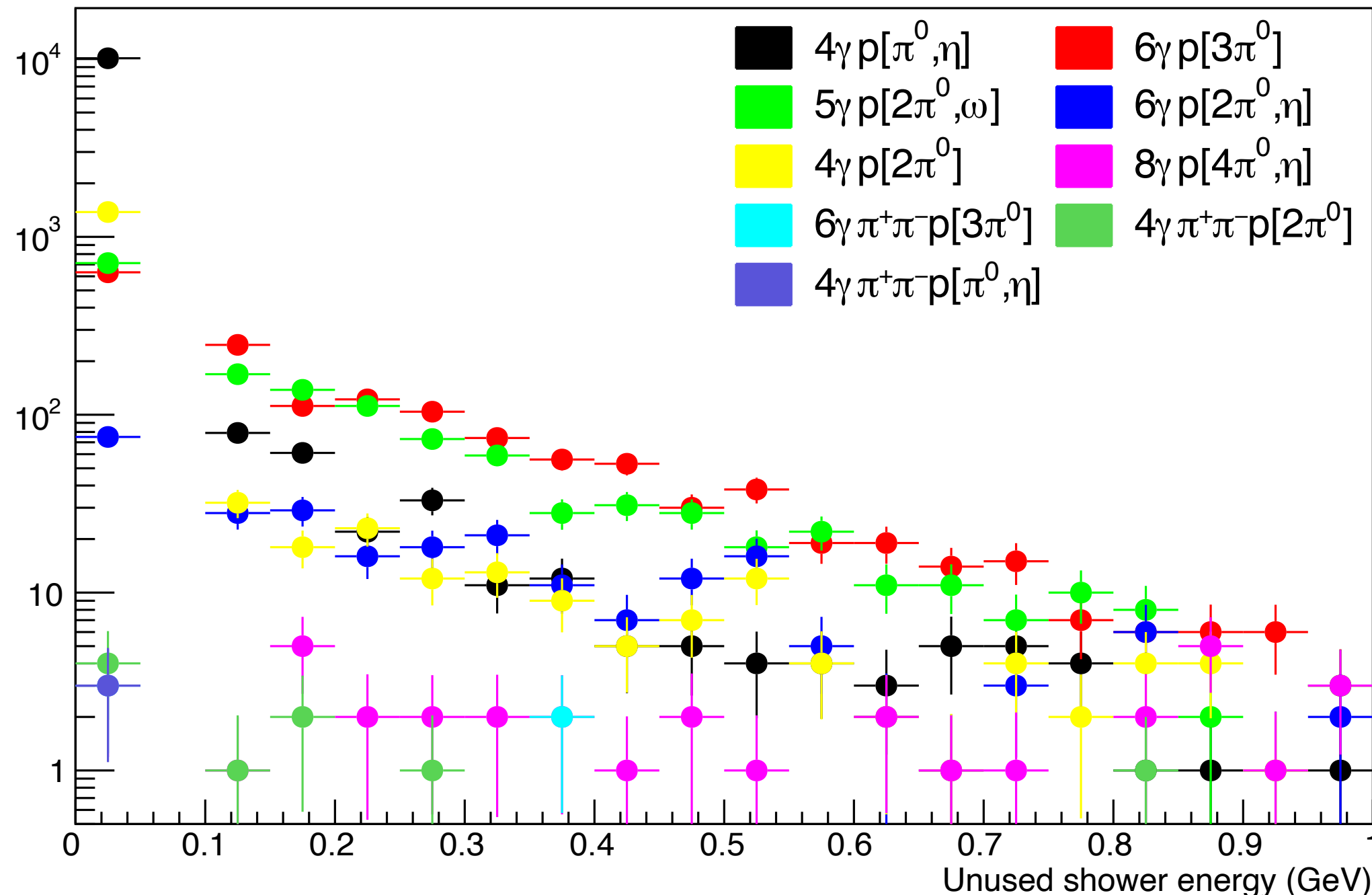
Identify variables to reject backgrounds

- * **Kinematic Fit χ^2/NDF** : background topologies less consistent with **4 γ p** final state



Identify variables to reject backgrounds

- ✱ **Unused Shower Energy:** many background topologies have extra showers leading to measured unused energy



Correctly paired photons $4\gamma p[\pi^0, \eta]$

//Step 1

```
TLorentzVector locPhoton1P4 = dPhoton1Wrapper->Get_P4();
```

```
TLorentzVector locPhoton2P4 = dPhoton2Wrapper->Get_P4();
```

//Step 2

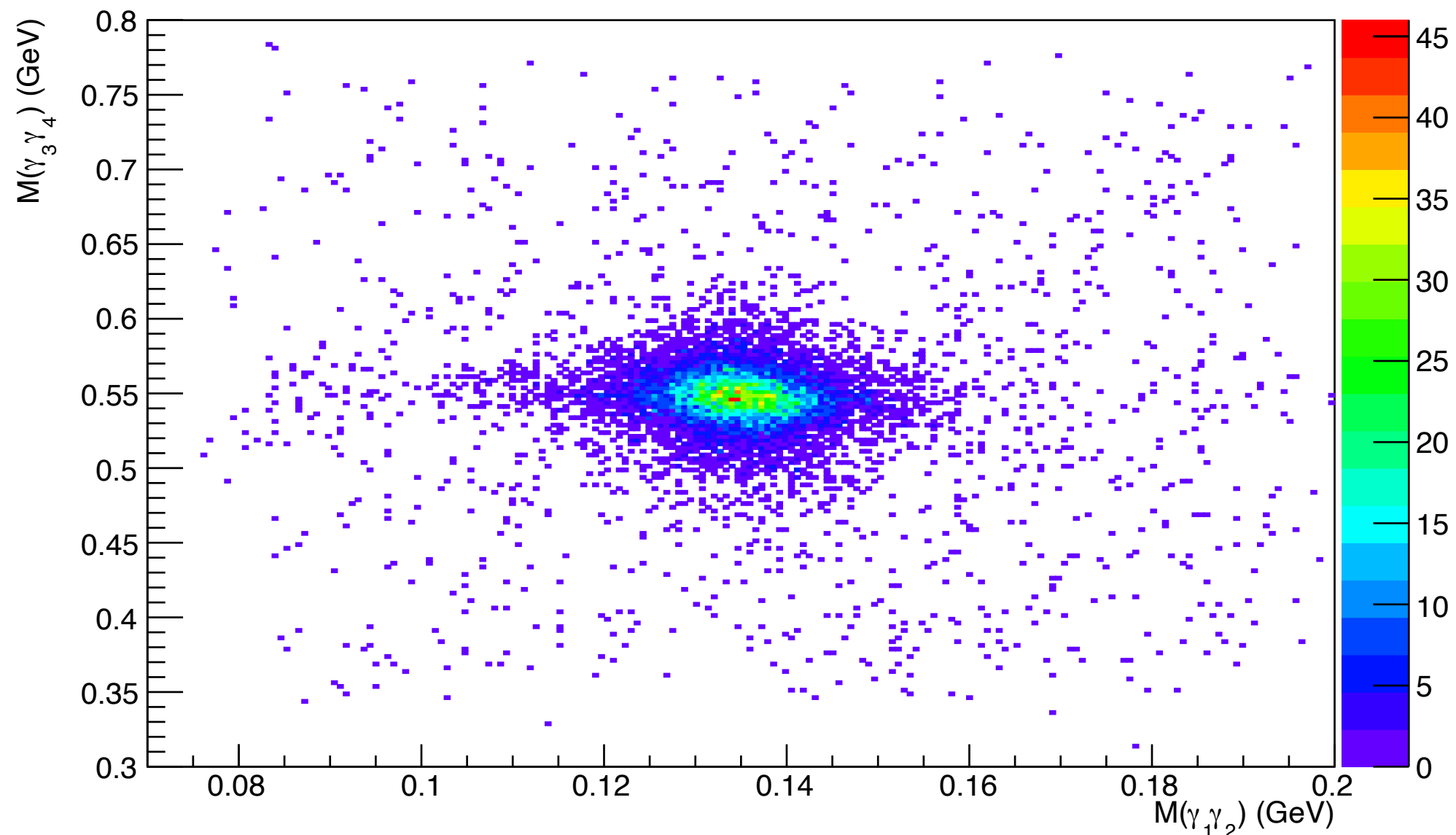
```
TLorentzVector locPhoton3P4 = dPhoton3Wrapper->Get_P4();
```

```
TLorentzVector locPhoton4P4 = dPhoton4Wrapper->Get_P4();
```

Assumed π^0

Assumed η

2D Invariant Mass: Topology $4\gamma p[\pi^0, \eta]$



“Correctly” paired photons $5\gamma p[2\pi^0, \omega]$

//Step 1

```
TLorentzVector locPhoton1P4 = dPhoton1Wrapper->Get_P4();
```

```
TLorentzVector locPhoton2P4 = dPhoton2Wrapper->Get_P4();
```

Assumed π^0

//Step 2

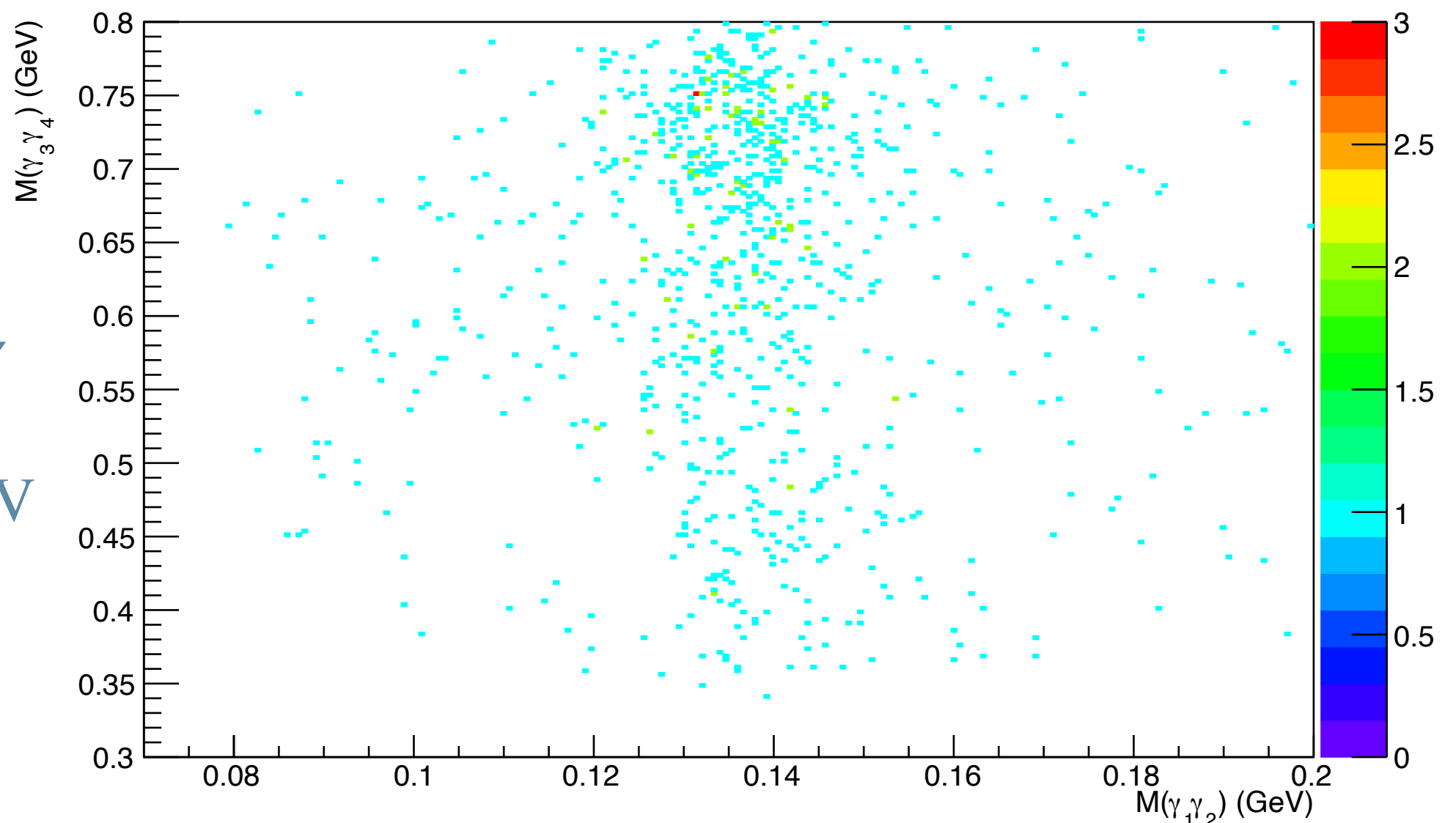
```
TLorentzVector locPhoton3P4 = dPhoton3Wrapper->Get_P4();
```

```
TLorentzVector locPhoton4P4 = dPhoton4Wrapper->Get_P4();
```

Assumed η

2D Invariant Mass: Topology $5\gamma p[2\pi^0, \omega]$

Lose extra γ in
 $\omega \rightarrow \pi^0 \gamma \rightarrow 3\gamma$
 $m_\omega = 0.782 \text{ GeV}$



Incorrectly paired photons $4\gamma p[2\pi^0]$

//Step 1

```
TLorentzVector locPhoton1P4 = dPhoton1Wrapper->Get_P4();
```

```
TLorentzVector locPhoton2P4 = dPhoton2Wrapper->Get_P4();
```

//Step 2

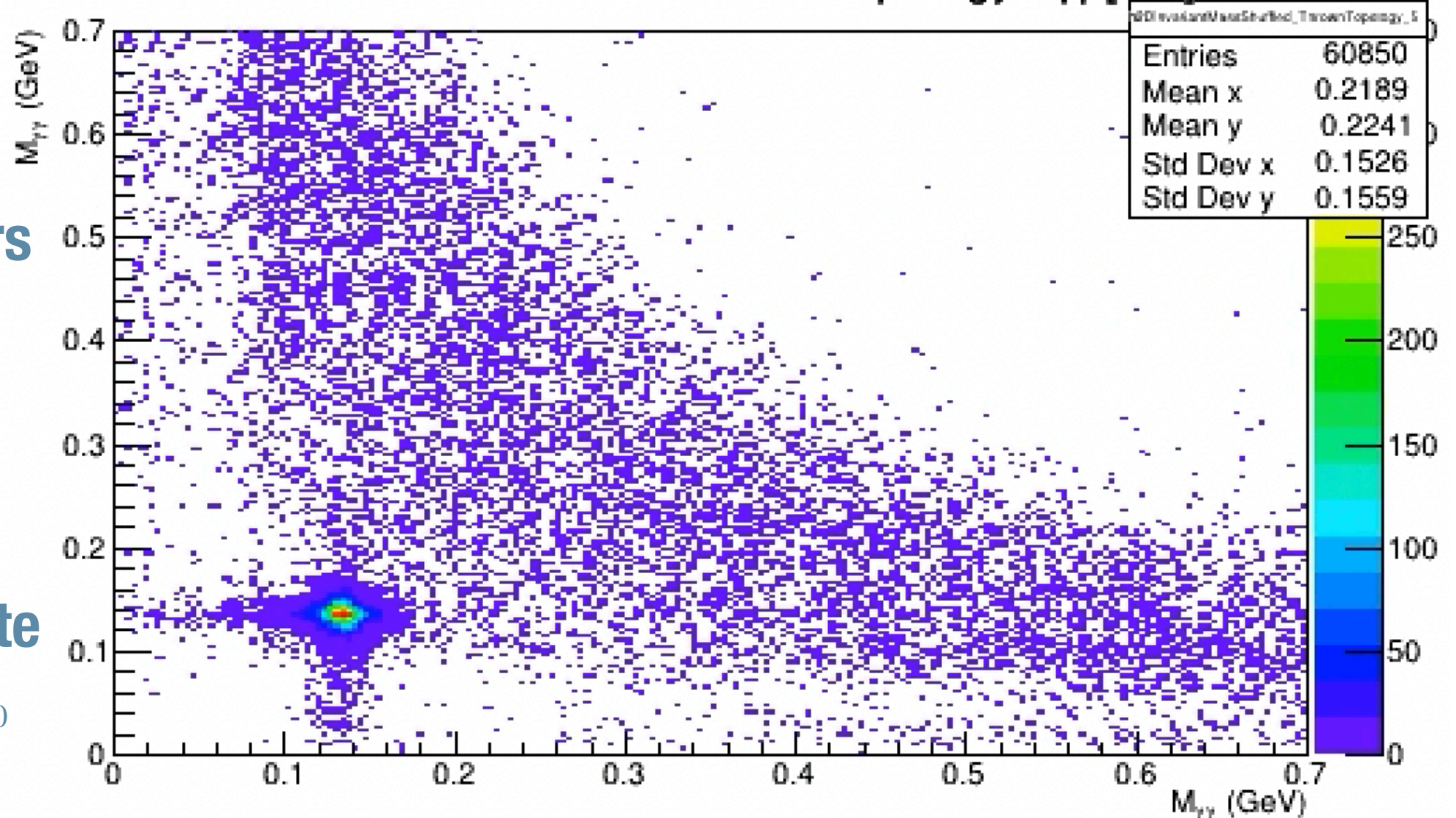
```
TLorentzVector locPhoton3P4 = dPhoton3Wrapper->Get_P4();
```

```
TLorentzVector locPhoton4P4 = dPhoton4Wrapper->Get_P4();
```

Assumed π^0

Assumed η

2D Invariant Mass Shuffled: Topology $4\gamma p[2\pi^0]$



Instead plot
alternative pairs

$\gamma_1\gamma_3$ **VS** $\gamma_2\gamma_4$

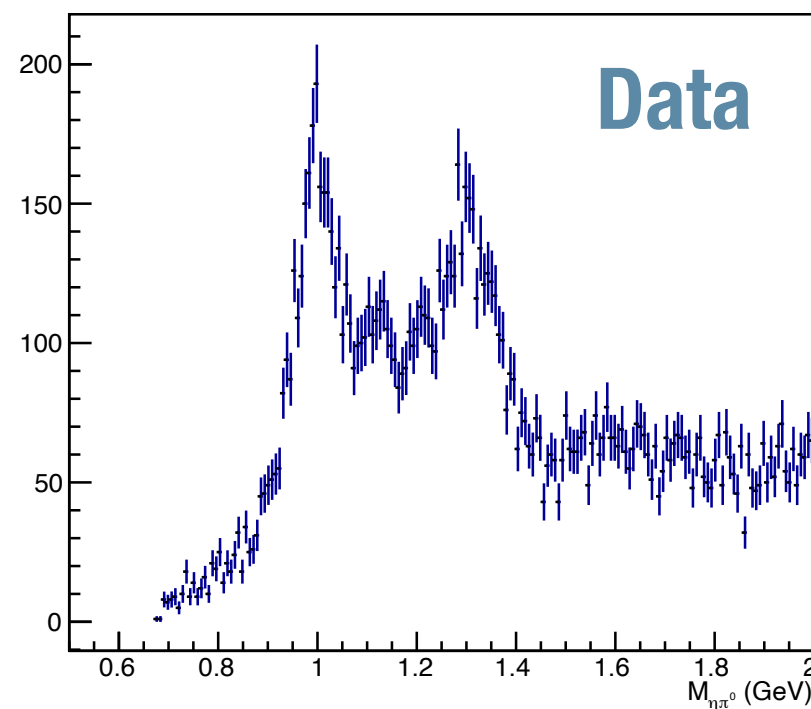
$\gamma_1\gamma_4$ **VS** $\gamma_2\gamma_3$

If these alternate
pairs have m_{π^0}
then reject

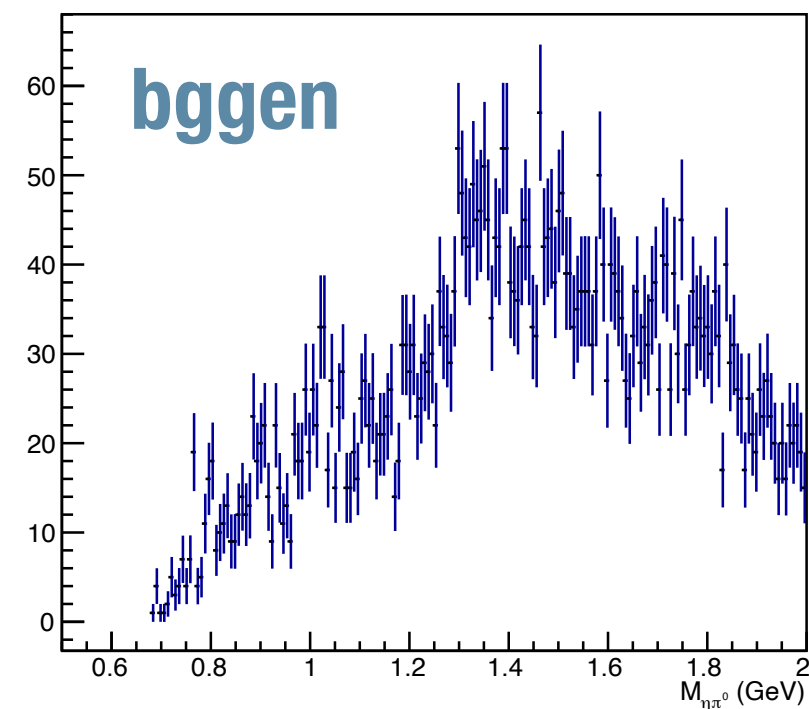
What might bggen be missing?

- * Meson resonances: a's, b's, f's, h's, etc.

Invariant Mass Topology: data

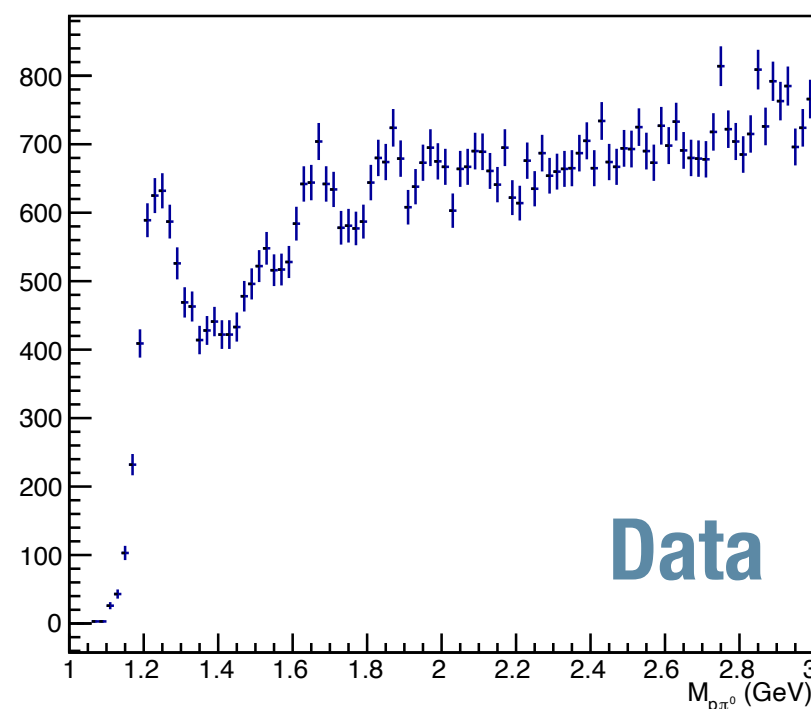


Invariant Mass Topology: $4\gamma p[\pi^0, \eta]$

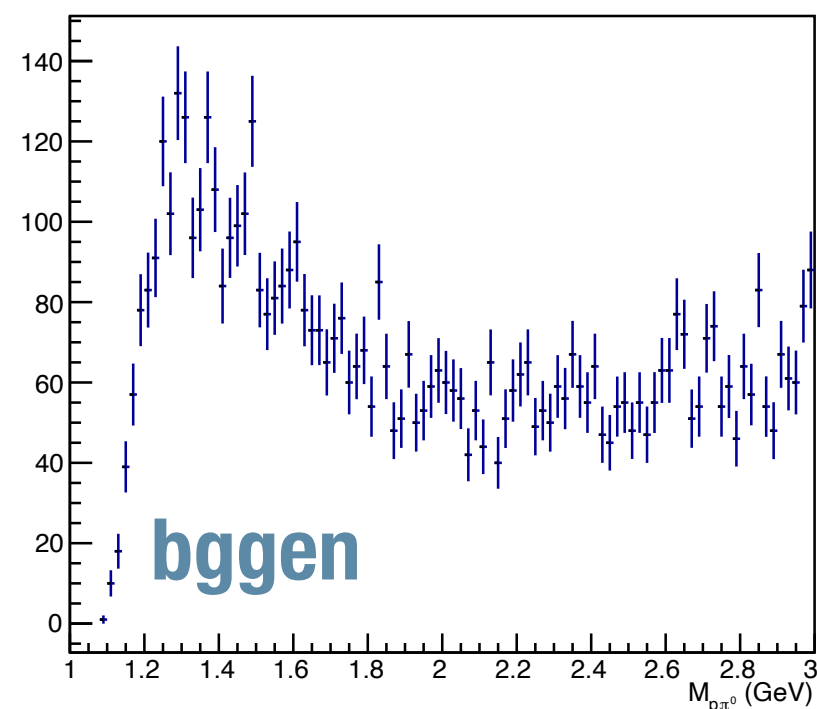


- * Baryon excitations: Δ , N^* , etc.

$p\pi^0$ Mass: Topology data



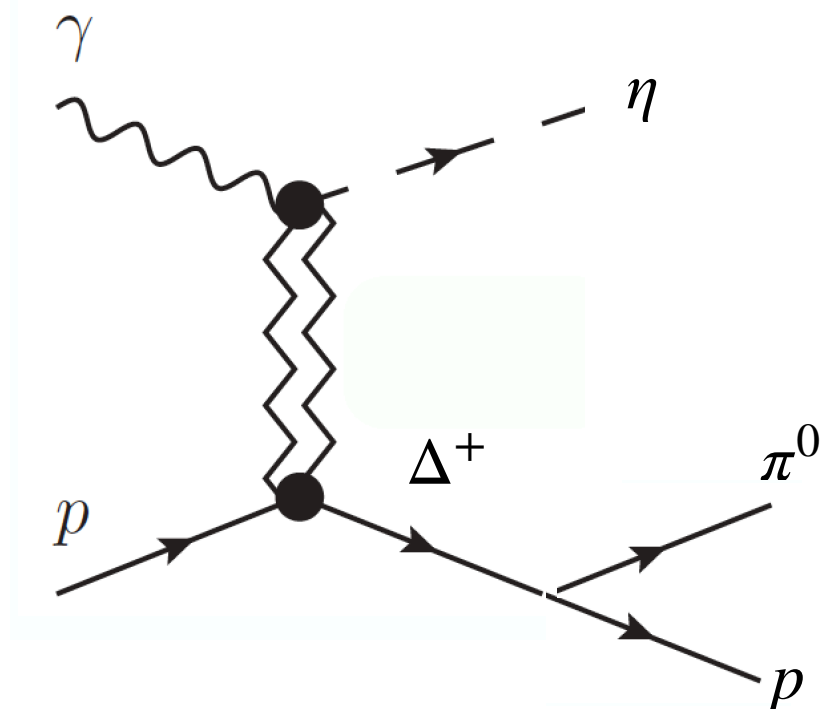
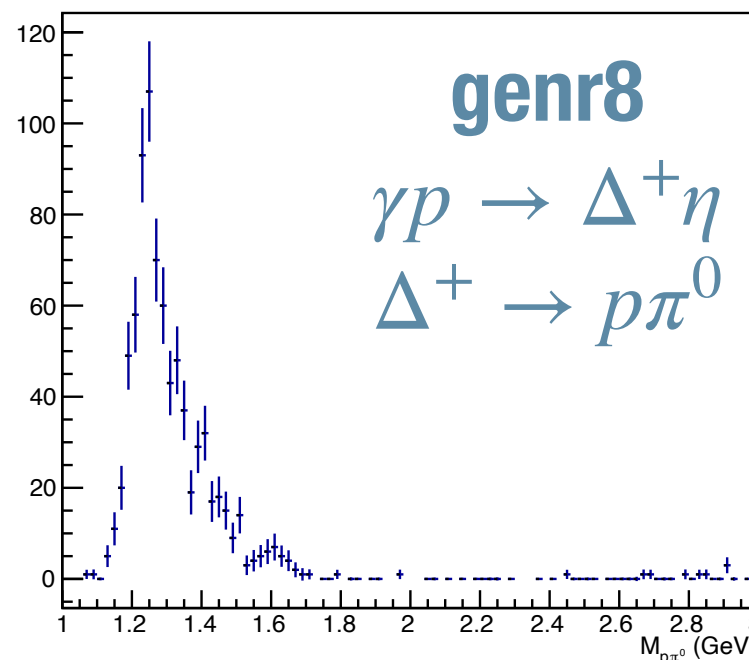
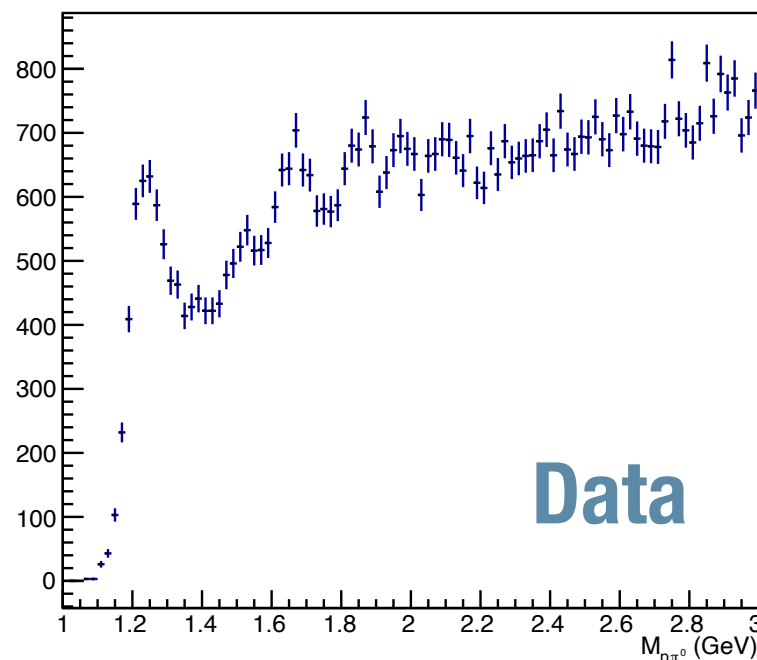
$p\pi^0$ Mass: Topology $4\gamma p[\pi^0, \eta]$



Simulate analysis-specific backgrounds

- ✳ If bggen isn't a good enough model for the background in your analysis, you can simulate them individually more accurately
- ✳ Use MCWrapper to generate samples (see Peter's talk)
 - ✳ Large scale - use web form, e.g. need ~10M+ events
 - ✳ Small scale - run interactively (ifarm or institution), e.g. ~10k events to study background distribution (~1 hour turnaround)

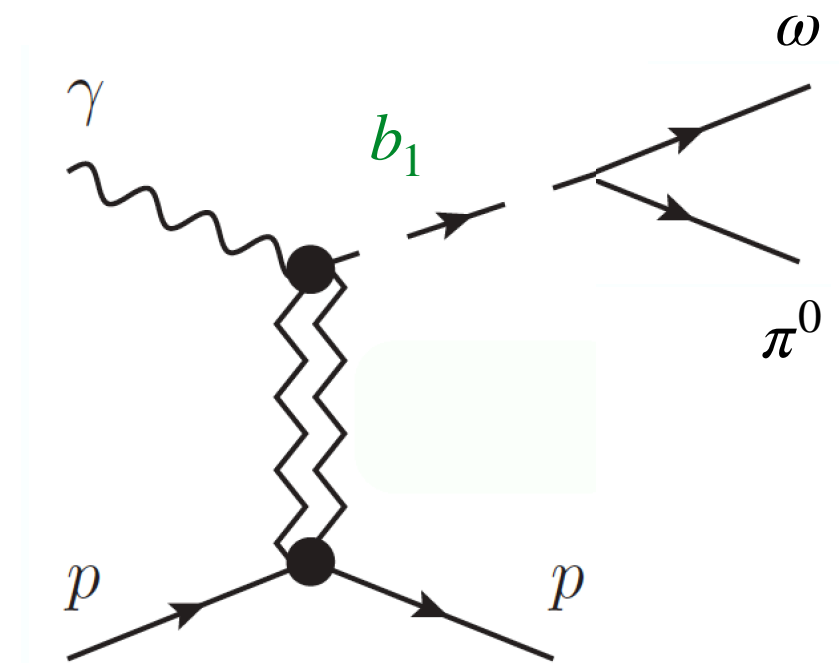
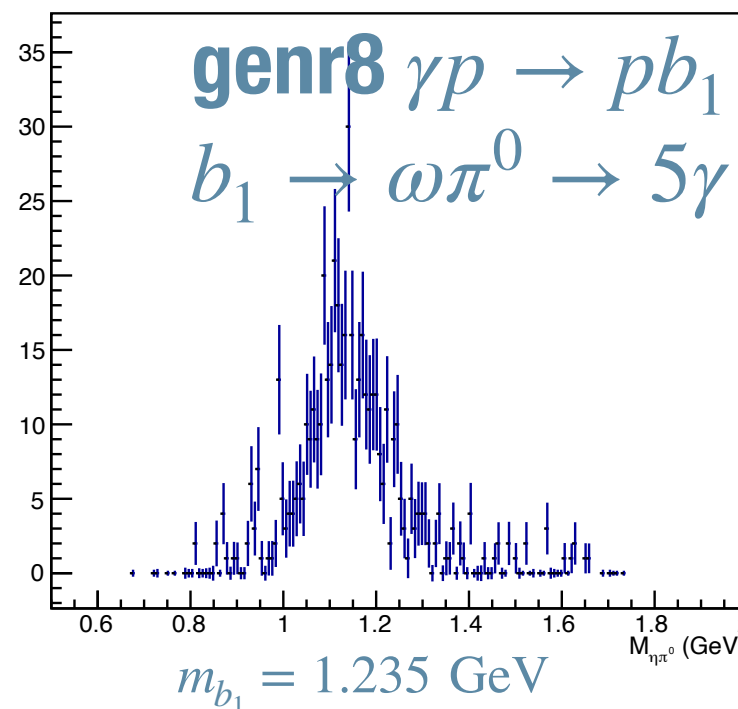
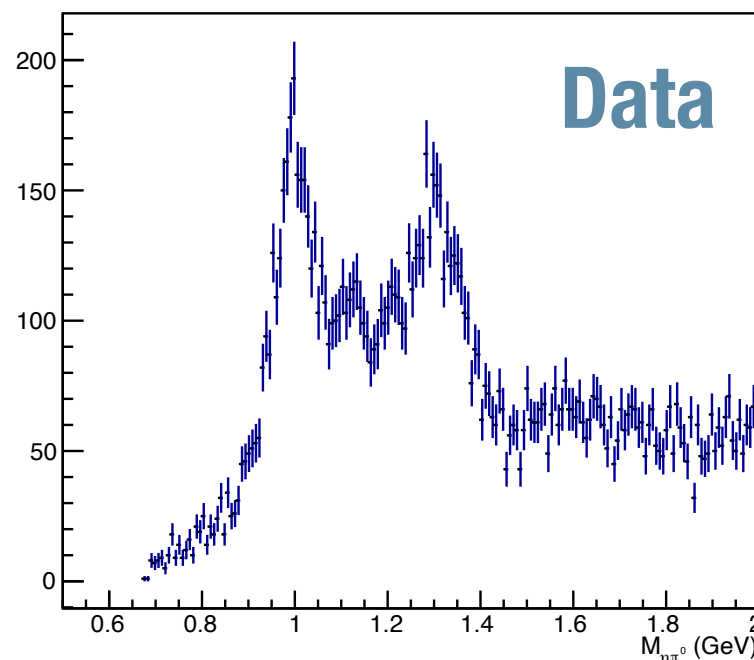
```
gluex_MC.py MC.config 30496 10000
```



Simulate analysis-specific backgrounds

- * If bggen isn't a good enough model for the background in your analysis, you can simulate them individually more accurately
- * Use MCWrapper to generate samples (see Peter's talk)
 - * Large scale - use web form, e.g. need $\sim 10\text{M}+$ events
 - * Small scale - run interactively (ifarm or institution), e.g. $\sim 10\text{k}$ events to study background distribution (~ 1 hour turnaround)

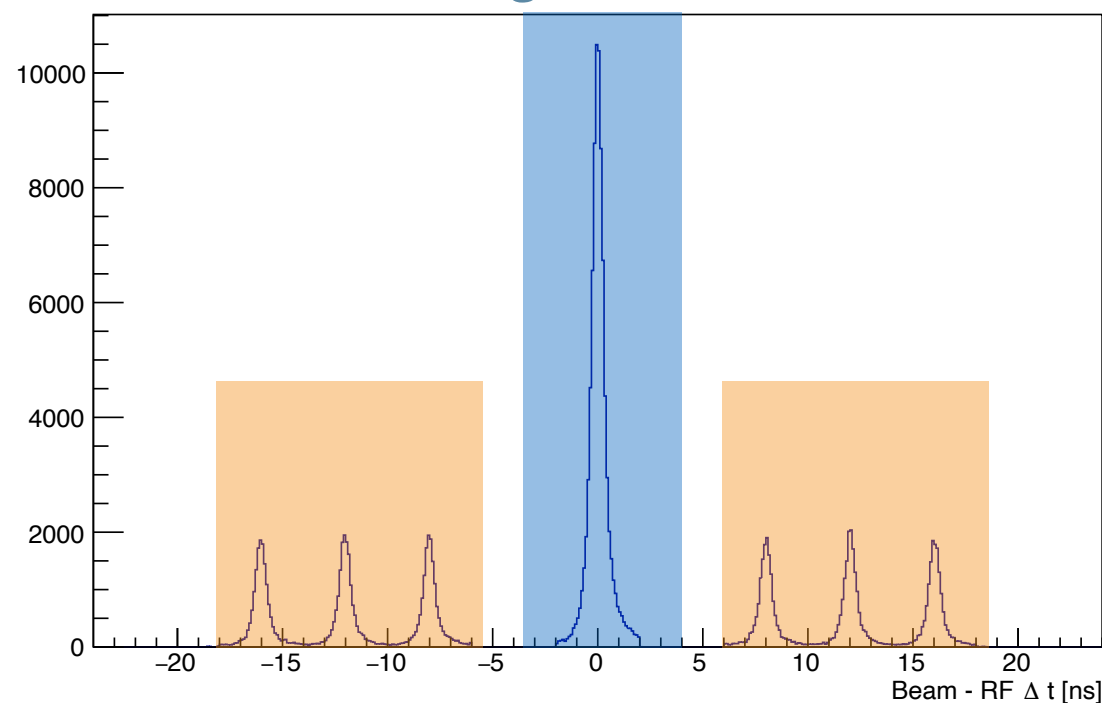
```
gluex_MC.py MC.config 30496 10000
```



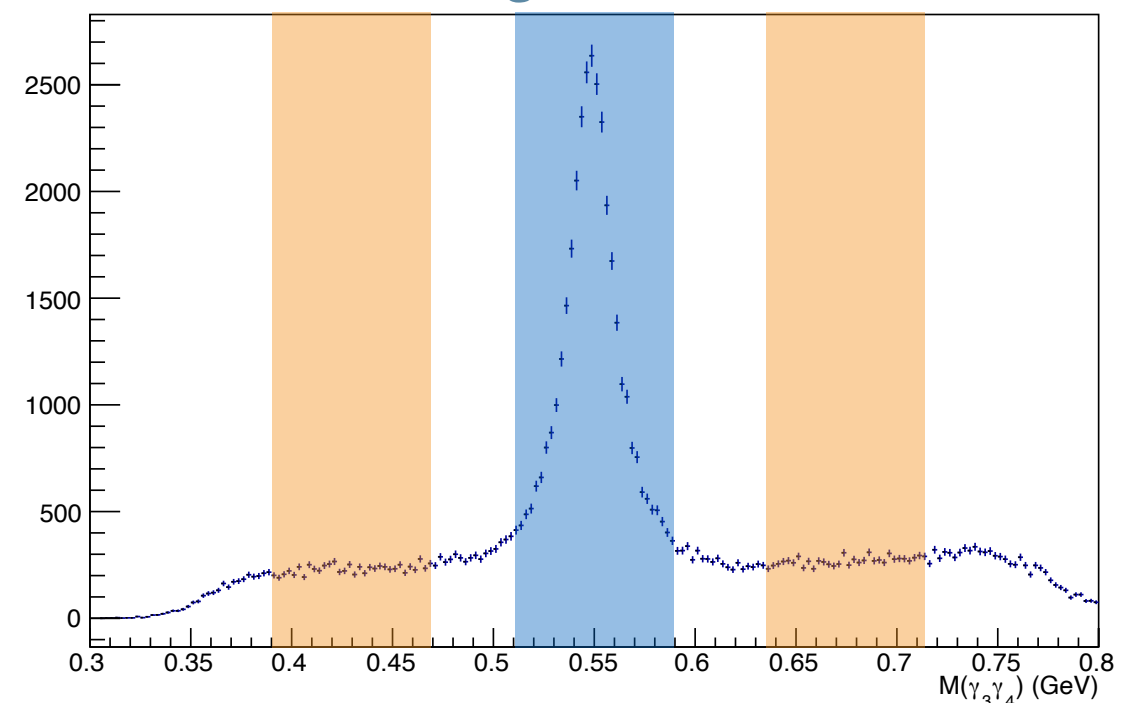
Subtracting remaining backgrounds

- * Some backgrounds will remain that we cannot reject on an event-by-event basis
- * Instead we statistically subtract them by either subtracting histograms or weighting events
- * e.g. accidental subtraction, mass sideband subtraction

weight = -1/6



weight = -1/2



- * After subtraction can compare signal MC and data

Simulate of signal process

- * We have better models for many physics processes than what's in bggen: realistic t -slope, beam energy dependence, angular distributions, etc.
- * Phasespace samples are needed for numerical integrals in amplitude analysis (see Matt's talk)
- * What can we learn from signal MC?

$$\epsilon(\vec{x}) = \frac{\# \text{ observed}(\vec{x})}{\# \text{ generated}(\vec{x})}$$

- * Efficiency corrections needed for cross sections and amplitude analysis
- * Reconstruction resolutions: mass, decay angles, etc.

What type of trees should I use?

- * **PART format tree** (1 entry per event): see Beni's talk
 - * Output of ReactionFilter, input to DSelector
- * **Flat tree** (1 entry per combo): see Lawrence's talk
- * **FSRoot** (1 entry per combo): see Malte's talk
- * Reduce dataset footprint whenever possible
 - * Write subset of analysis trees with first pass event selection with DSelector or FlattenFSRoot
 - * Goal is to make iterations quickly