UNIVERSITÄT HEIDELBERG
ZUKUNFT SEIT 1386

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How to Unfold Top Decays

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4 - Institut für Hochenergiephysik, Österreichische Akademie der Wissenschaft, Wien

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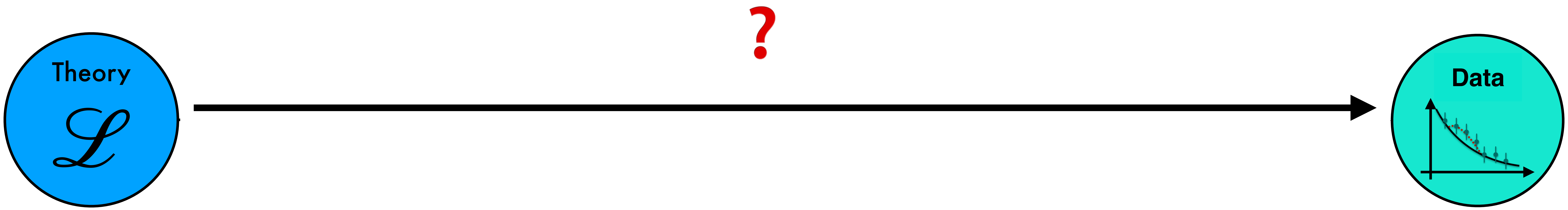
Simulation Chain



Cannot calculate testable predictions from first principles

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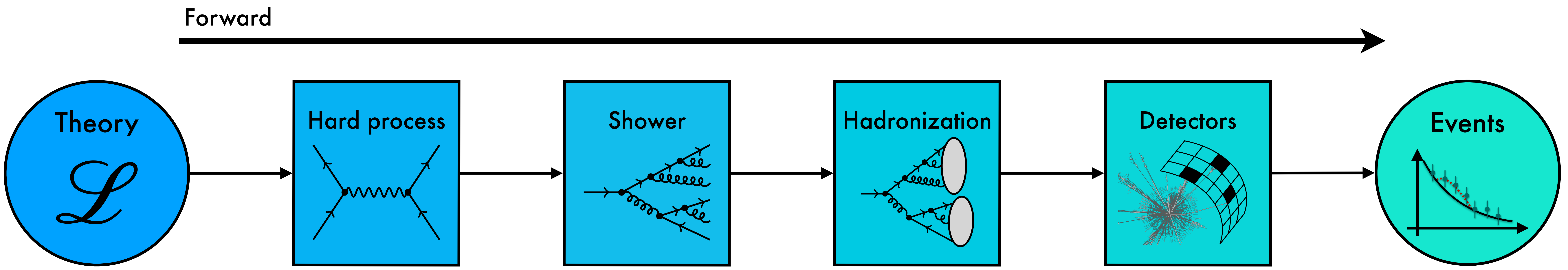
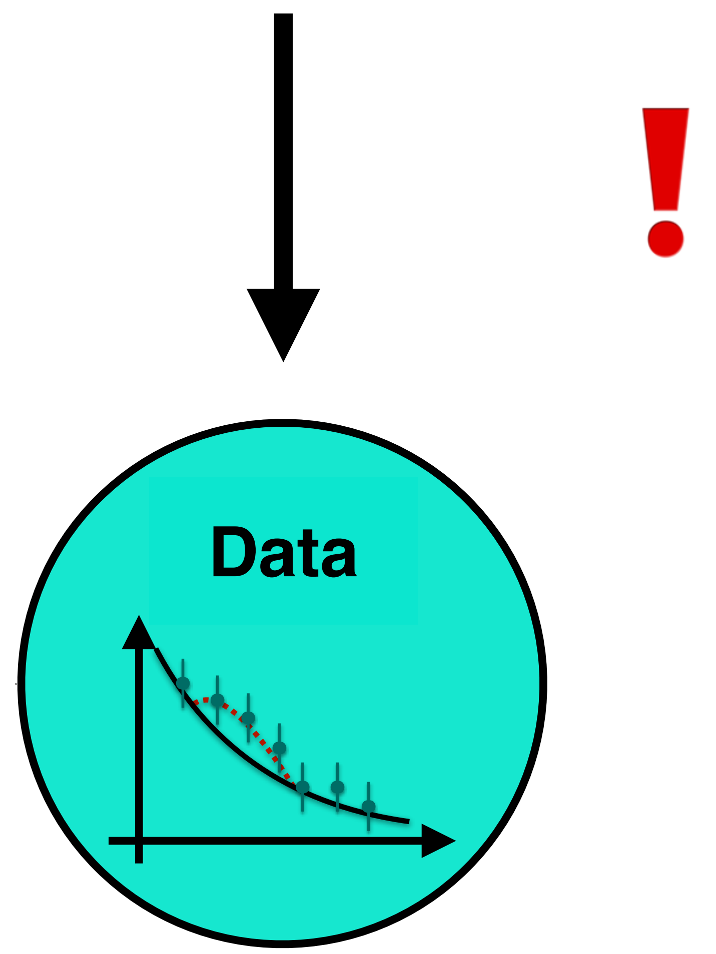




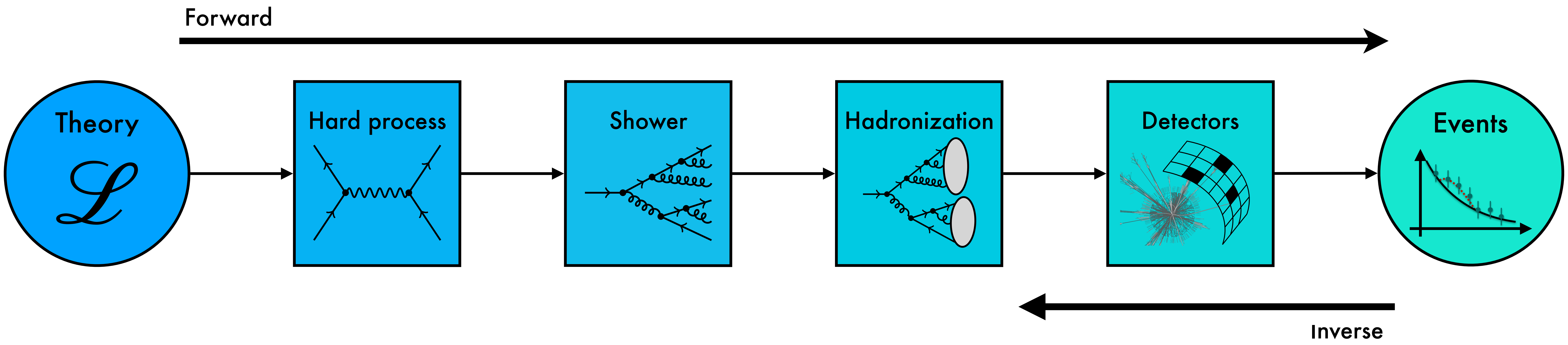
Cannot calculate testable predictions from first principles

Theory and Experiment connected via
non-deterministic simulation

After simulation chain: compare measured and simulated
distributions

Figure from A. Butter et al.: arXiv:2203.07460, R. Winterhalder

Simulation Chain — Inversion



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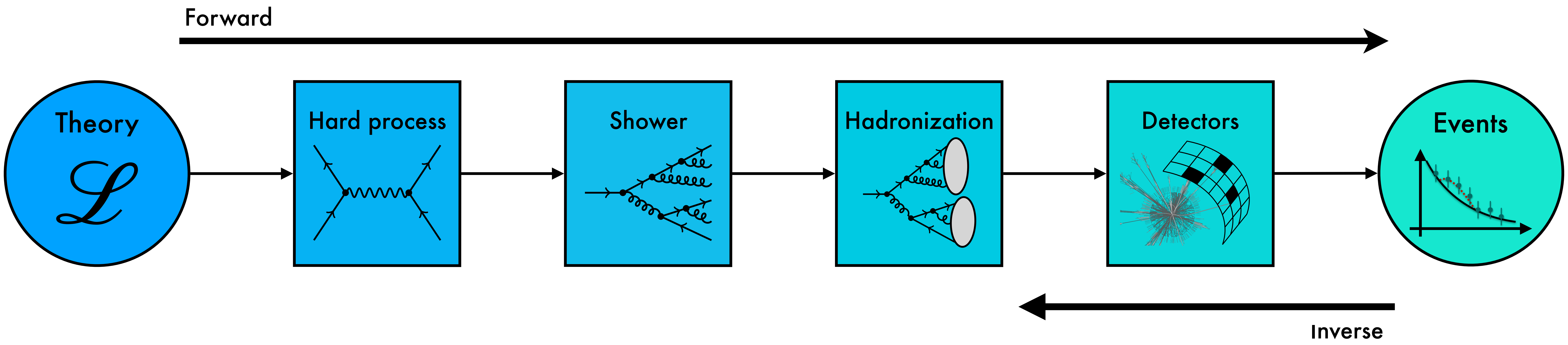
Why unfolding?



Theory analyses don't care about detectors

Comparing data from different experiments (Global Analysis)

For some analysis direct access to theory parameters

Resolution

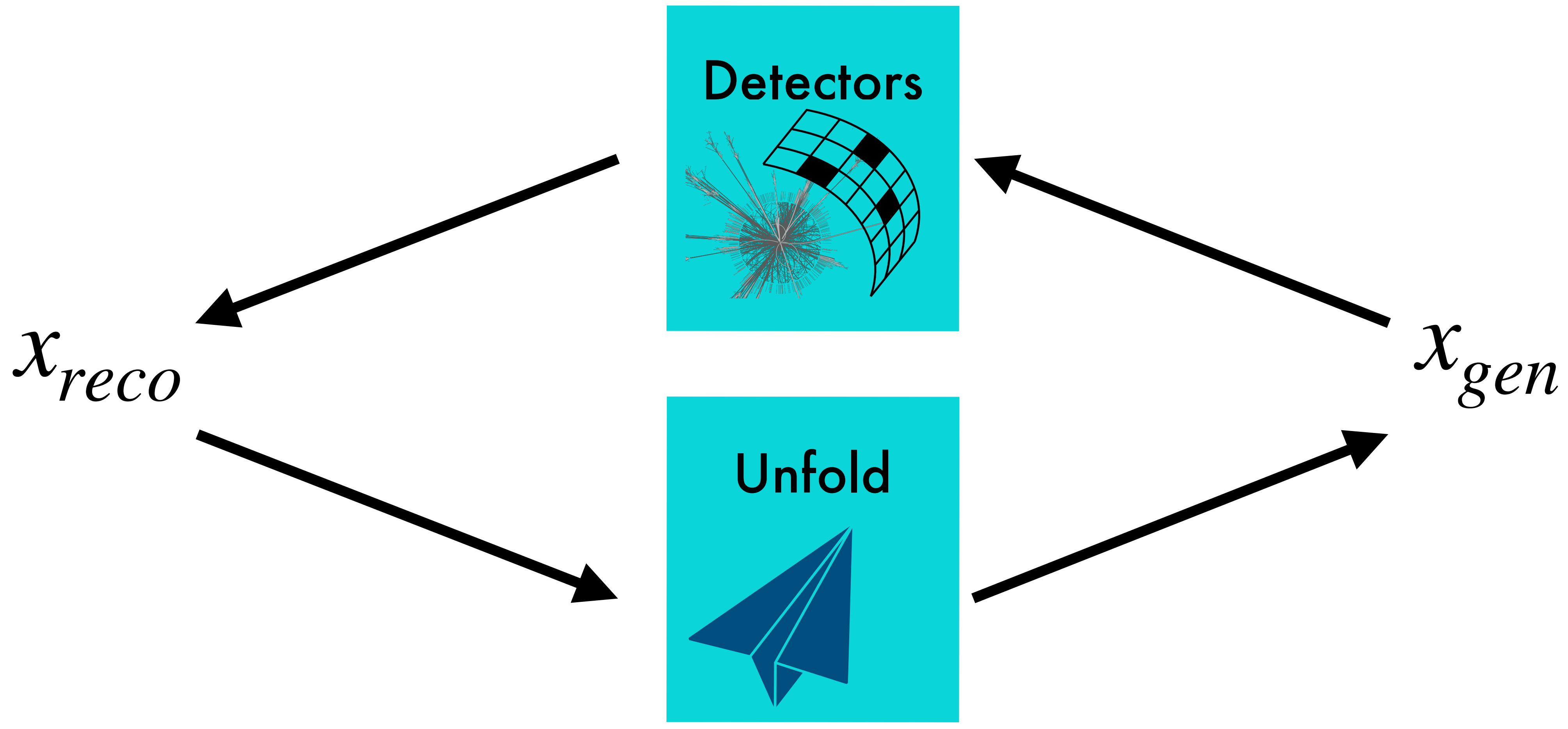
Data preservation

Figure from A. Butter et al.: arXiv:2203.07460, R. Winterhalder

Unfolding — unchained

$$p(x_{reco}) = \int p(x_{gen})R(x_{reco}, x_{gen})\ dx_{gen}$$

$$p(x_{gen}) = \int p(x_{reco})p(x_{gen} | x_{reco})\ dx_{reco}$$



x_{reco} x_{gen}

Unfolding — unchained

$$p(x_{reco}) = \int p(x_{gen}) \underbrace{R(x_{reco}, x_{gen})}_{\mathbf{p(x_{reco} | x_{gen})}} \, dx_{gen}$$

$$p(x_{gen}) = \int p(x_{reco}) p(x_{gen} | x_{reco}) \, dx_{reco}$$

Classical methods are restricted to binned, one-dimensional distributions

We would like to learn high-dimensional, unbinned unfolding probability

Unfolding — unchained

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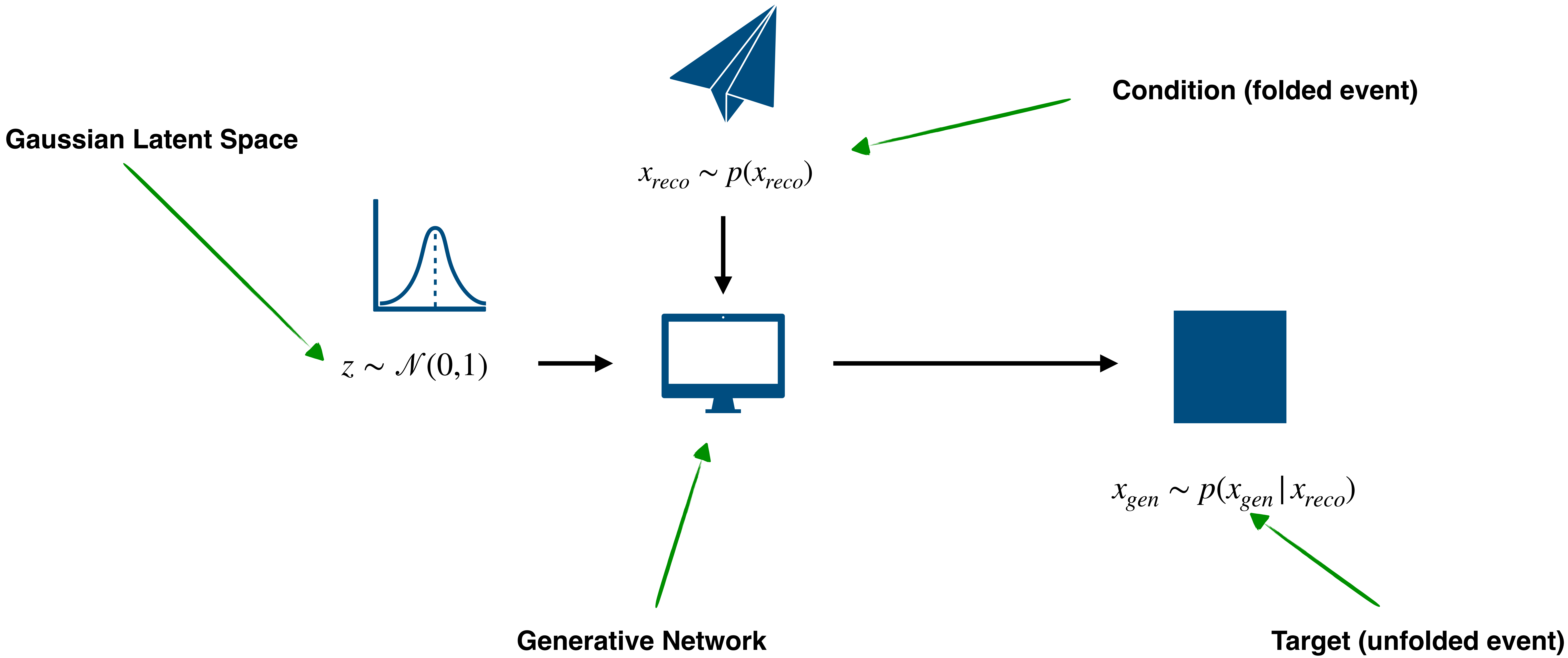
Unfolding — generative methods

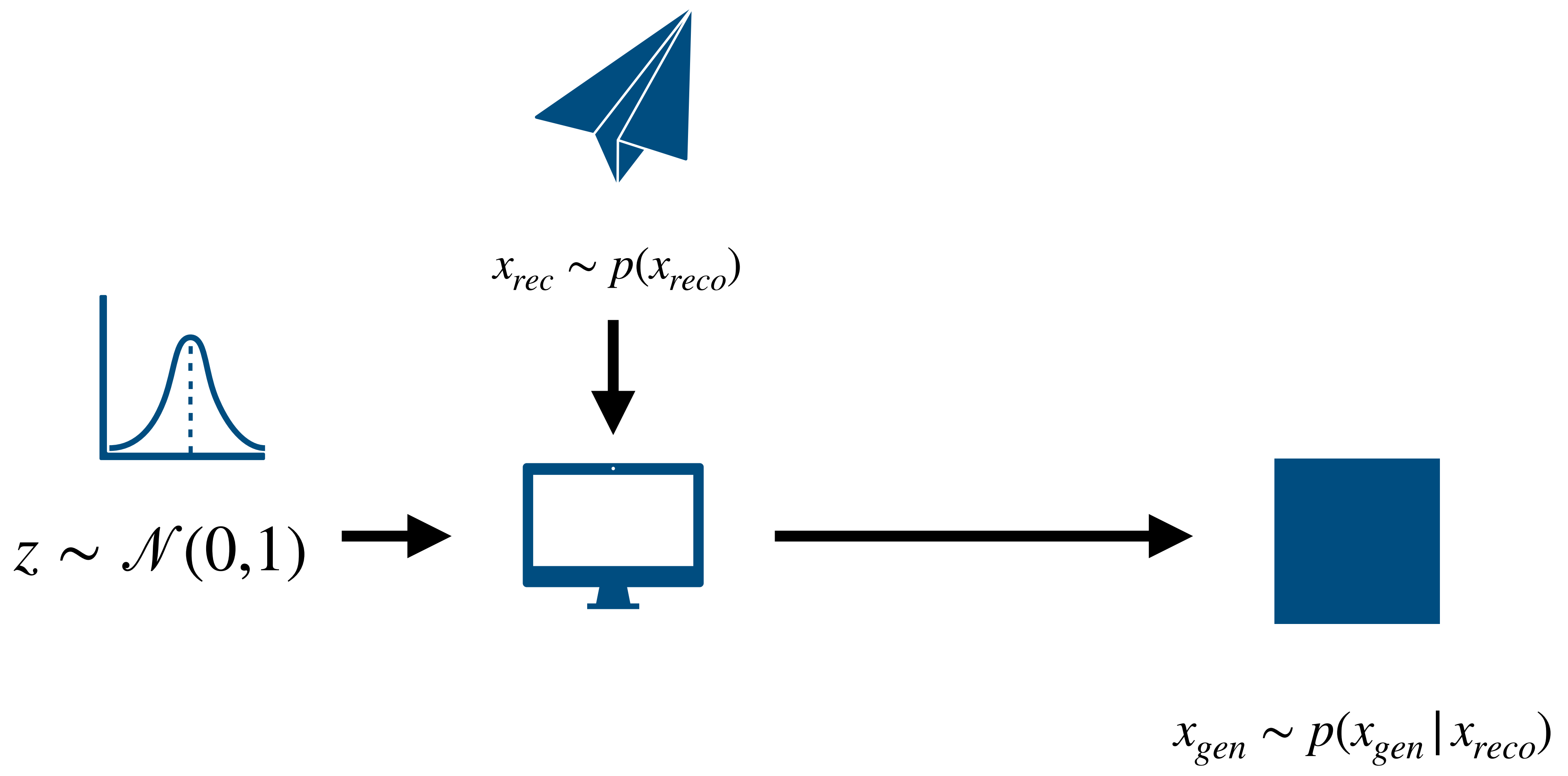


Unfolding — generative methods

Goal: learn transformation latent → gen phase space conditioned on reco event

During training, use paired events of forward simulation

After training, repeated sampling from latent space with constant condition allows probabilistic single event unfolding



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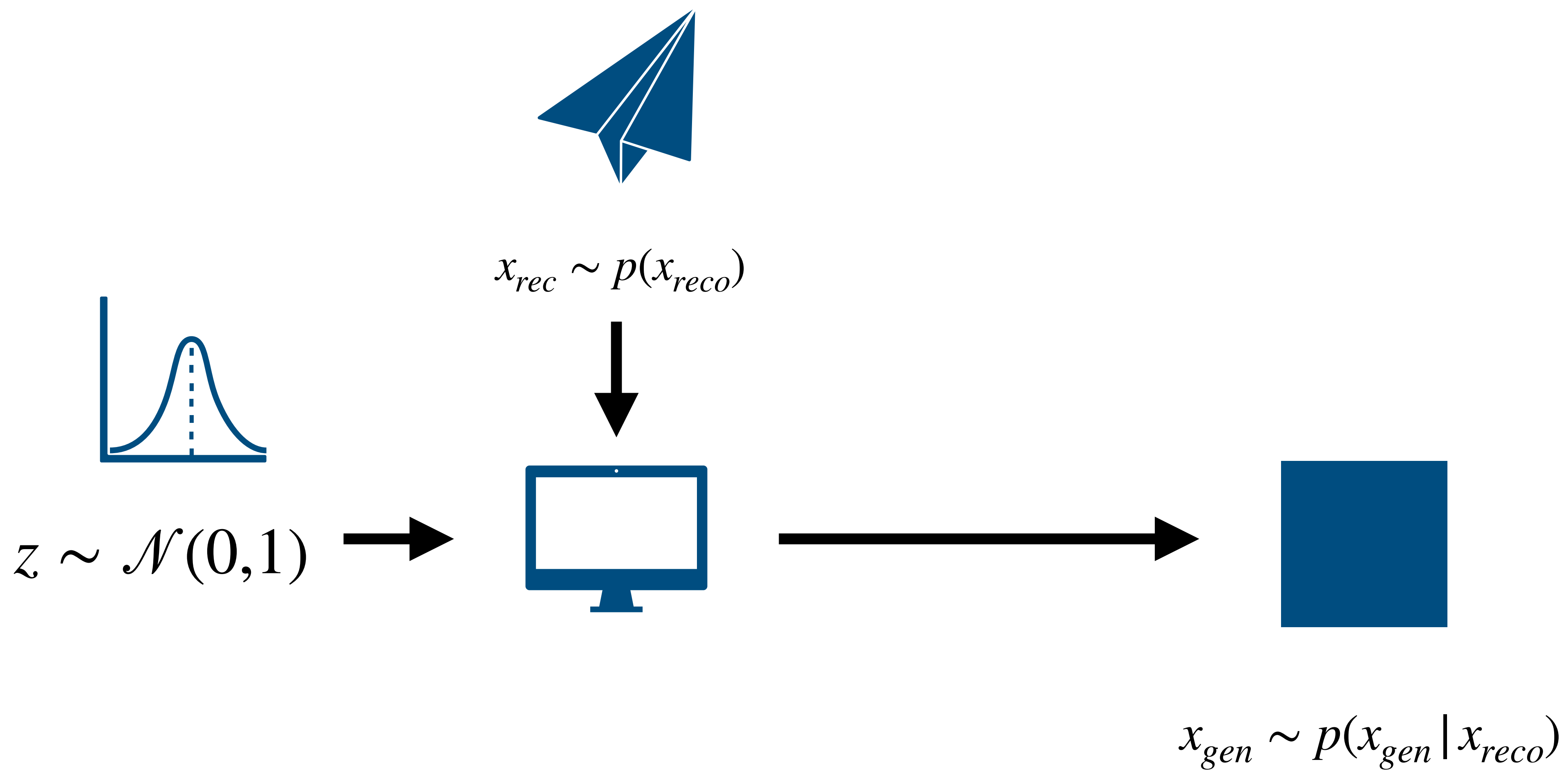
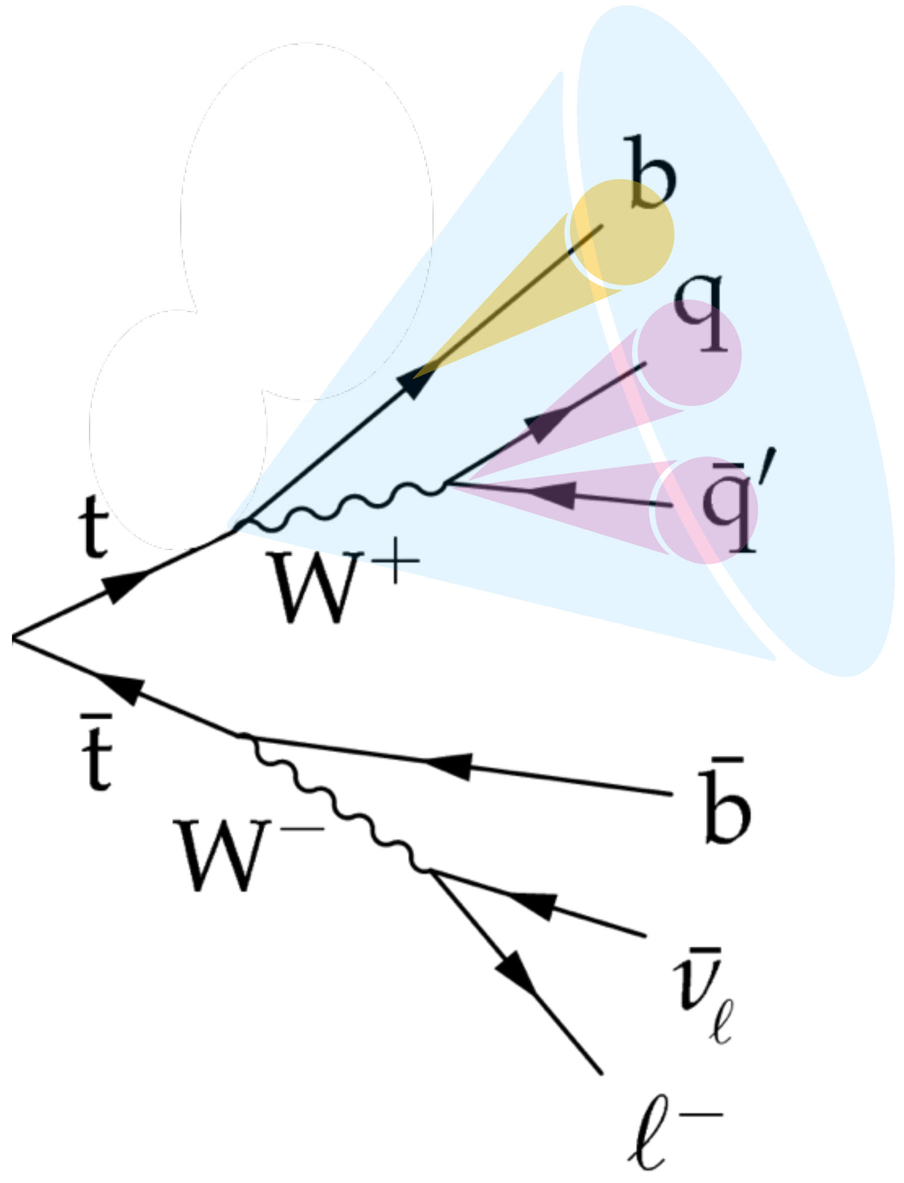


Bellagente et al. **1912.00477**
Bellagente et al. **2006.06685**
Backes et al. **2212.08674**
Huetsch et al. **2404.18807**

BOOSTed top decays

$p_{T,J} > 400$ GeV



Reconstruct triple jet mass M_{jjj} to measure m_t

Tag side

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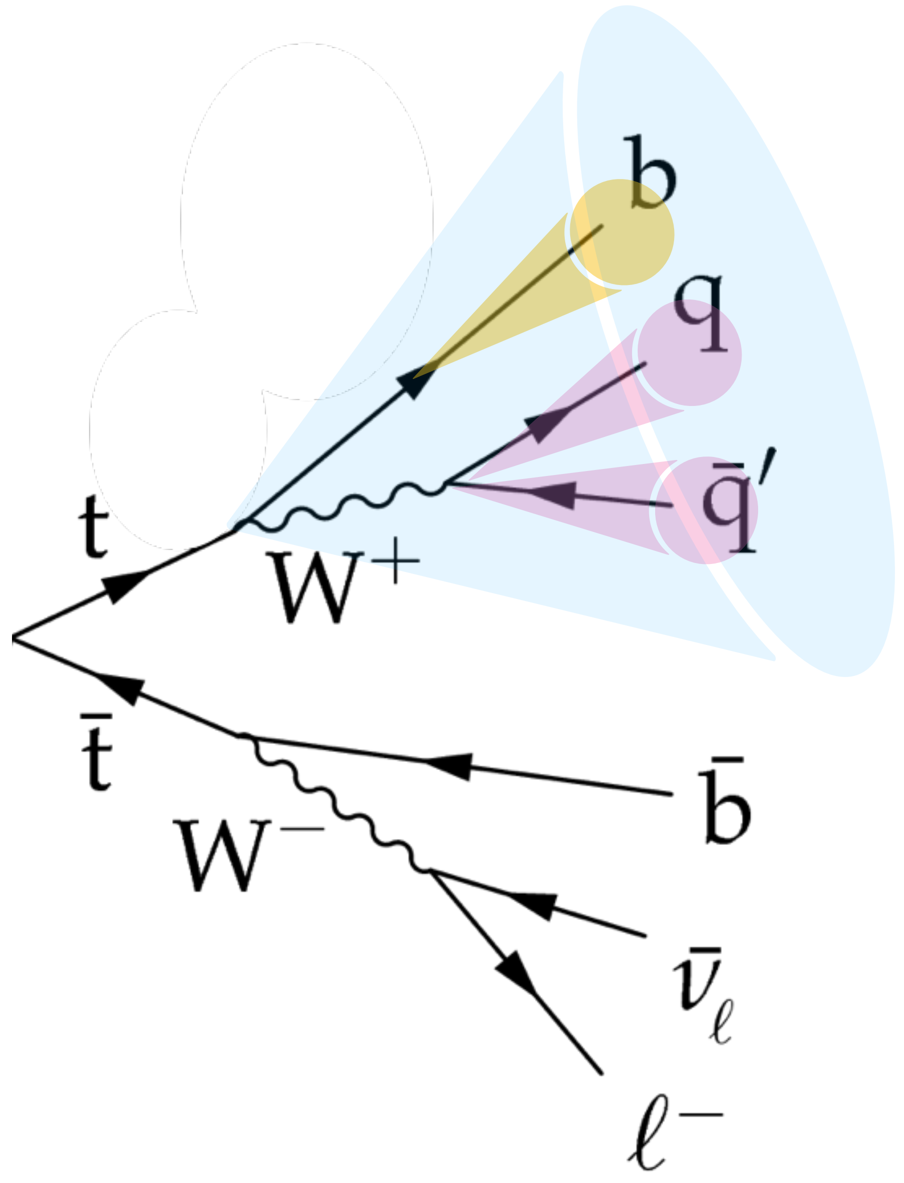

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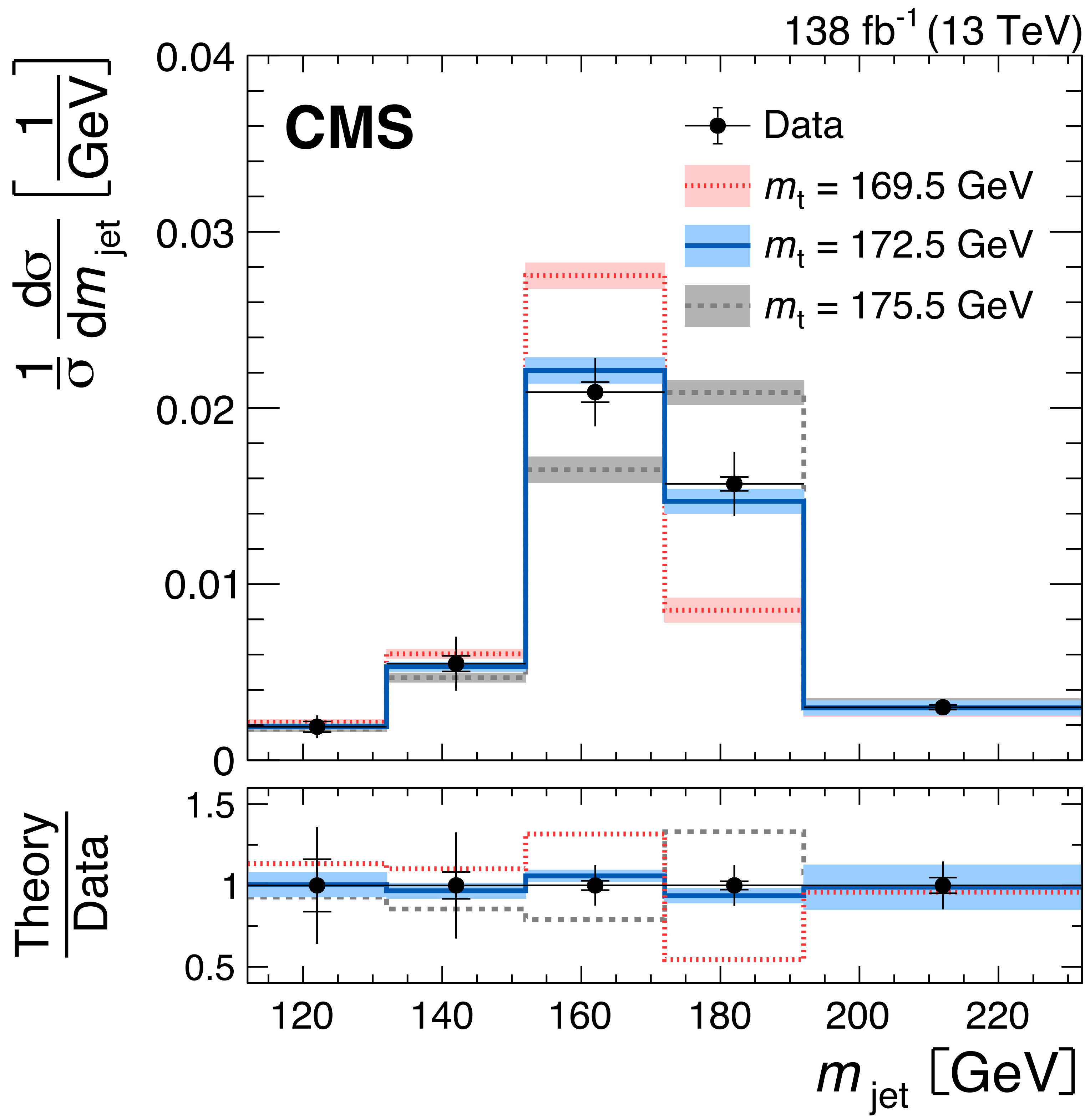
Previously done in CMS with TUnfold (classical binned unfolding algorithm)



CMS **2211.01456**

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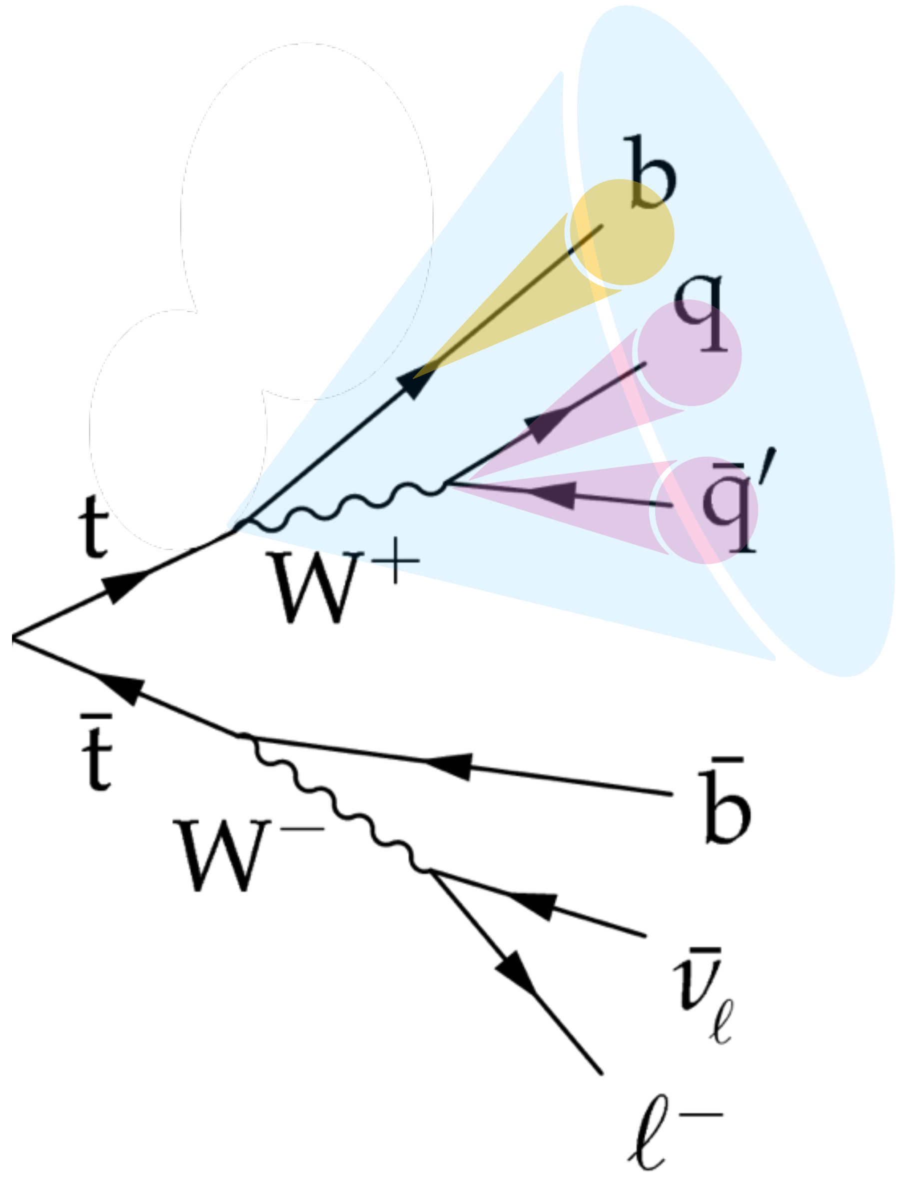

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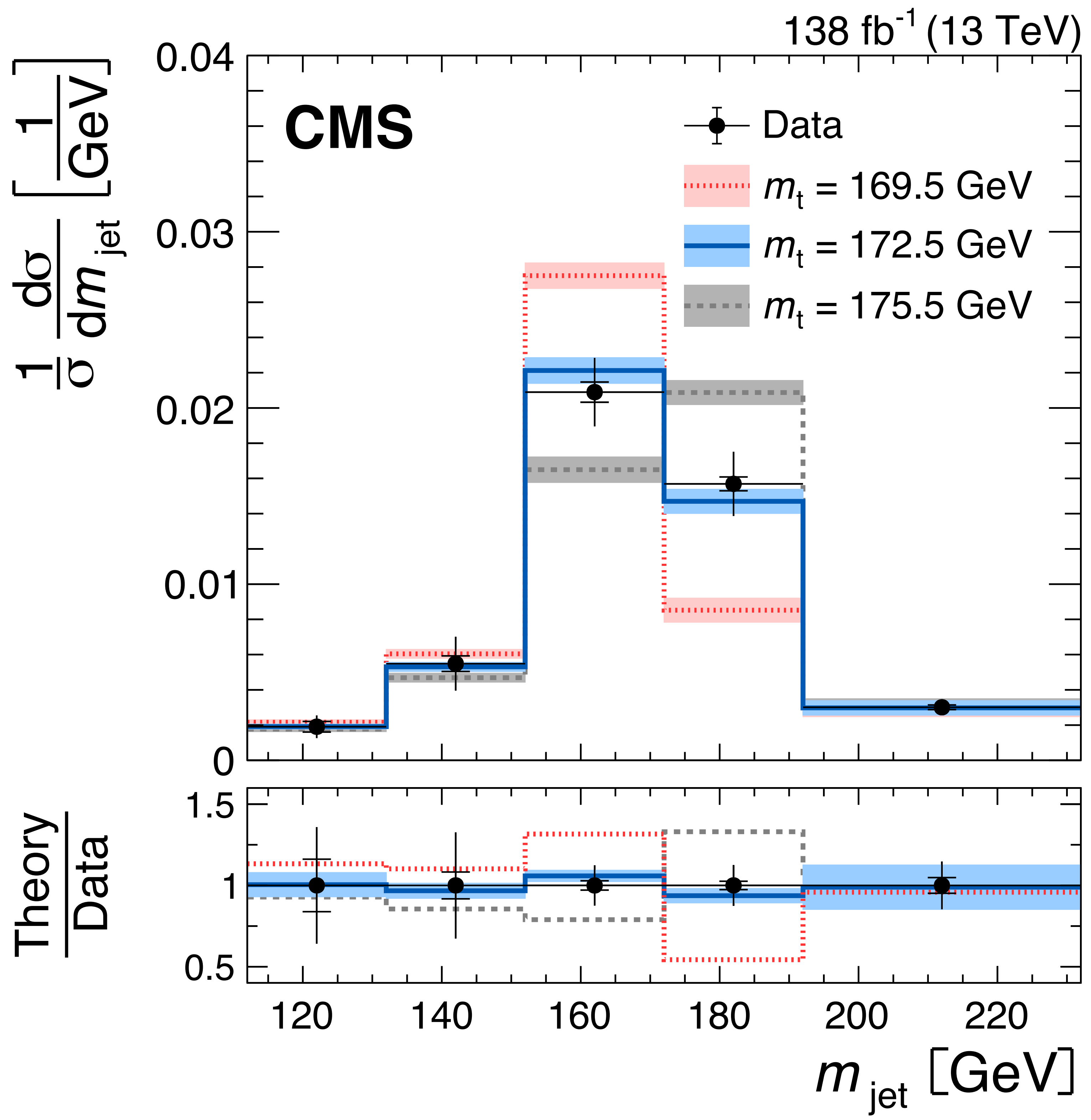


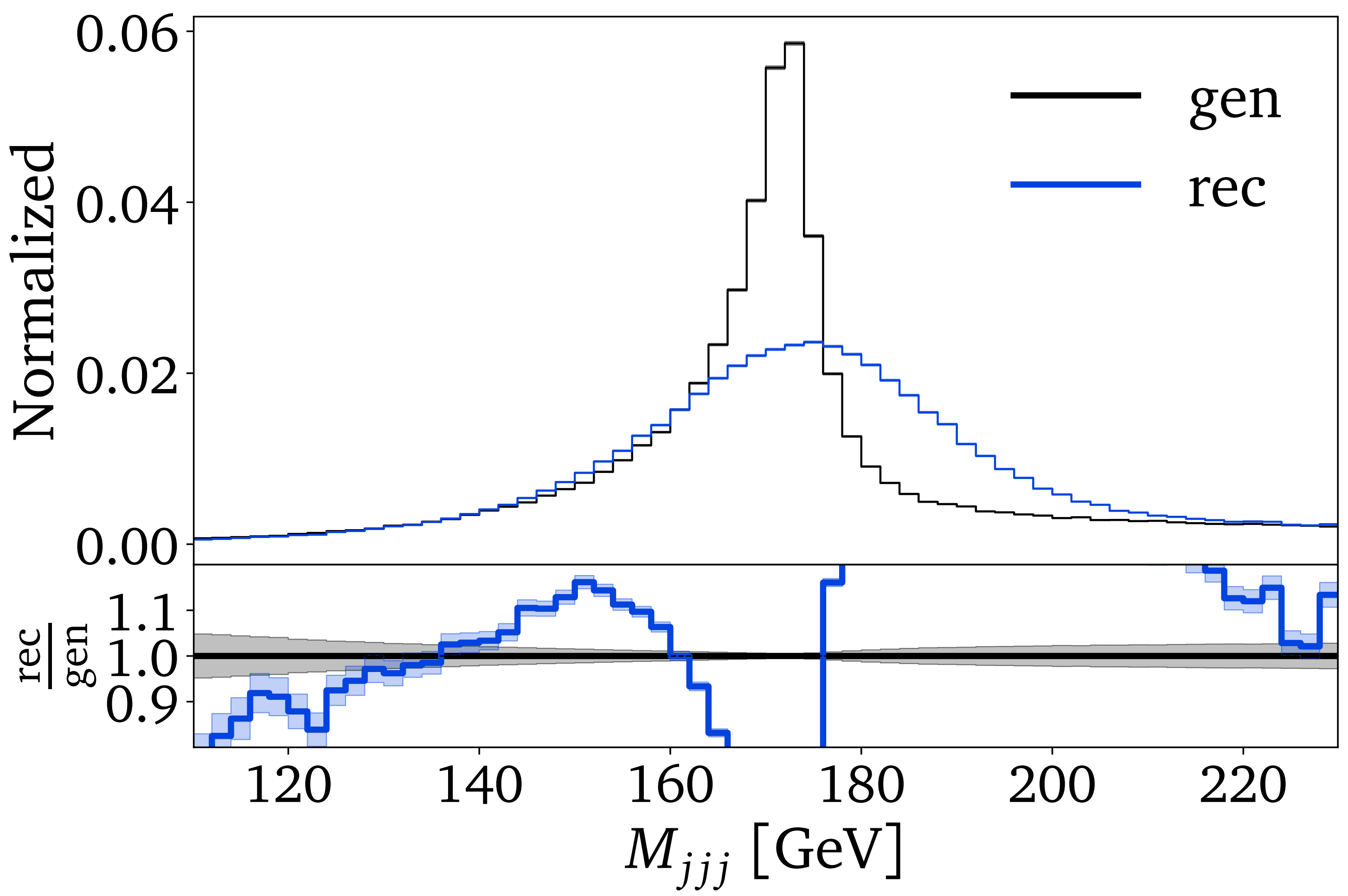
CMS **2211.01456**

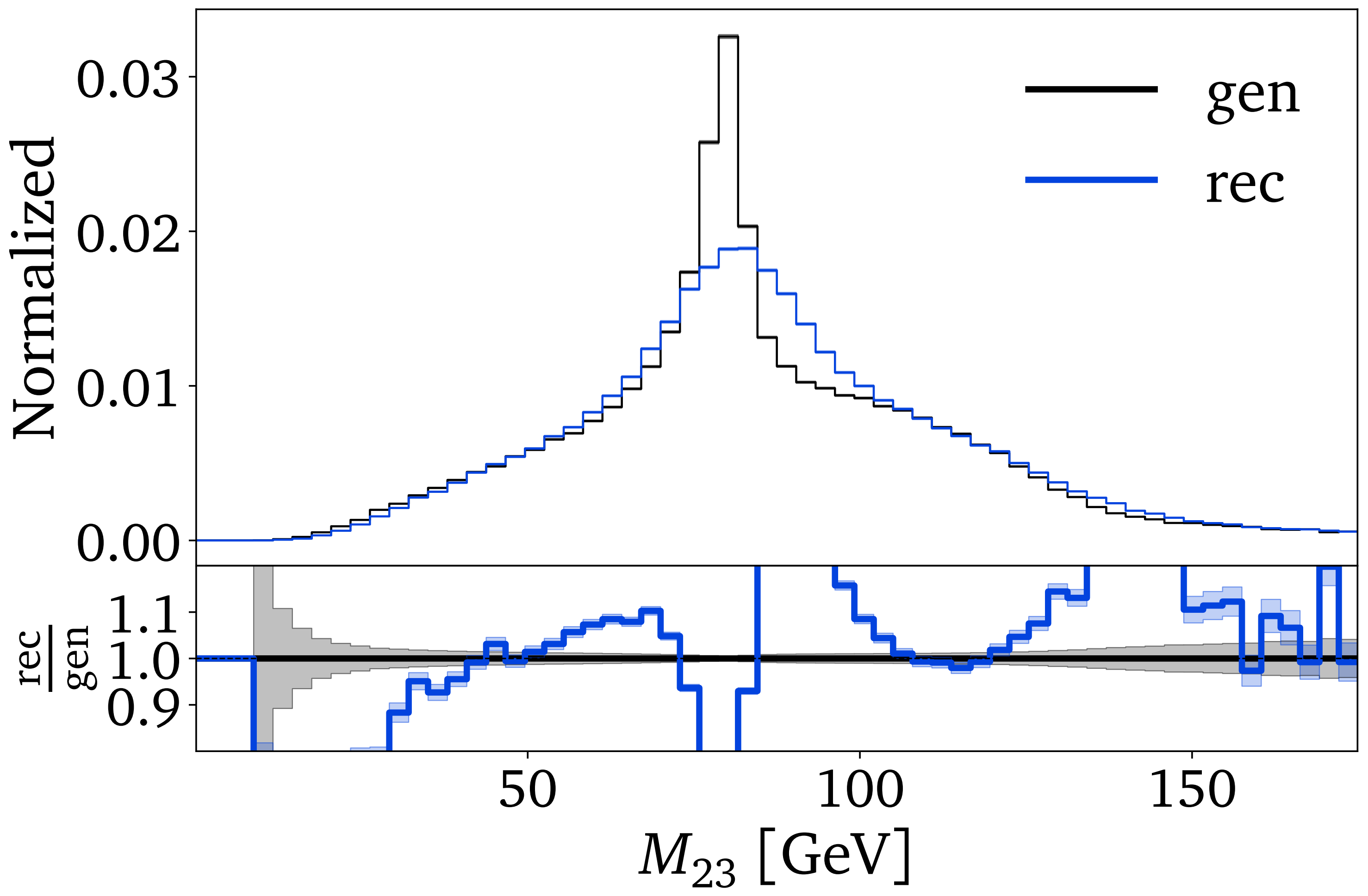
BUT leading uncertainty: choice of m_t in simulation + no access to full phase space

→ **Could generative unfolding help?**

Challenging aspects of top - unfolding

1. Mulitresonant phase space





Challenging aspects of top - unfolding

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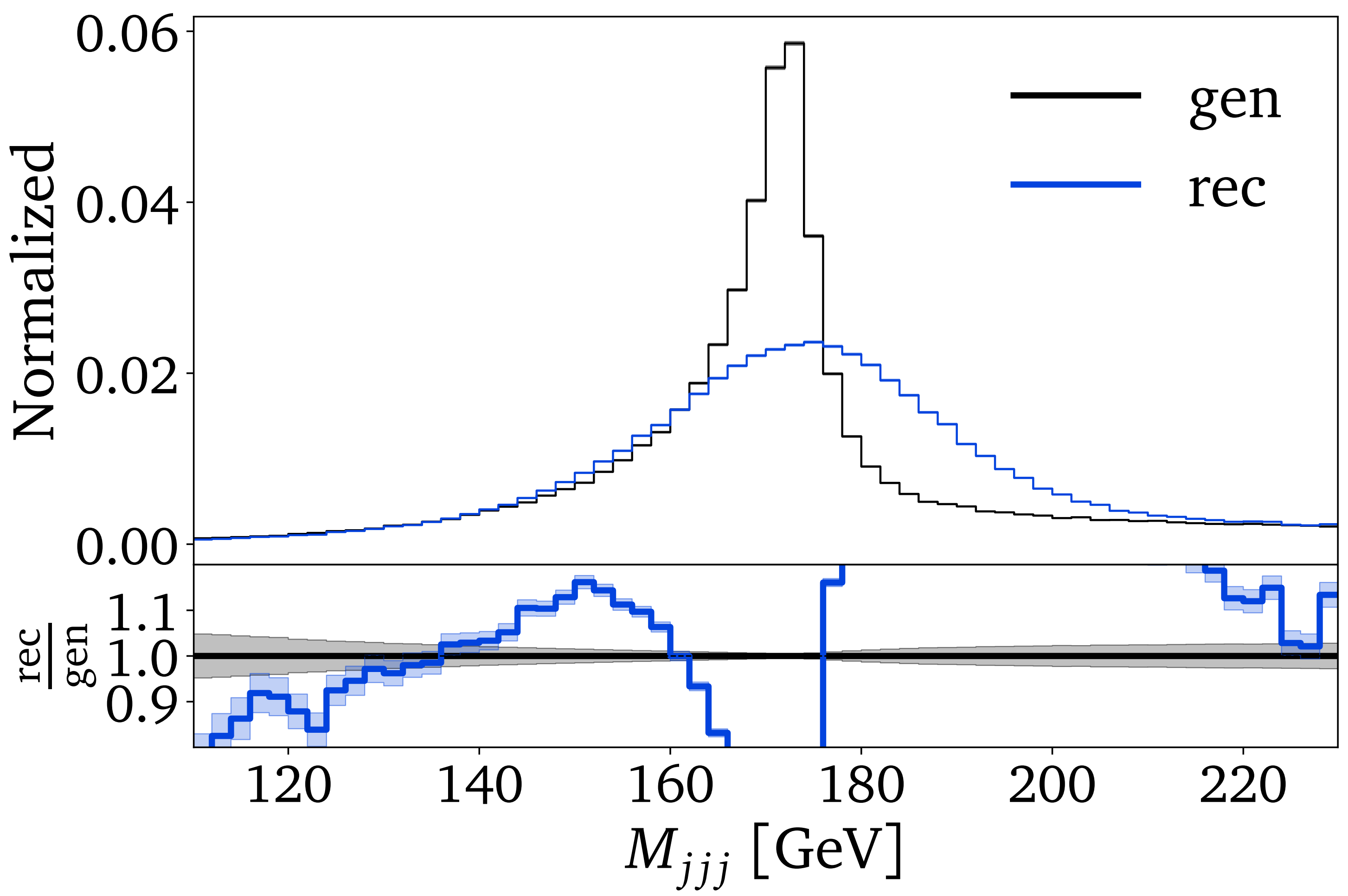
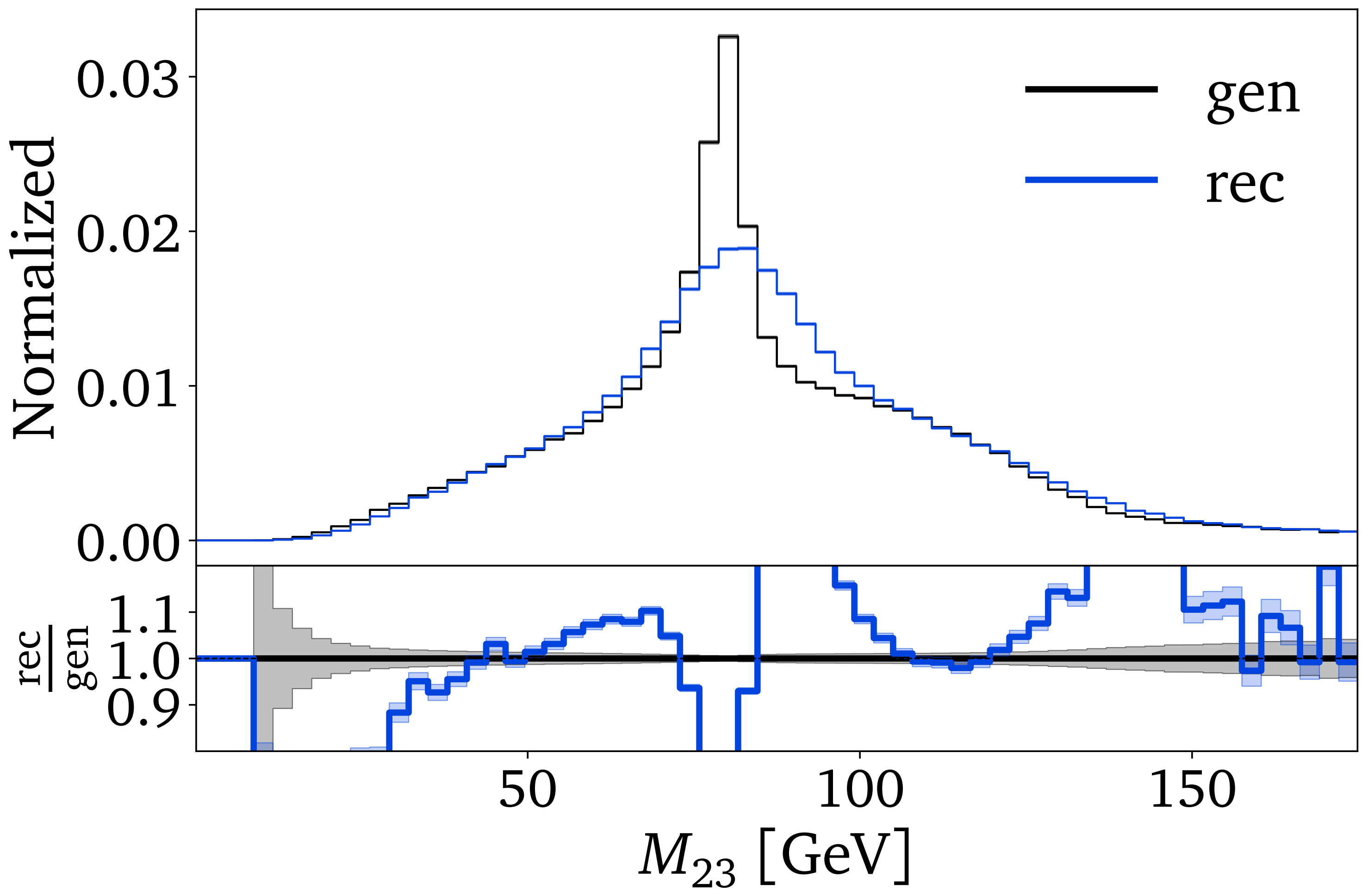
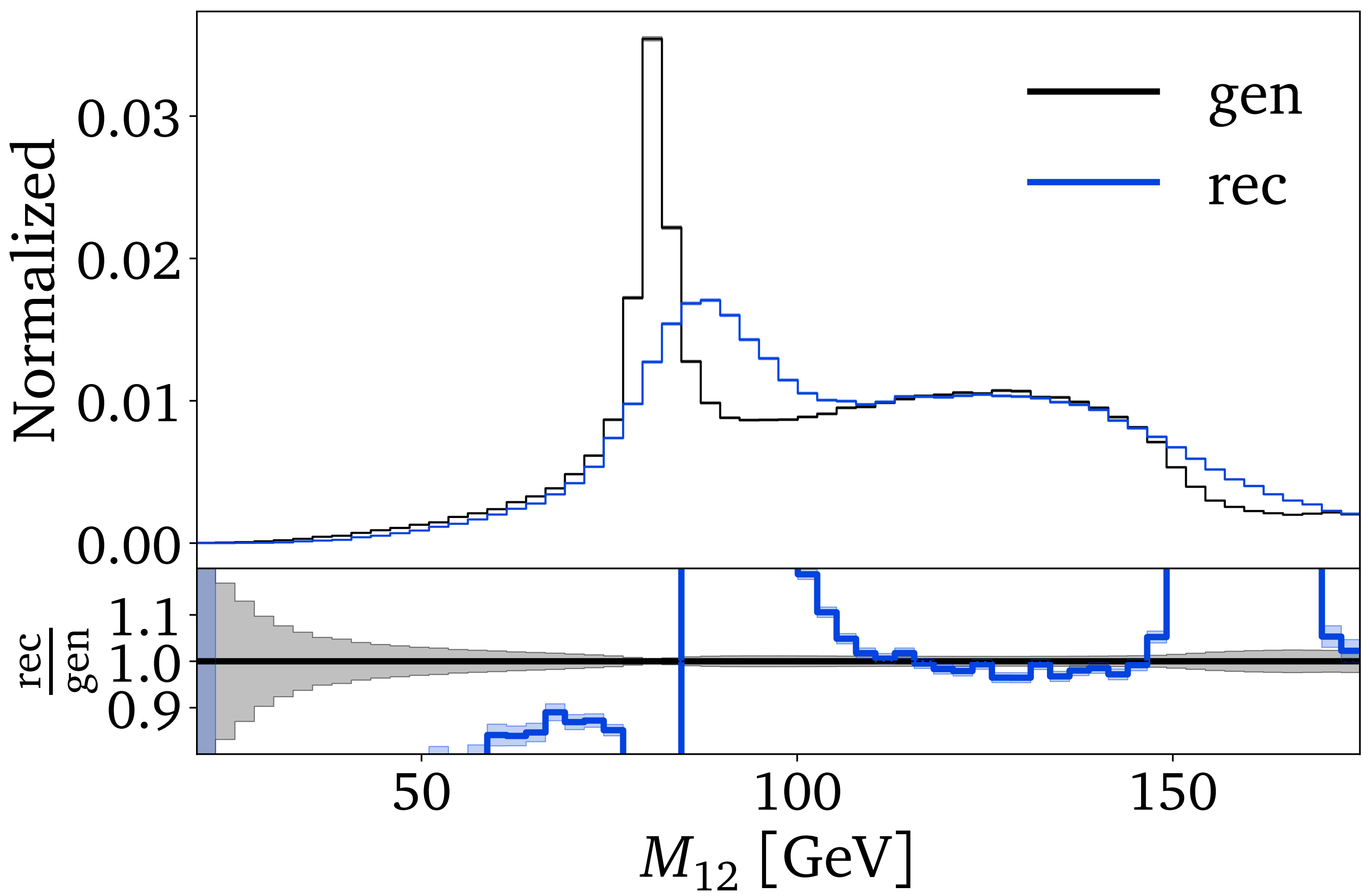
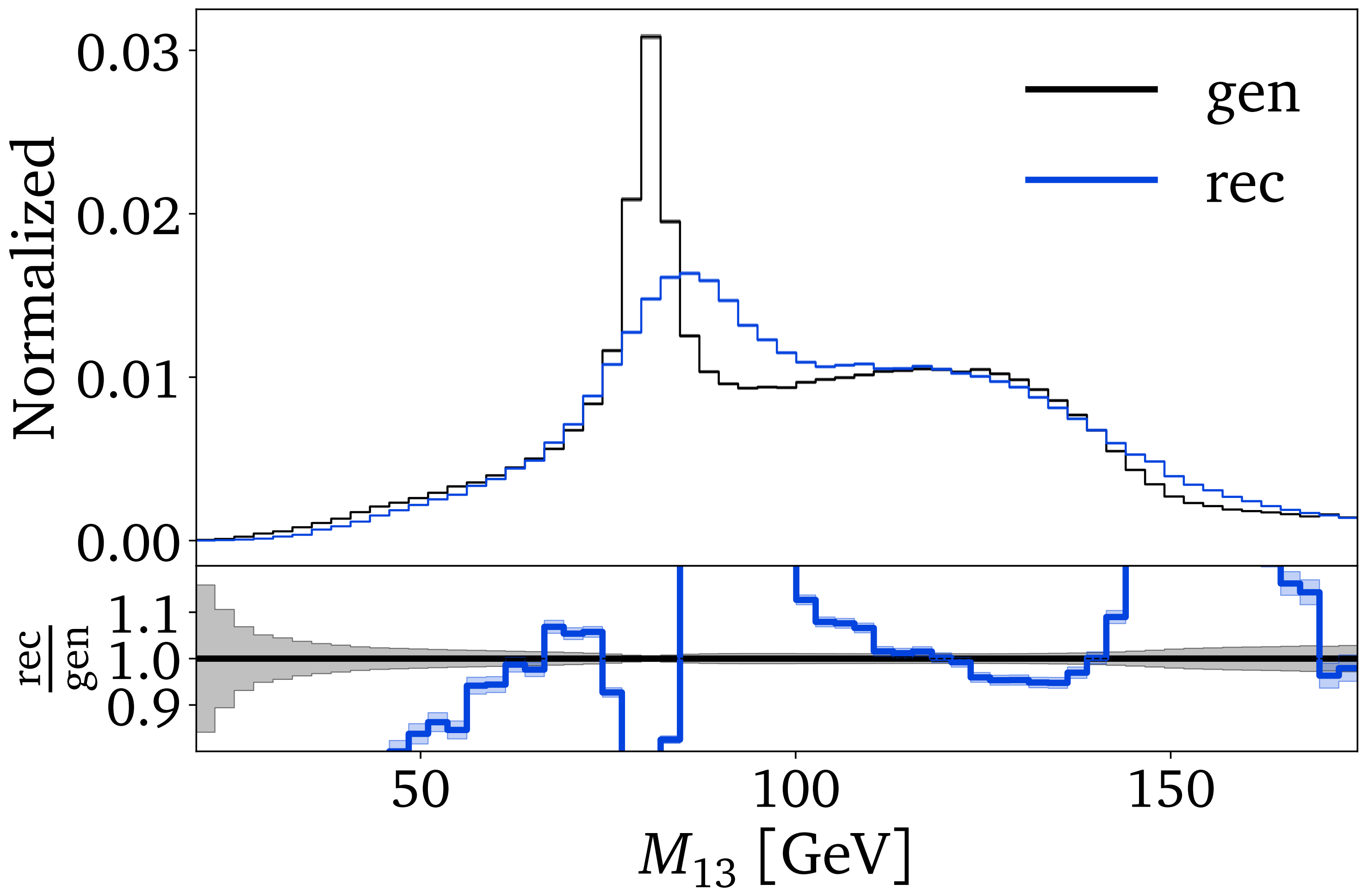




2. Combinatorics





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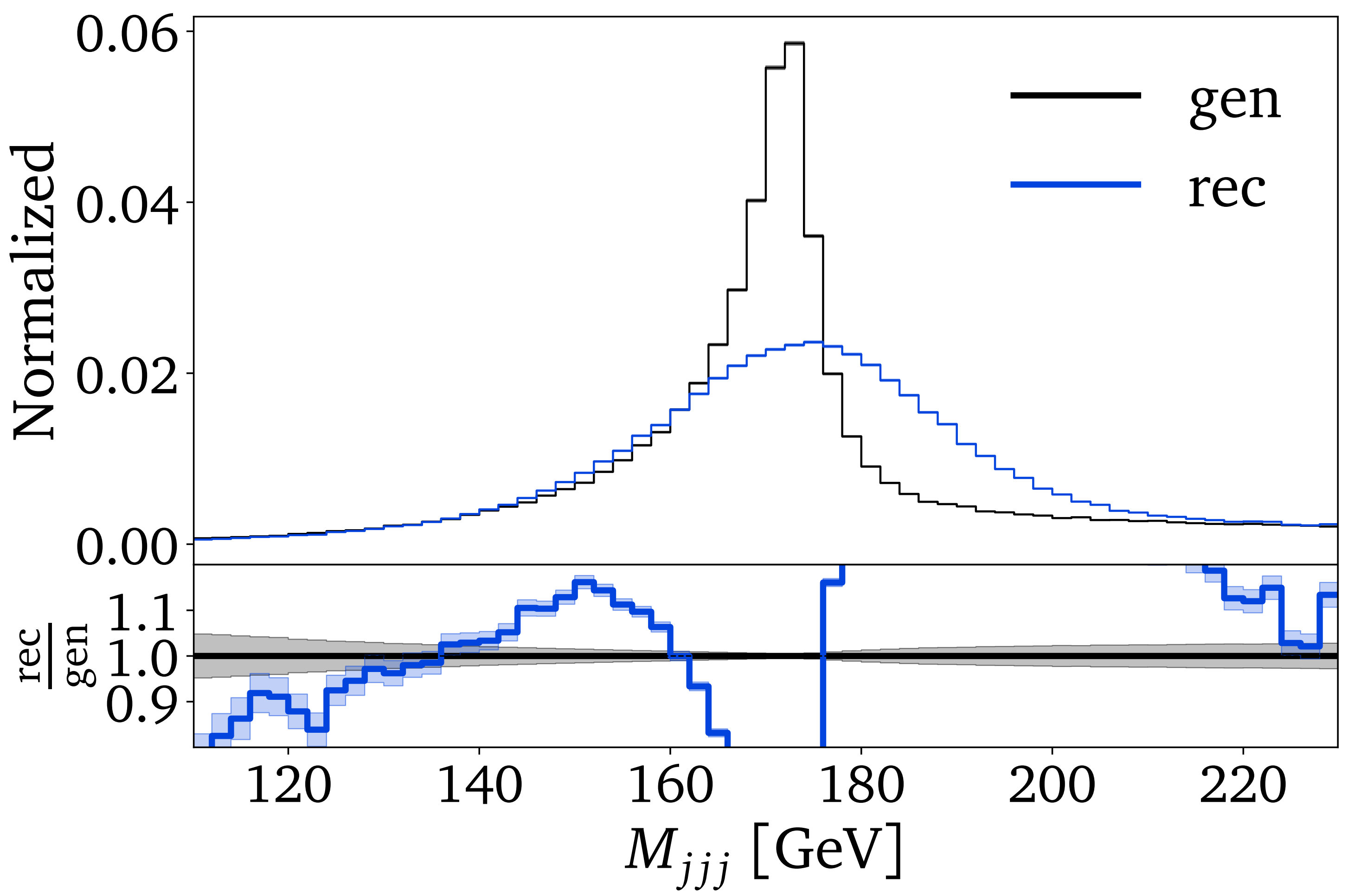

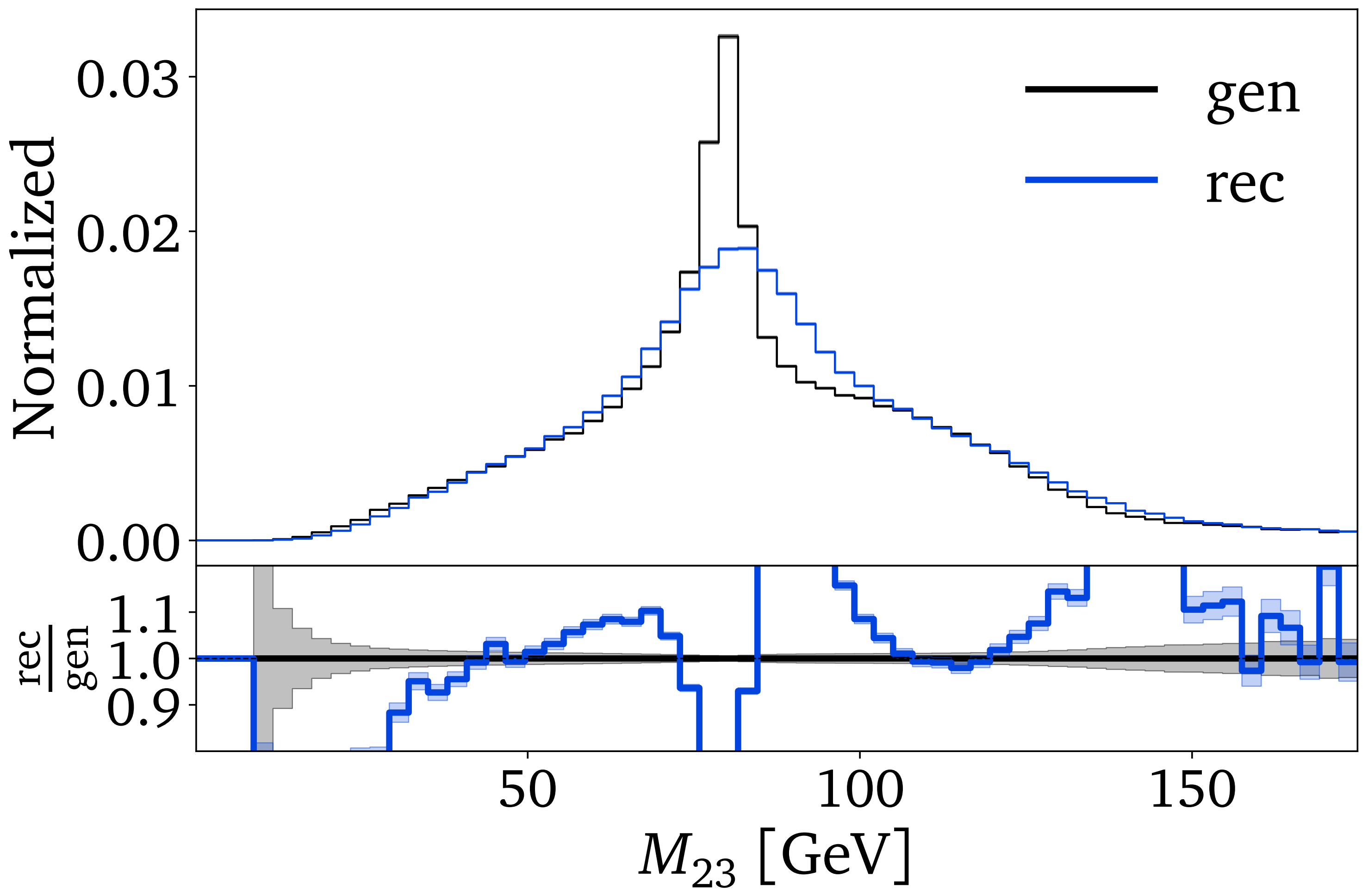

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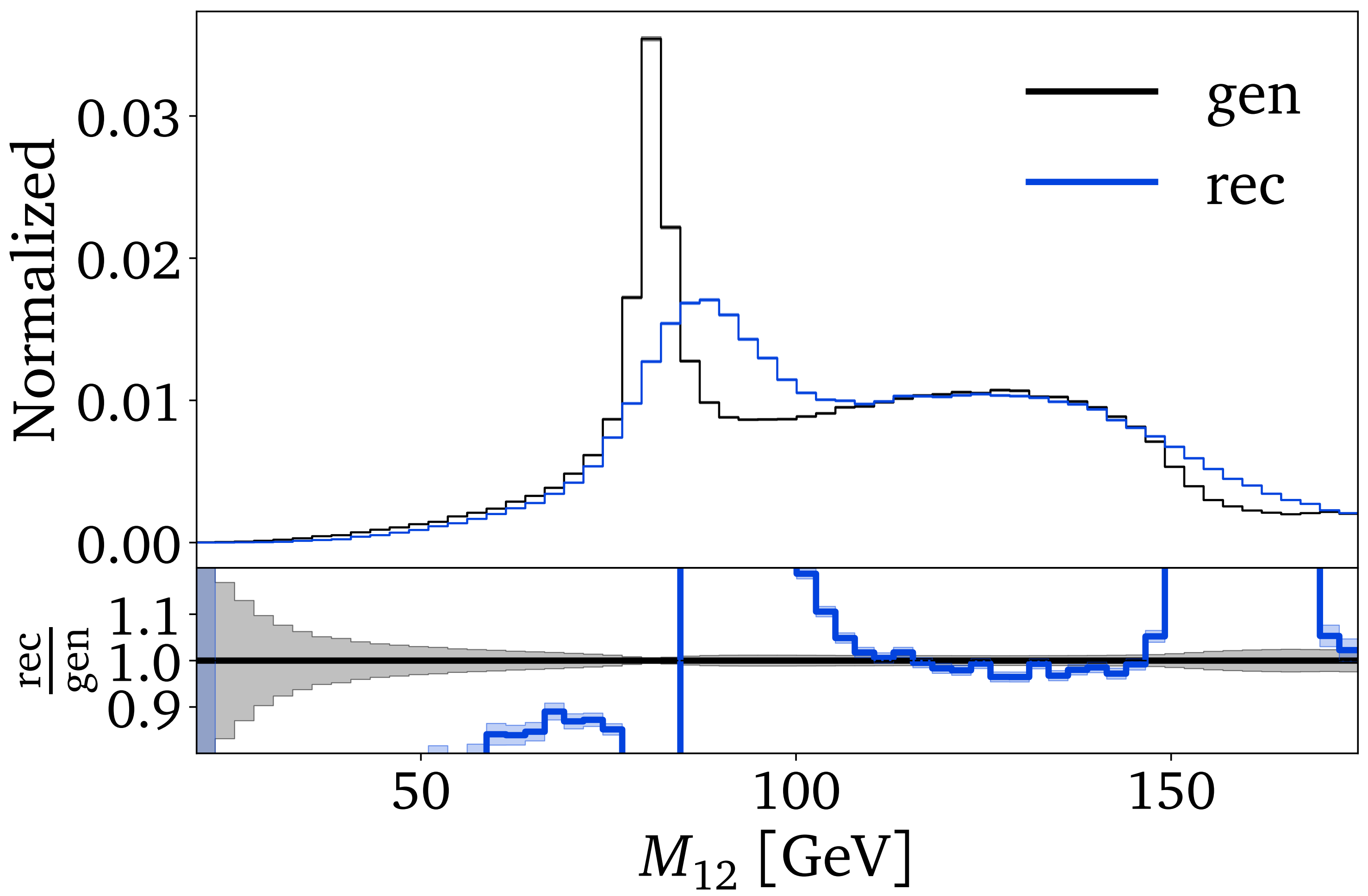
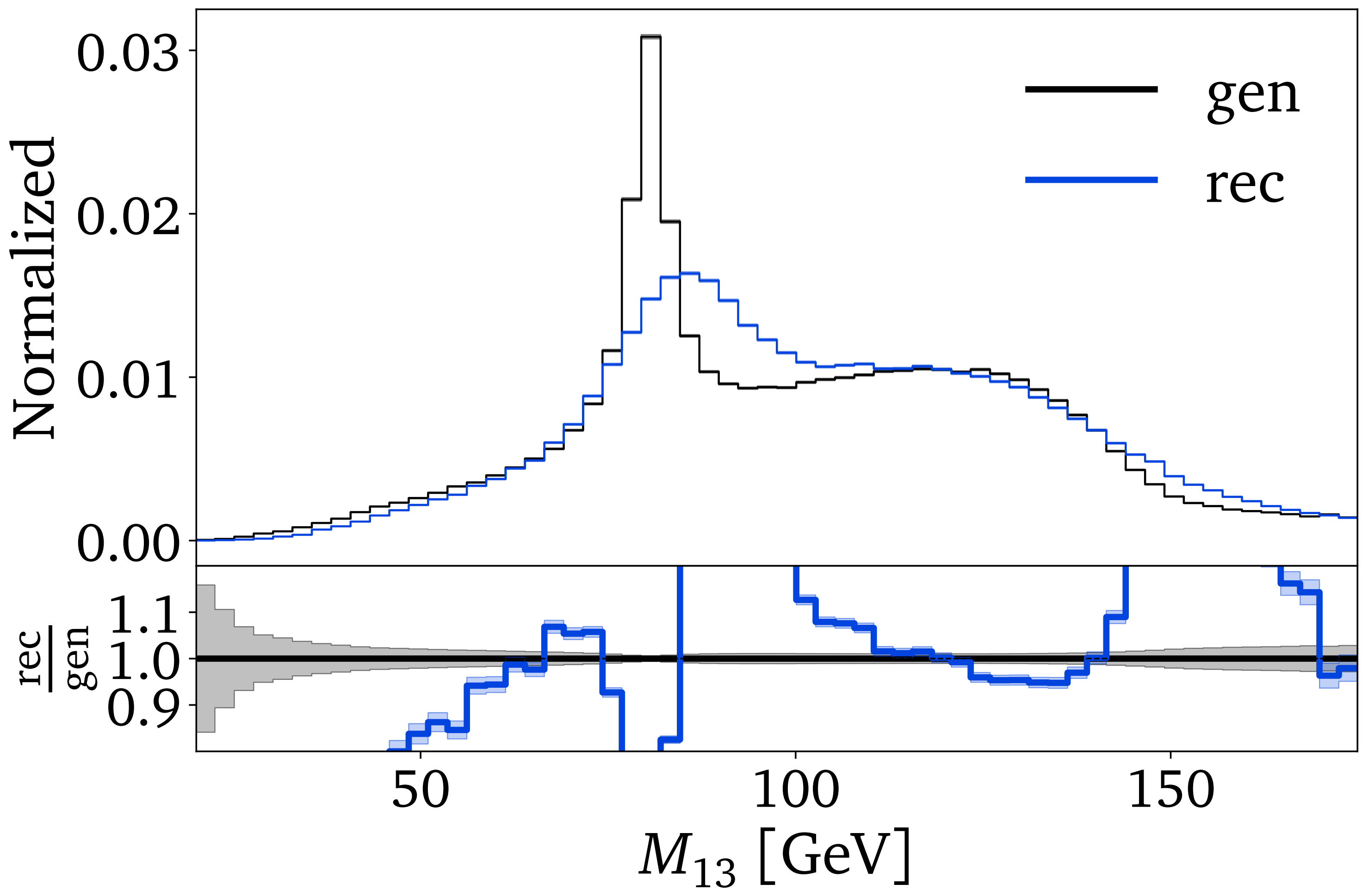
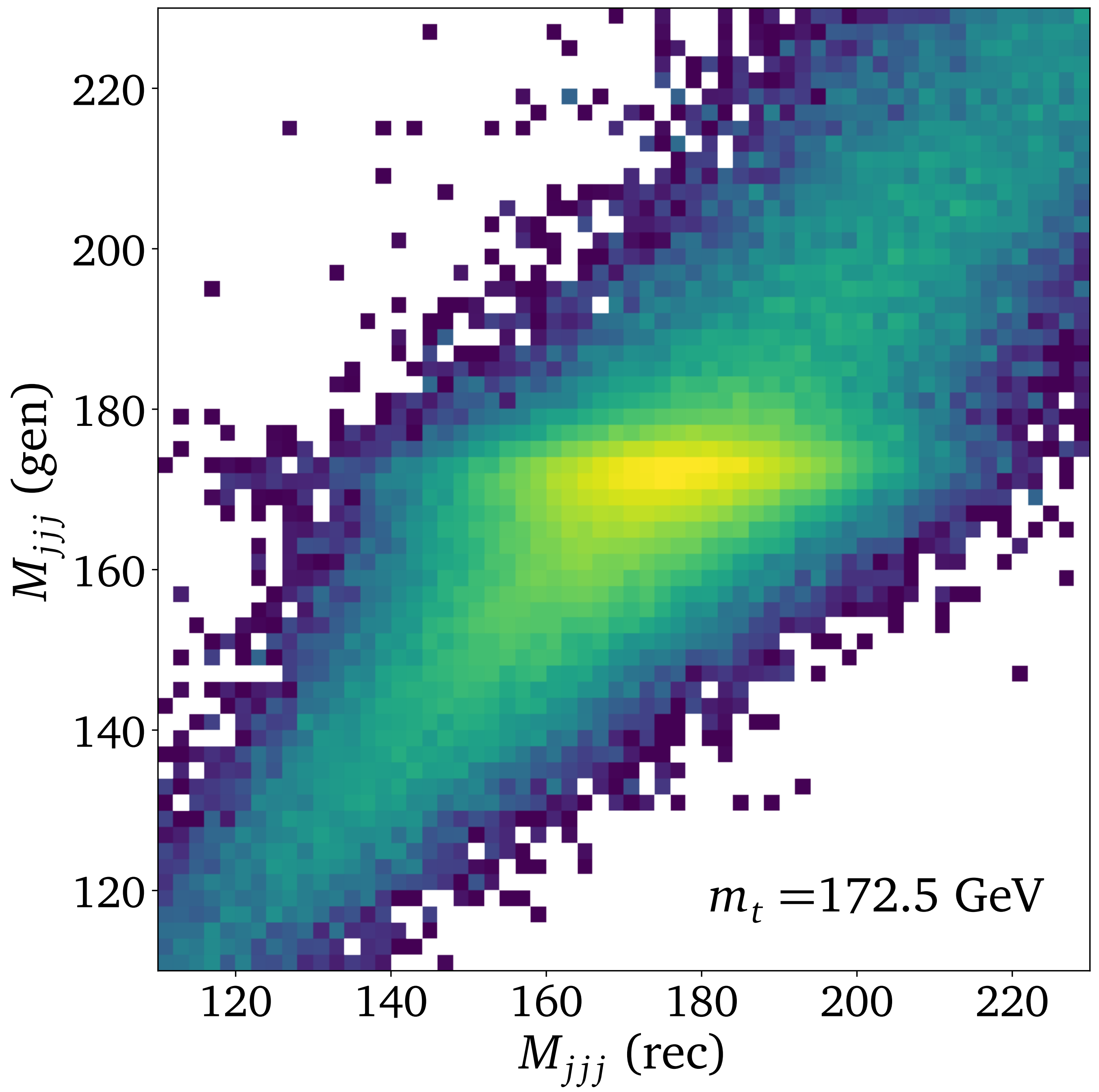




3. Detector Smearing



Choosing the right parametrization

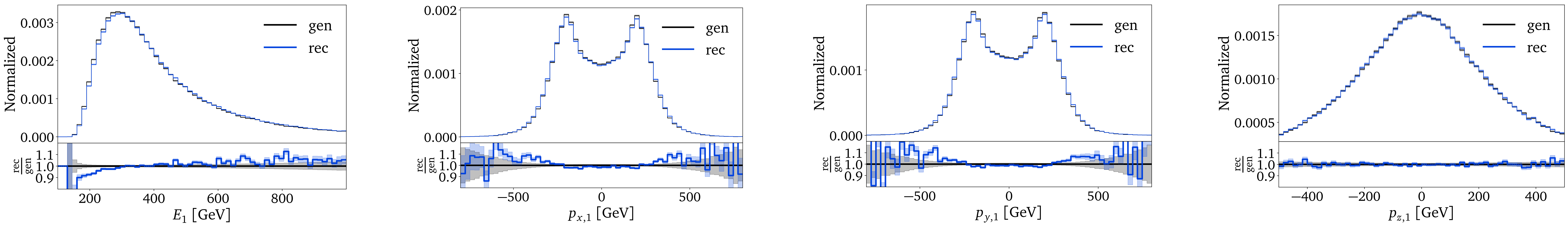
1. The naive

$$p_1 = (E_1, \vec{p}_1)$$
$$p_2 = (E_2, \vec{p}_2)$$
$$p_3 = (E_3, \vec{p}_3)$$

$M_{jjj}(p_1, p_2, p_3)$ ← 12 dimensional correlation

$M_{ij}(p_i, p_j)$ ← 8 dimensional correlation + combinatorics difficult

Reco and gen level difference not significantly visible, only in correlations



Choosing the right parametrization

2. The less naive

$$p_1 = (p_{T,1}, \phi_1, \eta_1, m_1)$$
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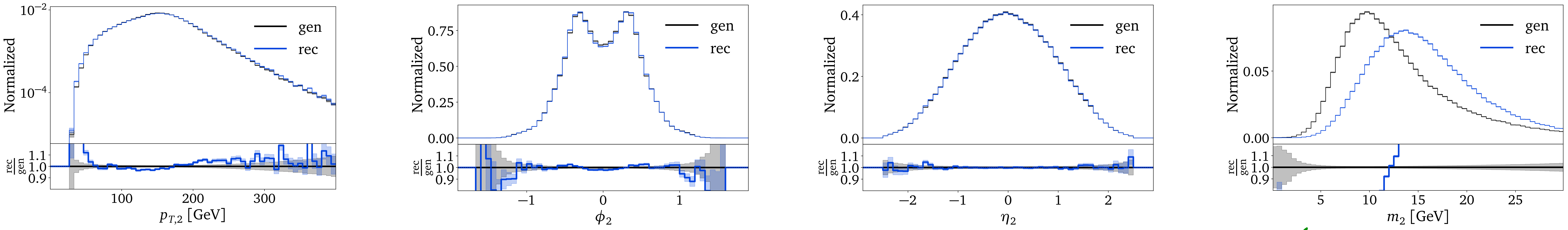


Reco and gen level difference visible

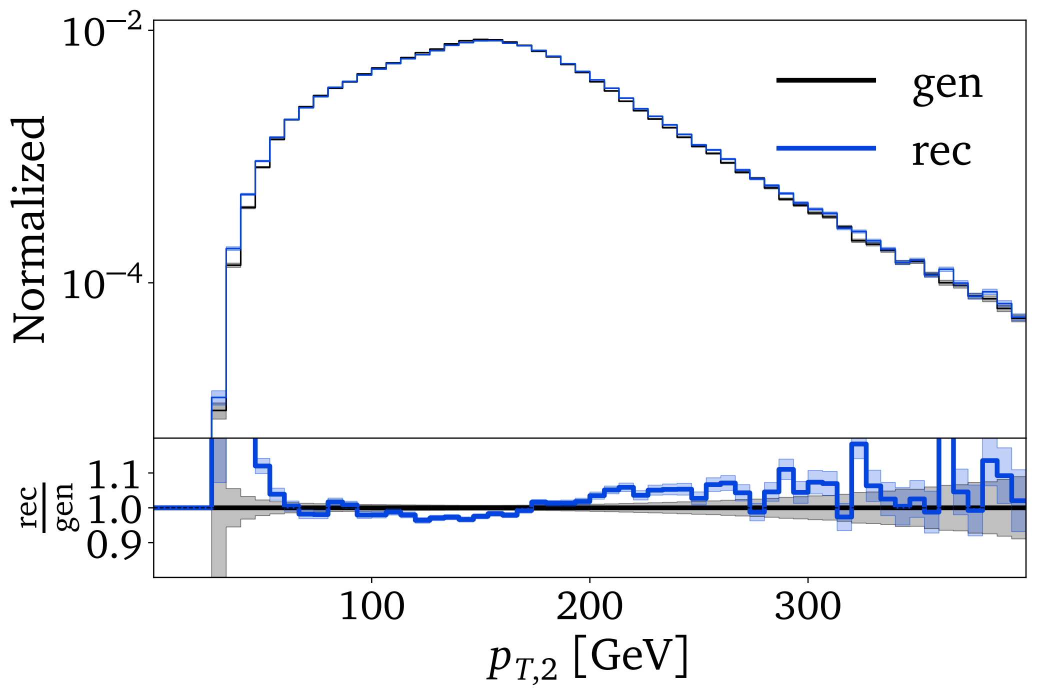
Choosing the right parametrization

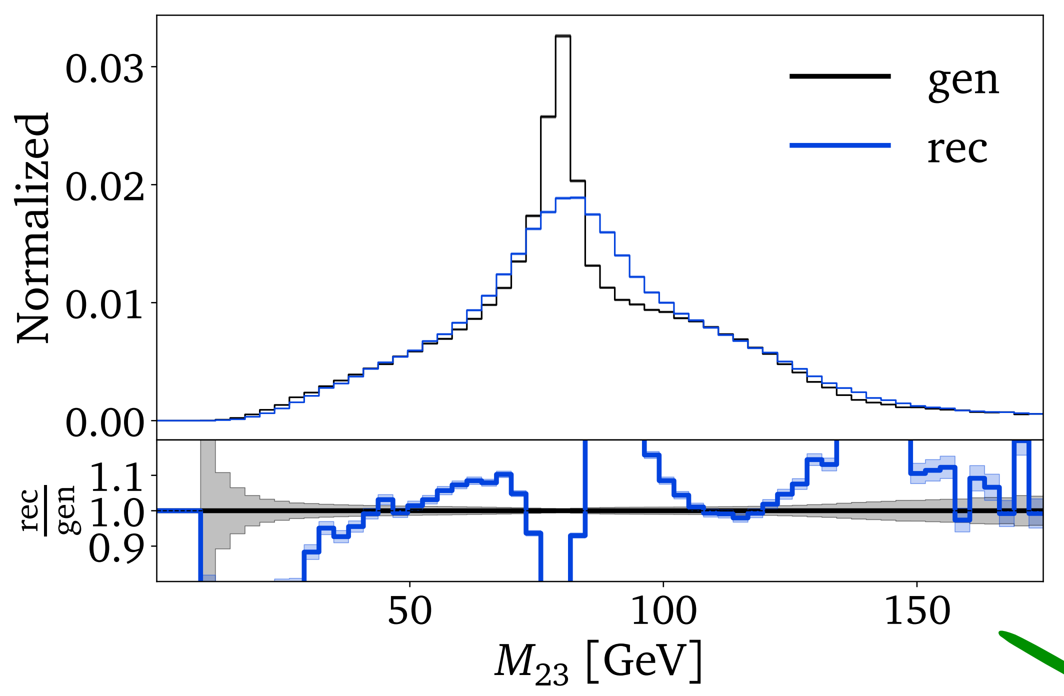
3. The least naive

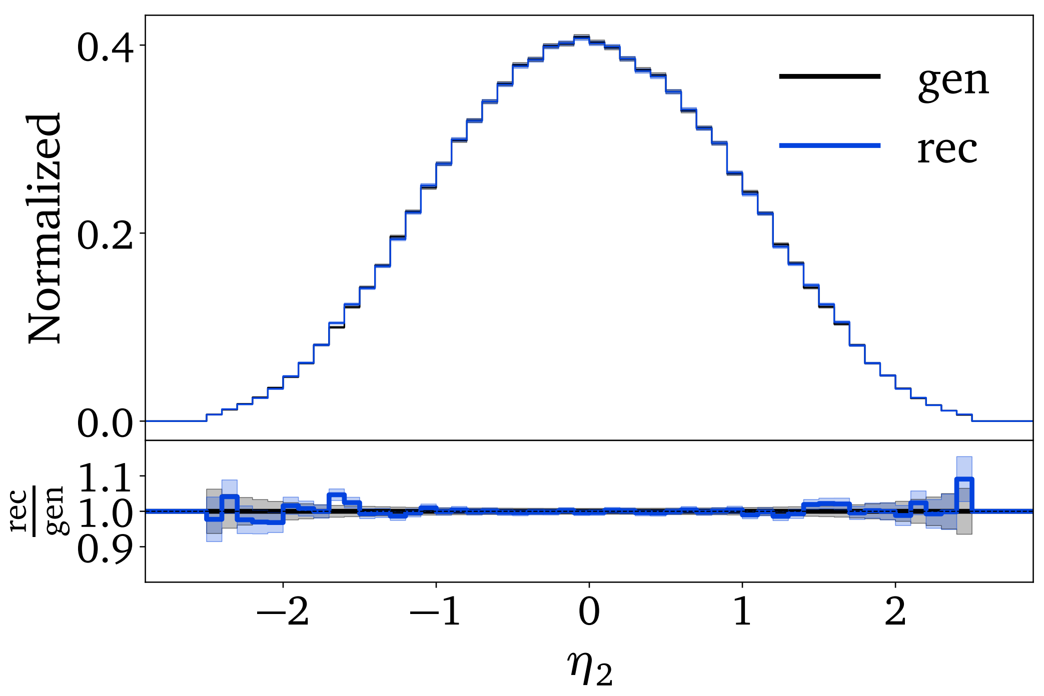
$$\left.\begin{aligned} p_1 &= (p_{T,1}, M_{12}, \eta_1, m_1) \\ p_2 &= (p_{T,2}, M_{23}, \eta_2, m_2) \\ p_3 &= (p_{T,3}, M_{13}, \eta_3, m_3) \end{aligned}\right\} \quad M_{jjj}^2 = \sum_{ij,i>j} M_{ij}^2 - \sum_i m_i^2$$

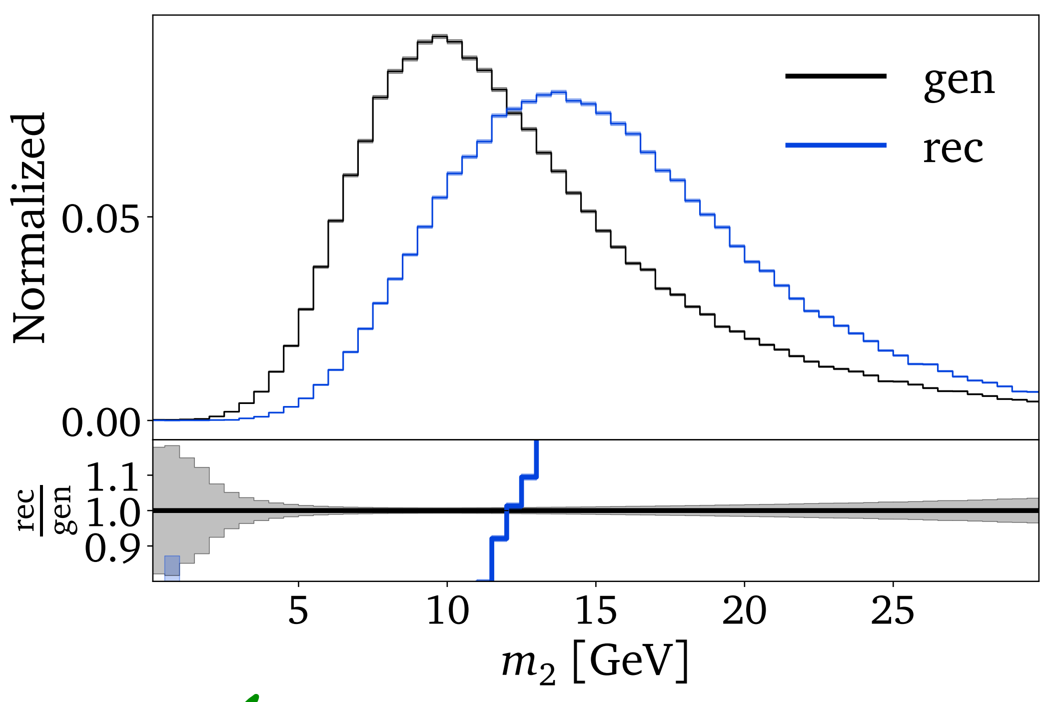
6 dimensional correlation

Direct input + combinatorics simple









Reco and gen level difference visible

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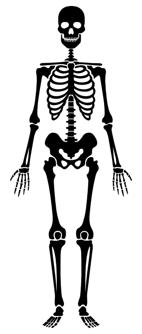

$|\Delta\phi_{ij}|$

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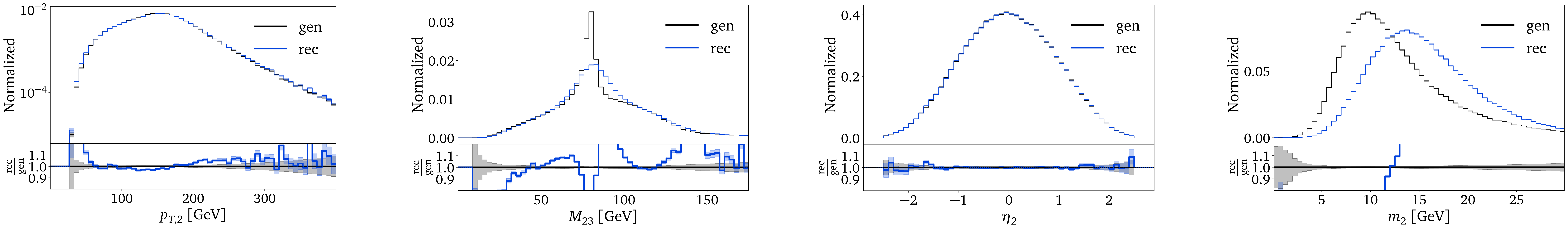

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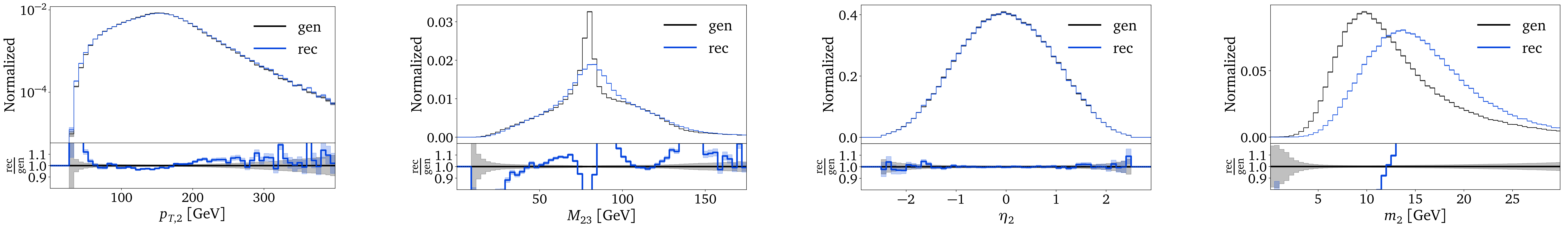

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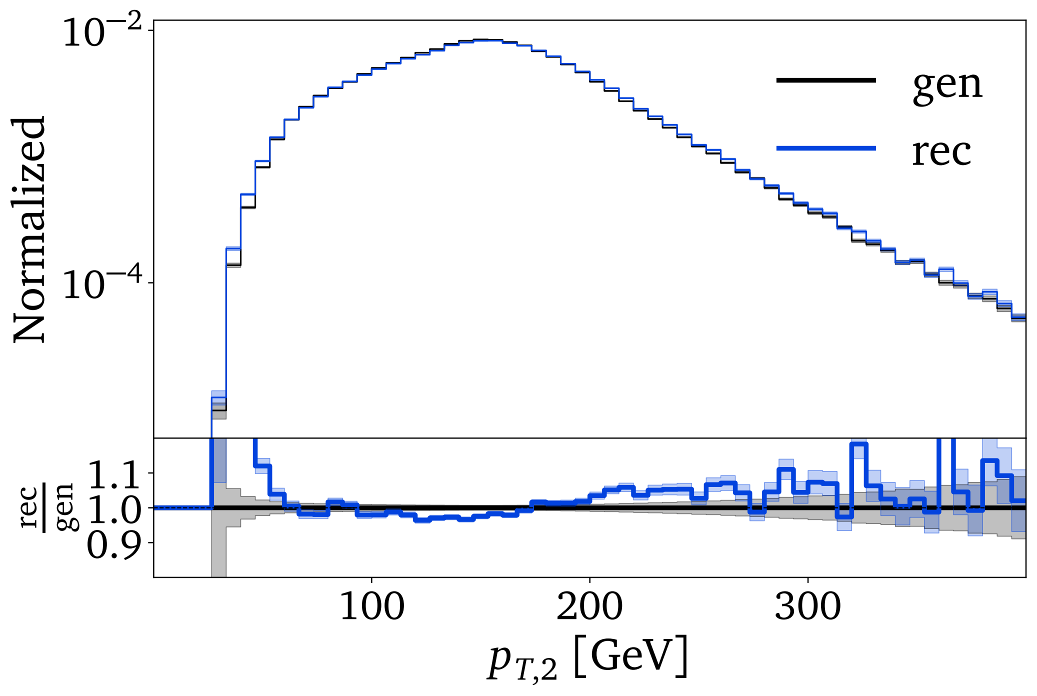
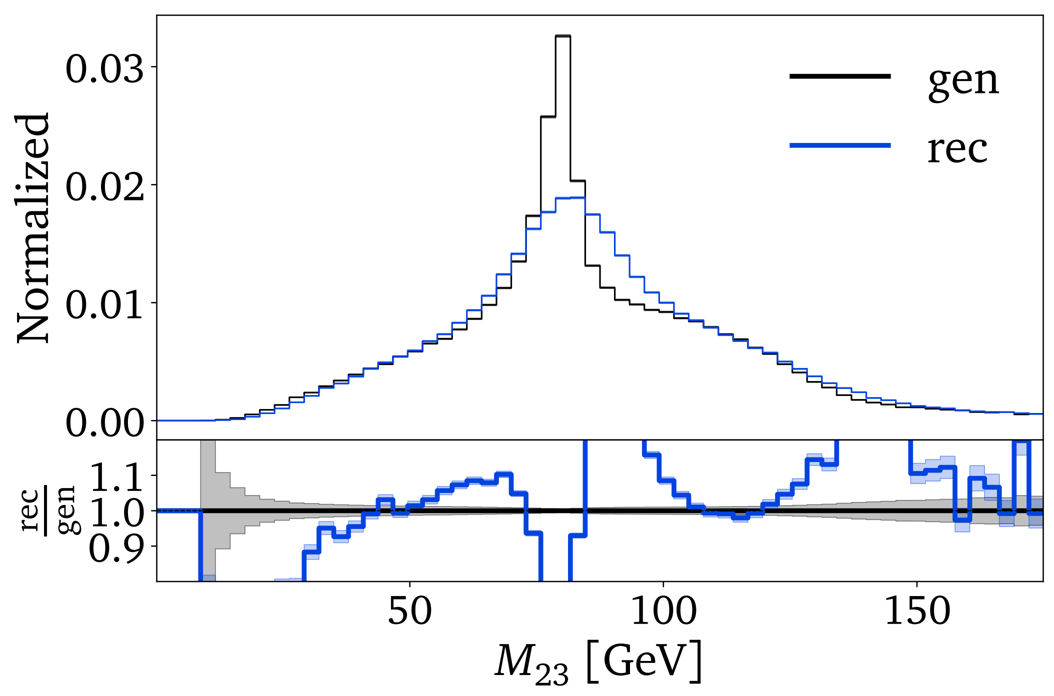
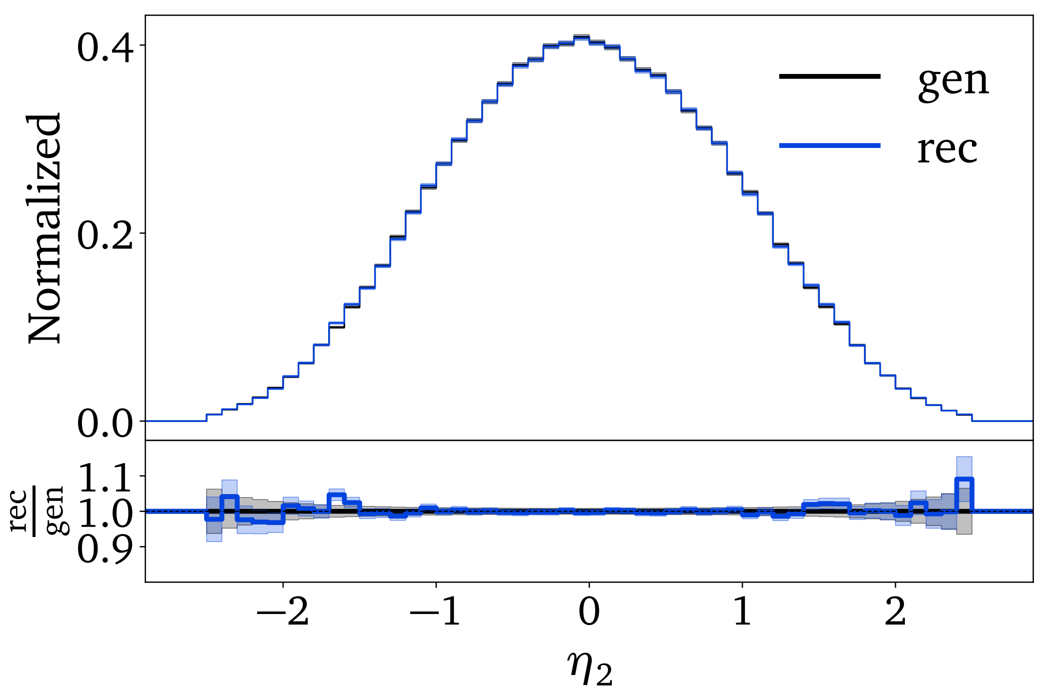
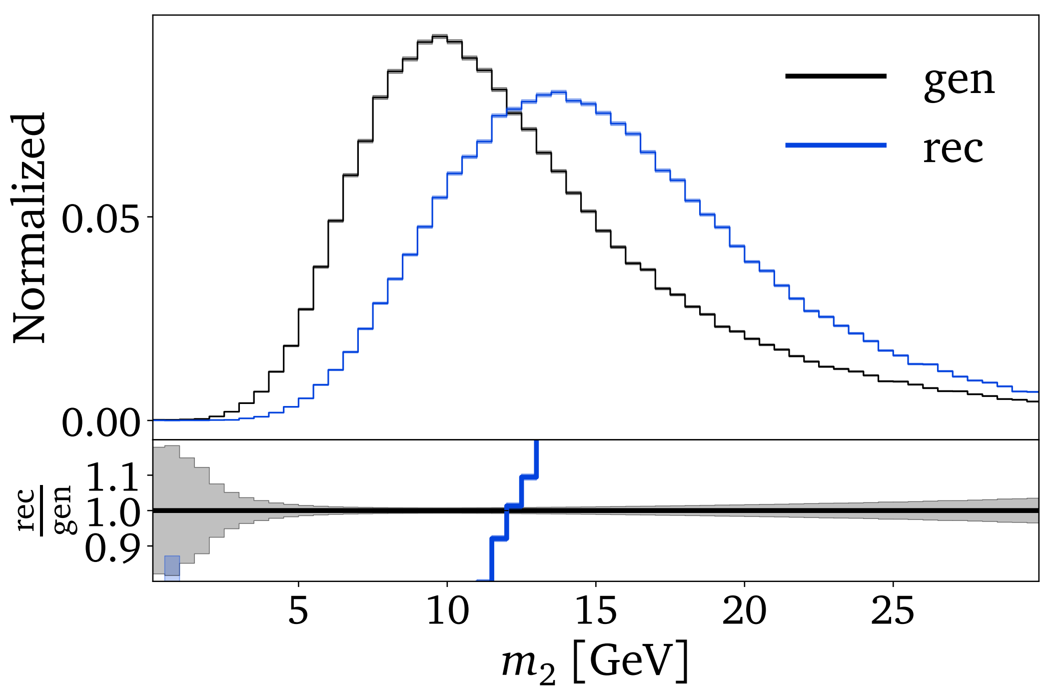
For mass measurement, we only use 6 dimensional subset of phase space to increase network performance

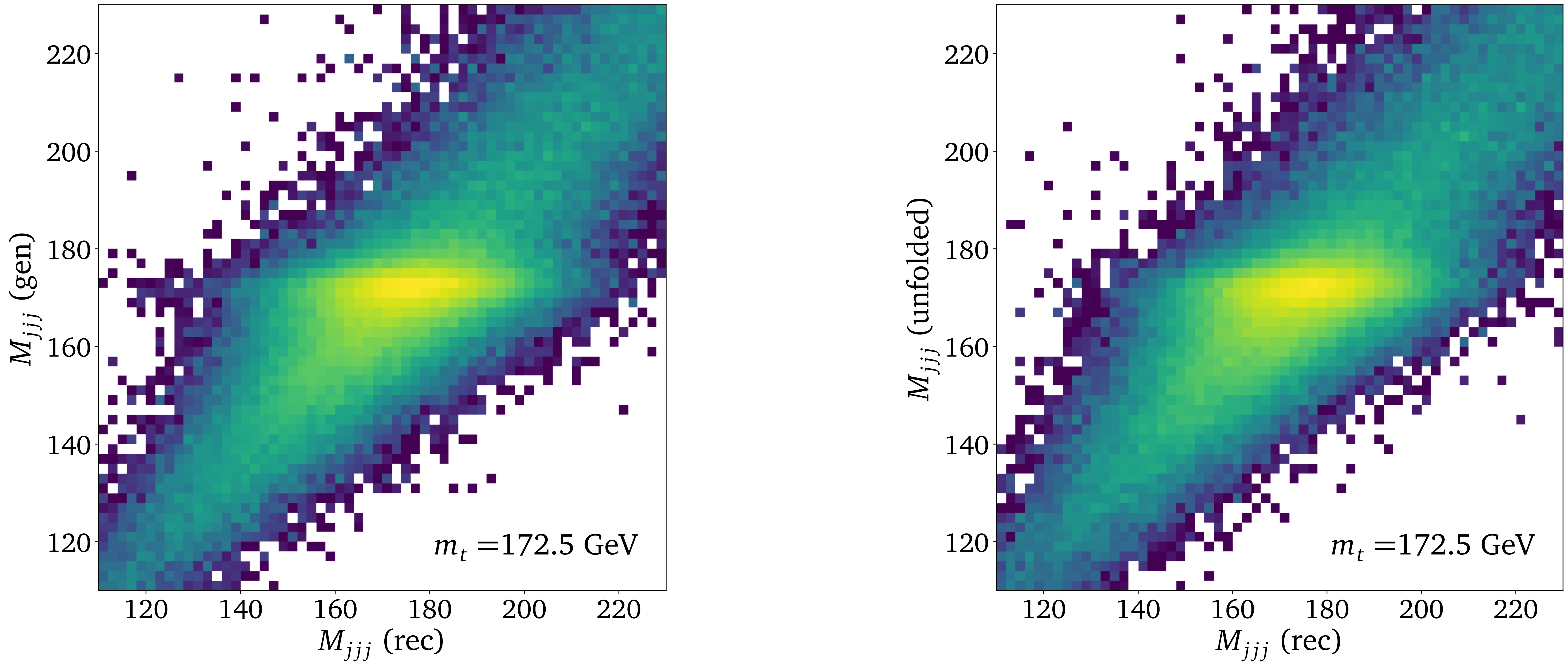








Model-Dependence



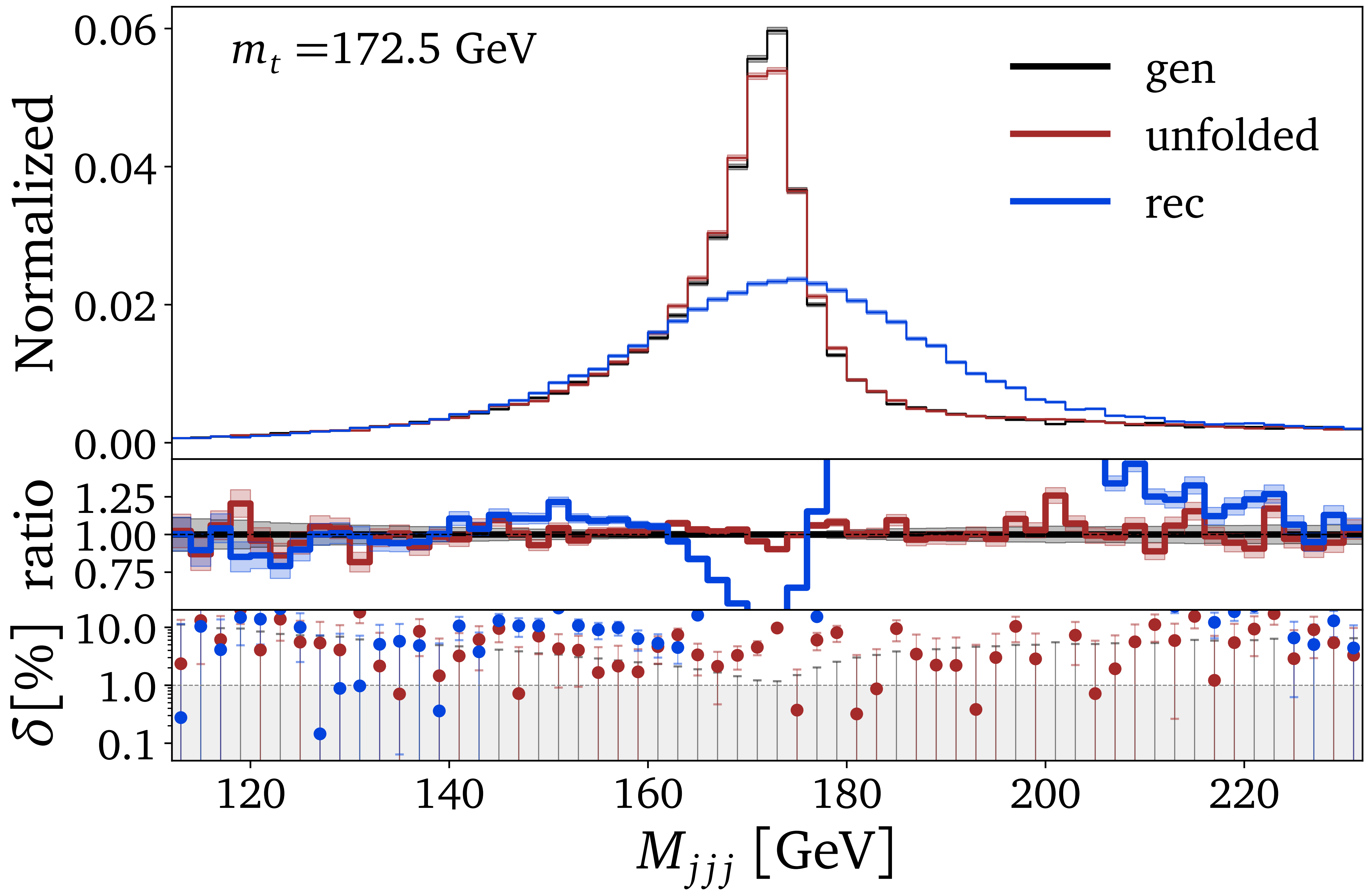
Correct migration learned?

Model-Dependence?

Train with full CMS simulation with
$m_t = 172.5$ GeV

Unfolded distribution of triple jet mass within
$\mathcal{O}(1\%)$ of truth gen level

BUT: Test data also simulation with
$m_t = 172.5$ GeV



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For pseudo-data with different top masses :
Algorithm falls back to prior ($m_t = 172.5$
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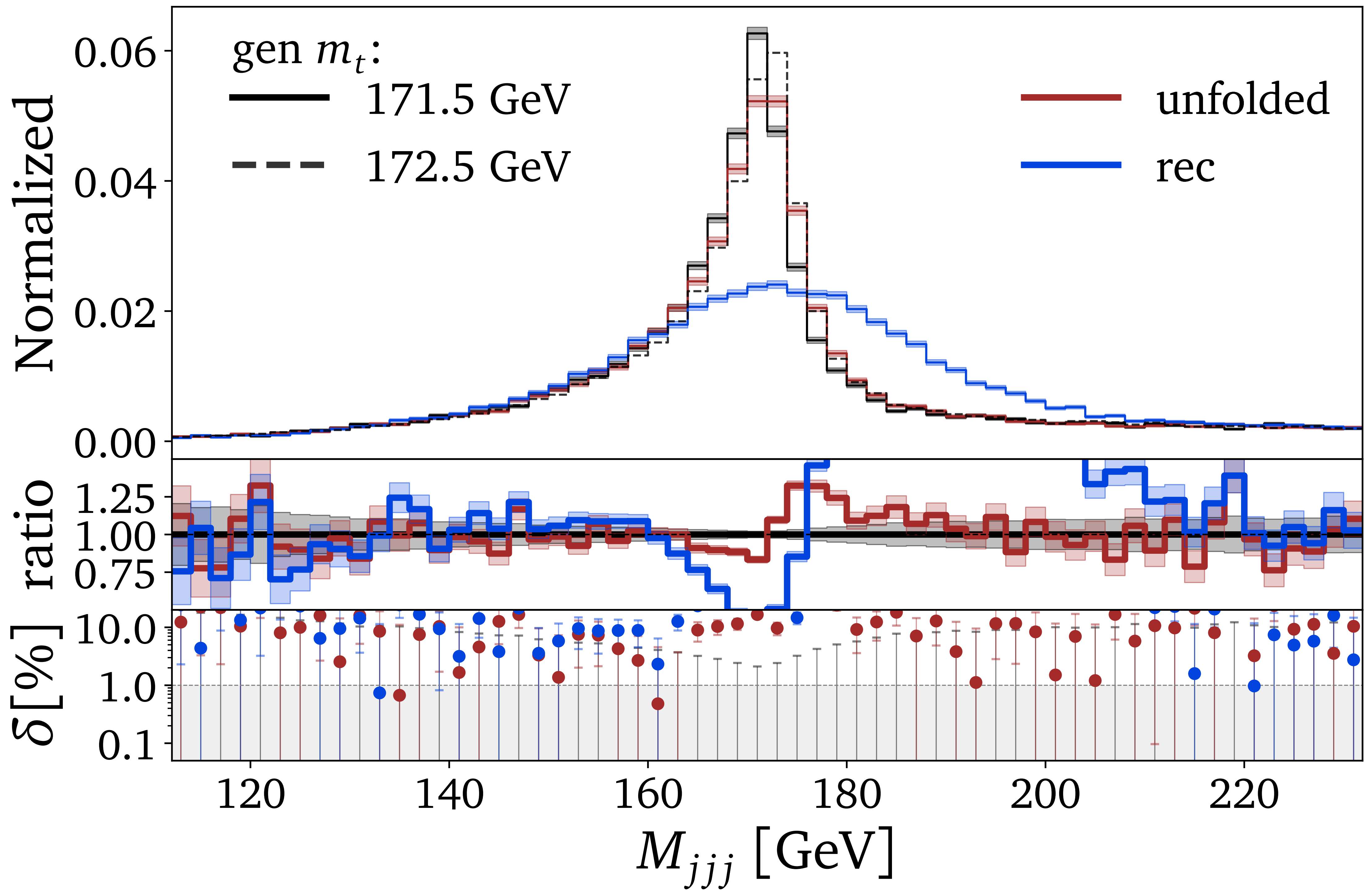

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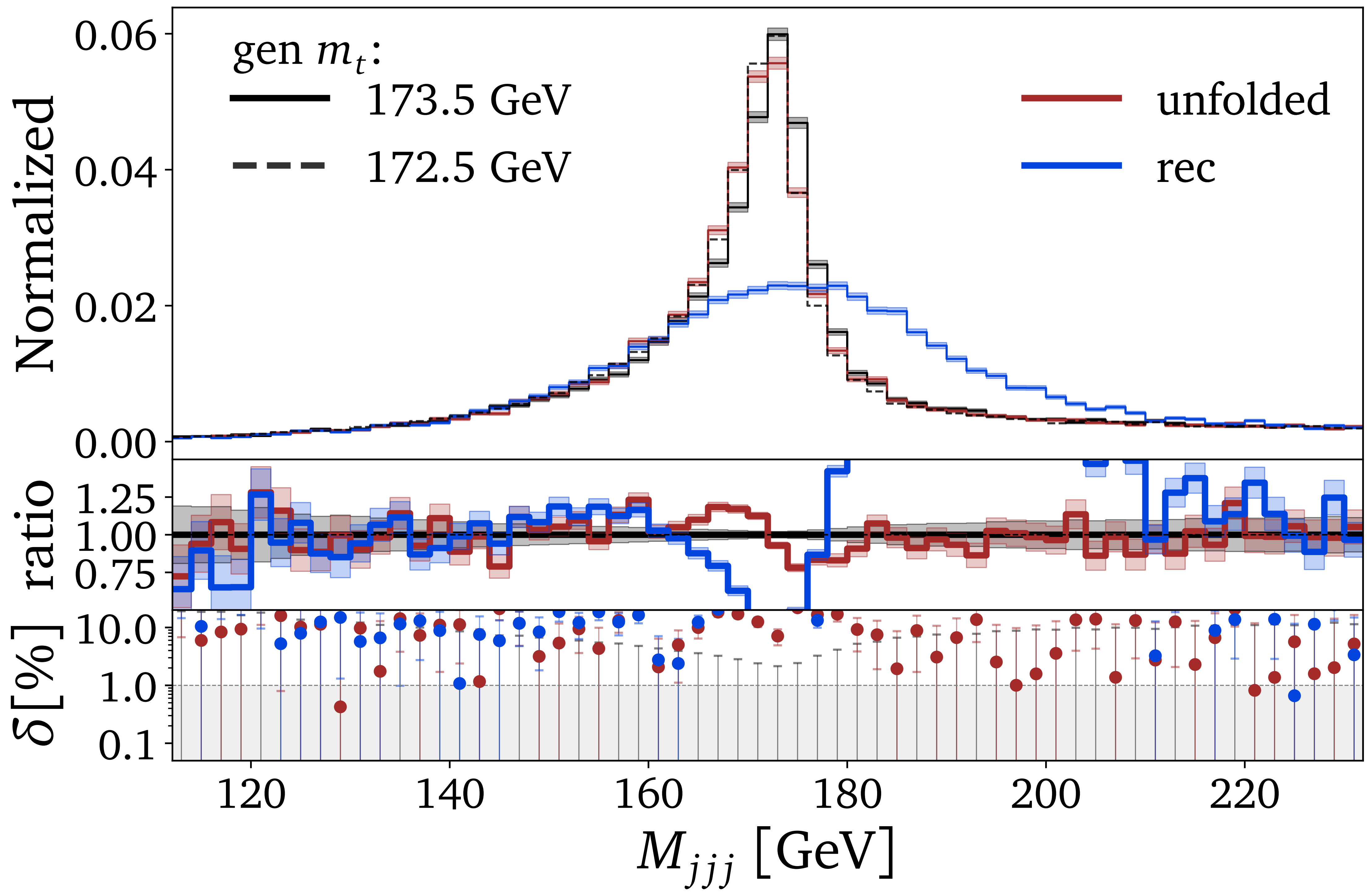


Removing Model-Dependence

$p_{sim}(x_{gen} | m_s)$

$p(x_{reco} | x_{gen})$

$p_{sim}(x_{reco} | m_s)$

correspondance

$p_{data}(x_{reco} | m_d)$

$p_{model}(x_{gen} | x_{reco}, m_s)$

$p_{unfold}(x_{gen} | m_s, m_d)$

Removing Model-Dependence

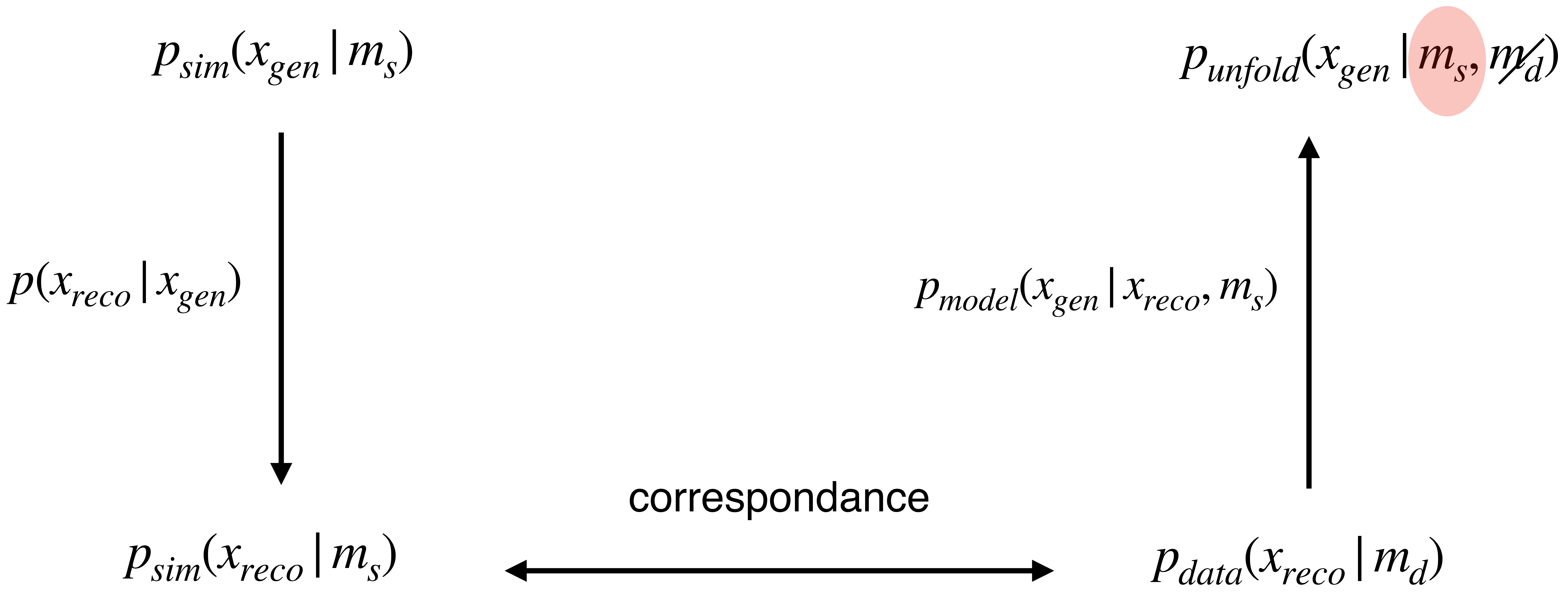
$p_{sim}(x_{gen} | m_s)$ → $p(x_{reco} | x_{gen})$ → $p_{sim}(x_{reco} | m_s)$

$p_{sim}(x_{reco} | m_s)$ ⟷ correspondance ⟷ $p_{data}(x_{reco} | m_d)$

$p_{data}(x_{reco} | m_d)$ → $p_{model}(x_{gen} | x_{reco}, m_s)$ → $p_{unfold}(x_{gen} | m_s, \cancel{m_d})$

→ **Solution: Strengthen m_d dependence, but how?**

Removing Model-Dependence



→ **Solution: Strengthen m_d dependence, but how?**

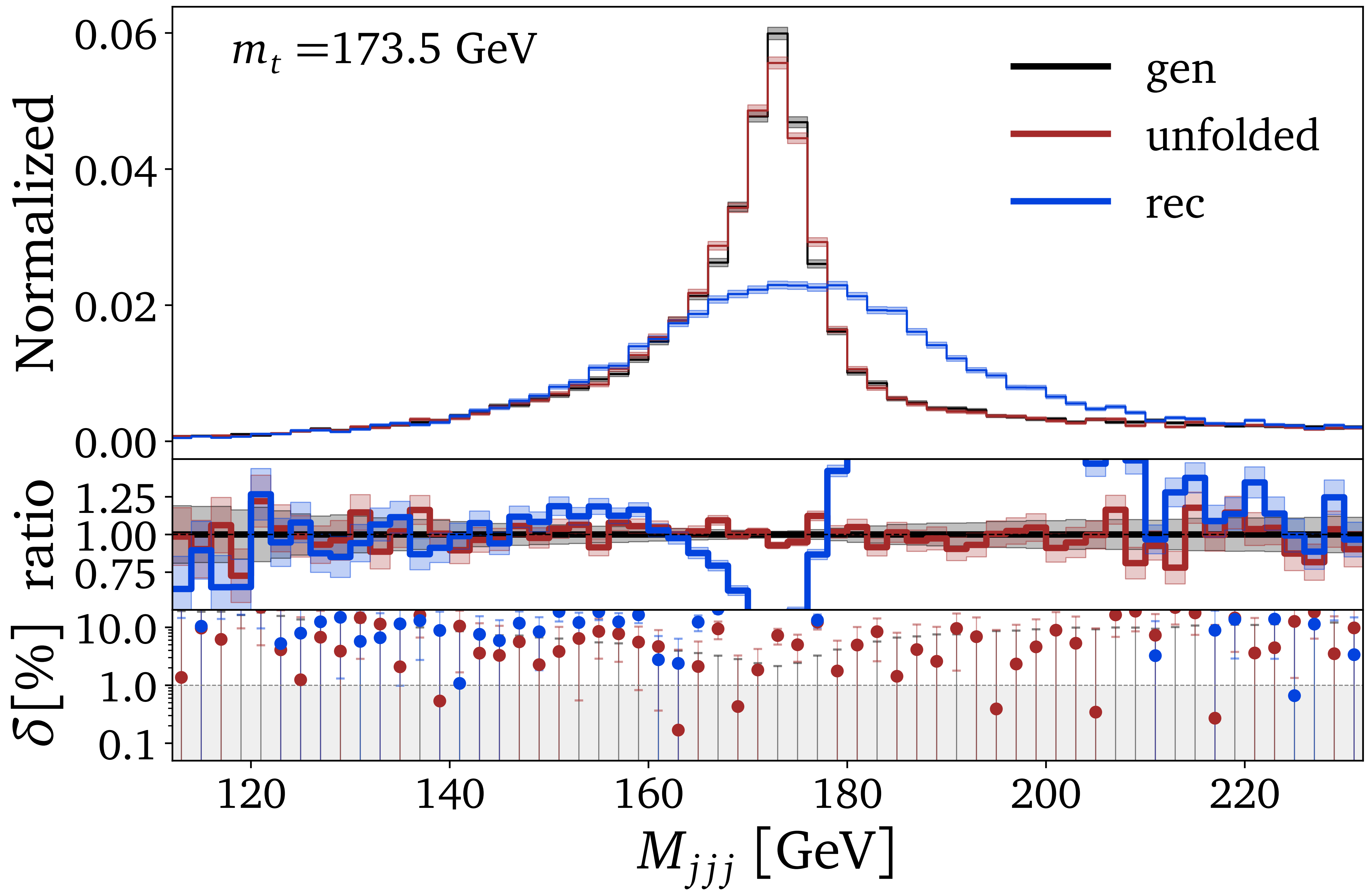
1. Augment training data with simulation from different top masses
2. Estimate batch-wise $m_d \approx$ weighted-median(M_{jjj}^{batch}) on reco level

Removing Model-Dependence!

Train with full CMS simulation with
$m_t = [172.5$ GeV, 169.5 GeV, 175.5 GeV$]$

Test by unfolding simulation with
$m_t = 171.5$ GeV & 173.5 GeV

Unfolded distribution of triple jet mass within
$\mathcal{O}(1\%)$ of truth gen level **without** bias



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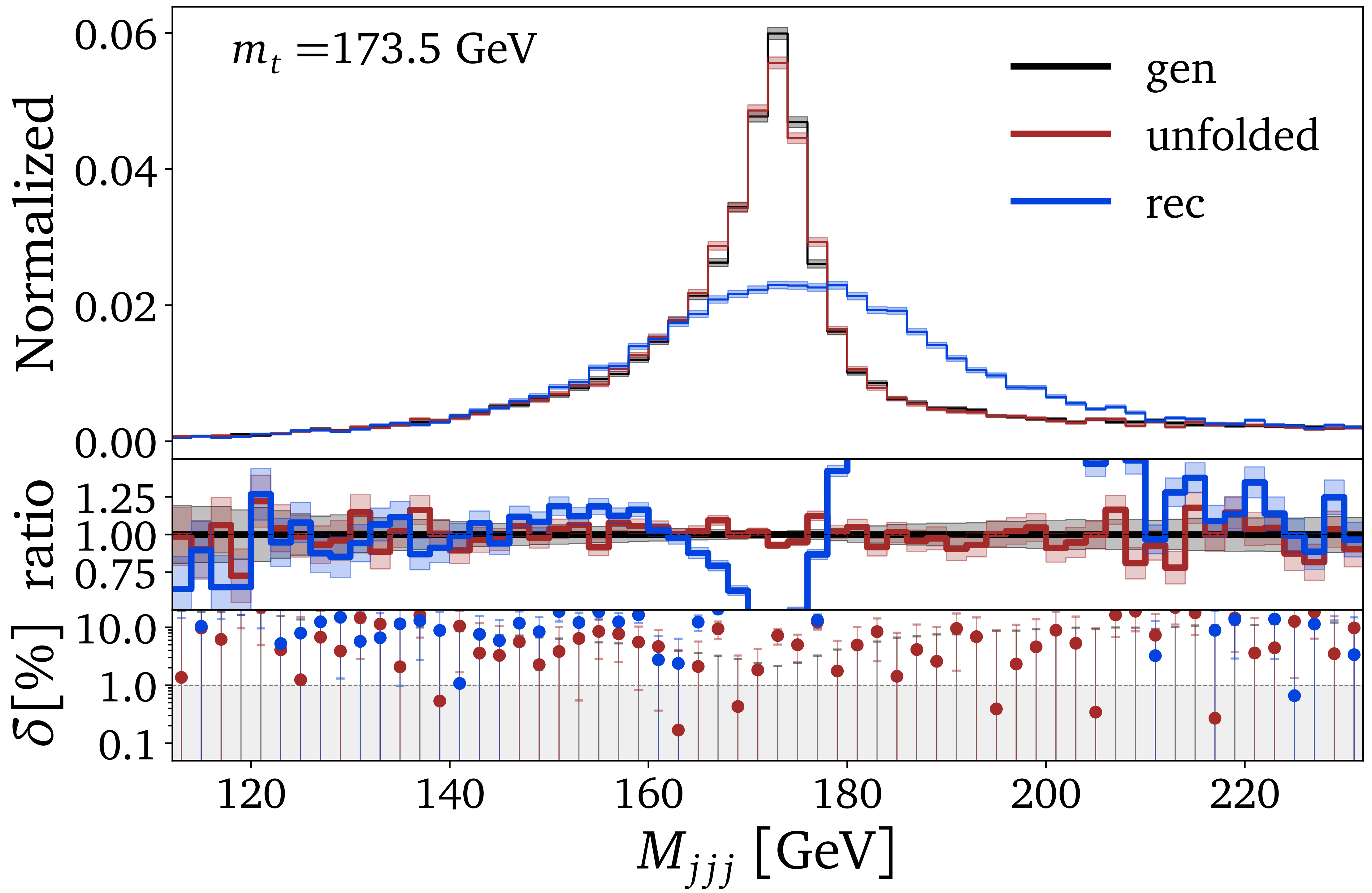


ML task becomes much harder

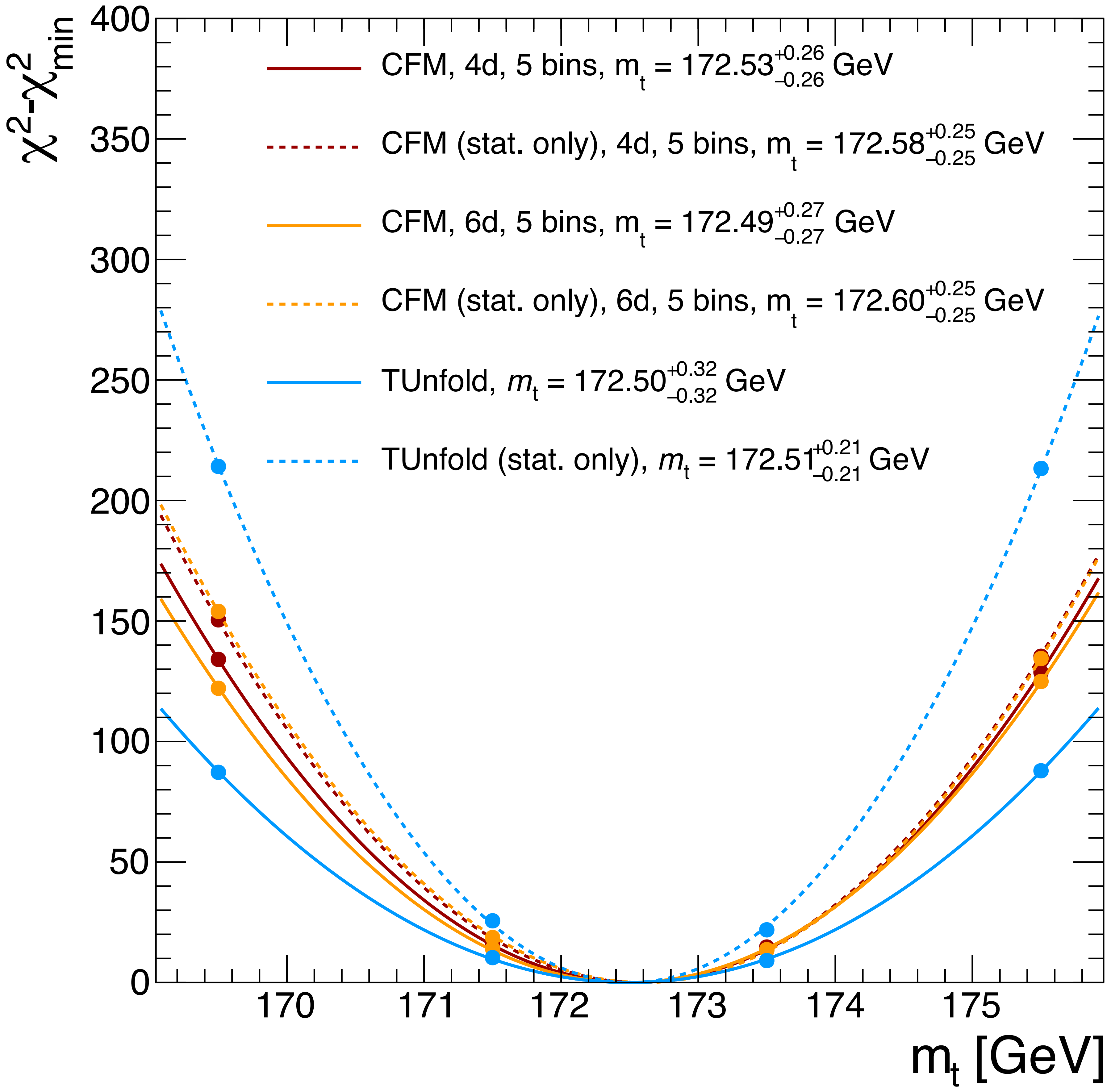
Mass Measurement

For a fixed top mass:

Choose subset of test data of 41000 reco level events

Unfolded 1000 bootstrapped replicas

Estimate covariance matrix and mean by 1000 different unfolded distributions



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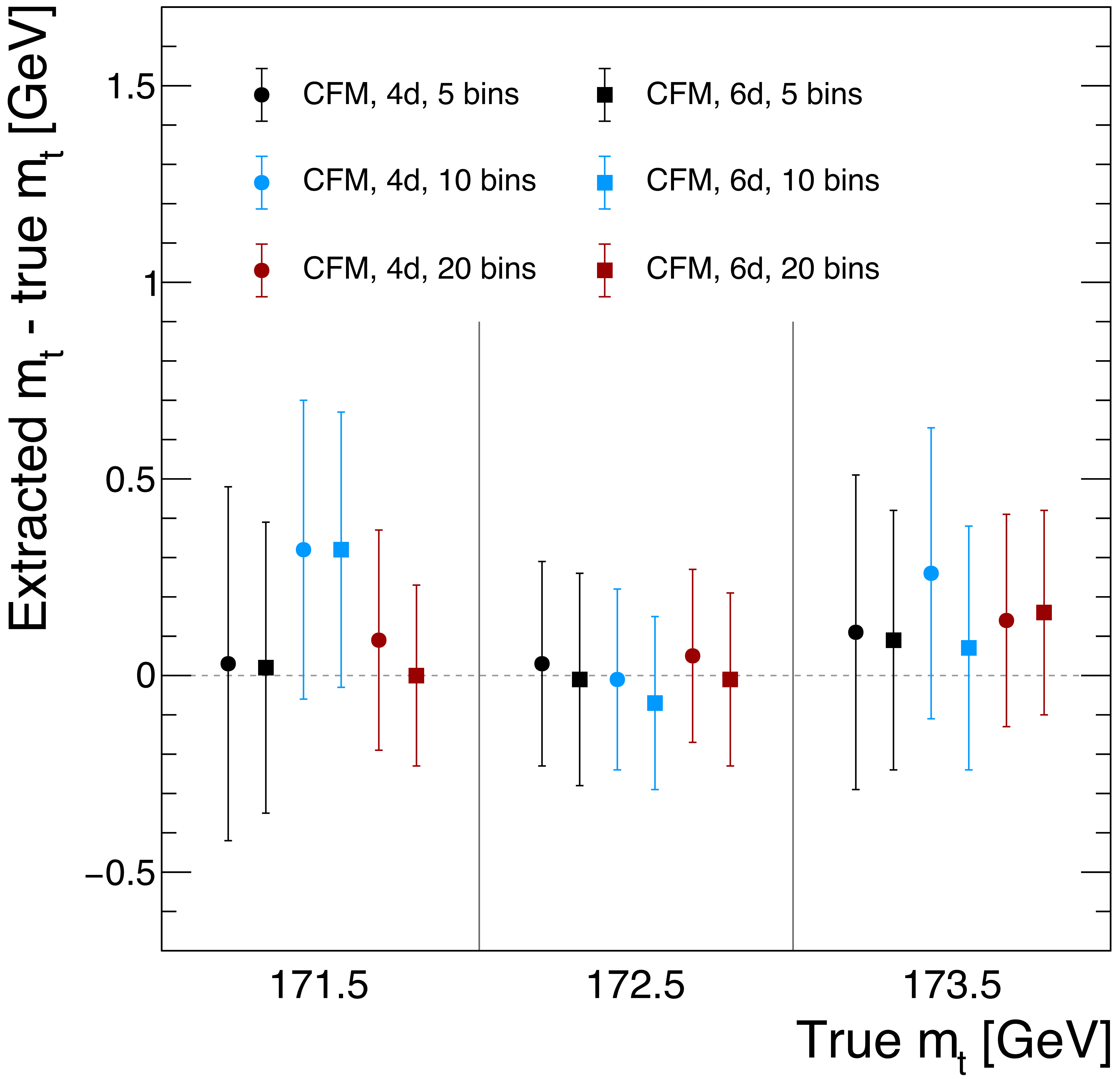

→ Reliably unfold triple jet mass without bias

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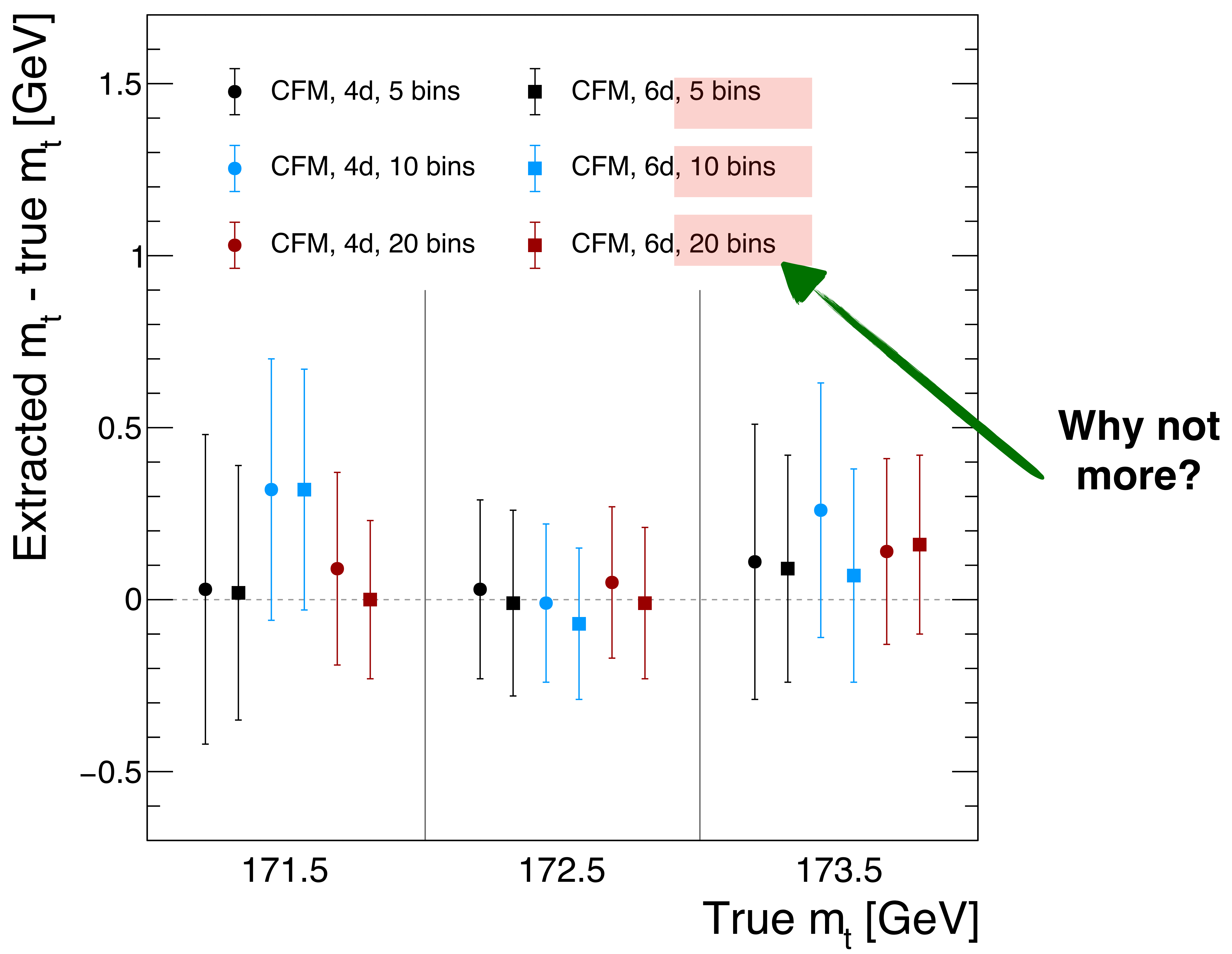

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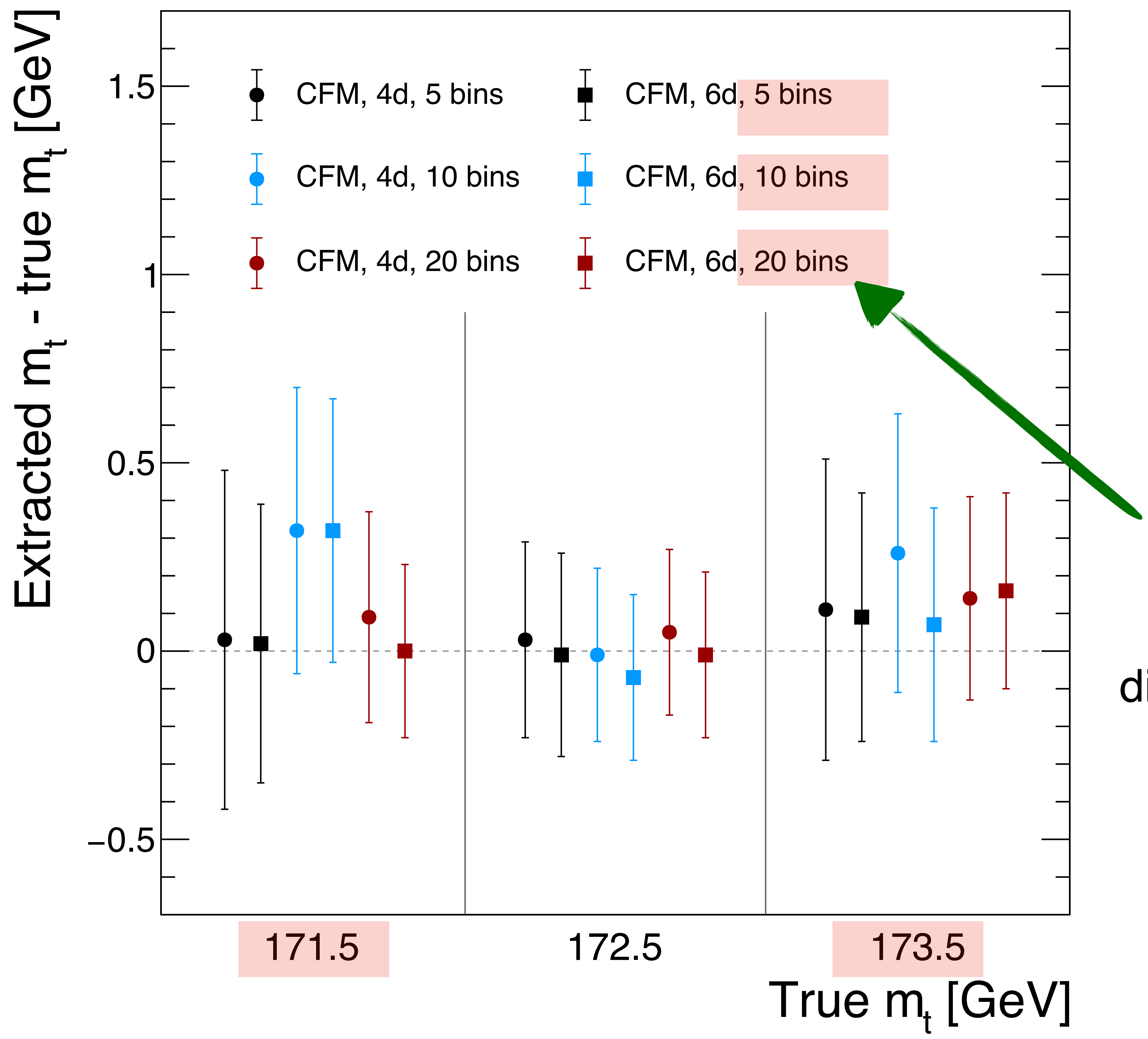
Unfolded 1000 bootstrapped replicas

Estimate covariance matrix and mean by 1000 different unfolded distributions



Why not more?

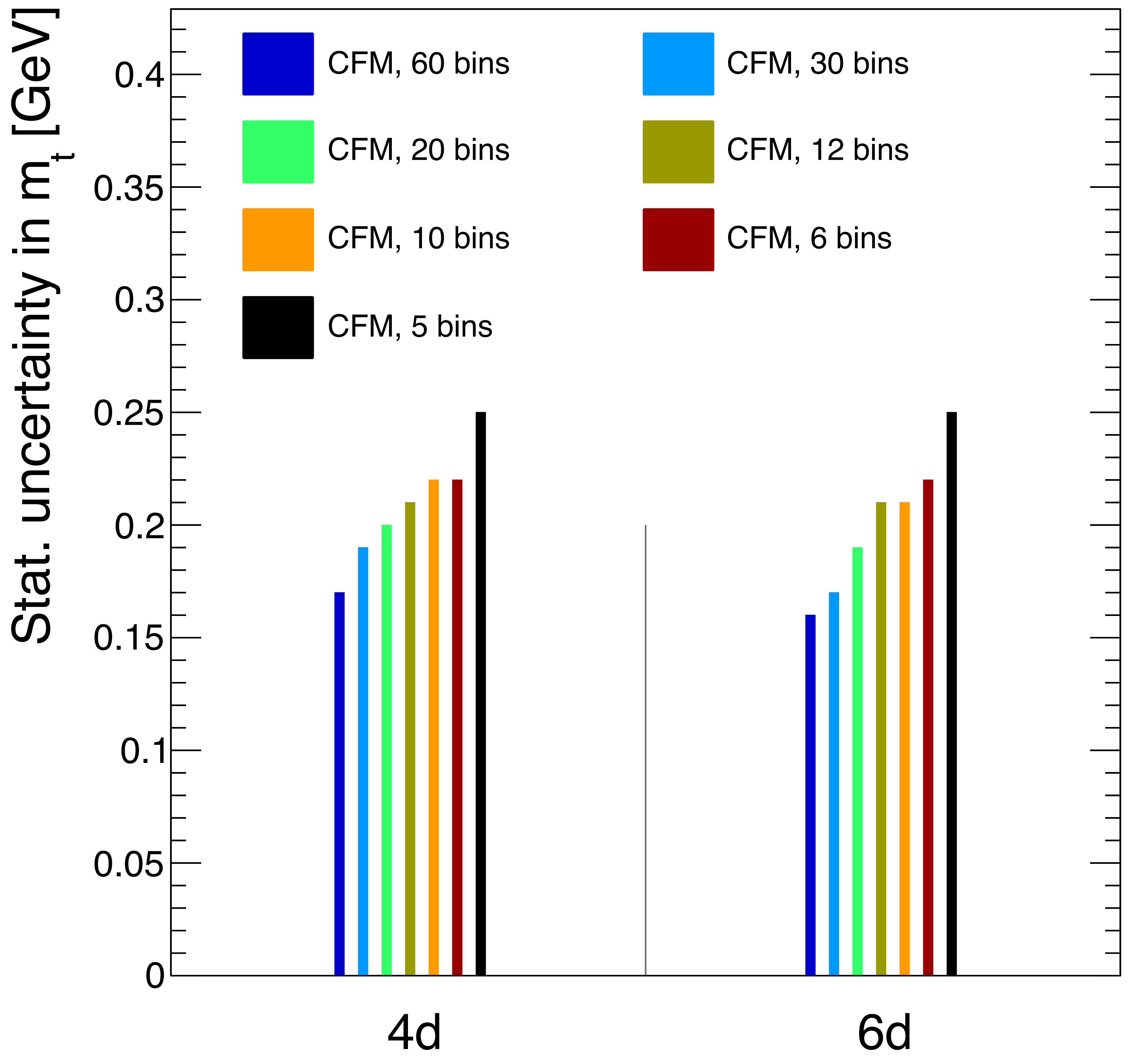
Limited by discrete grid of available m_t simulations

→ Reliably unfold triple jet mass without bias

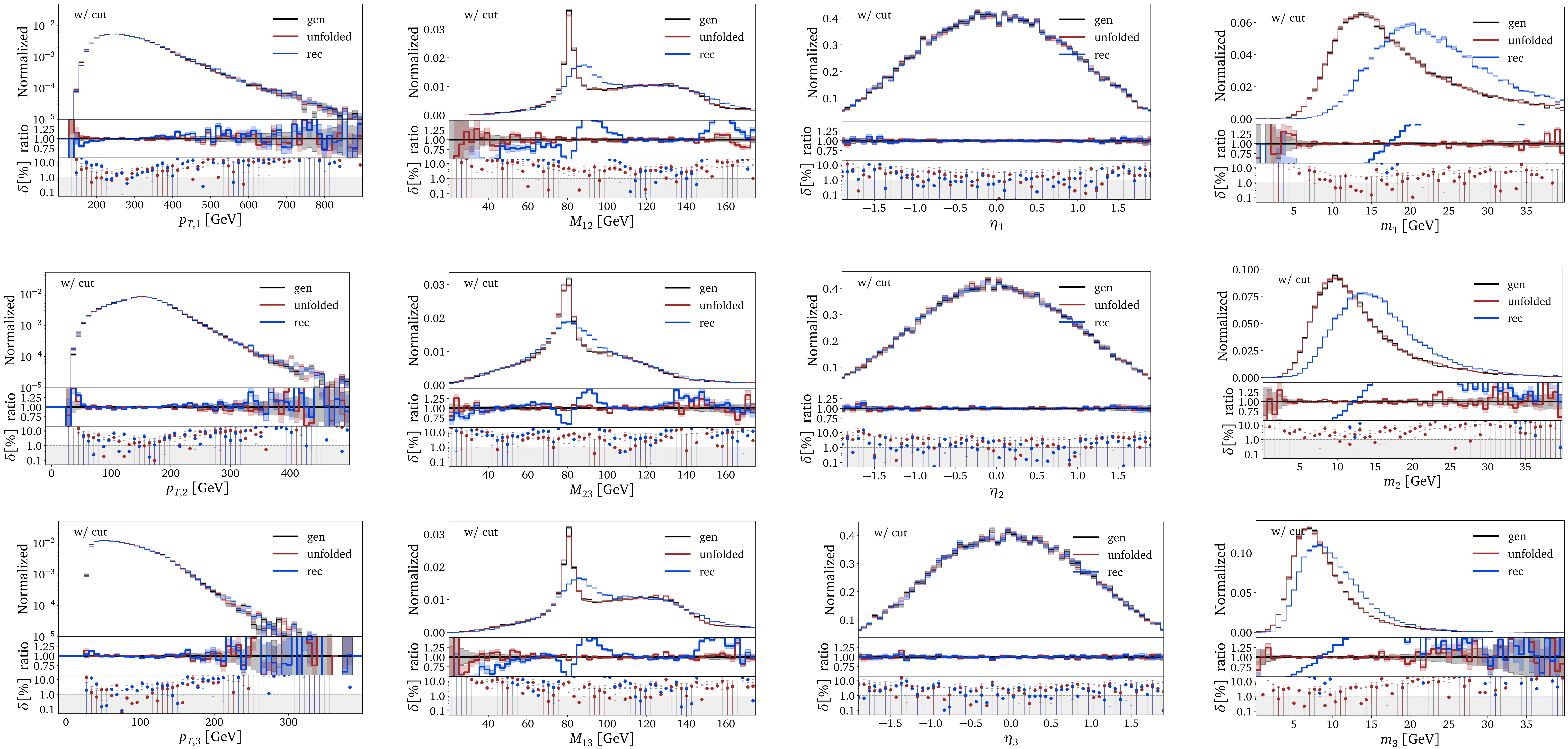
Mass Measurement

For $m_t = 172.5$ GeV, we have a close grid of available simulations (± 1 GeV)

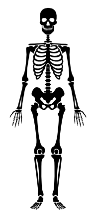
Statistical uncertainty for 60 bins decreases by 36%



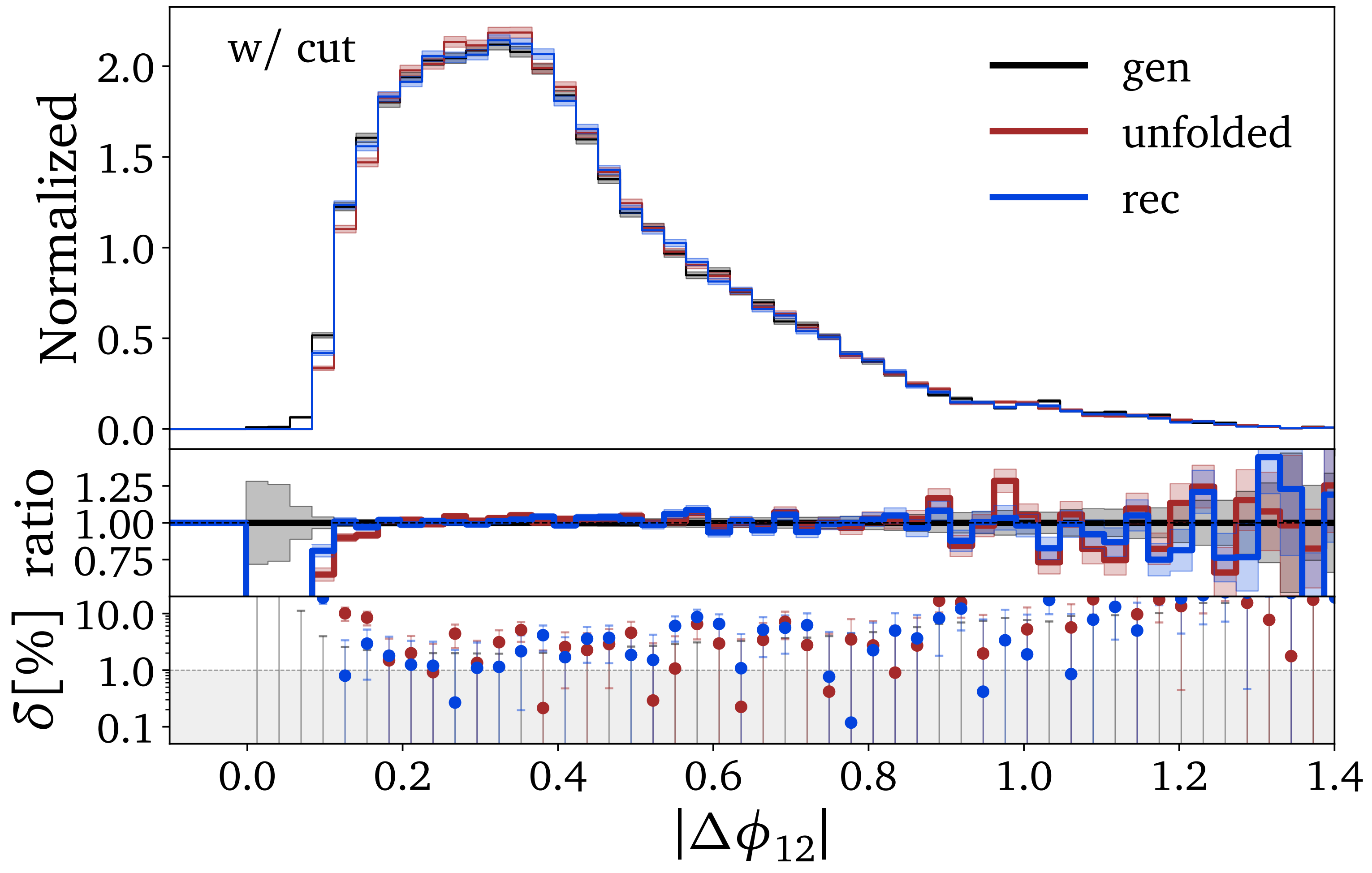
Full Phase Space Unfolding (12d)

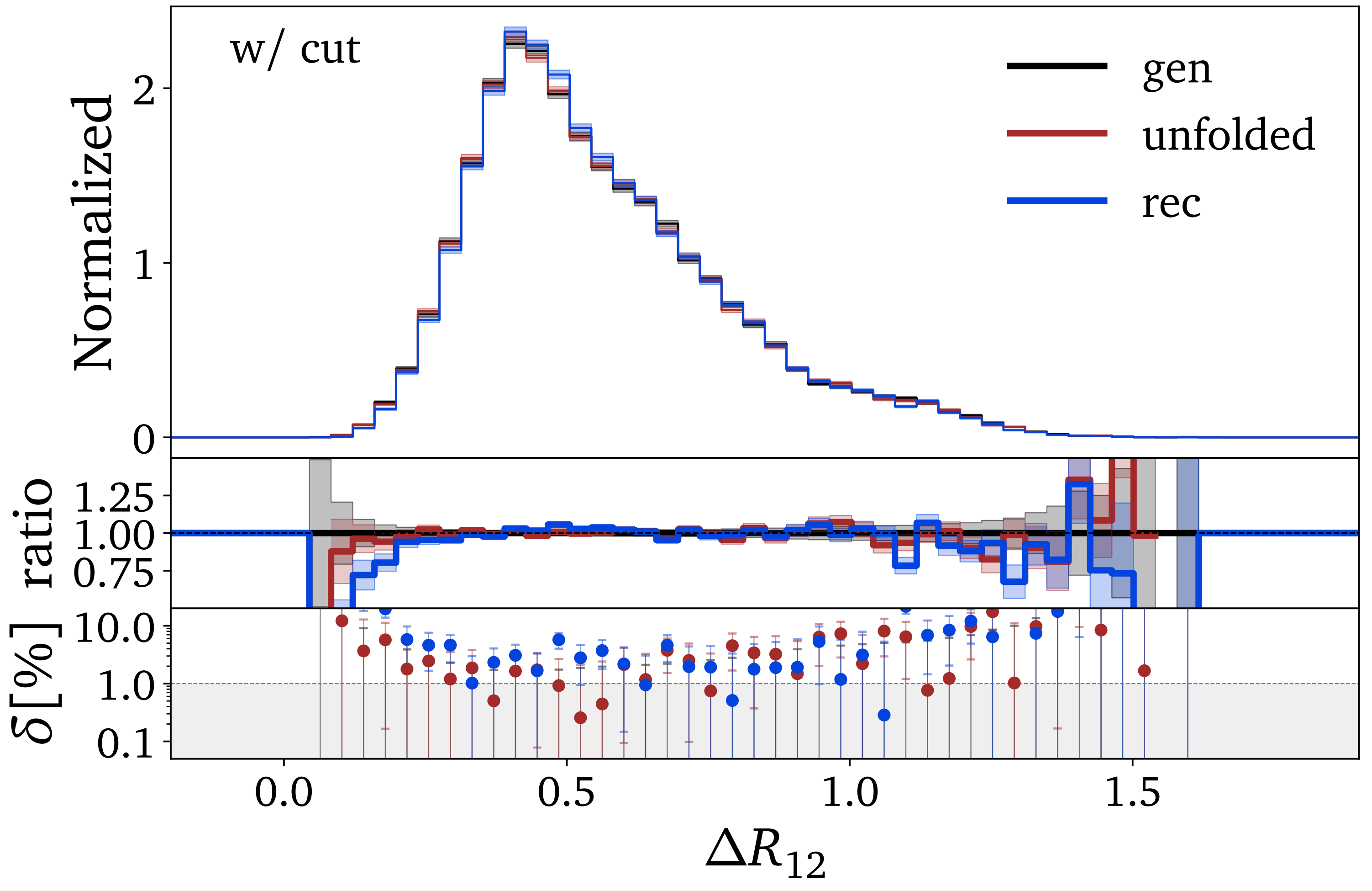


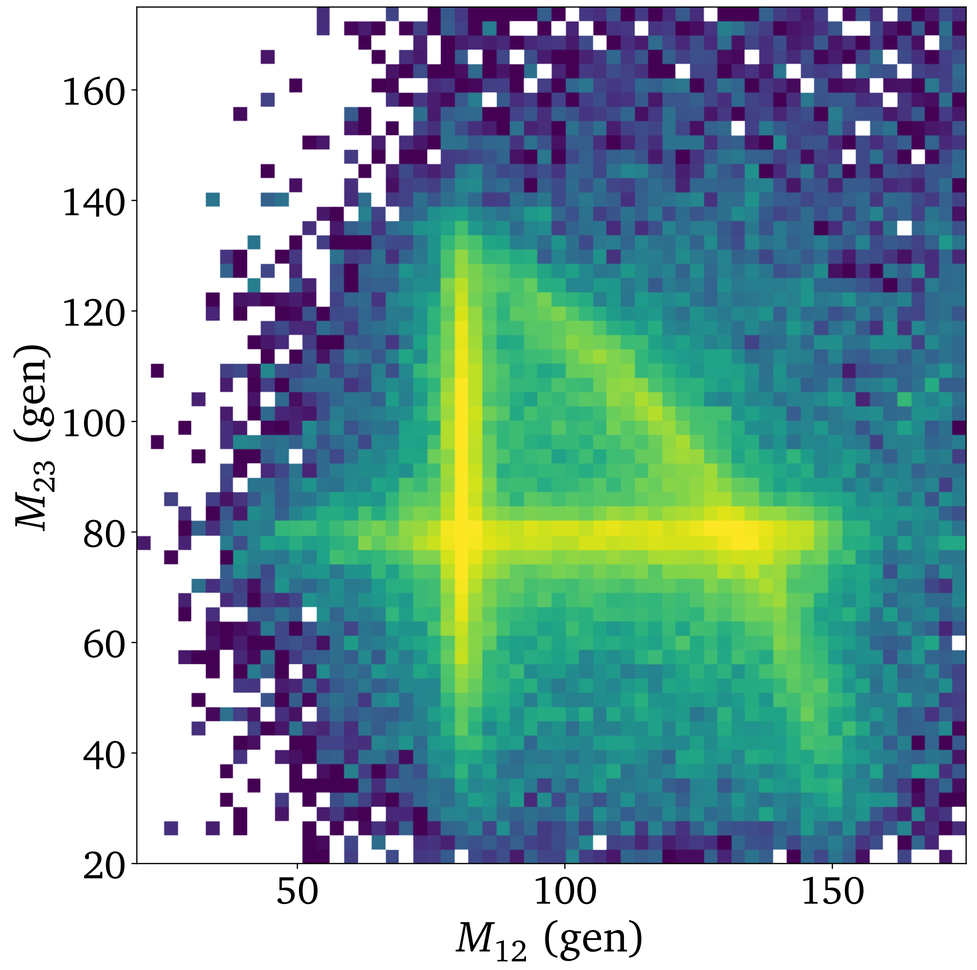
Full Phase Space Unfolding (12d) - Correlations

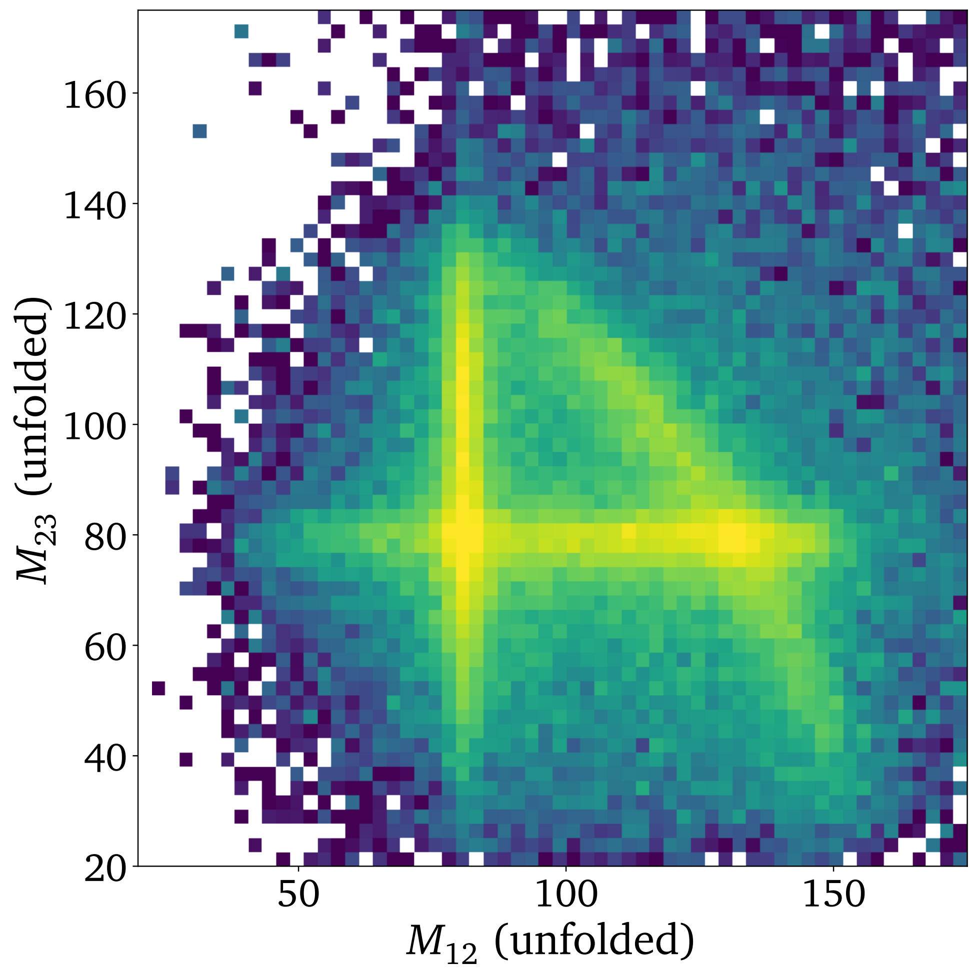


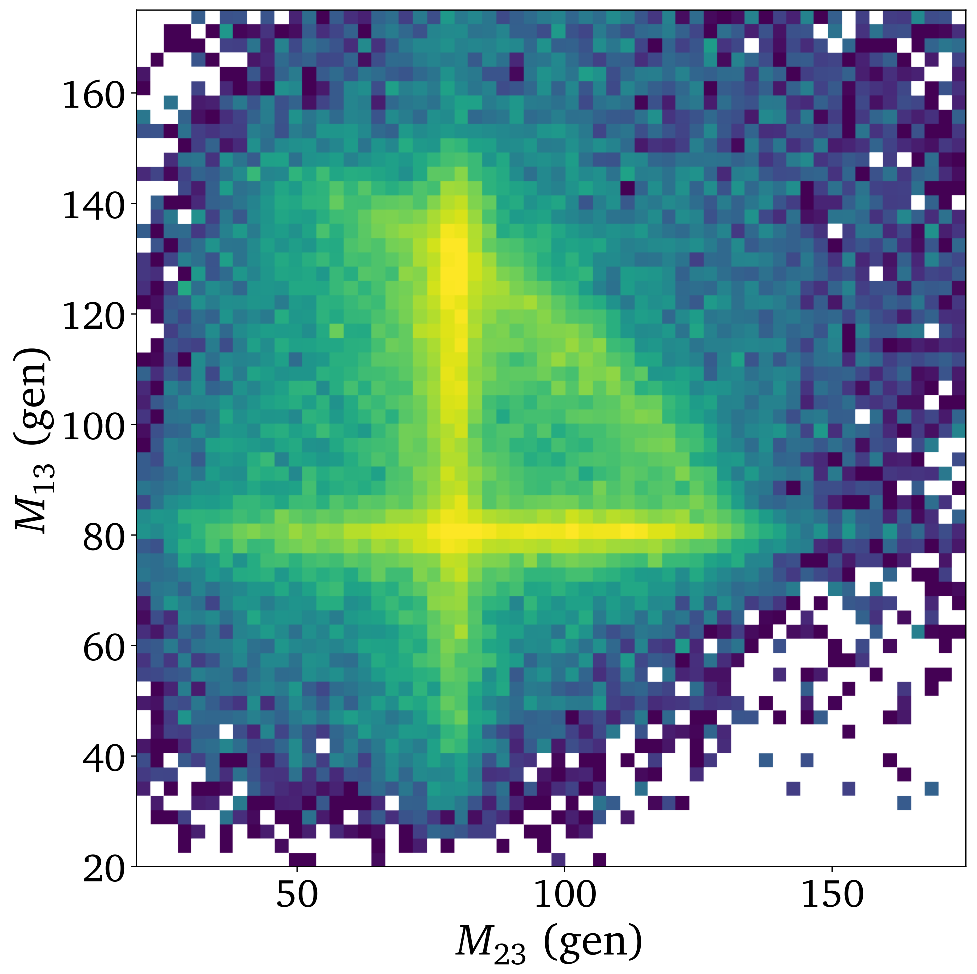
Cut at $|\Delta\phi_{ij}| > 0.1$

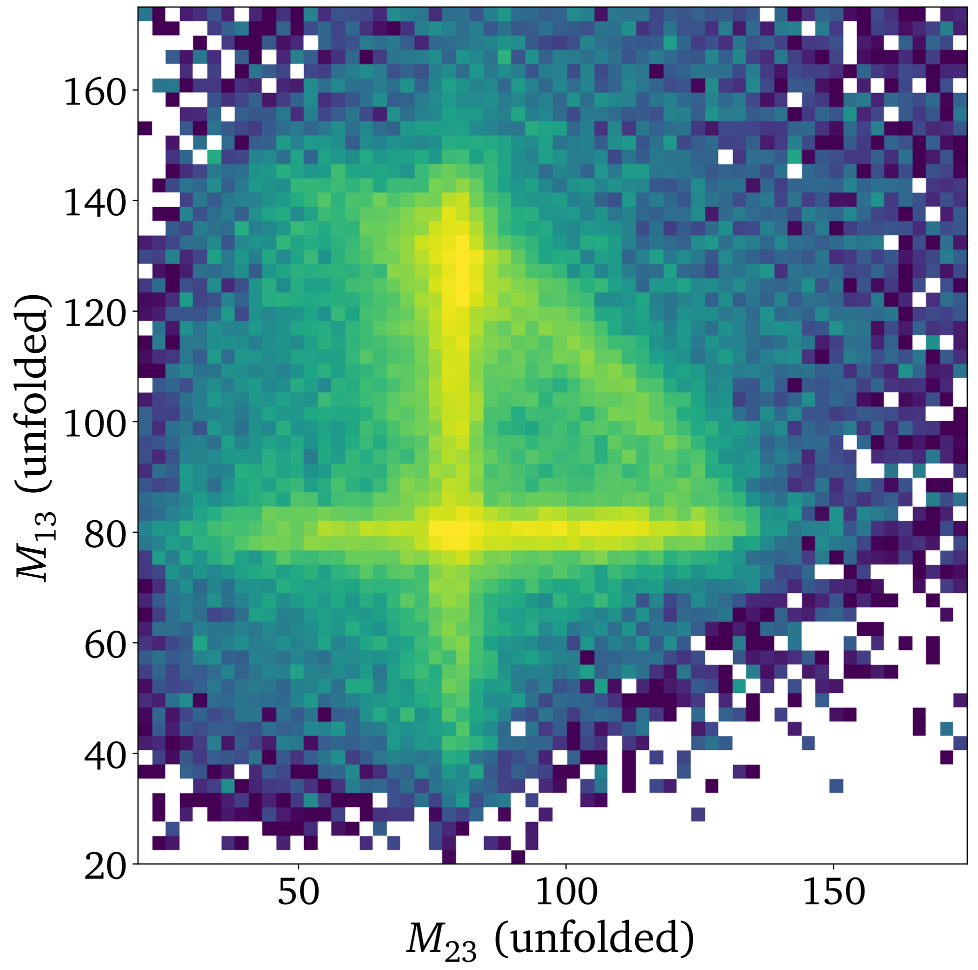












And now what?

Generative machine learning allows for unbinned, high dimensional unfolding

Unbiased networks can enhance precision in e.g. top mass measurement

Crucial step to build generative unfolding into existing LHC analysis

Proposal of analysis pipeline:

1. Event Selection
2. Unfold subset
3. Jet calibration
4. Measure top mass
5. Resimulate
6. Unfold full phasespace

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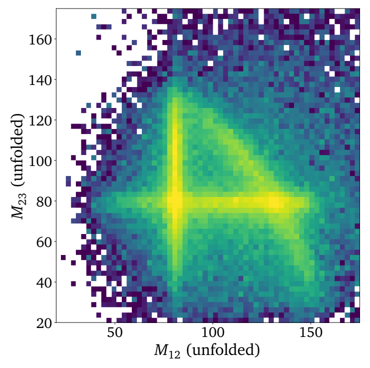

re there any questions?