UNIVERSITÄT HEIDELBERG
ZUKUNFT
SEIT 1386

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20.05.2025

How to Unfold Top Decays

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arXiv:2501.12363

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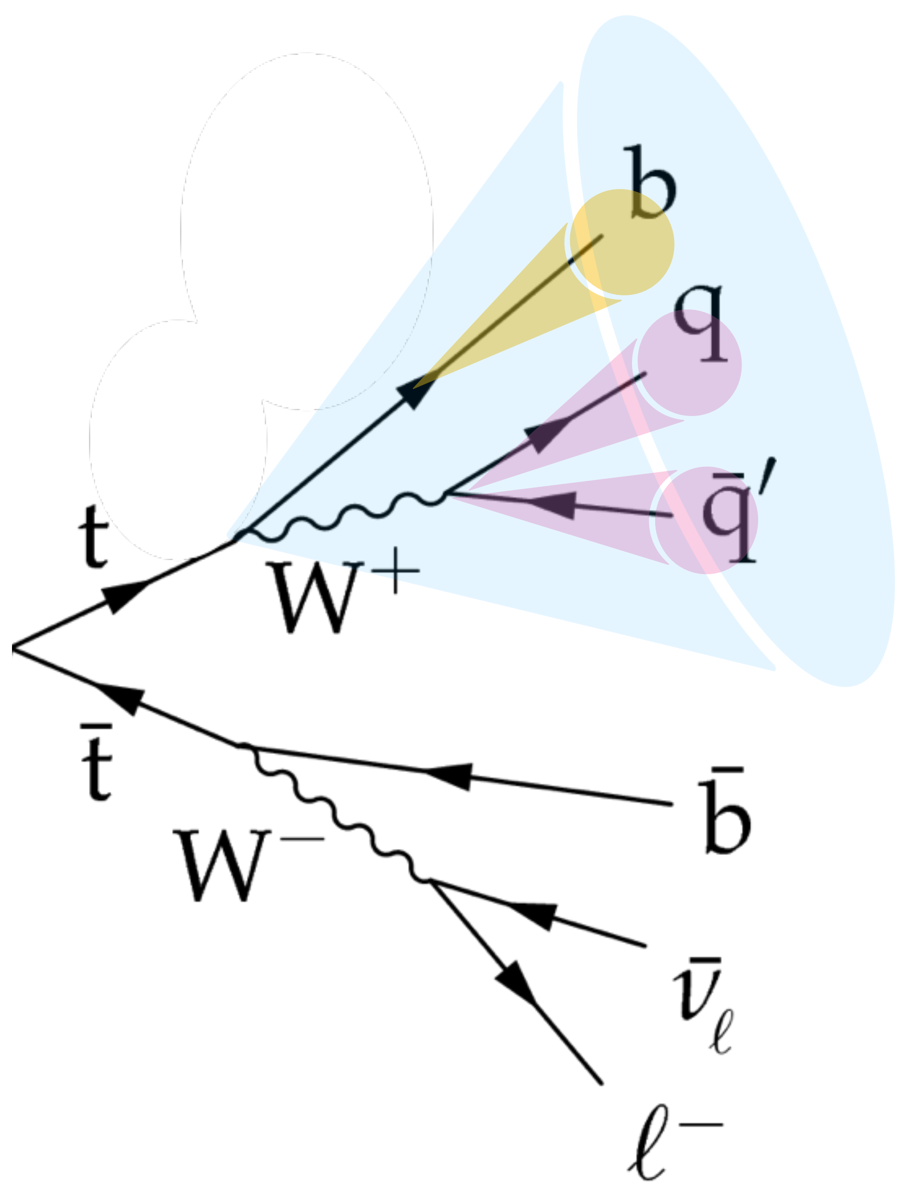
Boosted top decays (in theory)

$p_{T,J} > 750$ GeV



Reconstruct triple jet mass M_{jjj} to measure m_t

Tag side

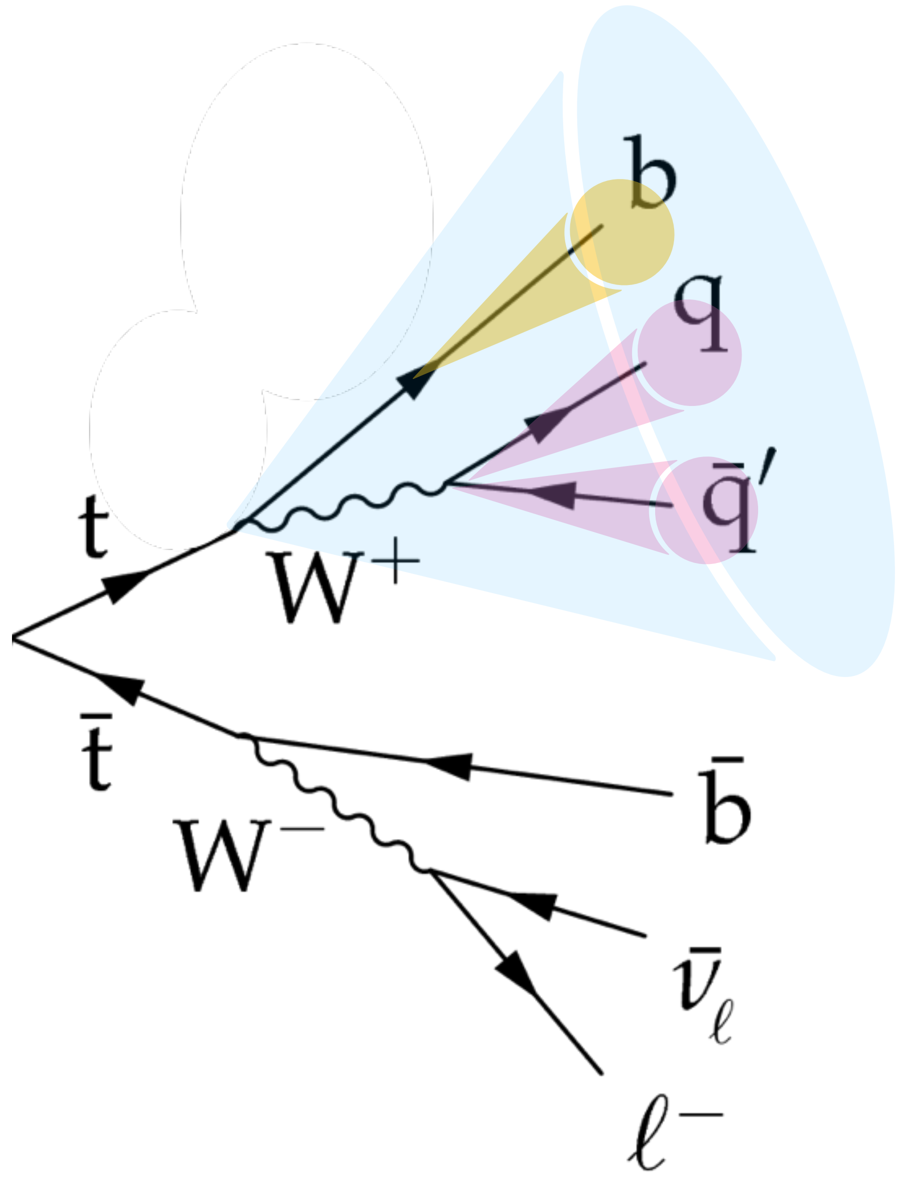
Hadron level factorization theorem for boosted top quark jet mass (arXiv:1708.02586)

→ at high $p_{T,J}$ top mass directly accessible through **unfolded** M_{jjj}

Boosted top decays (in practice)

Not there yet

$p_{T,J} > 750$ GeV



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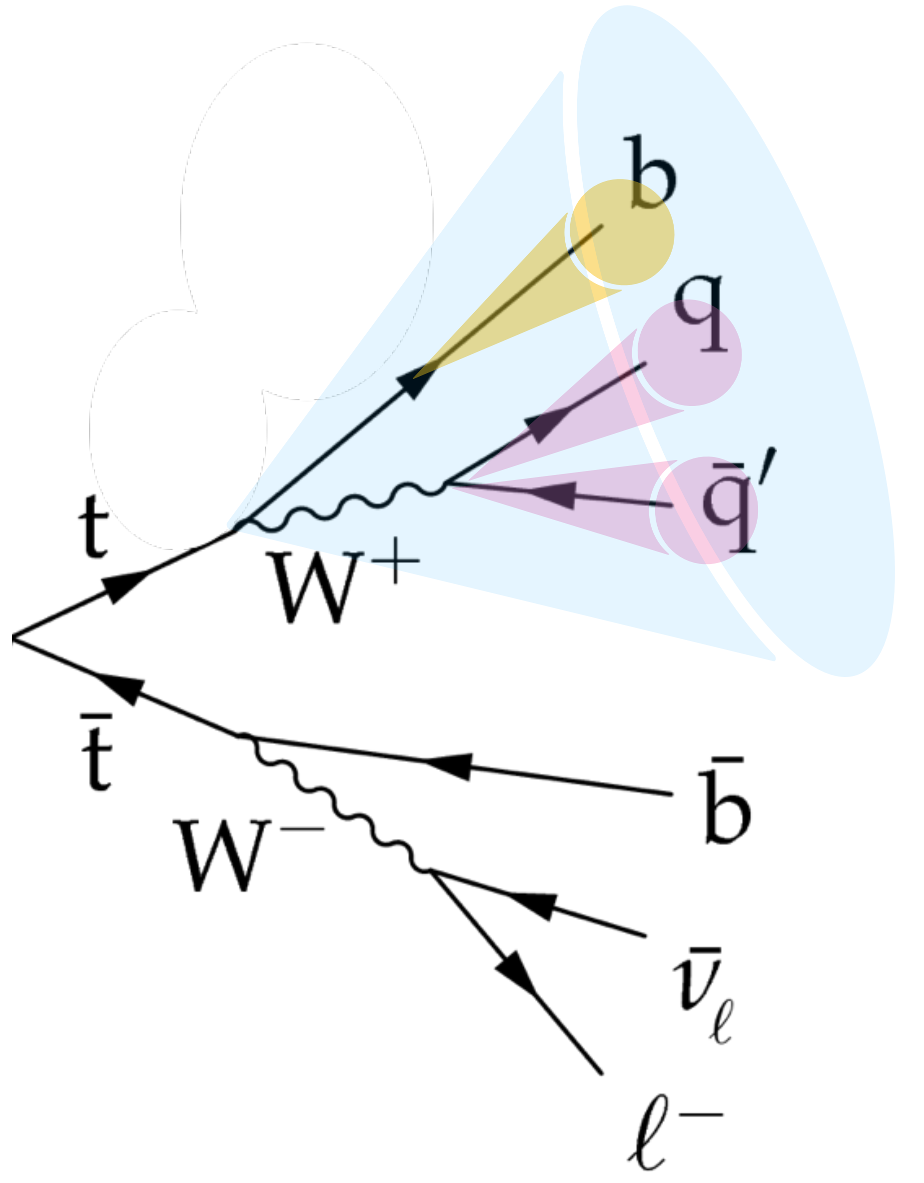
Boosted top decays (in practice)

$p_{T,J} > 400$ GeV



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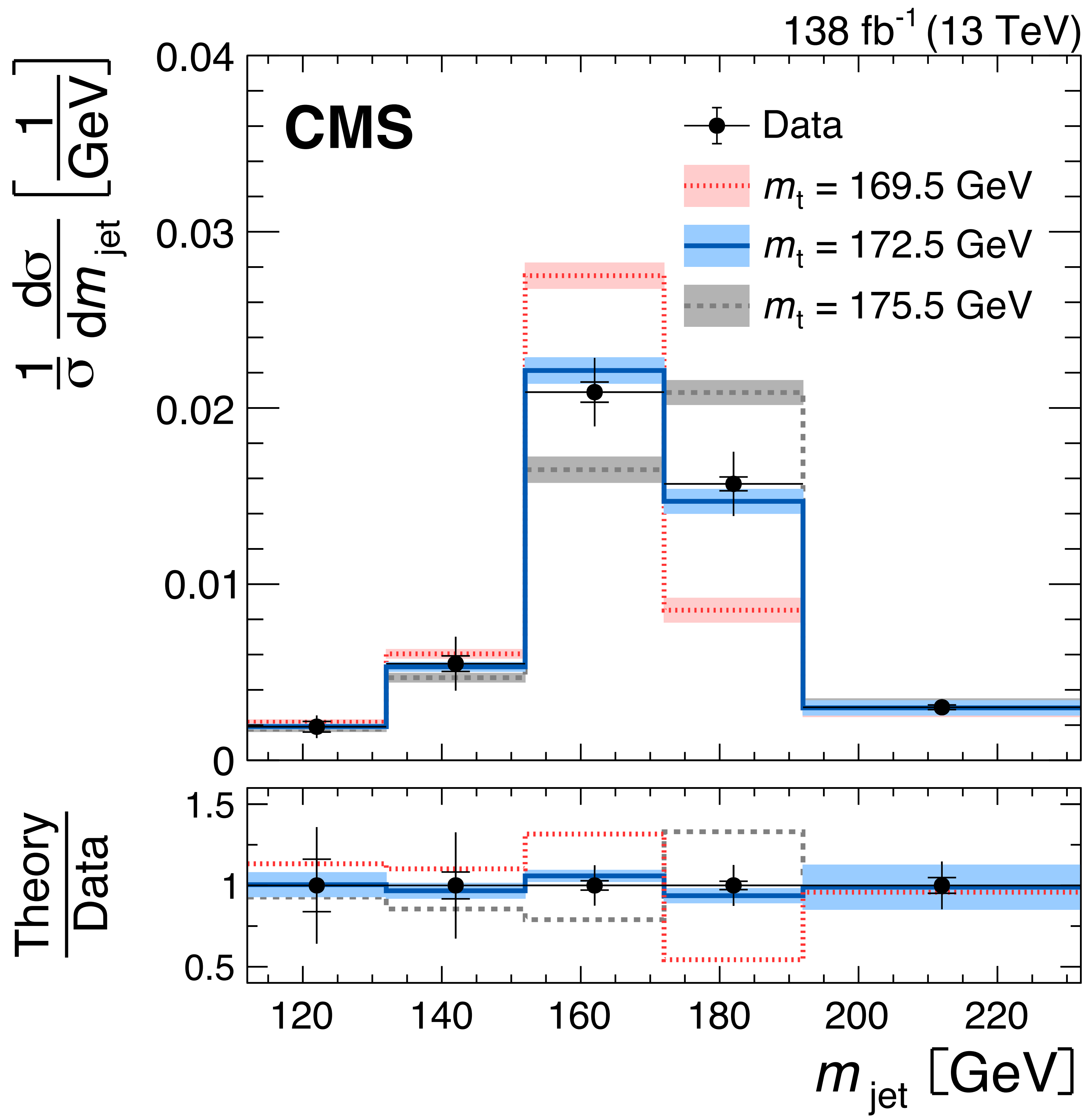
Previously done in CMS with TUnfold (classical binned unfolding algorithm)



CMS **2211.01456**

Boosted top decays (in practice)

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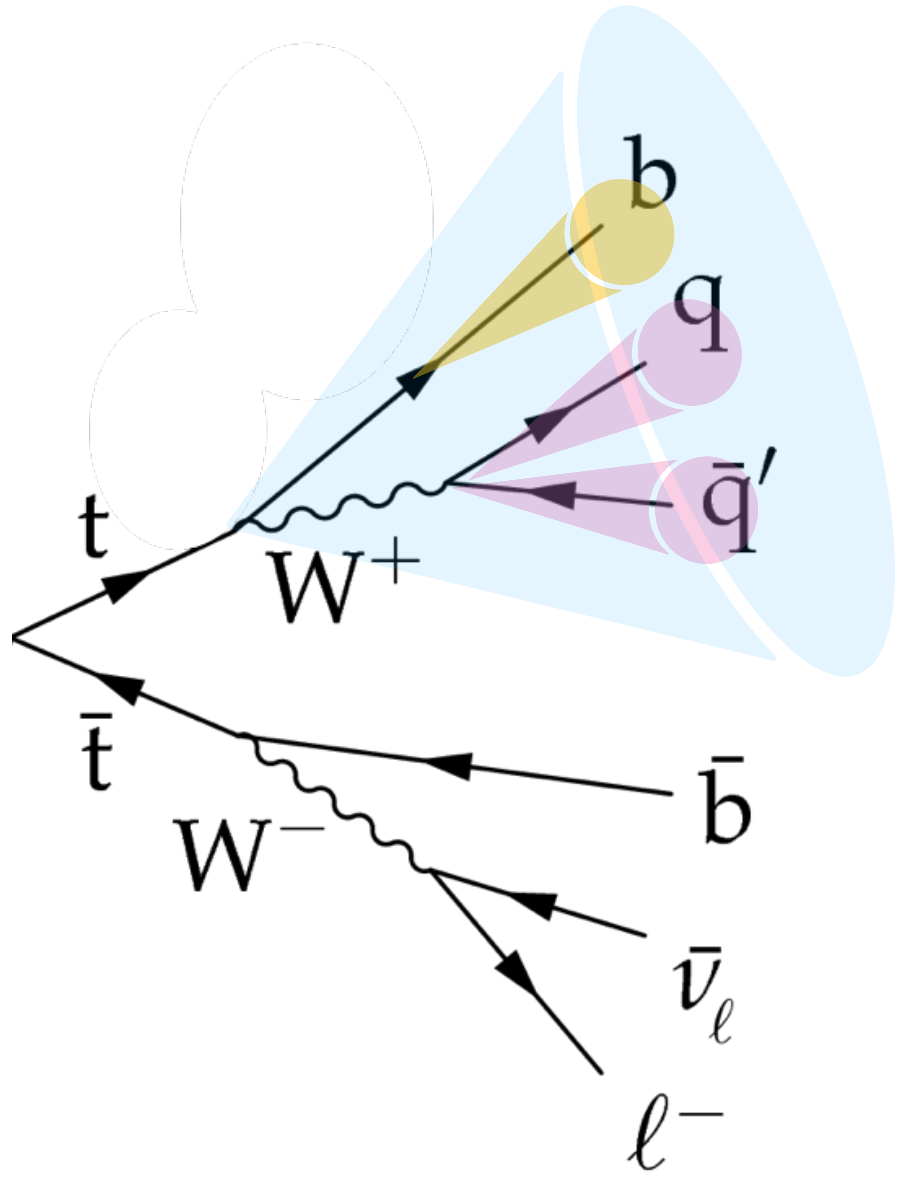

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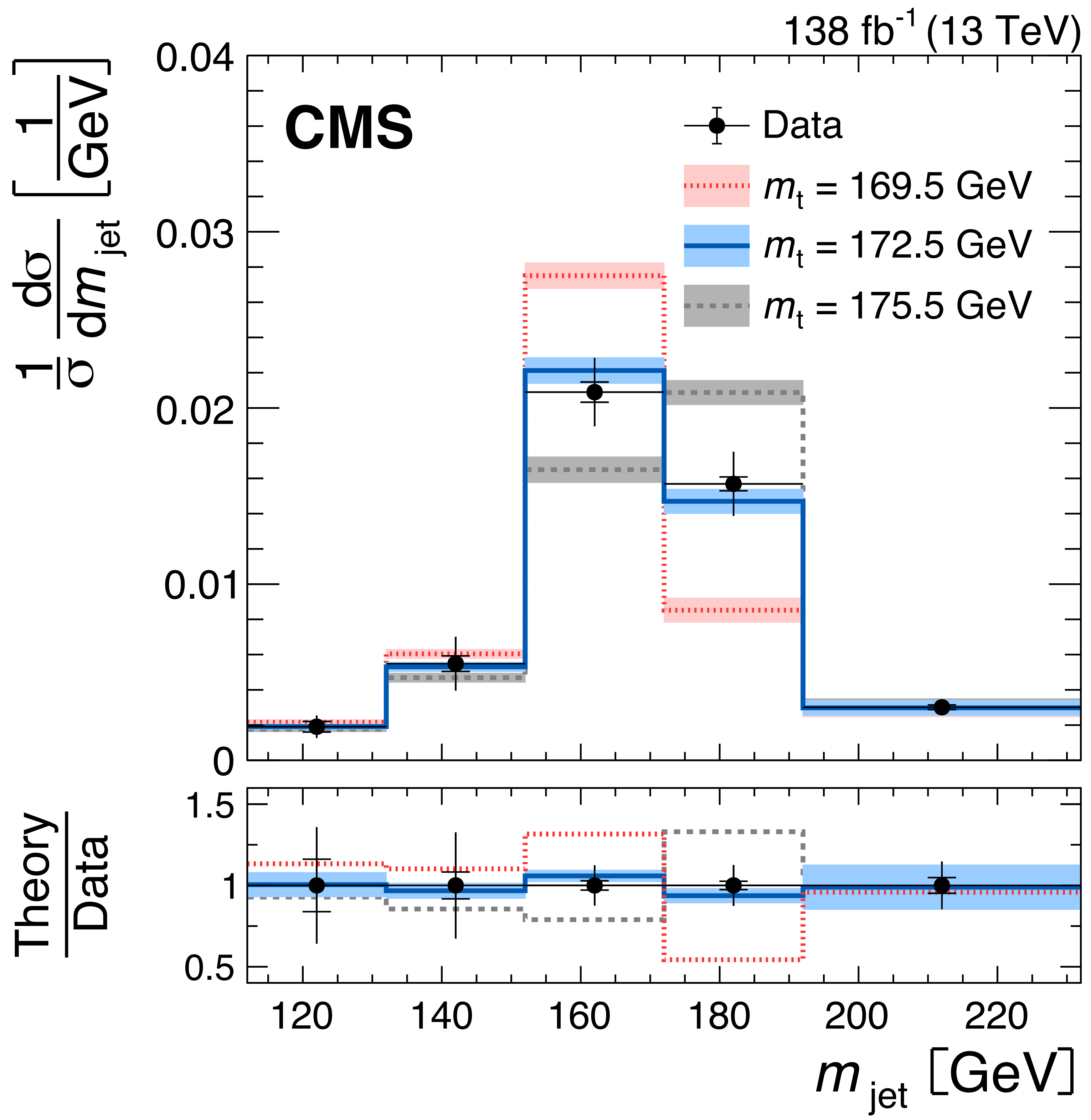


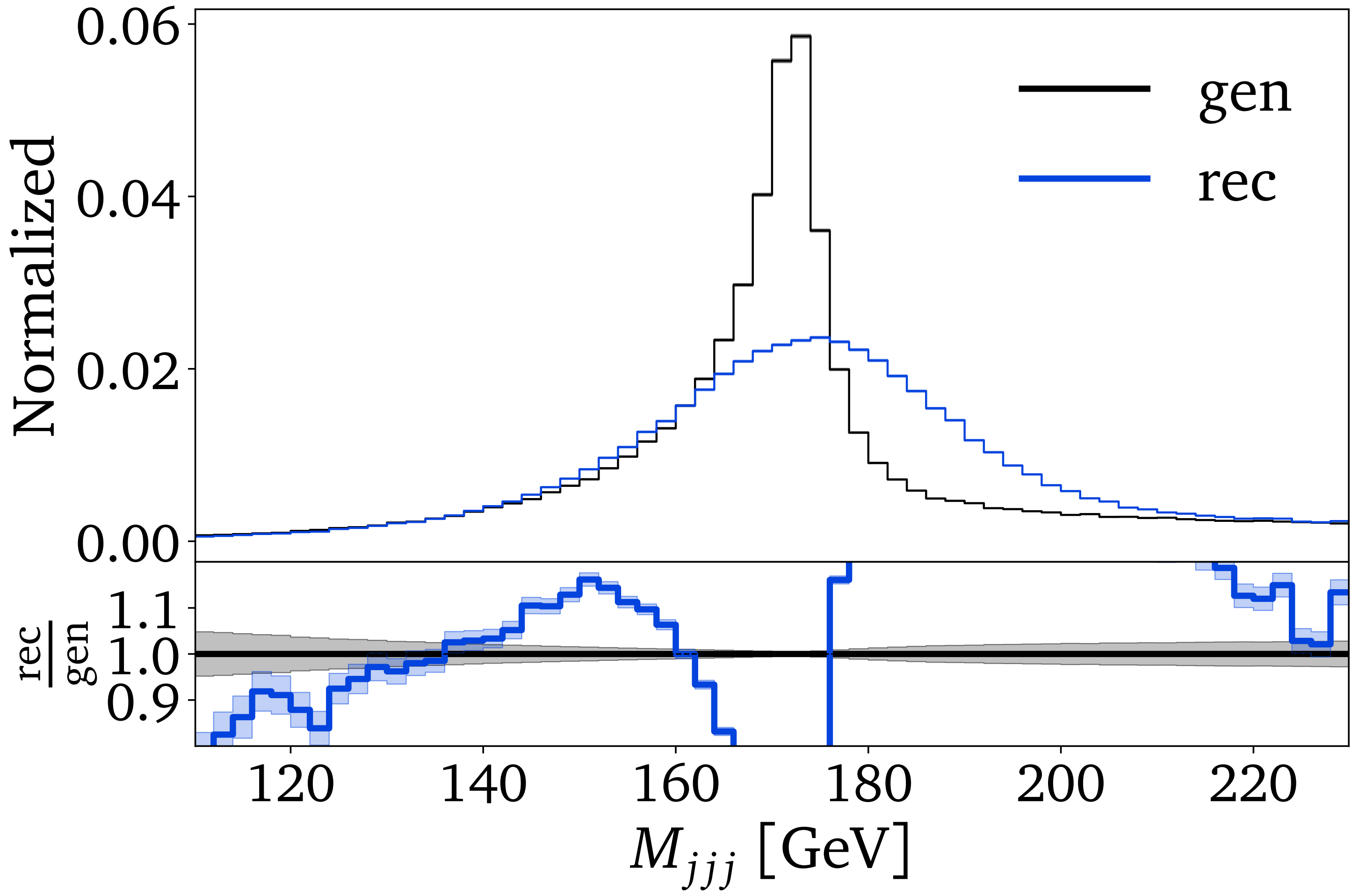
CMS **2211.01456**

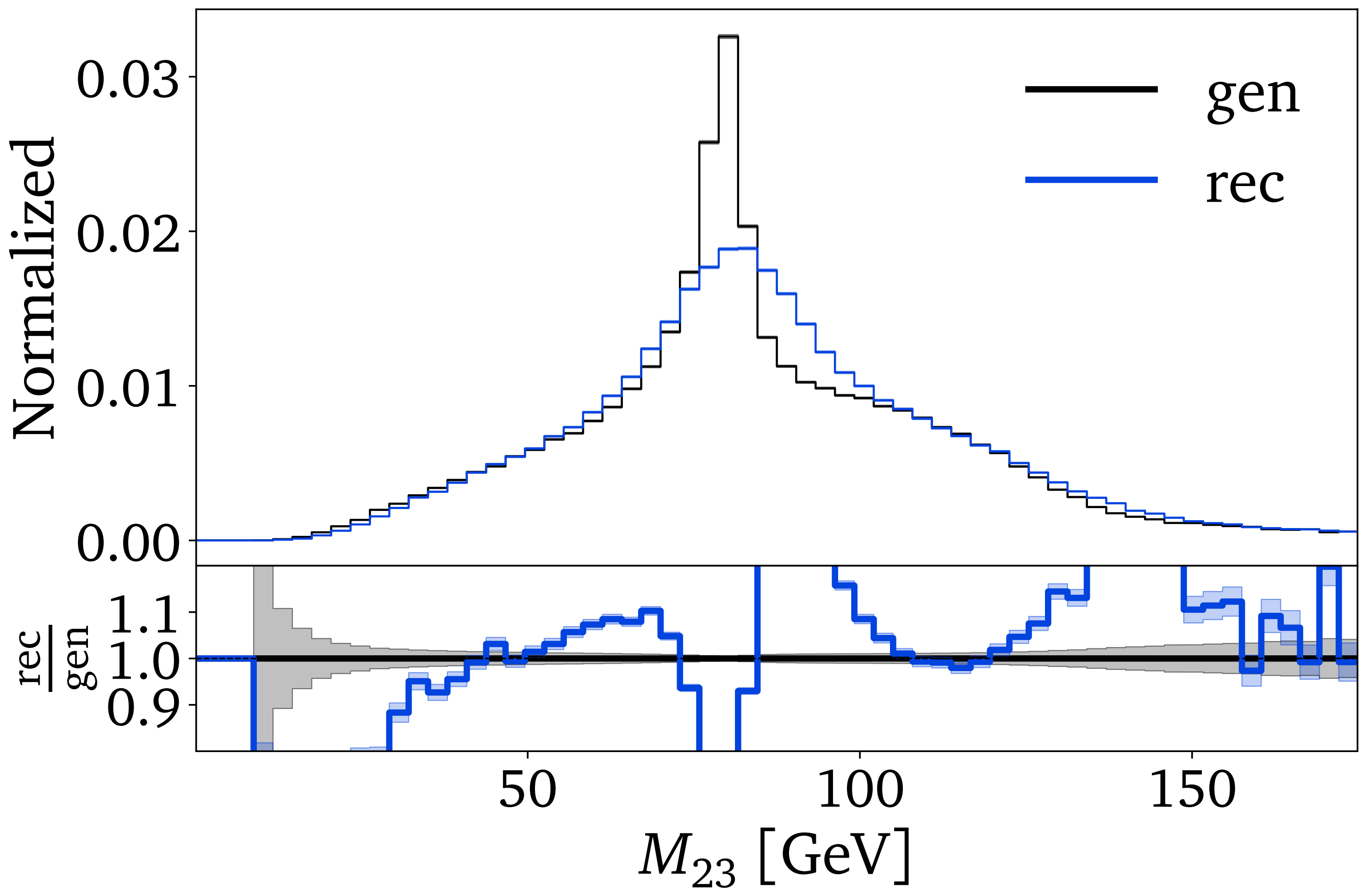
BUT leading uncertainty: choice of m_t in simulation + no access to full phase space

→ **Could generative unfolding help?**

Challenging aspects of top - unfolding

1. Mulitresonant phase space





Challenging aspects of top - unfolding

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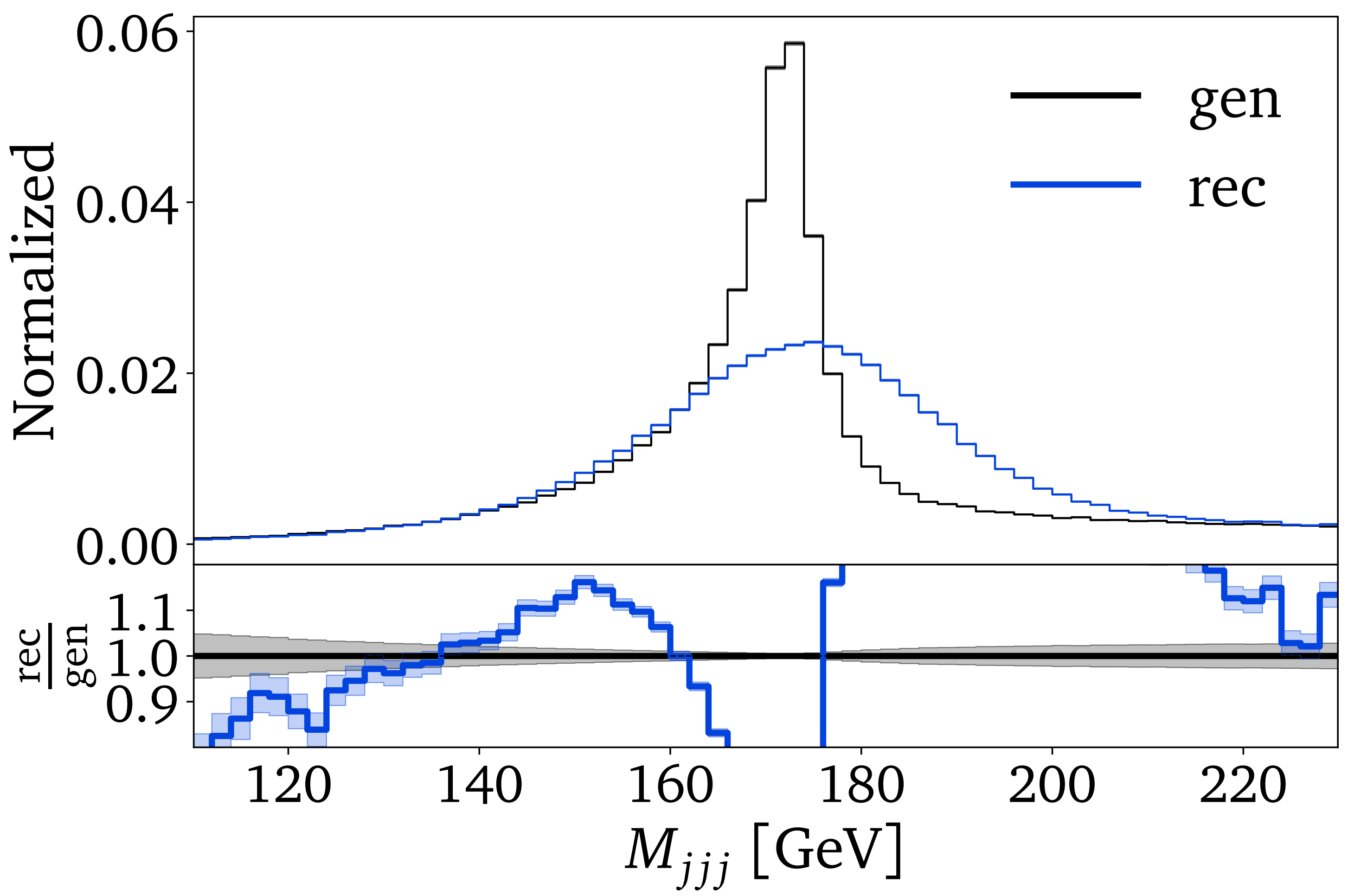
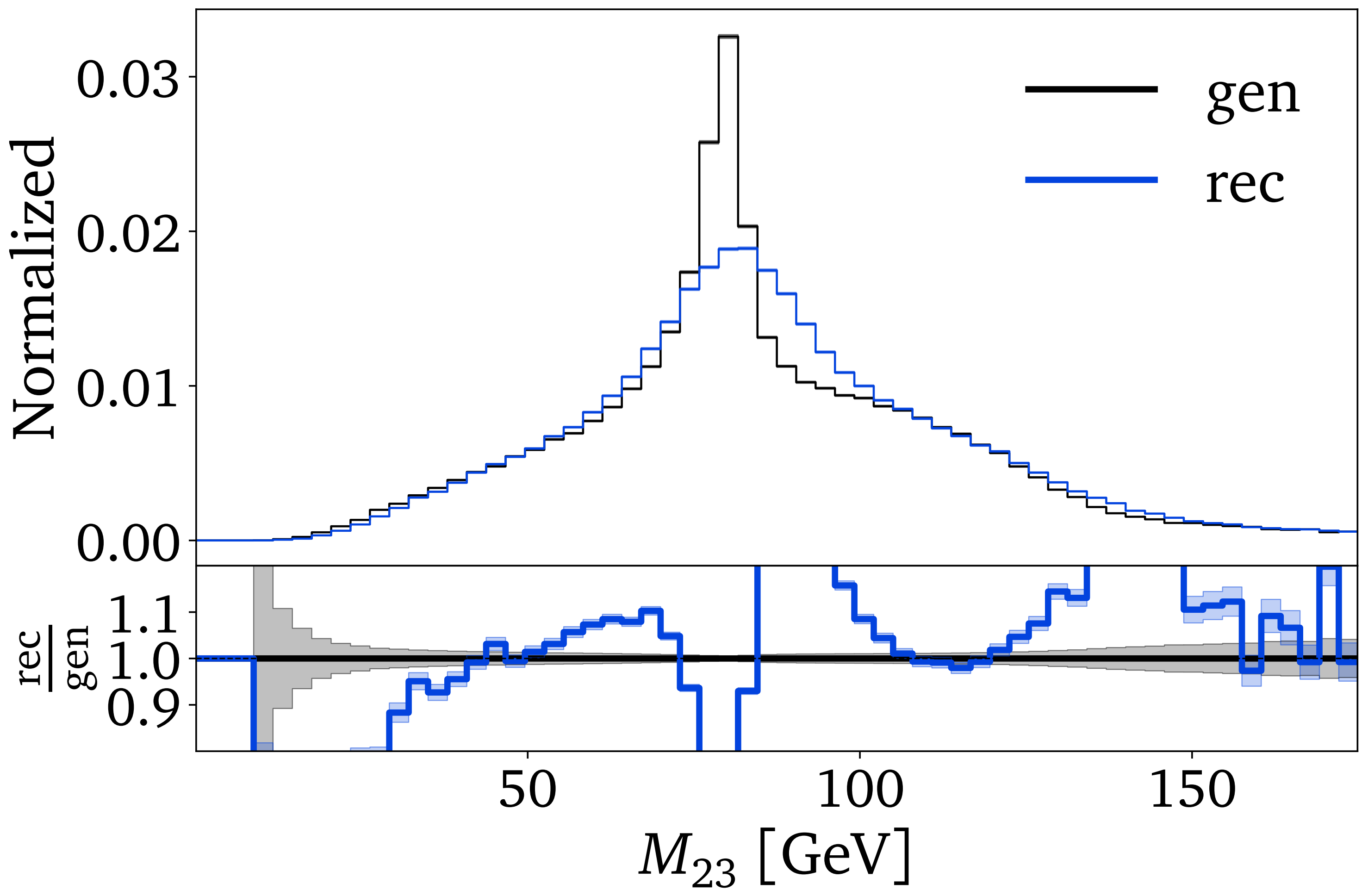
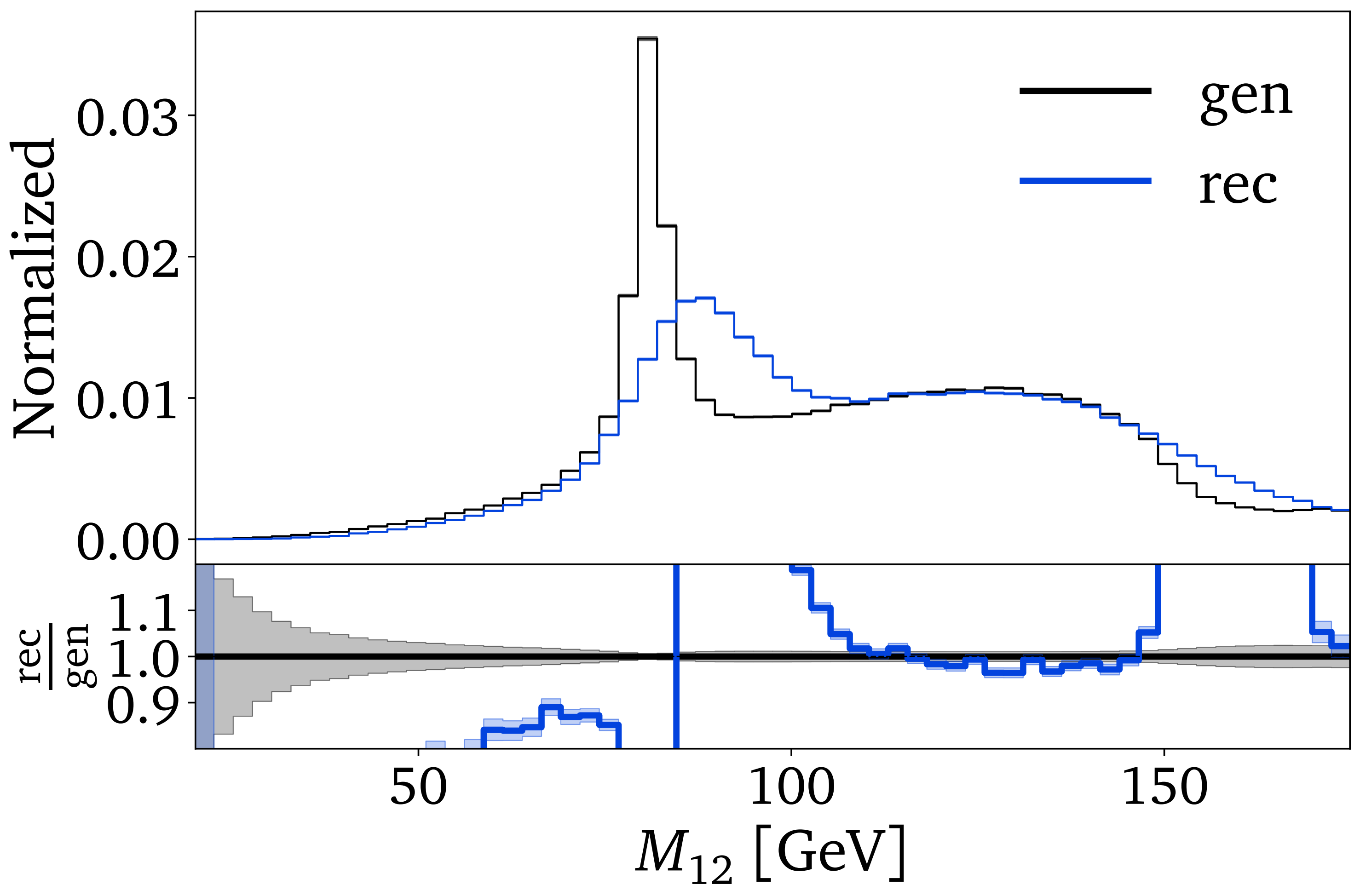
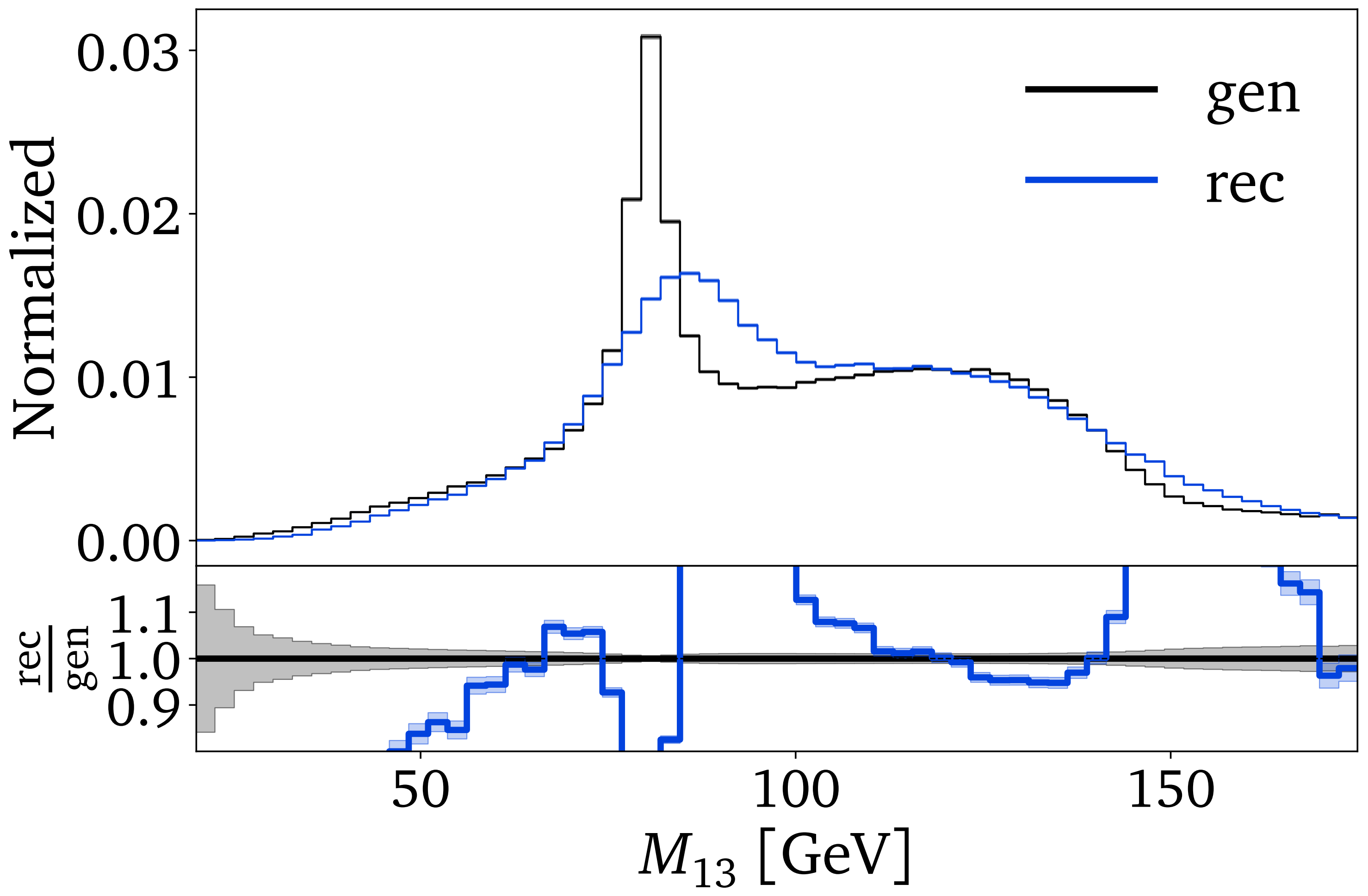




2. Combinatorics





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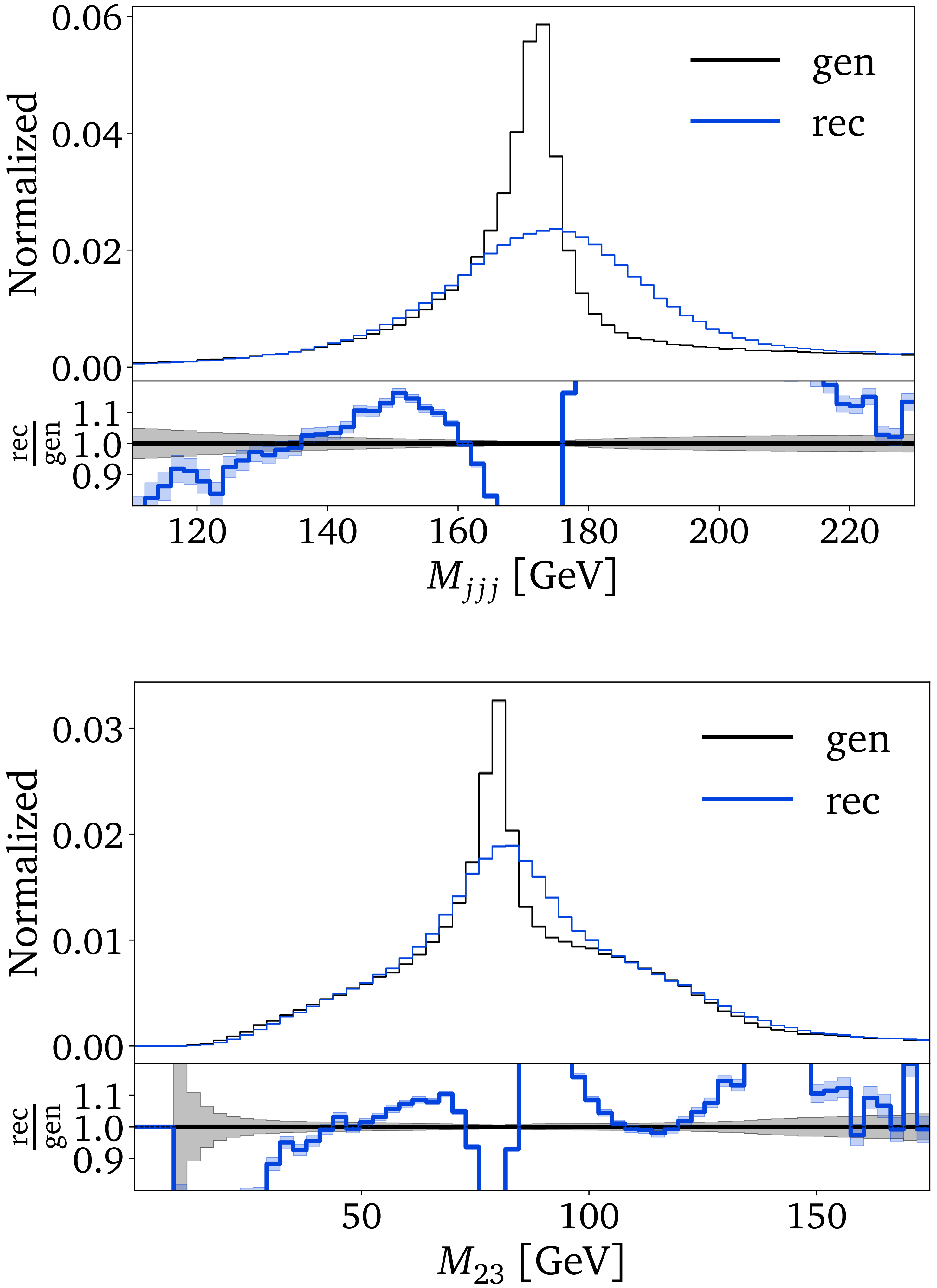

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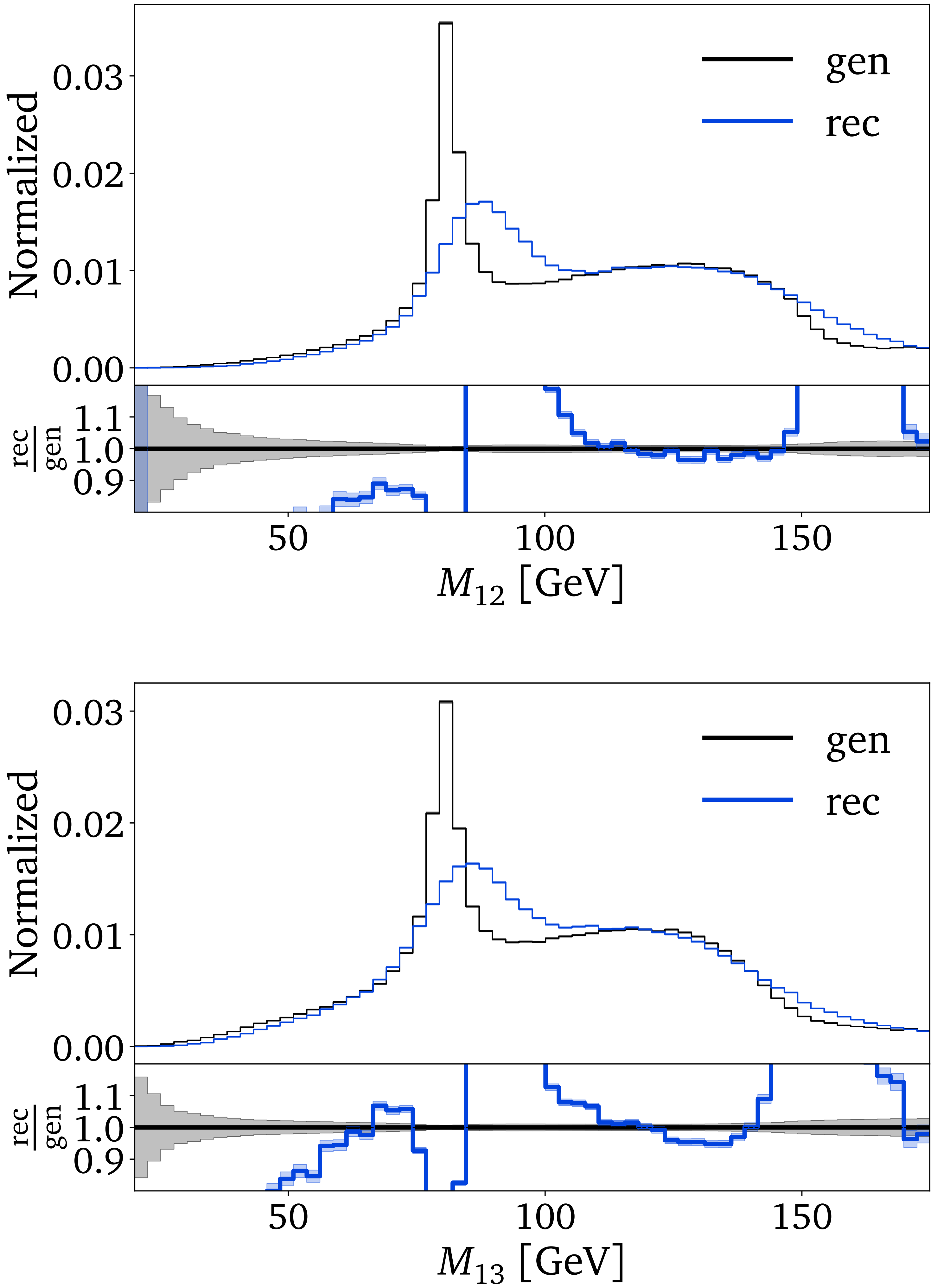
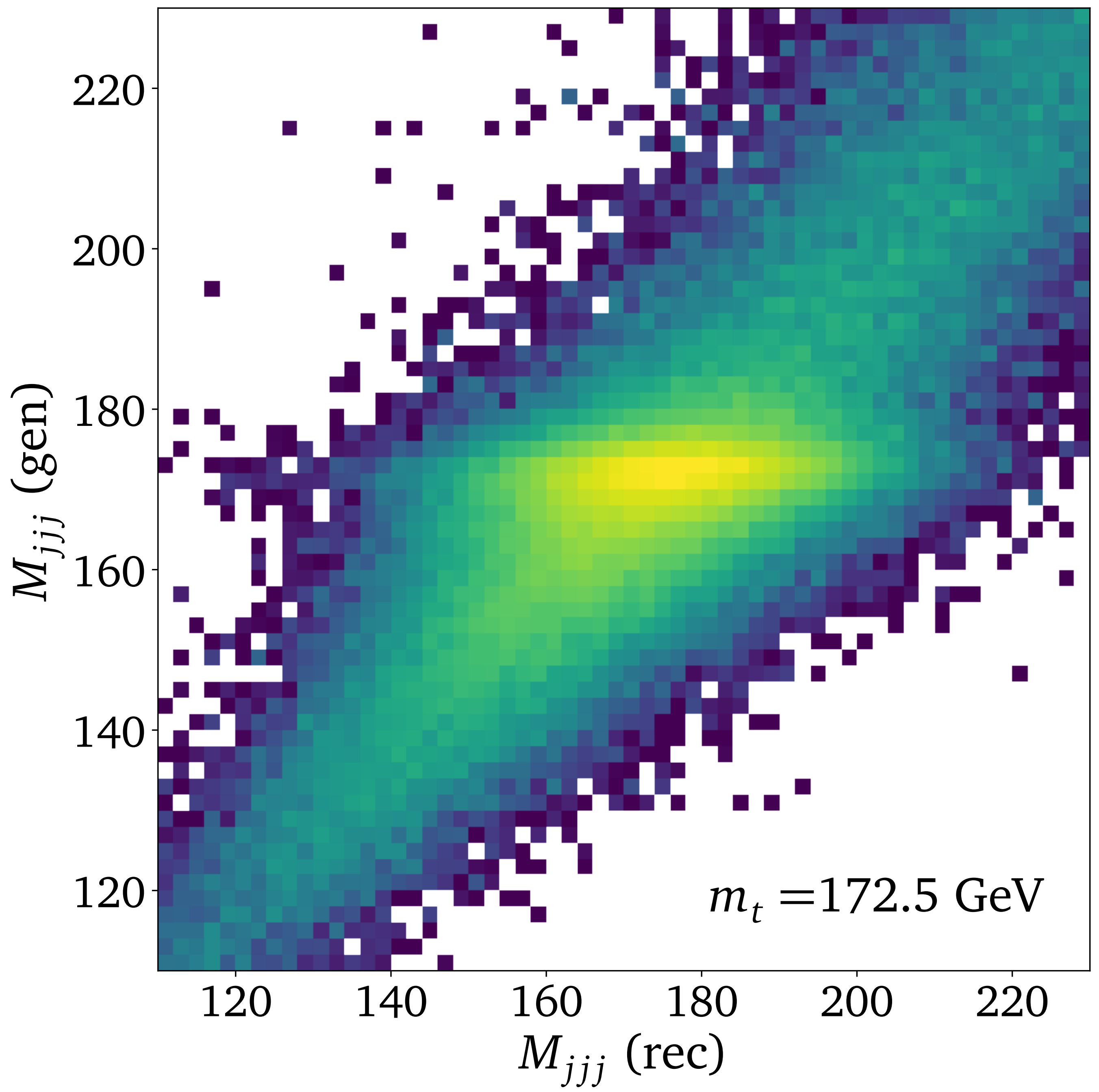


3. Detector Smearing



Choosing the right parametrization

1. The naive

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

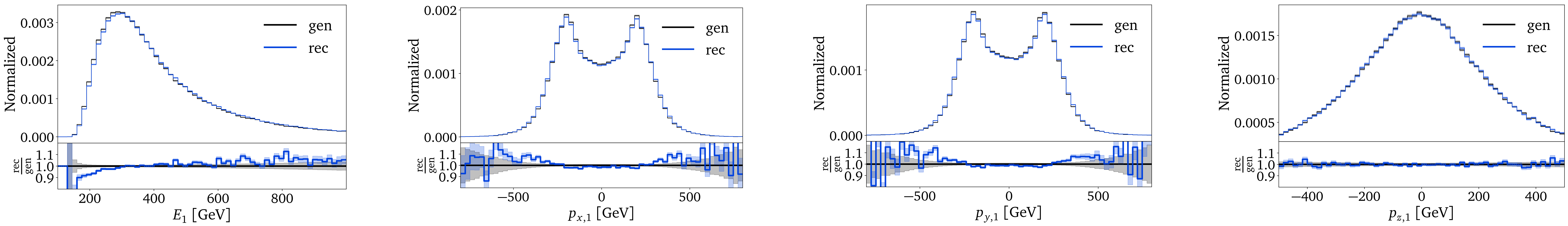
$$M_{jjj}(p_1, p_2, p_3)$$

$$M_{ij}(p_i, p_j)$$

12 dimensional correlation

8 dimensional correlation + combinatorics difficult

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



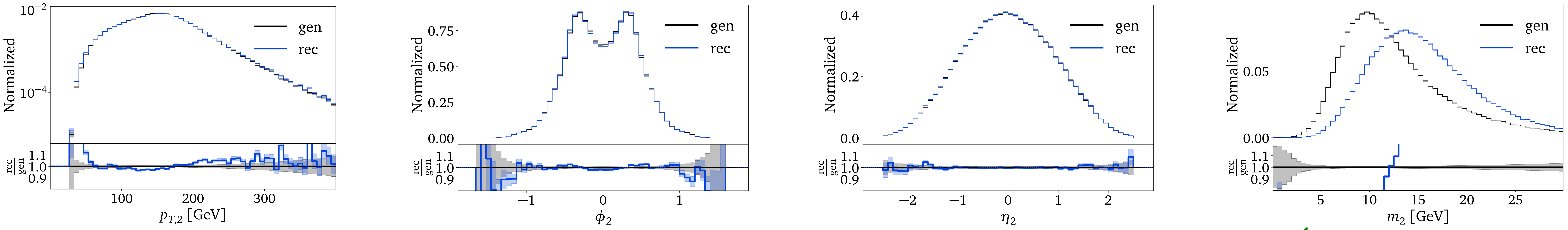
Choosing the right parametrization

2. The less naive

$$\left.\begin{aligned} p_1 &= (p_{T,1}, \phi_1, \eta_1, m_1) \\ p_2 &= (p_{T,2}, \phi_2, \eta_2, m_2) \\ p_3 &= (p_{T,3}, \phi_3, \eta_3, m_3) \end{aligned}\right\} \quad \begin{aligned} &M_{jjj}(p_1, p_2, p_3) \\ &M_{ij}(p_i, p_j) \end{aligned}$$

12 dimensional correlation

8 dimensional correlation + combinatorics difficult



Reco and gen level difference visible

Choosing the right parametrization

3. The least naive

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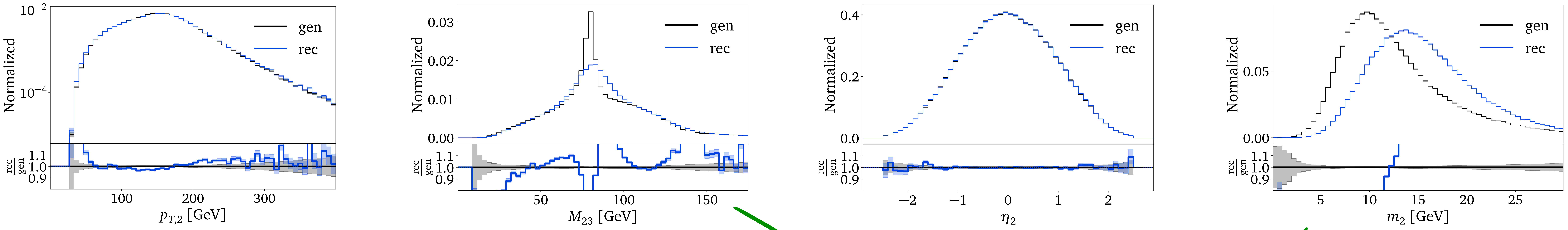
\end{aligned}\right\} \quad M_{jjj}^2 = \sum_{ij,i>j} M_{ij}^2 - \sum_i m_i^2
$$

6 dimensional correlation

Direct input + combinatorics simple



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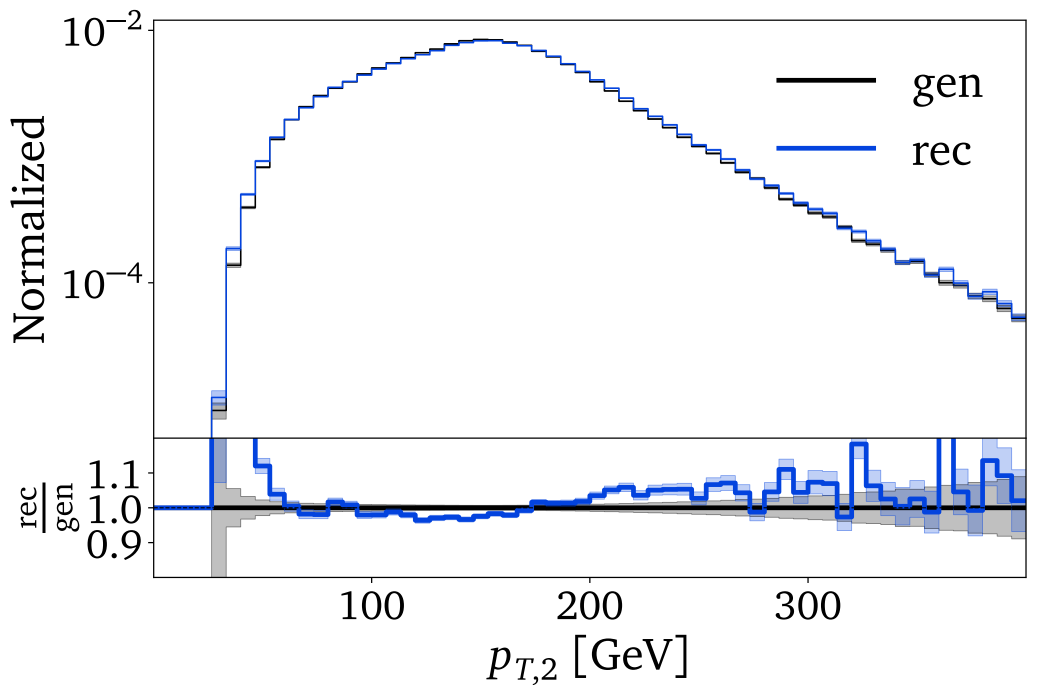

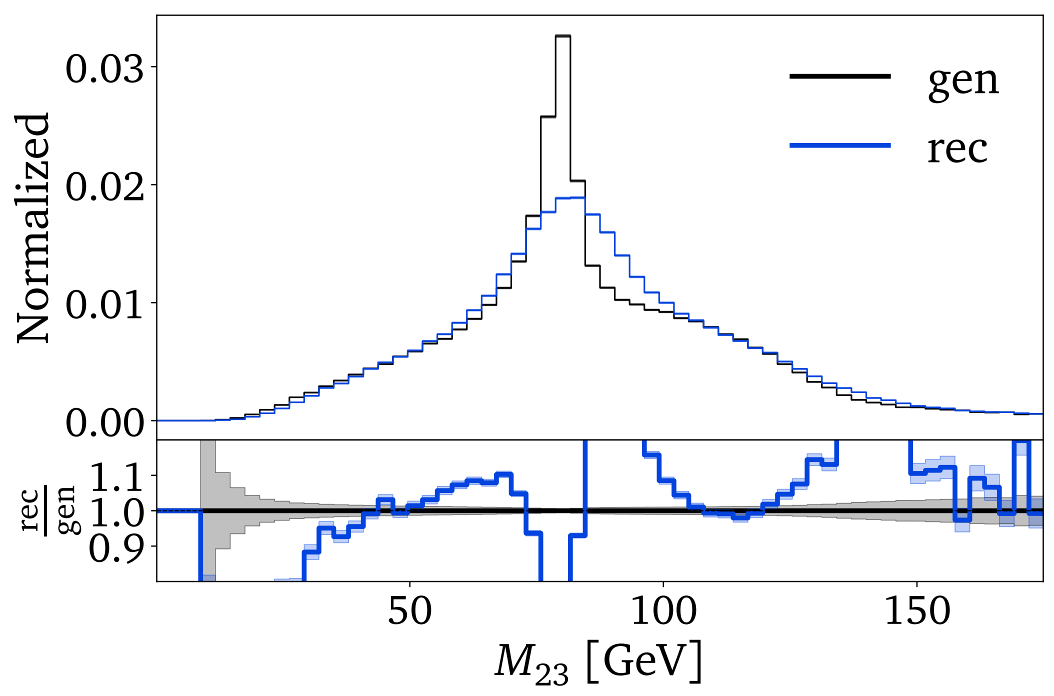

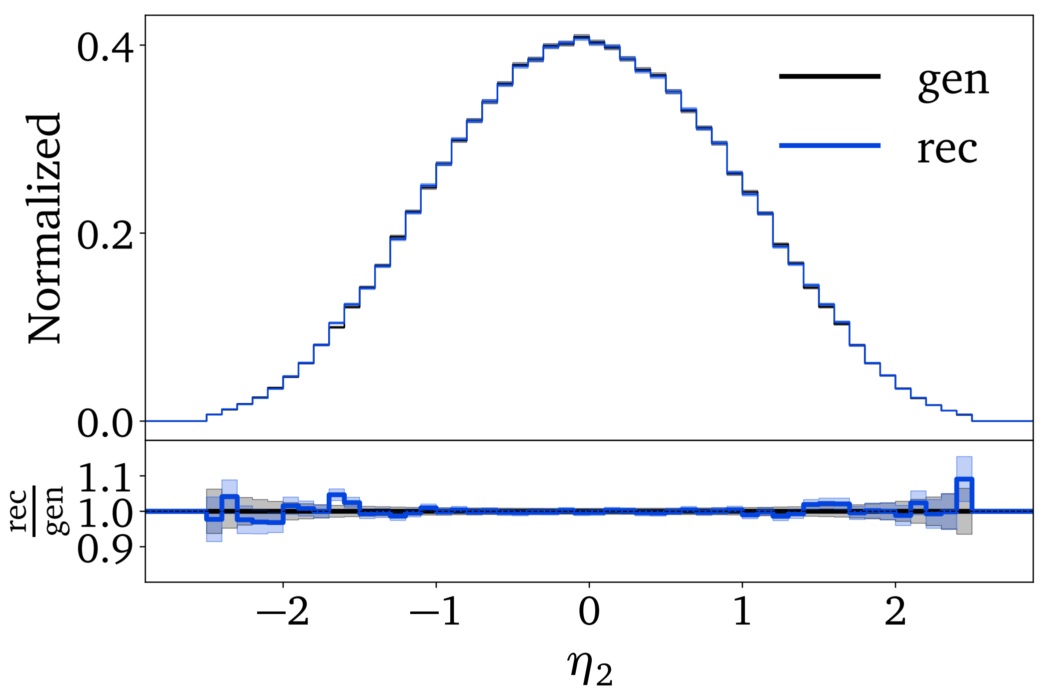

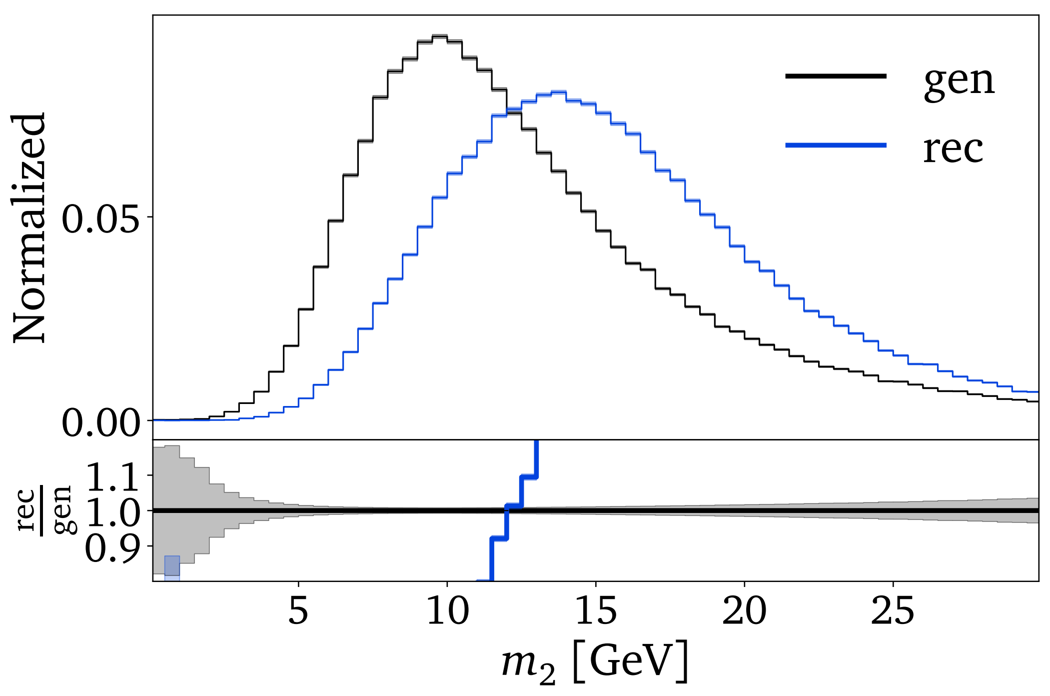

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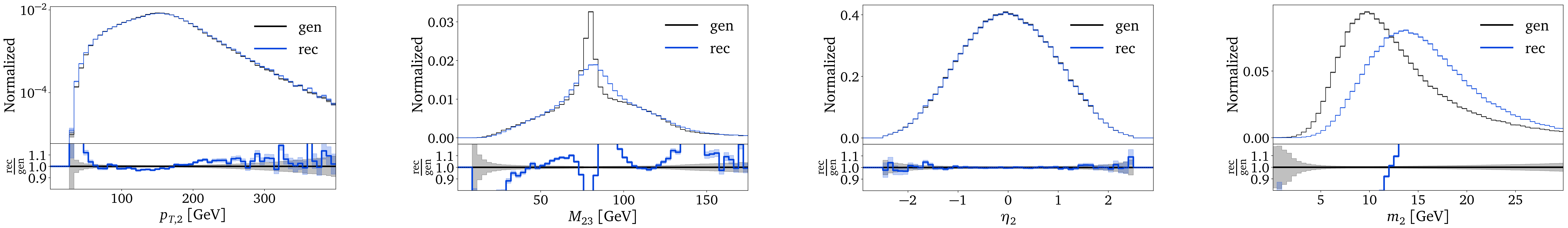
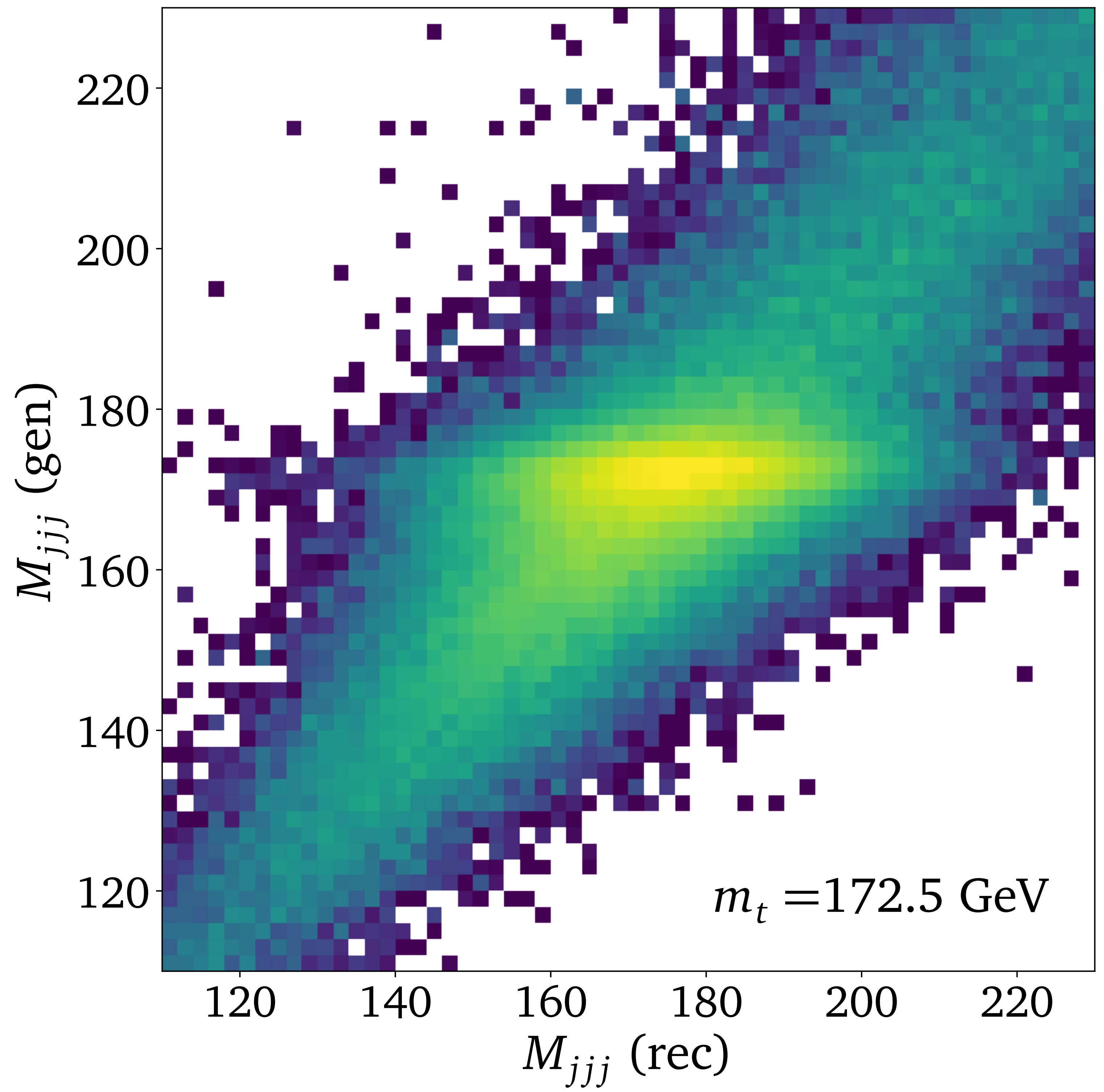
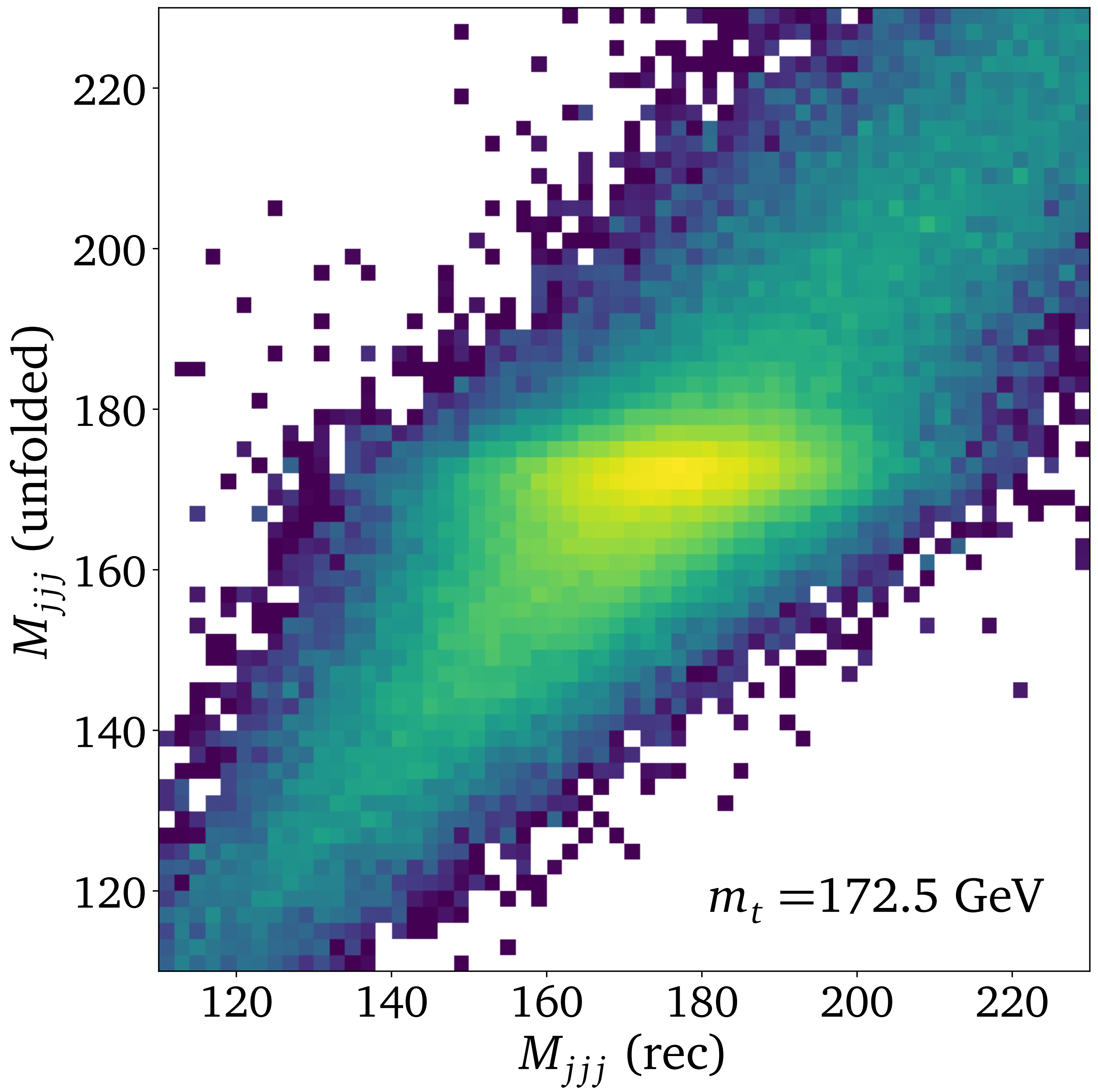
For mass measurement, we only use 6 dimensional subset of phase space to increase network performance



Model-Dependence





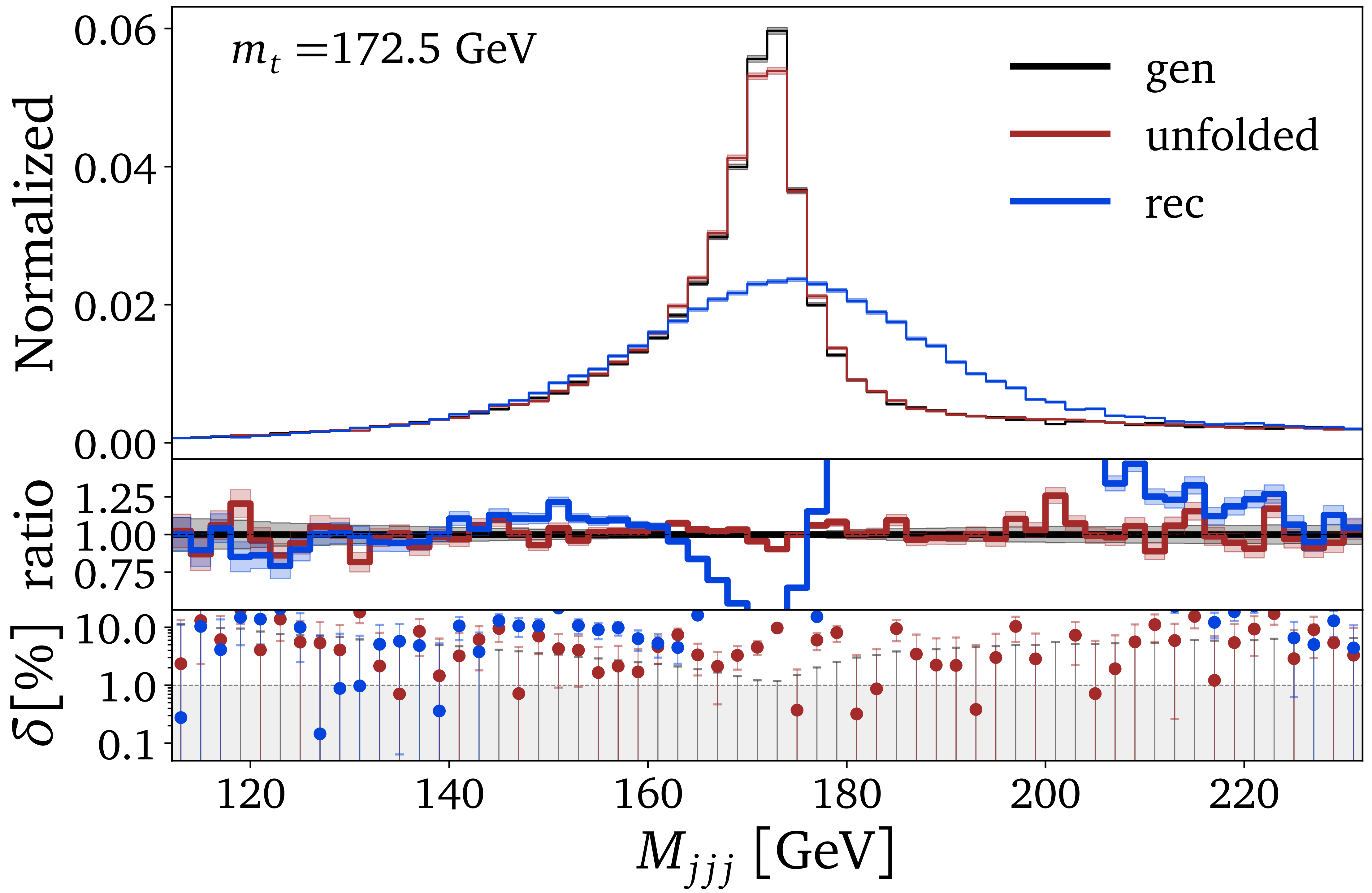
Correct migration learned?

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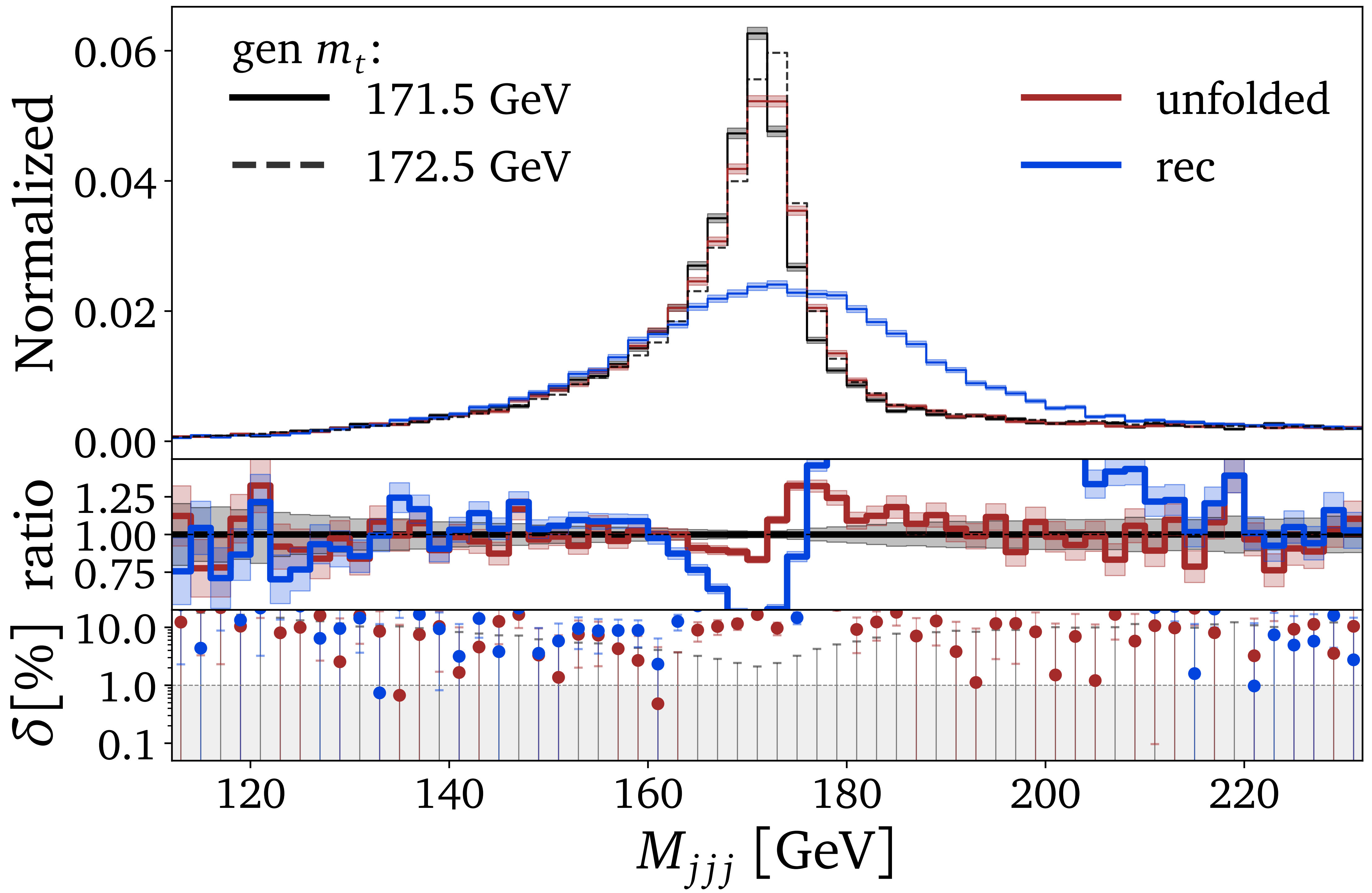
For pseudo-data with different top masses : Algorithm falls back to prior ($m_t = 172.5$ GeV)



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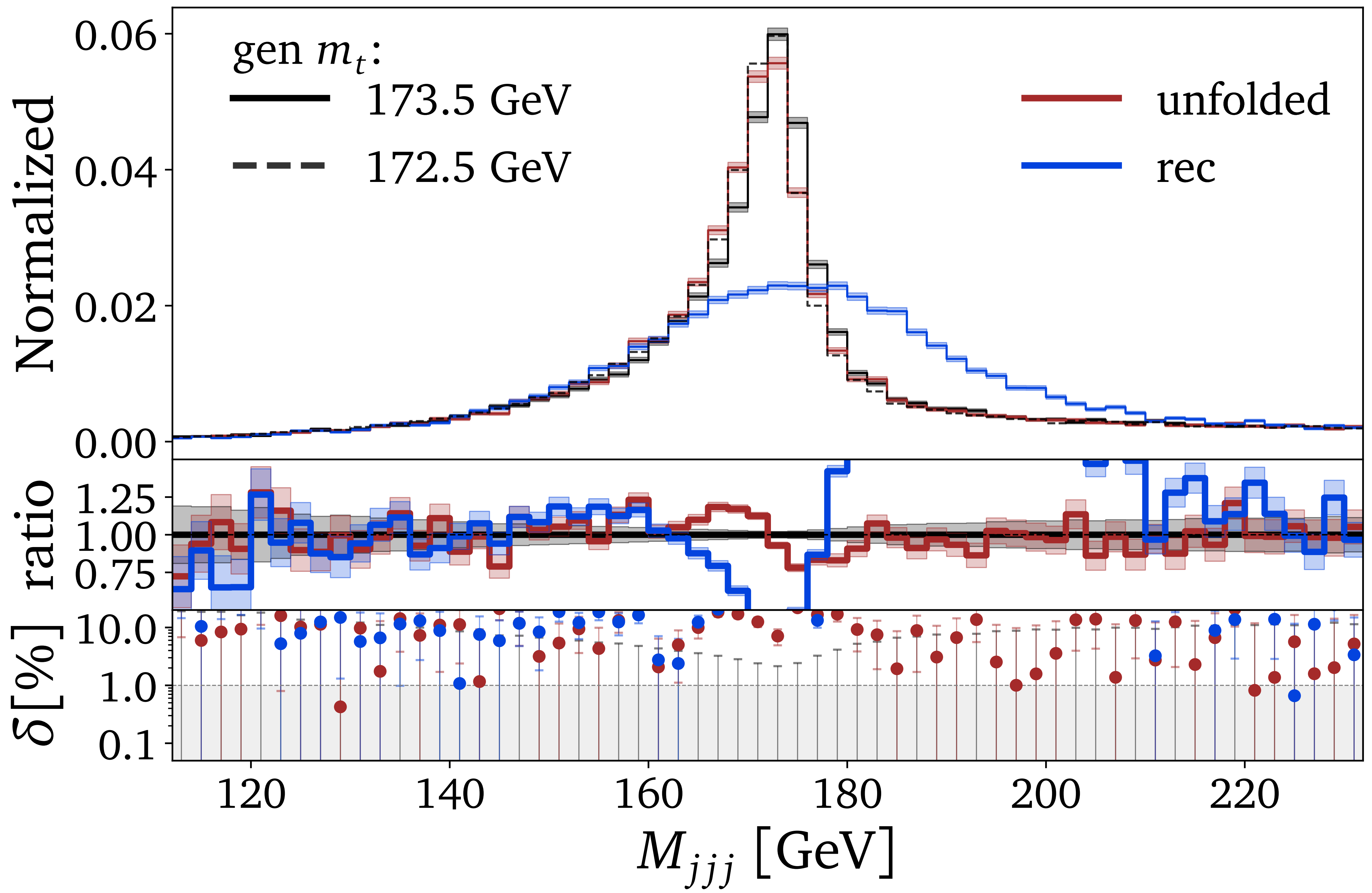

Removing Model-Dependence

$$
\begin{tikzcd}
p_{sim}(x_{gen} \,|\, m_s) \arrow[d, "p(x_{reco} \,|\, x_{gen})"'] & p_{unfold}(x_{gen} \,|\, m_s, m_d) \\
p_{sim}(x_{reco} \,|\, m_s) \arrow[r, leftrightarrow, "\text{correspondance}"] & p_{data}(x_{reco} \,|\, m_d) \arrow[u, "p_{model}(x_{gen} \,|\, x_{reco}, m_s)"']
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→ **Solution: Strengthen m_d dependence, but how?**

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\end{tikzcd}
$$

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

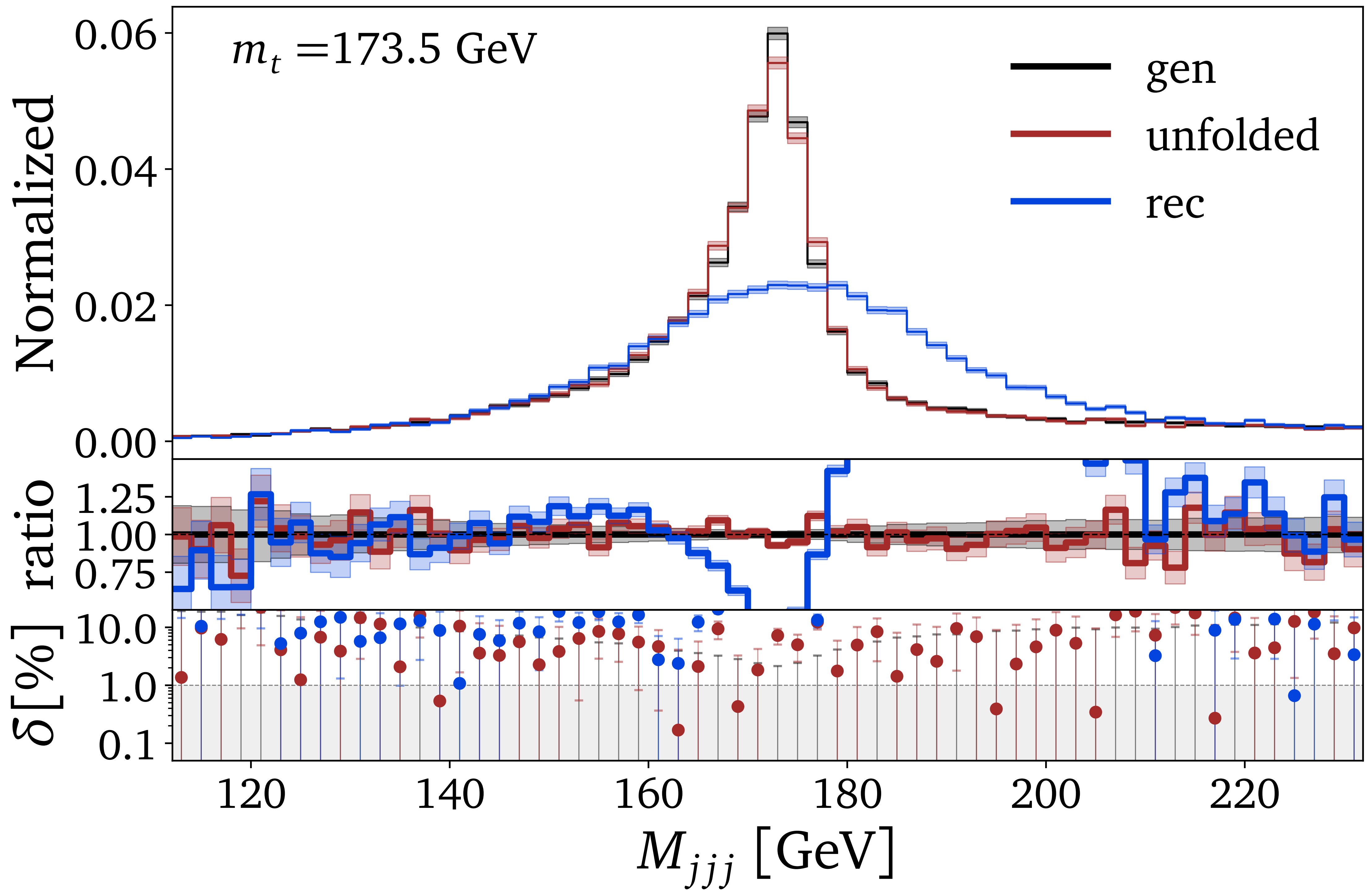
1. Augment training data with simulation from different top masses
2. Estimate batch-wise $m_d \approx$ weighted-median(M_{jjj}^{batch}) on reco level

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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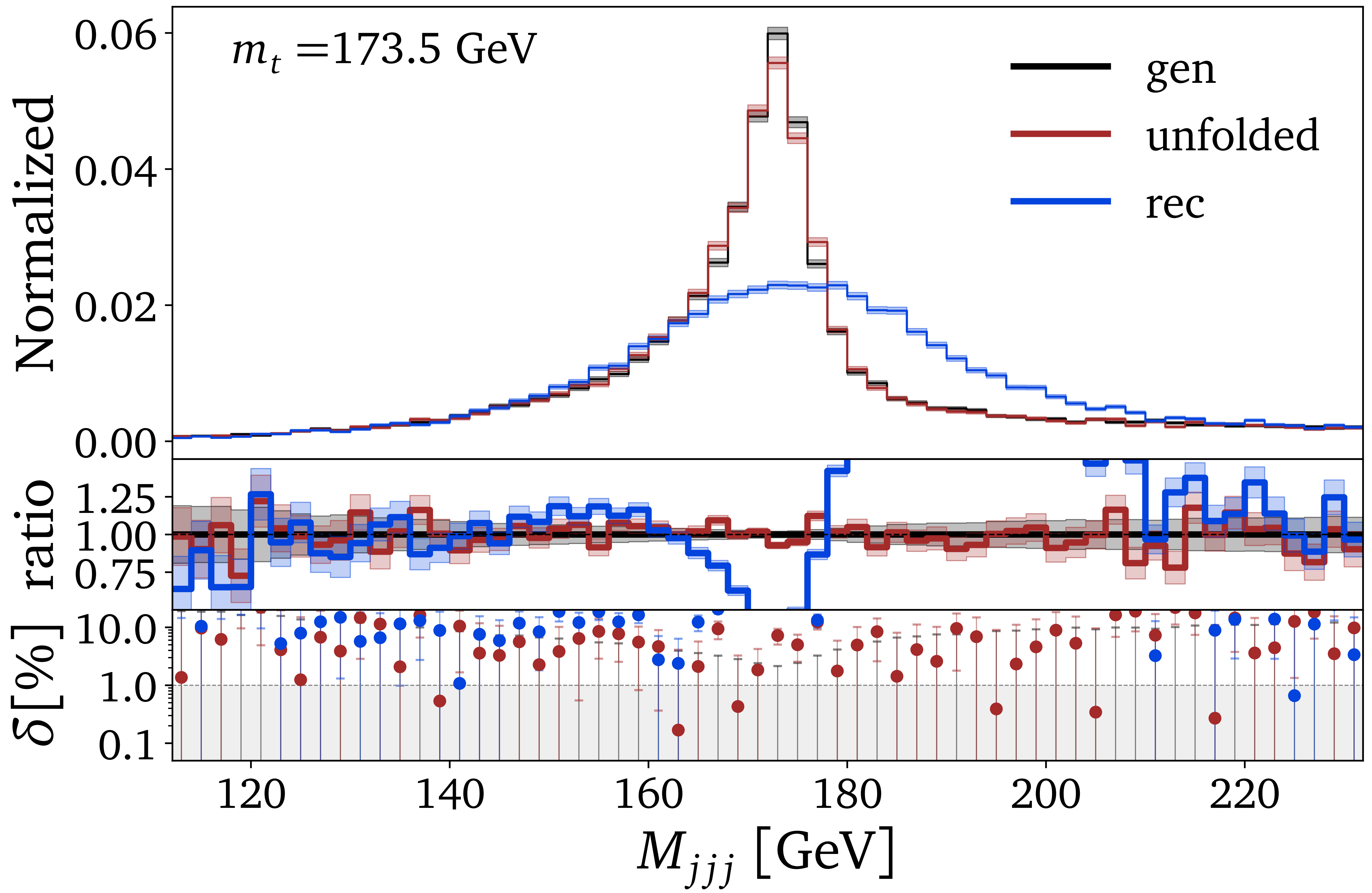

ML task becomes much harder

Removing Model-Dependence!

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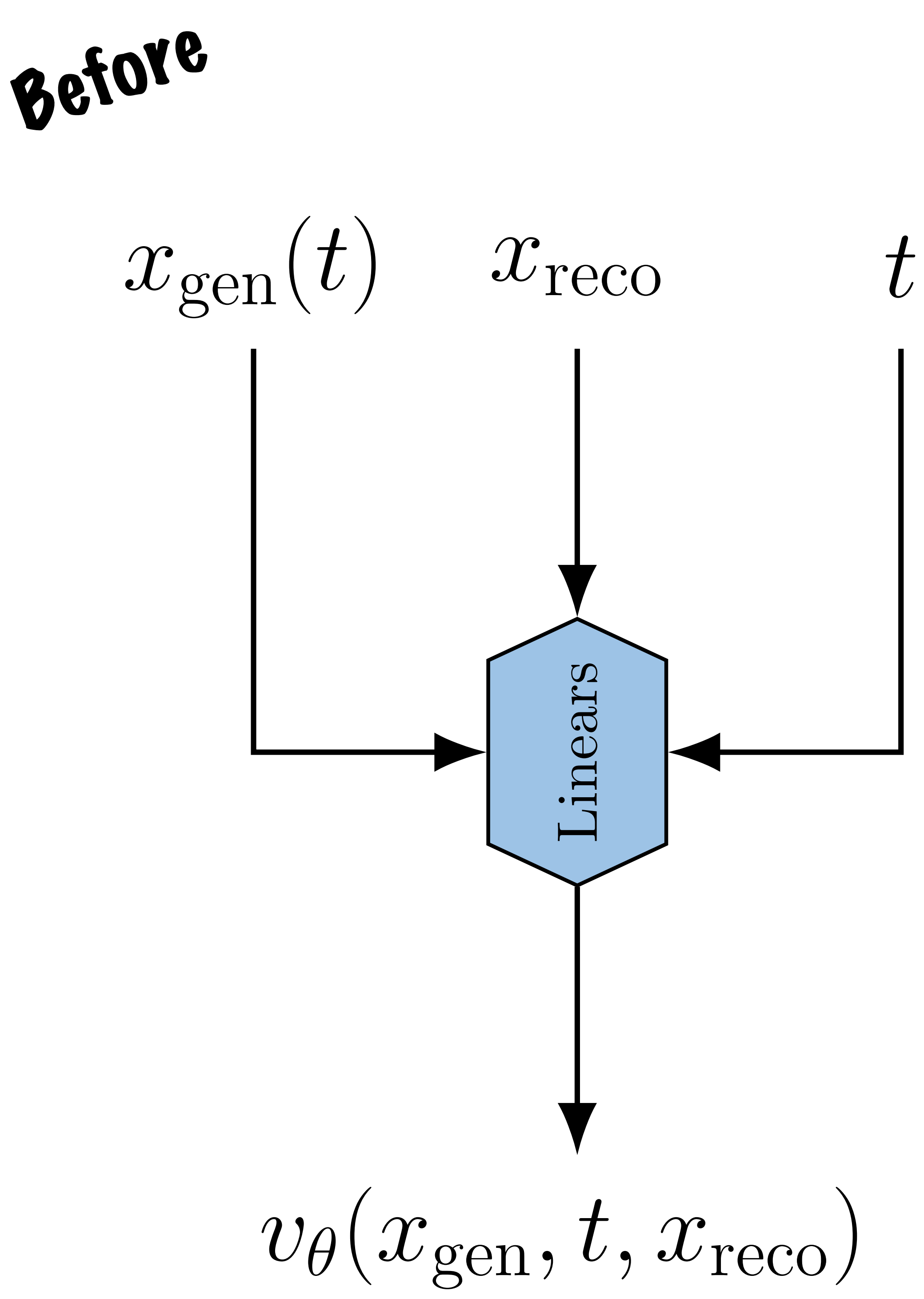
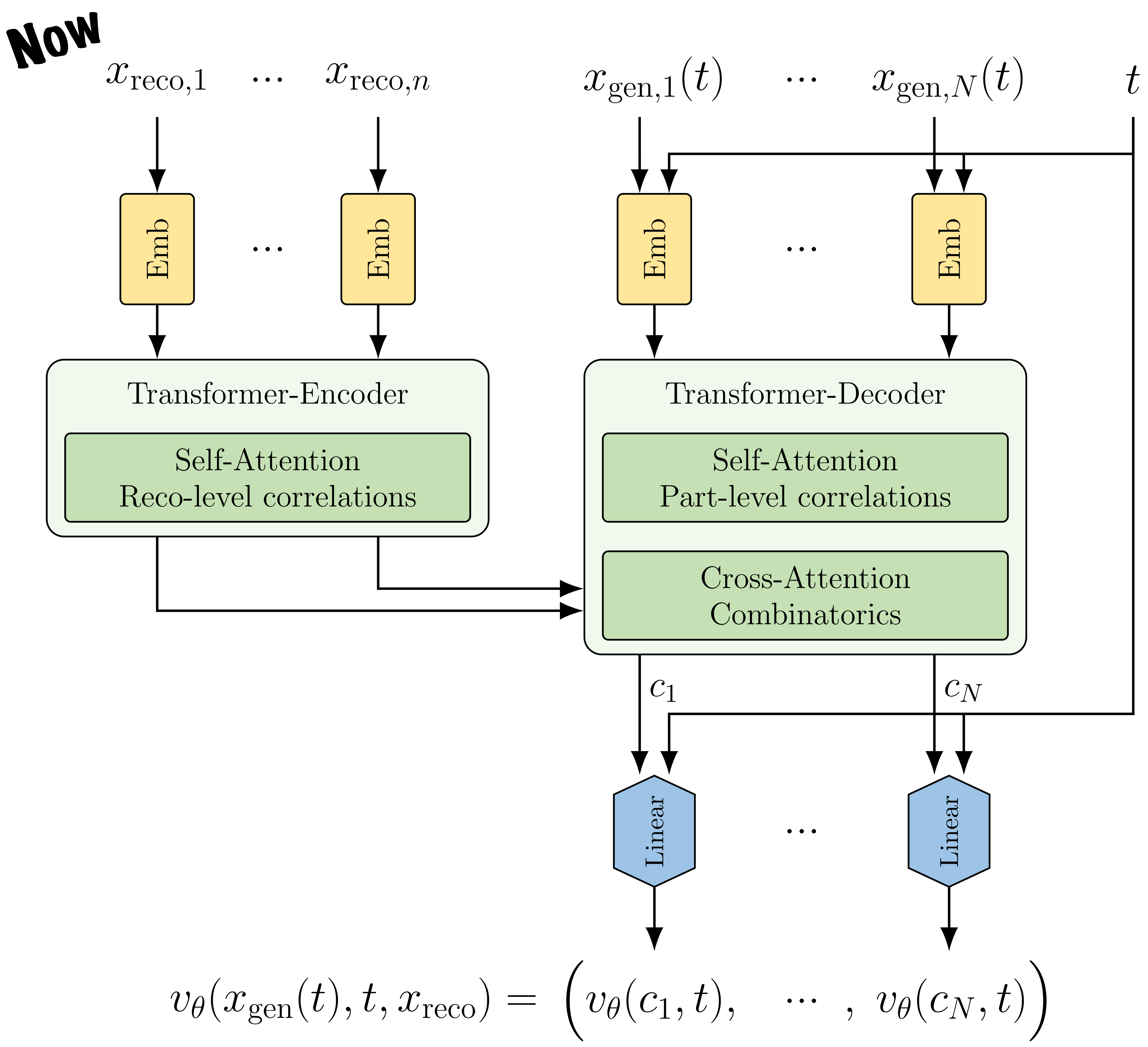


vs



Adapted from **arXiv:2310.07752**

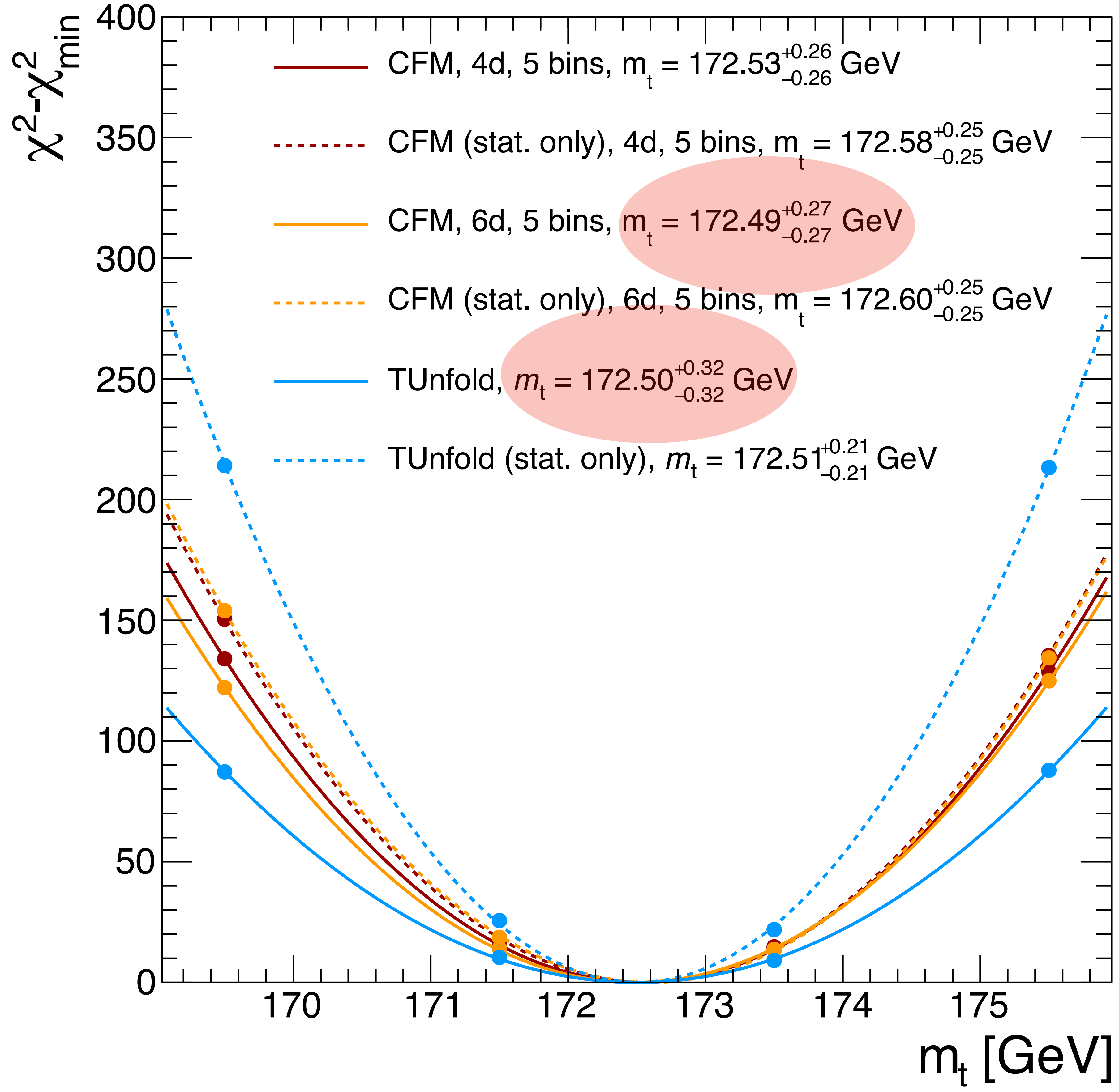
Mass Measurement

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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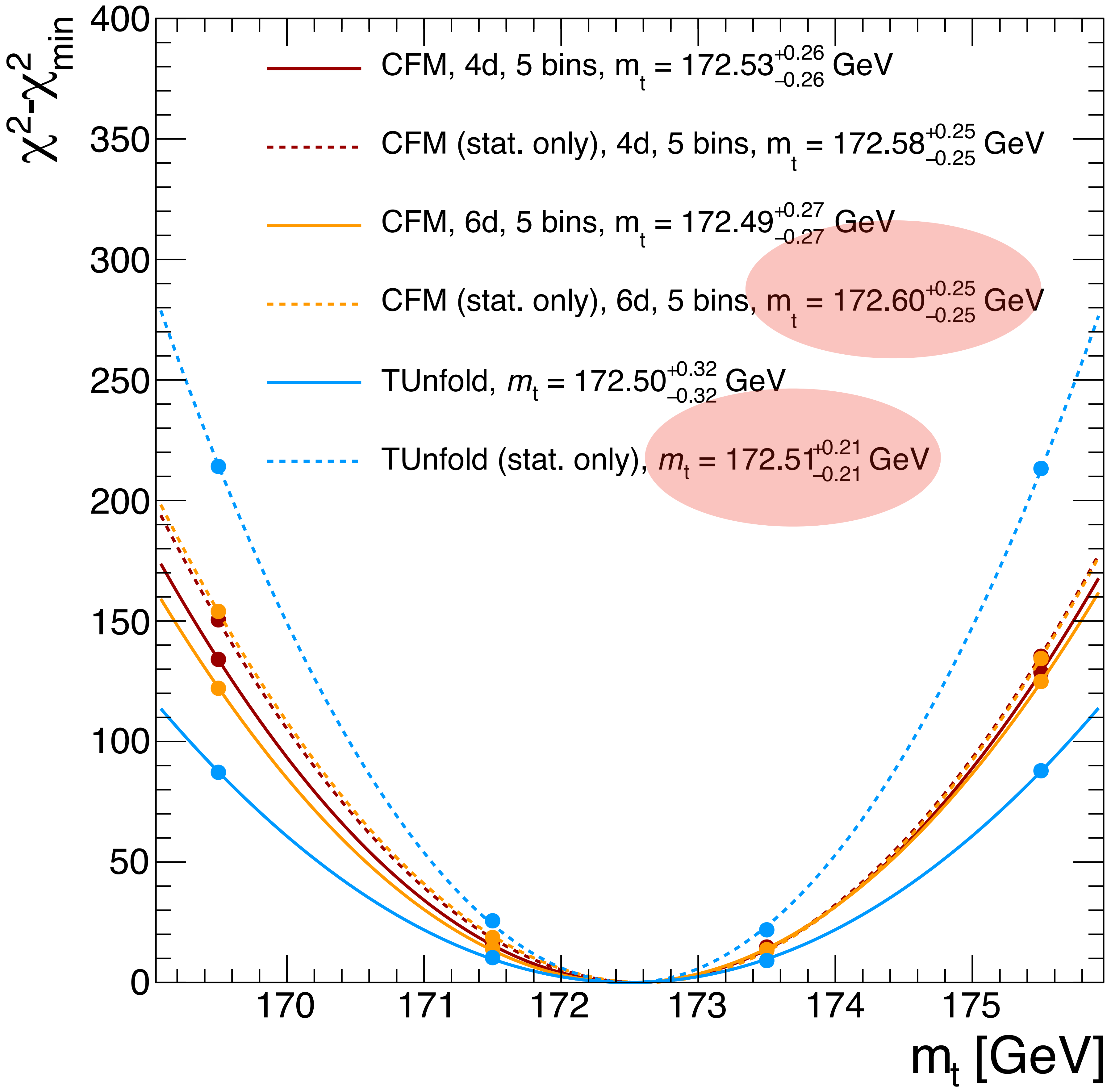

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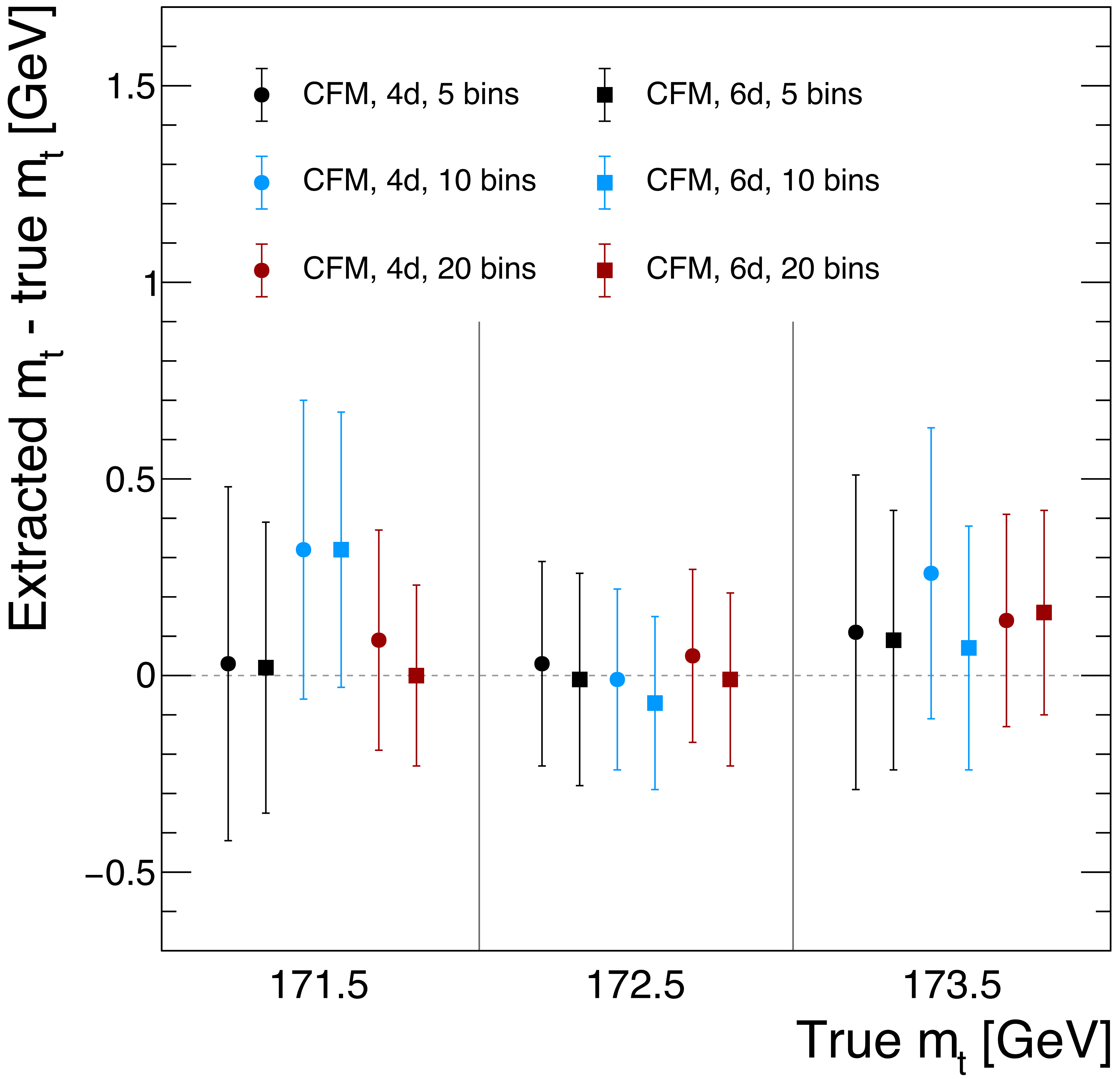

→ Reliably unfold triple jet mass without bias

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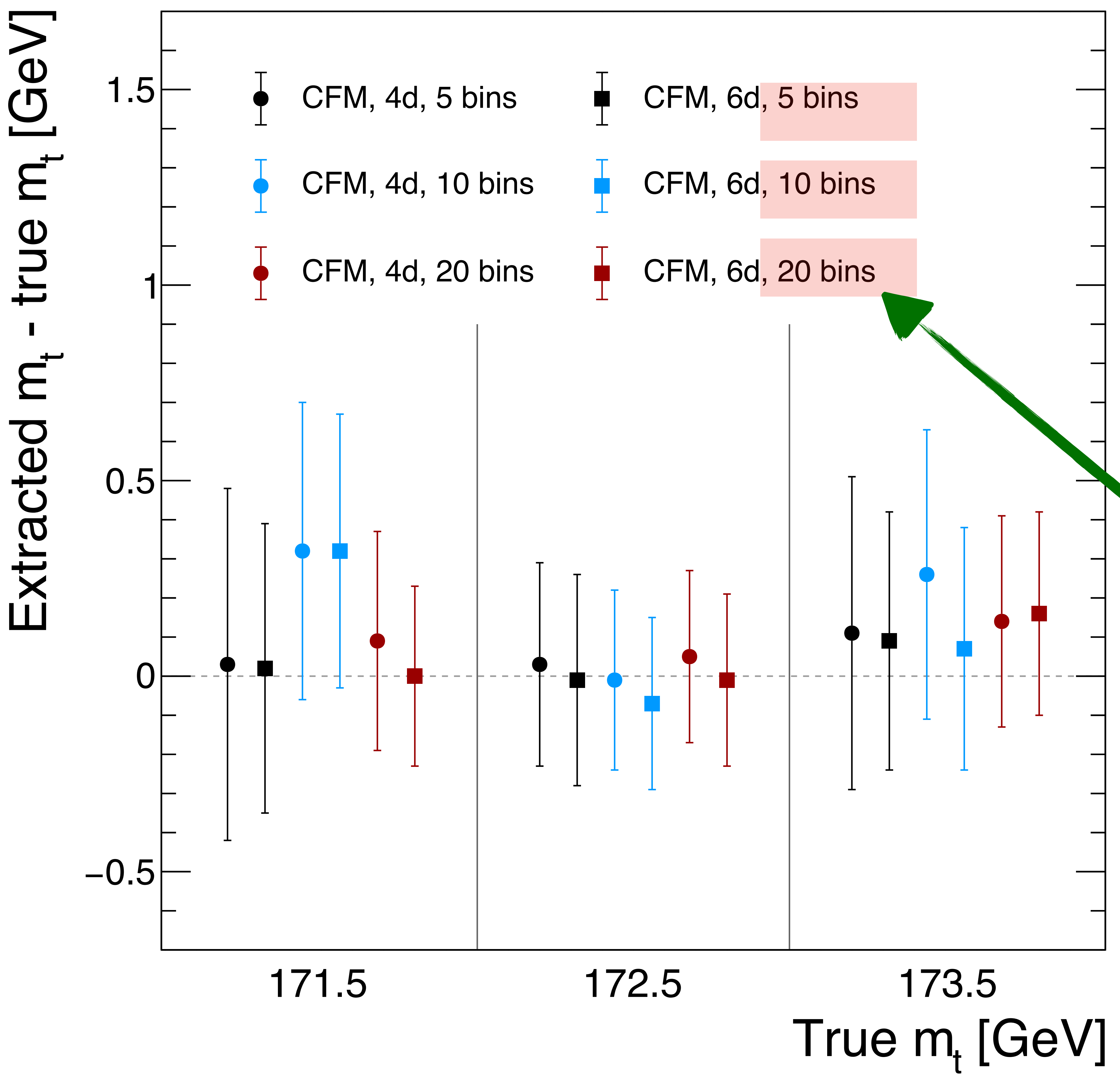

Why not more?

→ Reliably unfold triple jet mass without bias

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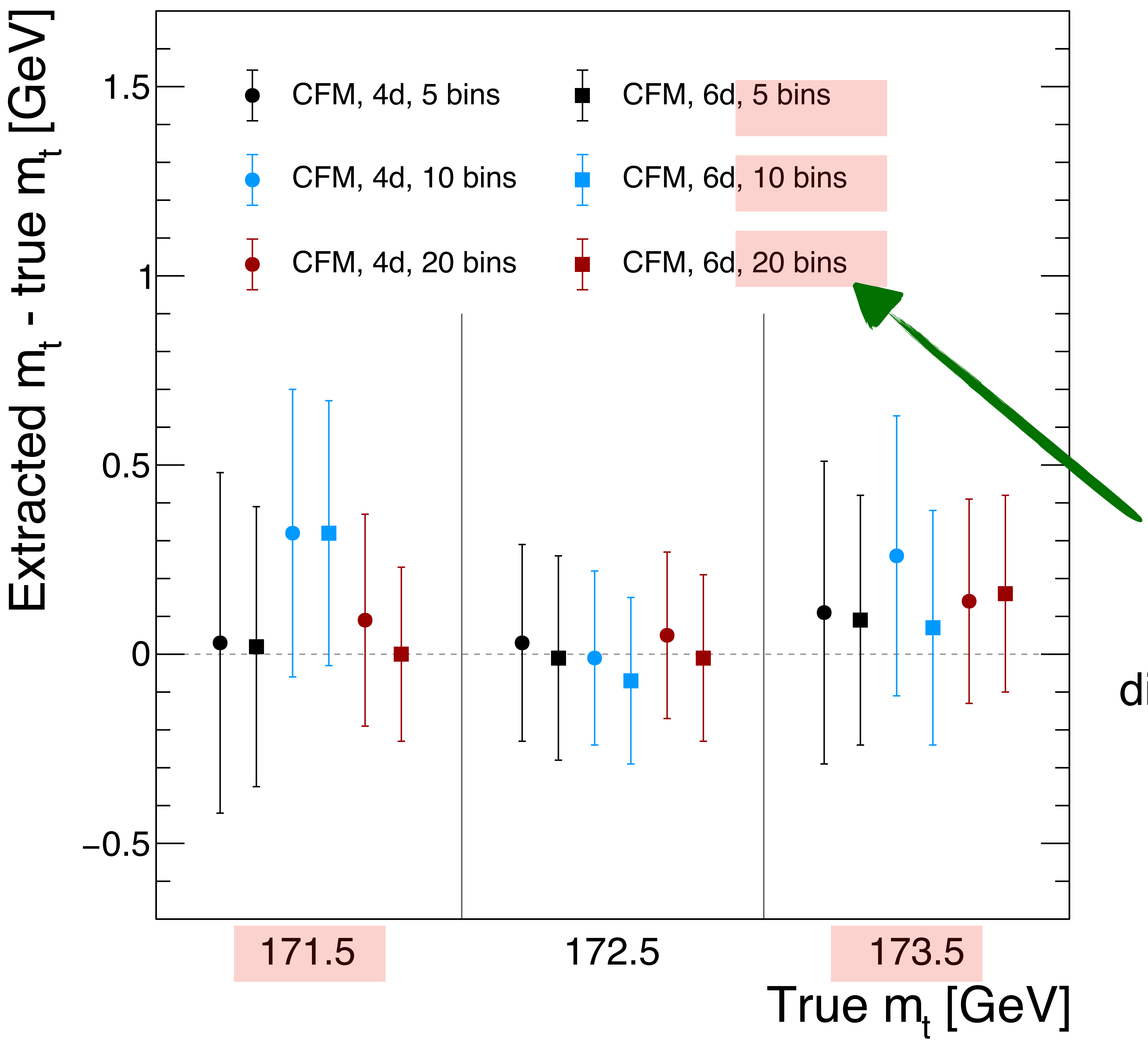


Why not more?

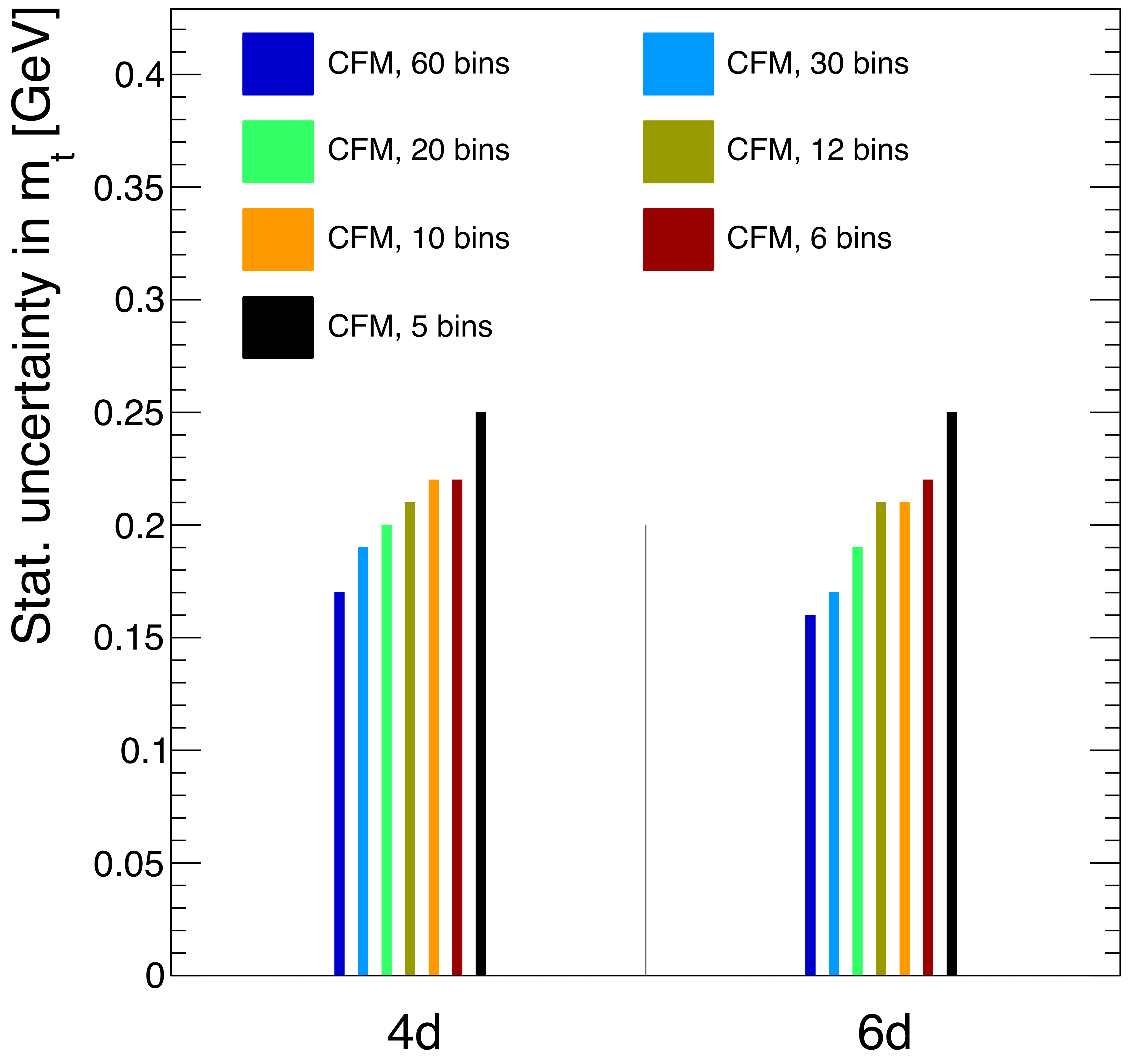
Limited by discrete grid of available m_t simulations

→ Reliably unfold triple jet mass without bias

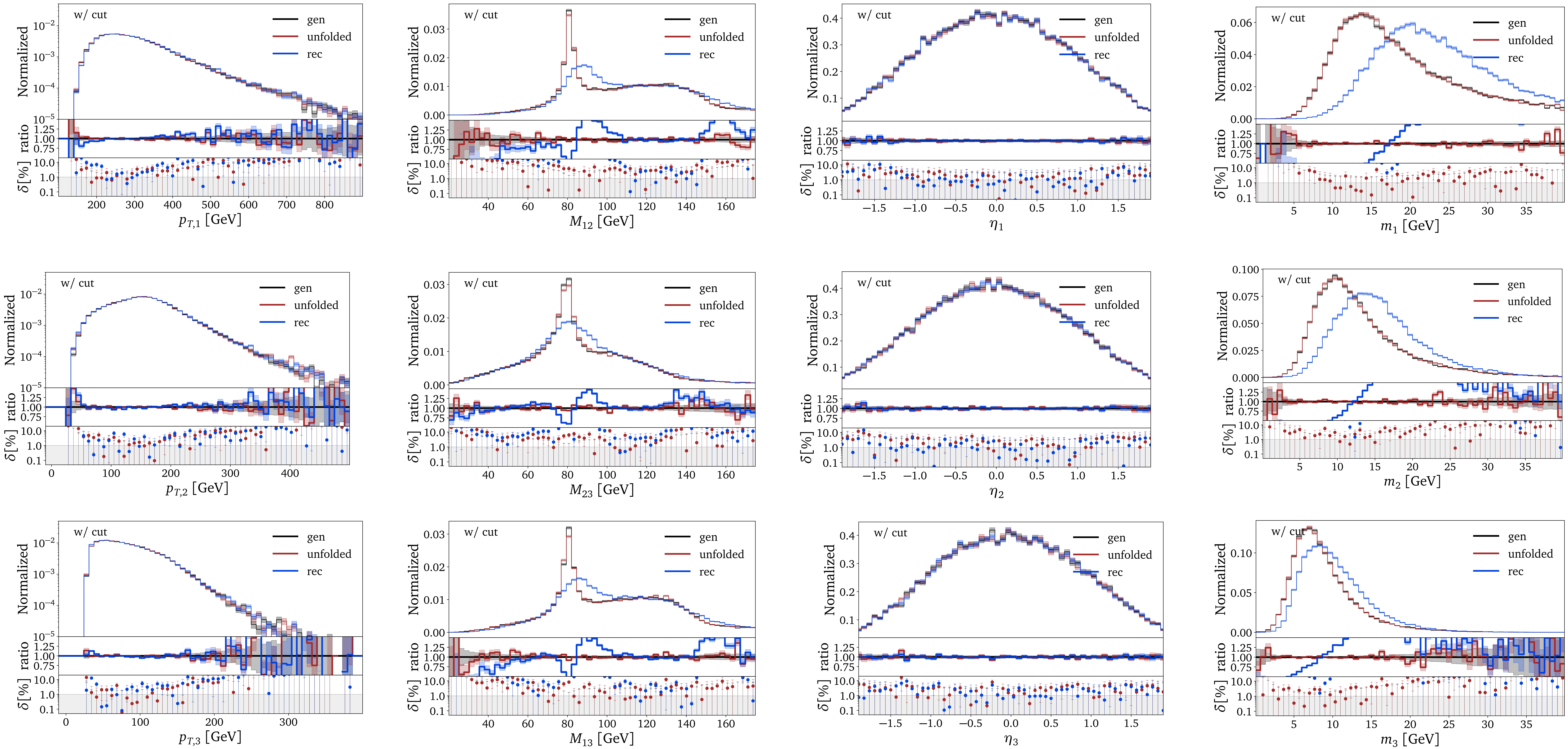
Mass Measurement

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

Statistical uncertainty for 60 bins decreases by 36%

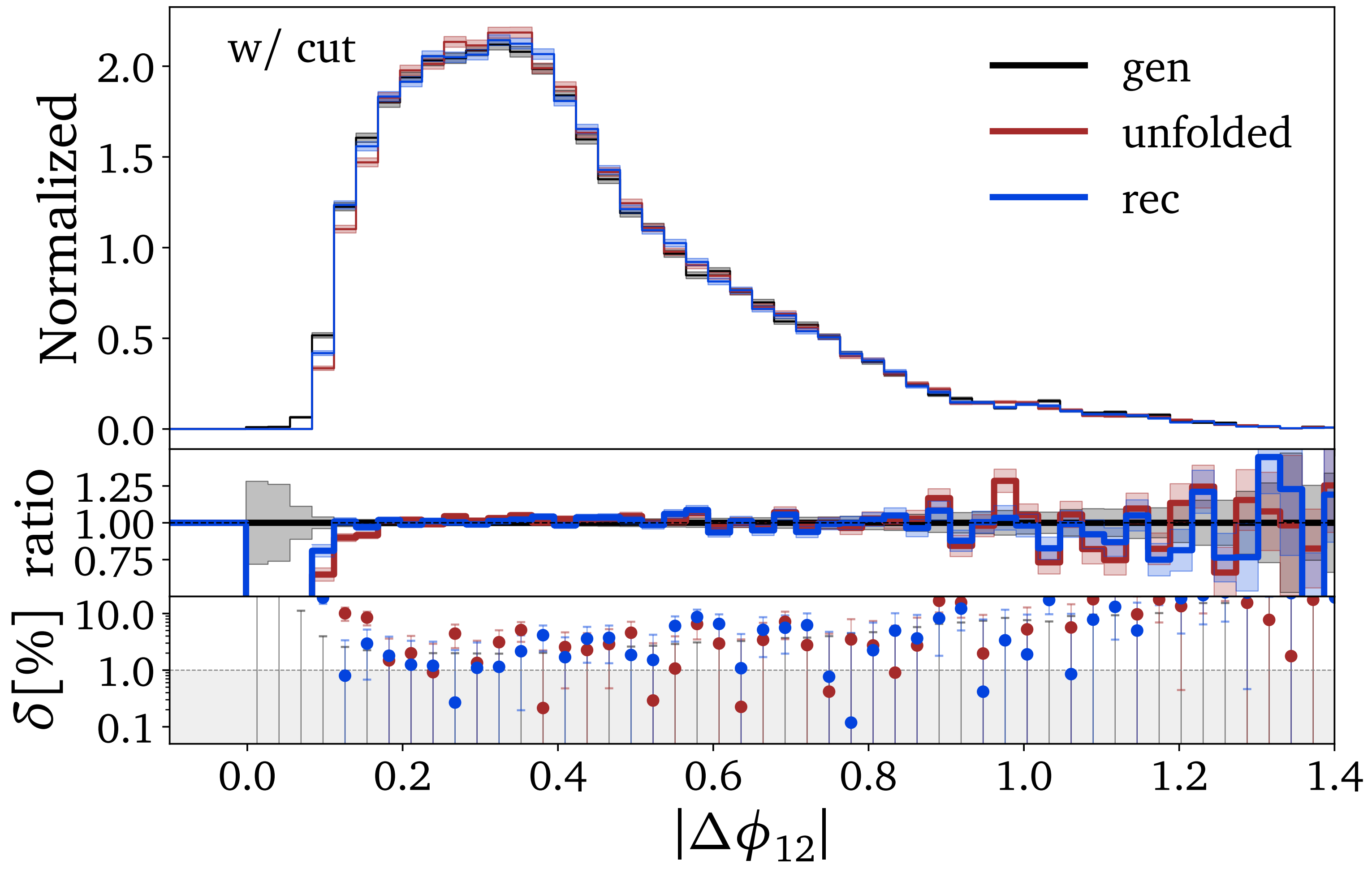


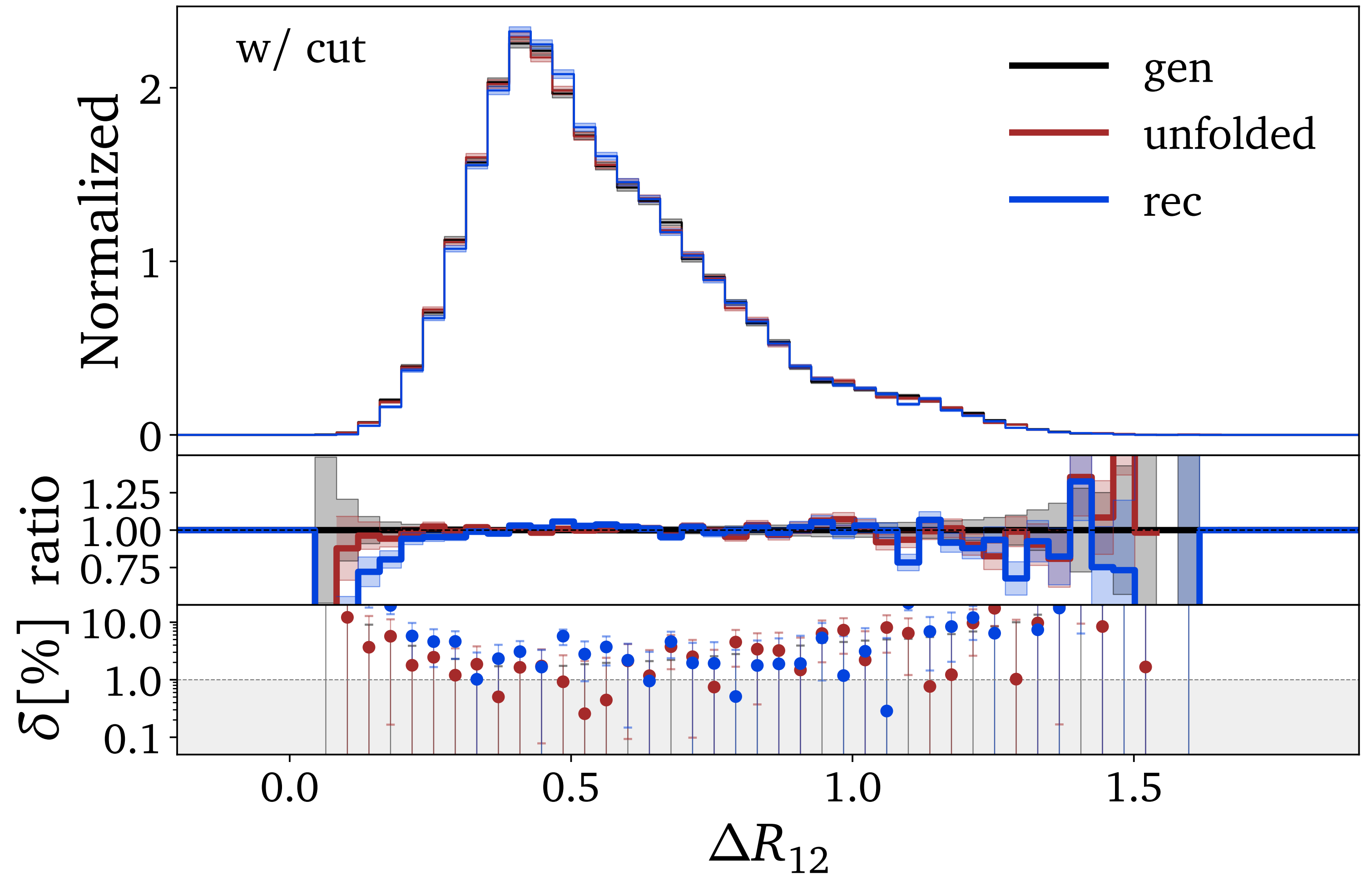
Full Phase Space Unfolding (12d)

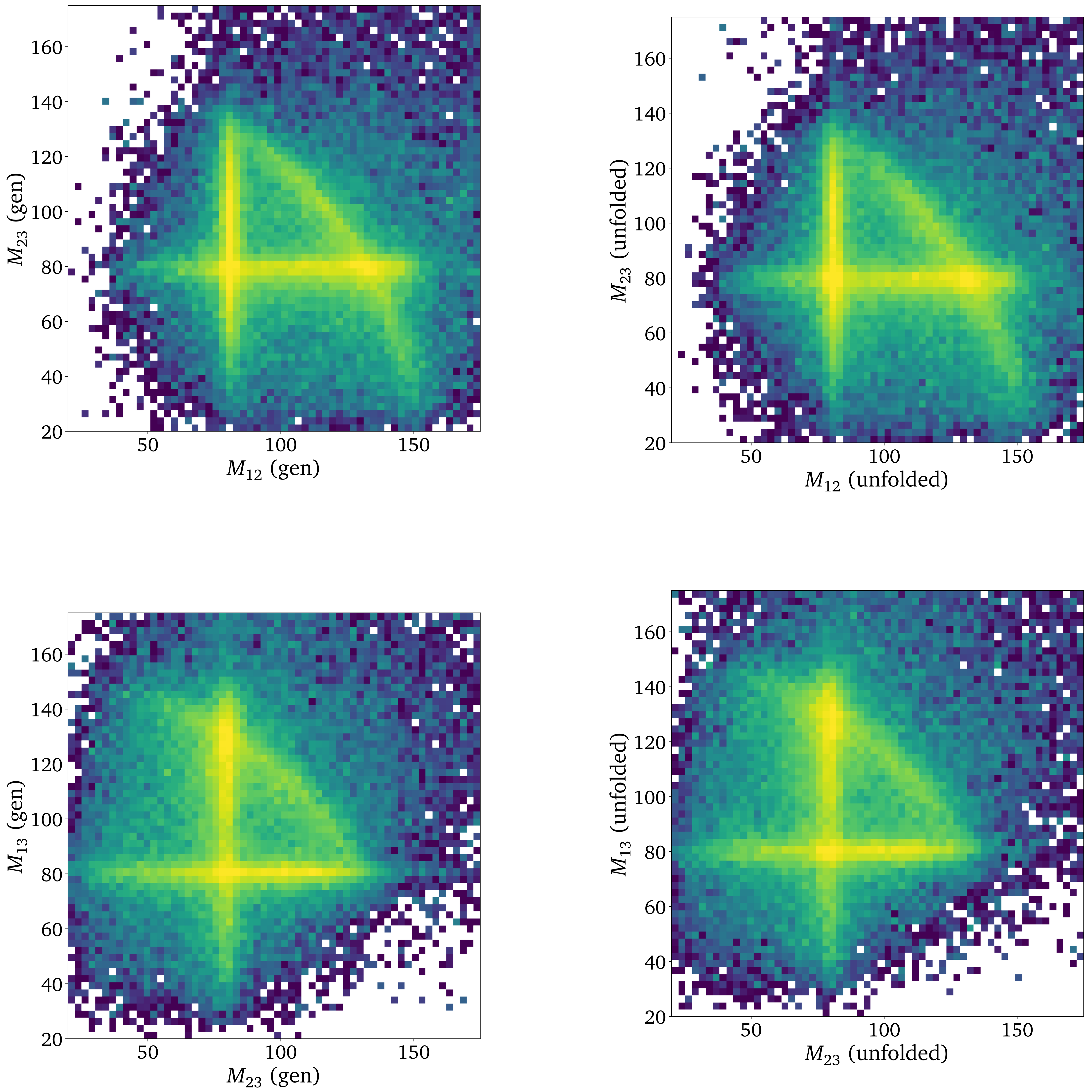


Full Phase Space Unfolding (12d) - Correlations

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. Jet calibration
3. Unfold subset
4. Measure top mass
5. Resimulate
6. Unfold full phasespace

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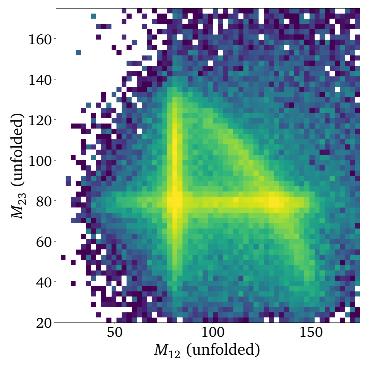

re there any questions?