Mass Minimization without Prejudice

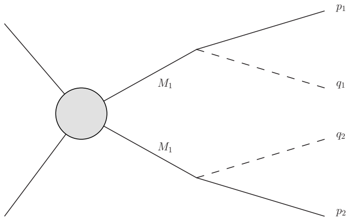
Lim, Sung Hak

Korea Advanced Institute of Science and Technology

September 7, 2015 @ IPMU, Kashiwa

to be appeared on arXiv soon

Pair Production of Semi-invisibly Decaying Particles and Cambridge-M_{T2}



M_{T2} is a mass variable designed for detect masses of identical pair of particles decaying semi-invisibly.

$$M_{T2} \equiv \min_{\substack{q_{1,T}, q_{2,T} \\ q_{1,T}+q_{2,T}=\not{E}_T}} \max[M_T(p_1, q_1), M_T(p_2, q_2)]$$

M_{T2} distribution is bounded above by mother particle's true mass, like M_T's case.

$$M_{T2} \leq \text{parent mass}$$

However, when we do an analysis at the beginning, we don't need to assume the parents are identical.

M_{T2} in Non-identical Pair Production

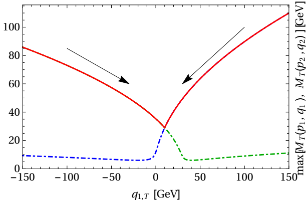
If we consider non-identical pair production, M_{T2} falls into several difficulties:

- The endpoint is only sensitive to the heavy one.

$$M_{T2} \leq \max(M_1, M_2)$$

- M_{T2} does not saturate to the expected endpoint.

These weakness of M_{T2} is originated from the fact that significant portion of the M_{T2} solutions are balanced in two transverse mass.



In the case of balanced configuration of transverse momenta, M_{T2} has an intrinsic constraint

$$M_T(p_1, q_1) = M_T(p_2, q_2)$$

Since the balancedness is encoded in the maximum function, we can try alternative objective functions to get away from symmetric intrinsic constraint.

Minimization of Generalized Mean: Power Mean

As a continuous and smooth generalization of maximum, we considered a power mean μ_p.

$$\hat{\mu}_p(f_1, \cdots, f_n) = \left(\frac{1}{n} \sum_{i=1}^{n} f_i^p \right)^{\frac{1}{p}}$$

p	function
∞	Maximum
2	Root mean square
1	Mean
0	Geometric Mean
-1	Harmonic Mean
$-\infty$	Minimum

- One can define a *minimized power mean*, to construct mass-bounding variables.

$$\mu_p[f] = \min \hat{\mu}_p(f(1), \cdots f(n))$$

- As $p \to \infty$, they converges to their maximum variant such as

$$\lim_{p\to\infty} \mu_p[M_T] = M_{T2} \equiv \min_{\substack{q_{1,T}, q_{2,T} \\ q_{1,T}+q_{2,T}=\not{E}_T}} \max[M_T(p_1, q_1), M_T(p_2, q_2)]$$

$$\lim_{p\to\infty} \mu_p[M] = M_2 \equiv \min_{\substack{q_1, q_2 \\ q_{1,T}+q_{2,T}=\not{E}_T}} \max[M(p_1, q_1), M(p_2, q_2)]$$

Endpoint of μ_p and the Intersection

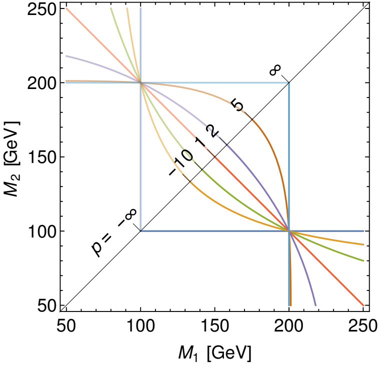
- μ_p also has upper bound originated from its functional form.

$$\mu_p[M_T] \leq \hat{\mu}_p(M_1, M_2), \quad \mu_p[M] \leq \hat{\mu}_p(M_1, M_2)$$

- Each endpoints of power means μ_p distribution constrains distinct region of mass spectrum.

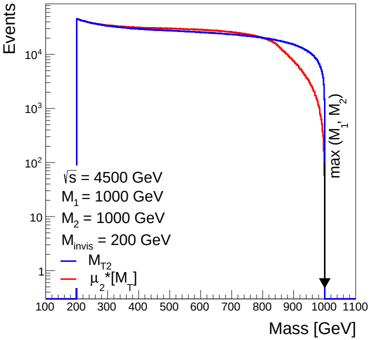
$$\hat{\mu}_p(M_1, M_2) = \mu_p[M_T]^{\max}$$

- The constrained regions eventually intersect around the true parents masses.
- We can pin down the mass spectrum by the endpoint analysis of μ_p's.

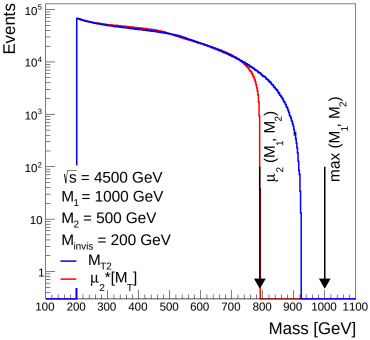


Distribution of μ_p : Two-body Decay

Identical pair production

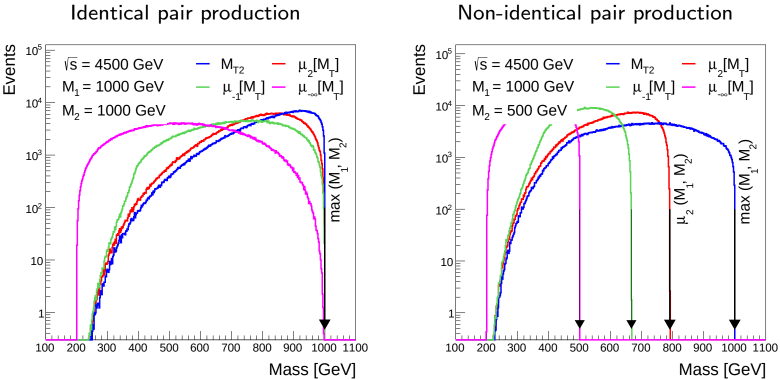


Non-identical pair production



- Sample events are generated from Monte Carlo simulation assuming constant cross section. ISR is not considered.
- Balanced configurations are dominates.

Distribution of μ_p^* : Three-body Decay

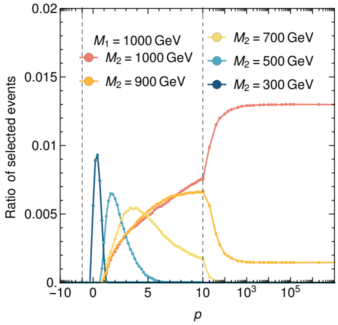


- Sample events are generated from Monte Carlo simulation assuming constant cross section. ISR is not considered.
- Unbalanced configurations contributes to endpoint region becase of rich invariant mass spectrum of net visible momenta in one decay chain.

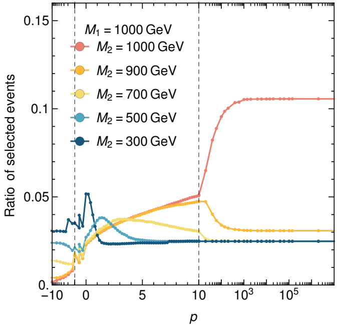
Endpoint Saturation of μ_p

- The fingerprint for distinguishing true mass spectrum is the endpoint region of Histogram.
- The saturation depends on type of configuration:
  - Balanced configuration sensitive to compatibility between intrinsic constraint and true mass spectrum
  - Unbalanced configuration sensitive to the invariant mass of net visible momenta on each decay chain

Two-body decay



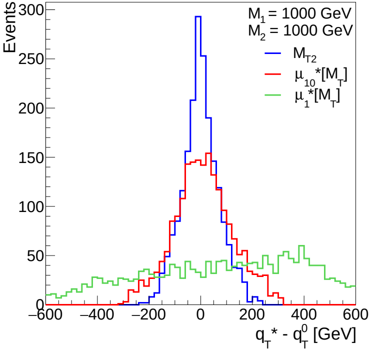
Three-body decay



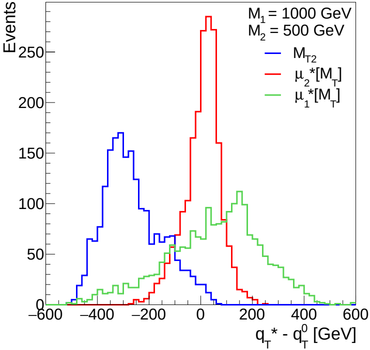
- Ratio of selected events having mass value at least 95% of expected endpoint mass

Event Reconstruction of μ_p

Identical pair production



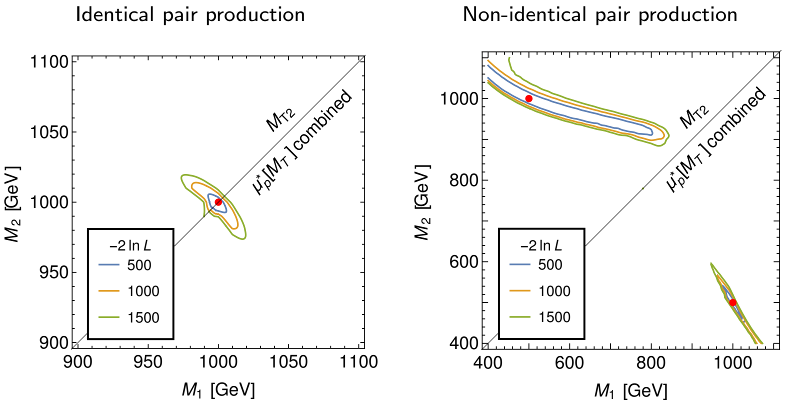
Non-identical pair production



Difference of reconstructed transverse momentum q_T^* and exact transverse momentum q_T^0 of missing particles. Events having the top 0.1% M_{T2} or μ_p are selected.

Likelihood Analysis of μ_p

- To estimate resolving power of each mass variable, we calculated Poisson log-likelihood between a reference sample and a template



- Red point is reference mass spectrum used as a sample.
- From 90% of M_{T2} or μ_p value to endpoint region on template is considered.
- μ_p with $p = 1, 2, 5, 10, 100, 1000$ and M_{T2} is used for combined analysis

Conclusion

- We developed a class of mass functions. which is based on power means, in multiple resonace decay system, which to be minimized over invisible missing momenta with minimal kinematic constraints.
- We show and emphasize that mass variables in the general class can provide significantly enhanced resolving power of measuring generally *a*symmetric resonance masses, which should be complementary to the M_{T2} where its expected endpoint becomes mass-sensitive only when symmetric and identical mother particle masses are assumed.