A New Method for Resolving Combinatorial Ambiguities at Hadron Colliders

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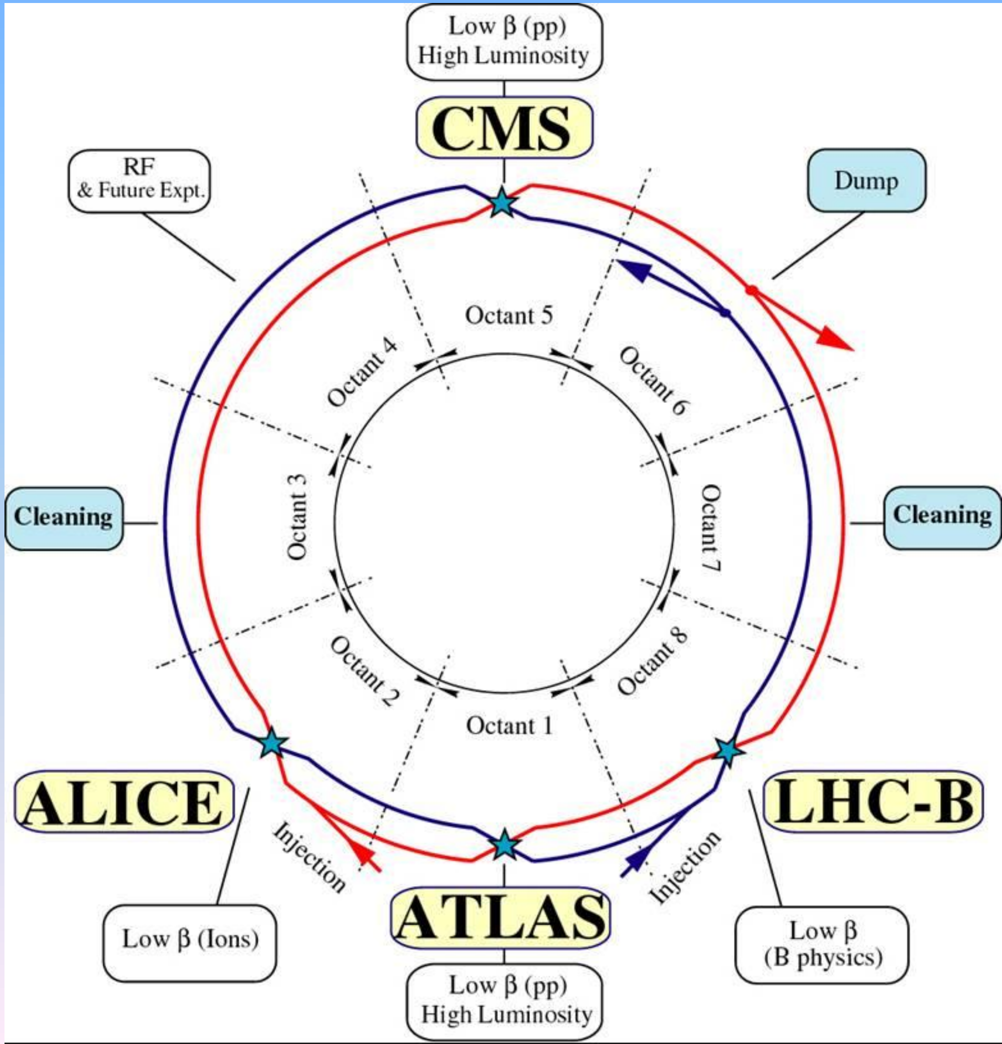
The LHC Era is here!

- The current 7 TeV run will finish in 2011 with ≈1 fb^{-1}
- Potential for new physics (cf. Workshop on Topologies for Early LHC Searches, SLAC, Sept. 22-26, 2010)
- One hope is for the direct production of dark matter



Motivation

- Collider signals of SUSY, UED
  - Cascade decay chains ending in LSP, LKP
  - Z_2 symmetry ensures the LSP, LKP is stable
    - If neutral, is usually a good dark matter candidate
  - Z_2 symmetry ensures the kinematics of the event are not readily measurable
- Many kinematic methods have been developed to aid determination of the LSP, LKP mass

Motivation

- Kinematic edges
  - Thresholds and maximums of invariant mass distributions provide algebraic expressions relating underlying cascade decay chain masses
- Polynomial method
  - Solve momentum conservation equations
  - Use non-linear constraints to solve for LSP, LKP momenta
- m_{T2}, m_{CT2} method
  - m_{T2} Kink
  - Sub-system m_{T2}
  - m_{T2} as a discovery variable

Baer, Chen, Paige, Tata, Hinchliffe
Allanach, Lester, Parker, White
Barr, Gripaios, Nojiri, Cheng, Gunion, Han, Marandella, McElrath, …

Motivation

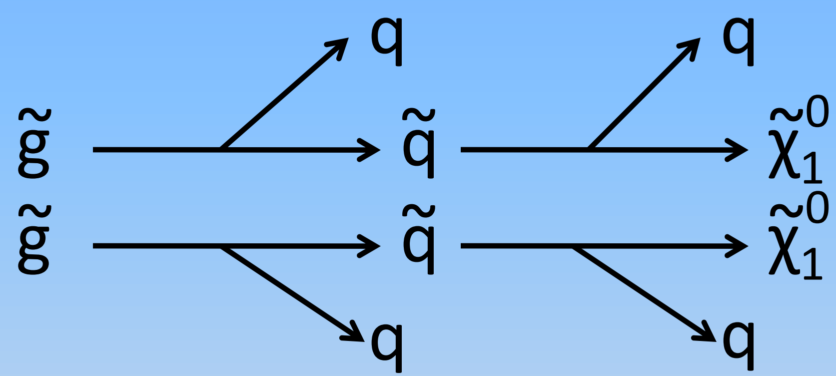
- Need the LSP, LKP mass to determine the mass scale
  - Differences in masses are easy
- Usual procedure to solve for LSP, LKP mass:
  1. Use cuts to isolate some collection of objects (*e.g.* 4 jets inclusive + 0 leptons + MET), eliminate background
  2. Hypothesize an underlying decay chain topology (*e.g.* pair-produced gluinos decaying to neutralinos via squarks)
  3. Assign objects to decay chains (ordered, if possible)
  4. Apply your favorite mass reconstruction technique

Motivation

Method	Decay chain assignment? (Combinatorial ambiguity)	Ordering required? (Permutative ambiguity)
H_T, M_{eff}	No	No
Kinematic edges	Yes	Yes/No
Polynomial	Yes	Yes
m_{T2}	Yes	No
m_{CT2}	Yes	No
Subsystem m_{T2}	Yes	Yes

Motivation

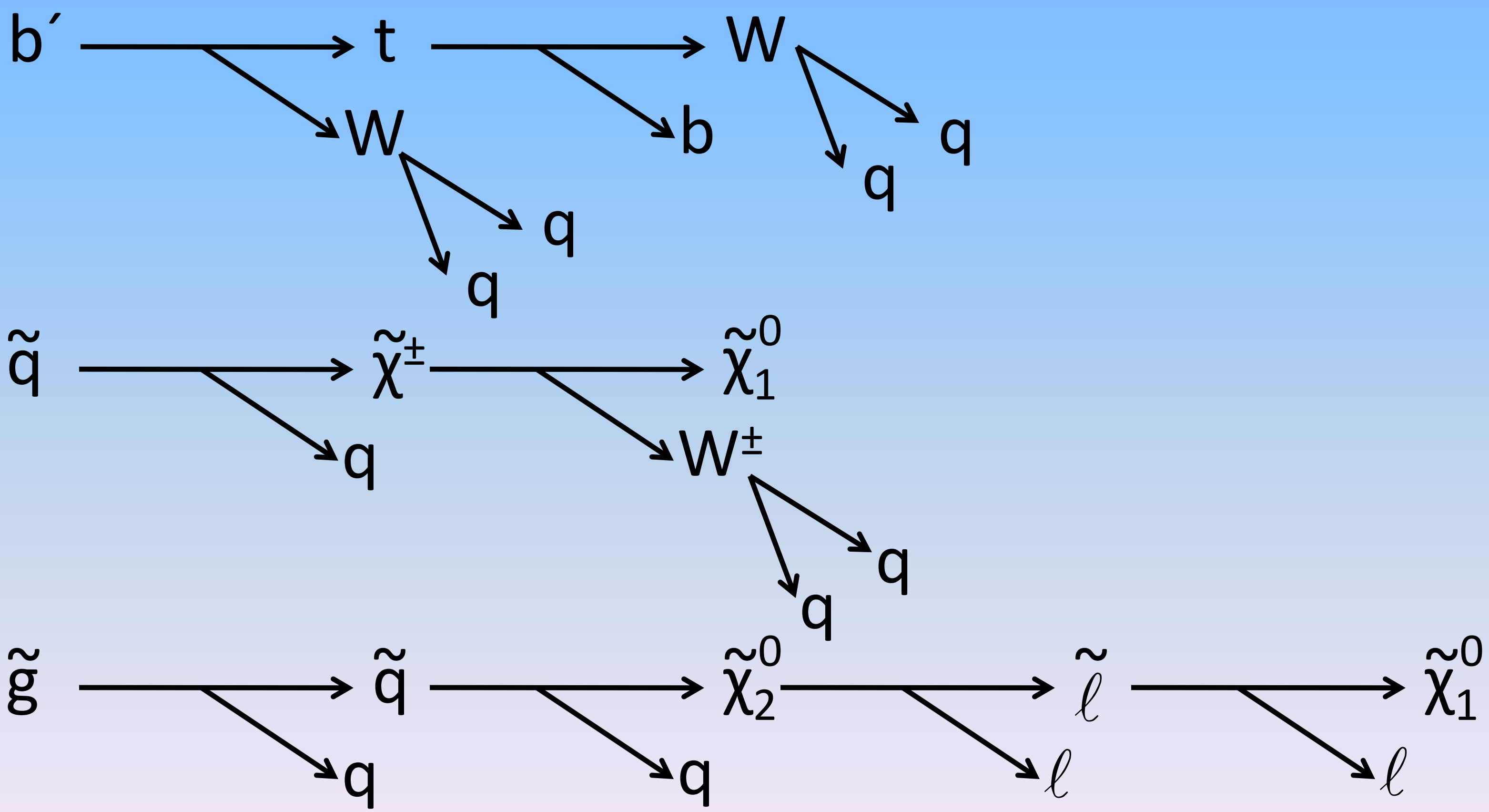
- Decay chain assignments must deal with combinatorial ambiguities



- For pair-produced gluinos decaying to LSPs via squarks, we have 4 quarks that can be grouped into 3 pair-pair combinations
  - Important note: this combinatorial ambiguity is present even if dealing with only signal events

Motivation

- Other possibilities: in busy cascade decay chains, it is important to associate particles correctly
- Usually, there are additional tools to eliminate wrong combinations



Outline

- Motivation
- Our simple models
- Brief review of basic kinematics
- The well-studied hemisphere method
- The new p_T v. M method
- Comparison
- Conclusions

Models

- Consider gluino pair-production in a 7 TeV LHC or 14 TeV LHC, both decay identically via on-shell or off-shell squarks to LSP neutralino

	Gluino Mass	Squark Mass	Neutralino Mass	Kinematic Edge
Model A	600 GeV	400 GeV	100 GeV	433 GeV
Model B	600 GeV	800 GeV	100 GeV	500 GeV

- Generate 100,000 events using MadGraph/MadEvent 4.4.26, decay using BRIDGE
  - No ISR/FSR, hadronization
  - Only consider parton level

Kinematic edge in invariant mass

- An oft-used feature of cascade decay chain kinematics is the invariant mass edge
- On-shell squark – characteristic triangular shape

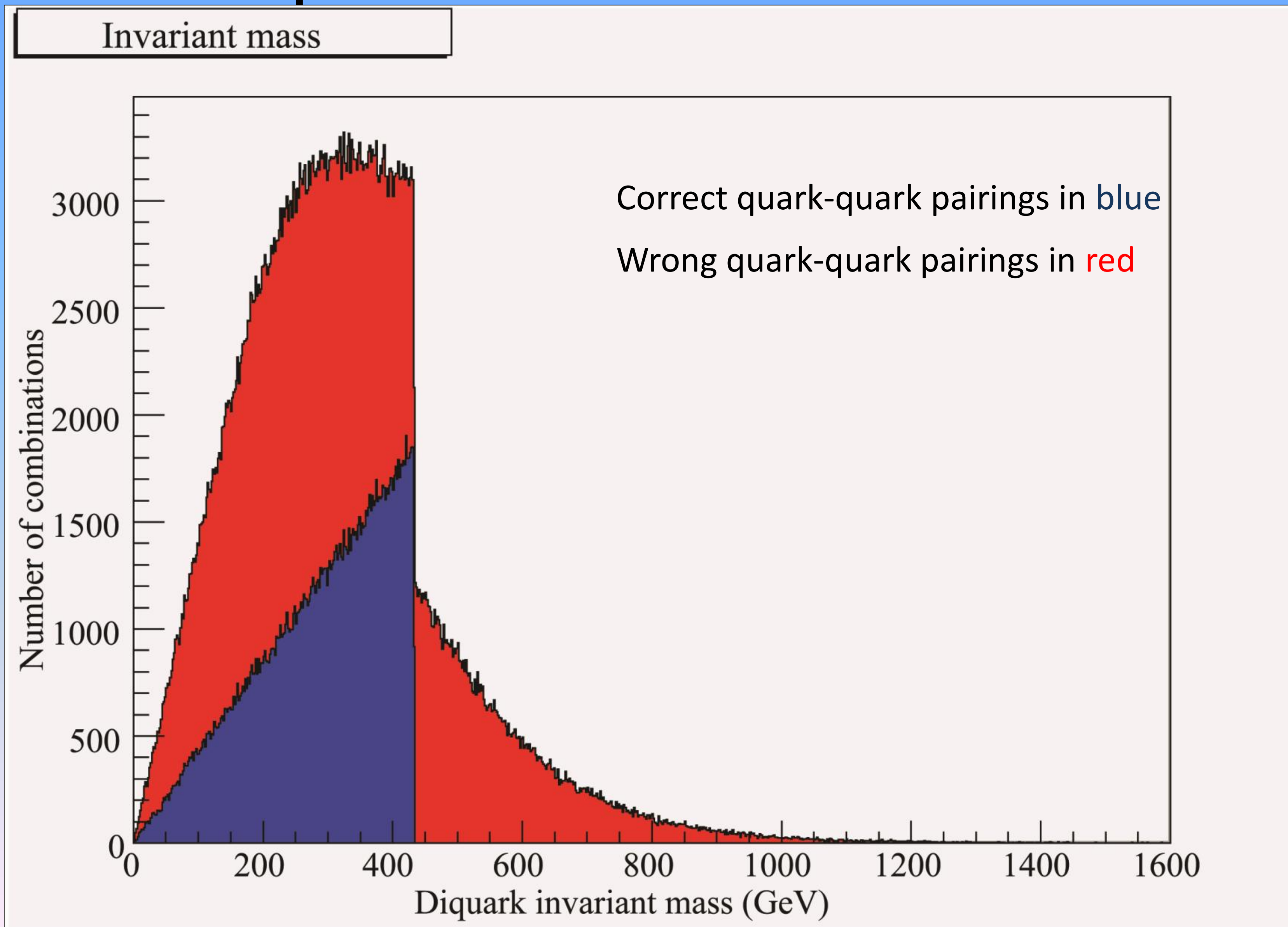
$$m_{qq}\big|_{\mathrm{edge}} = \sqrt{\frac{(m_{\tilde{g}}^2 - m_{\tilde{q}}^2)(m_{\tilde{q}}^2 - m_{\tilde{\chi}_1^0}^2)}{m_{\tilde{q}}^2}}$$

- Off-shell squark – small number of events near edge

$$m_{qq}\big|_{\mathrm{edge}} = m_{\tilde{g}} - m_{\tilde{\chi}_1^0}$$

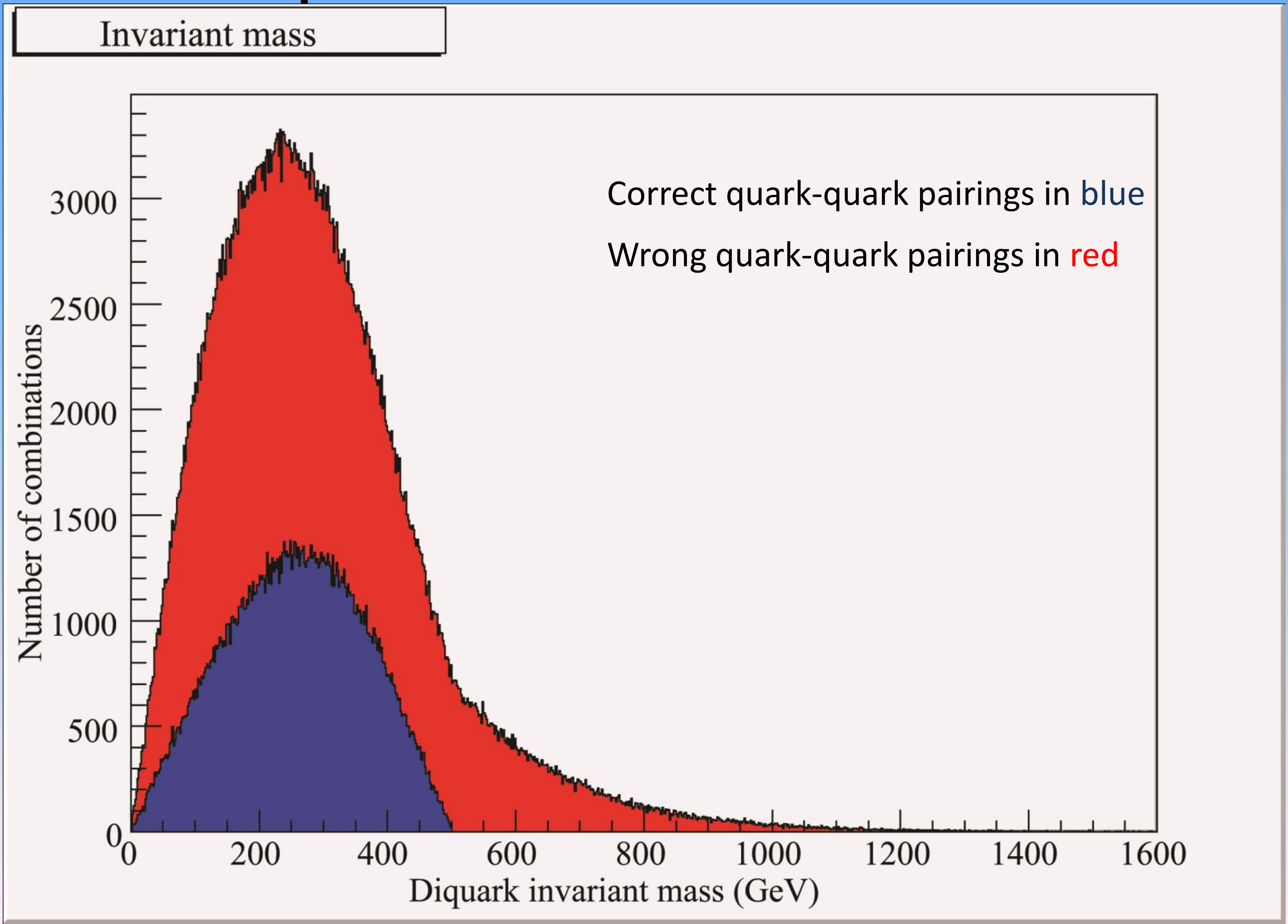
Kinematic edge in invariant mass

On-shell squark scenario



Kinematic edge in invariant mass

Off-shell squark scenario



The Hemisphere Method

- Basic idea: divide an event into hemispheres where each decay chain falls entirely into separate hemispheres
- Two steps
  - Step 1: Choose 2 seeds
    - These are the central axes for the hemisphere clusters
  - Step 2: Cluster remaining objects with the given seeds
    - Figure of merit is minimum pdR: roughly, a momentum-weighted angular separation

      $pdR \equiv (|\Delta p|\ \Delta R)$, where $\Delta R \equiv \sqrt{[(\Delta\phi)^2 + (\Delta\eta)^2]}$

The Hemisphere Method

- Our implementation

1. Choose highest p_T object as seed 1
2. **PDR1**. Of the remaining objects, choose the maximum pdR object as seed 2

   PDR2. Of the remaining objects, choose the maximum invariant mass object as seed 2
3. For each remaining objects, calculate pdR w.r.t seed 1 and w.r.t. seed 2. Cluster the object with whichever seed has the smaller pdR, *i.e.* the closer seed in momentum-weighted angle space.

The Hemisphere Method

- Our cuts

  Cut 1. The highest p_T object must have $p_T \geq 200$ GeV

  PDR1 Cut 2. The minimum pdR between seed 1 and seed 2 must be 1800 GeV

  PDR2 Cut 2. The invariant mass of seed 1 and seed 2 must be larger than the kinematic edge value

  Cut 3. Discard all singlet-triplet events

  Cut 4. The maximum seed-object invariant mass must be less than or equal to the kinematic edge value

The Hemisphere Method

- Our cuts do not include realistic detector cuts (η-acceptance, minimum p_T, isolation requirements)

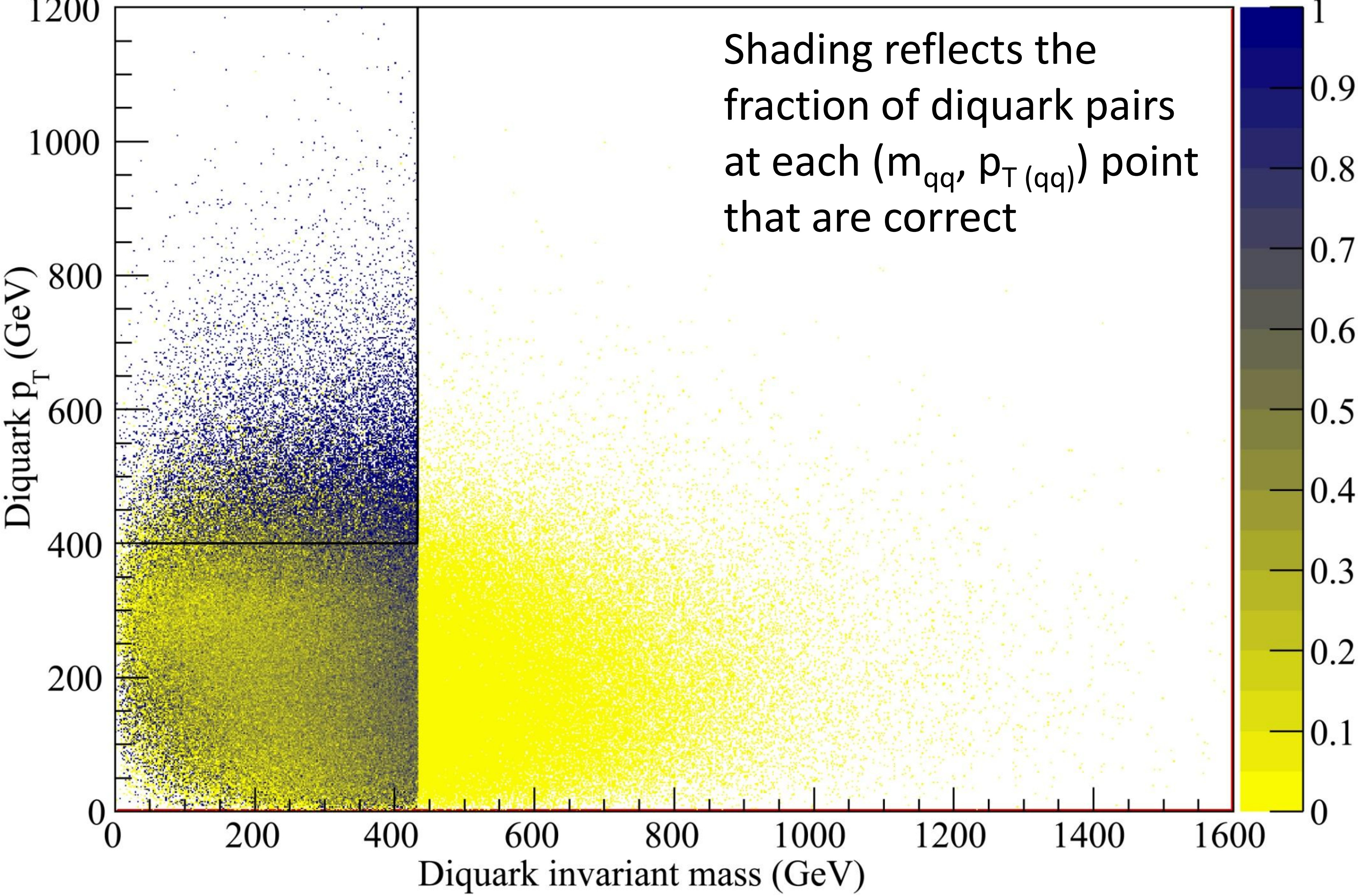
PDR 1 Cut Performance	Cut 1	Cuts 1-2	Cuts 1-3	Cuts 1-4
Model A – 7 TeV	78.8%	25.2%	12.4%	12.2%
Model A – 14 TeV	81.7%	35.8%	18.5%	18.2%
Model B – 7 TeV	81.8%	27.1%	13.4%	13.3%
Model B – 14 TeV	83.9%	37.5%	19.2%	18.7%

PDR 2 Cut Performance	Cut 1	Cuts 1-2	Cuts 1-3	Cuts 1-4
Model A – 7 TeV	78.8%	51.4%	26.1%	25.7%
Model A – 14 TeV	81.7%	58.1%	30.5%	30.1%
Model B – 7 TeV	81.8%	38.5%	19.6%	19.6%
Model B – 14 TeV	83.9%	46.1%	24.4%	24.4%

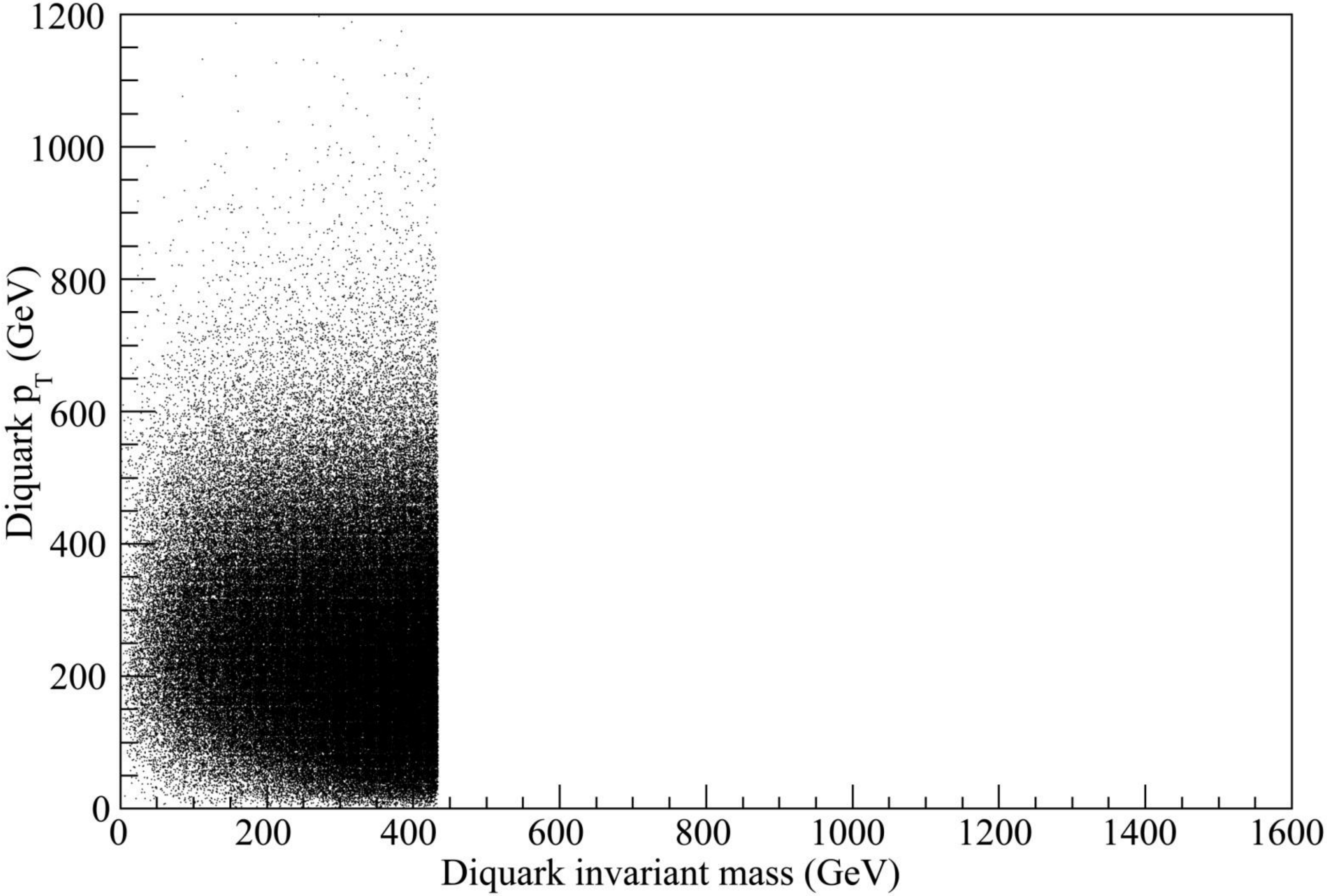
The New p_T v. M Method

- Plot p_T v. M for each qq pair of the event
  - Each event has 6 unique qq pairs; 2 pairs are correct, 4 pairs are wrong
  - The 6 qq pairs can be grouped into 3 unique pair-pair combinations, one of which is correct
  - We want to isolate the correct pair-pair combination
- Observe excesses at high invariant mass (wrong diquark pairs) and high p_T (correct diquark pairs)

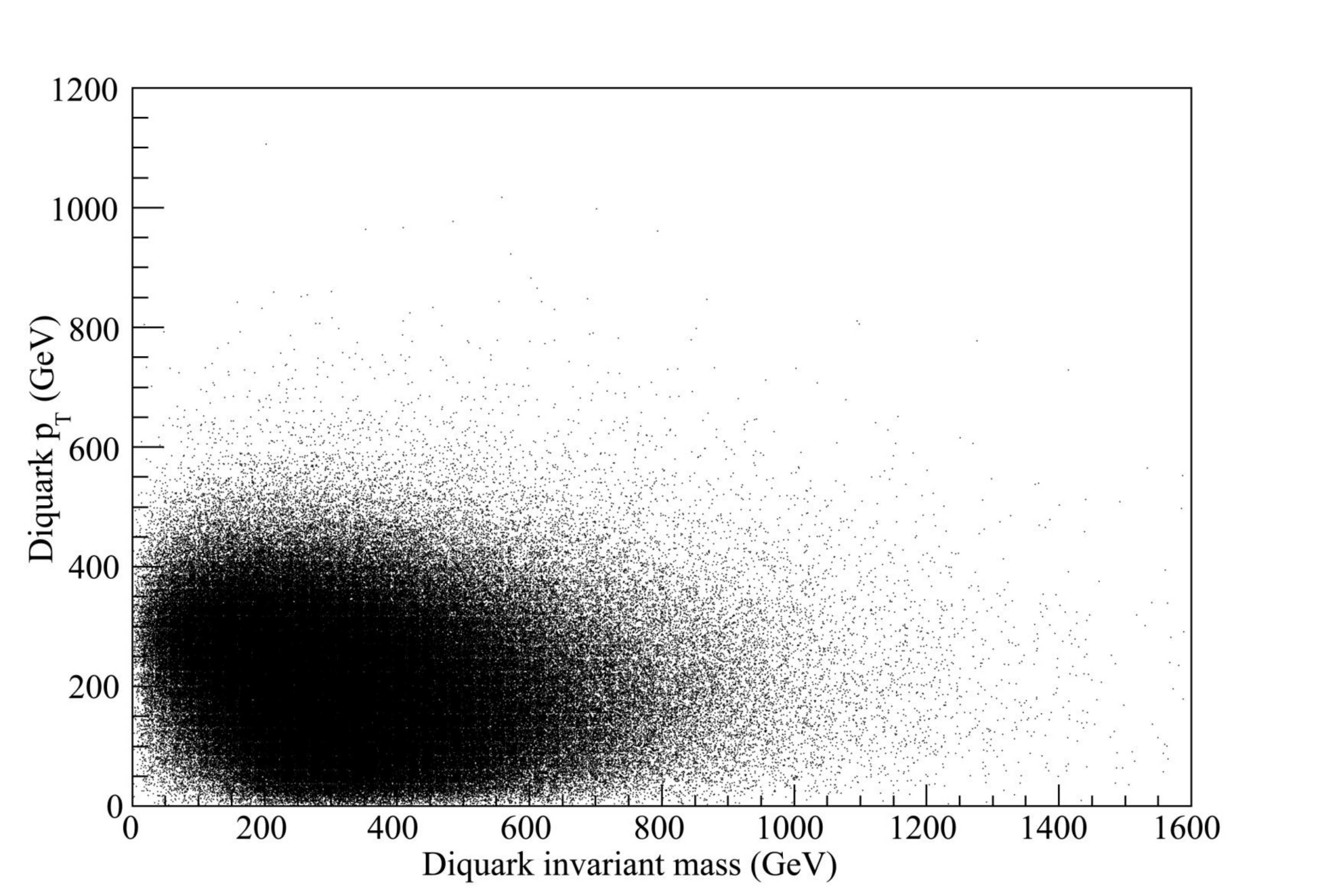
The p_T v. M method – Model A 7 TeV



The p_T v. M method – Model A 7 TeV – **Correct** Diquark Pairs Only



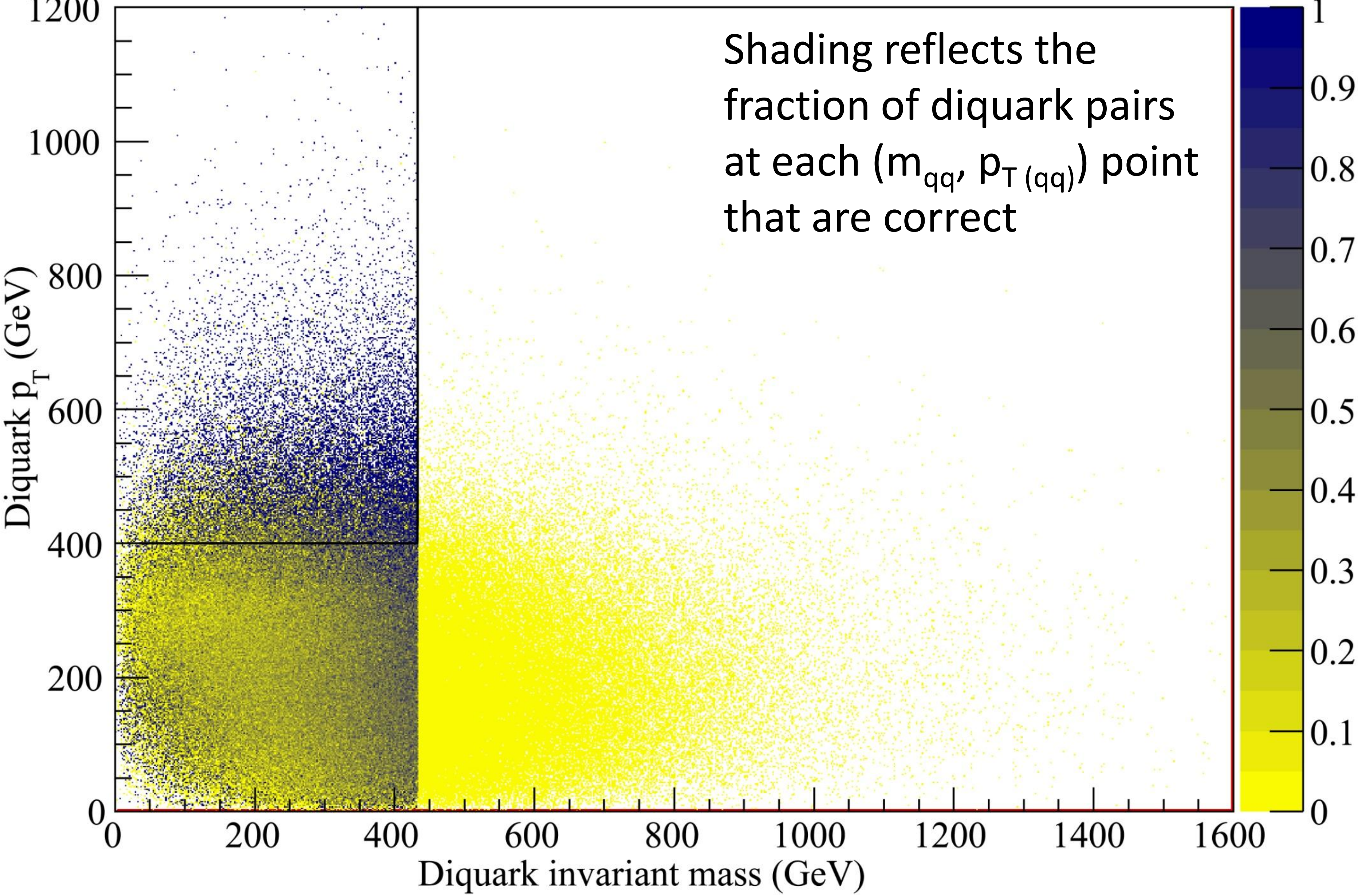
The p_T v. M method – Model A 7 TeV – **Wrong** Diquark Pairs Only



The p_T v. M Implementation

- Plot p_T v. M for each qq pair of the event
  - If possible, observe the invariant mass edge
  - For the (wrong) pairs with invariant masses larger than the edge value, gradually increase the p_T cut such that the survival rate of pairs drops below 5%
  - Extrapolate this cut to the upper left region with high p_T and low invariant mass
    - This region will characteristically have high purity, *i.e.* be dominated by correct diquark pairs
    - Only use pair-pair combinations where both diquark pairs lie in the boxed region

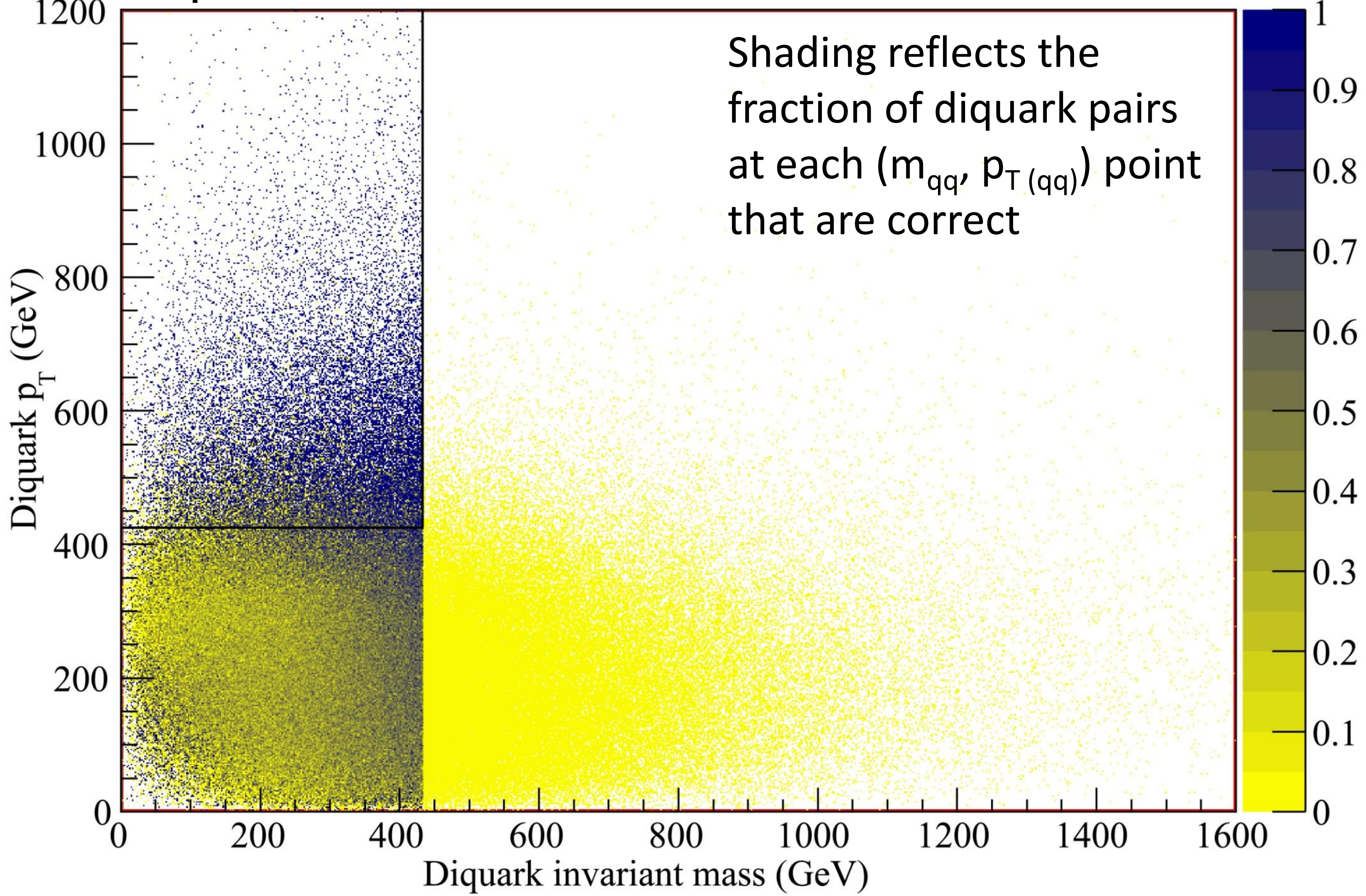
The p_T v. M method – Model A 7 TeV



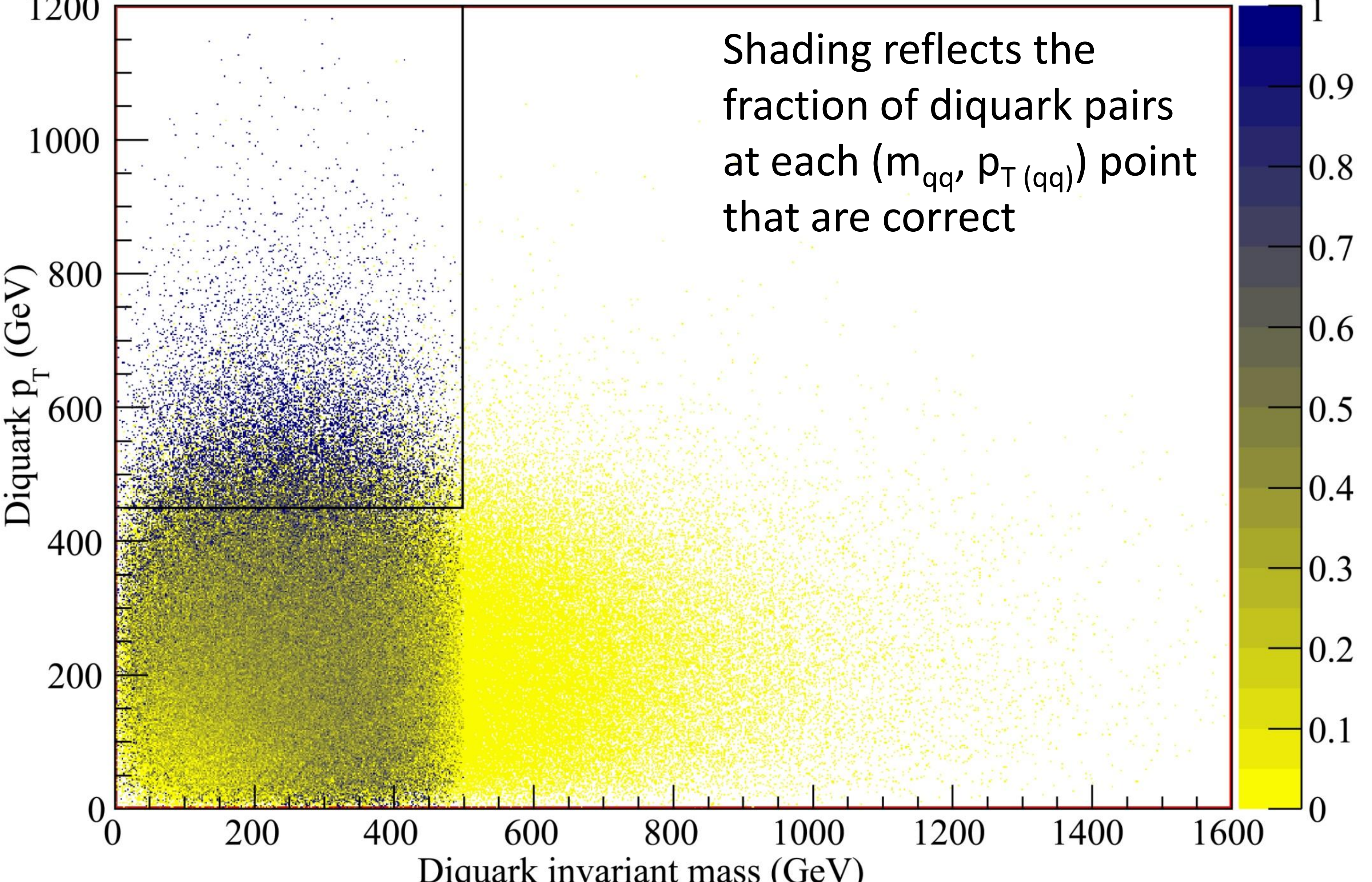
Survival Probability

Cut on min p_T	Survival %
0	100.000%
25	98.525%
50	94.402%
75	88.347%
100	80.857%
125	72.162%
150	62.948%
175	53.796%
200	44.963%
225	36.548%
250	29.014%
275	22.481%
300	16.960%
325	12.398%
350	8.982%
375	6.275%
400	**4.378%**
425	3.007%
450	2.077%
475	1.427%
500	0.994%

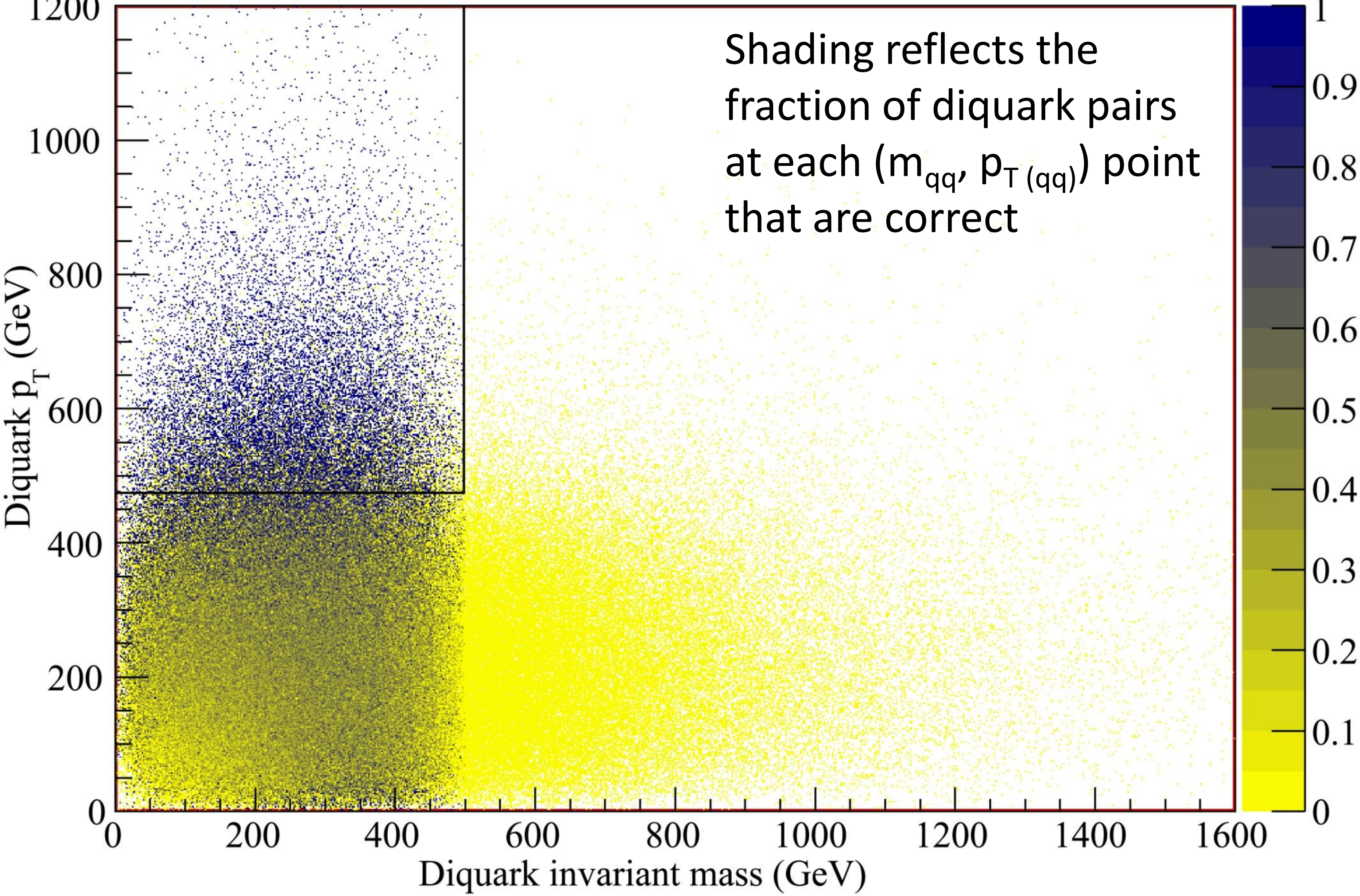
The p_T v. M method – Model A 14 TeV



The p_T v. M method – Model B 7 TeV

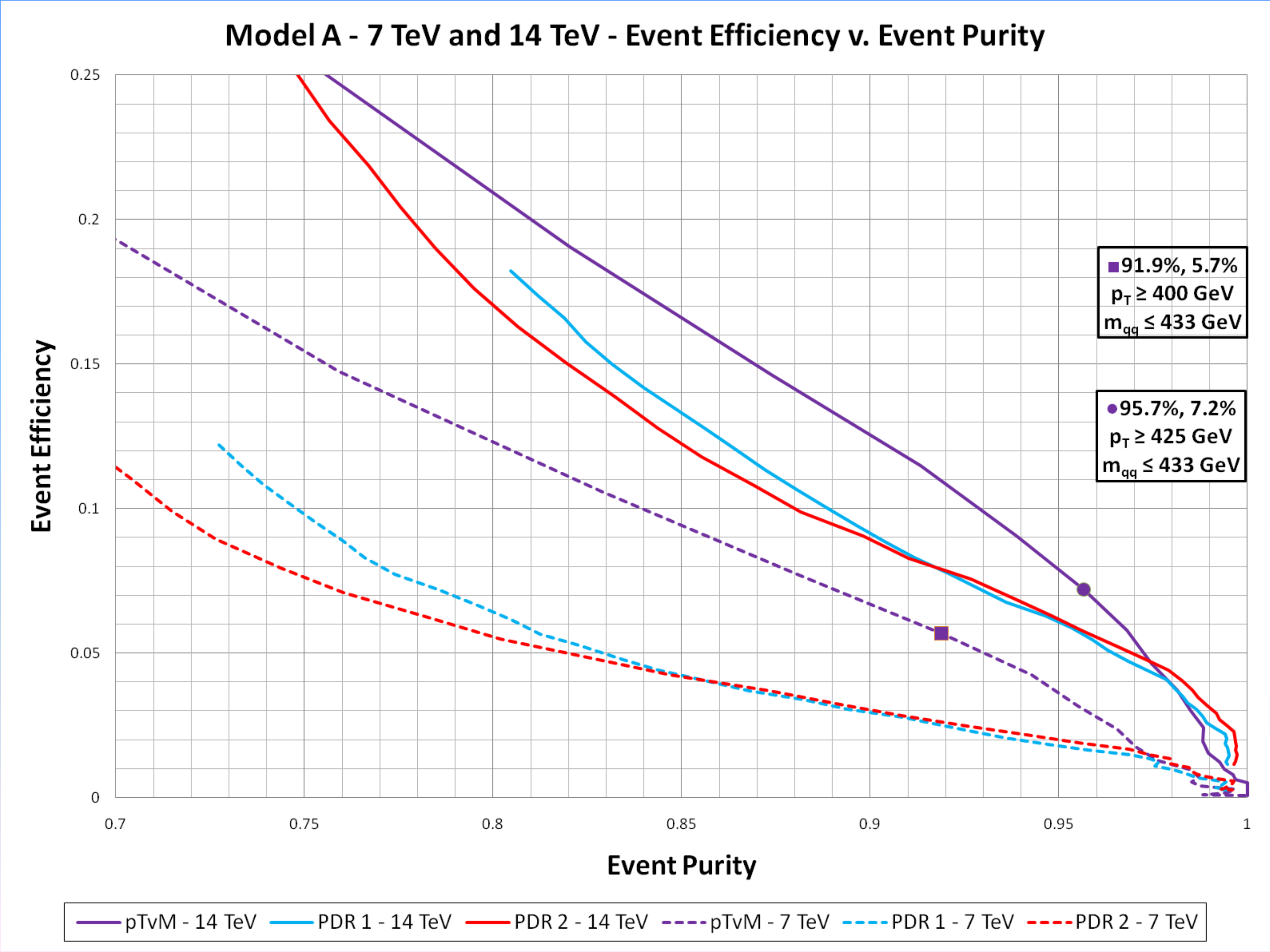


The p_T v. M method – Model B 14 TeV



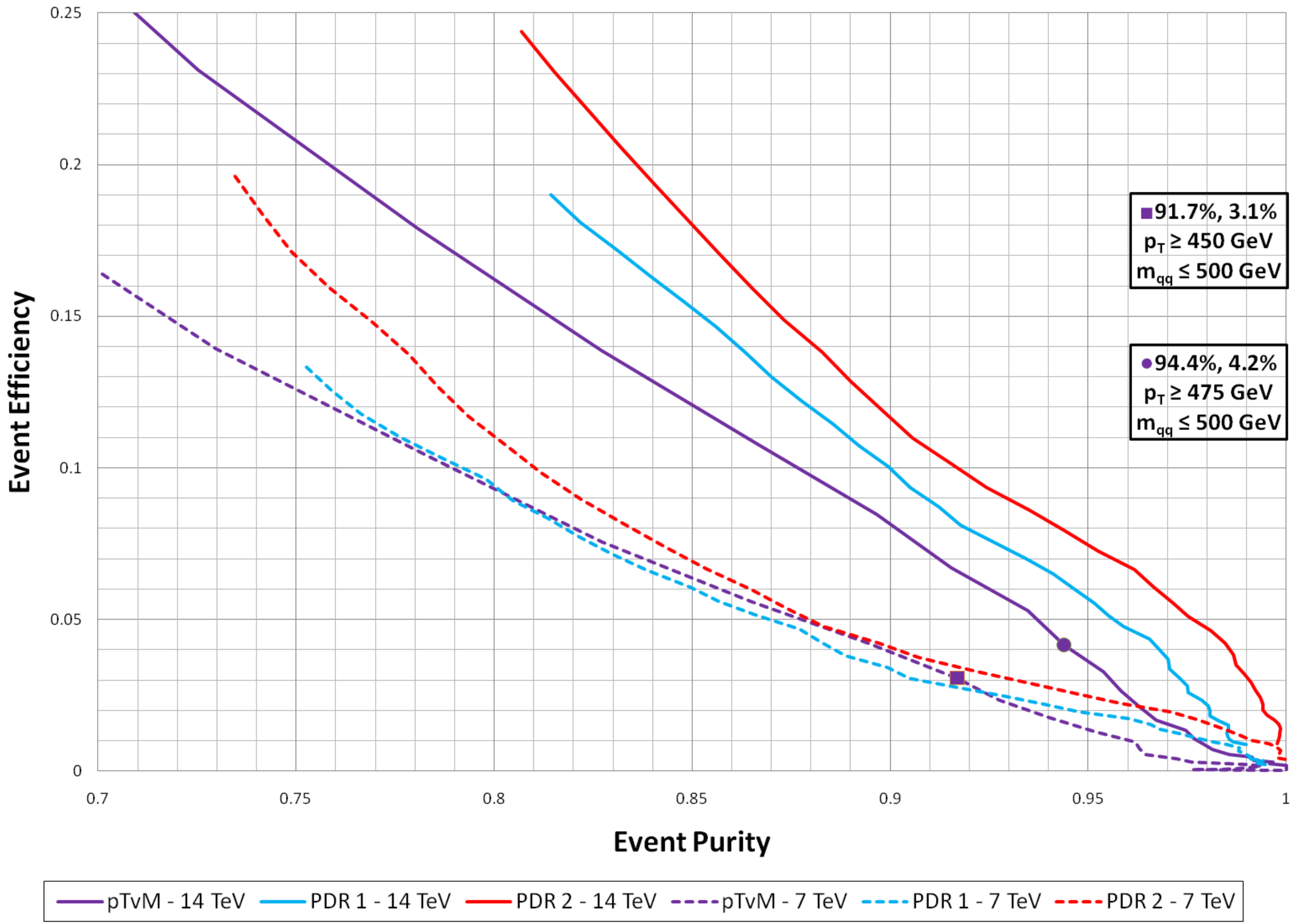
Comparison between the hemisphere method and the p_T v. M method

- Will use event efficiency v. event sample purity
  - Event efficiency is the percentage of events that pass cuts
  - Event purity is the percentage of remaining events that are fully correctly assigned
- Variable cut
  - Hemisphere method: Vary the object-seed pdR difference
    - Example: For a given object, its pdR w.r.t seed 1 is 500 GeV, and its pdR w.r.t seed 2 is 505 GeV. By the pdR measure, it could equally well be clustered with seed 1 or 2. By imposing an increasing pdR difference cut (a minimum difference in pdR between an object and the two seeds), we can gradually eliminate these ambiguous assignment scenarios.
  - p_T v. M method: Vary the survival probability in the (wrong) diquark pairs region at high invariant mass
    - Equivalently, require a higher p_T cut



Model A - 7 TeV and 14 TeV - Event Efficiency v. Event Purity
0.25
0.2
0.15
0.1
0.05
0
Event Efficiency
0.7
0.75
0.8
0.85
0.9
0.95
1
Event Purity
■91.9%, 5.7%
$p_T \geq 400$ GeV
$m_{qq} \leq 433$ GeV
●95.7%, 7.2%
$p_T \geq 425$ GeV
$m_{qq} \leq 433$ GeV
pTvM - 14 TeV
PDR 1 - 14 TeV
PDR 2 - 14 TeV
pTvM - 7 TeV
PDR 1 - 7 TeV
PDR 2 - 7 TeV

Model B - 7 TeV and 14 TeV - Event Efficiency v. Event Purity



Discussion

- On-shell decay chains
  - p_T v. M is significantly better than the hemisphere method in retaining more event efficiency for a given event purity
- Off-shell decay chains
  - p_T v. M is marginally to moderately worse than the hemisphere method
    - Possibly because of the flexibility in choosing second hemisphere axis

Discussion

- p_T v. M is more flexible
  - No distinction between choosing seeds and clustering
  - If seed 1 and seed 2 are incorrect, the hemisphere method fails
    - Requires strict cuts to ensure seed 1 and seed 2 are from different decay chains
- p_T v. M and the hemisphere method are readily generalized
  - Multi-jets, leptons, complicated decay chains including W and Z bosons

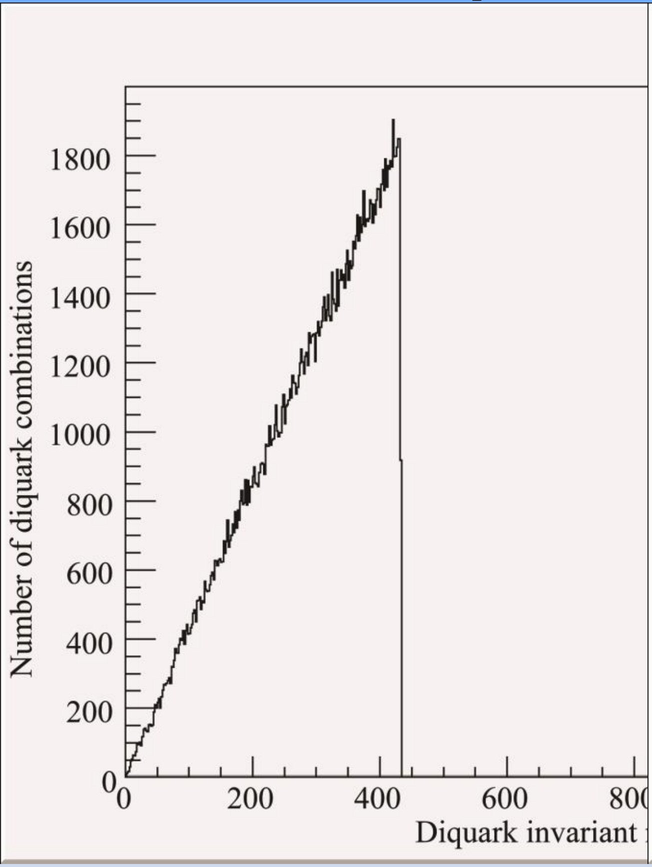
Future Work

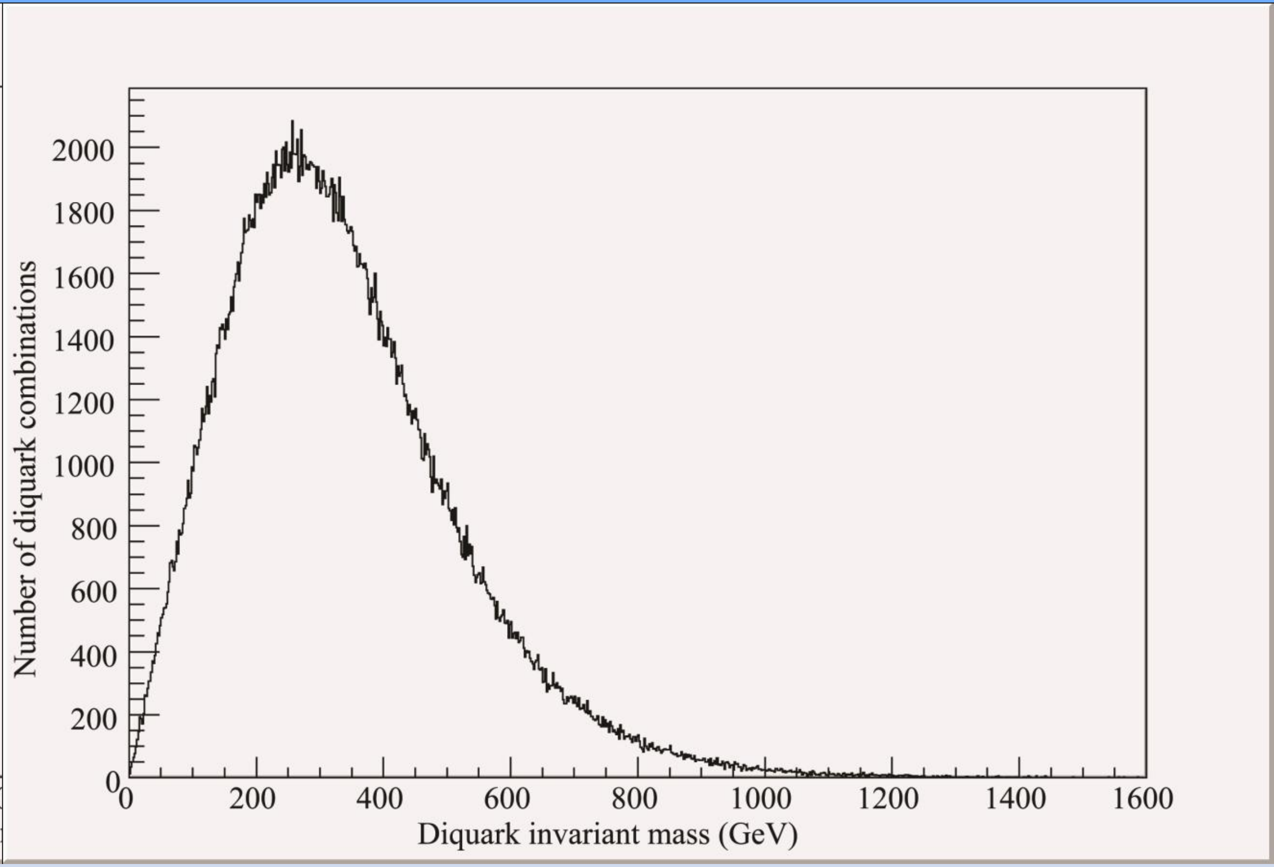
- Apply p_T v. M at reconstruction level
  - SPS1a including ISR/FSR, detector simulation
- Perform shape analysis of p_T v. M
  - Optimize the p_T v. M cut
- Reorganize p_T v. M to be an event-by-event variable
- Perform a detailed study of p_T v. M and the hemisphere method in off-shell cases
  - Should use both in parallel since it is not known a priori whether the decay chain is on-shell or off-shell

Conclusions

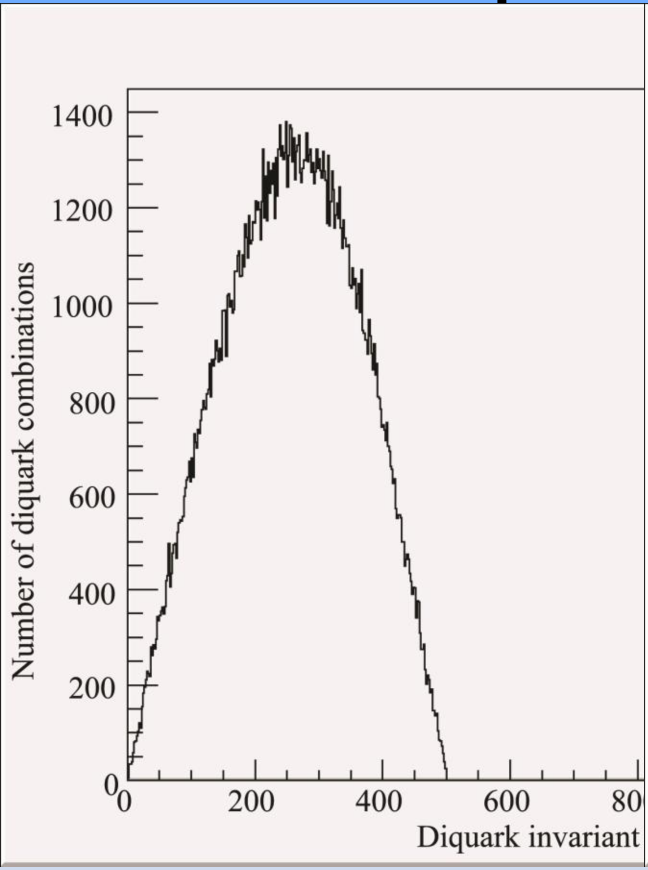
- Distinguishing combinatorial ambiguities is important for new physics searches at the LHC
- The p_T v. M method is better than the hemisphere method for on-shell decay chains in delivering high purity event samples
  - The hemisphere method is better suited for off-shell decay chains
- The p_T v. M method is easy to implement and flexible
  - A "robustness" study in a simulated collider environment is underway

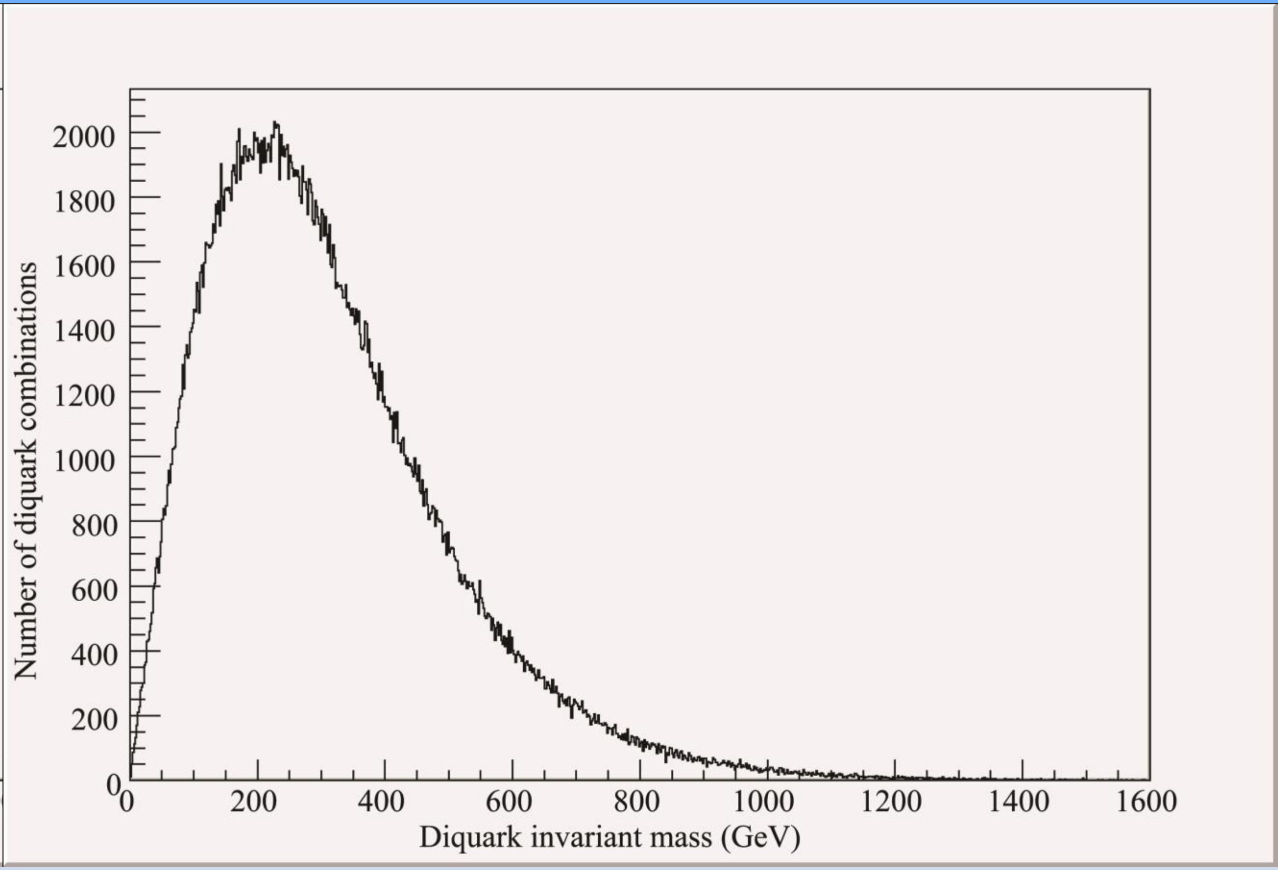
Kinematic edge in invariant mass
On-shell squark scenario





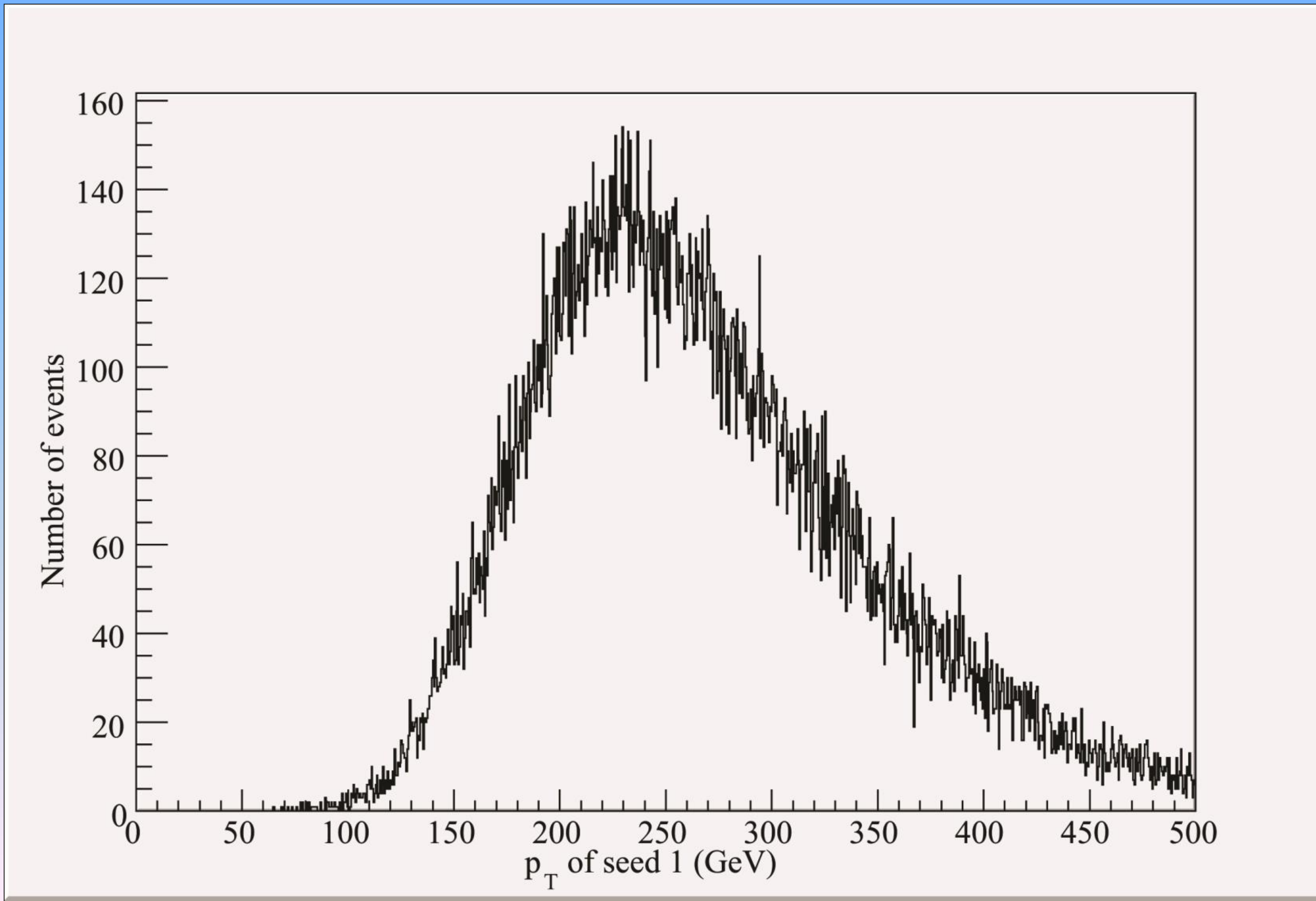
Kinematic edge in invariant mass
Off-shell squark scenario





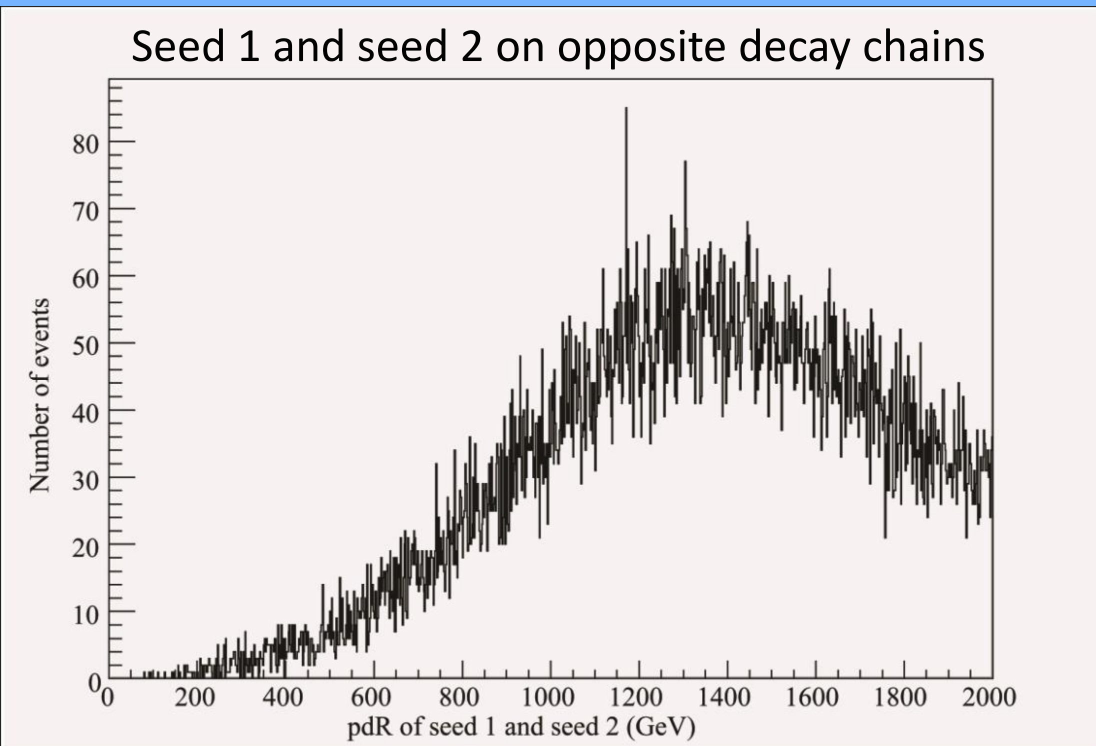
The Hemisphere Method – Cut 1

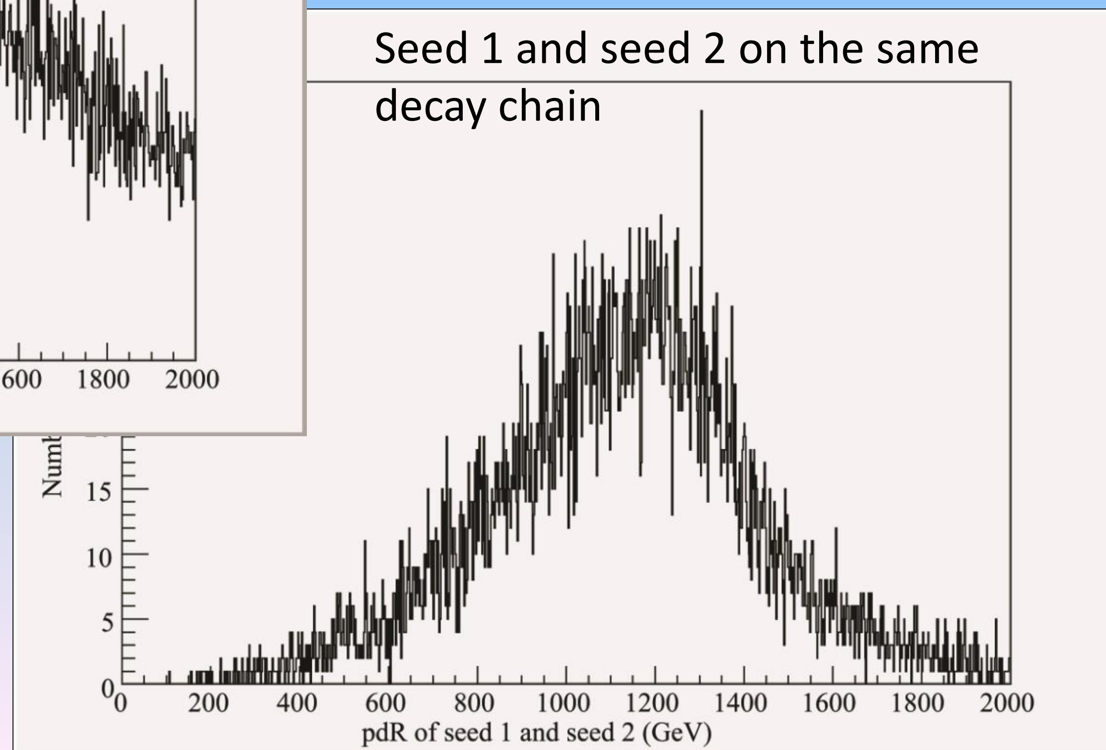
p_T (of seed 1) ≥ 200 GeV



The Hemisphere Method – PDR 1 Cut 2

pdR (of seed 1 and seed 2) ≥ 1800 GeV

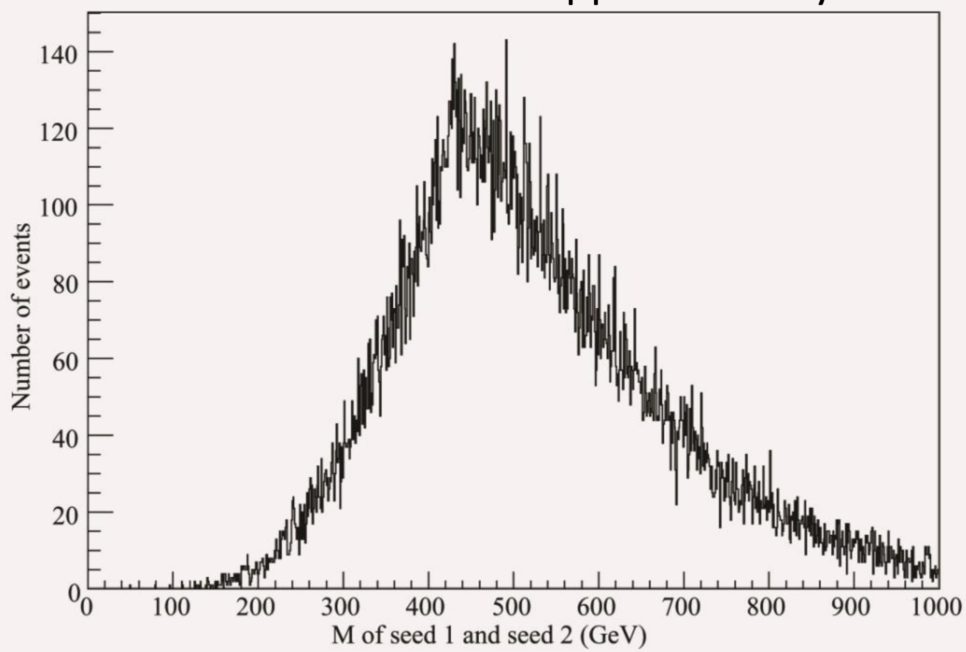




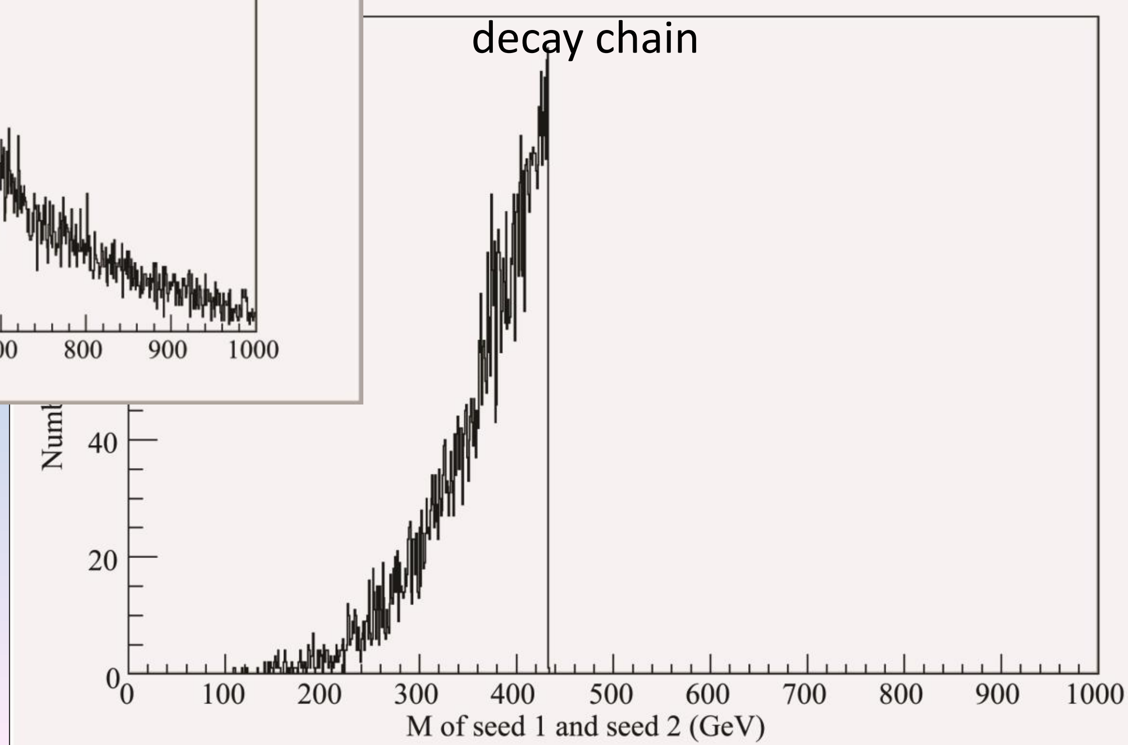
The Hemisphere Method – PDR 2 Cut 2

M (of seed 1 and seed 2) > M_{edge}

Seed 1 and seed 2 on opposite decay chains



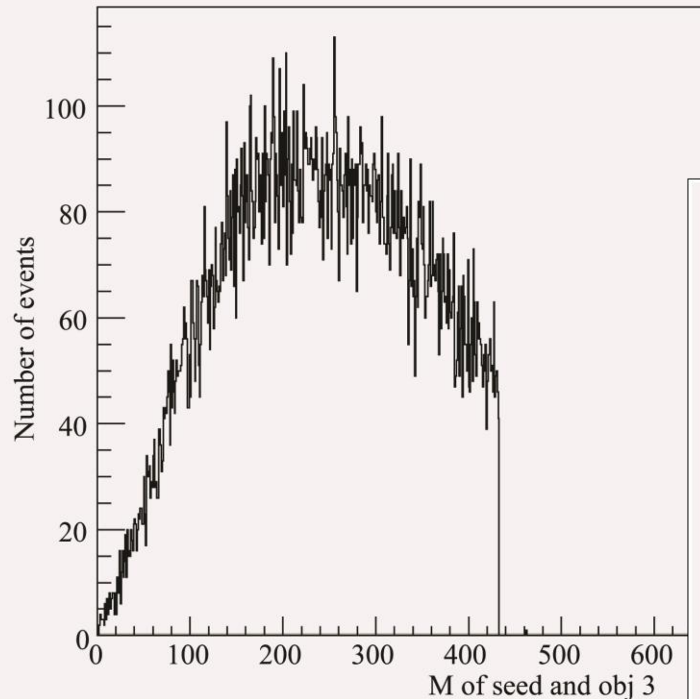
Seed 1 and seed 2 on the same decay chain



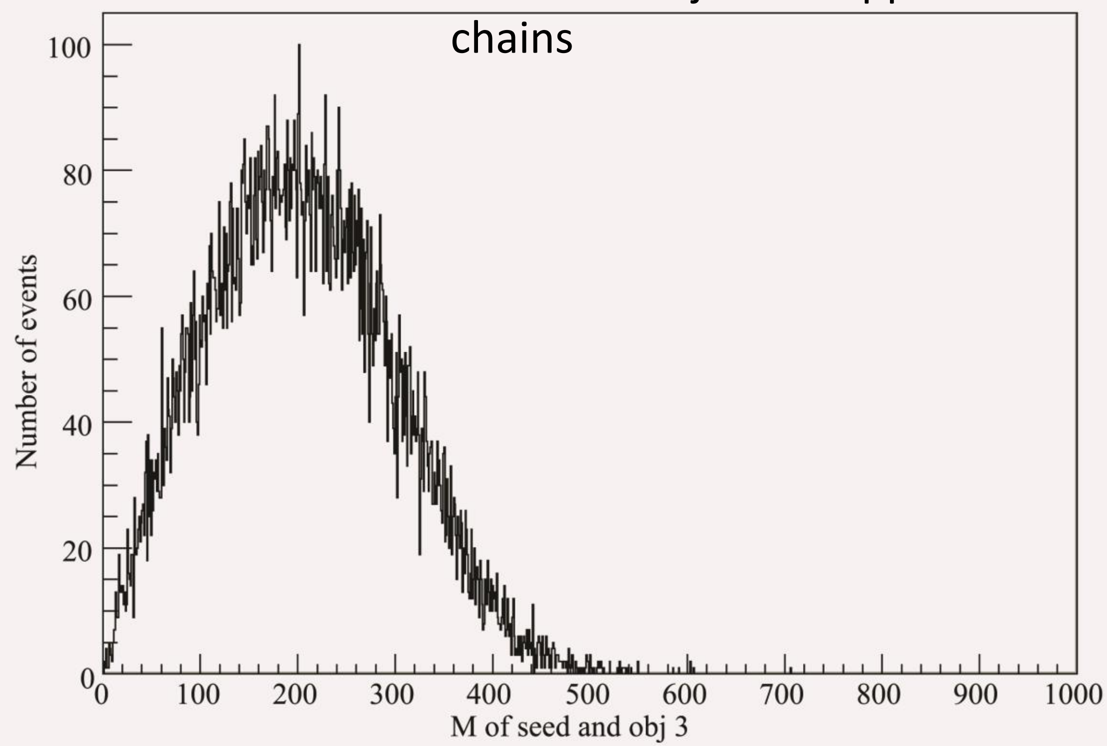
The Hemisphere Method – PDR 1 Cut 4

M (of seed and object) $\leq M_{edge}$

Seed and object on the same decay chain



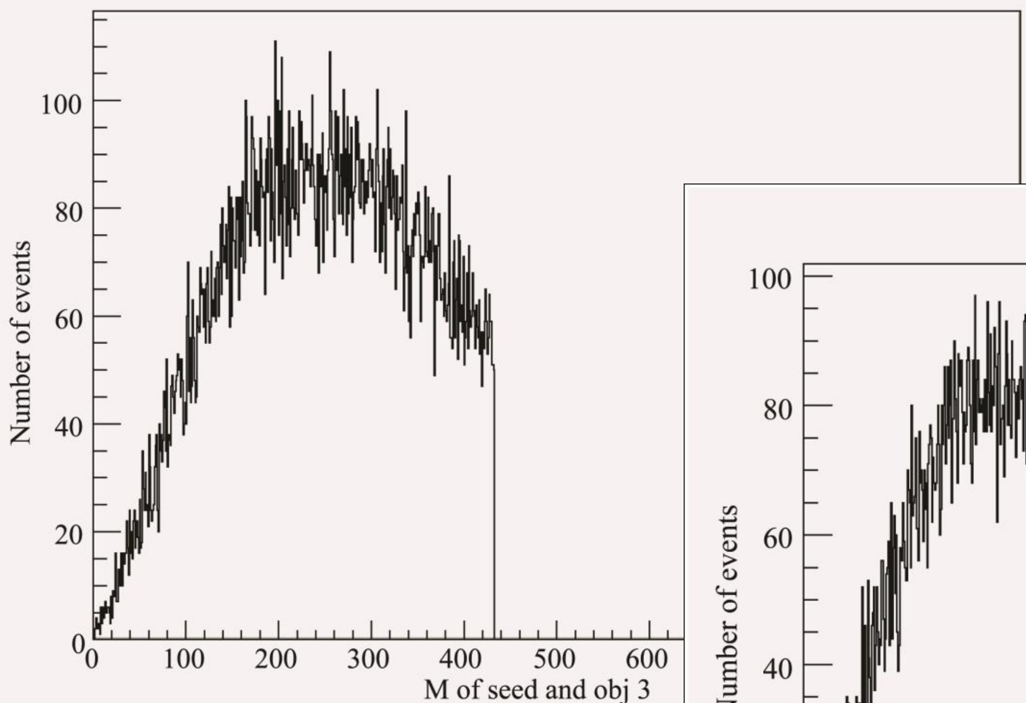
Seed and object on opposite decay chains



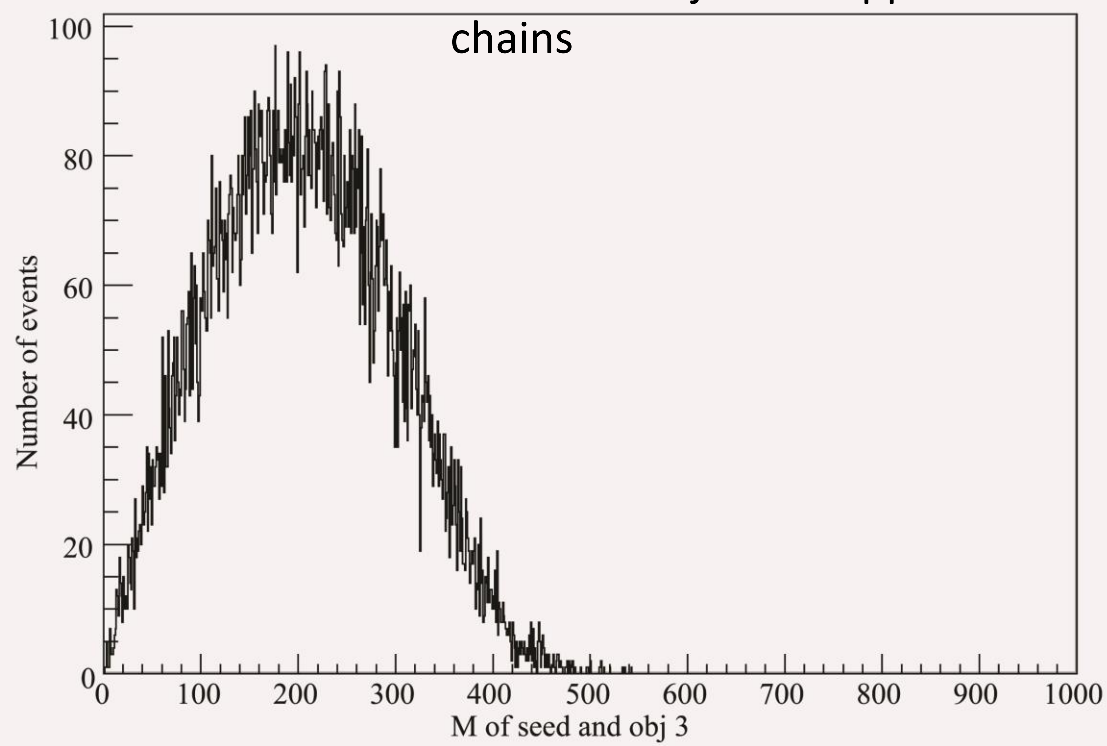
The Hemisphere Method – PDR 2 Cut 4

M (of seed and object) ≤ M_{edge}

Seed and object on the same decay chain



Seed and object on opposite decay chains



Alternative cut: maximum dR cut

- Constraining dR differences does not work