

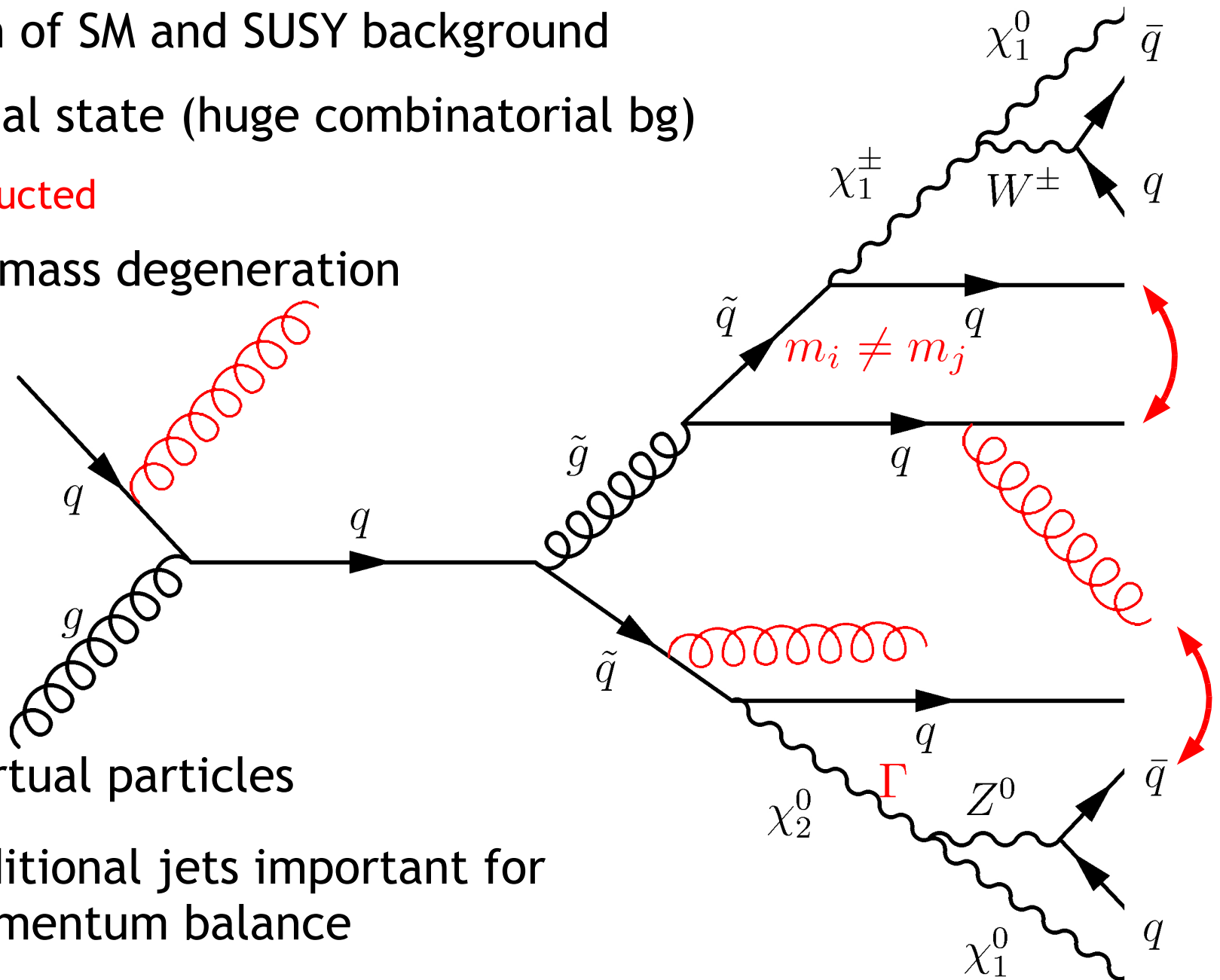


Update on Kinematic Fits

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Uni HH - Susy Group Meeting - 21st February 09

- Suppression of SM and SUSY background
- 7 jets in final state (huge combinatorial bg)
 - all reconstructed
- No perfect mass degeneration



- Width of virtual particles
- +FSR } additional jets important for momentum balance
- +ISR }

- Constrained fitting via Lagrangian Multiplier

$$\sum_{i=1}^{N_m} \left(\frac{m_i - t_i}{\sigma_i} \right)^2 + 2 \cdot \sum_{i=1}^{N_c} \lambda_i \cdot f_i$$

- Find extremum where all derivatives vanish
- If constraints are linear find perfect solution within one Gauss-Newton step
- Invariant mass constraints are (highly) non-linear → linearization and iterative approach
- **General problem:** Fit can converge at local (and not global) minimum

- Formulation of constraints as additional χ^2 term \rightarrow “cost function”
- To interpret cost function as χ^2 all correlations have to be taken into account

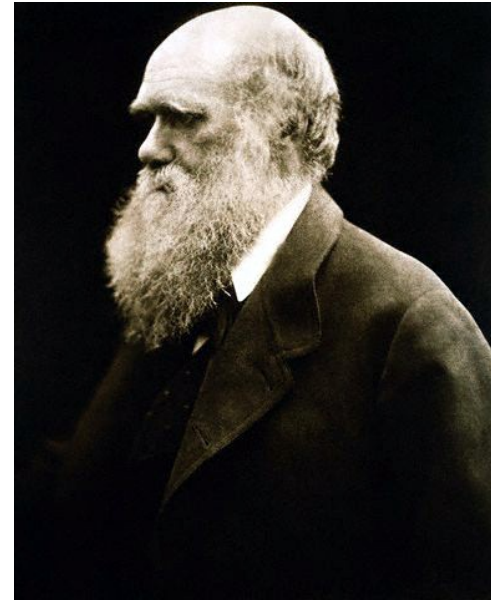
$$\left(\frac{M_{\text{inv}}(j_1, j_2, j_3) - M}{\sigma} \right)^2$$

with

$$\sigma^2 = \sum_{i=1}^{N_m} \left(\frac{\partial M_{\text{inv}}}{\partial i} \right)^2 \cdot \sigma_i^2 + \Gamma_m^2$$

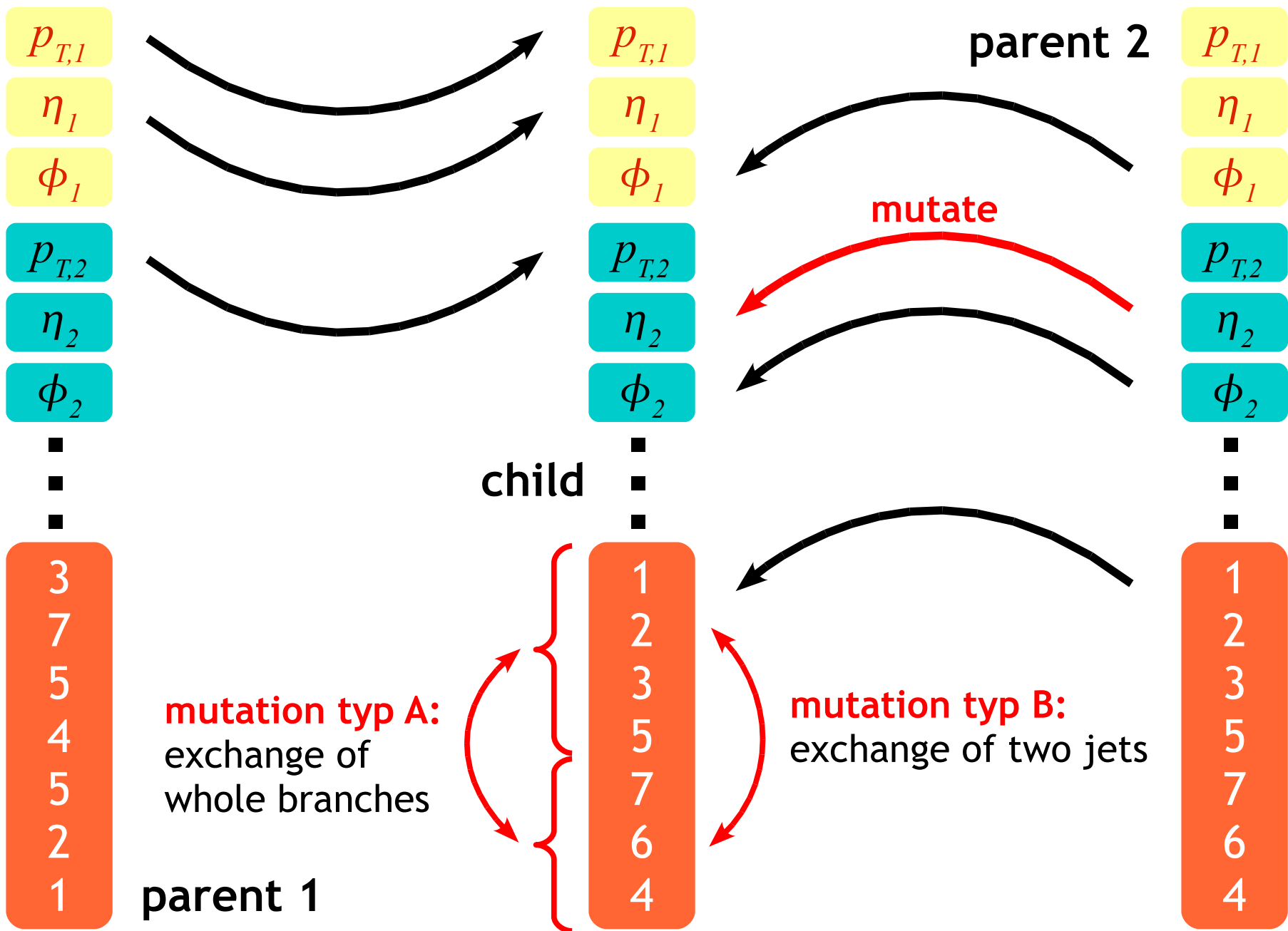
- Minimize cost function: many possible algorithms (gradient, simplex, LBFGS, simulated annealing ... genetic algorithm)

- Final state 4-momenta are properties (*genes*) of *individuum*; jet combination is one additional *gene*
 - A fitness function (here χ^2) defines if a *individuum* is *fittest*
- 1) Starting from starting values create a first *generation* of *individua* (starting *population*): use all possible jet combinations (1260 for 7 jets)
 - 2) Select N best fitting *individua* (here 20)
 - 3) Create M (here 1000) new *individua* by selecting randomly two *parents* and take randomly the *genes* from either one or the other *parent*
 - 4) *Mutate* (variation within the measurement errors) each *gene* (except jet combination) with a given probability (here 10 %)
 - 5) Back to step 2) until convergence is reached (here: no change within 3 *generations*) or fixed iteration number is reached (here 200)



Charles Darwin
(1809 - 1882)

On the origin of species (1859)



- In typical Susy scenarios: $m_{\chi_1^\pm} - m_{\chi_1^0} \gtrsim m_W$

→ small relative momentum of W and χ^0

- Assume same direction of W and χ^0 and adjust χ^0 momentum to fulfill mass constraint

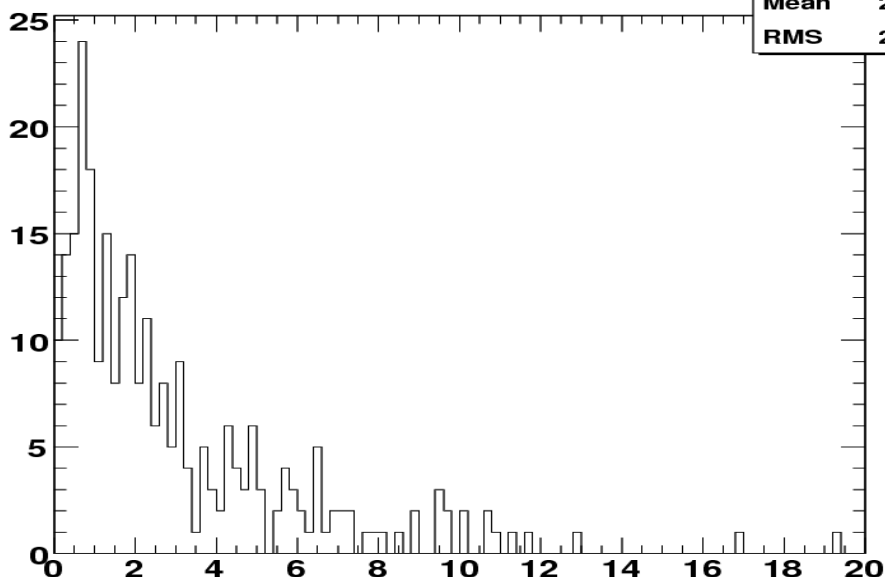
$$0 \stackrel{!}{=} f(x) = m_{\chi_1^\pm}^2 - \left(\left(E_W + \sqrt{m_{\chi_1^0}^2 + (x \cdot p_W)^2} \right)^2 - (1+x)^2 p_W^2 \right)$$

- Solve analytically or numerically by Newtons method

$$x_{n+1} = x_n - \frac{f(x_n)}{f'(x_n)}$$

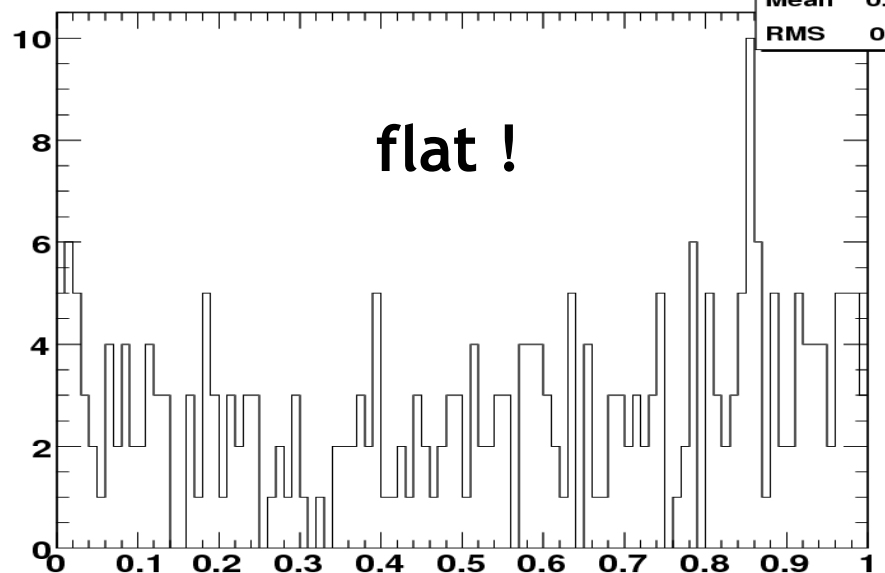
Chi2 distribution

Entries	269
Mean	2.939
RMS	2.958



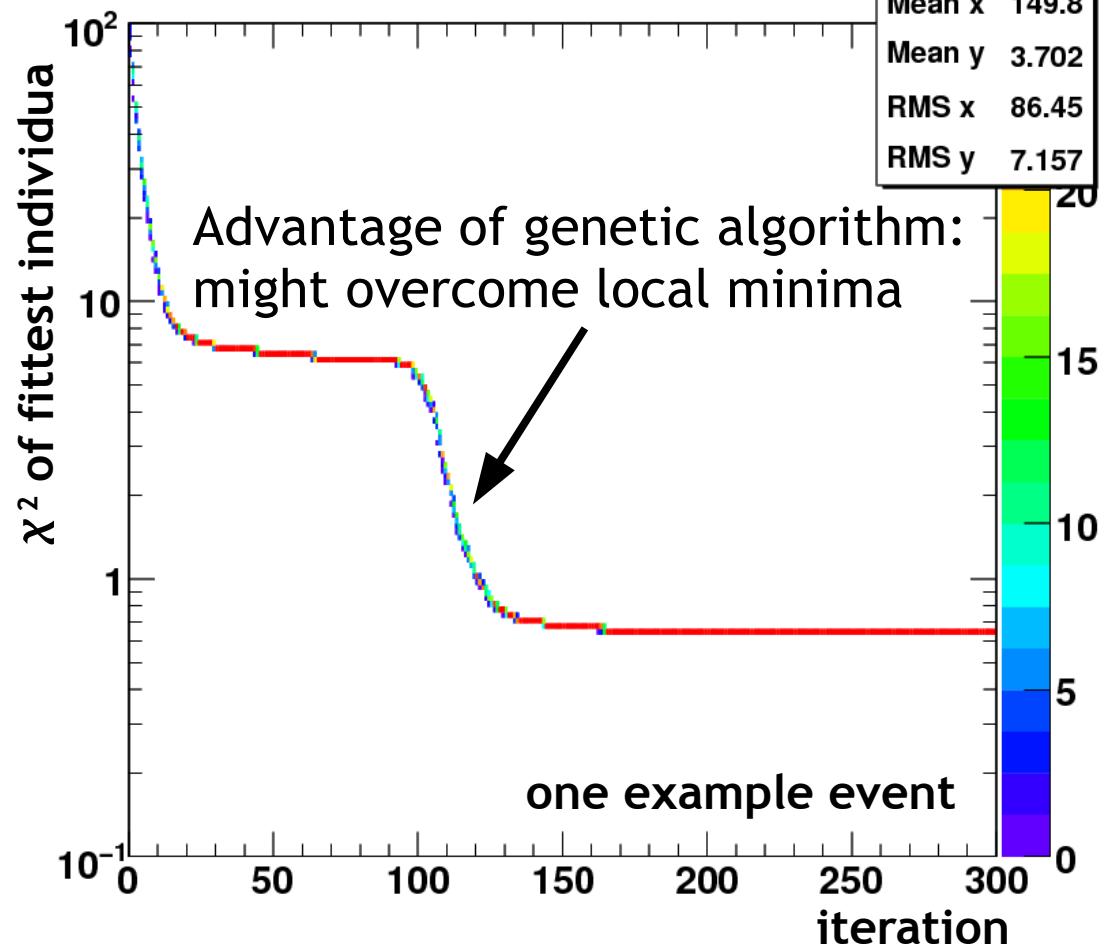
Prob. distribution

Entries	269
Mean	0.5419
RMS	0.3141



Evolution of Fitness

Entries	7500
Mean x	149.8
Mean y	3.702
RMS x	86.45
RMS y	7.157



Input:

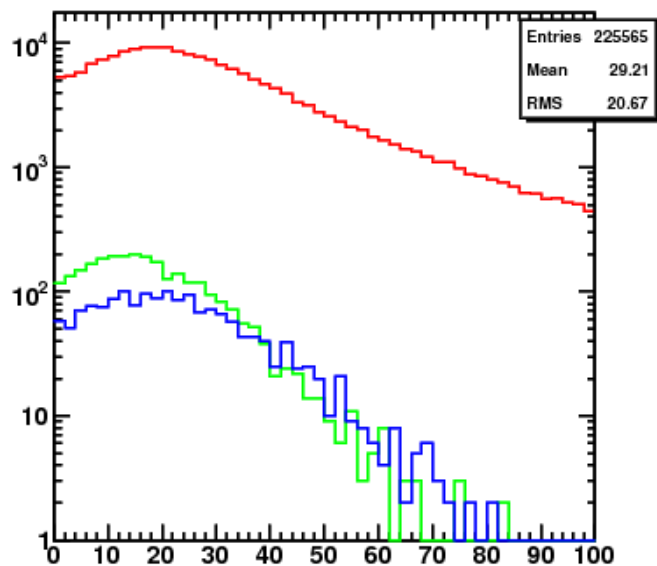
no combinatorial bg

no SUSY bg

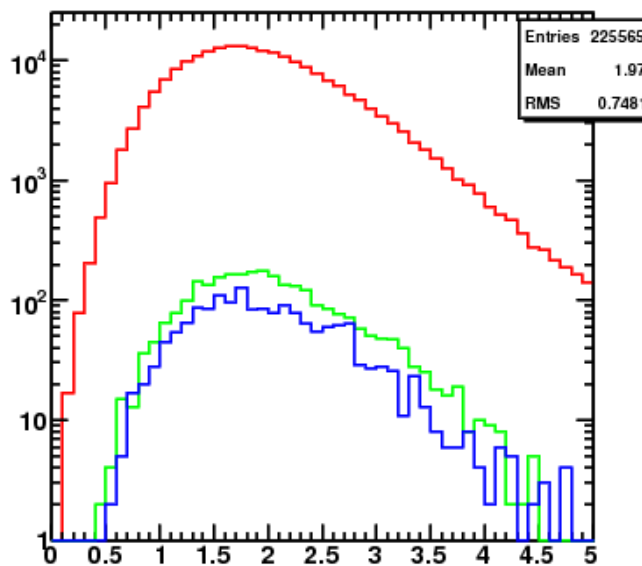
ISR for momentum balance from MC

- Demand exactly 7 jets with:
 - $p_T > 20$ GeV
 - $|\eta| < 3.0$
- This will reject many signal events with hard ISR or FSR, but combinatorics is reduced

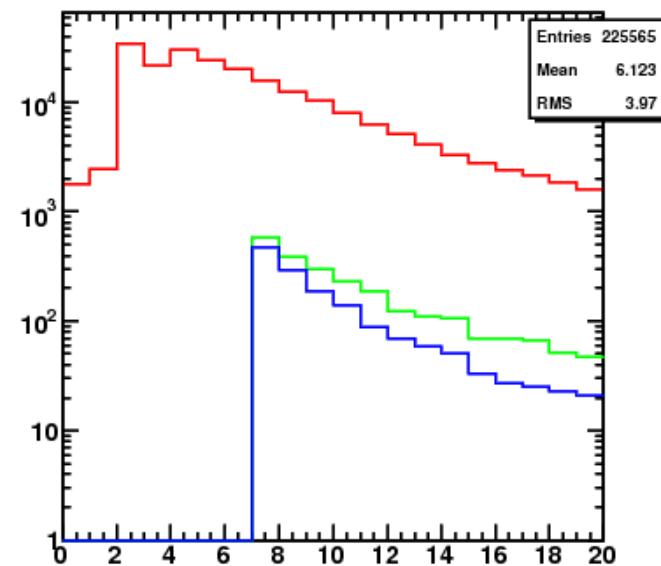
pT of softest jet (wrong)



largest abs(eta) of jet (wrong)



position of softest jet (wrong)



Before genetic algorithm:

Chi2 (starting values, no combinatorics) = 18.6535

probability = 1.56763e-05

Chi2 (KinFitter, no combinatorics) = 4.09197

probability = 0.251702

After genetic algorithm:

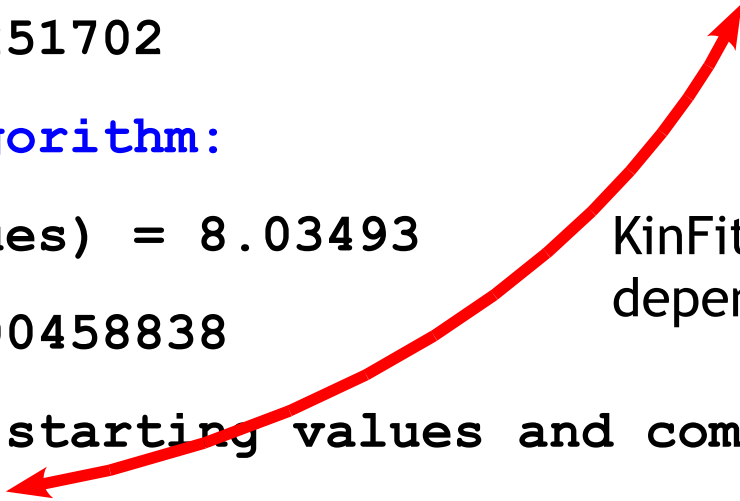
Chi2 (fitted values) = 8.03493

probability = 0.00458838

Chi2 (KinFitter, starting values and combinatorics from gen.
fit) = 1.15671

probability = 0.763404

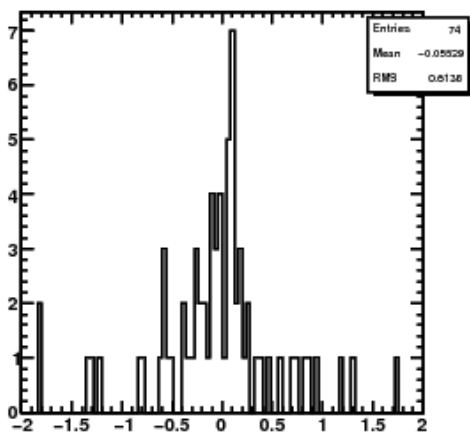
KinFitter result (and convergence)
depends strongly on starting values



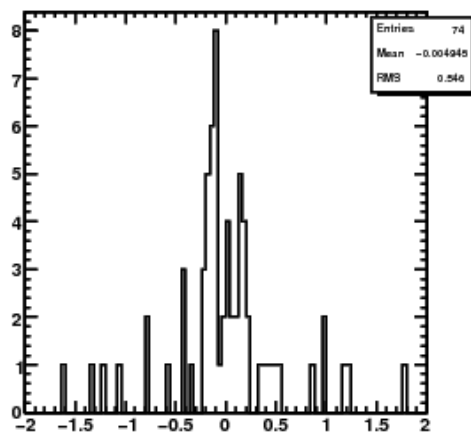
χ^2 of genetic Fit and KinFitter not directly comparable (different treatment of mass constraints)

- Genetic algorithm: $RMS(\Delta R) = 0.56$

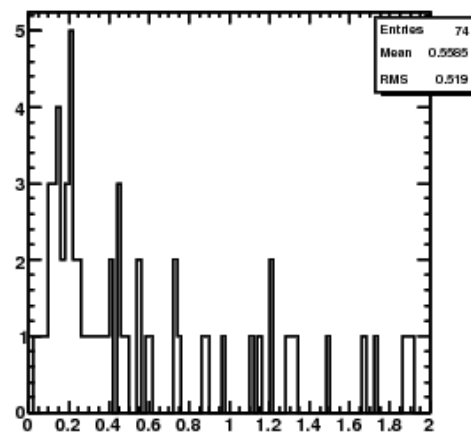
1: Delta Phi Neutralino



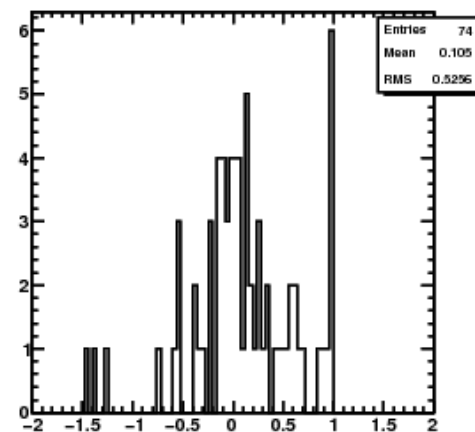
1: Delta Eta Neutralino



1: Delta R Neutralino

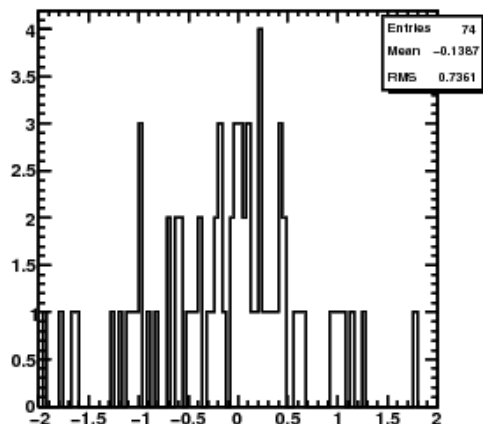


1: Delta Pt (rel) Neutralino

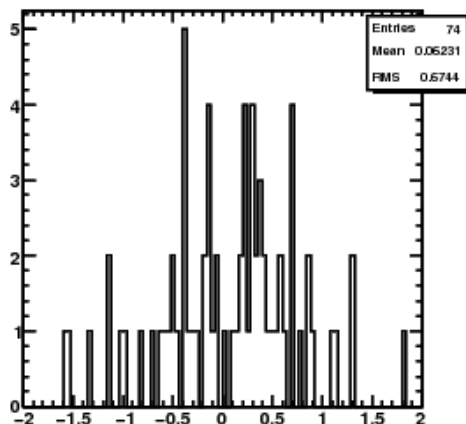


- KinFitter (with starting values from genetic fit): $RMS(\Delta R) = 0.50$

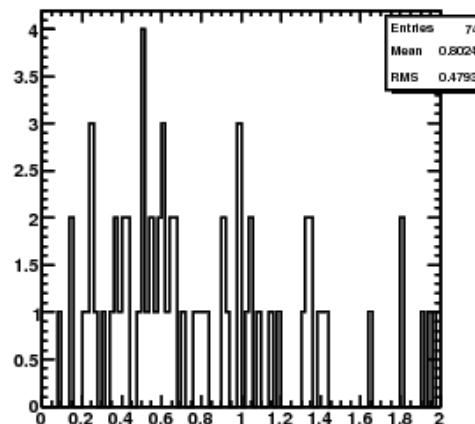
1: Delta Phi Neutralino (KF)



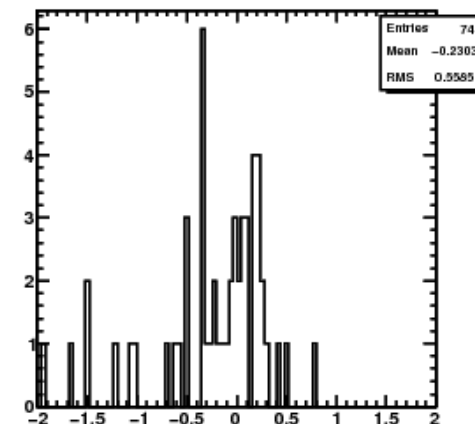
1: Delta Eta Neutralino (KF)



1: Delta R Neutralino (KF)



1: Delta Pt (rel) Neutralino (KF)



- Included backgrounds:

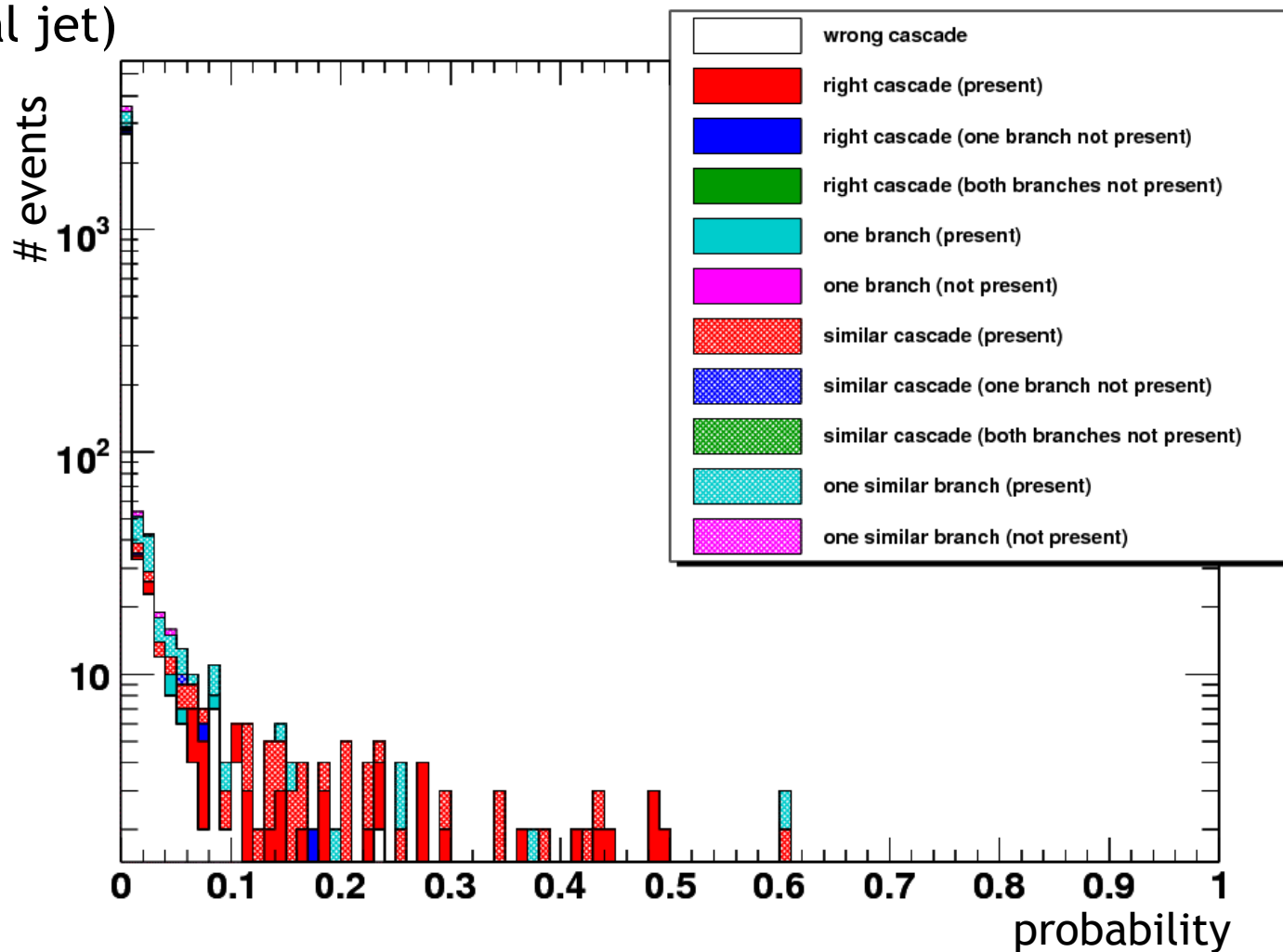
- SUSY
- signal cascades but not all signal jets selected (at least one ISR or FSR jet is harder than one signal jet)

Signal cascade:
only left handed
squarks of first two
generations

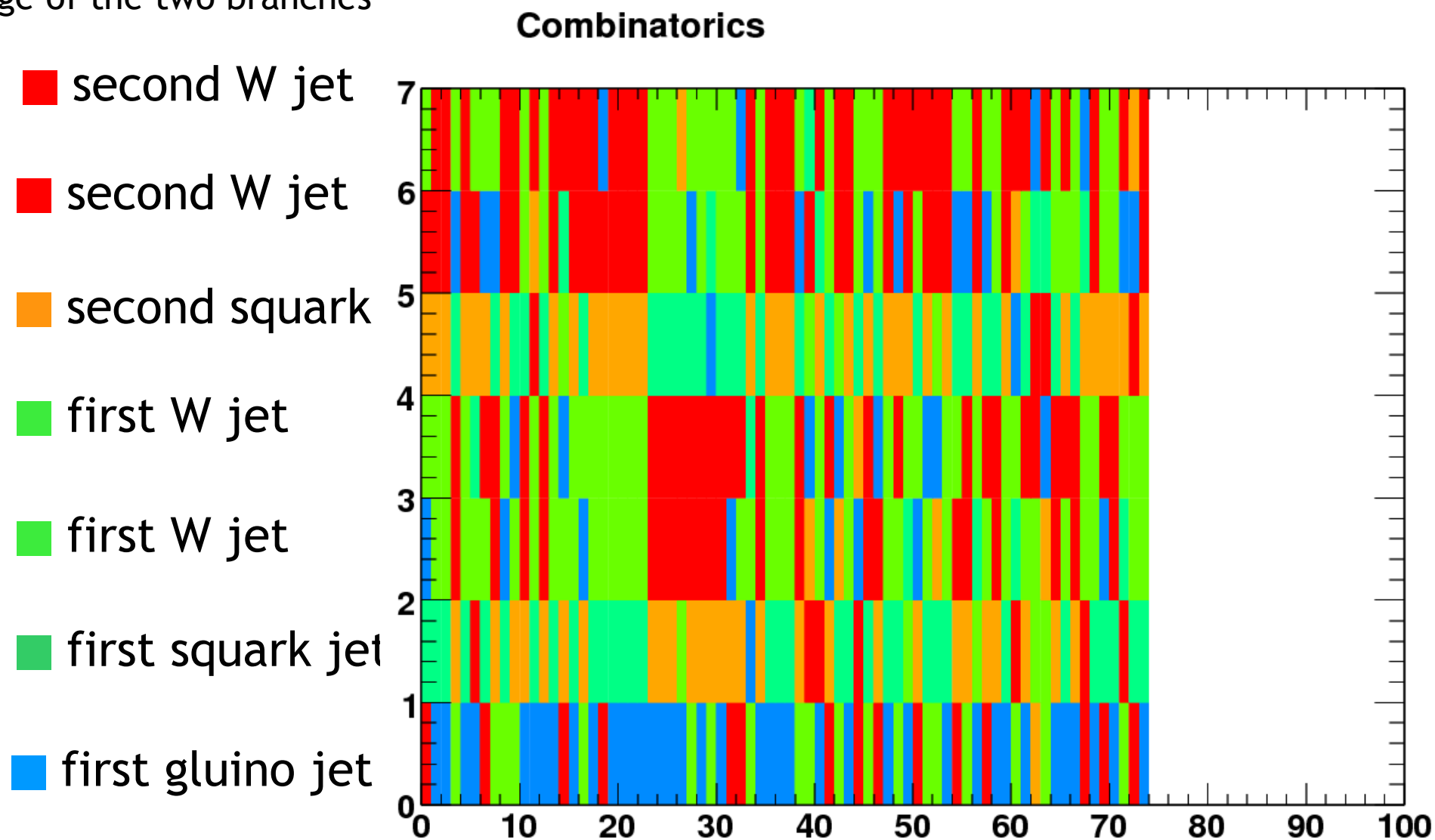
Similar cascades:
other squarks


→ Prob. distribution
not flat due to
missing ISR

→ SUSY bg peaks at
small probabilities



~ 20% complete right cascade
most wrong combinations are
exchange of the two branches



- Scan over mass hypothesis or mSUGRA parameters
 - Use NAF 
 - First try with: $M_1 : M_2 : M_3 = 1 : 2 : 6$
- Use leptonic Z -decays (smaller combinatorics, bg, and statistics)
- Include ISR jets in event selection (treat higher statistics vs. larger combinatorial bg) (maybe not for SUSY09)
- Include systematic uncertainties (likely not for SUSY09)
- Think about “dynamic hypothesis selection” (surely not for SUSY09)

