$J/\psi \rightarrow e^+e^-$ Reconstruction In ID

E. Bouhova-Thacker

Lancaster University, UK

ATLAS-UK Physics Meeting, 18 - 20/09/06

J/ψ Reconstruction in ATLAS

- Most of the B-Physics programme uses $J/\psi \to \mu^+\mu^-$

  $J/\psi \to e^+e^-$ difficulties due to

  - Bremsstrahlung radiation
  - Trigger issues

- EM Calorimeter not covered here

- Track Reconstruction in ID
  - iPatRec
  - xKalman
  - New Tracking KalmanFitter

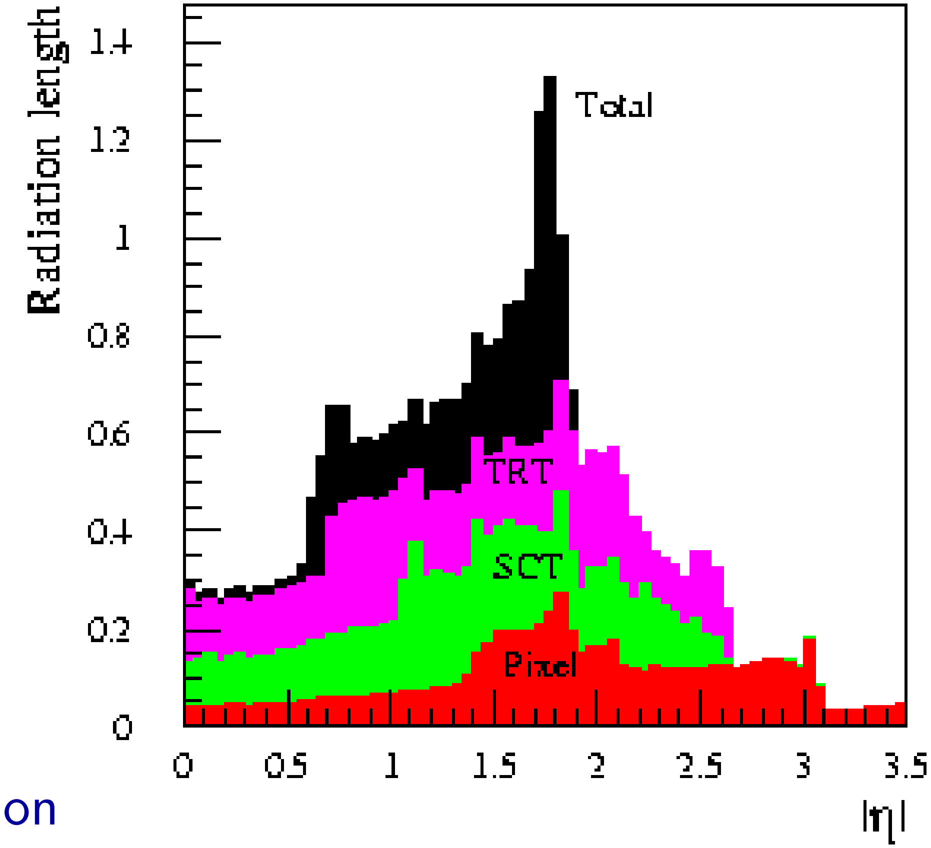
Electron Reconstruction in ID

Kalman Filter

Assumes Gaussian distribution
for measurement noise and
process noise

Multiple scattering

Bremsstrahlung:



$$f(z) = \frac{(-\ln(z))^{c-1}}{\Gamma(c)}$$ Bethe-Heitler distribution

$$c = \frac{t}{\ln 2}$$ amount of material traversed in radiation lengths

Dynamical Noise Adjustment (DNA) during Kalman filtering

- Default Kalman Fitter uses Gaussian distribution with width and rms equal to that of the true bremsstrahlung distribution
- Gaussian Sum Filter
- DNA method developed at Lancaster University by V. Kartvelishvili, E. Bouhova-Thacker, D. Price
- Use a (fairly simple) algorithm to locate and flag hits which may be associated with a (strong) brem
- Brem search only performed in Pixel and SCT (TRT hits produce too many fake flags)
- If no brem was flagged, continue as before (i.e. default New Tracking KalmanFitter)
- When flagged, estimate z — the fraction of energy retained by the electron

Dynamical Noise Adjustment (DNA) during Kalman filtering

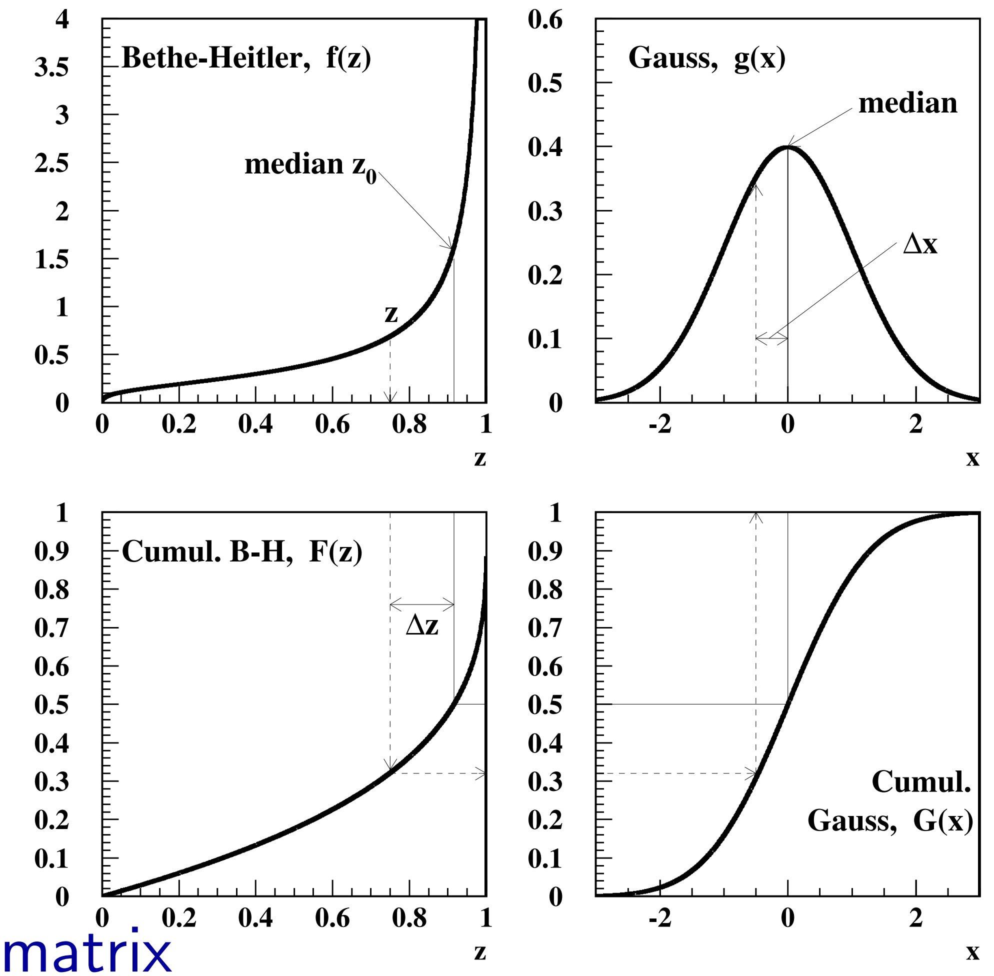
- Calculate the effective $\sigma(\text{noise})$ which matches the probability of such z when the (cumulative) Bethe-Heitler distribution is mapped onto the normal error function

$$z = z_0 + v\sigma(z)$$

$$G(v) = F(z) \equiv \int_{-\infty}^{z} dz' f(z')$$

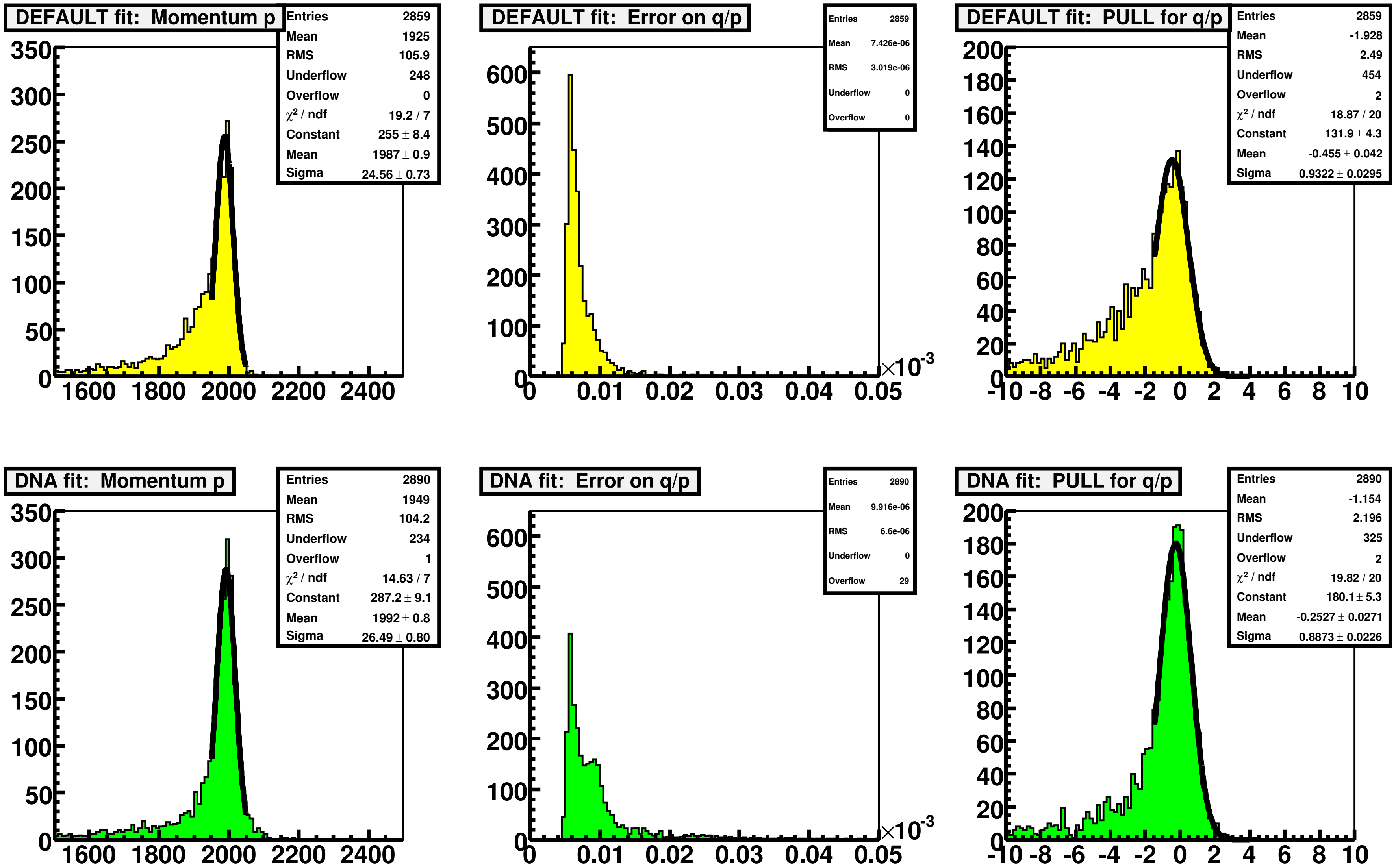
$$v = G^{-1}(F(z))$$

$$\sigma(z) = \frac{z - z_0}{G^{-1}(F(z))}$$

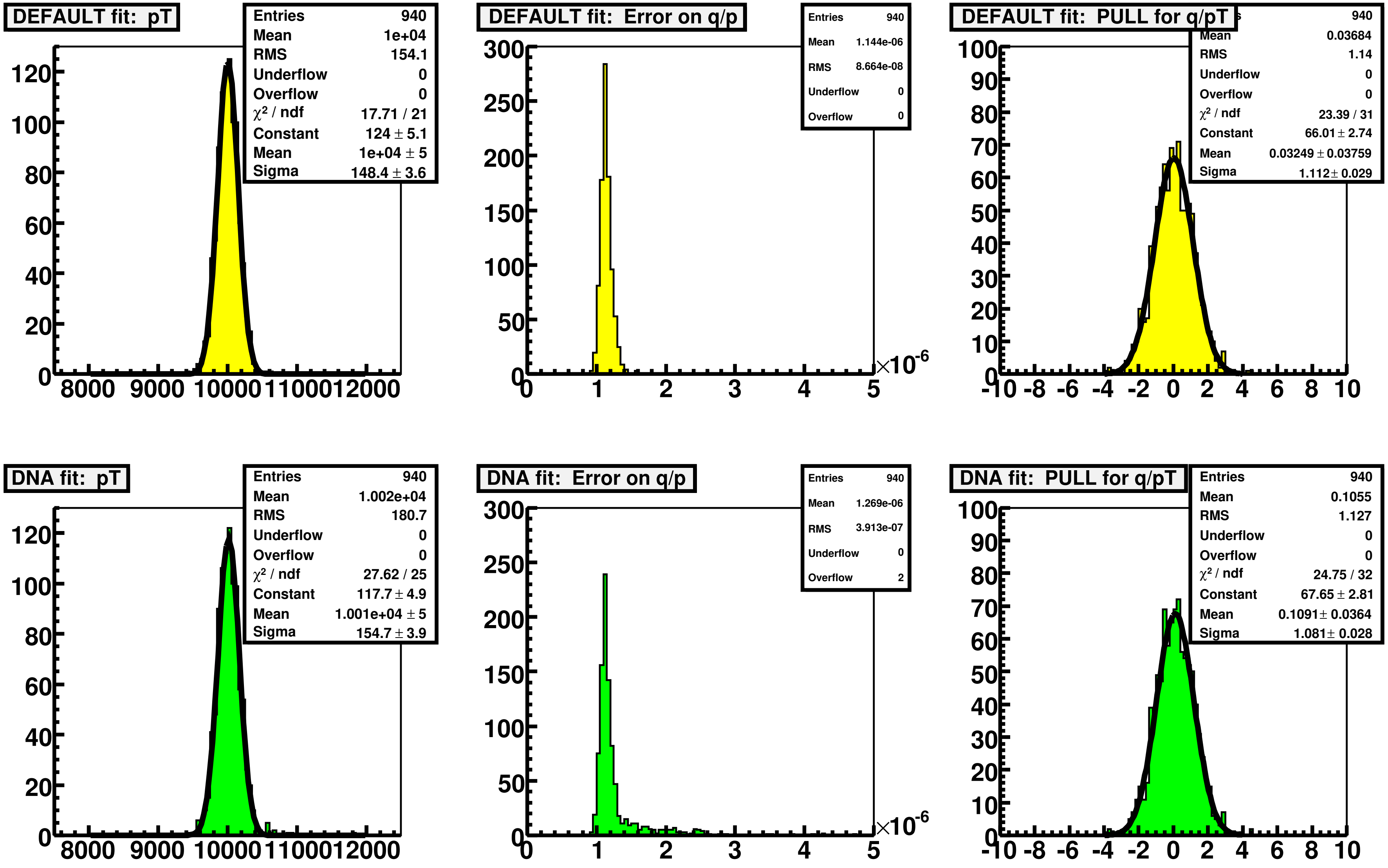


- Adjust the Kalman covariance matrix

2 GeV single electrons, barrel only



$p_T = 10$ GeV single muons, $|\eta| < 1$



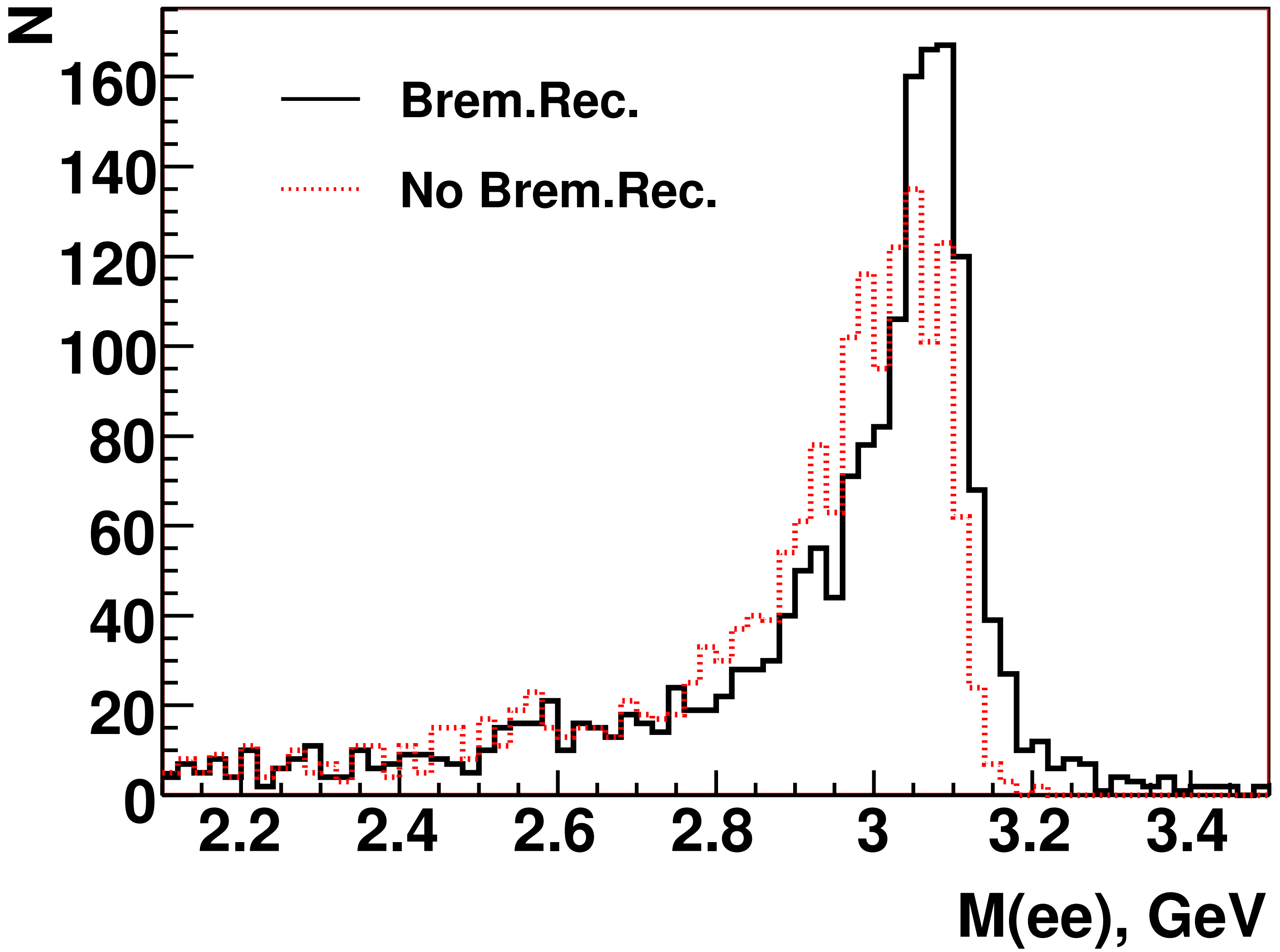
$J/\psi \to e^+e^-$ Reconstruction

- Pairs of reconstructed opposite-charge electrons from J/ψ decays fitted to a common vertex
- χ^2/n.d.f < 6
- Fitted transverse decay length of reconstructed $J/\psi > 250\ \mu m$
- Efficiency assessed separately for the barrel region (both tracks with true pseudorapidity within ± 0.7), the endcap region (at least one with $|\eta| > 0.7$) and for the full η range

  Invariant mass within an asymmetric window around the nominal J/ψ mass, $M_{J/\psi} = 3096$ MeV
  - $[-5\sigma, +3\sigma]$ for $|\eta| < 0.7$, $\sigma = 60$ MeV
  - $[-7\sigma, +3\sigma]$ for $|\eta| > 0.7$

- Distributions fitted using an asymmetric Gaussian function with different values of σ, σ_{left} and σ_{right}

$J/\psi \rightarrow e^+e^-$ invariant mass distributions



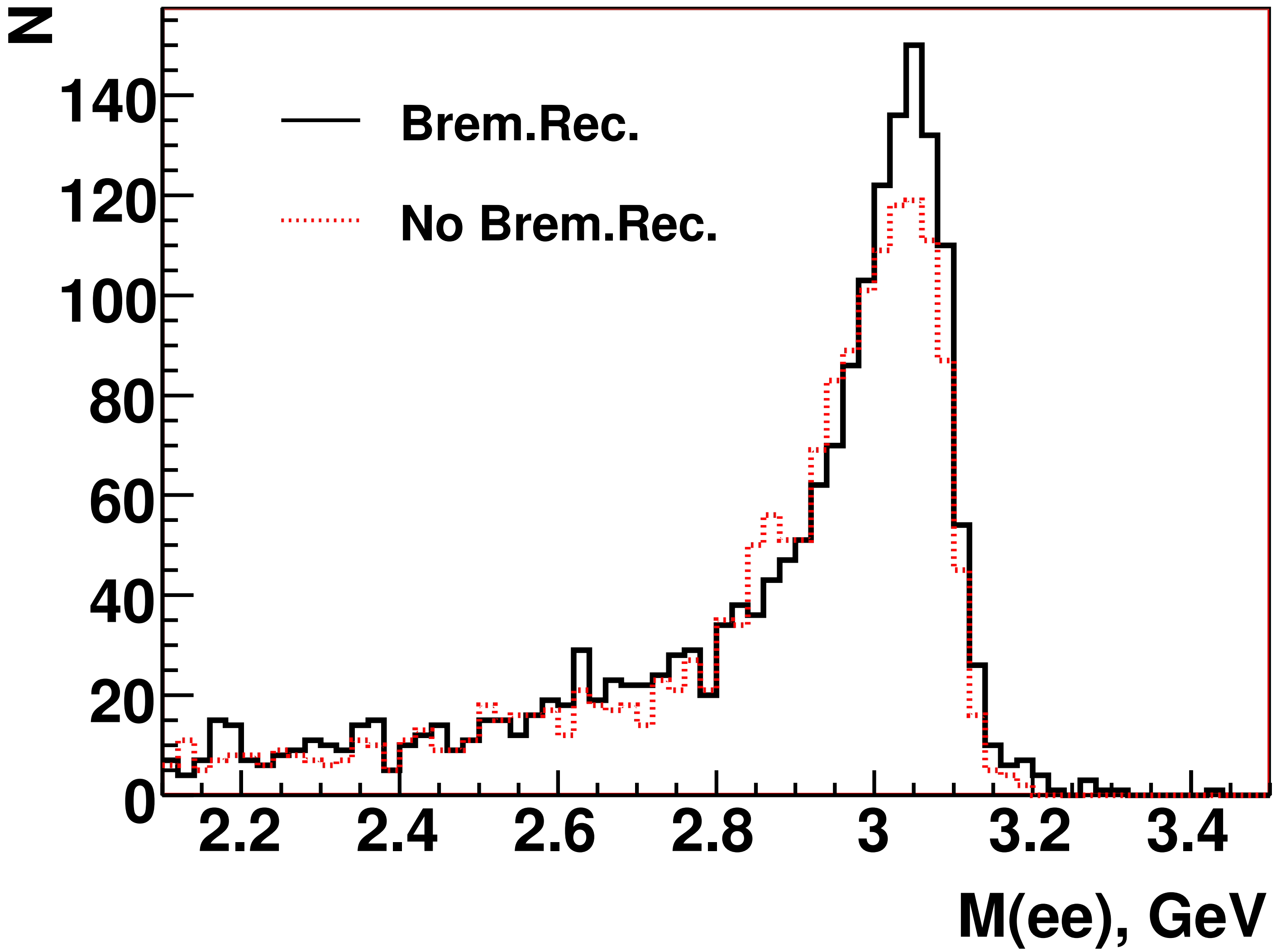
$J/\psi \to e^+e^-$ results, New Tracking

	NT, barrel	DNA, barrel
J/ψ mass, from fit	3.087 ± 0.006	3.093 ± 0.007
σ_{left}	0.100 ± 0.008	0.068 ± 0.007
σ_{right}	0.026 ± 0.004	0.030 ± 0.005
Efficiency, %	59.5	60.1
	NT, endcap	DNA, endcap
J/ψ mass, from fit	3.060 ± 0.010	3.084 ± 0.008
σ_{left}	0.155 ± 0.014	0.113 ± 0.011
σ_{right}	0.038 ± 0.007	0.041 ± 0.007
Efficiency, %	42.6	46.8
	NT, all η	DNA, all η
J/ψ mass, from fit	3.080 ± 0.010	3.085 ± 0.005
σ_{left}	0.145 ± 0.008	0.083 ± 0.006
σ_{right}	0.028 ± 0.003	0.038 ± 0.004
Efficiency, %	46.5	49.9

$J/\psi \to e^+e^-$, xKalman

	xK, barrel	xK 61, barrel	TDR, barrel
J/ψ mass	3.077 ± 0.008	3.072 ± 0.008	3.082 ± 0.005
σ_{left}	0.105 ± 0.018	0.070 ± 0.008	0.094 ± 0.005
σ_{right}	0.028 ± 0.004	0.032 ± 0.004	0.042 ± 0.004
Efficiency, %	58.4	59.5	66.6
	xK, endcap	xK 61, endcap	TDR, endcap
J/ψ mass	3.048 ± 0.009	3.048 ± 0.009	3.072 ± 0.006
σ_{left}	0.129 ± 0.021	0.094 ± 0.017	0.141 ± 0.008
σ_{right}	0.040 ± 0.005	0.043 ± 0.005	0.046 ± 0.005
Efficiency, %	39.8	44.2	58.5
	xK, all η	xK 61, all η	TDR, all η
J/ψ mass	3.060 ± 0.010	3.058 ± 0.006	3.078 ± 0.002
σ_{left}	0.117 ± 0.011	0.086 ± 0.010	0.122 ± 0.003
σ_{right}	0.035 ± 0.004	0.039 ± 0.004	0.043 ± 0.002
Efficiency, %	44.1	47.7	61.0

$J/\psi \to e^+e^-$ invariant mass distributions, xKalman



Comments

- Dynamical Noise Adjustment during Kalman filtering produces a significant improvement in the reconstruction of single electrons
- The q/p distribution becomes more symmetric, with no dramatic low-energy tail
- Improves error estimation
- Single muons mostly unaffected, with a small percentage of tracks reconstructed with an increased error

- DNA gives significantly better $J/\psi \rightarrow e^+e^-$ mass resolutions (even compared to the TDR results)
- Improves mean values
- Improves reconstruction efficiency