Optimising top-quark pair-production threshold scan at future e+e- colliders

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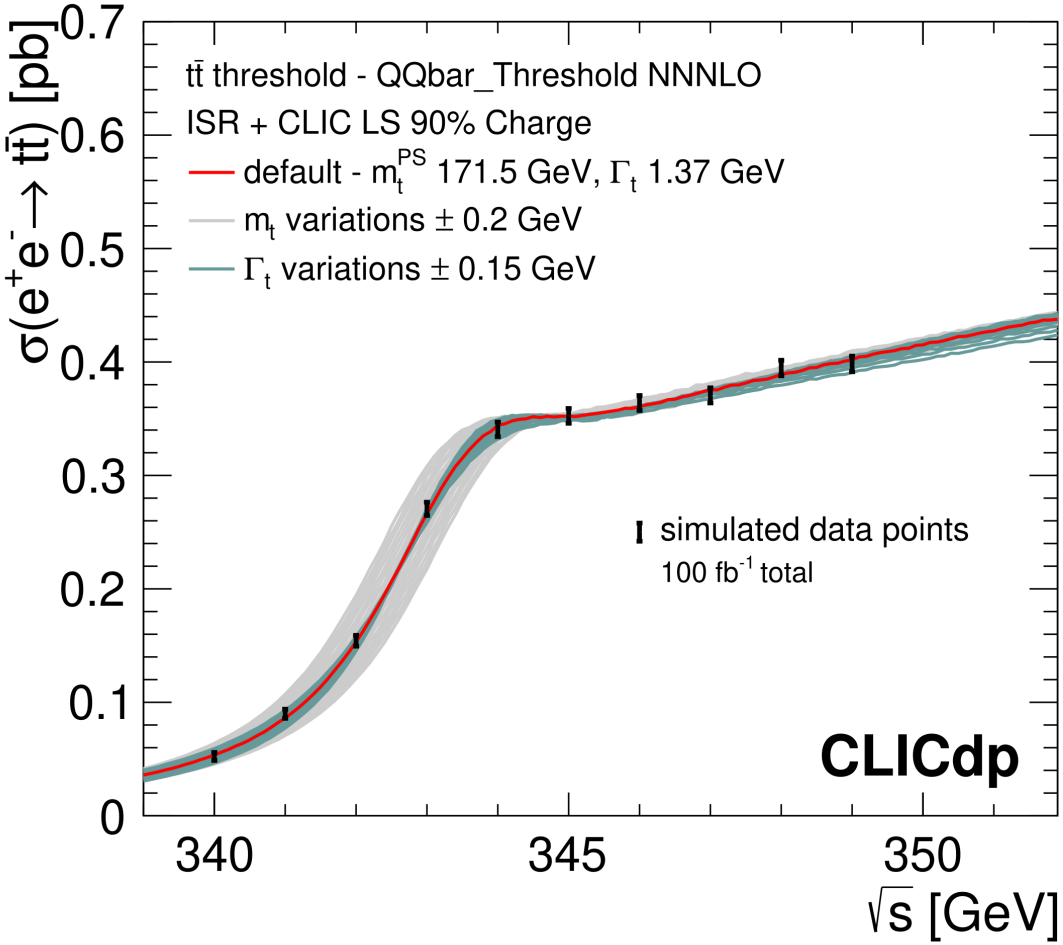
Motivation

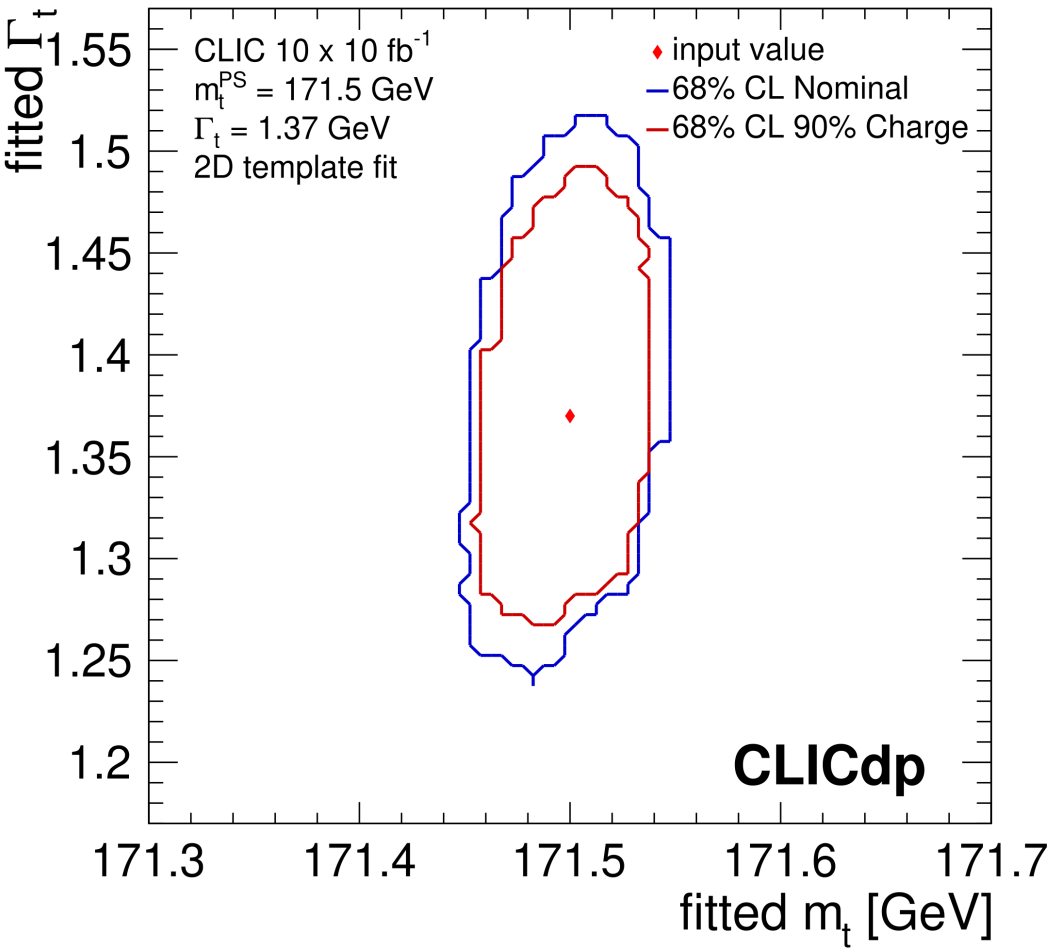


Threshold scan is assumed to be the most precise method to determine the top quark mass.

Baseline scenario assumes 10 scan points with 10 fb^{-1} each

H.Abramowicz et al. (CLICdp Collaboration), *Top-Quark Physics at the CLIC Electron-Positron Linear Collider*, **JHEP 11 (2019) 003, arXiv:1807.02441**,

Motivation

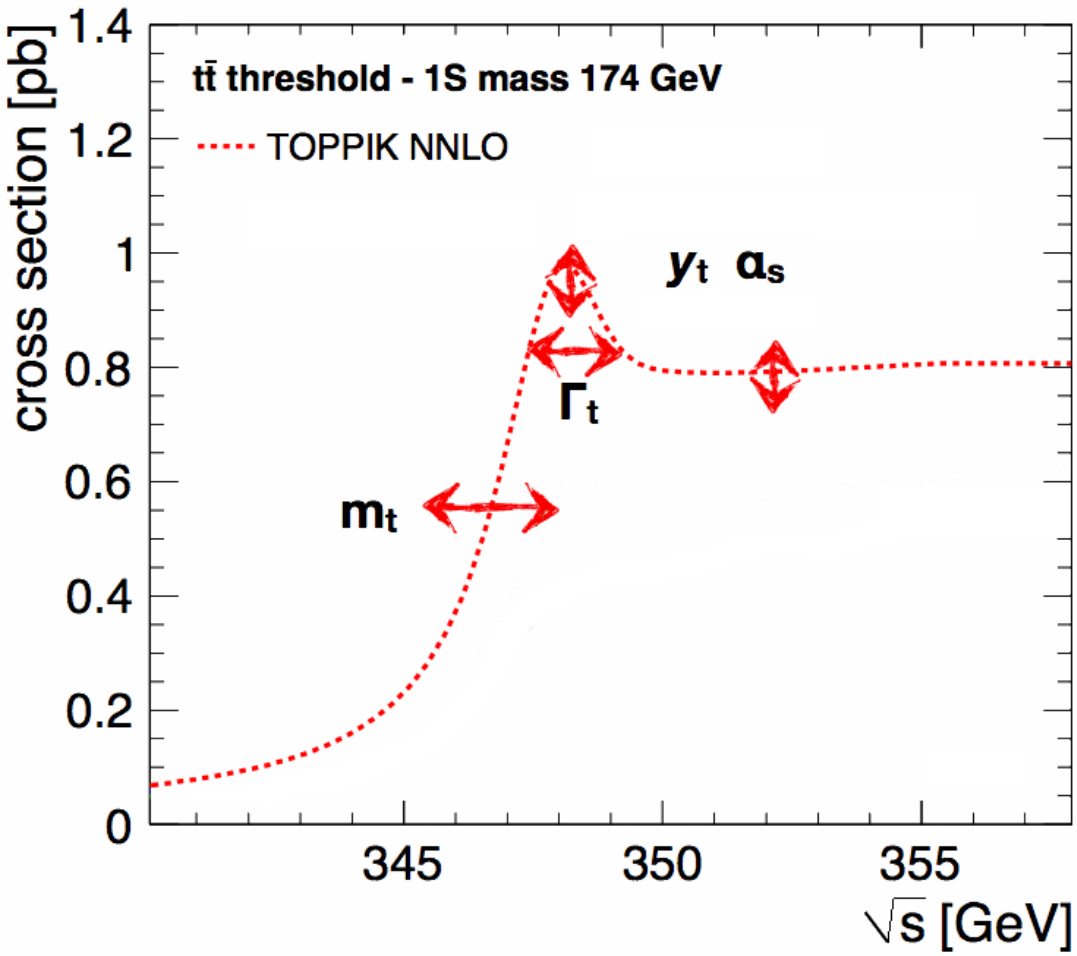


Dedicated study for CLIC indicates that the statistical precision of the measurement is around 20 MeV

However, this is based on a 2-D mass-width fit...

H.Abramowicz et al. (CLICdp Collaboration), *Top-Quark Physics at the CLIC Electron-Positron Linear Collider*, **JHEP 11 (2019) 003, arXiv:1807.02441**,

Motivation

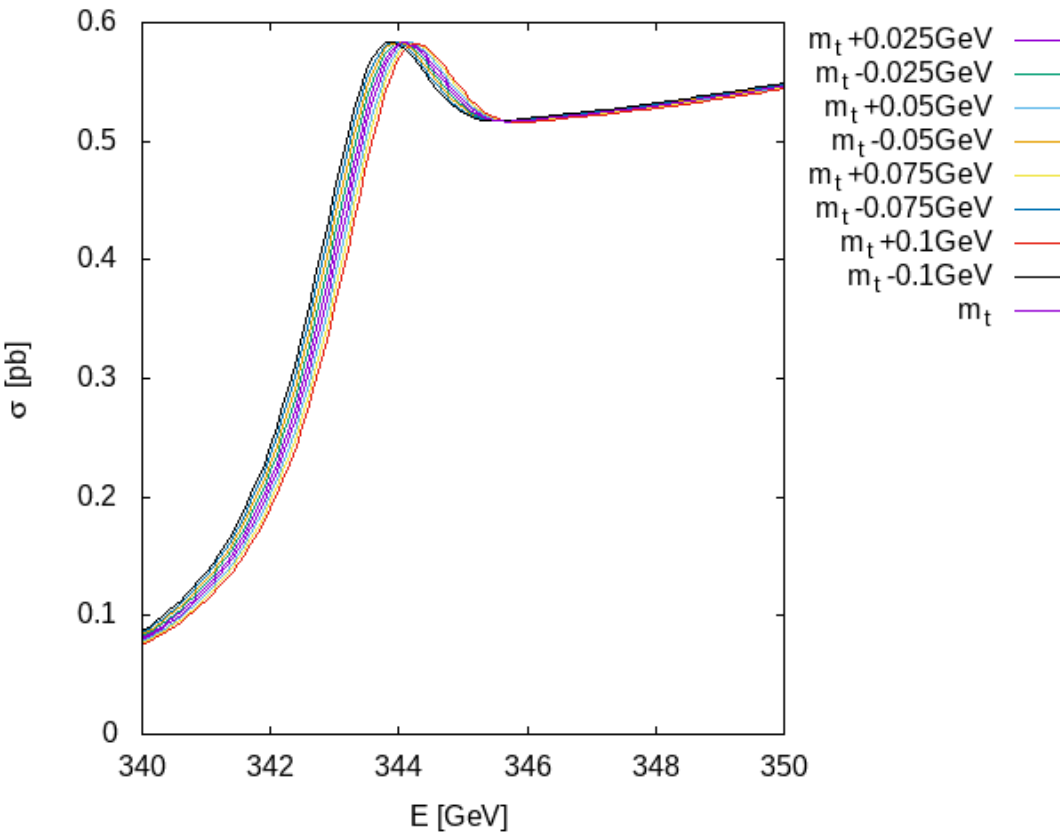


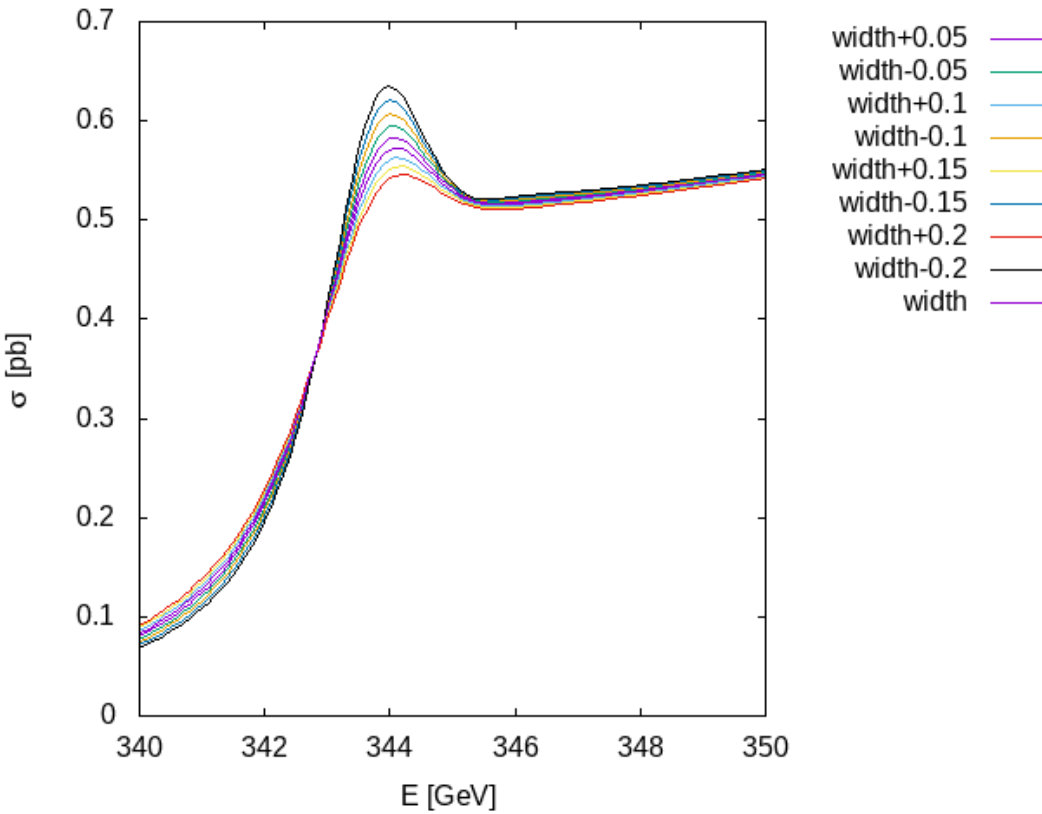
Threshold cross section depends on other model parameters as well…

Does it influence m_t determination precision?

Can the scan procedure be optimized?

Cross-section templates

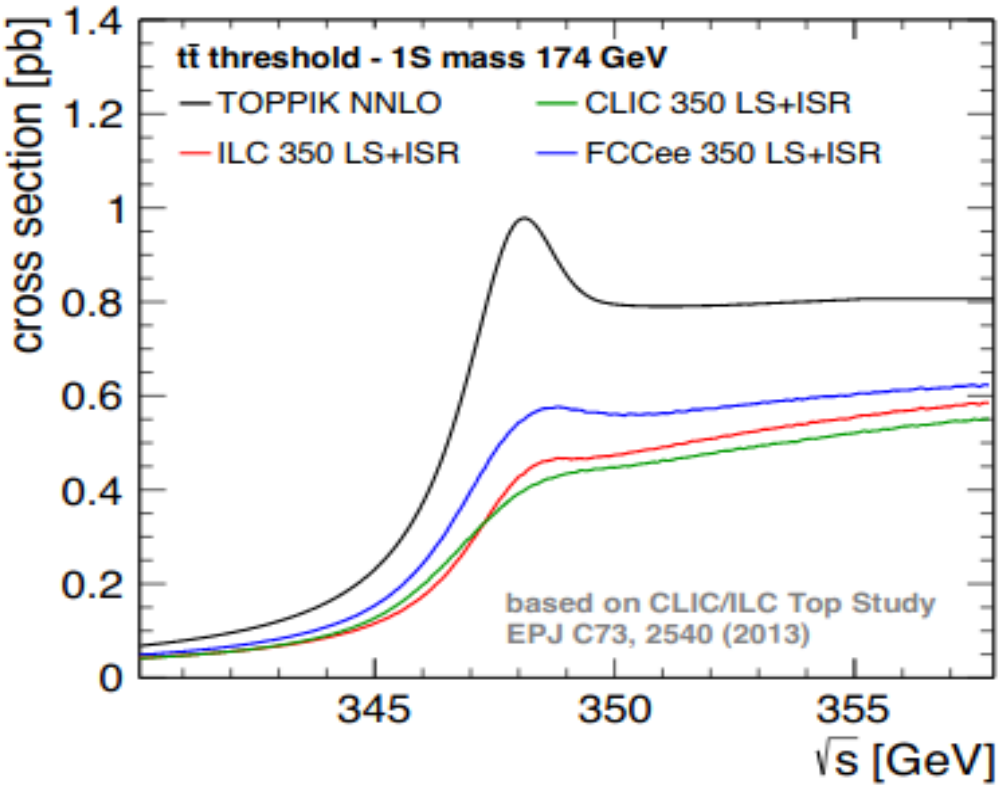


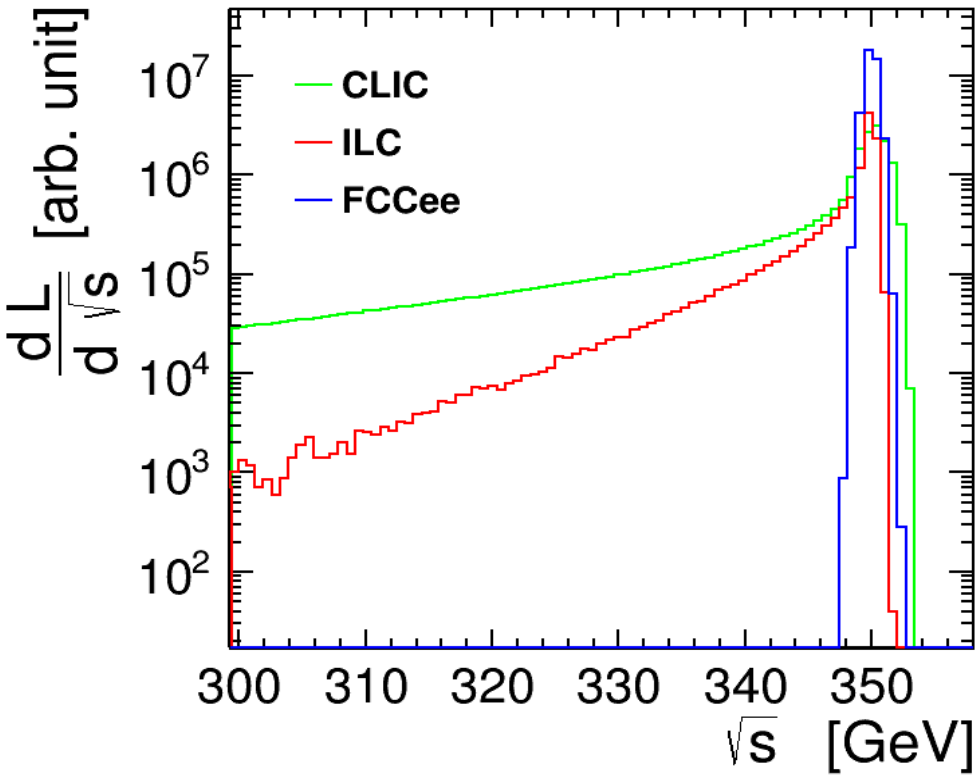


Templates generated with **Qqbar_threshold**

Beneke, M. et al. “Near-threshold production of heavy quarks with QQbar_threshold,” Comput. Phys. Commun. 209, 96–115 (2016).

Luminosity spectra

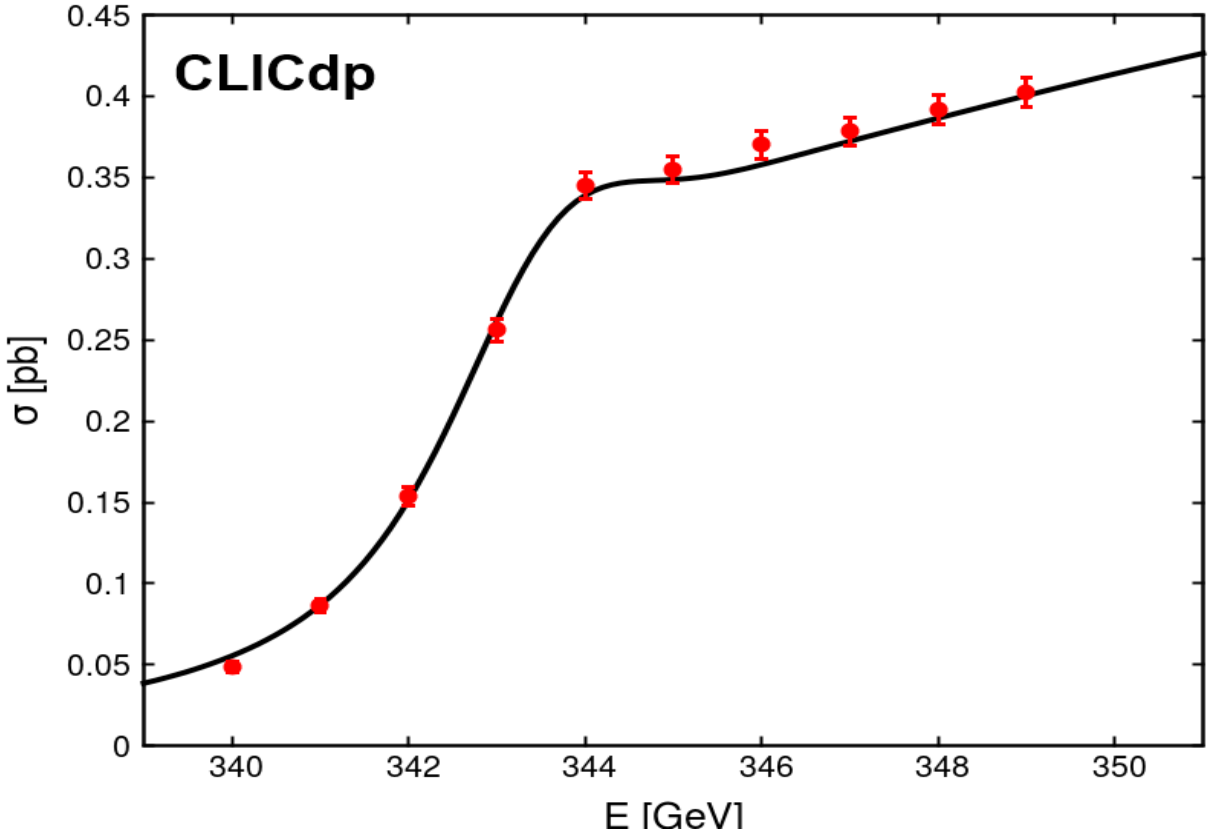




For CLIC we use luminosity spectra with 90% bunch charge

Benchmark scenario

Assume 10 measurements at the threshold, with 1 GeV step in energy, with 10 fb^{-1} taken at each energy point (100 fb^{-1} total).



Generate statistical fluctuation assuming 70.2% event reconstruction efficiency and background level (remaining after cuts) corresponding to the 73 fb

K. Seidel et al., Eur. Phys. J. C 73 (2013) 2530 [arXiv:1303.3758]

Fit procedure

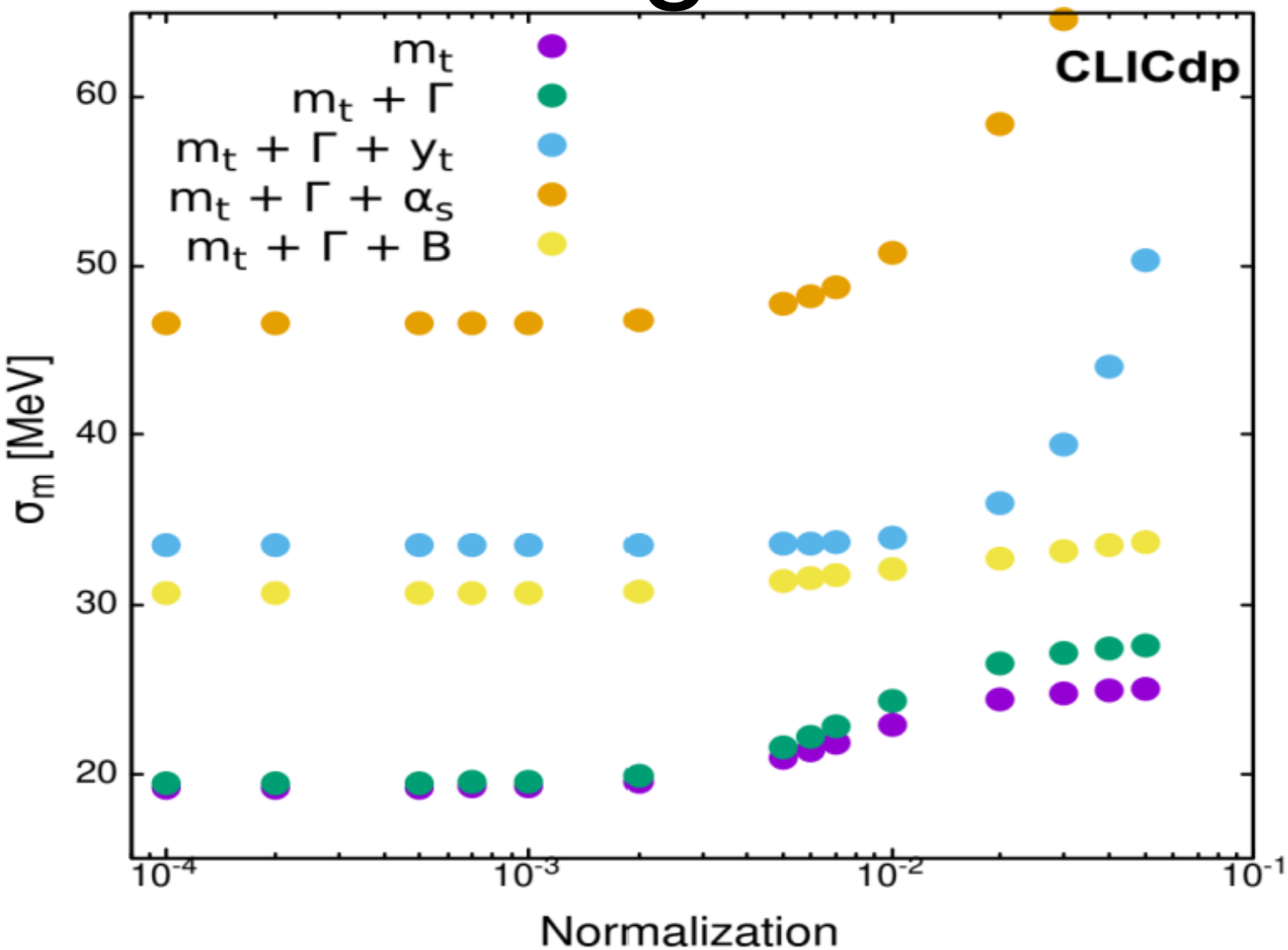
For each generated data set (pseudo-experiment) χ^2 value is calculated for different parameter values (different templates)

Quadratic dependence of the χ^2 value on the model parameters is fitted to find the best fit parameter values and the estimated uncertainty (corresponding to $\Delta\chi=1$)

Fits resulting in the parameter values outside the range used to generate templates are ignored.

More details on the fit method: **arXiv:2103.00522**

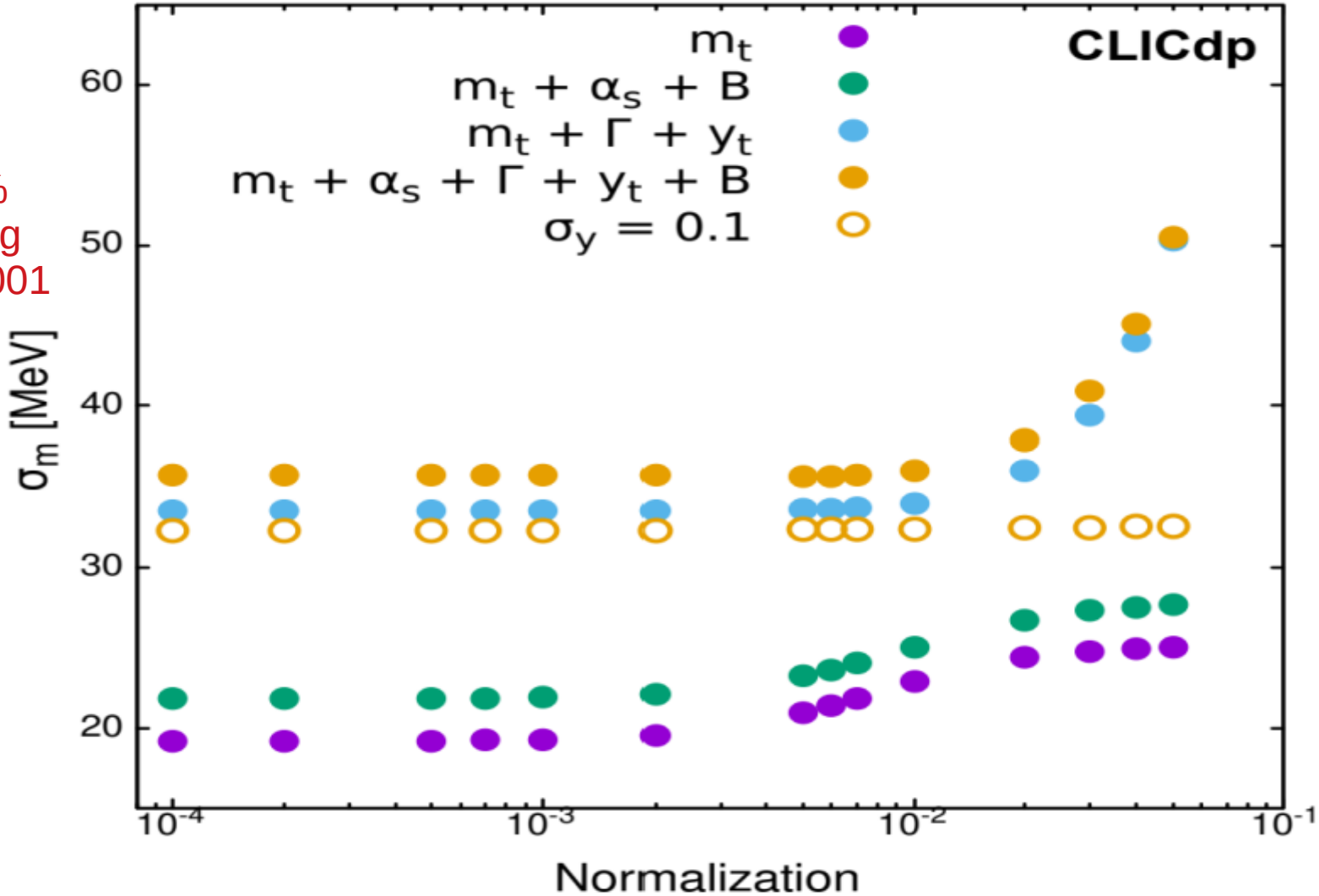
Fit configuration



Expected top quark mass uncertainty for different choices of free fit parameters

Systematic uncertainties

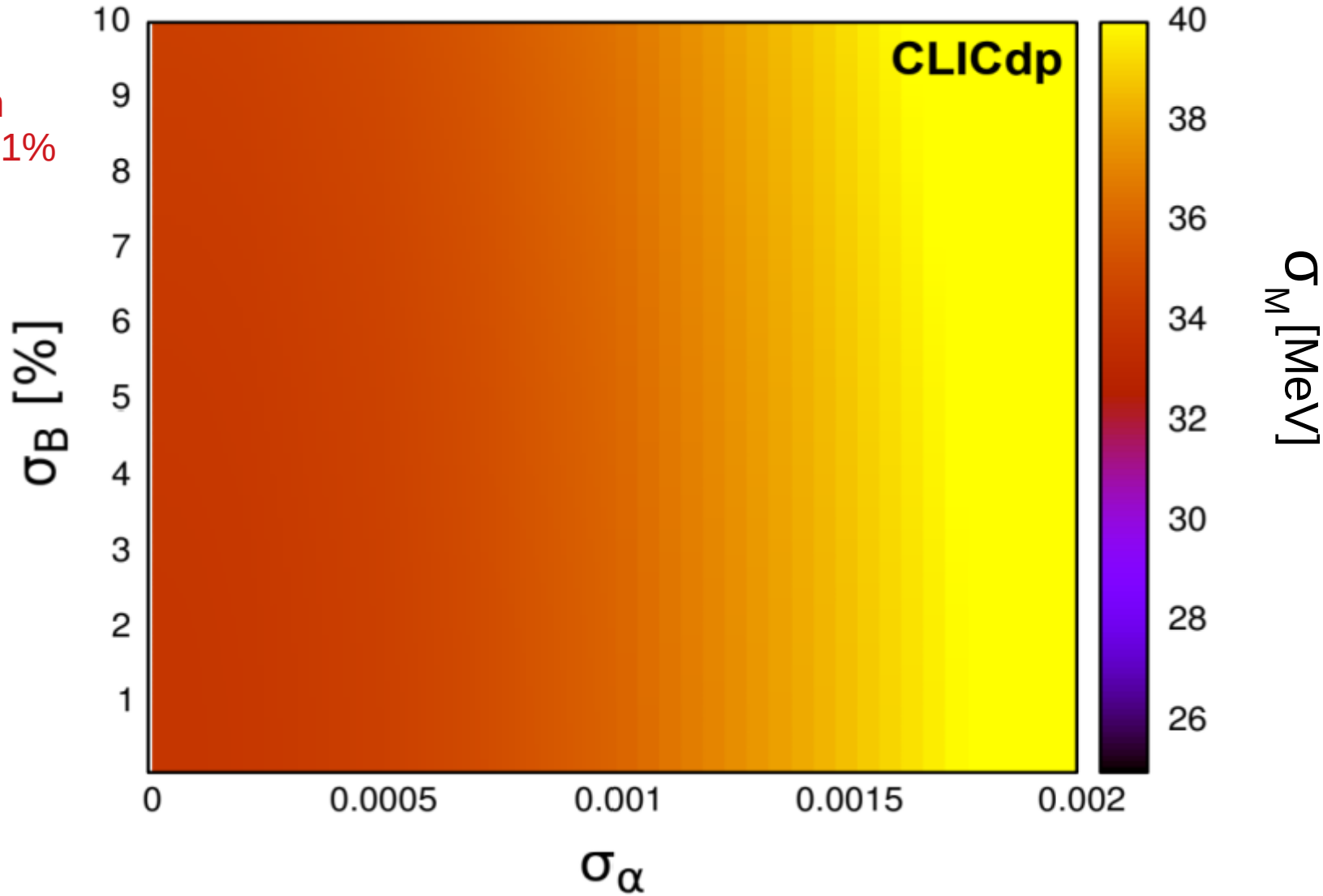
Assuming
Background
uncertainty 2%
Strong coupling
uncertainty 0.001



Systematic effects described by constrained fit parameters

Baseline fit results

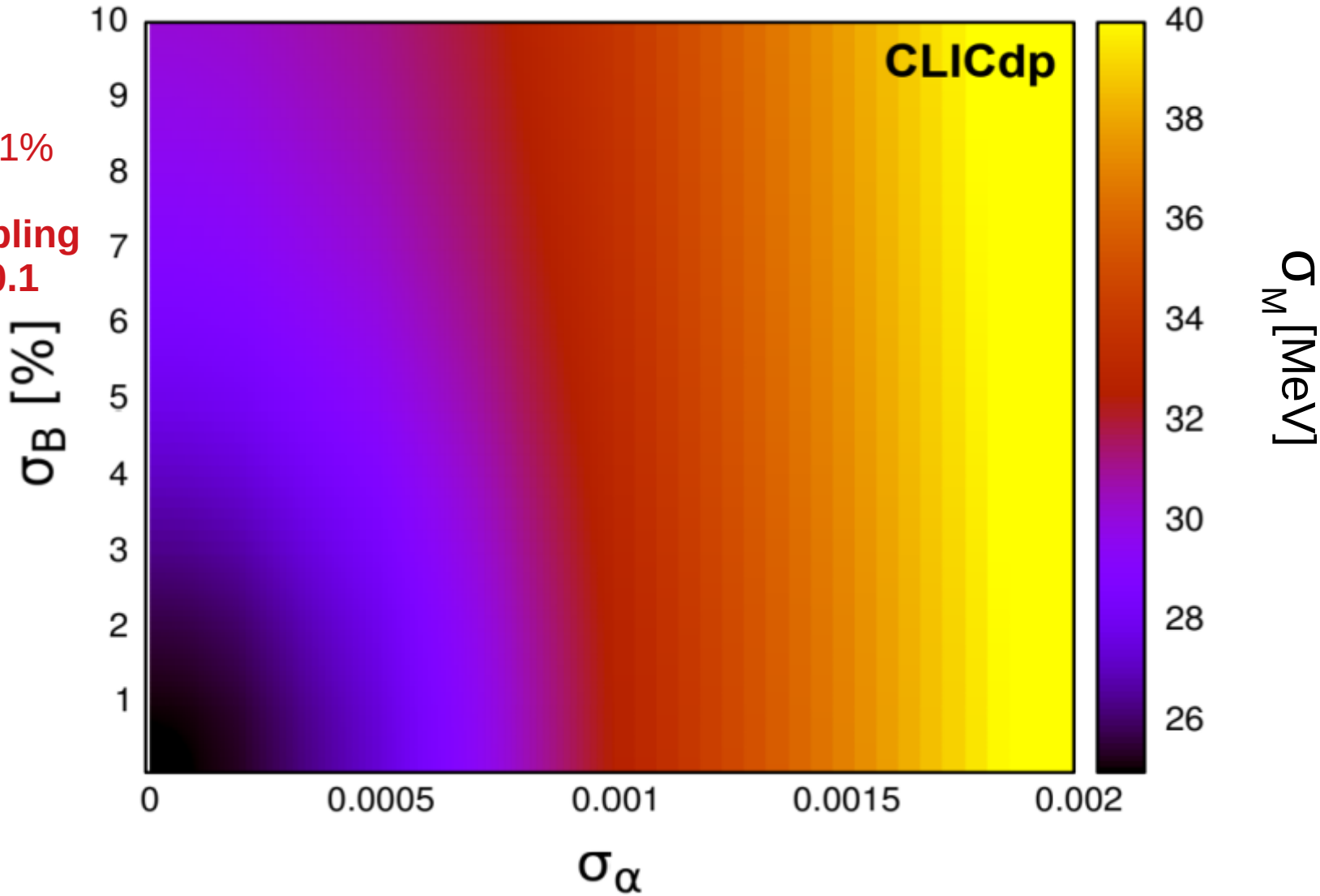
Assuming Normalization uncertainty 0.1%



Baseline fit results

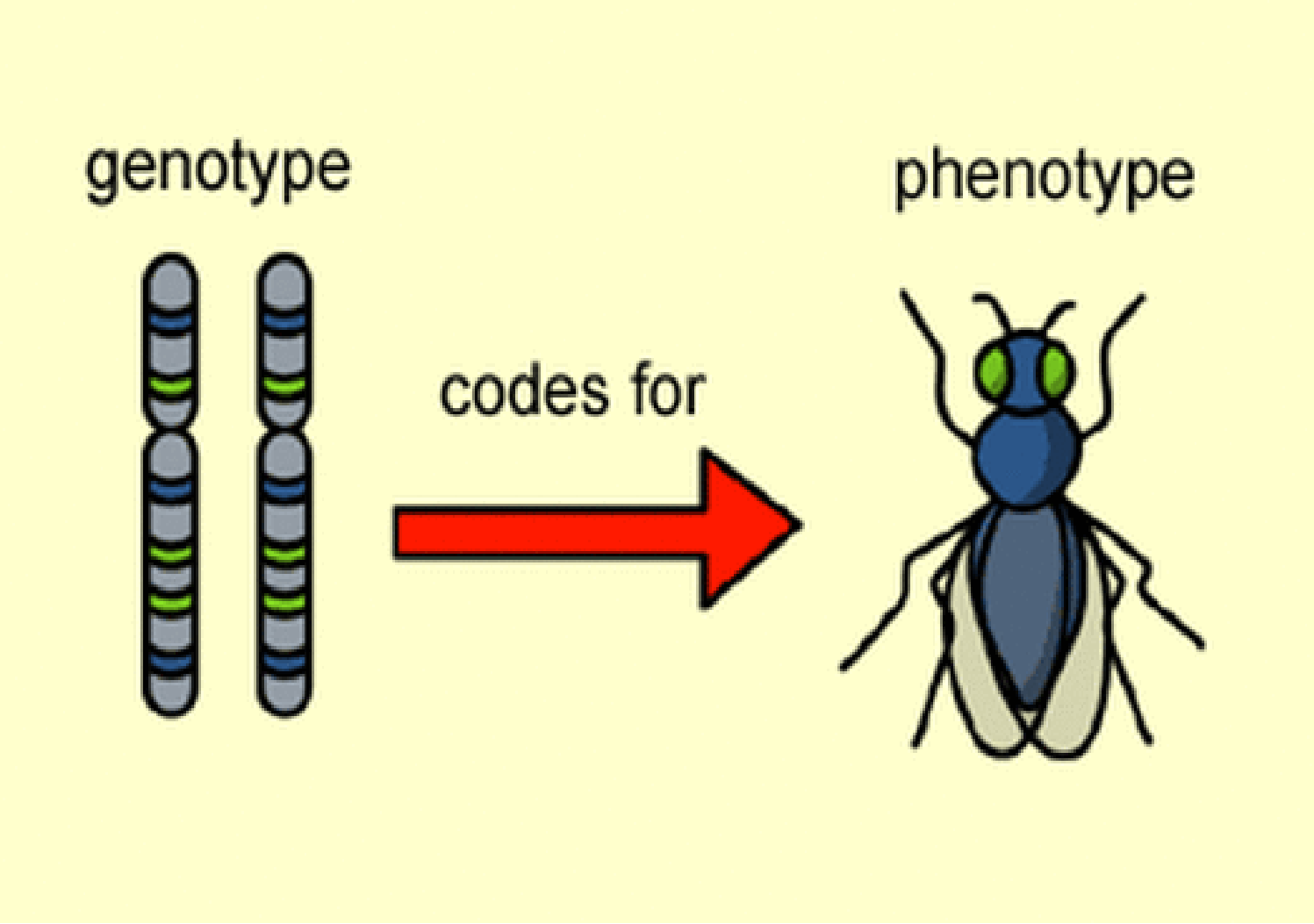
Assuming Normalization uncertainty 0.1%

Yukawa coupling uncertainty 0.1



Scan optimization

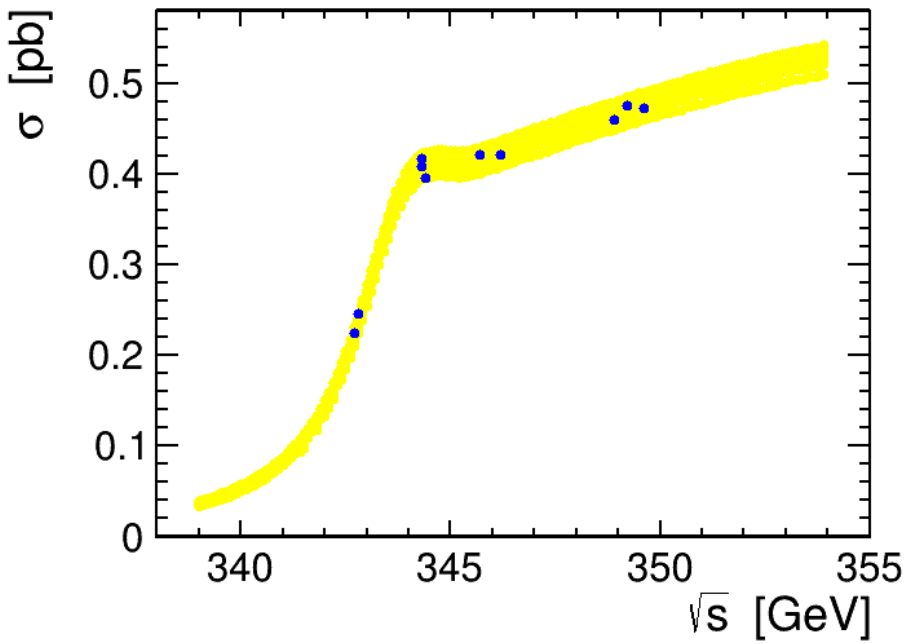
Genetic algorithm



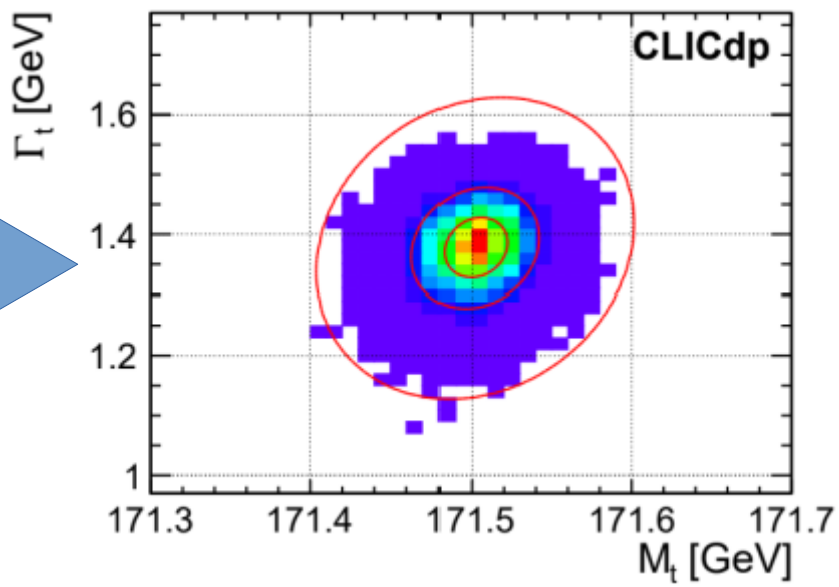
Genetic algorithm

Each measurement point makes a chromosome.
We assume total luminosity is always 100 fb^{-1} and is equally distributed.

Genotype



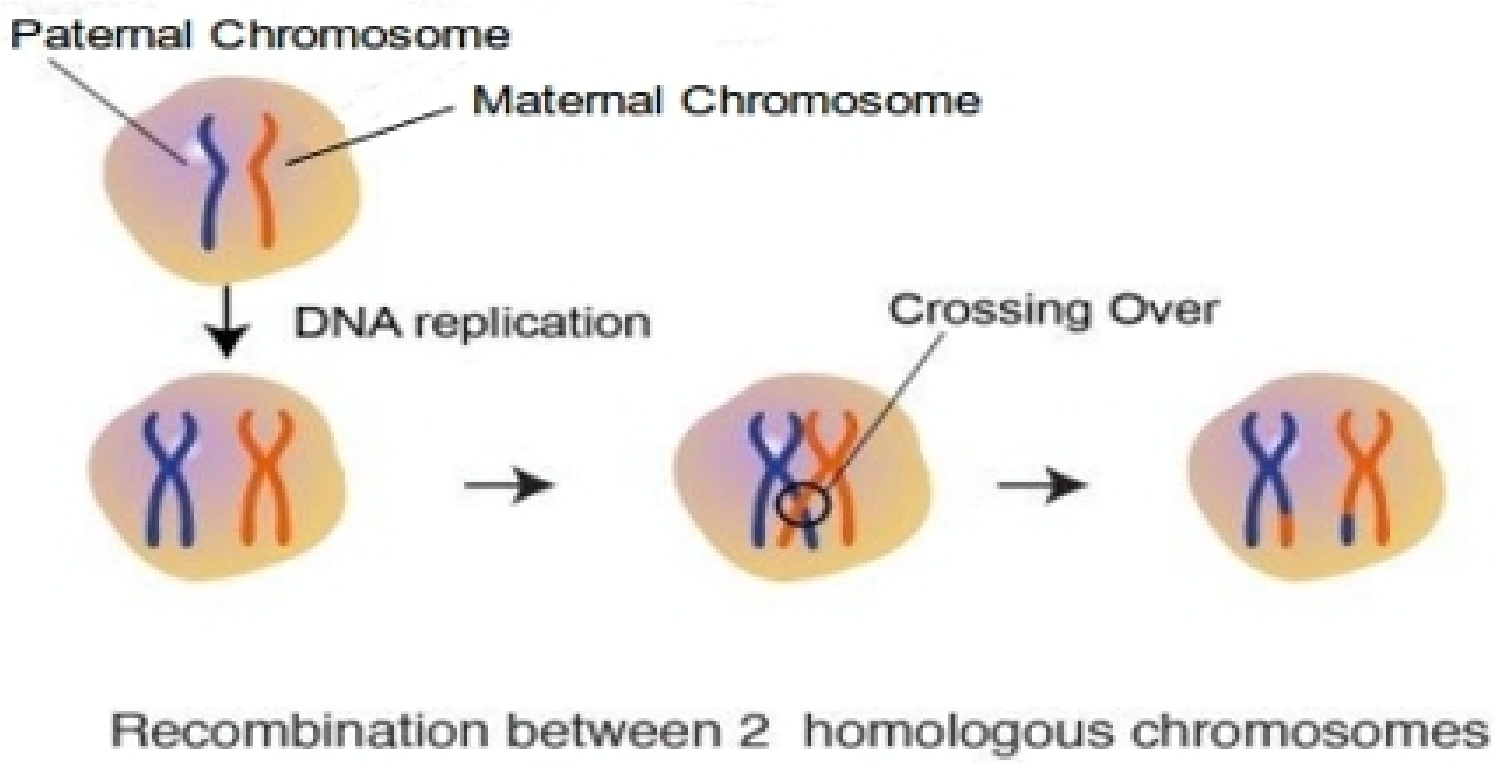
Phenotype



Fits resulting in the parameter values outside the range used to generate templates are ignored.

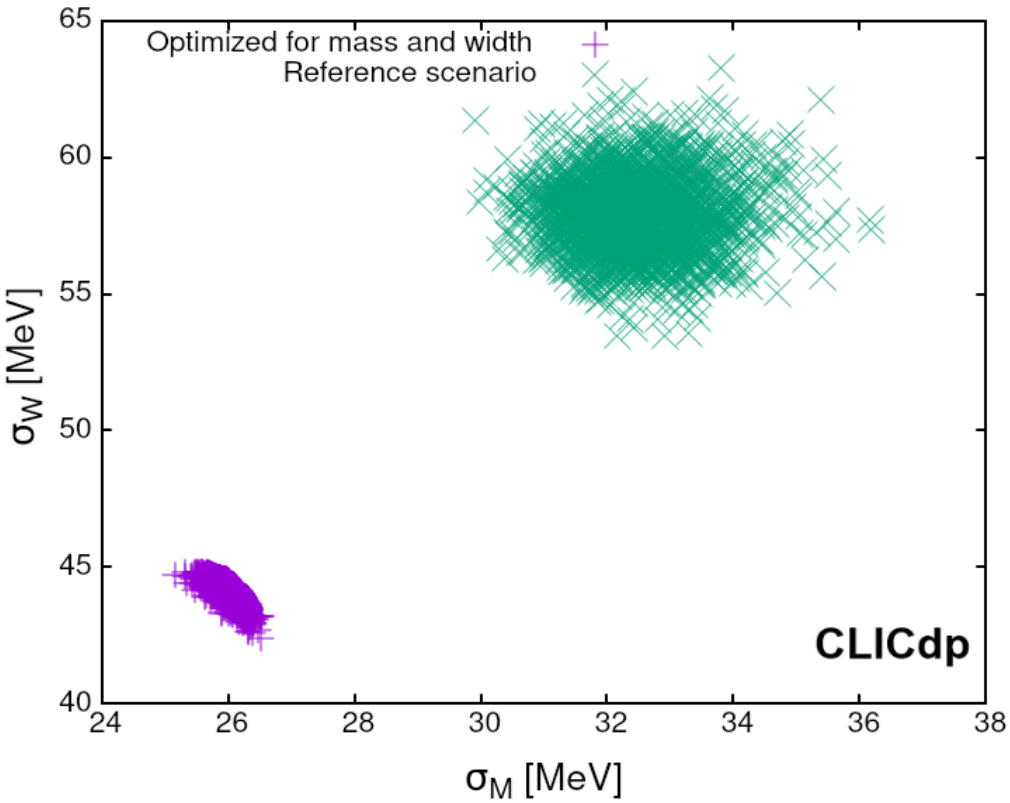
Creating new individuals

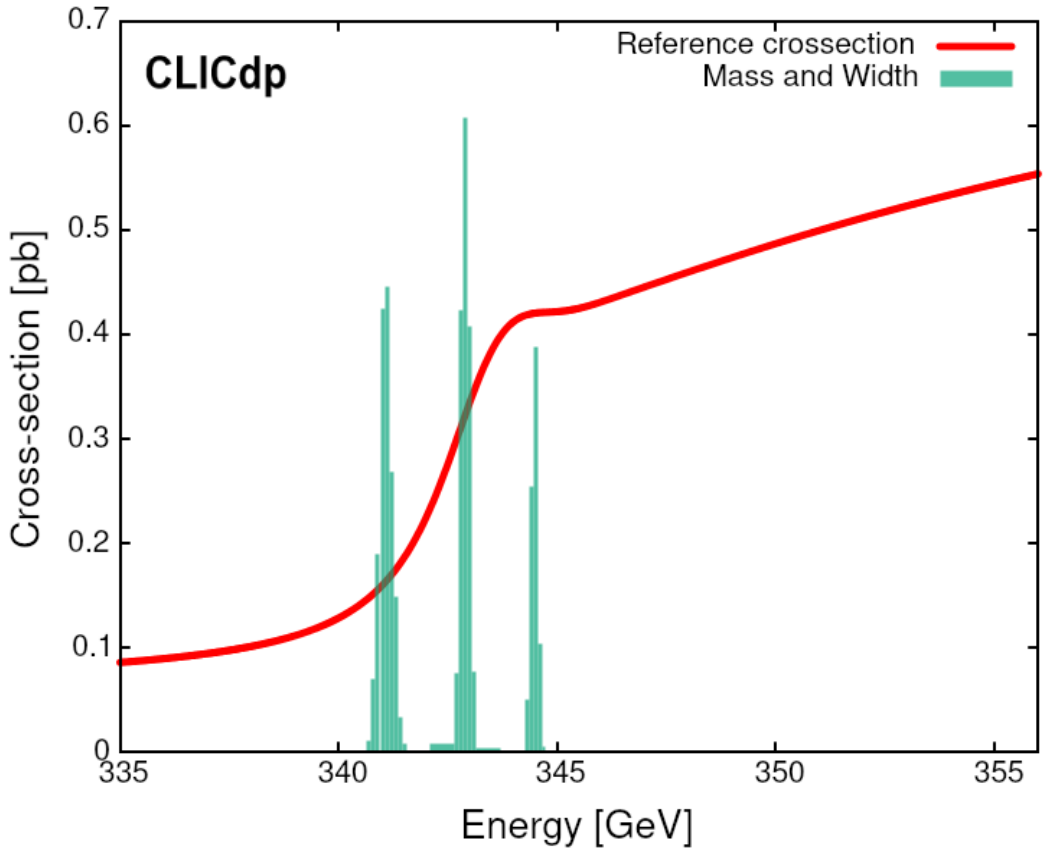
Randomly choosing parts of parents genotype and add random mutation +/- 0.5 GeV



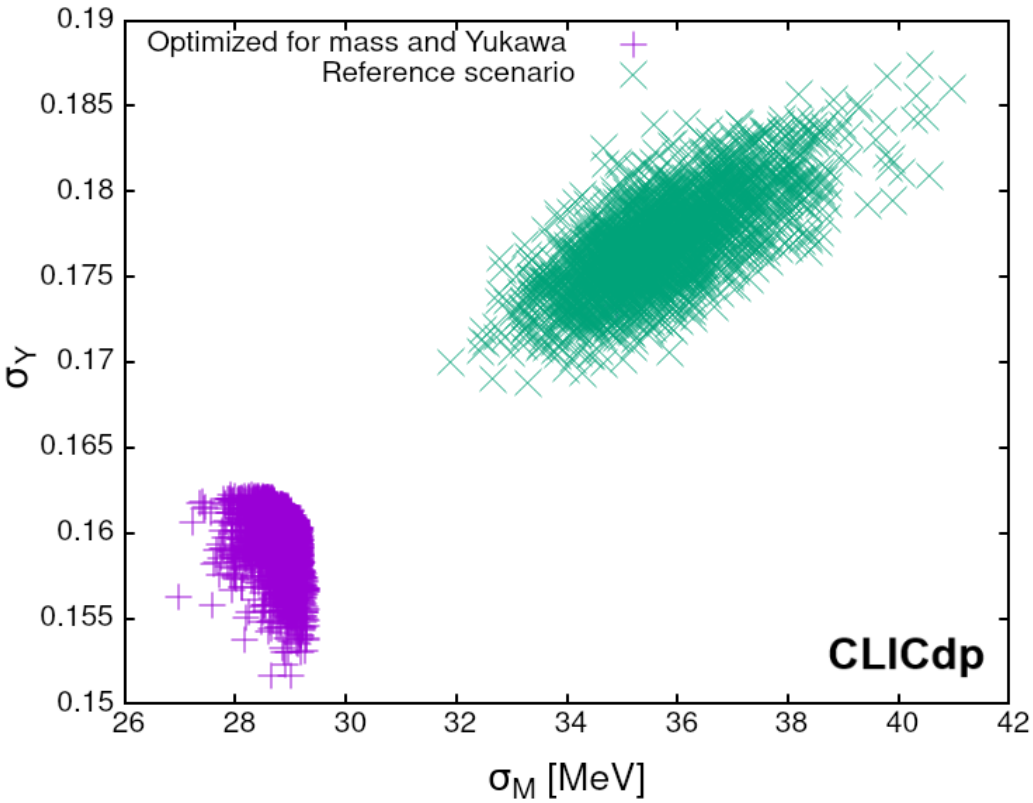
We add 5% chance to drop any of measurement points.

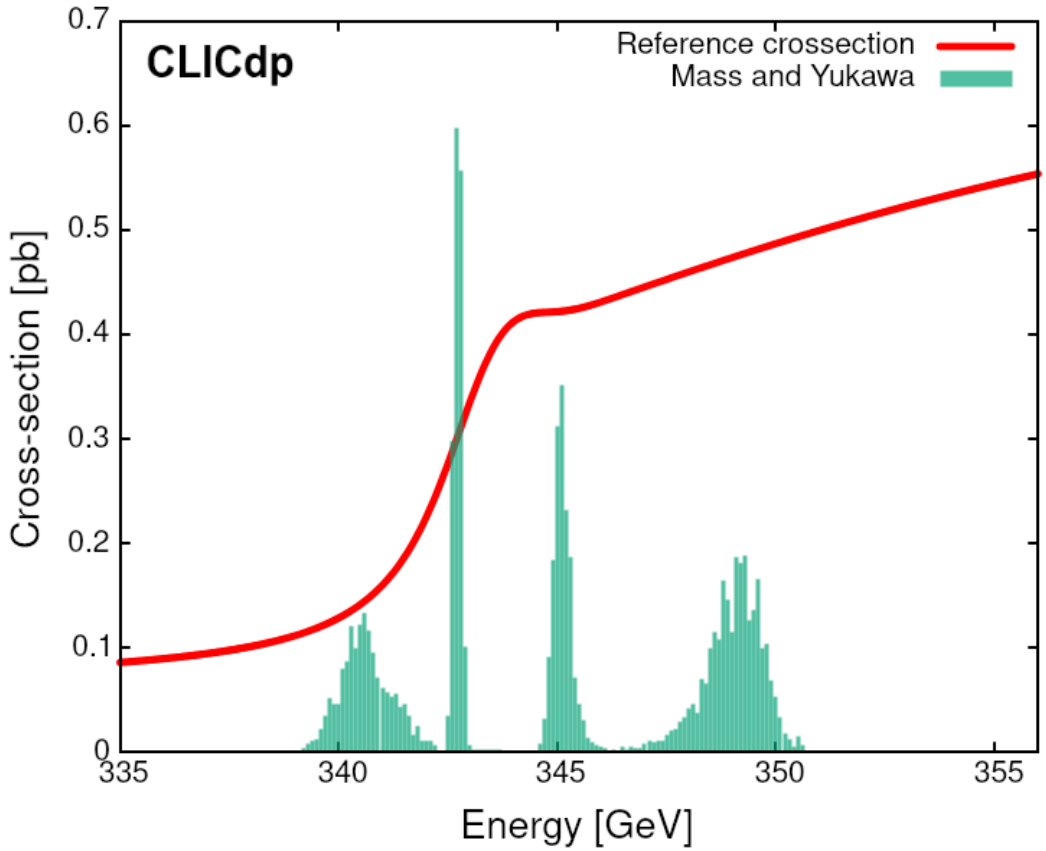
Mass and Width optimization





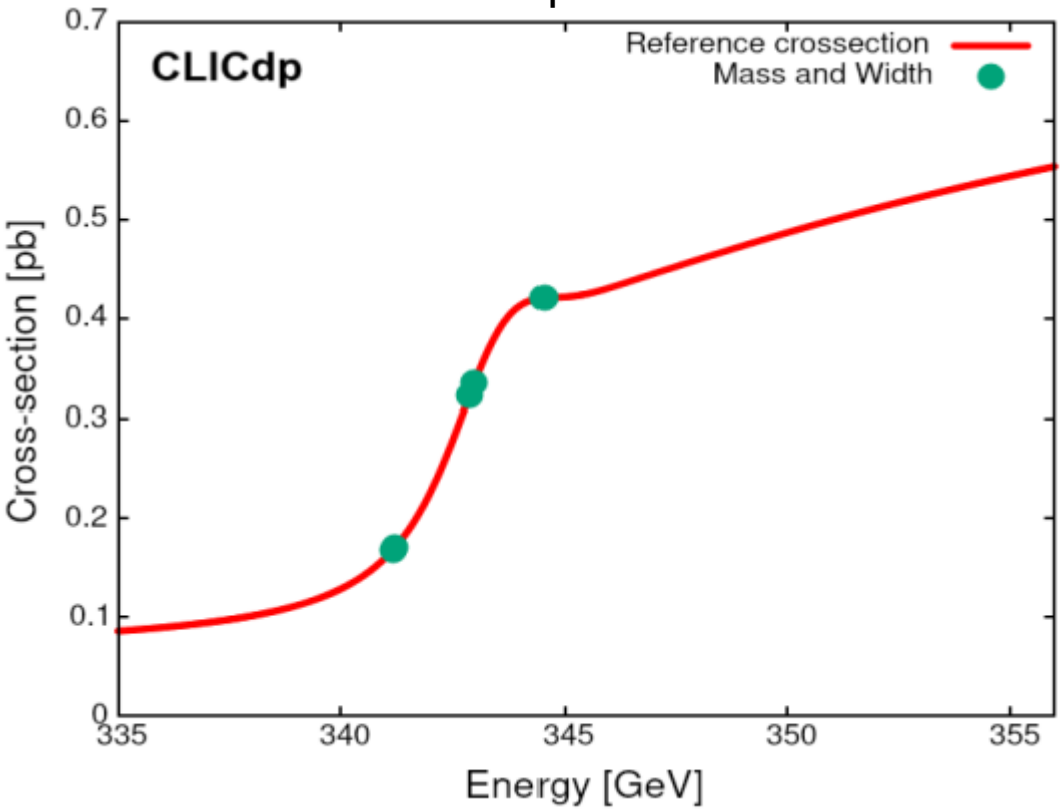
Mass and Yukawa optimization



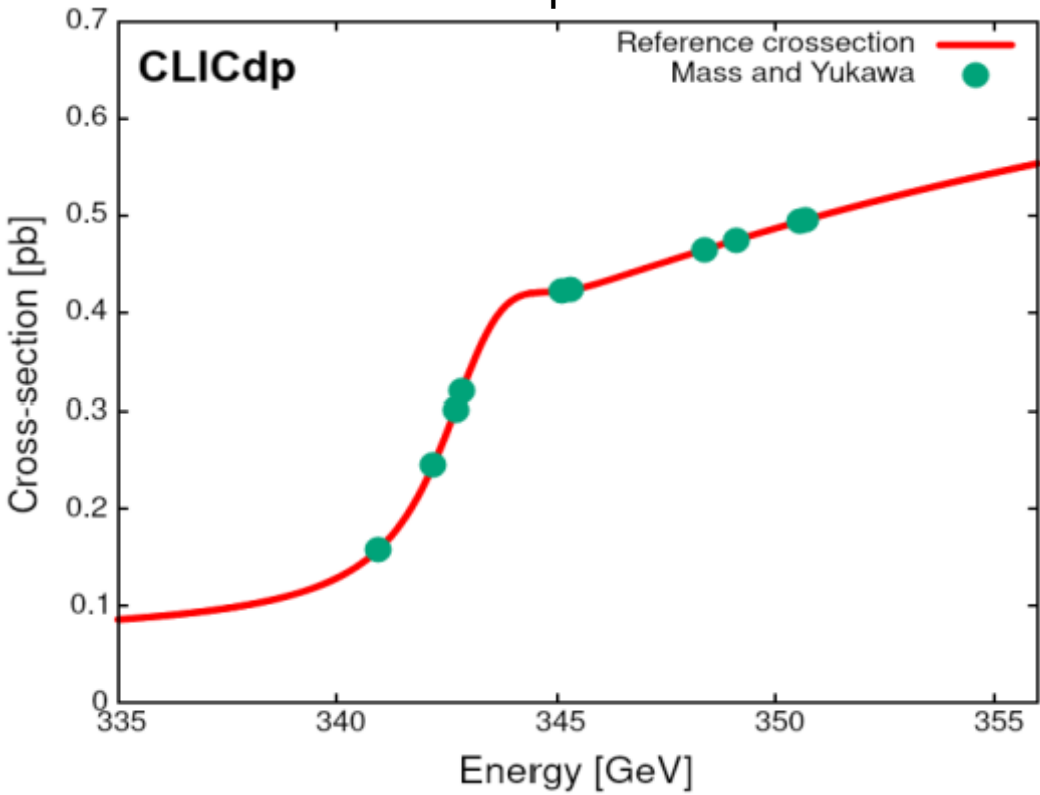


Optimized scenarios

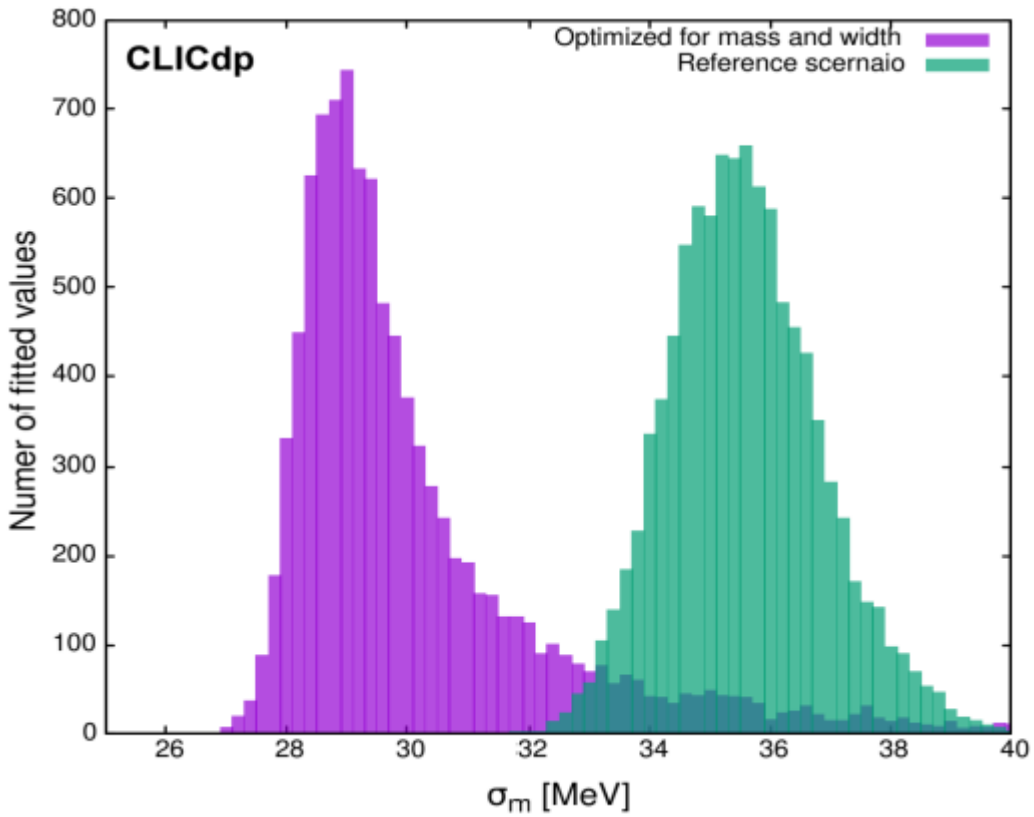
Mass and Yukawa
5 points

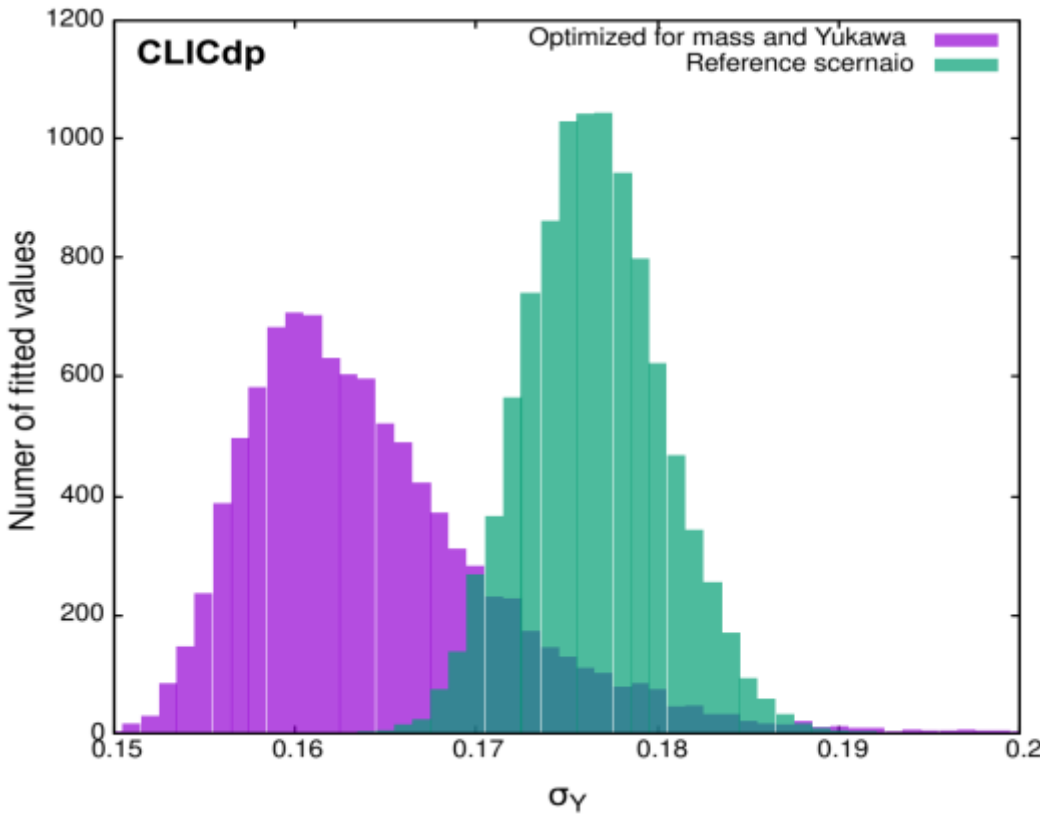


Mass and Width
10 points



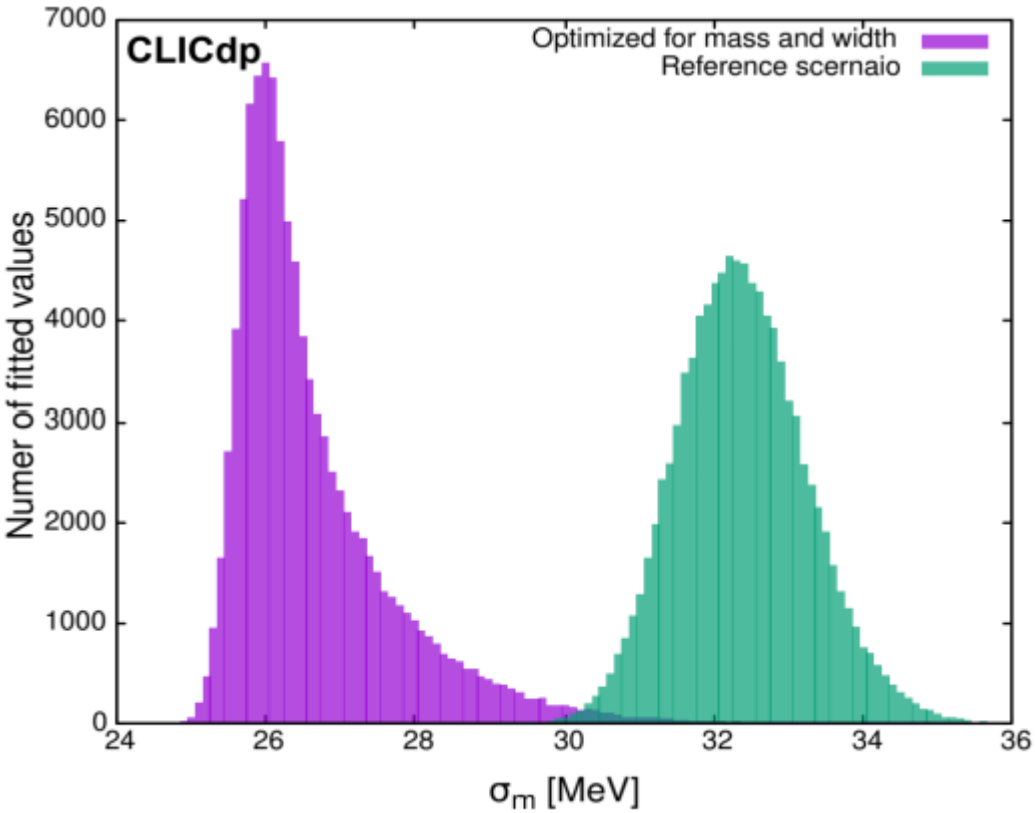
Mass and Yukawa scenario

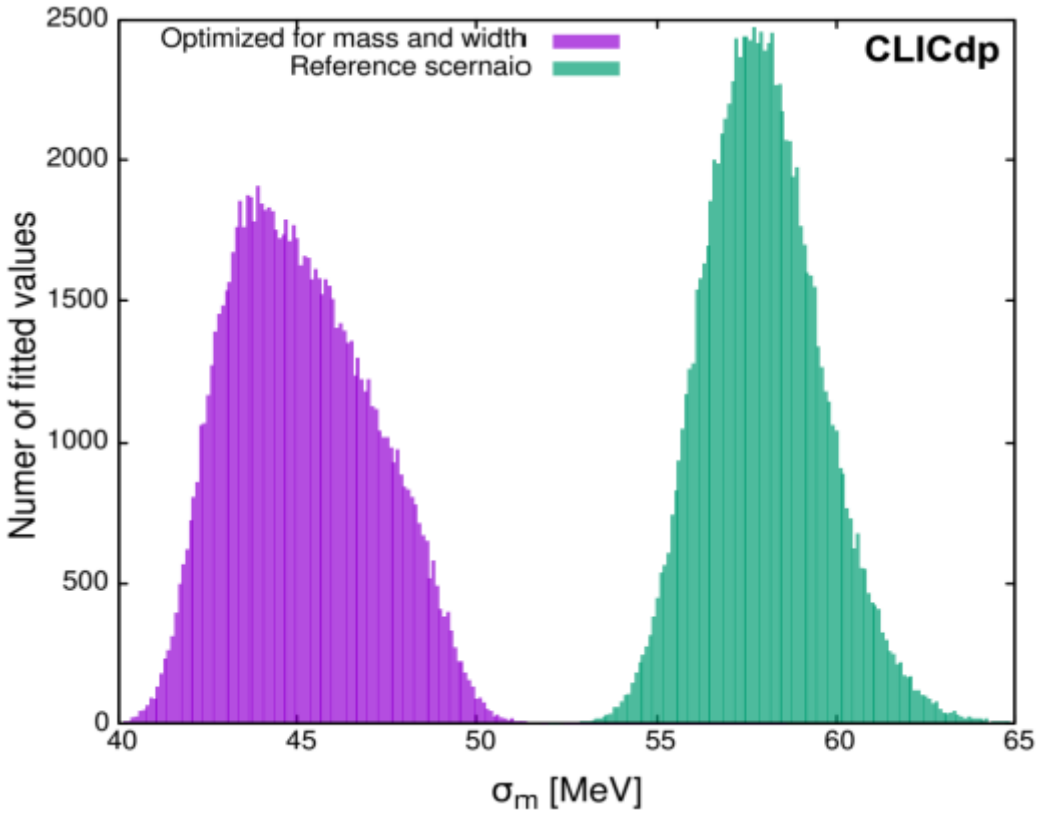




Normalization uncertainty 1%
Strong coupling uncertainty 0.001
Background uncertainty 2%

Mass and width scenario



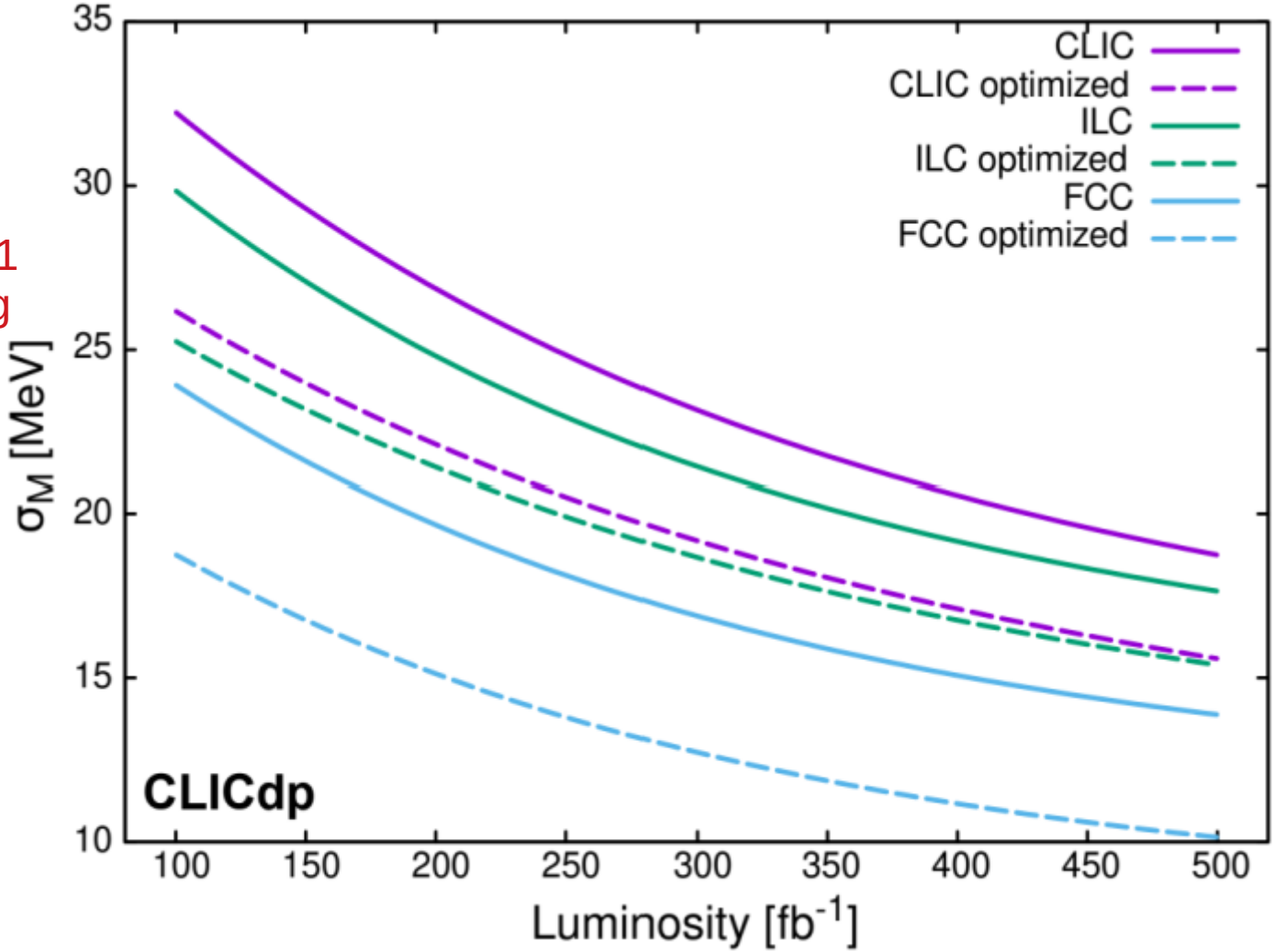


Normalization uncertainty 1%
Strong coupling uncertainty 0.001
Yukawa coupling uncertainty 0.1
Background uncertainty 2%

Influence of luminosity spectra

Normalization uncertainty 1%
Strong coupling uncertainty 0.001
Yukawa coupling ucertainty 0.1

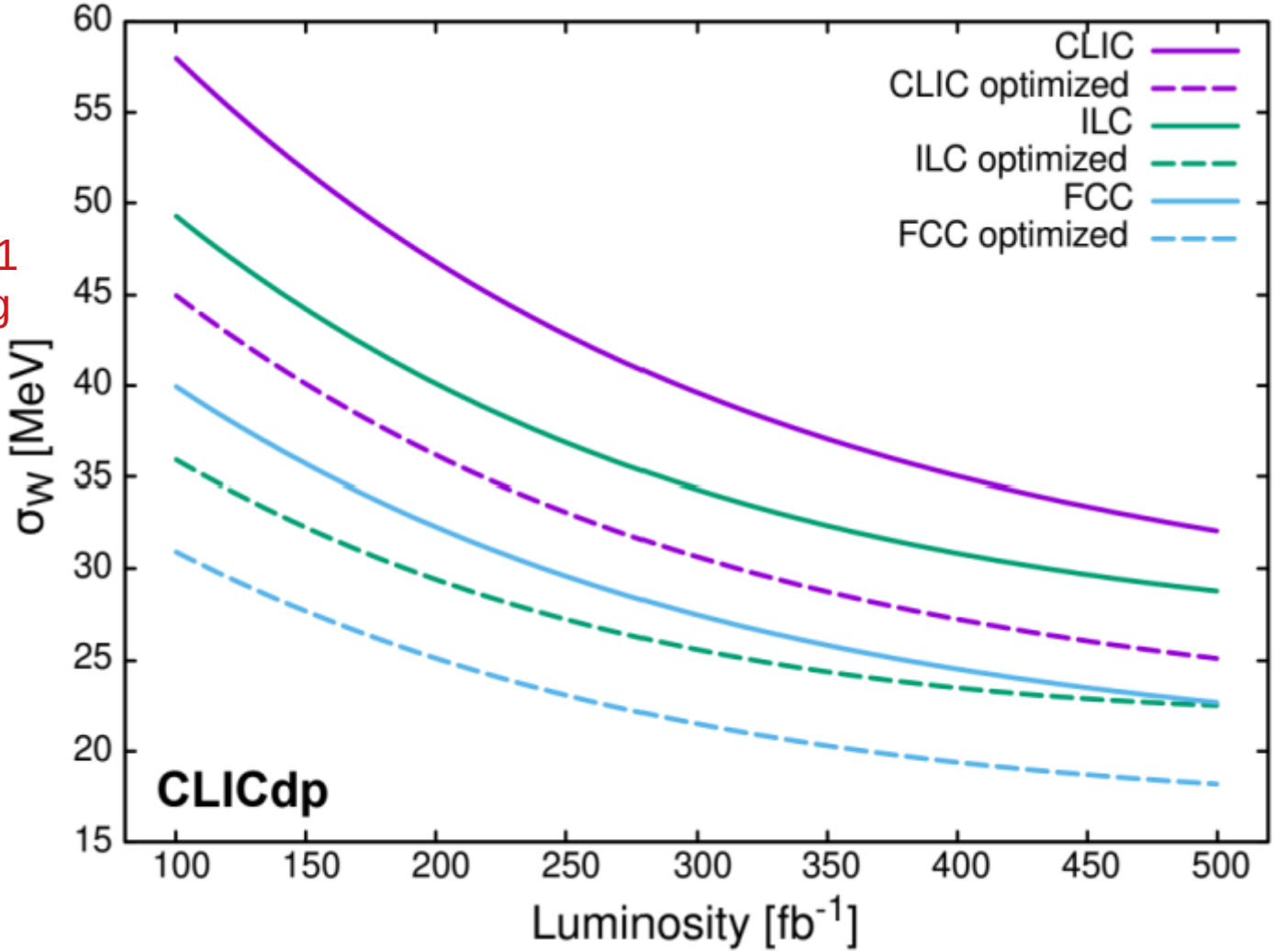
Optimized for mass and width determination precision



Assuming **same** background and efficiency, **no polarisation**

Influence of luminosity spectra

Normalization uncertainty 1%
Strong coupling uncertainty 0.001
Yukawa coupling ucertainty 0.1



Optimized for mass and width determination precision

Assuming **same** background and efficiency, **no polarisation**

Conclusions

Top-quark mass

can be extracted with ~25 MeV statistical uncertainty even in the most general approach, when expected parameter constraints are taken into account.

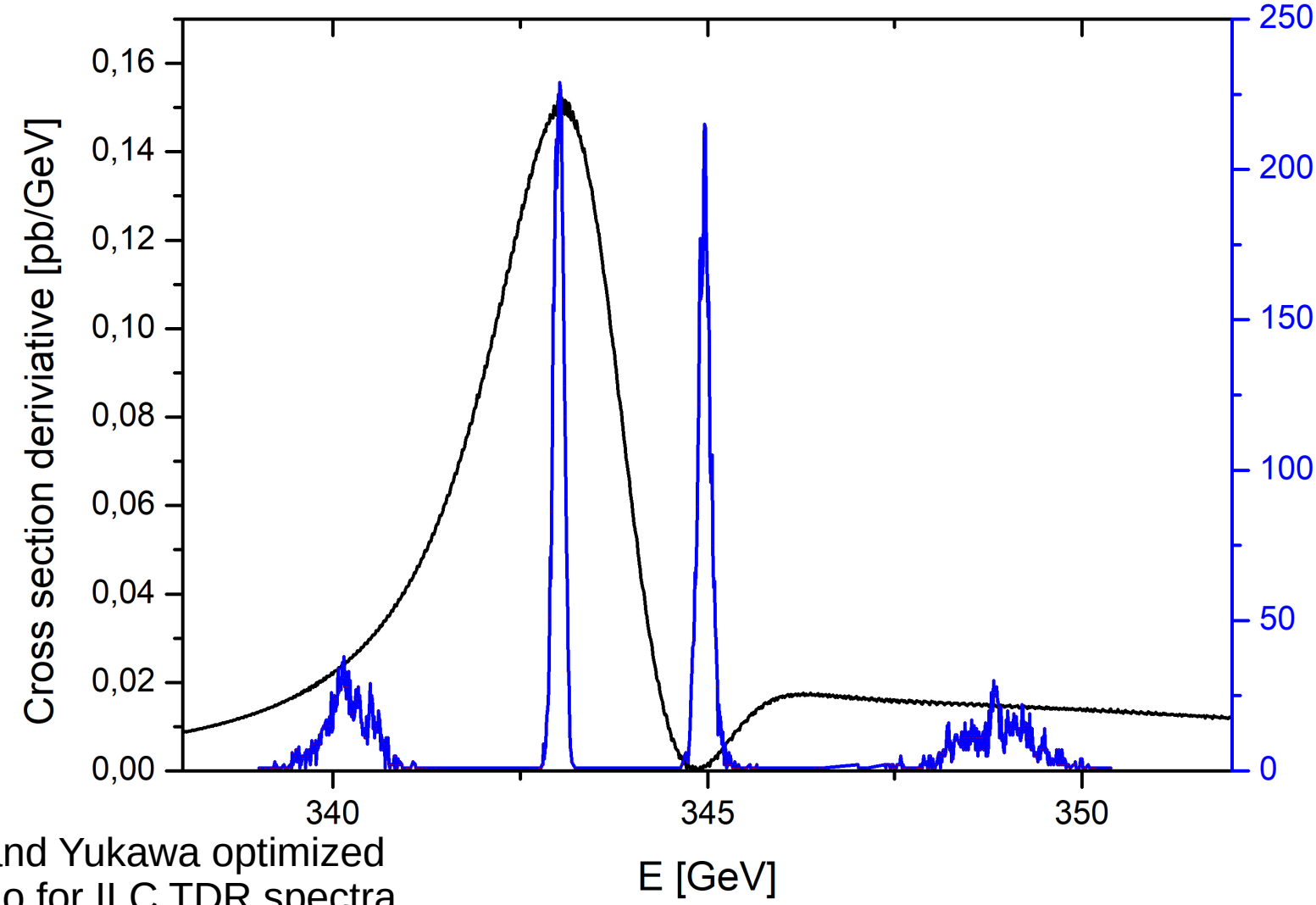
Scan optimization

Statistical uncertainty of the extracted top-quark mass can be reduced by ~25%, without losing precision in width or Yukawa determination

For more results see **arXiv:2103.00522**

Backup slides

What is the algorithm looking for?



Mass and Yukawa optimized scenario for ILC TDR spectra