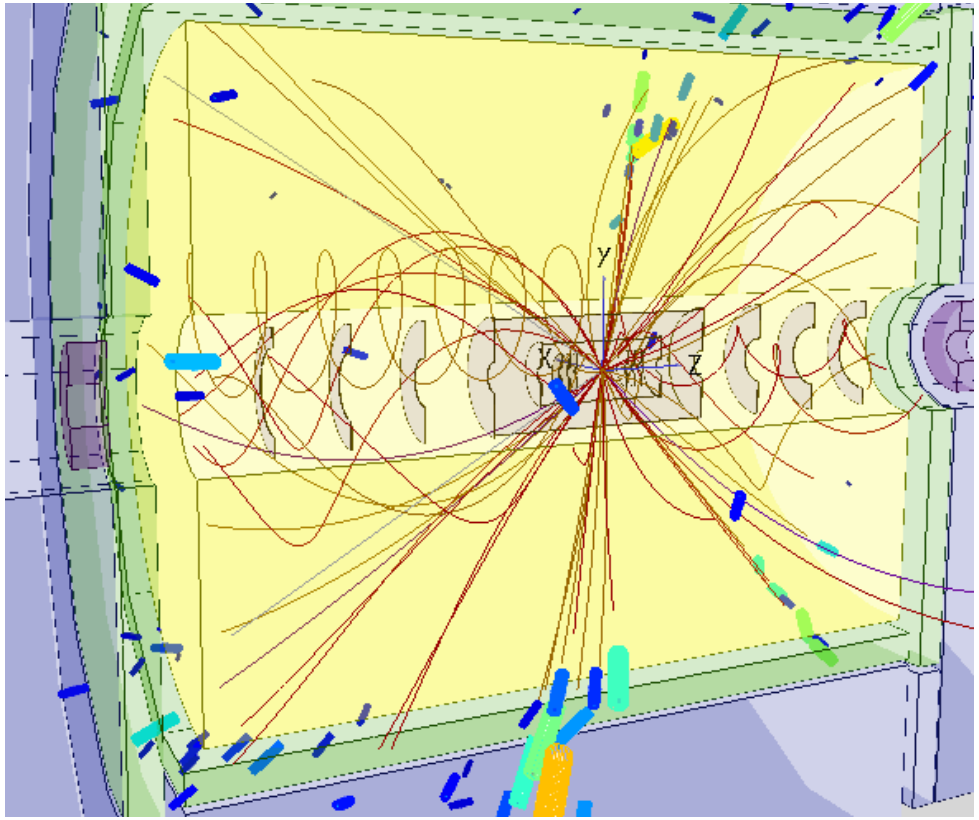
Optimising top-quark pair-production threshold scan at future e^+e^- colliders



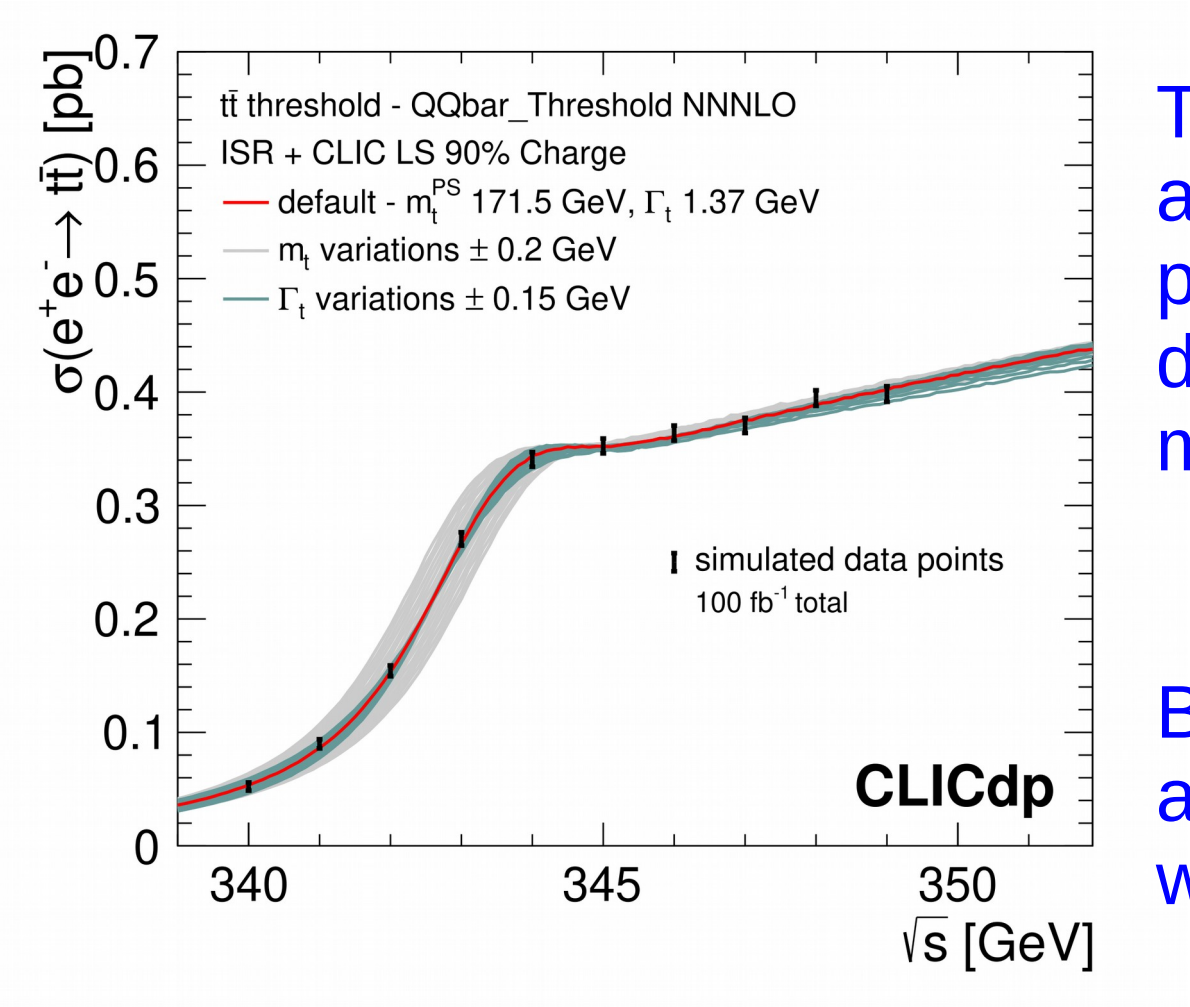
ICHEP 2020, July 31, 2020

Kacper Nowak, Aleksander Filip Żarnecki

FACULTY OF PHYSICS UW

Motivation

Motivation

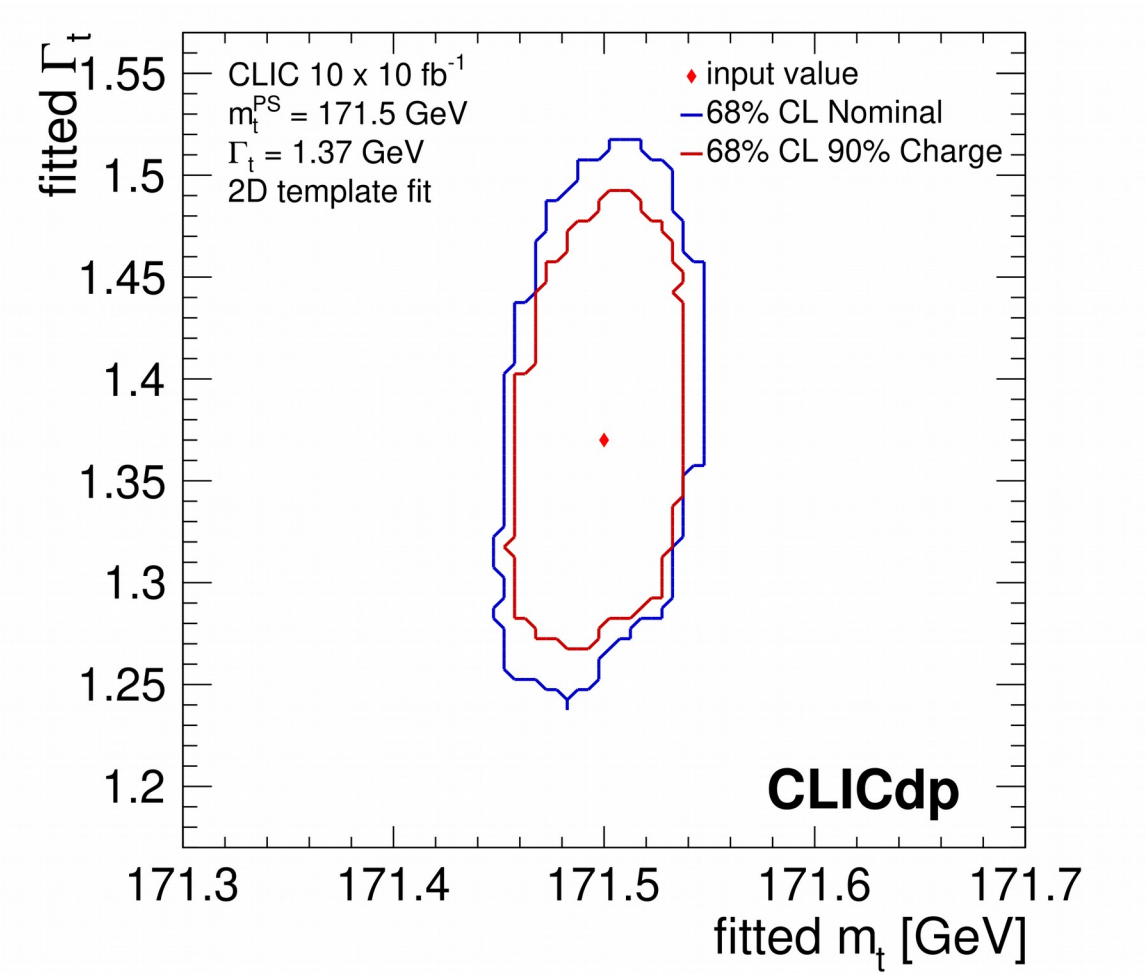


Threshold scan is assumed to be the most precise method to determine the top quark mass.

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

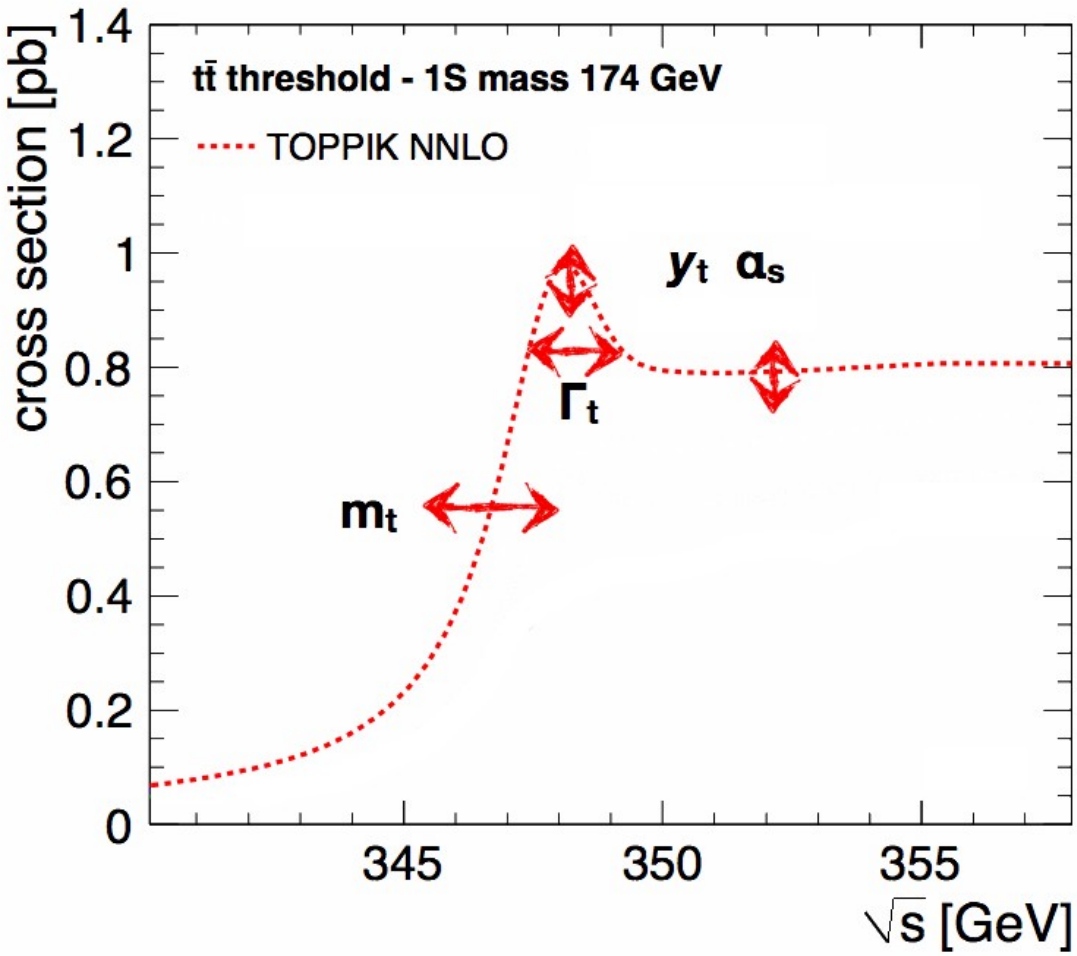


Dedicated study for CLIC indicates that the statistical precision of the measurement is around 20 MeV

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



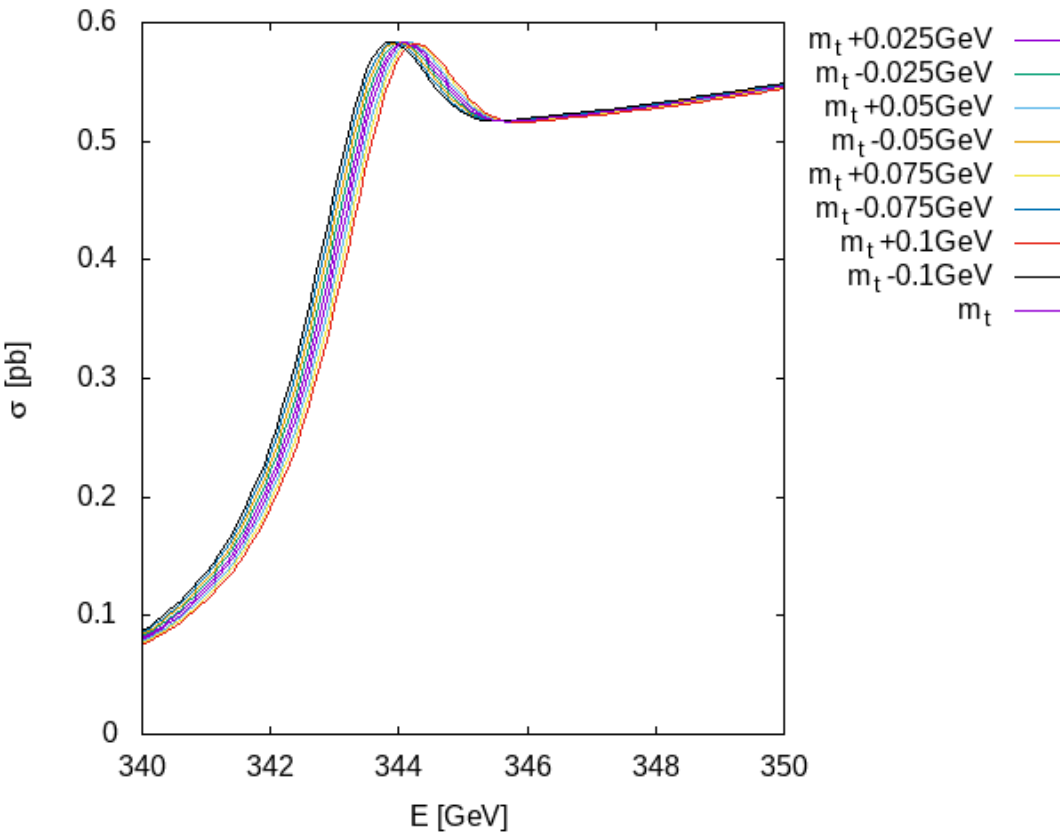
Threshold cross section depends on other model parameters as well…

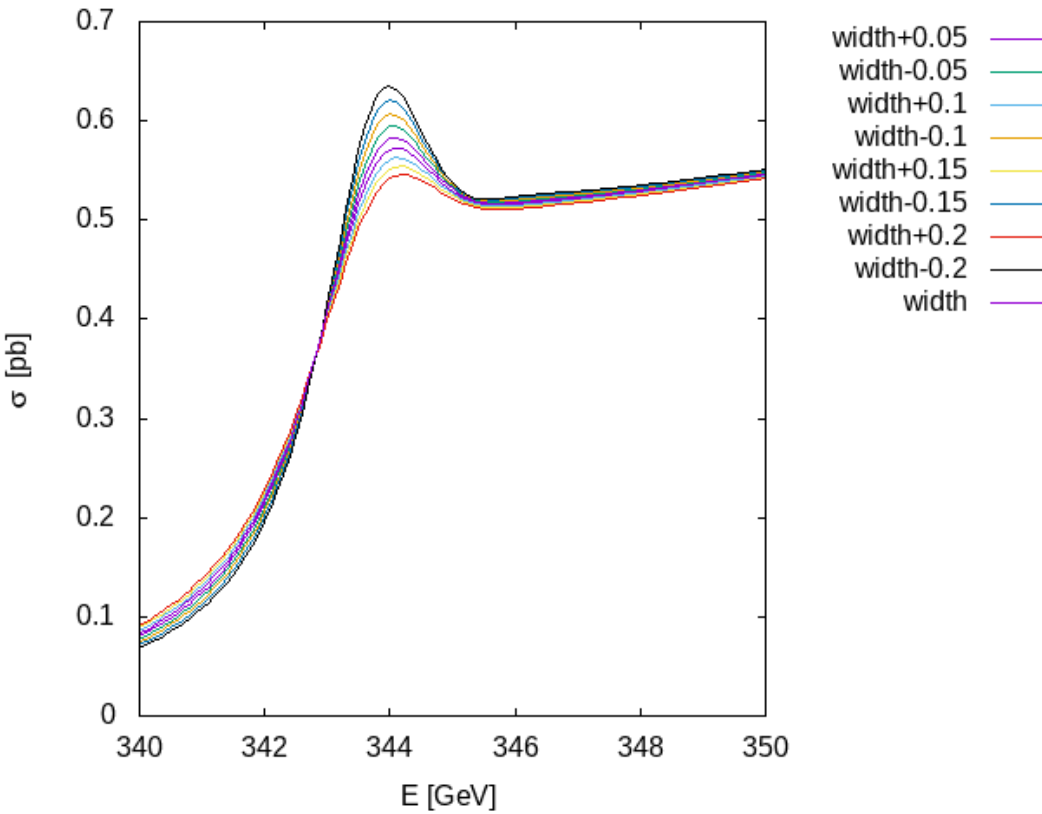
Does it influence m_t determination precision?

Can the scan procedure be optimized?

Fit method

Cross-section templates

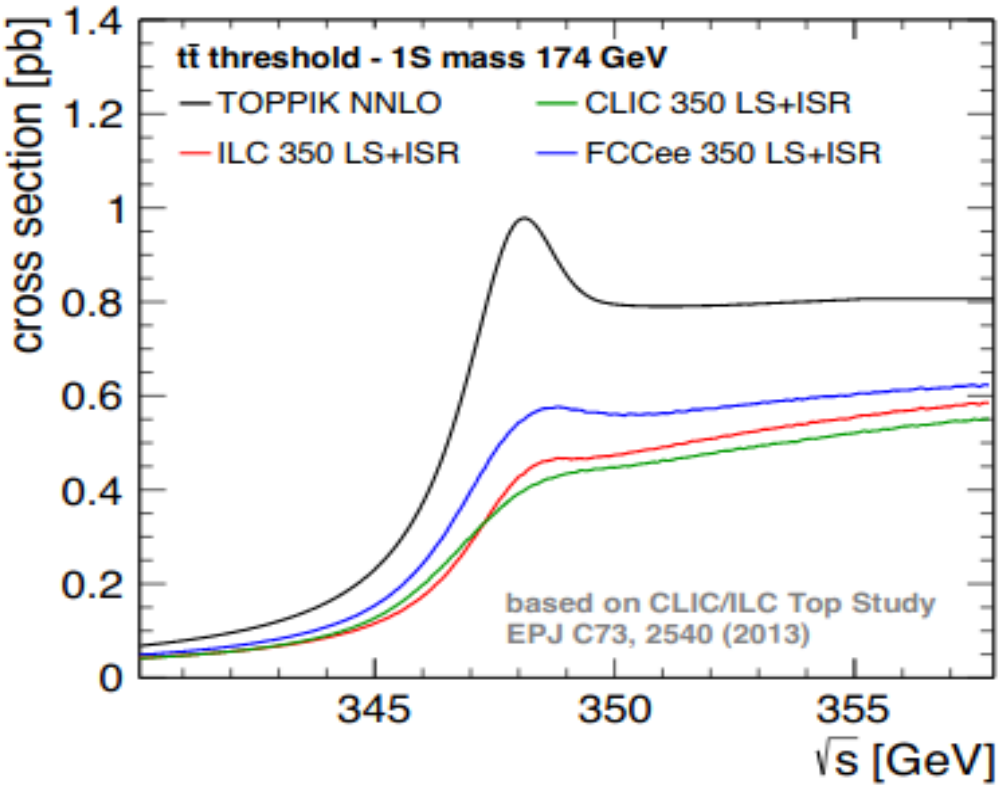


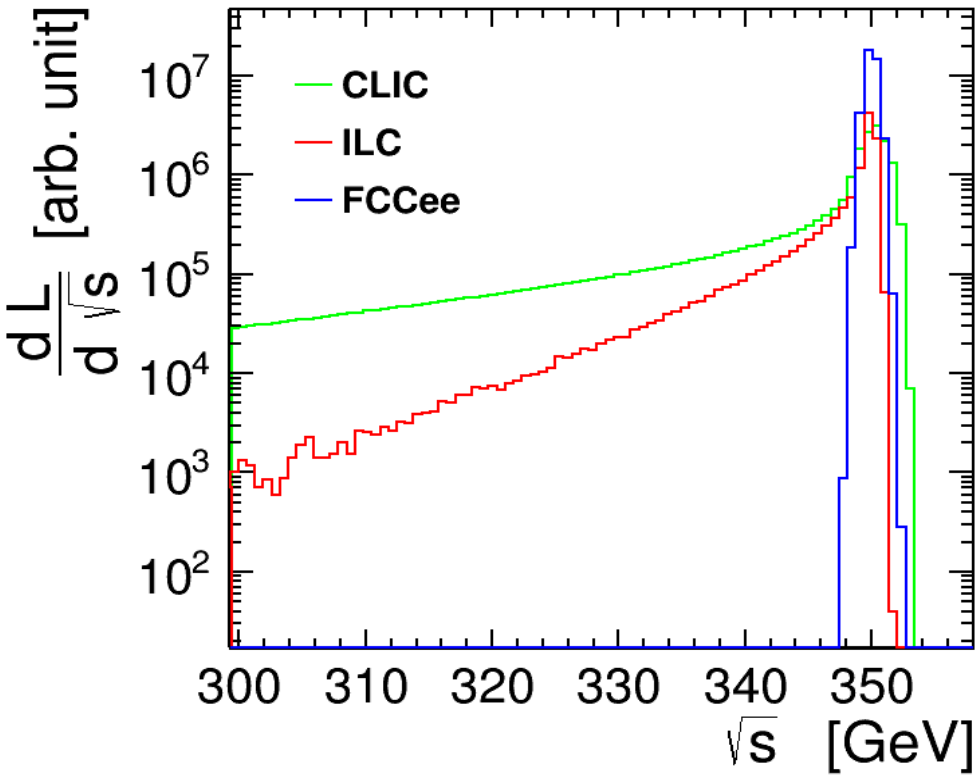


Templates generated with **Qqbar_threshold**

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

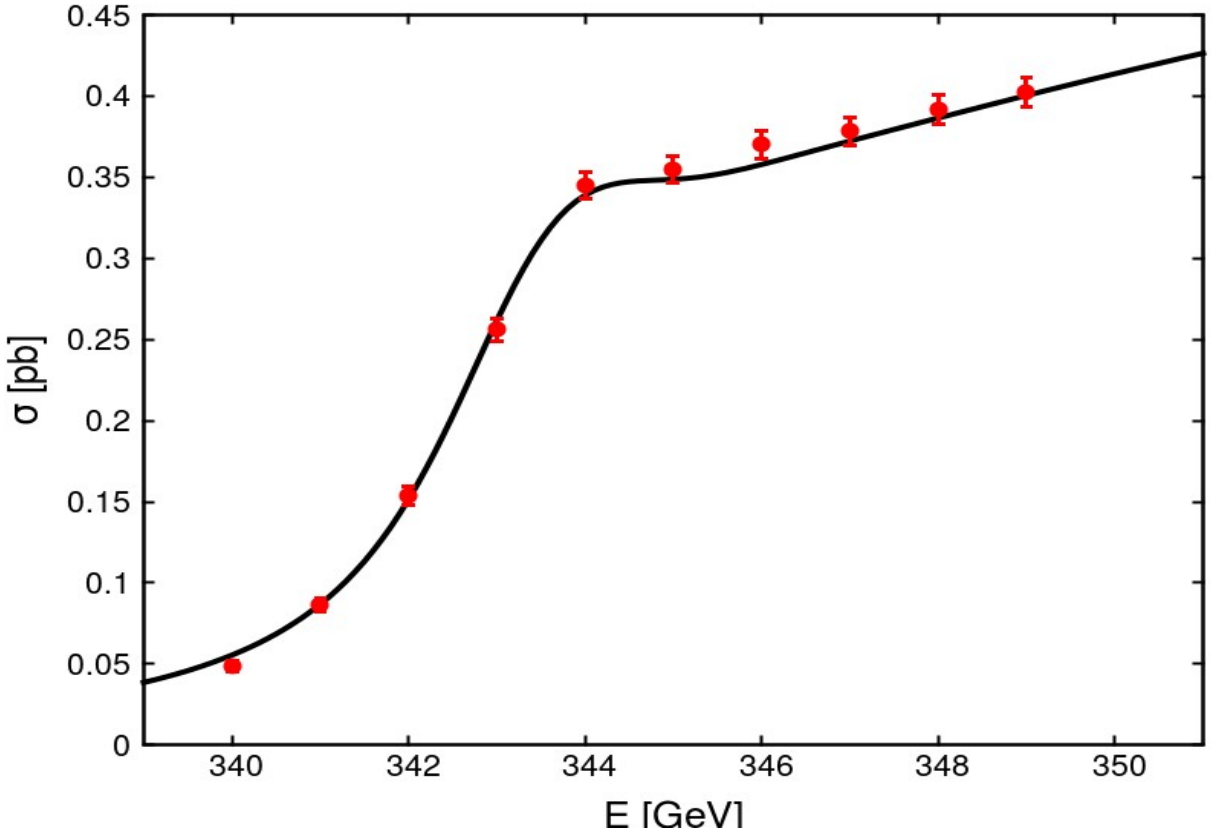
Luminosity spectra





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)

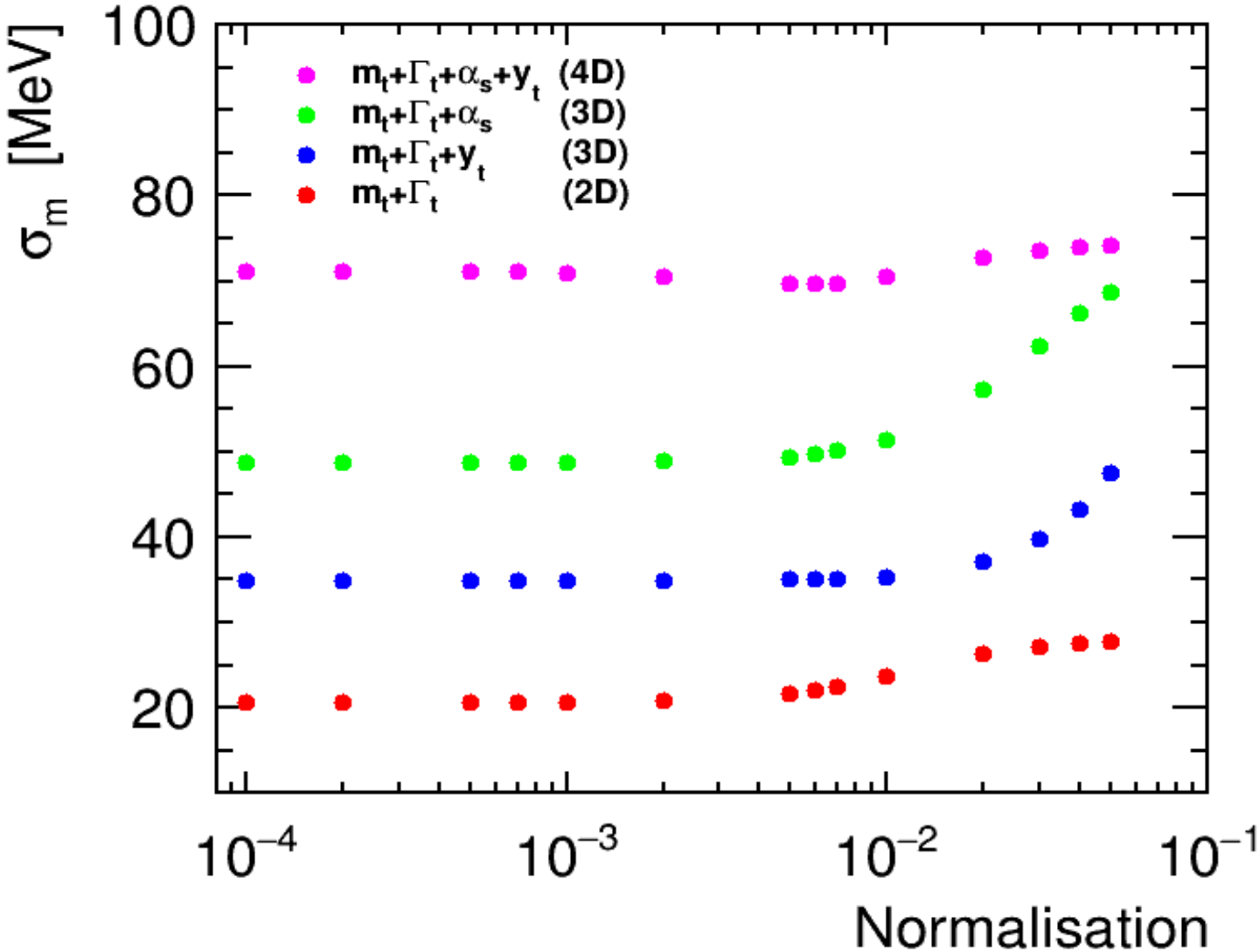
Quadratic dependence of the χ^2 value on the model parameters is fitted to find the best fit parameter values and the estimated uncertainty (corresponding to $\Delta\chi=1$)

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

More details on the fit method: Proc.SPIE Int.Soc.Opt.Eng. 11176 (2019) 1117648, CLICdp-Conf-2019-011

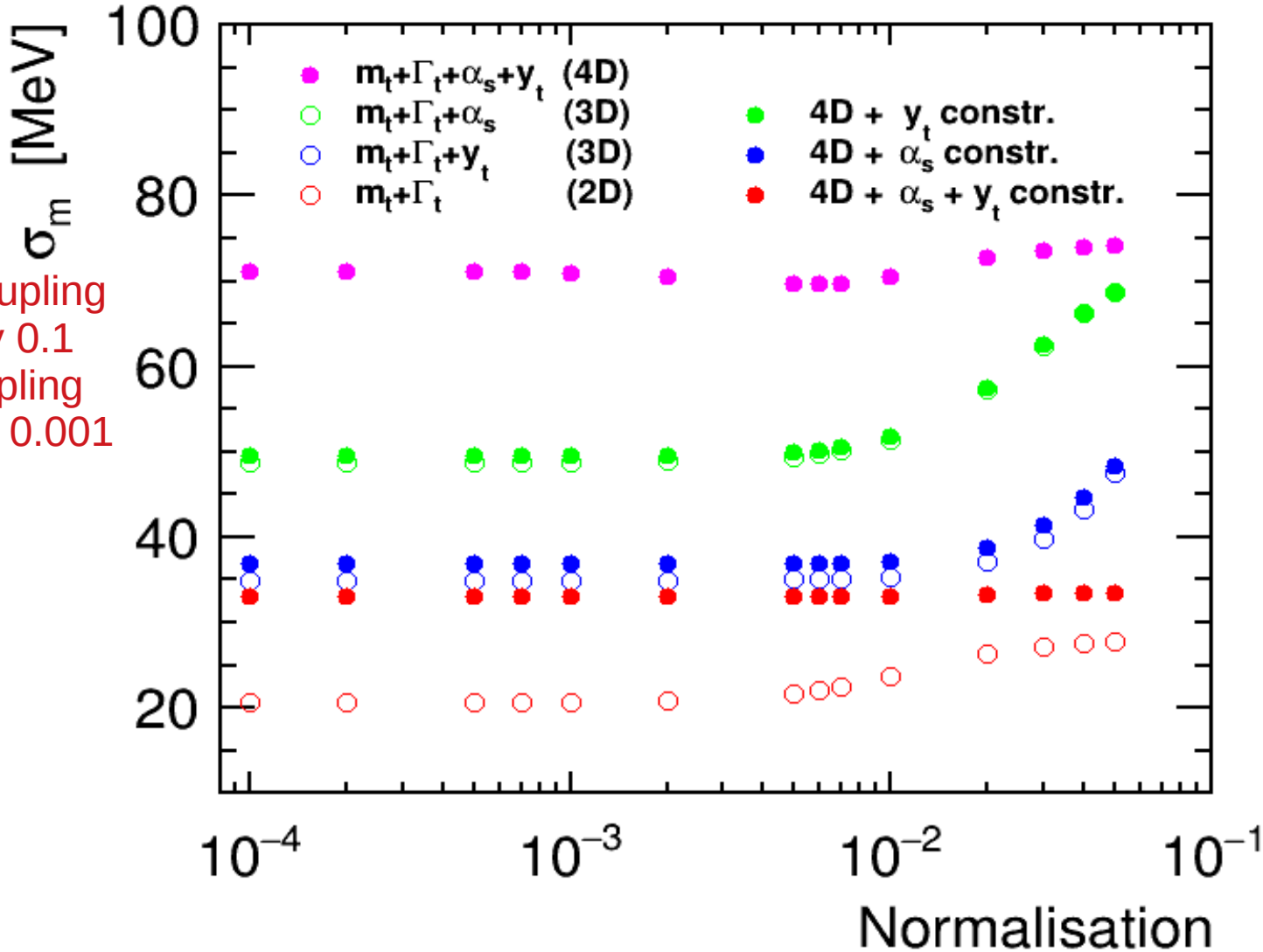
Baseline Fit Results

Fit configuration



Parameter constrains

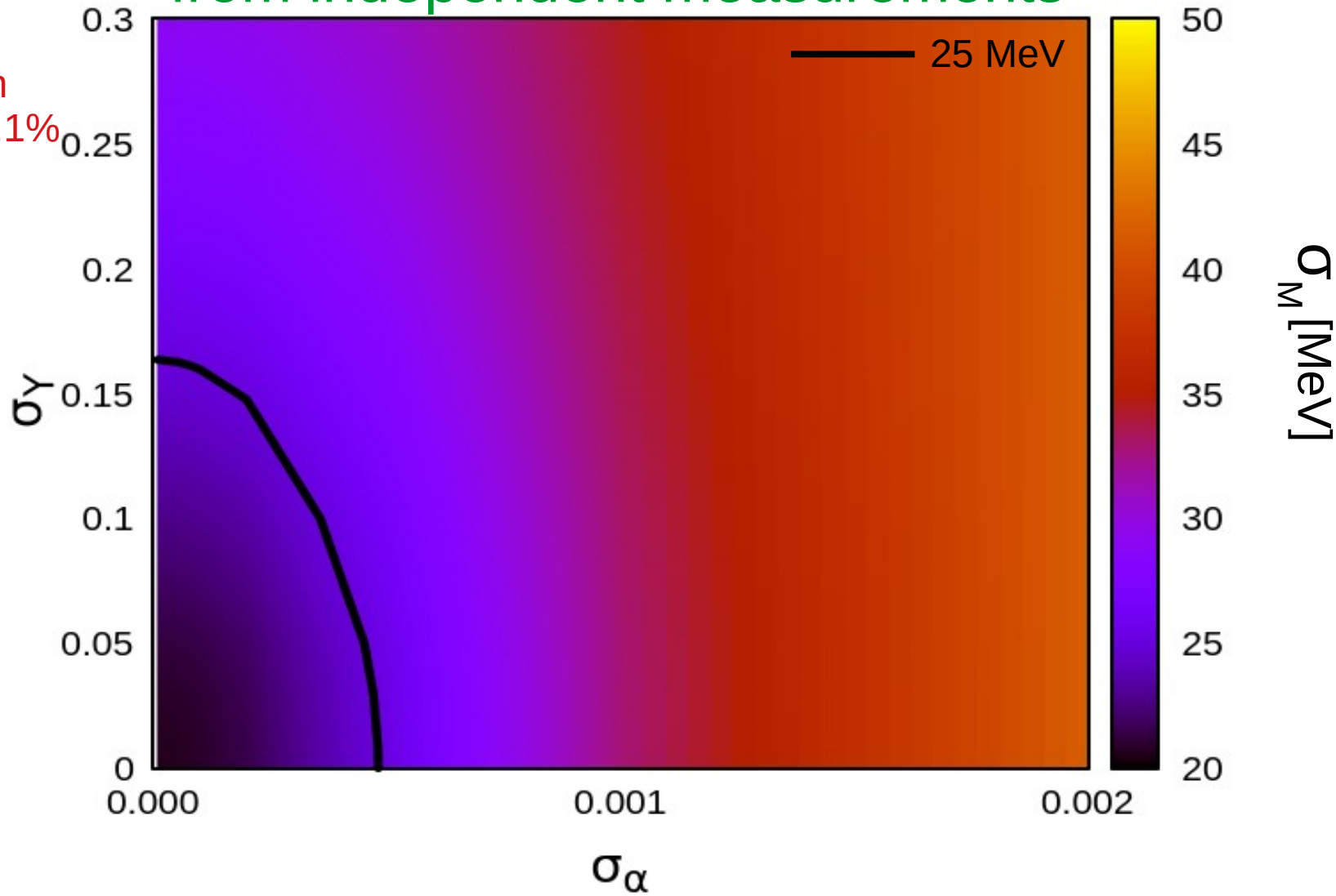
Yukawa coupling
Uncertainty 0.1
Strong coupling
uncertainty 0.001



Statistical uncertainty on top-quark mass vs Yukawa and strong coupling uncertainties

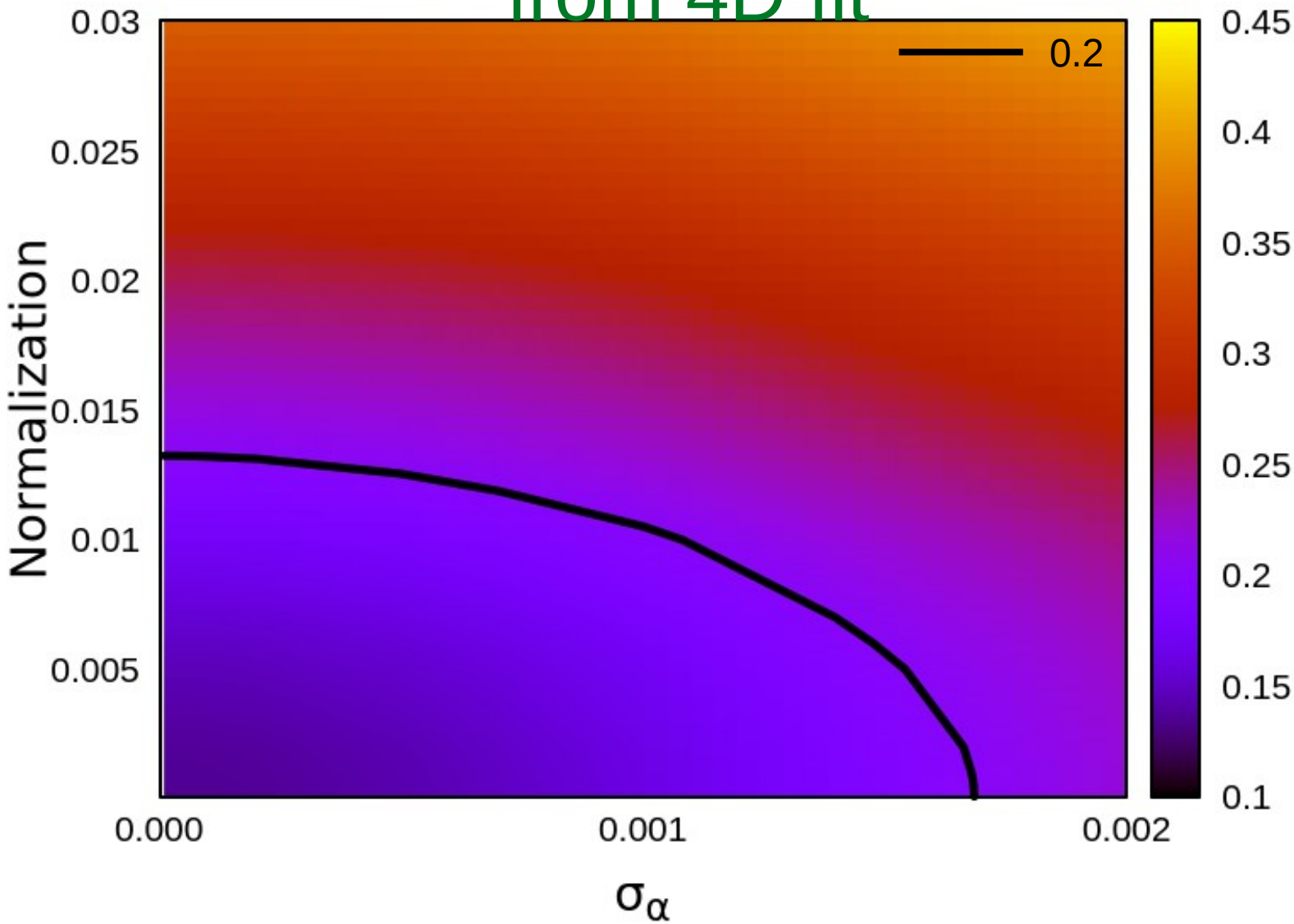
from independent measurements

Normalization uncertainty 0.1%



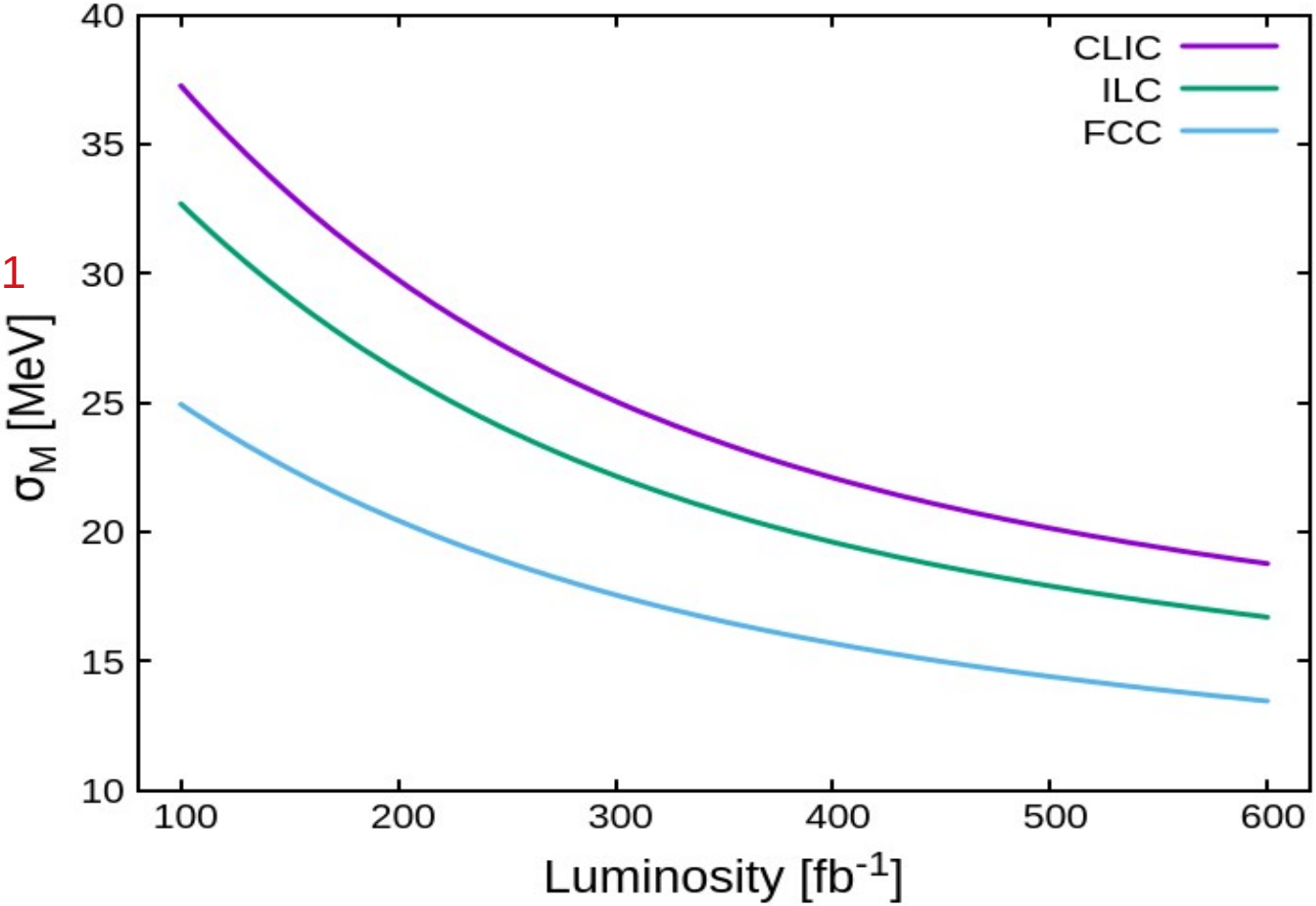
Yukawa uncertainty

from 4D fit



Influence of luminosity spectra

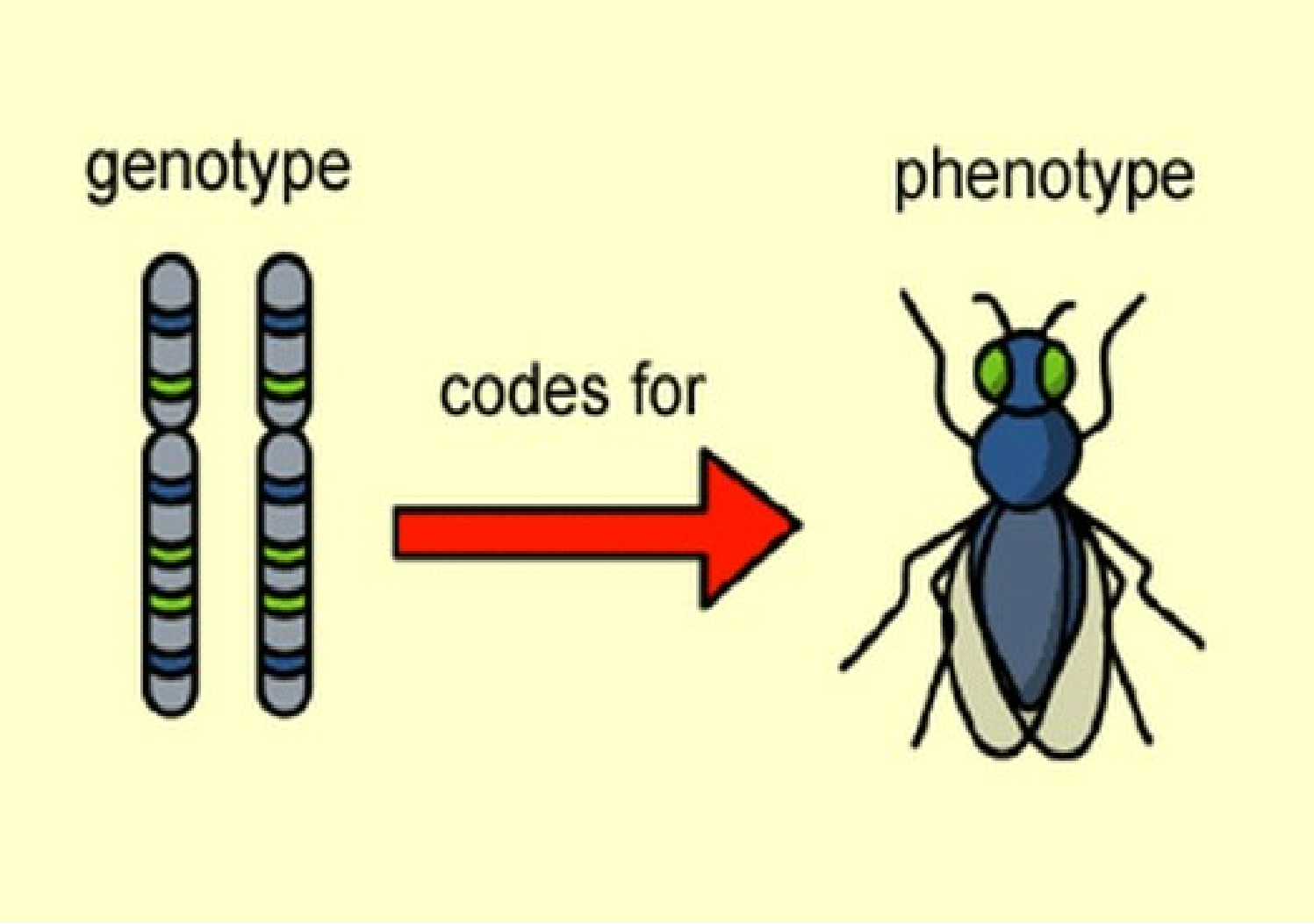
Normalization uncertainty 1%
Strong coupling uncertainty 0.001



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

Scan optimization

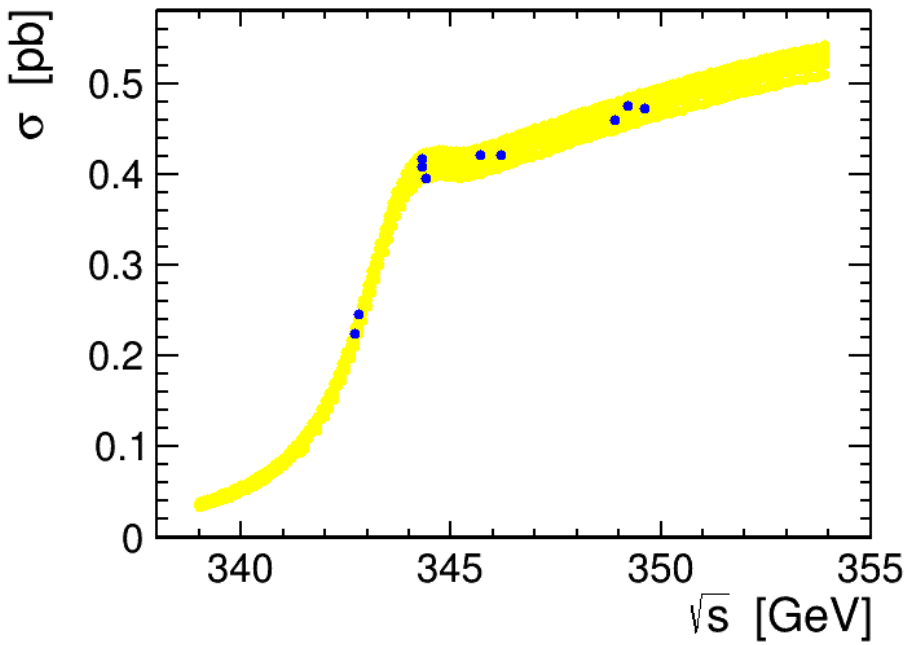
Genetic algorithm



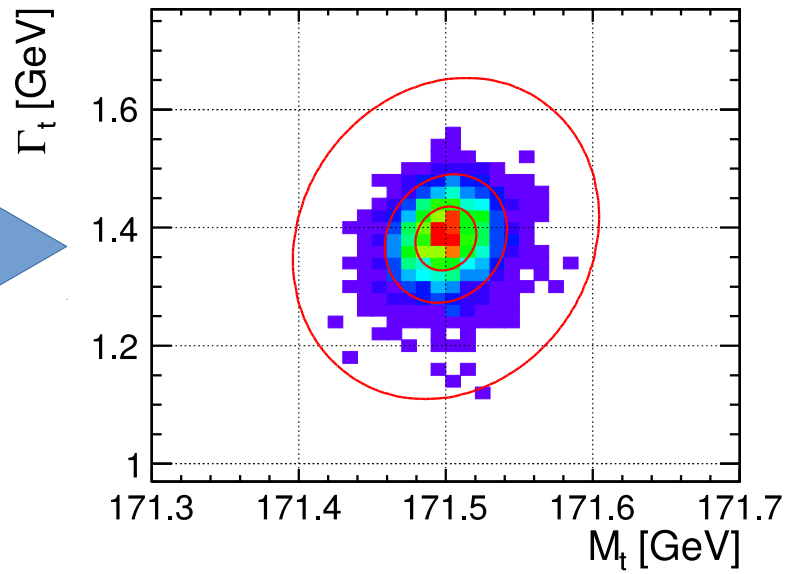
Genetic algorithm

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

Genotype



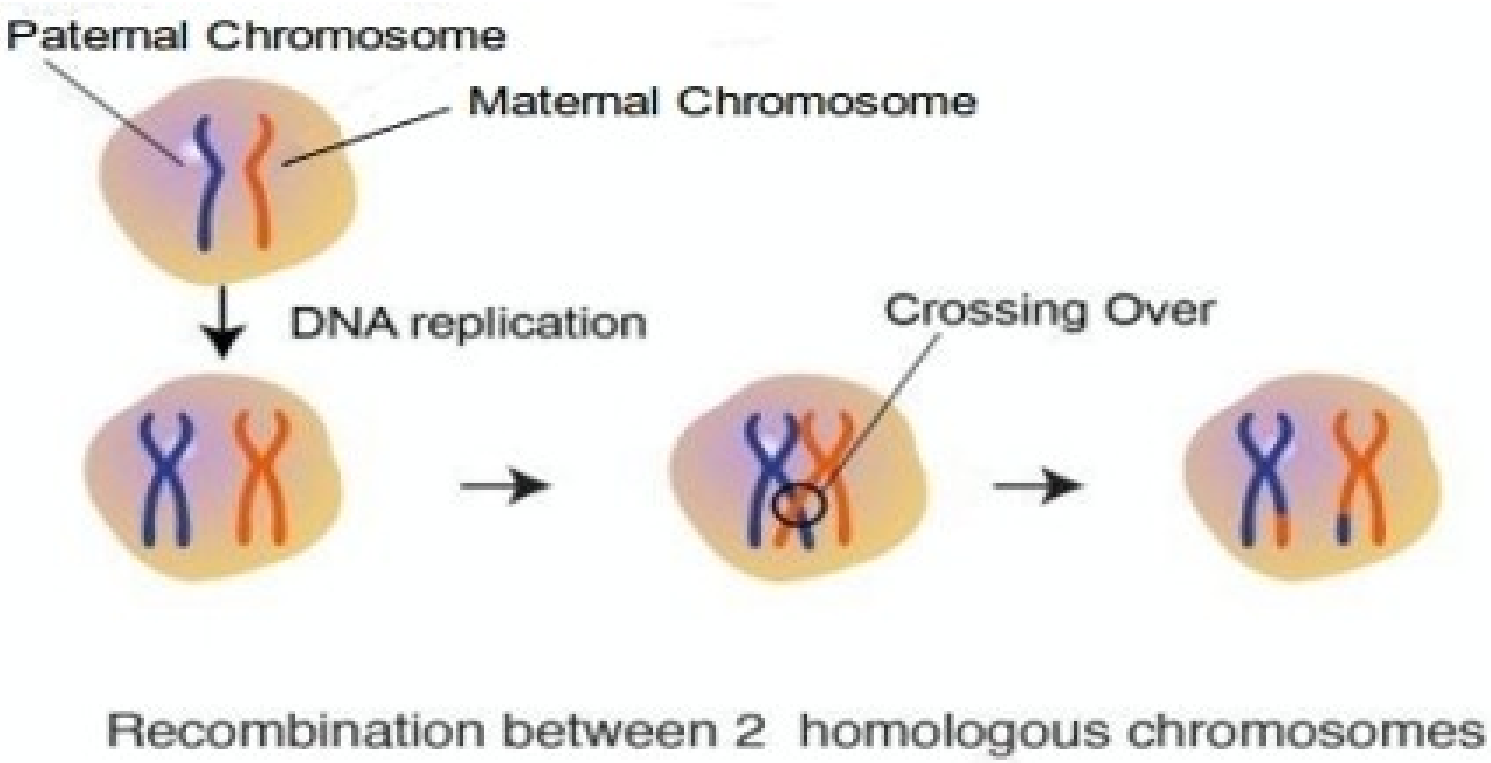
Phenotype



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

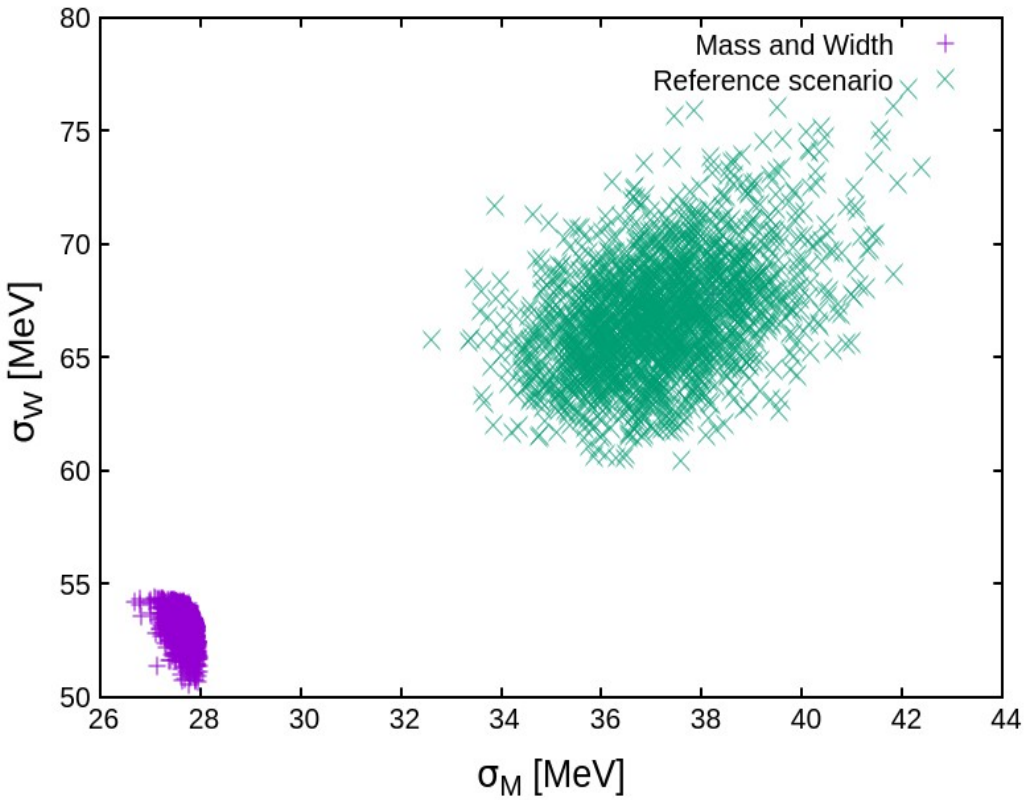
Creating new individuals

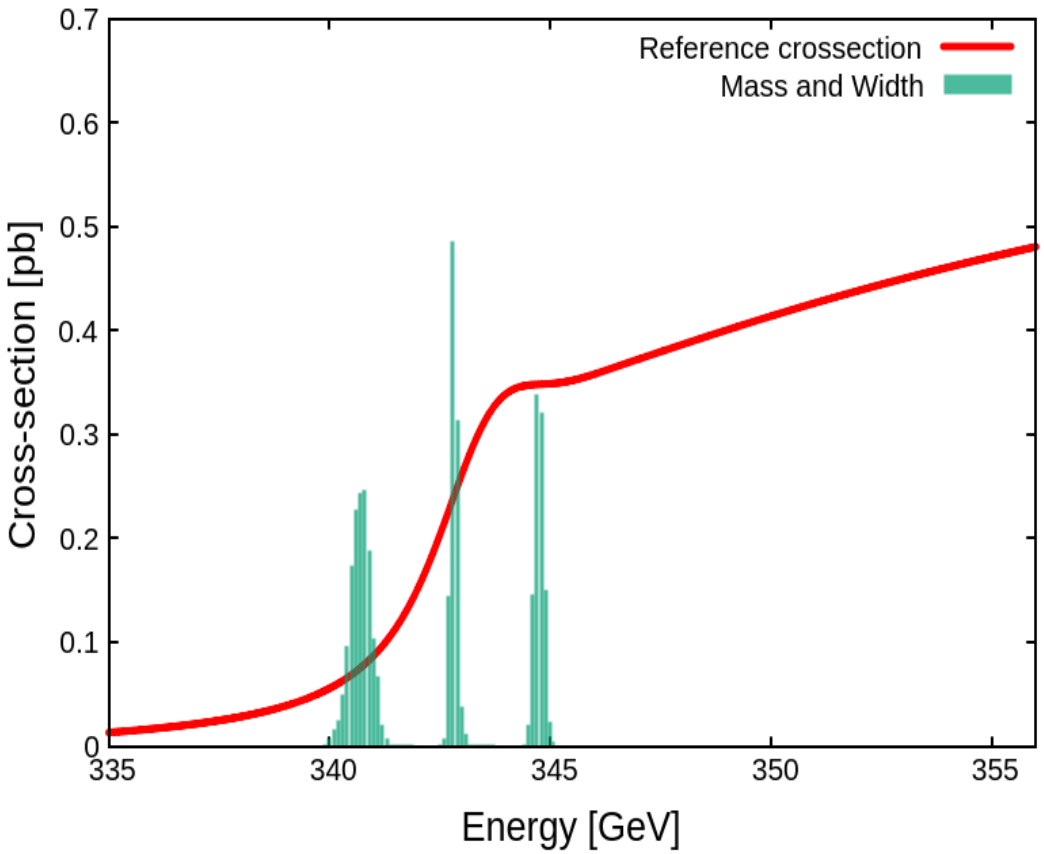
Randomly choosing parts of parents genotype and add random mutation +/- 0.5 GeV



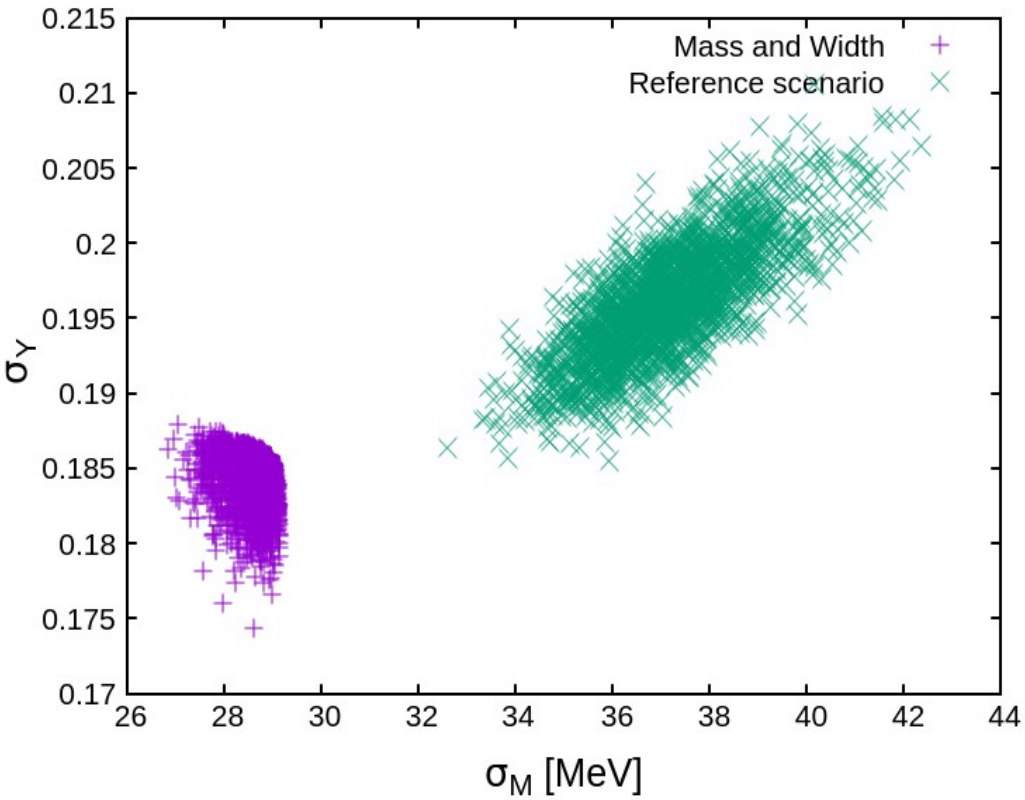
We add 5% chance to drop any of measurement points.

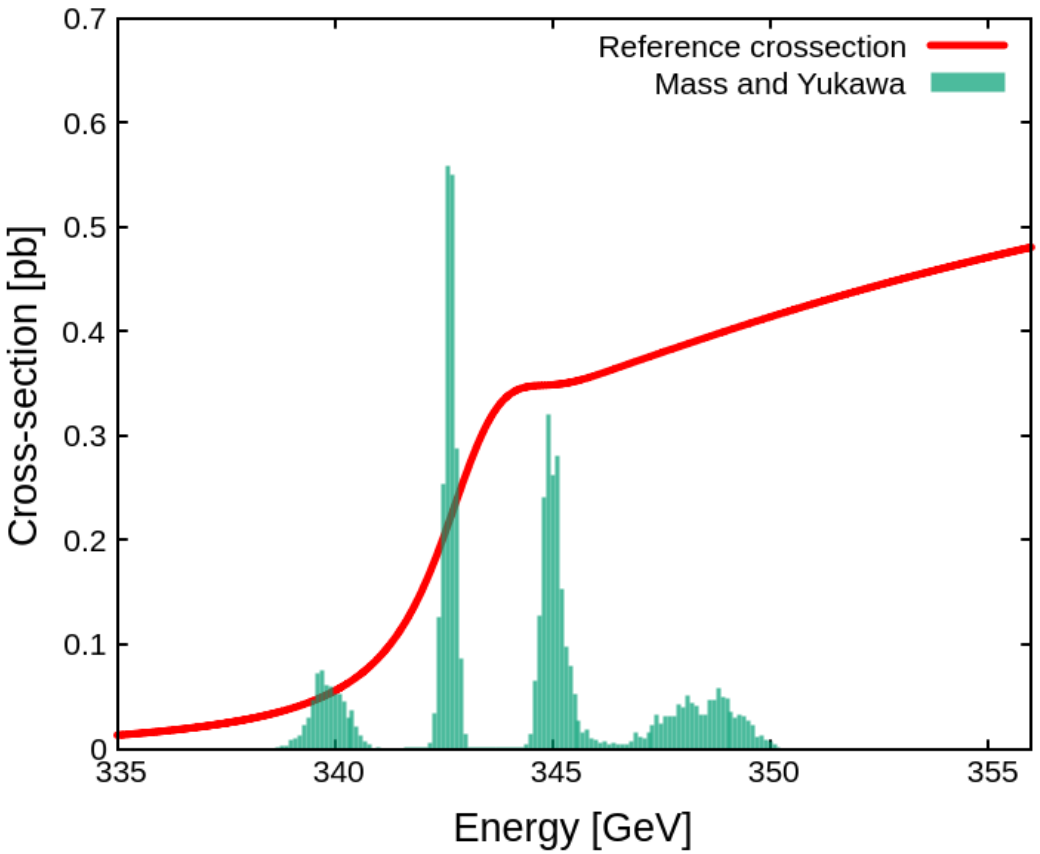
Mass and Width optimization





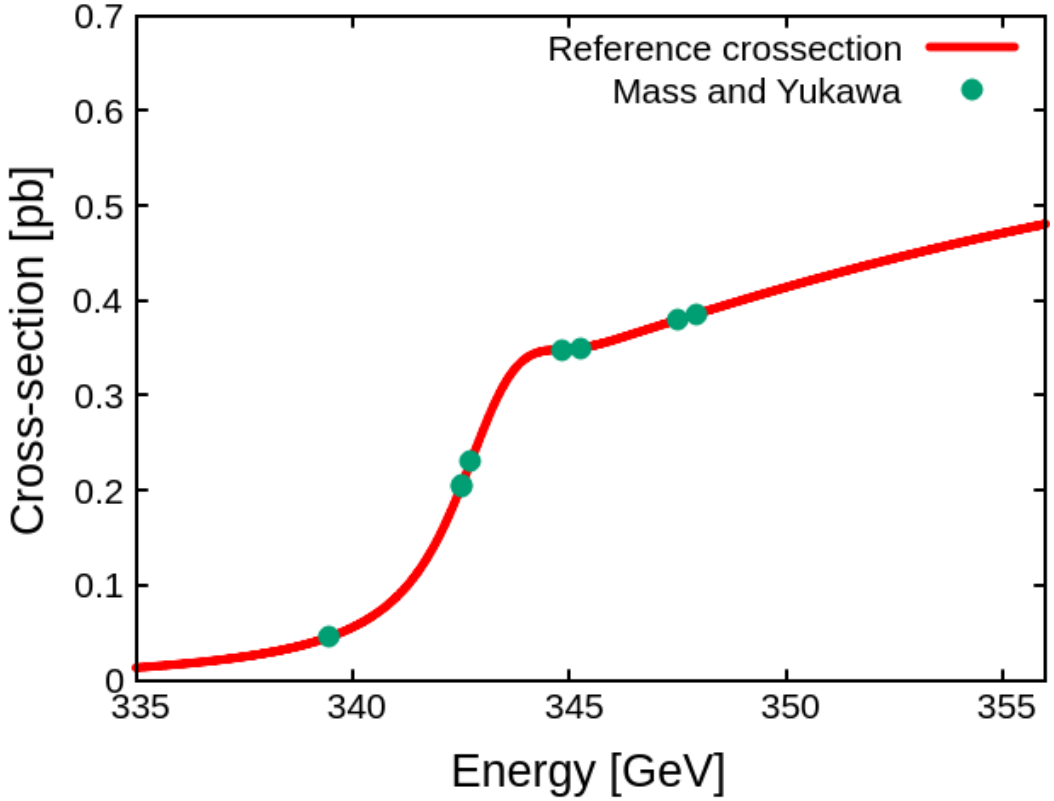
Mass and Yukawa optimization



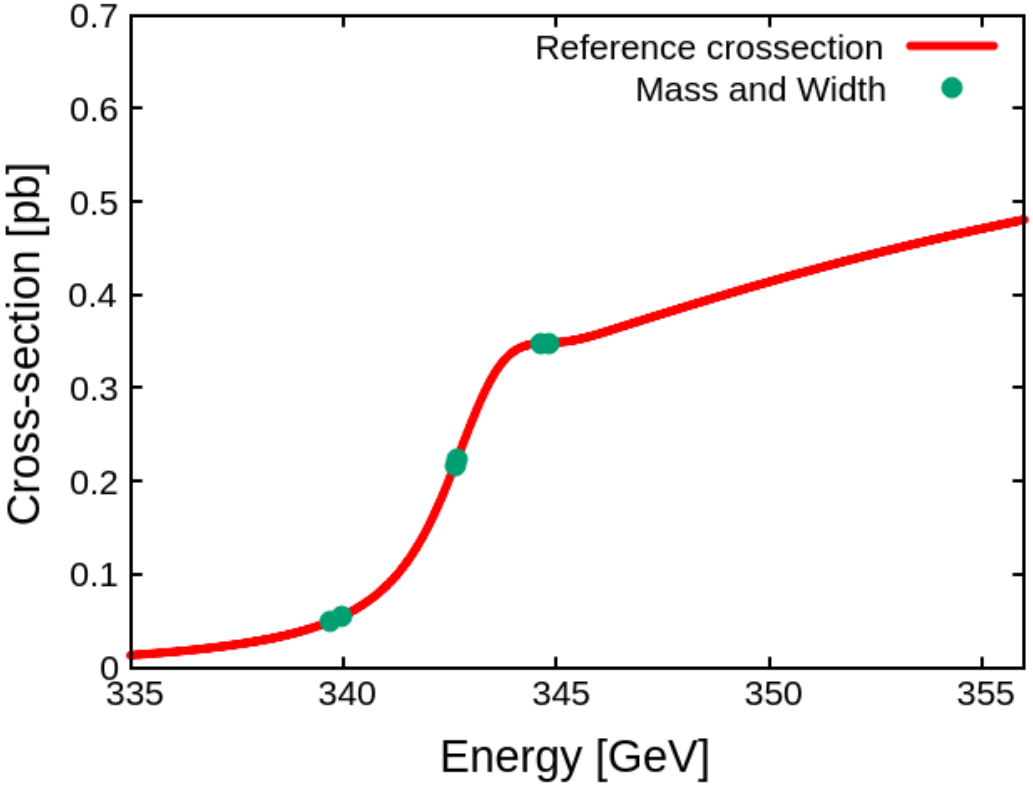


New scenarios

Mass and Yukawa
8 points

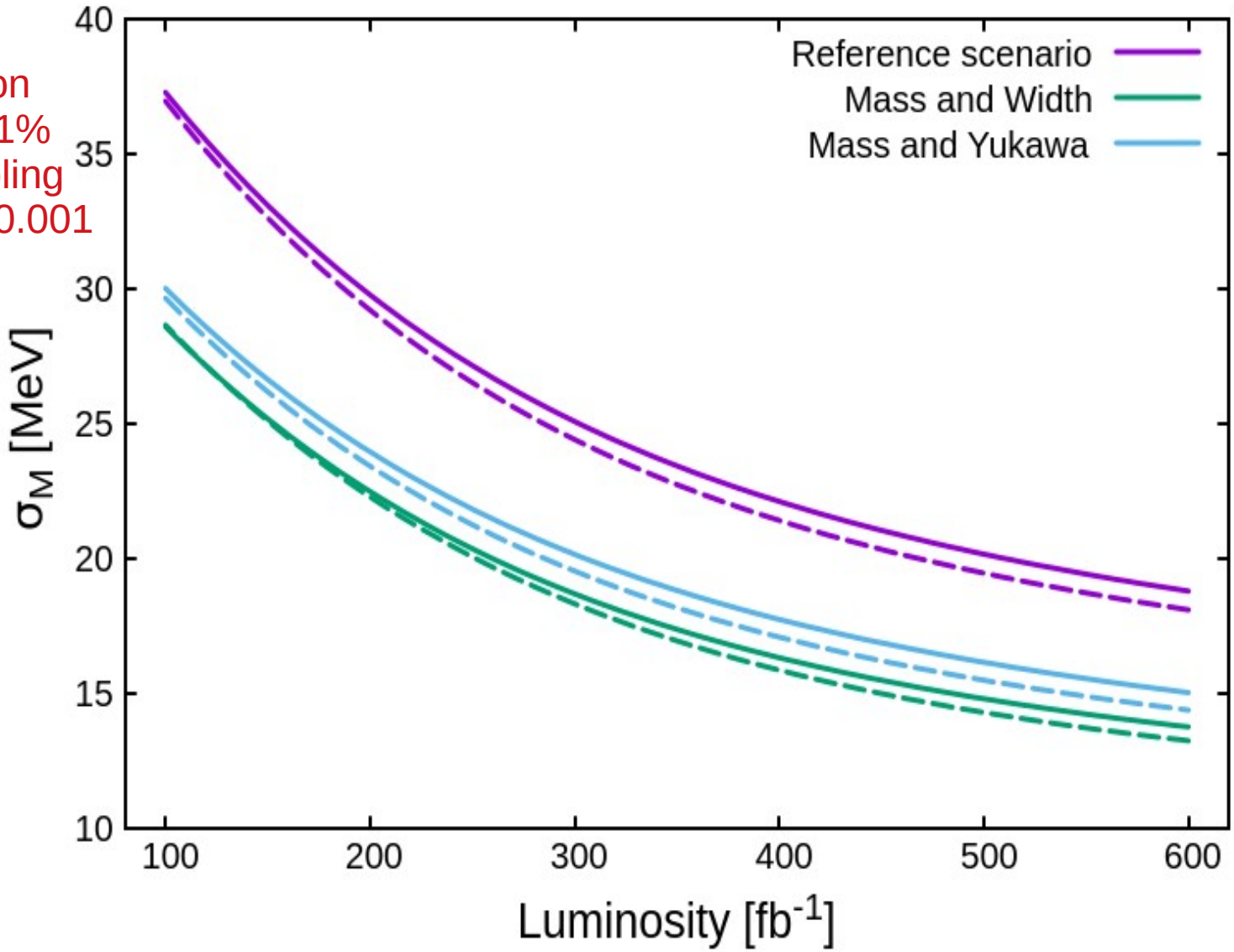


Mass and Width
6 points



Total luminosity

Normalization uncertainty 1%
Strong coupling uncertainty 0.001



Influence of luminosity spectra

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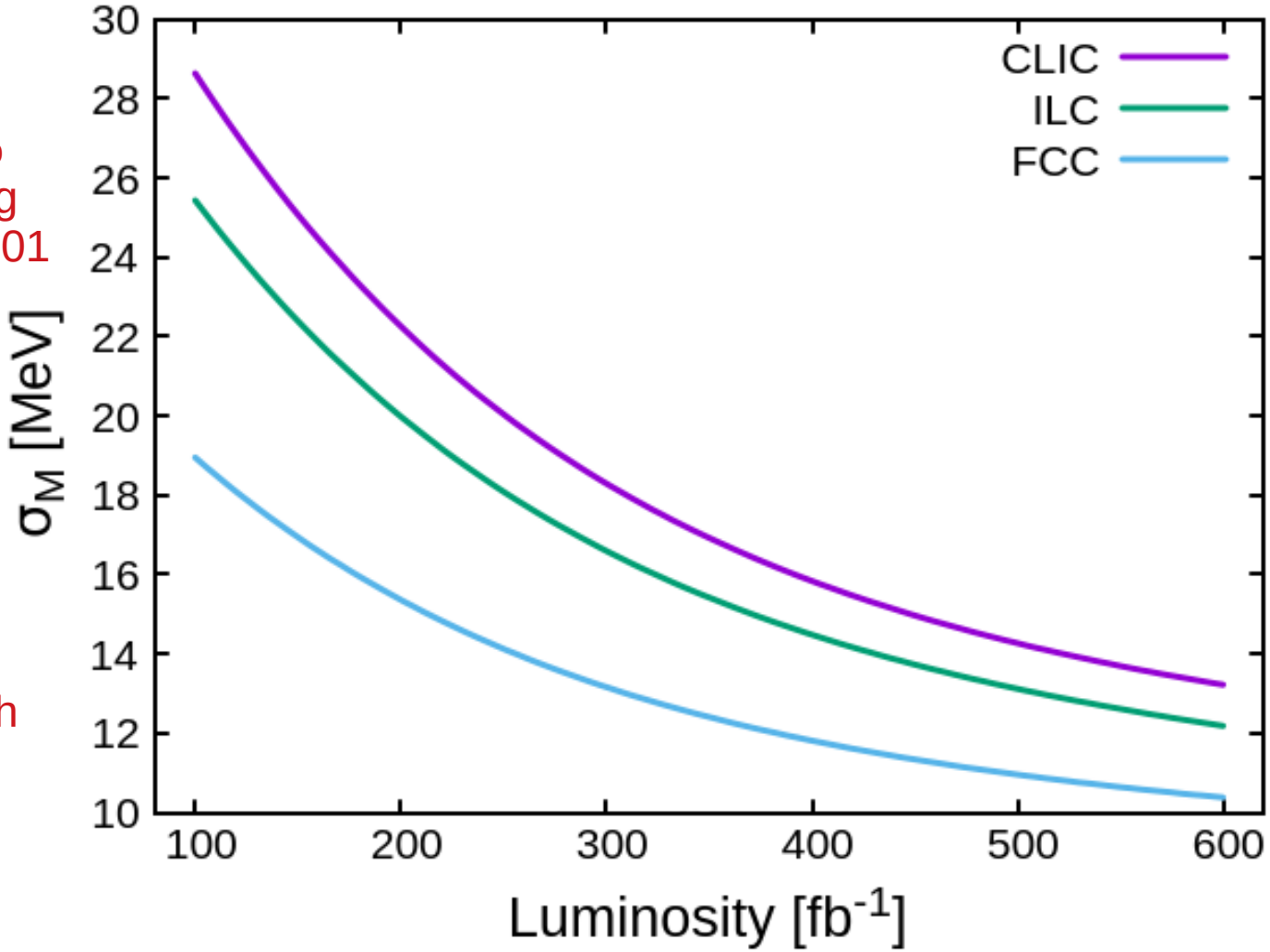


Optimized for mass and width determination precision

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.

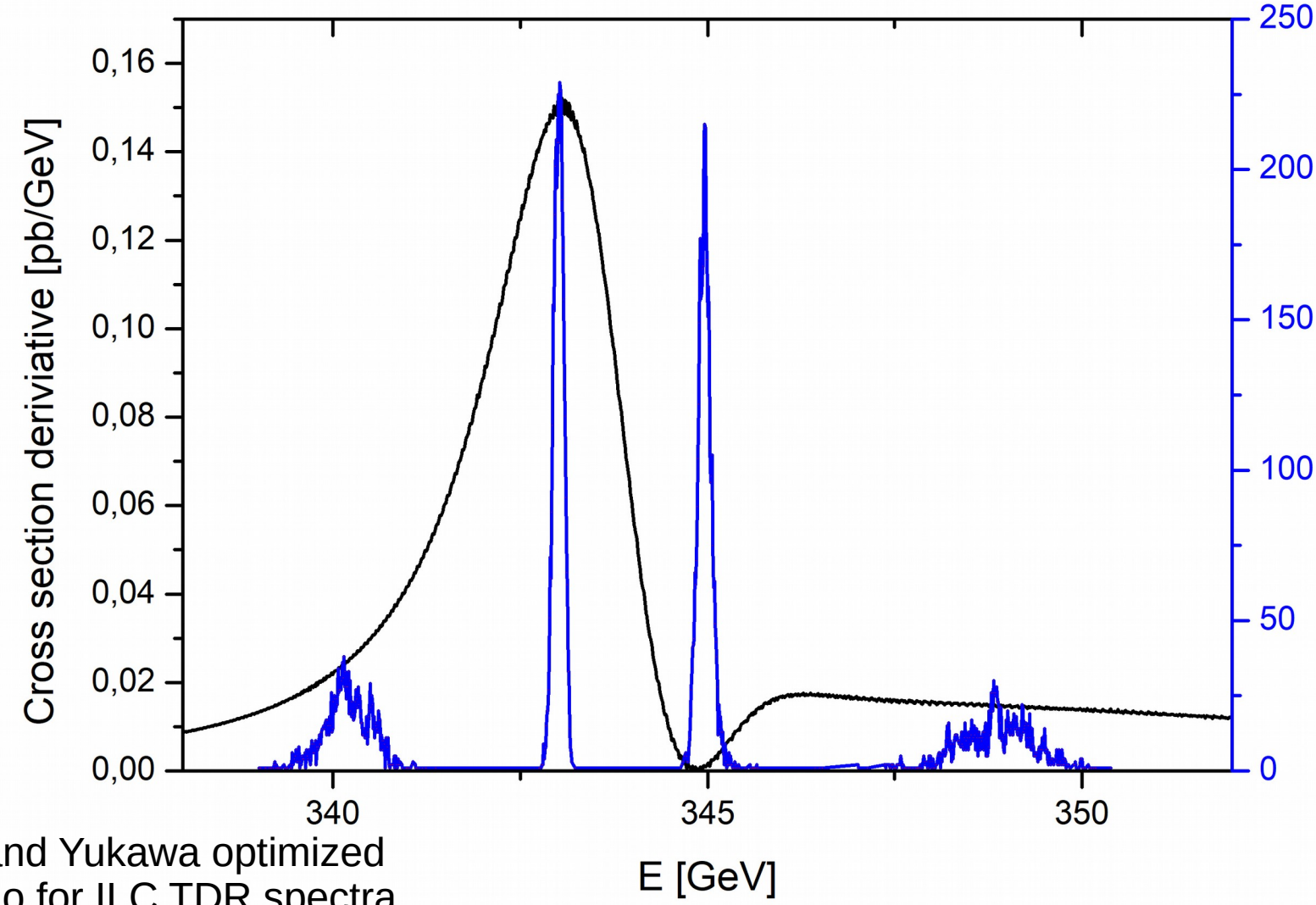
Scan optimization

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

Further improvement

Possible when taking beam polarisation and other observables into account - to be studied

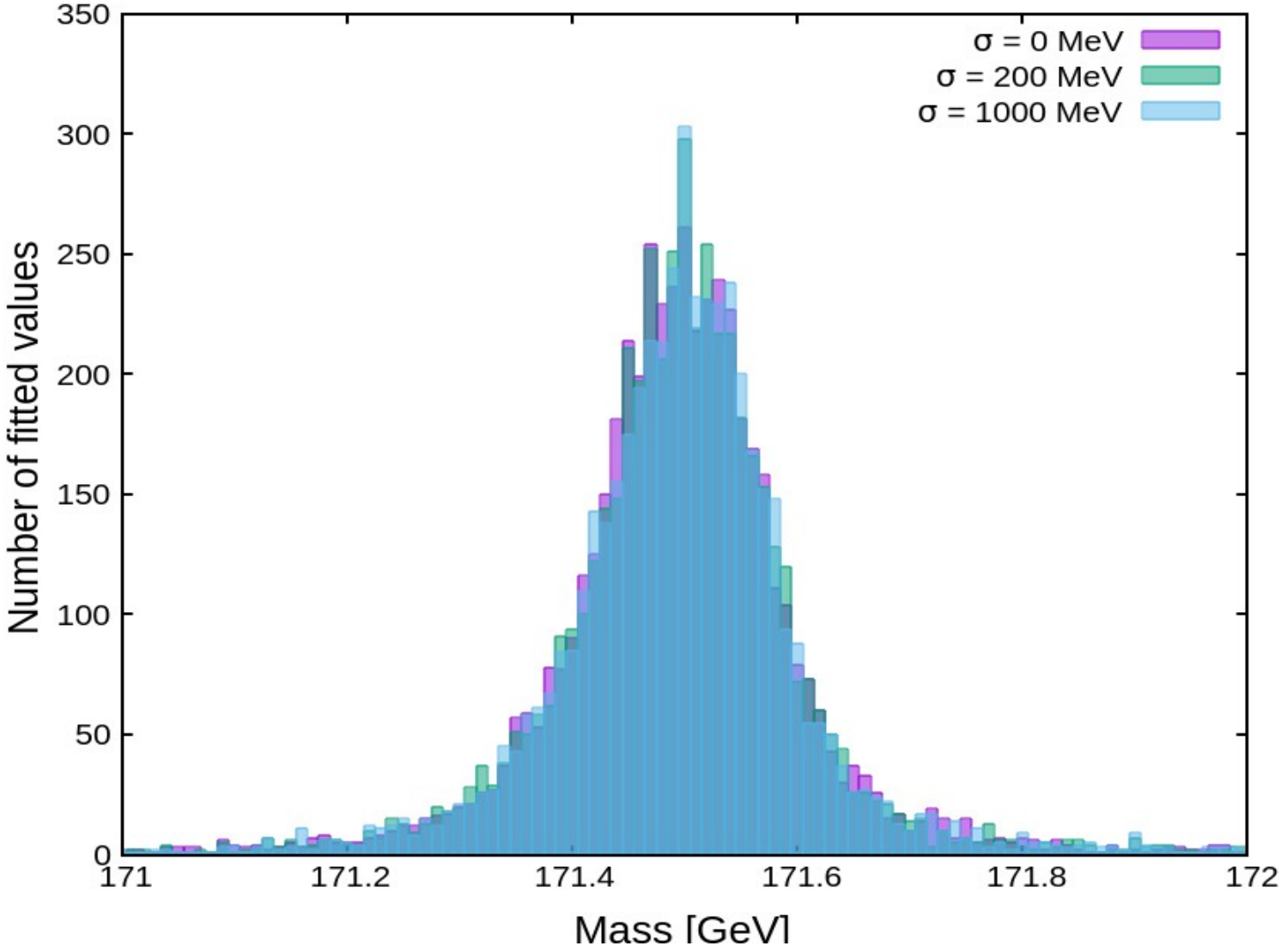
What is algorithm looking for?



Mass and Yukawa optimized scenario for ILC TDR spectra

(Initial) mass uncertainty

Assumed true mass value from normal distribution



Background level uncetrainty

Change background normalization in pseudo-experiment generation by ±2%

Influence on Yukawa coupling determination