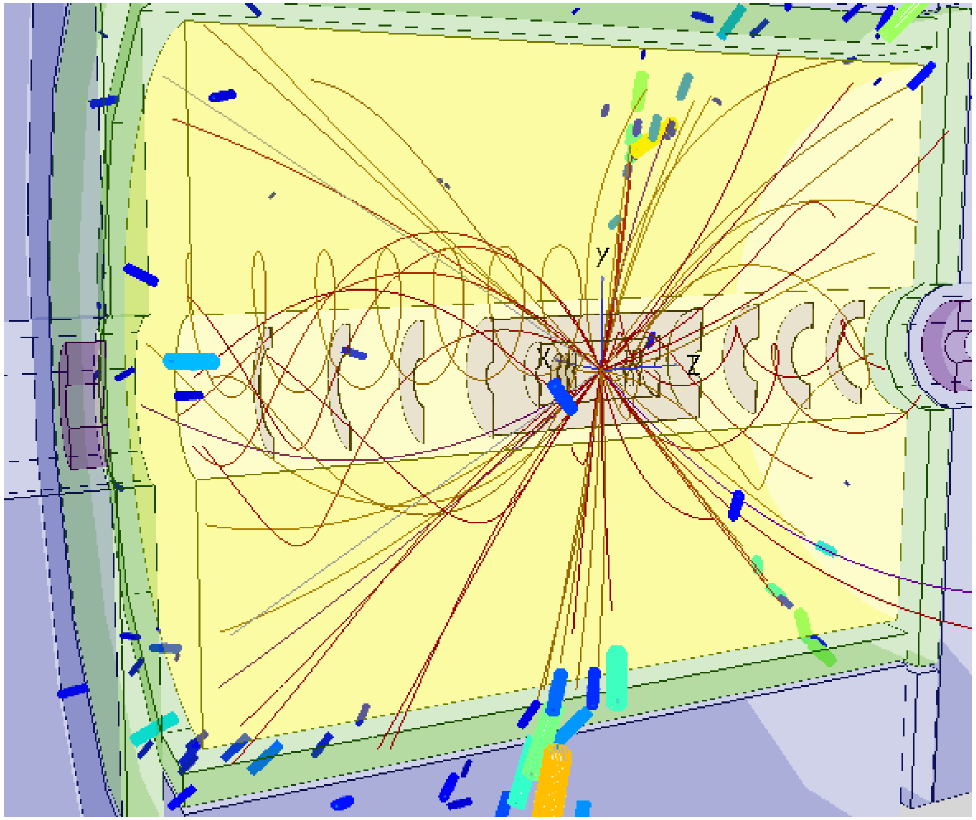
Optimizing top-quark threshold scan at future e^+e^- colliders



Preparatory Joint Sessions on "Open questions and News Ideas"
July 7, 2020

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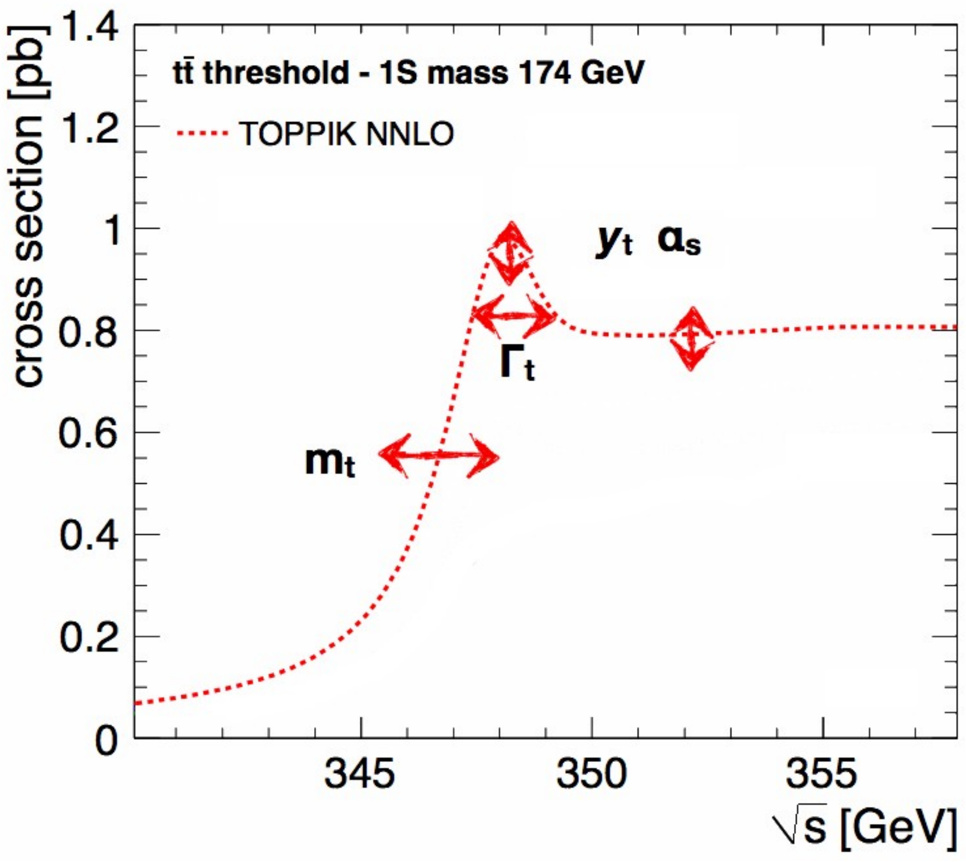
Motivation



Top-quark mass is one of the fundamental parameters of the Standard Model.

Measurement of the pair production threshold:

$$e^+e^- \rightarrow t\,\bar{t}$$

is the most precise method to extract it.

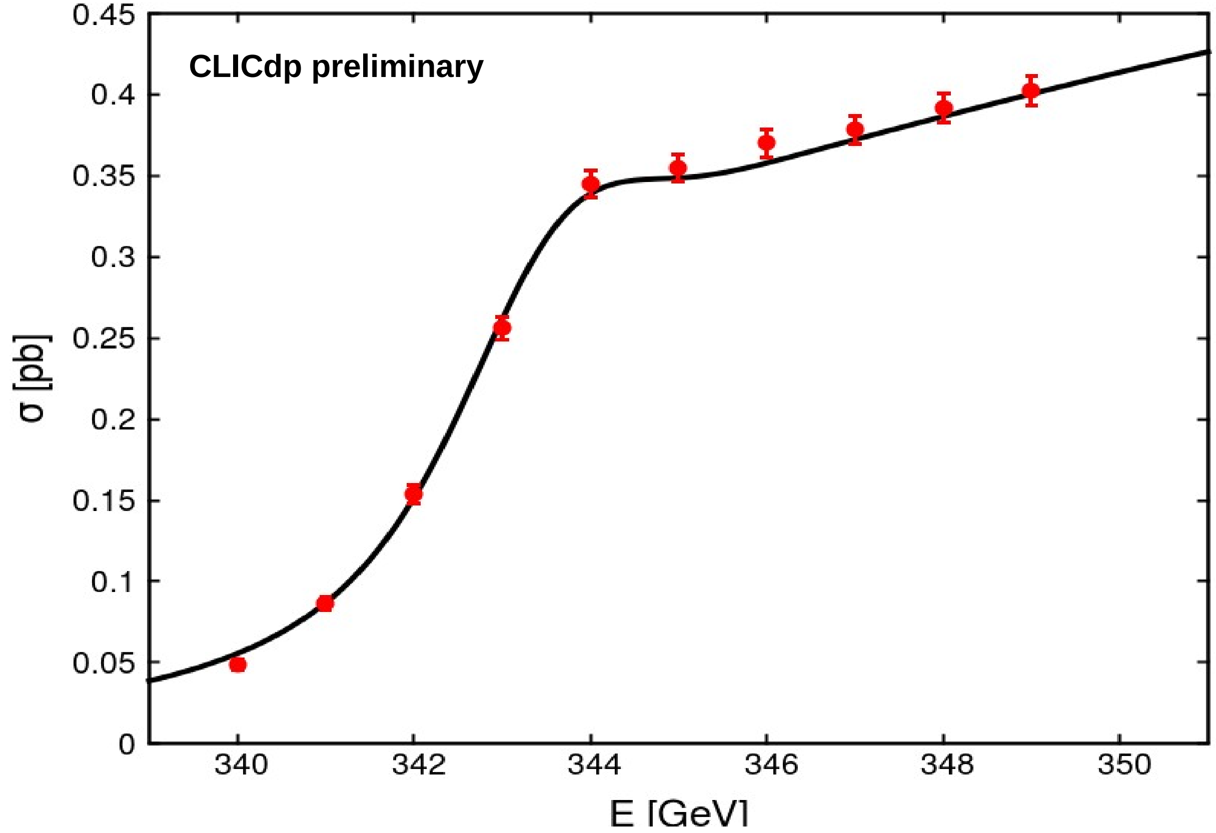
However, cross section depends also on other model parameters…

How this influences m_t determination?

Can the threshold scan procedure be optimized?

Benchmark scenario

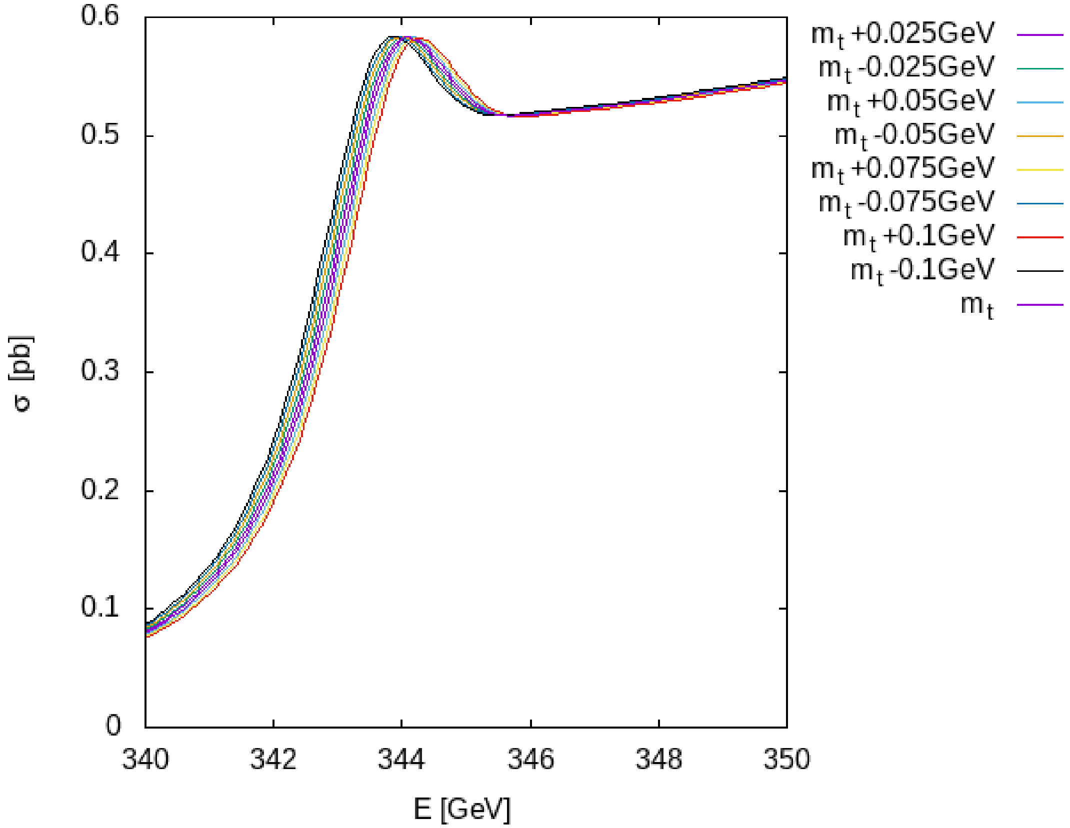
Assume 10 measurements at the threshold, with 1 GeV step in energy, with 10 fb^{-1} taken at each energy point (100 fb^{-1} total).

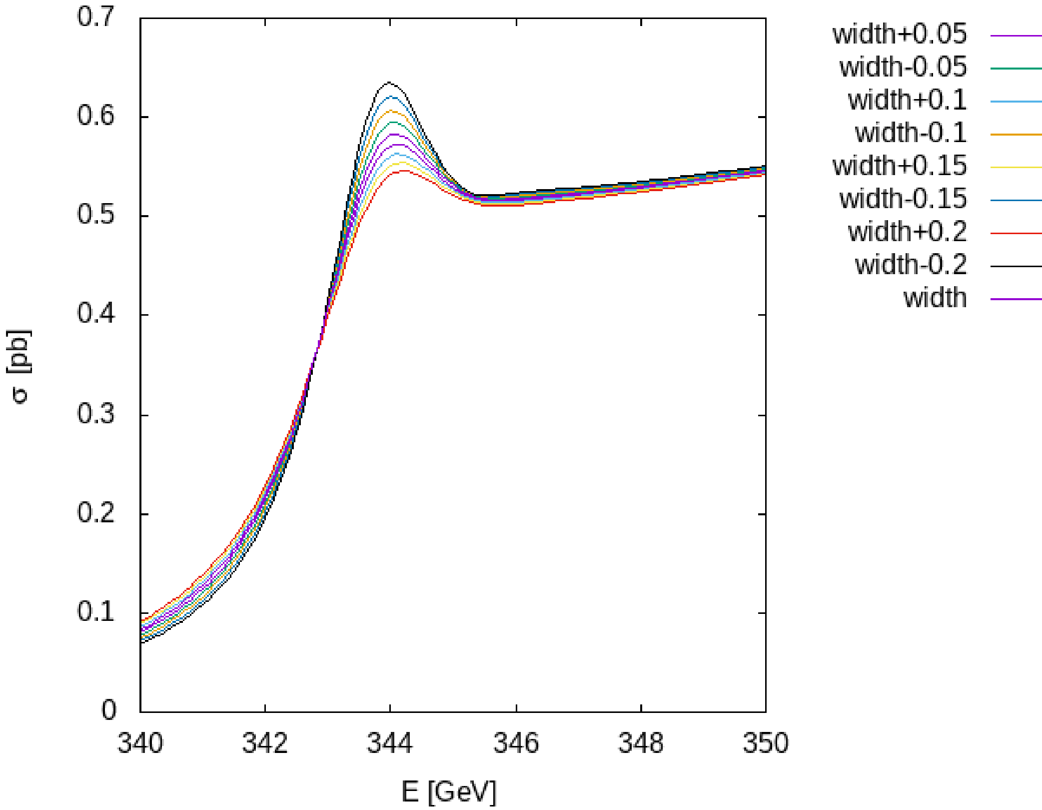


Generate statistical fluctuation assuming 70.2% event reconstruction efficiency and background level (remaining after cuts) corresponding to the 73 fb

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

Cross-section templates

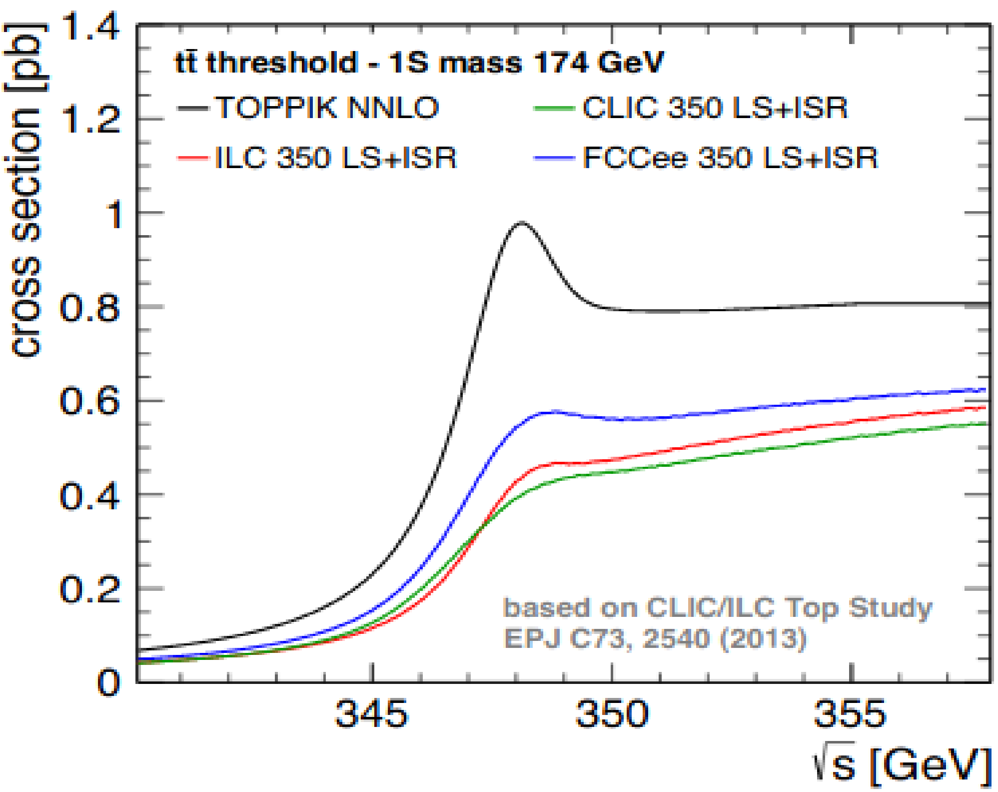


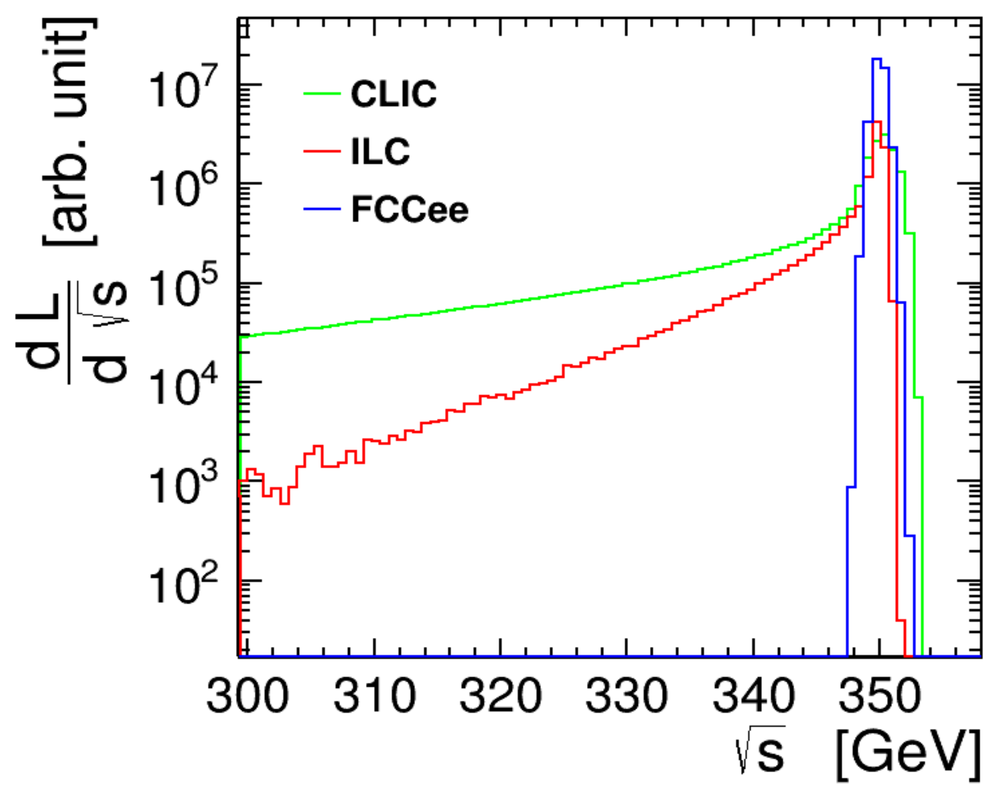


Templates generated with **Qqbar_threshold**

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

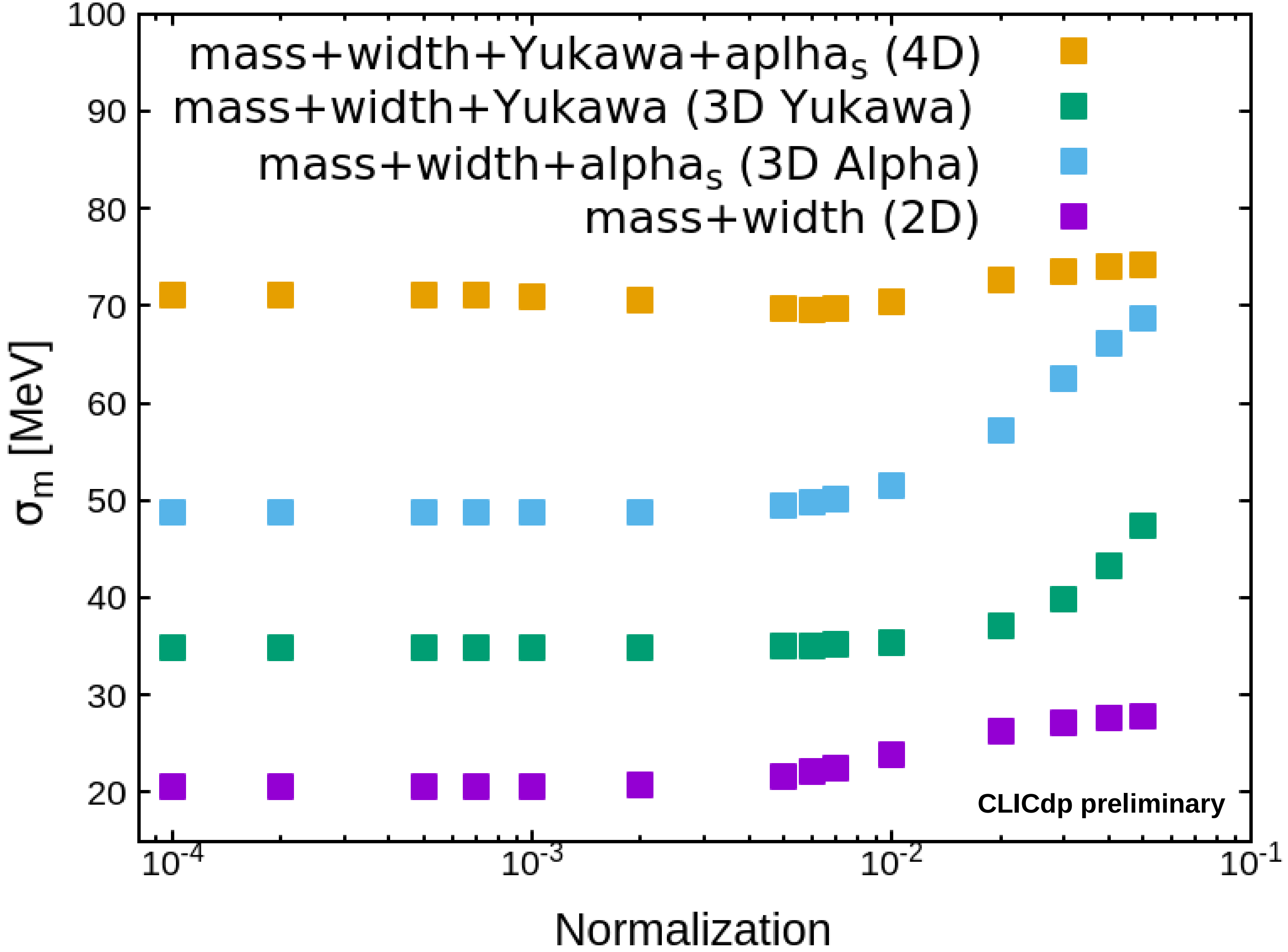
Luminosity spectra



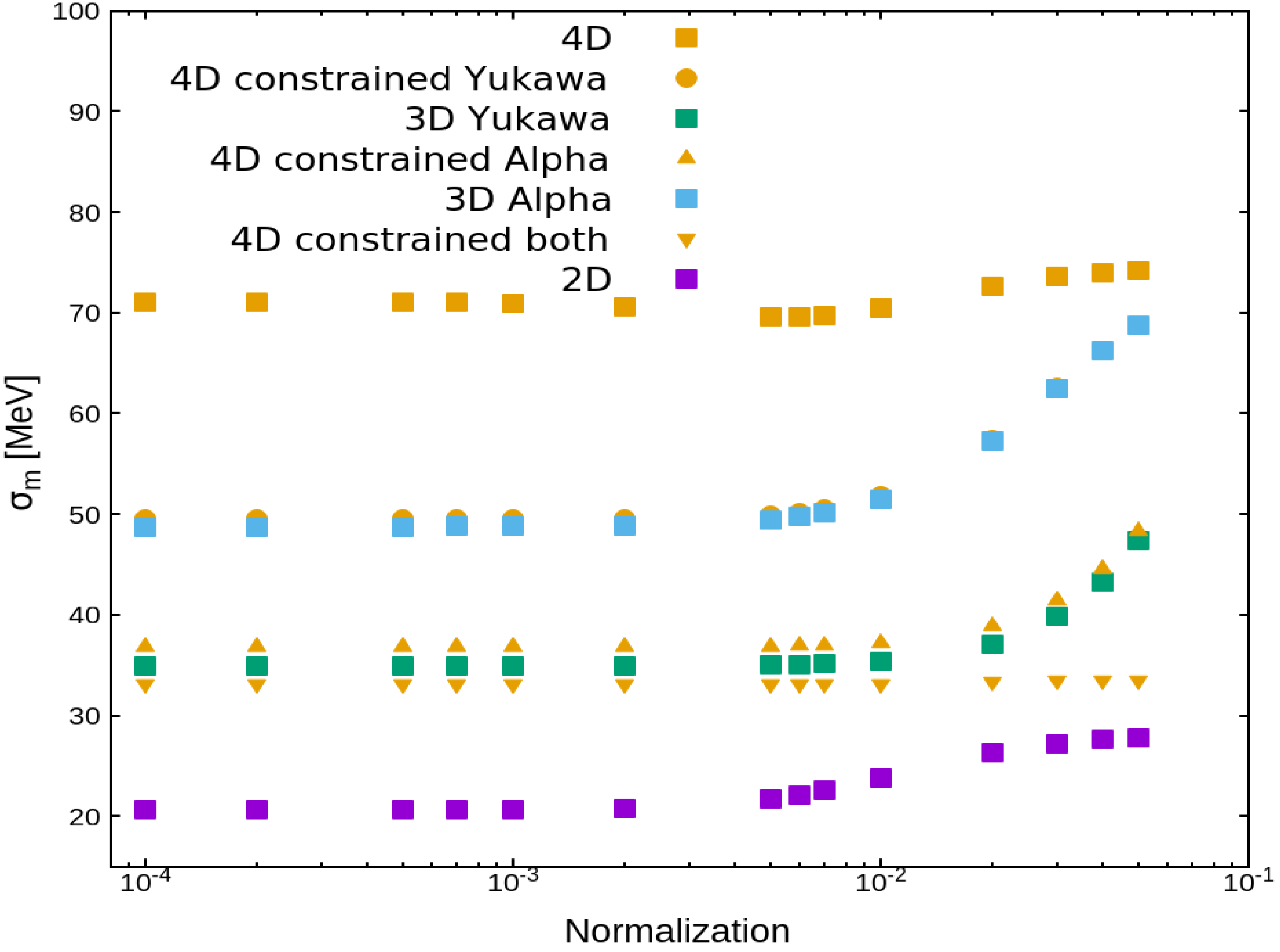


Baseline Fit Results

Fit configuration



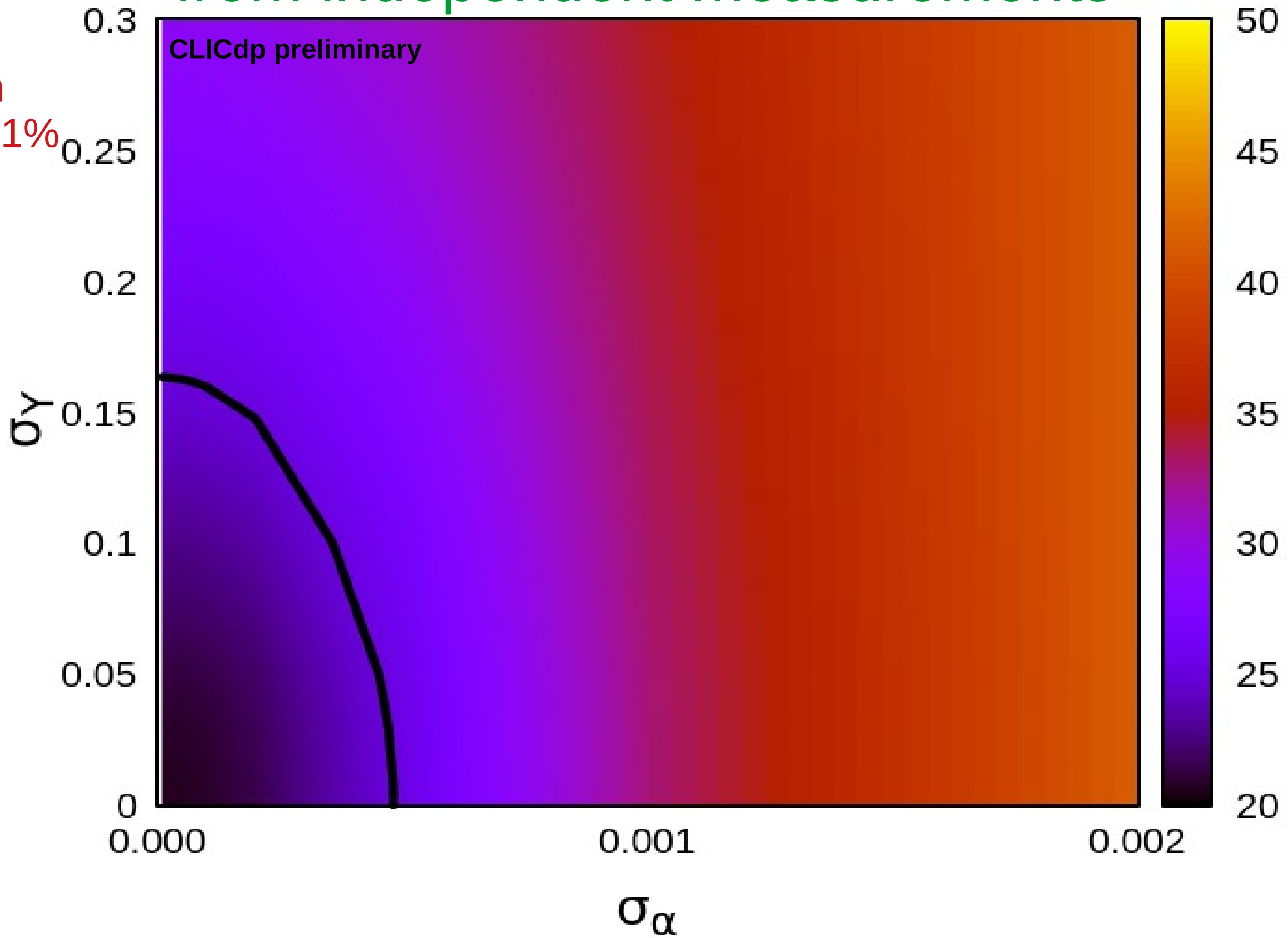
Parameter constrains



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

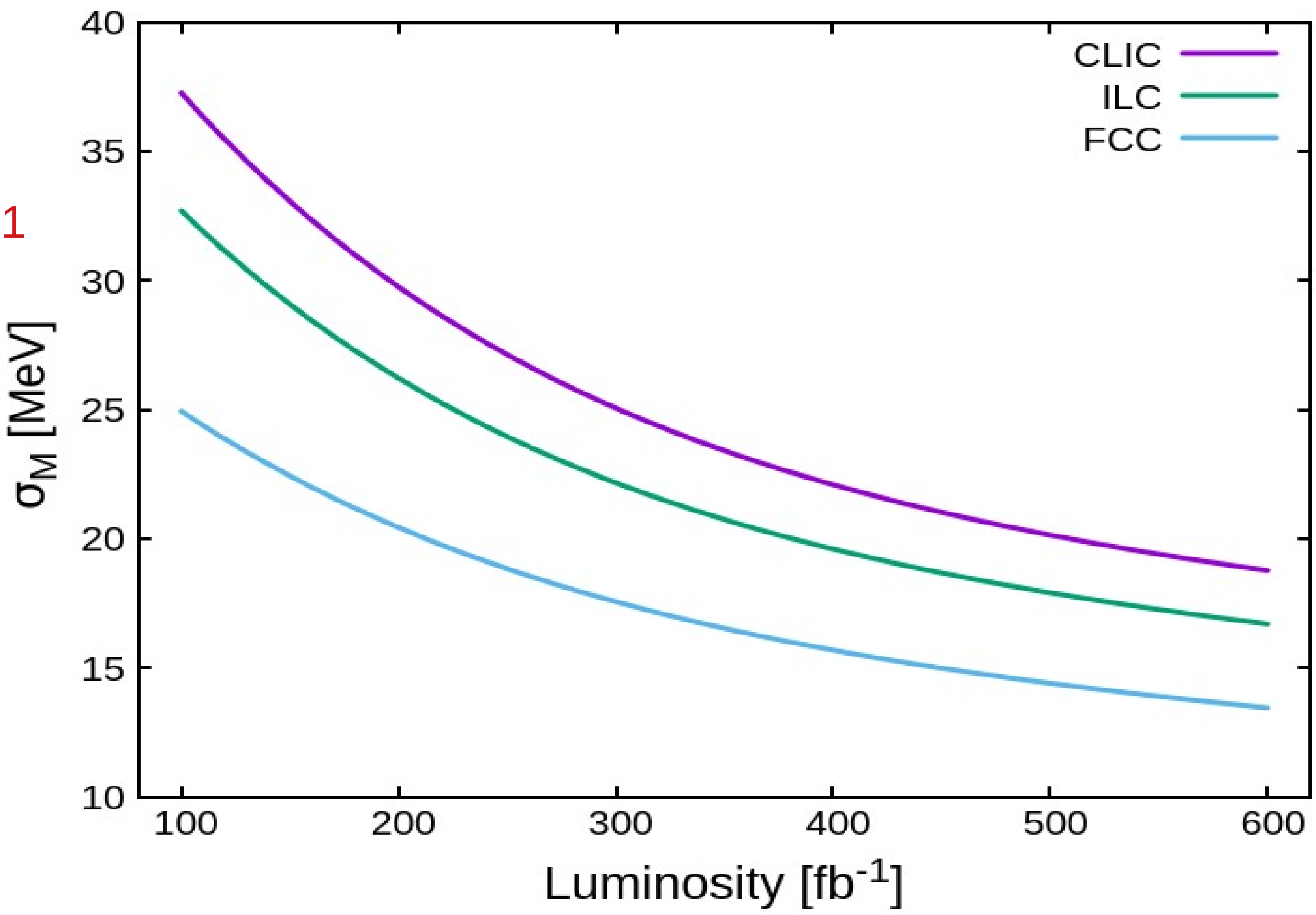
from independent measurements

Normalization uncertainty 0.1%



Influence of luminosity spectra

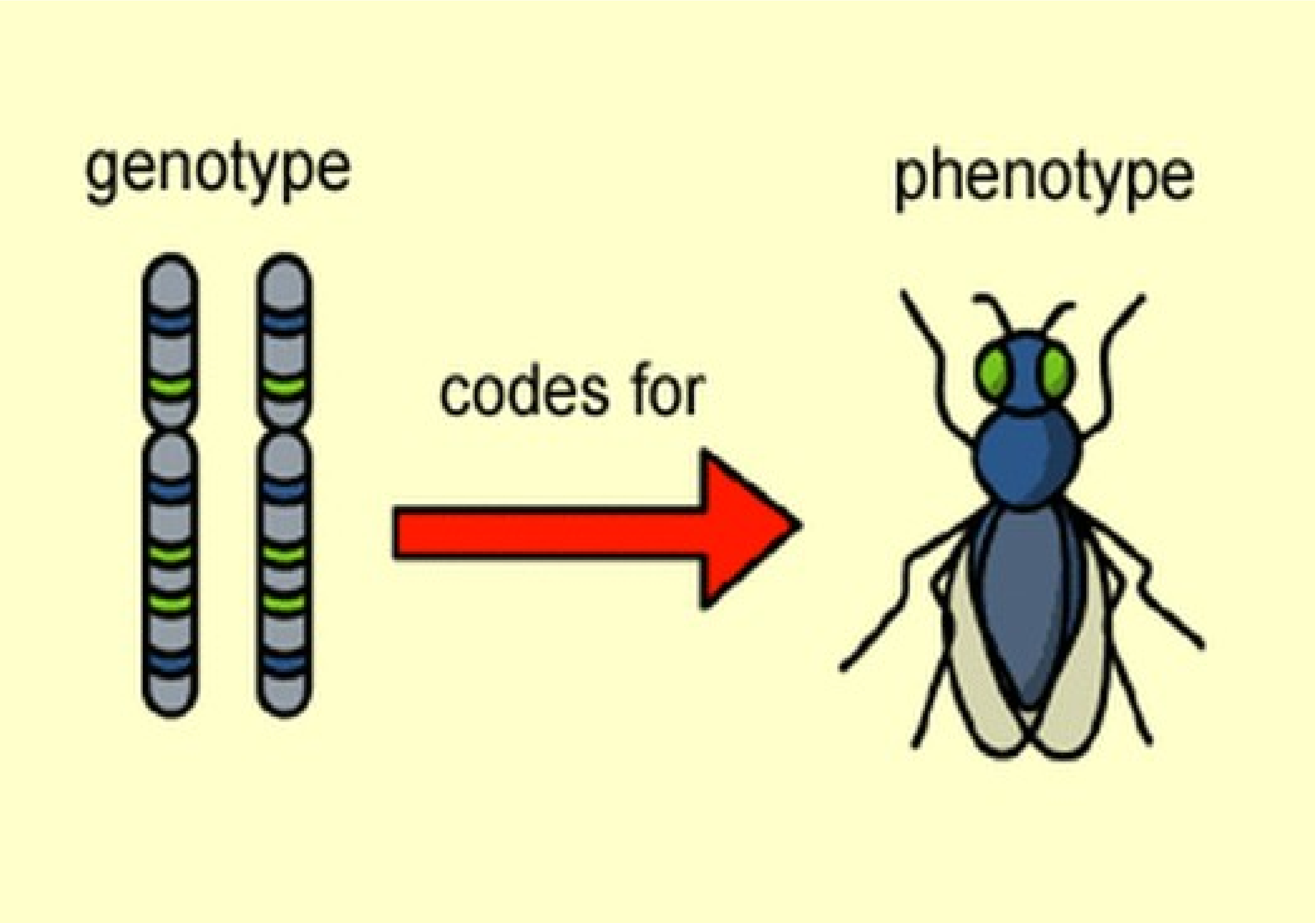
Normalization uncertainty 1%
Strong coupling uncertainty 0.001



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

Scan optimization

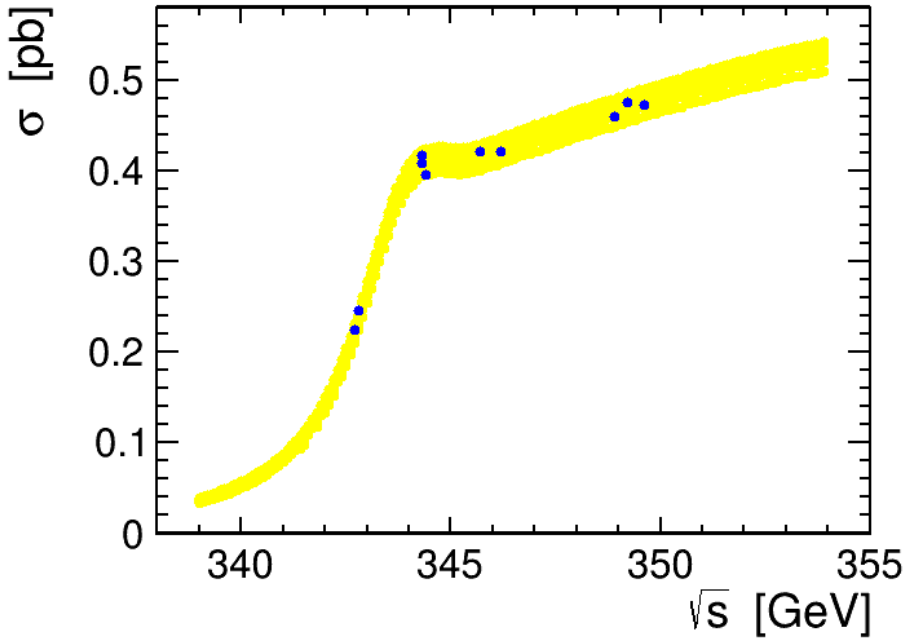
Genetic algorithm



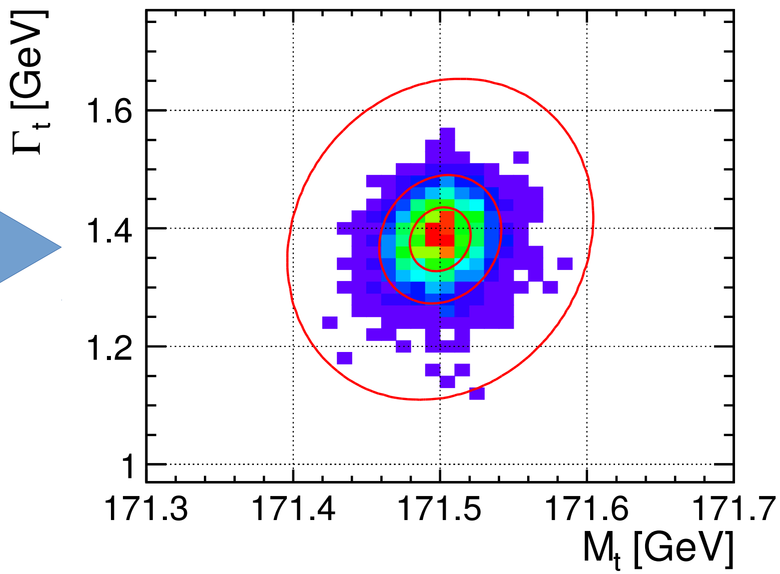
Genetic algorithm

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

Genotype



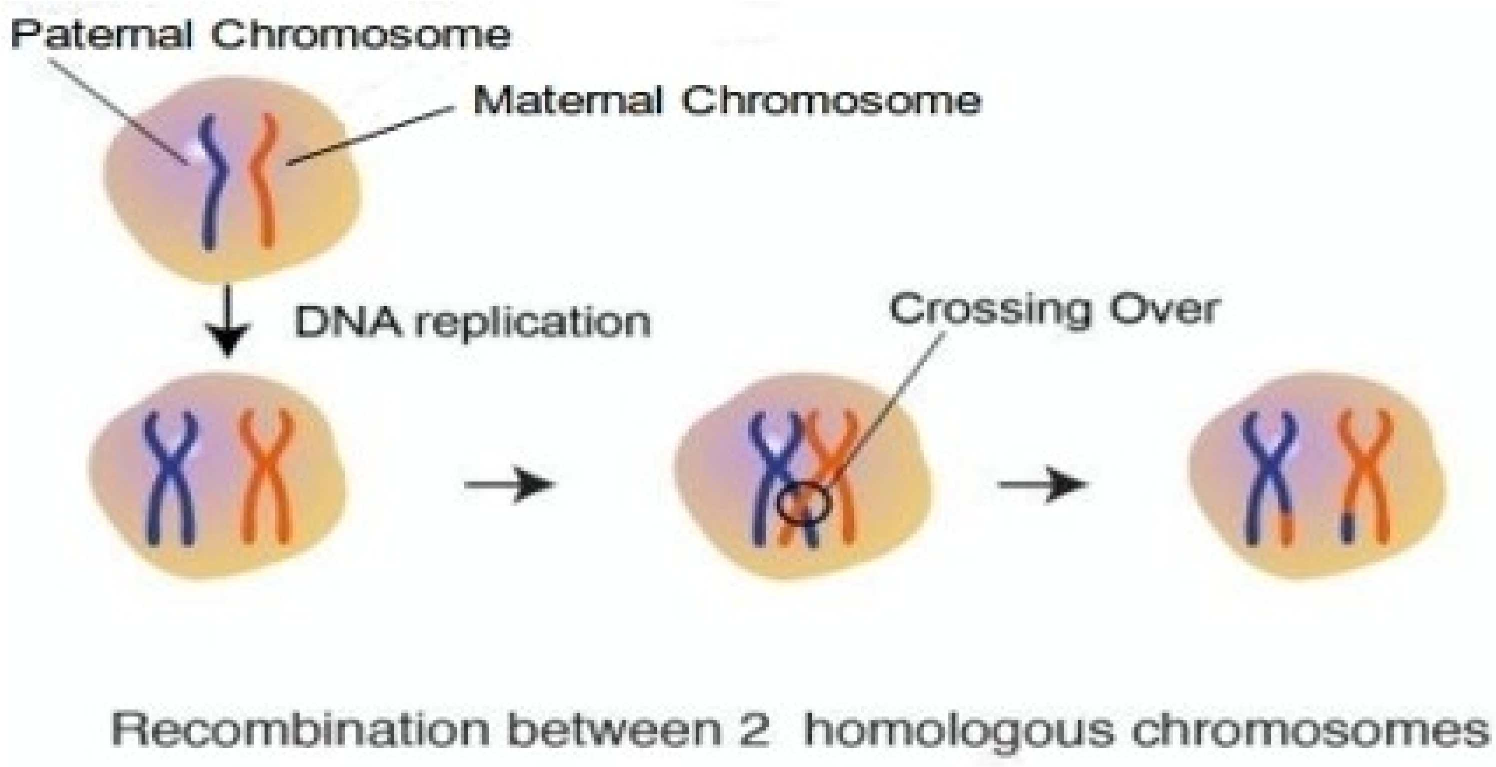
Phenotype



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

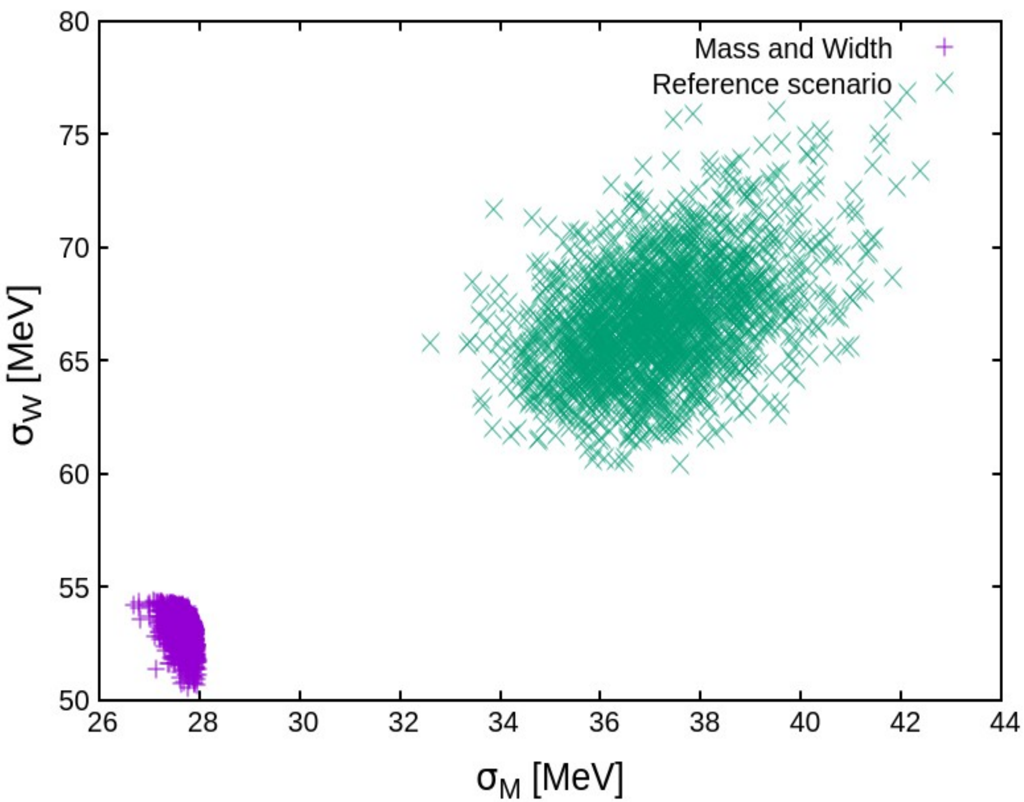
Creating new individuals

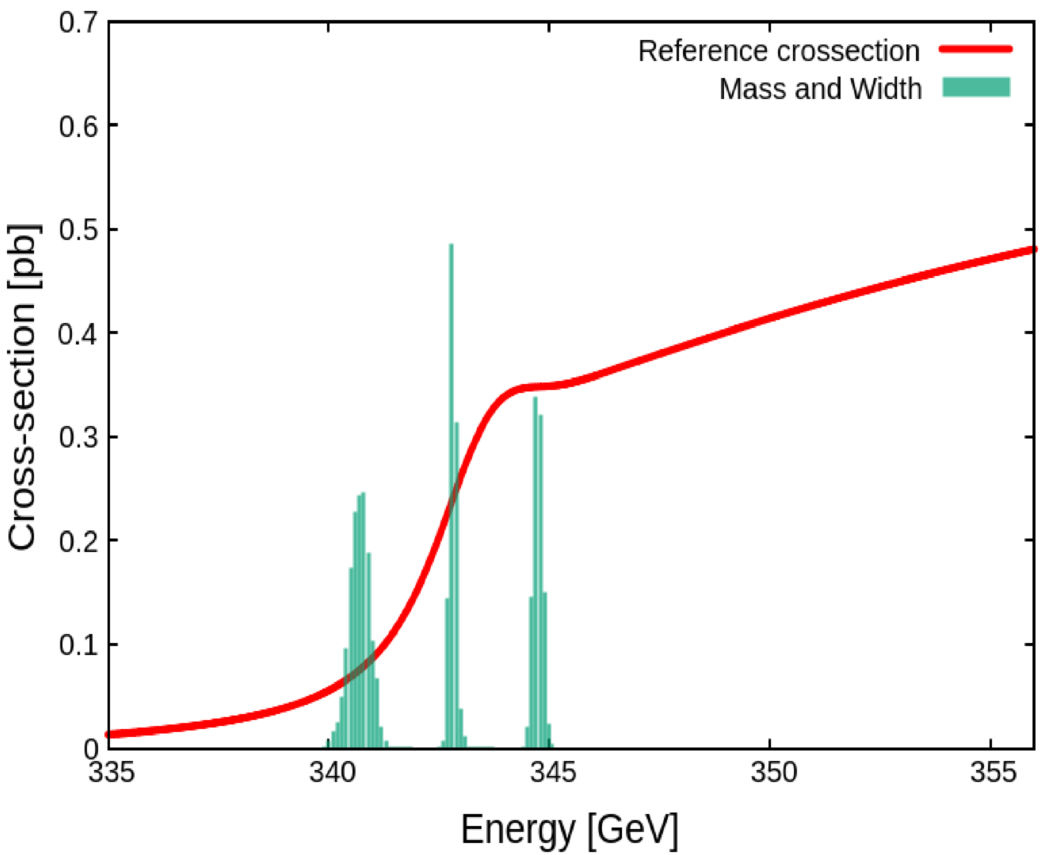
Randomly choosing parts of parents genotype and add random mutation +/- 0.5 GeV



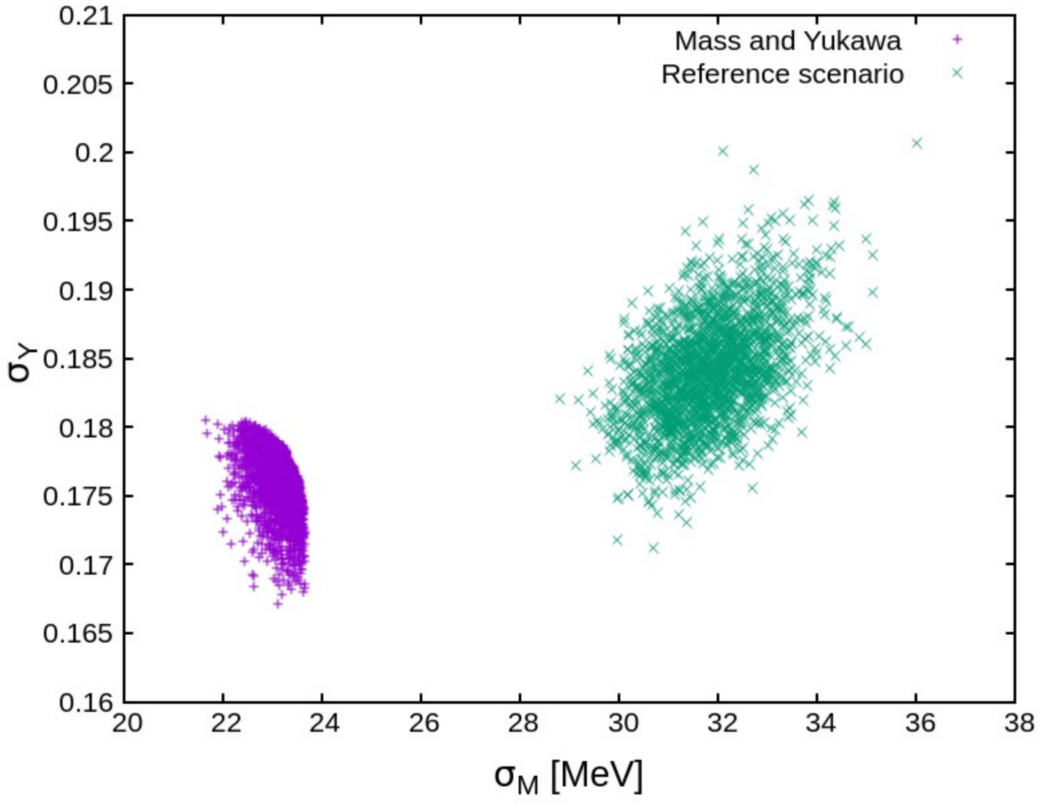
We add 5% chance to drop any of measurement points.

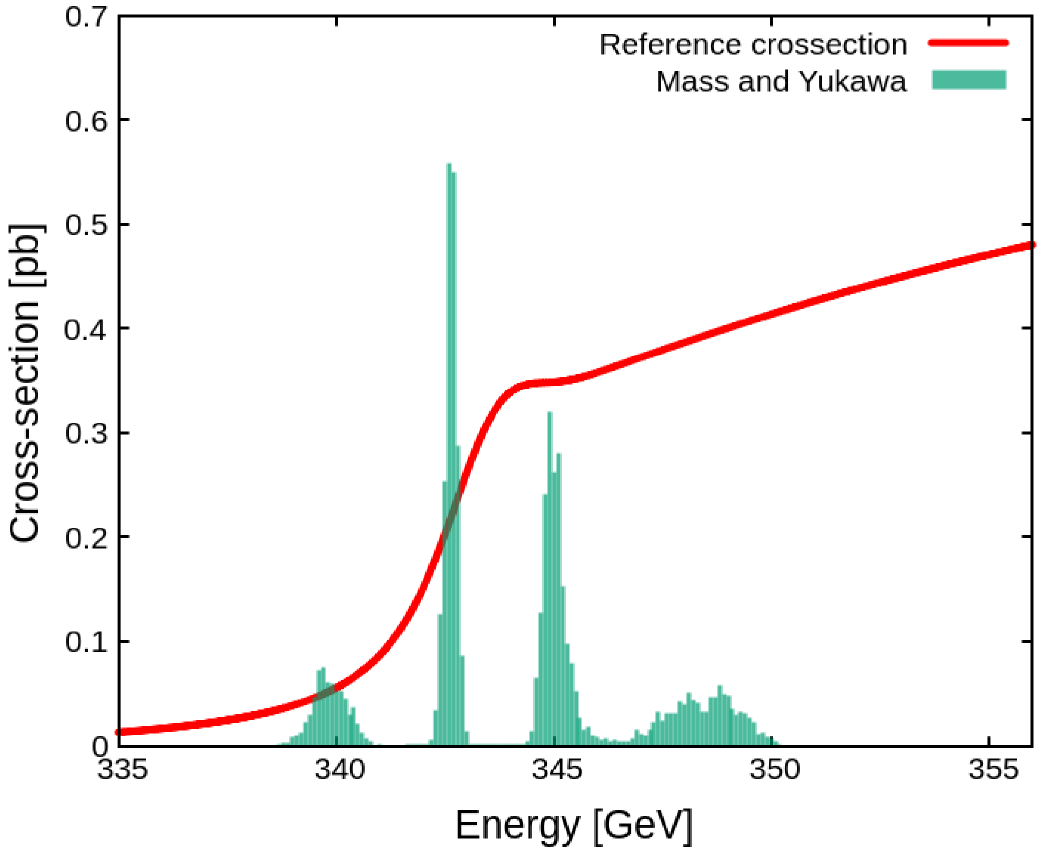
Mass and Width optimization





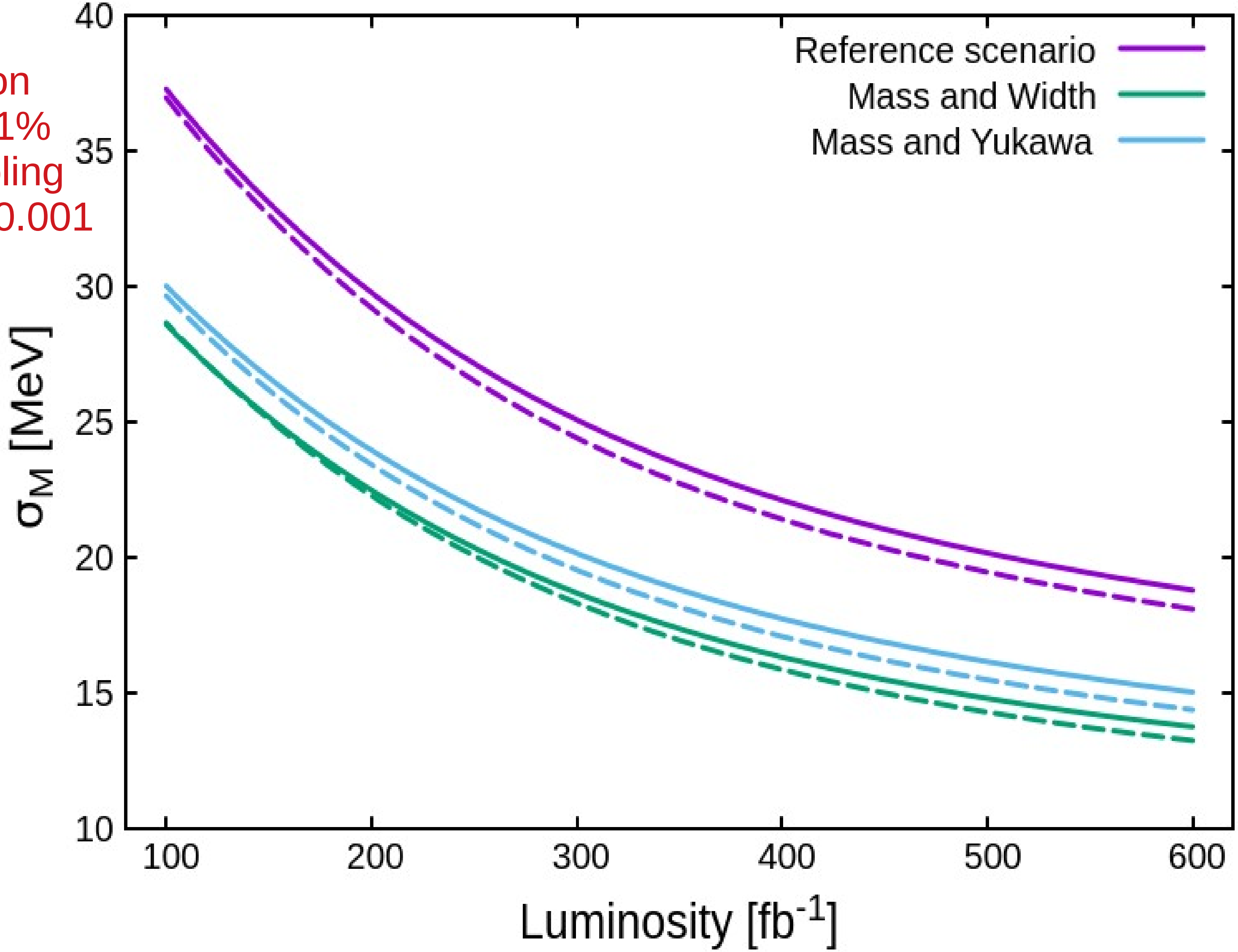
Mass and Yukawa optimization





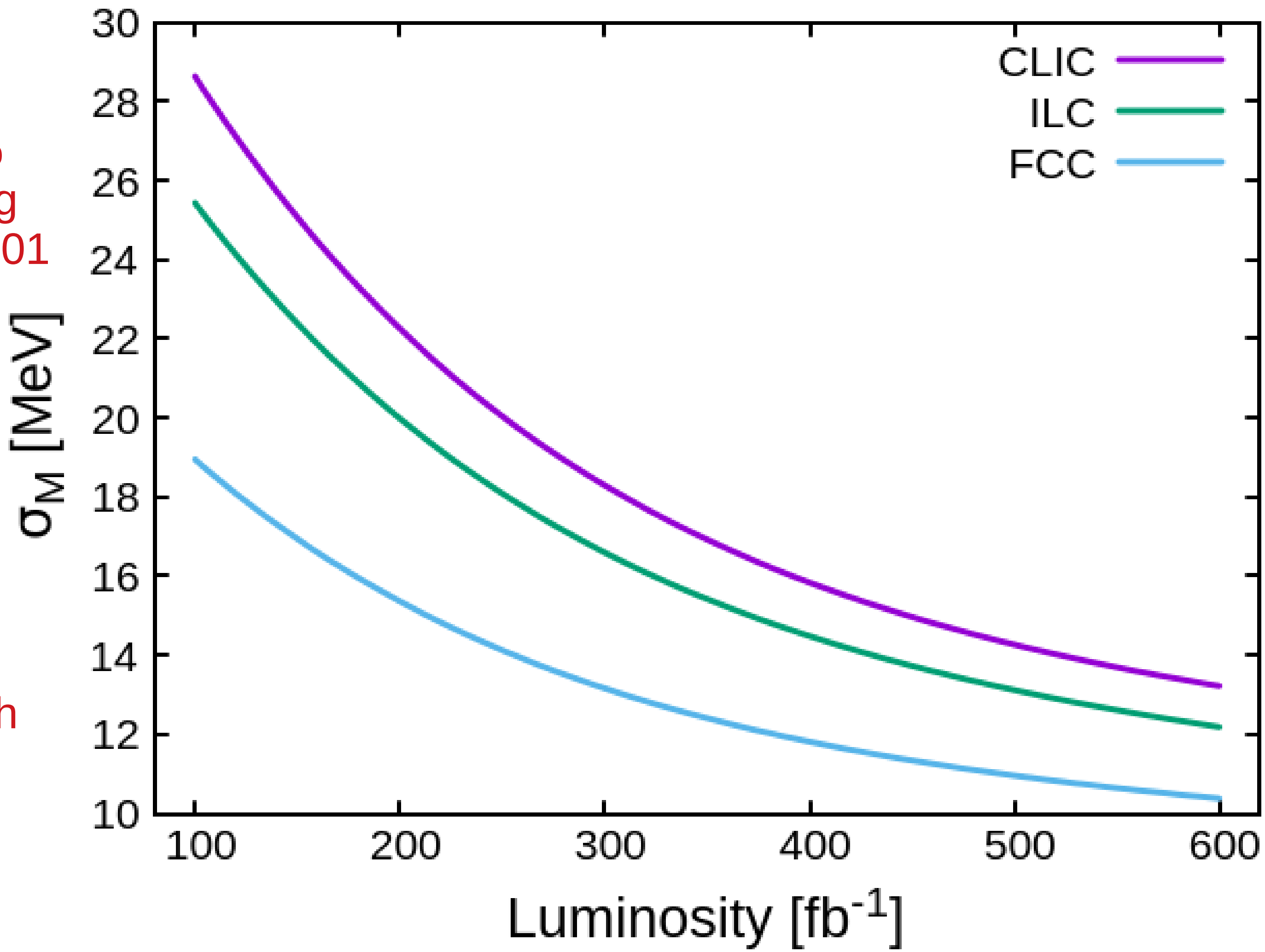
Total luminosity

Normalization uncertainty 1%
Strong coupling uncertainty 0.001



Influence of luminosity spectra

Normalization uncertainty 1%
Strong coupling uncertainty 0.001



Optimized for mass and width determination precision

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

Future plans

and possible contribution to Snowmass’2021

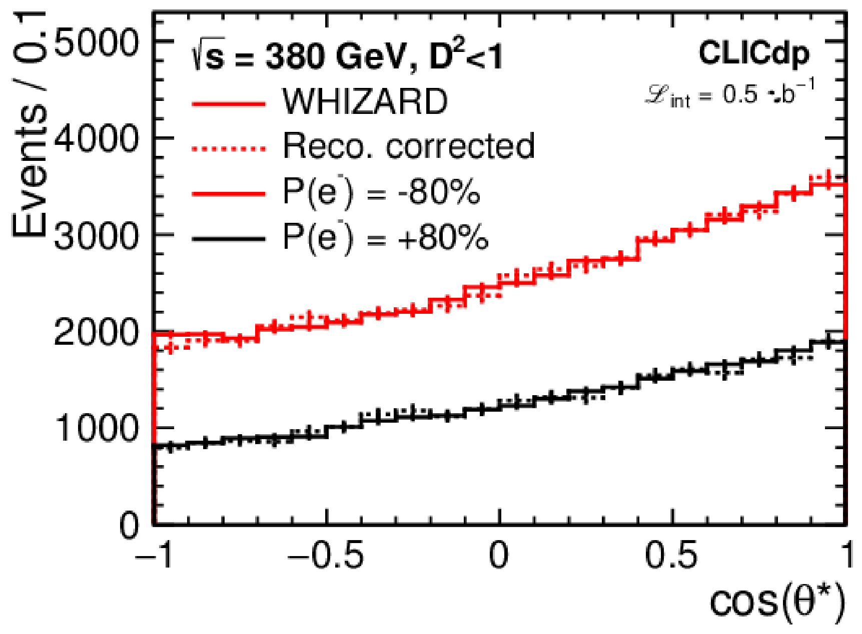
We plan to move to a more advanced approach, including:

- **impact of beam polarisation**
- **additional observables**
- **more detailed analysis of backgrounds and systematic uncertainties**

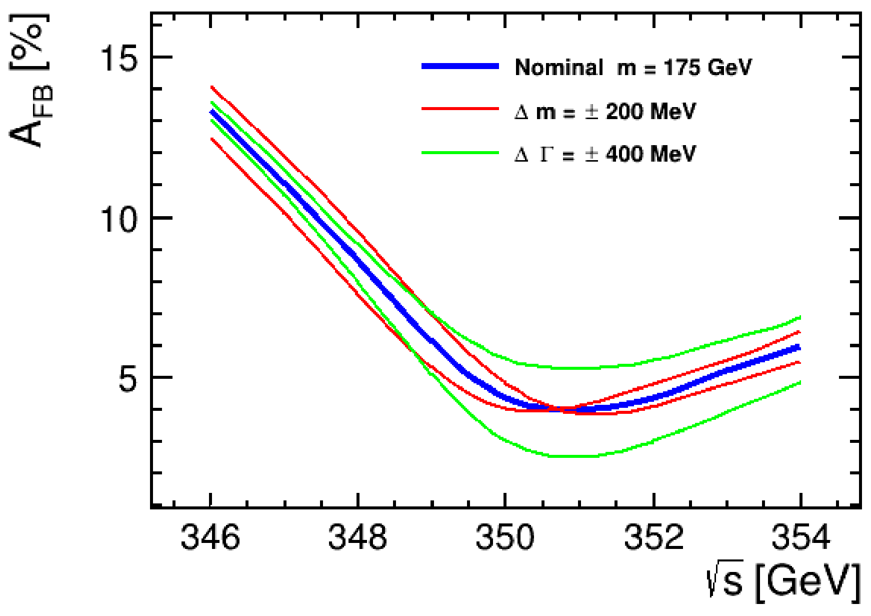
Additional observables

When reconstructing top pair production events, much more information can be extracted than just the production cross section.

Top-quark polar angle distribution
can be used to reconstruct **forward-backward asymmetry A_{FB}**



JHEP 1911 (2019) 003 [arXiv:1807.02441]

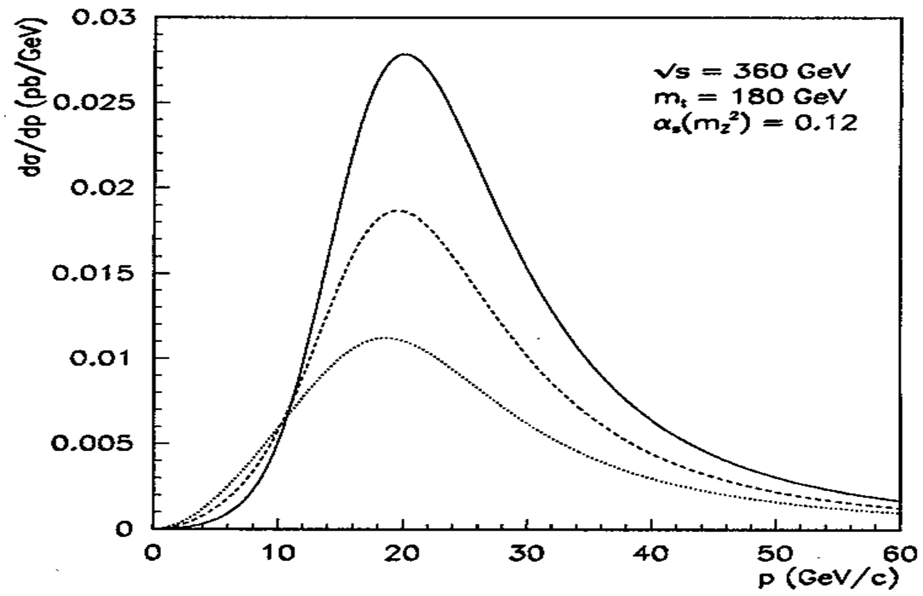


Adapted from arXiv:hep-ph/0207315

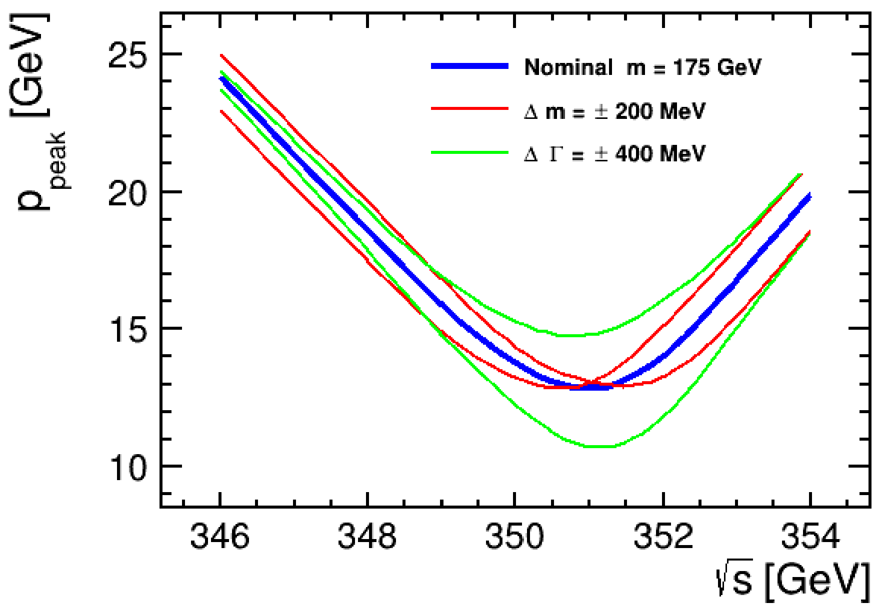
Additional observables

When reconstructing top pair production events, much more information can be extracted than just the production cross section.

Peak position of the **top-quark momentum distribution** is also sensitive to top quark mass and other paramaters



CERN-PPE-96-040
http://cds.cern.ch/record/300417



Adapted from arXiv:hep-ph/0207315

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.

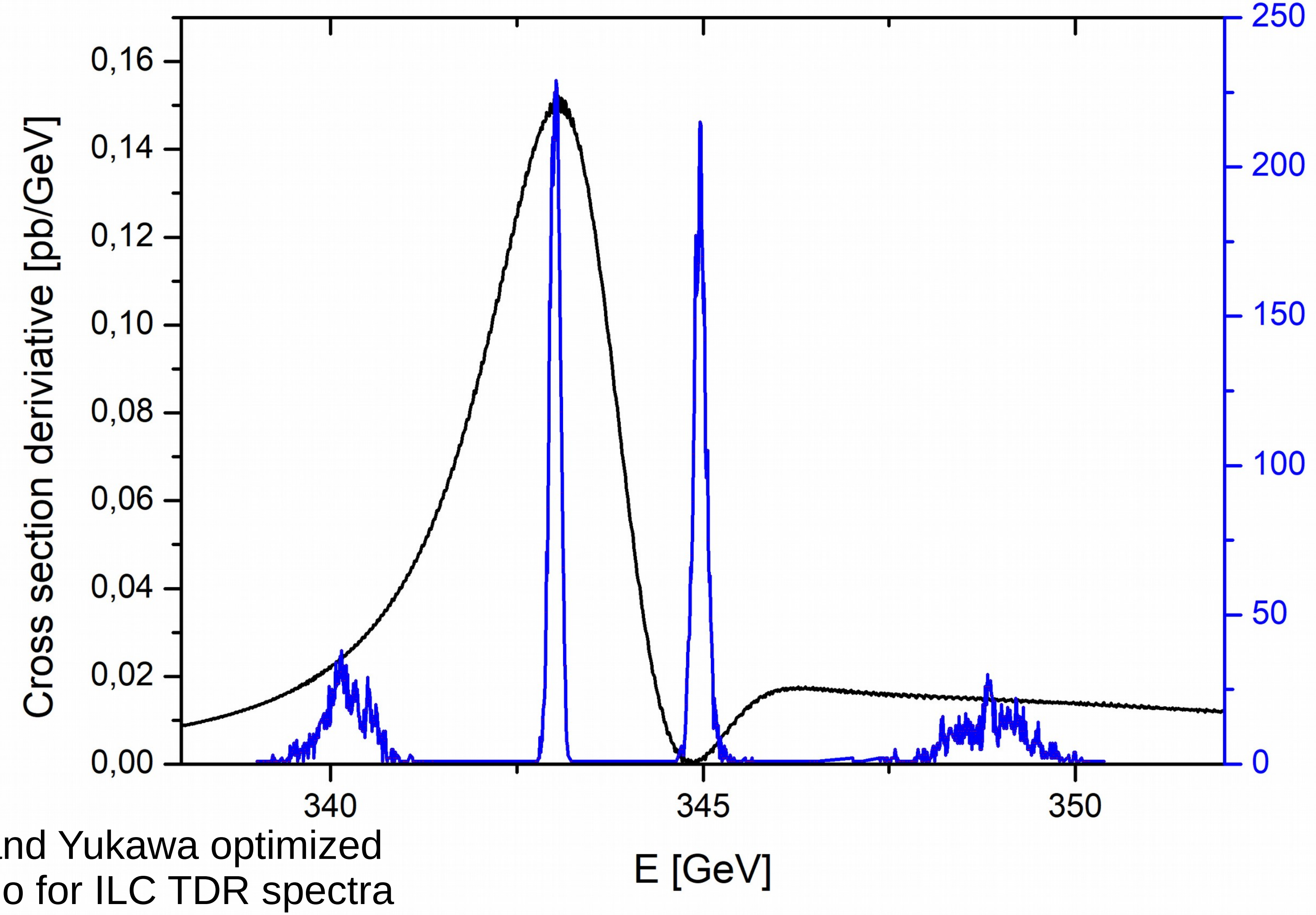
Scan optimization

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

Plans for Snowmass contribution:

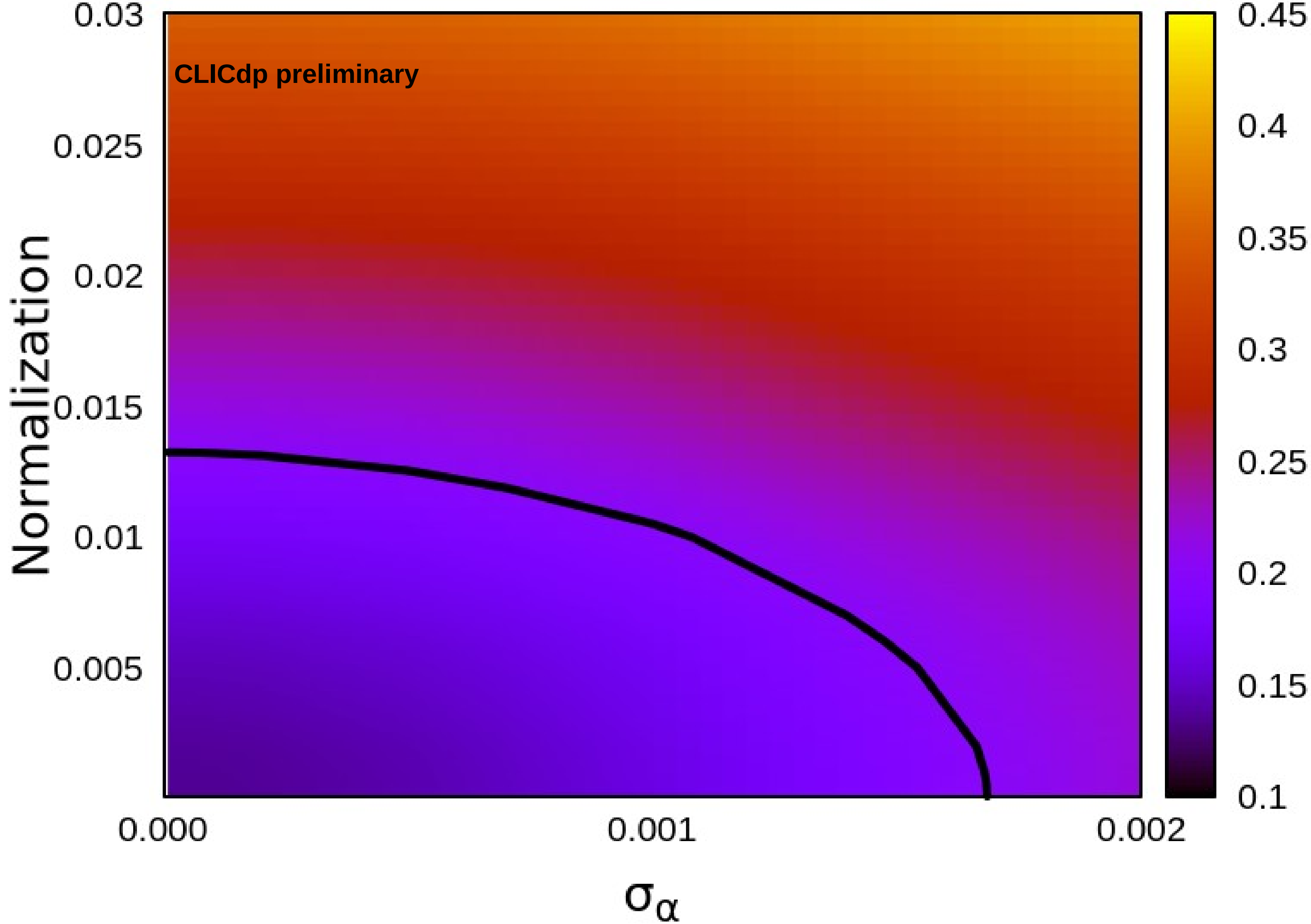
- impact of beam polarisation
- additional observables
- more detailed analysis of backgrounds and systematic uncertainties

What is algorithm looking for?



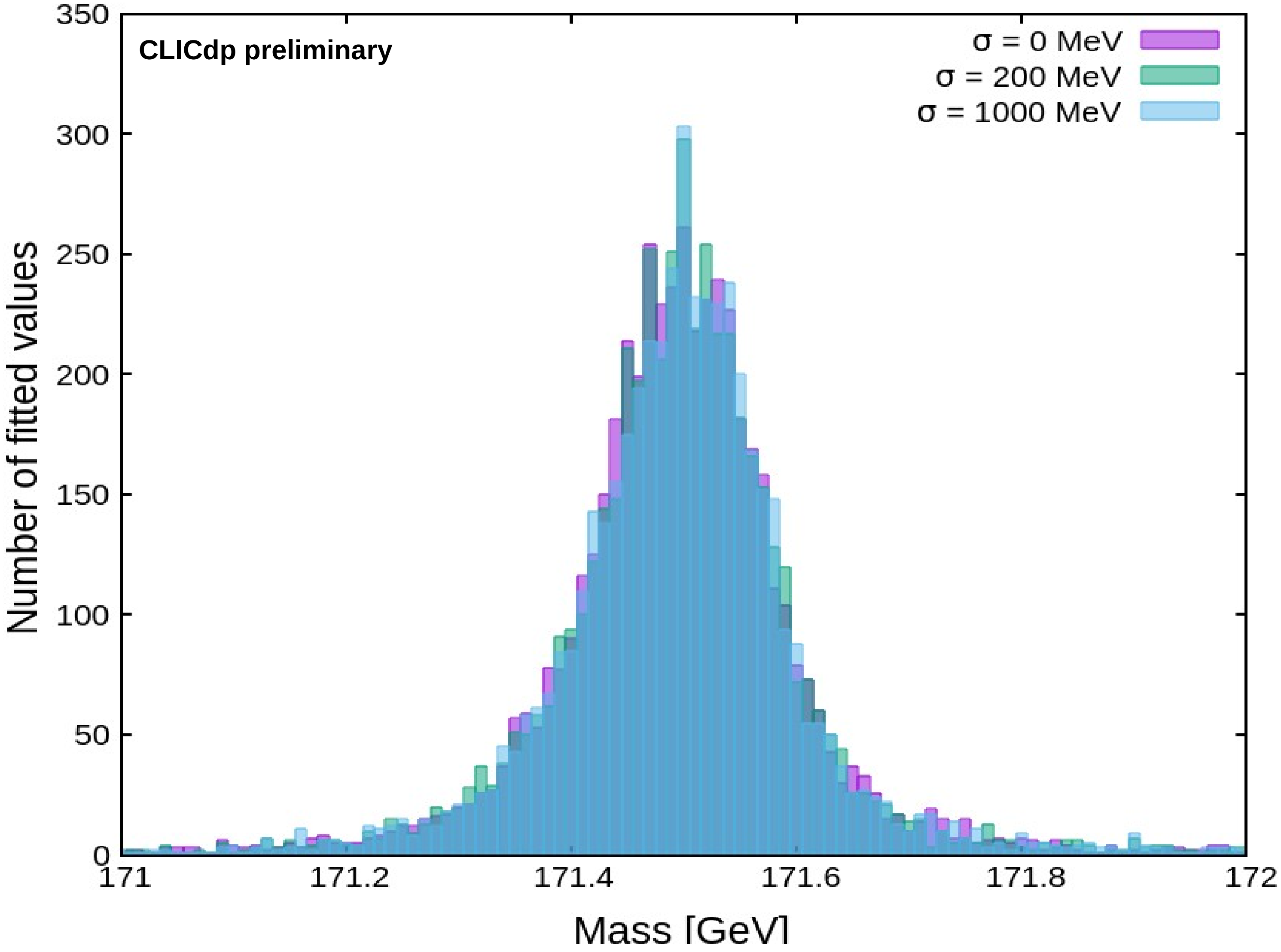
Mass and Yukawa optimized
scenario for ILC TDR spectra

Yukawa uncertainty
from 4D fit



(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