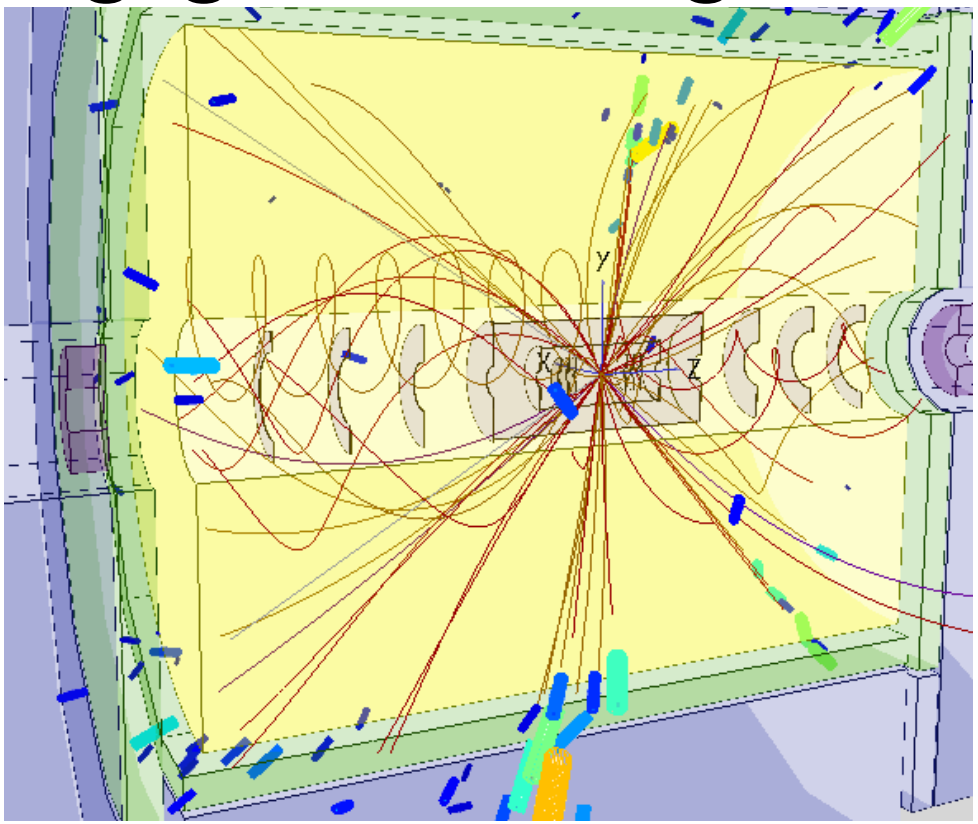
Optimizing top-quark threshold scan using genetic algorithm



Snowmass 2021, EF03 meeting, June 11, 2020

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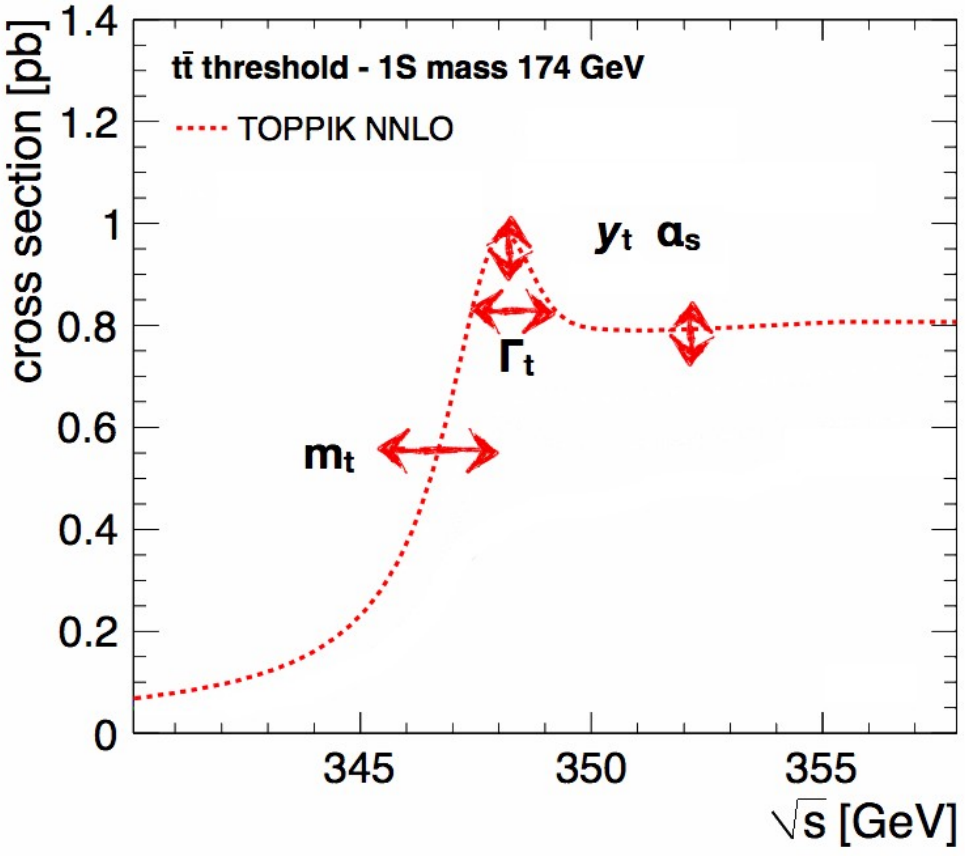
Motivation



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.

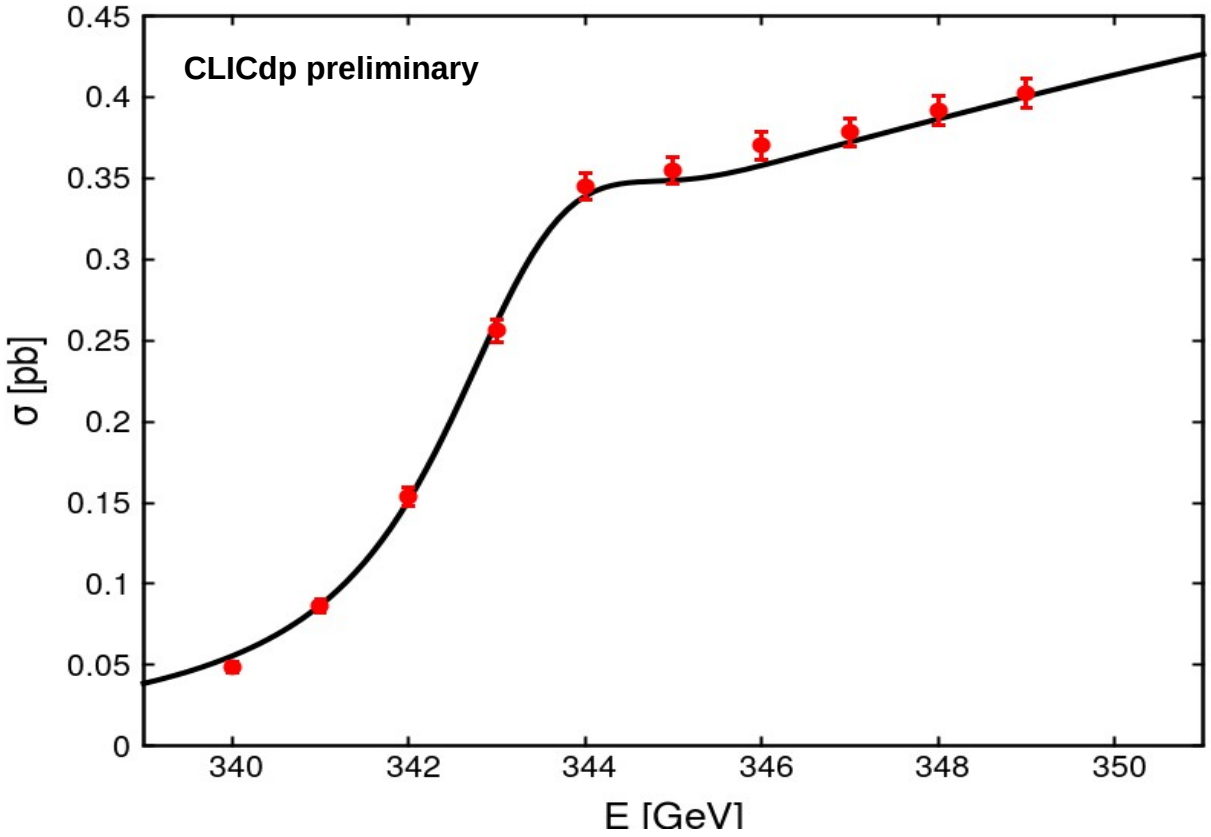
However, cross section depends also on other model parameters…

How this influences m_t determination?

Can the threshold scan procedure be optimized?

Benchmark scenario

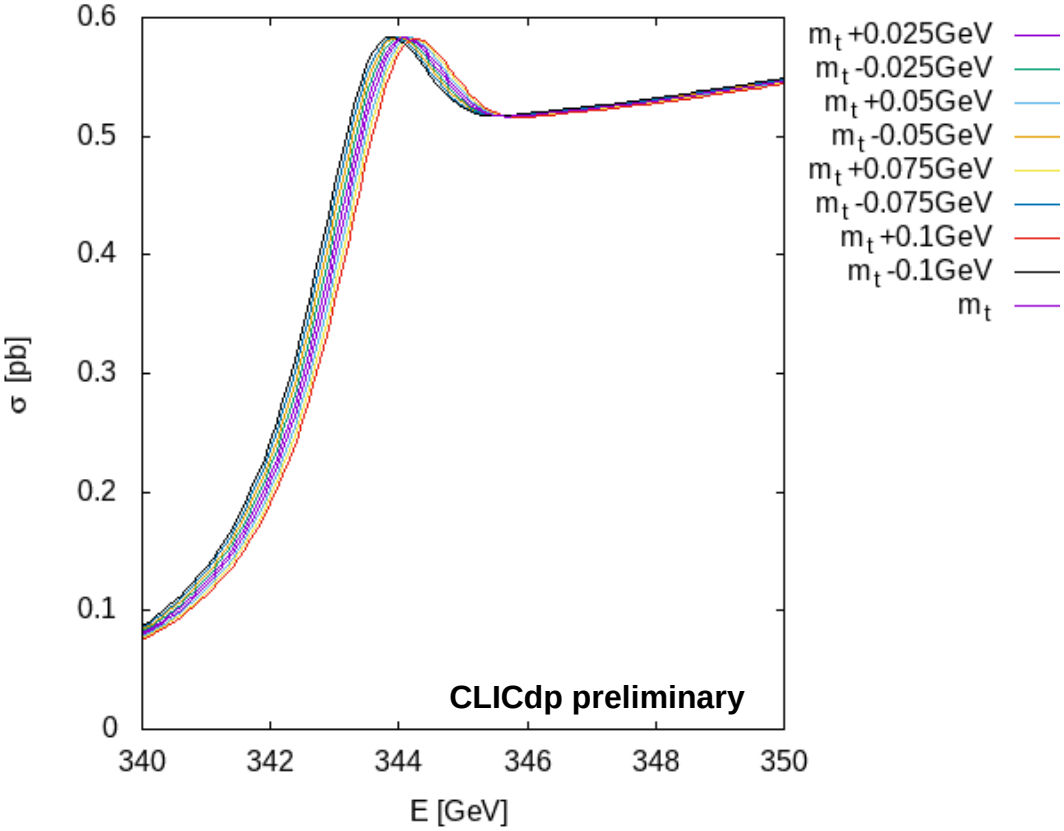
Assume 10 measurements at the threshold, with 1 GeV step in energy, with 10 fb^{-1} taken at each energy point (100 fb^{-1} total).

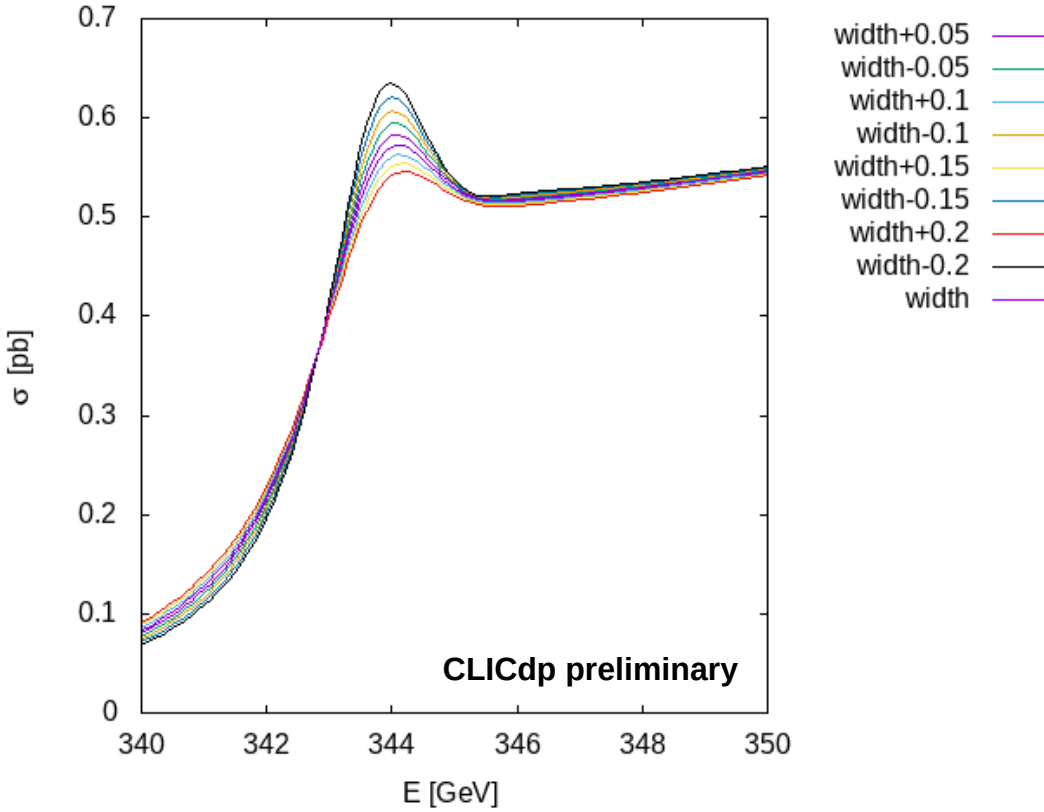


Generate statistical fluctuation assuming 70.2% event reconstruction efficiency and background level (remaining after cuts) corresponding to the 73 fb

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

Cross-section templates



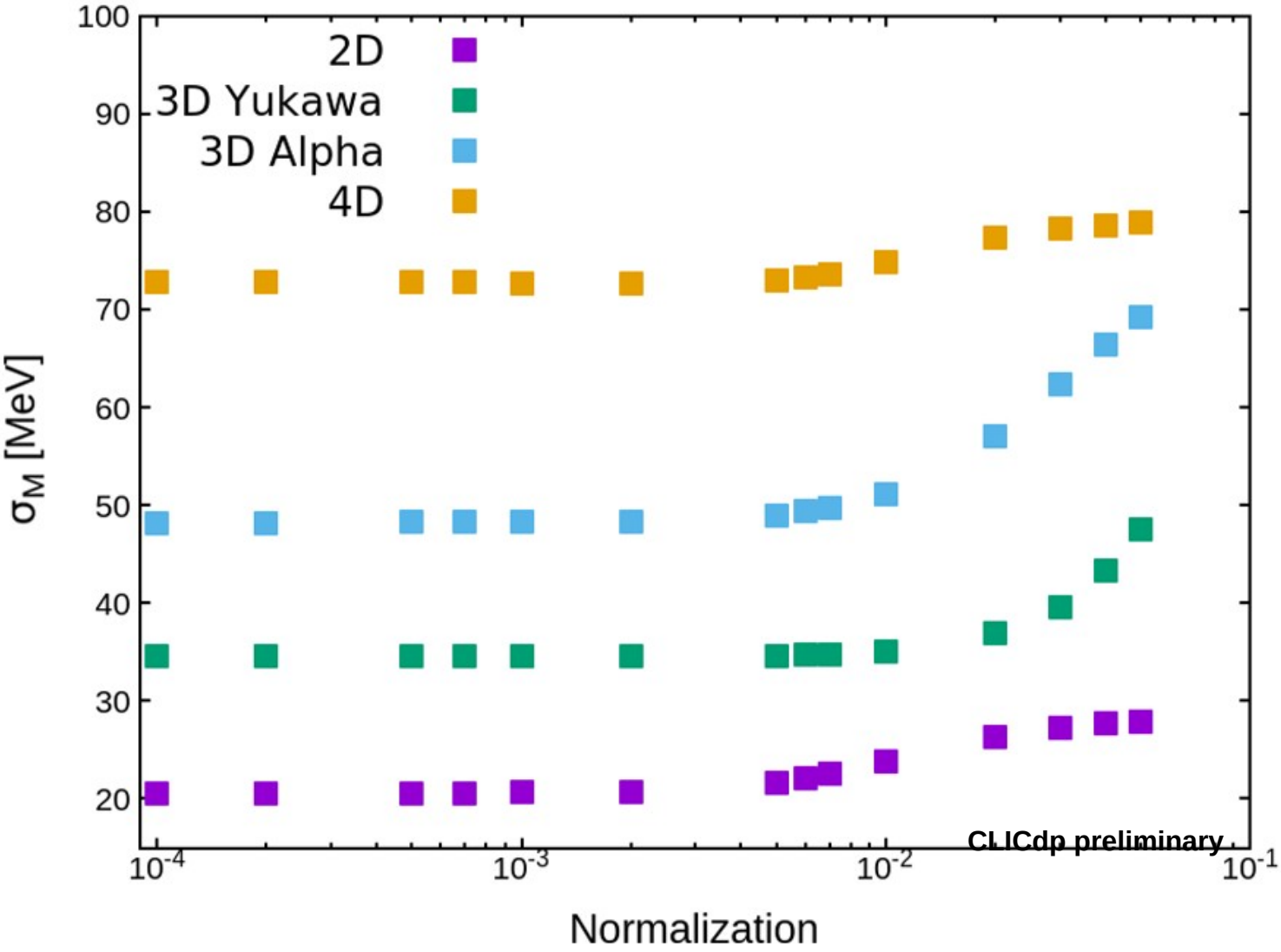


Templates generated with **Qqbar_threshold**

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

Baseline Fit Results

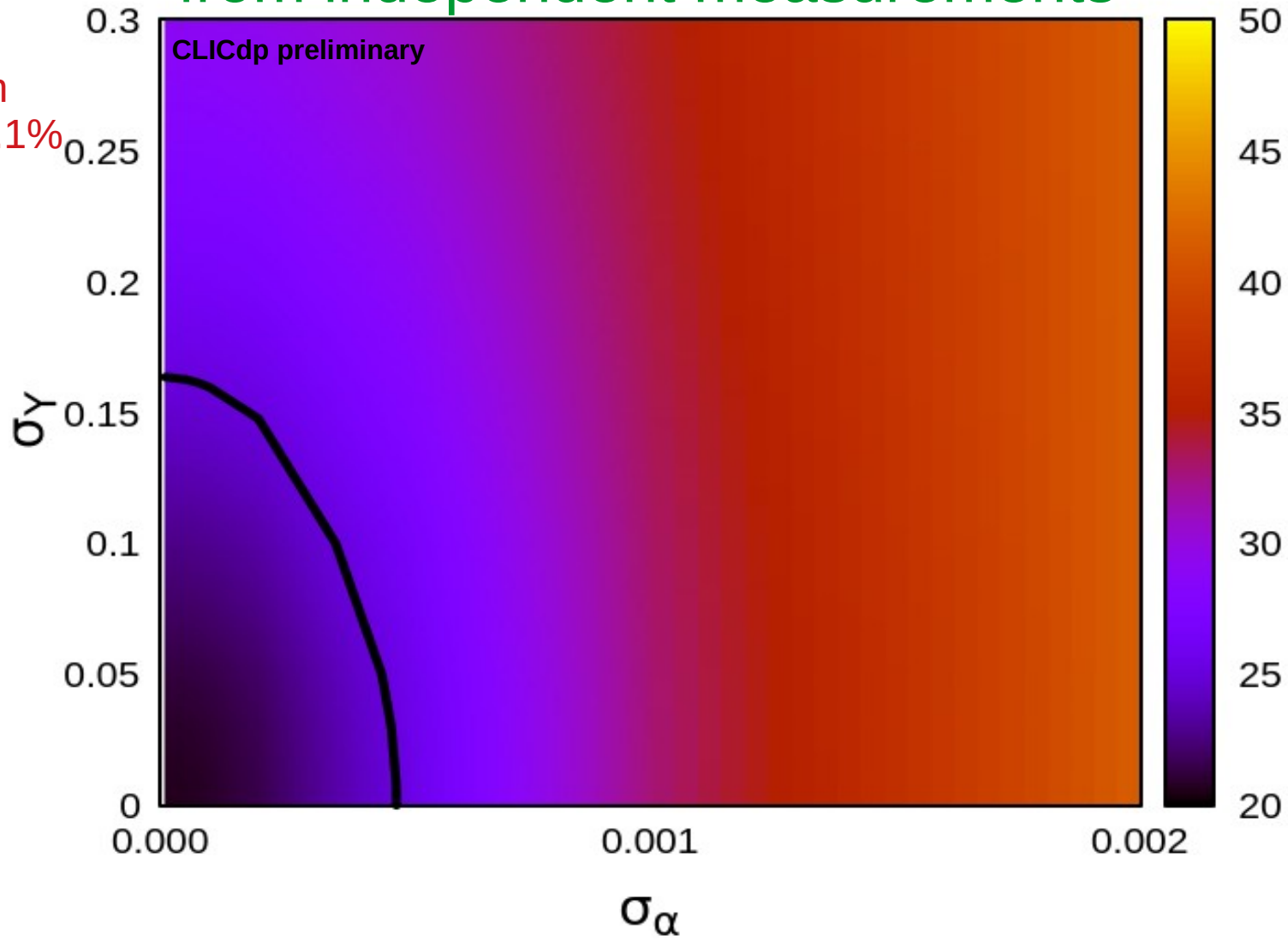
Fit configuration



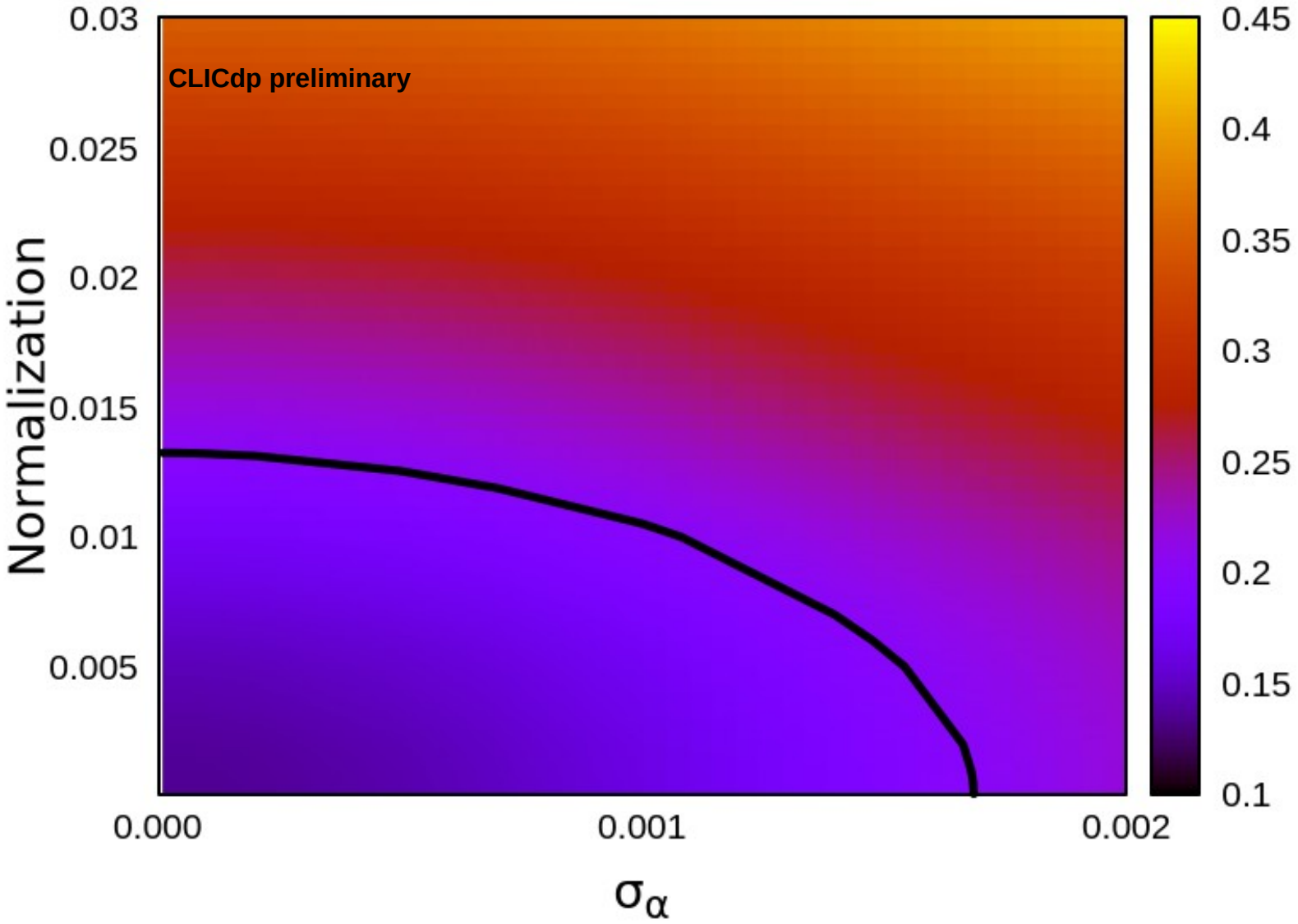
Statistical uncertainty on top-quark mass vs Yukawa and strong coupling uncertainties

from independent measurements

Normalization uncertainty 0.1%

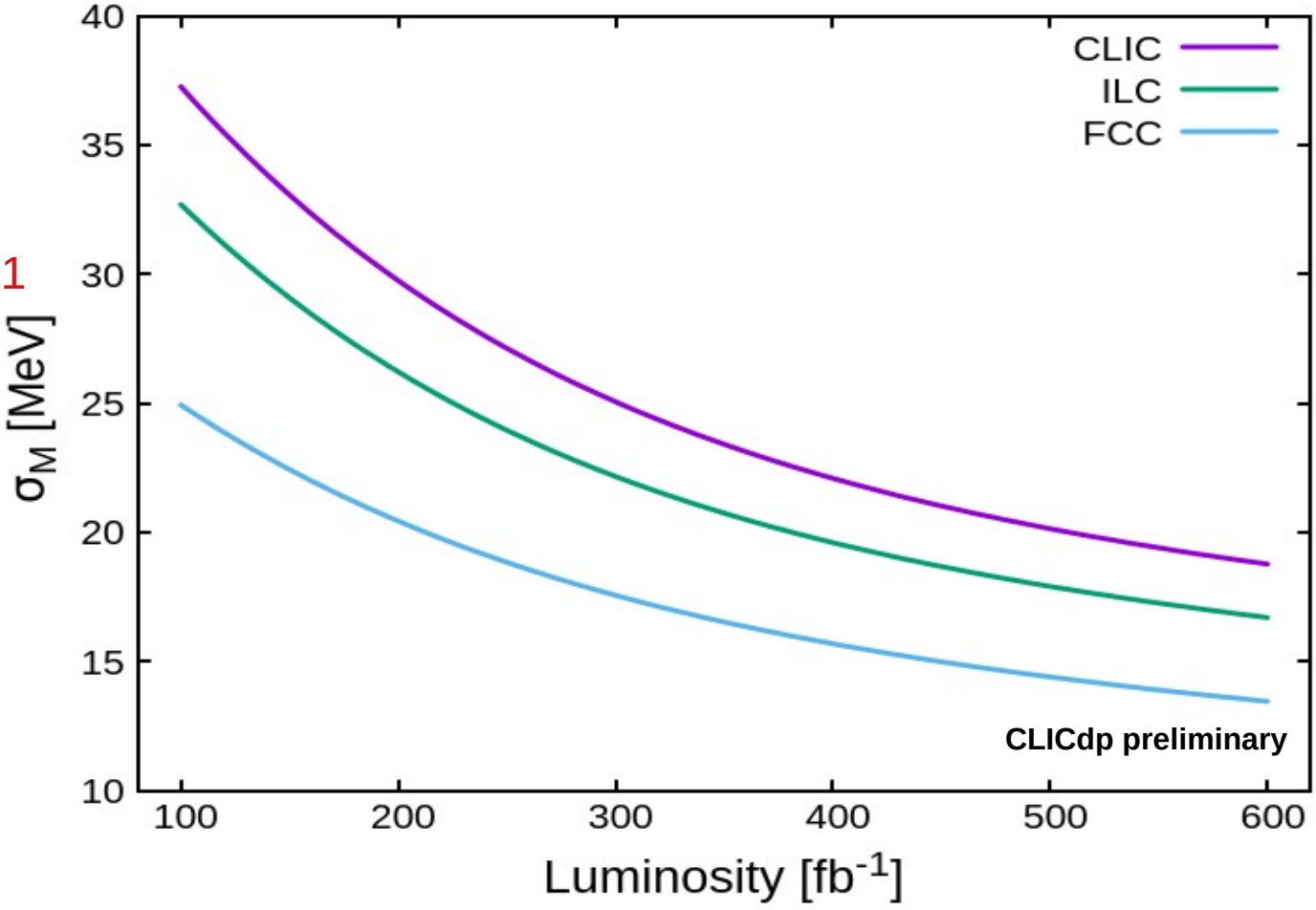


Yukawa uncertainty
from 4D fit



Influence of luminosity spectra

Normalization uncertainty 1%
Strong coupling uncertainty 0.001



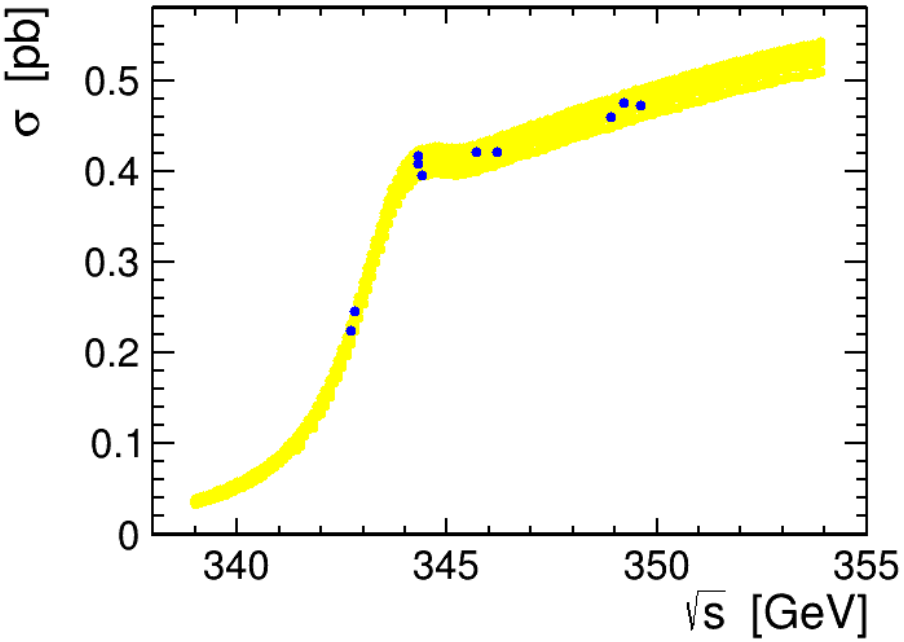
Assuming **same** integrated luminosity, **same** background and efficiency, **no polarisation**

Scan optimization

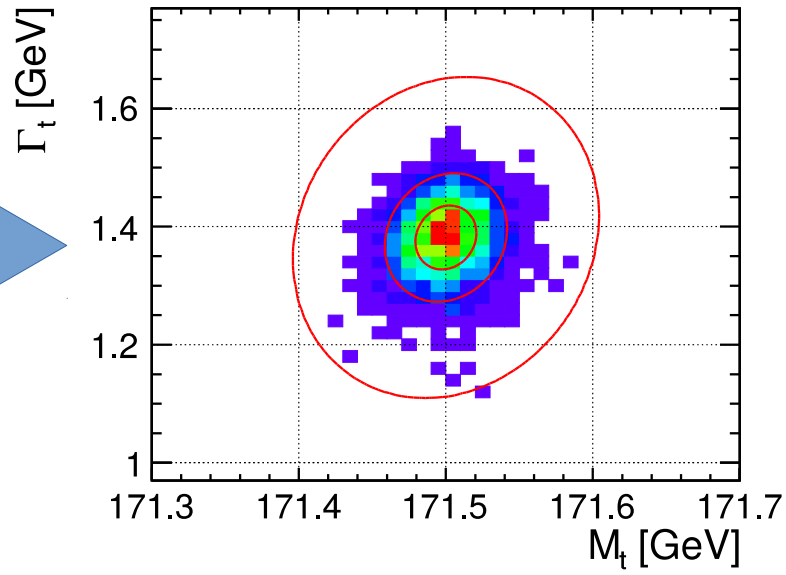
Genetic algorithm

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

Genotype

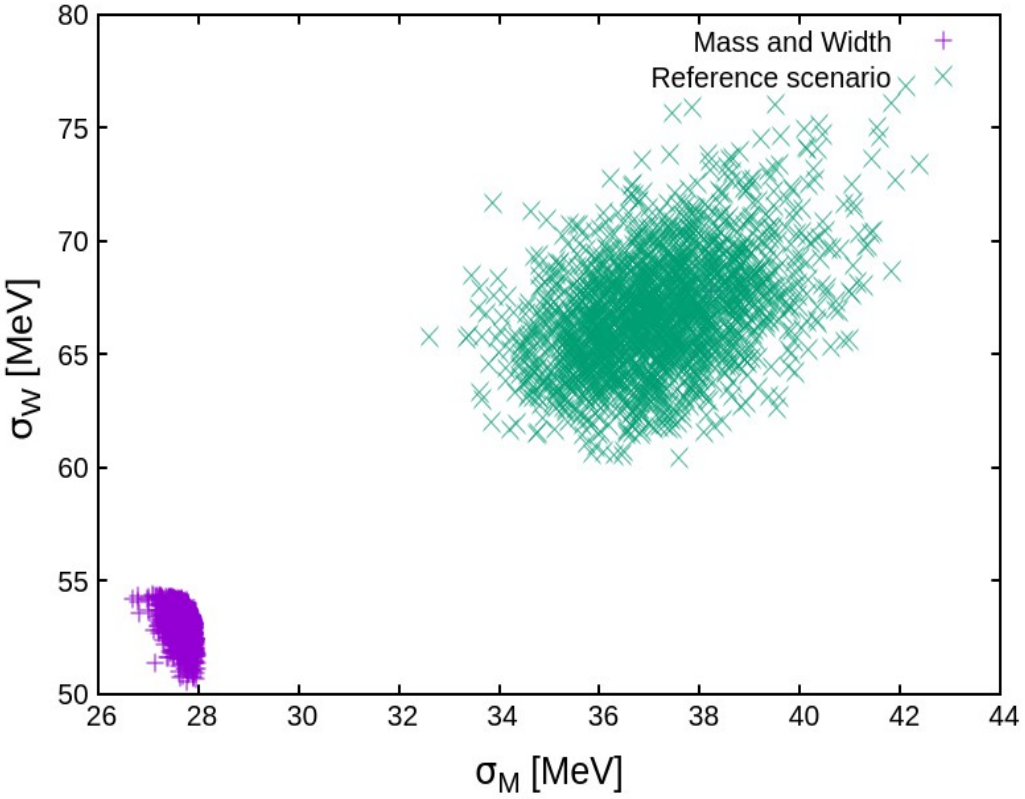


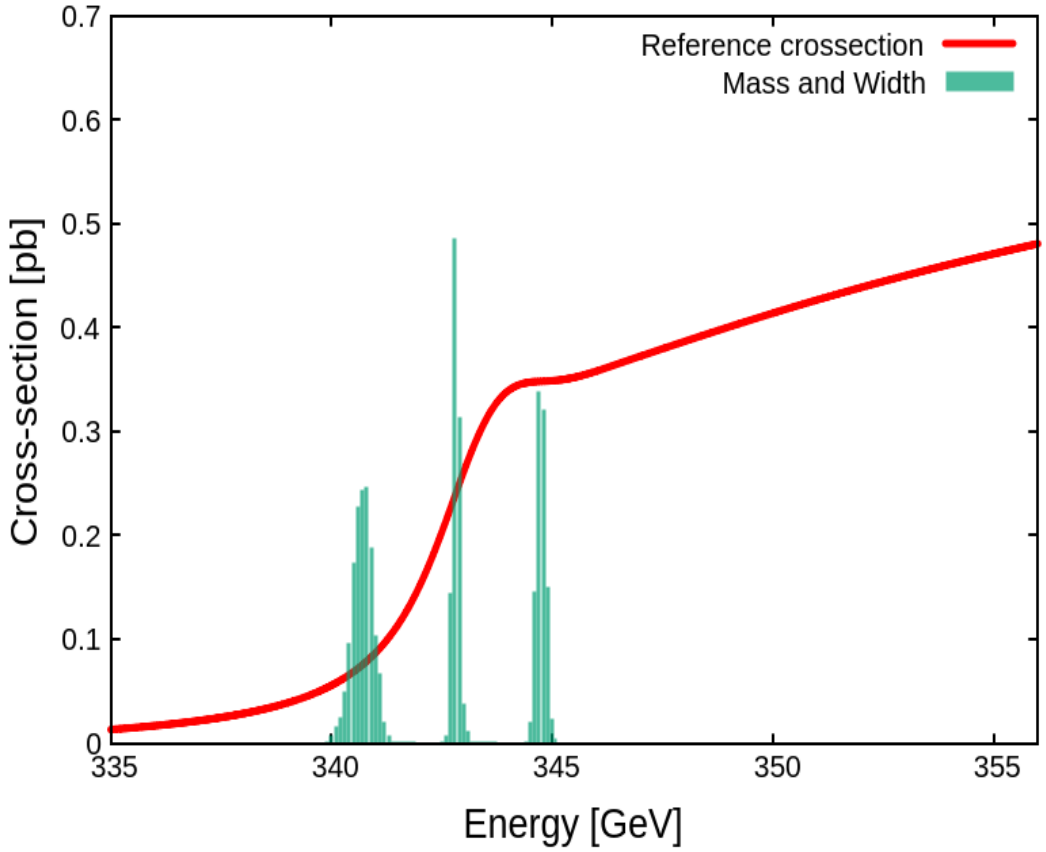
Phenotype



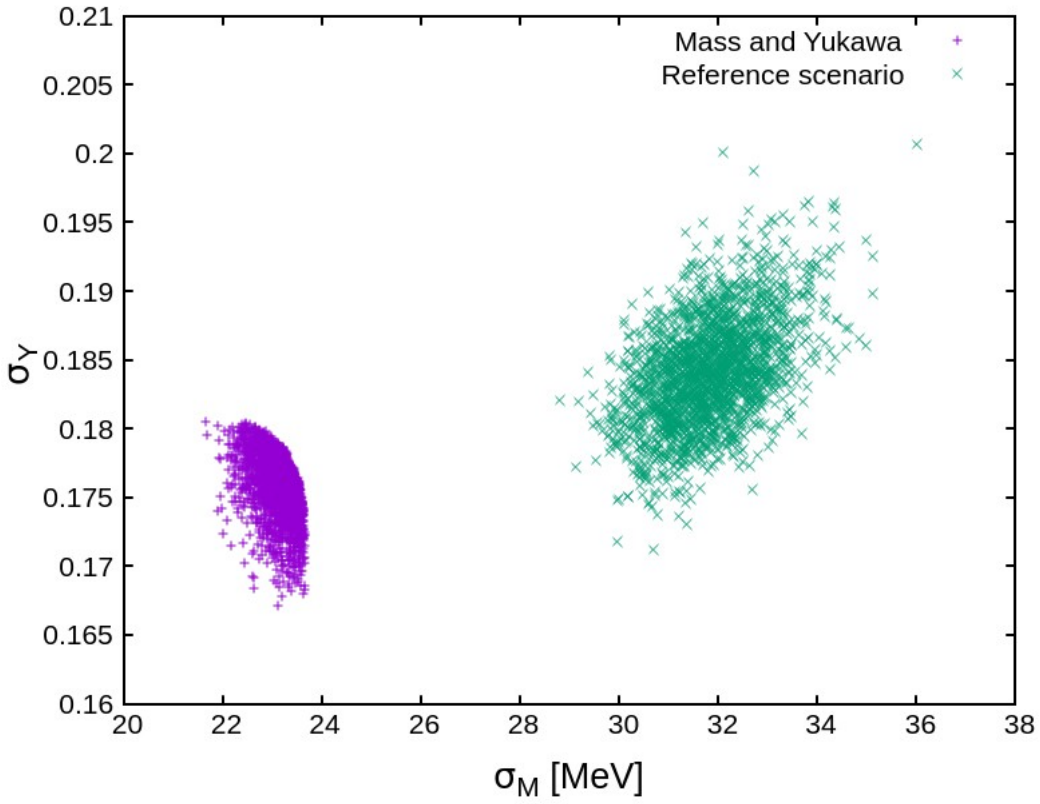
Fits resulting in the parameter values outside the range used to generate templates are ignored.

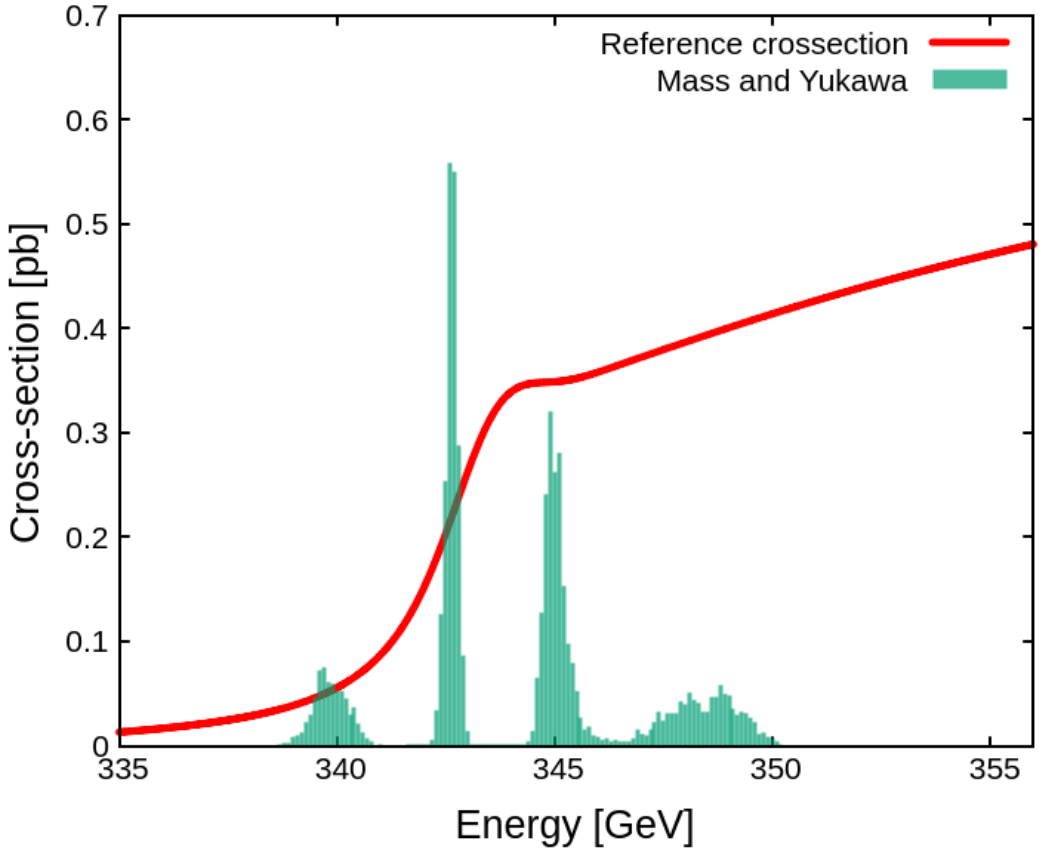
Mass and Width optimization





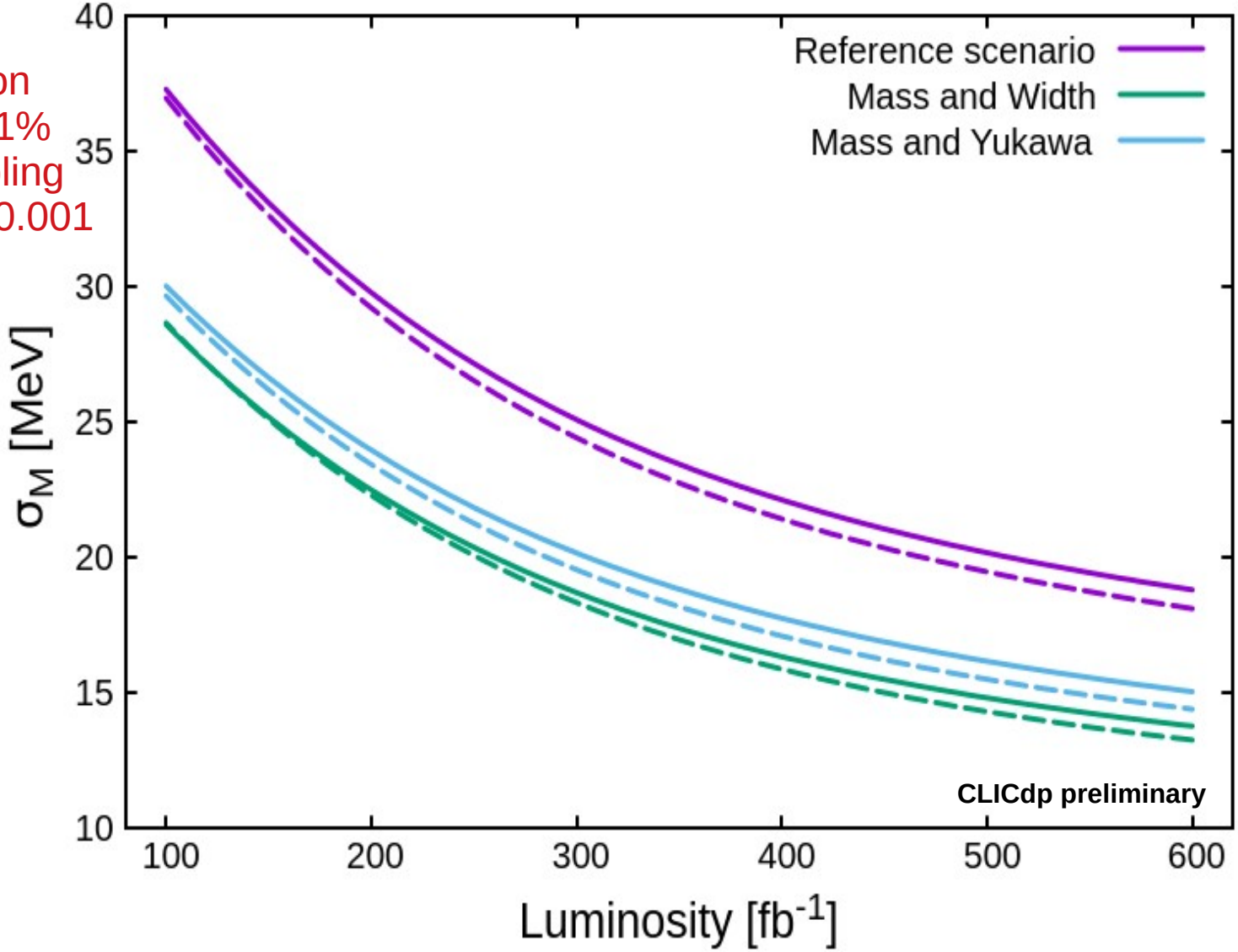
Mass and Yukawa optimization





Total luminosity

Normalization uncertainty 1%
Strong coupling uncertainty 0.001



Conclusions

Top-quark mass

can be extracted with ~25 MeV statistical uncertainty, provided $\sigma_\alpha < 0.0005$, $\sigma_\Upsilon < 0.05$ and normalization ~0.1%.

Top-quark Yukawa coupling

Contribution to the top pair-production can be observed with significance > 5σ

Systematic uncertainties are very important.

Scan optimization

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

Our results were accepted for ICHEP 2020

Future

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

- **impact of beam polarisation**
- **additional observables, eg. angular distributions**
- **more detailed analysis of backgrounds and systematic uncertainties**

and submit it as a contribution to Snowmass'2021

Comparing with other projects