PROCEEDINGS OF SCIENCE

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

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One of the main goals of the future e^+e^- colliders is to measure the top-quark mass and width in a scan of the pair production threshold. Yet, the shape of the threshold cross section depends also on other model parameters as the top Yukawa coupling and the strong coupling constant. We study the expected precision of the top-quark mass determination from the threshold scan at CLIC, ILC and FCCee. We use the most general fit approach with all relevant model parameters and expected constraints from earlier measurements taken into account. We demonstrate that even in the most general approach the top-quark mass can be extracted with statistical precision of the order of 20 to 30 MeV. Additional improvement is possible, if the running scenario is optimised. We propose the optimisation procedure based on the genetic algorithm. When optimising the mass measurement the statistical uncertainty can be reduced by about 25%, corresponding to factor of 2 increase in the integrated luminosity.

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1. Motivation

Precise measurement of the top-quark mass is essential for the understanding of the Higgs mechanism, electroweak symmetry breaking and for constraining many “new physics” scenarios. The top-quark pair-production threshold scan at an $\mathrm{e^+e^-}$ collider is expected to be the most precise way to measure it. Scan scenario with ten energy points separated by 1 GeV, with 10 $\mathrm{fb^{-1}}$ of data collected at each energy is considered as a baseline scenario for future e^+e^- colliders. Recent study [1] showed that expected statistical uncertainty in the mass is around 21 MeV and in the top-quark width 51 MeV. However the analysis took only the two model parameters, top-quark mass and width, into account. The main goal of the presented study was to quantify the influence of additional model parameters, the top Yukawa coupling and the strong coupling constant, and related uncertainties, on the statistical precision of top-quark mass determination. As the baseline running scenario seems to be conservative, possible reduction of the statistical uncertainties when using the optimised running scenario is also considered.

This work was carried out in the framework of the CLIC detector and physics (CLICdp) study. Results included in this contribution supersede results presented previously in [2, 3]. For more details interested reader is referred to [4].

2. Modelling of the threshold scan

2.1 Cross-section templates

The proposed procedure of threshold scan data fit is based on a set of the cross section templates generated using `QQbar_threshold` [5, 6], assuming different values of top quark parameters. Each template consists of 300 points representing cross-section values calculated for given set of model parameters, for collision energies from 330 to 360 GeV. Nominal cross section template was generated first, four parameters considered in the study: top-quark mass, m_t, top-quark width, Γ_t, top-quark Yukawa coupling relative to SM prediction, y_t, and strong coupling constant, α_s, were then varied in small steps, corresponding to the expected experimental sensitivities, resulting in additional cross section templates. Total of 274 “theoretical” templates generated with `QQbar_threshold` for different variations of model parameters were then convoluted with the expected collider luminosity spectra to obtain final cross-section templates used in the analysis. CLIC spectra with the reduced bunch charge (90% charge) was used assuming its shape is independent on the collision energy.

2.2 Reference scenario

At the first energy stage CLIC is assumed to run at 380 GeV, which was selected for optimising both the Higgs boson and top quark measurements. With 1 $\mathrm{ab^{-1}}$ of total integrated luminosity at this stage, a dedicated scan of 100 $\mathrm{fb^{-1}}$ is planned at the $\mathrm{t\bar{t}}$ threshold. As already mentioned above, the baseline scenario of the threshold scan assumes running at 10 equidistant energy points taking 10 $\mathrm{fb^{-1}}$ of data for each value of $\sqrt{s}$. When generating simulated measurements (pseudo-data), the overall top-pair event reconstruction efficiency of 70.2% (including the relevant branching fractions) was assumed, and the background contribution remaining after the event selection procedure corresponding to the cross section of 73 fb [7]. Reconstruction efficiency is assumed to be independent on the collision energy (in the considered energy range) and on the model parameters.

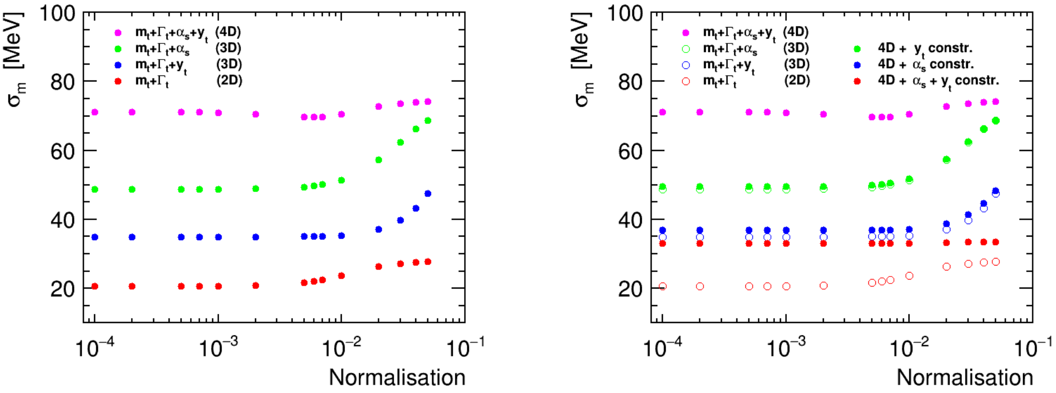

Figure 1: Statistical uncertainty in the top-quark mass expected from the fit of model parameters, as a function of the assumed normalisation uncertainty. Left: for different number of model parameters included in the fit, without parameter constrains. Right: for fit including all model parameters (4D), with different sets of parameter constrains taken into account. Assumed uncertainties on the strong coupling constant and the top Yukawa coupling are: $\sigma_\alpha = 0.001$ and $\sigma_y = 0.1$

2.3 Fit procedure

For each simulation of the threshold scan measurement, one of the cross section templates (convoluted with the luminosity spectra) is selected as the base for pseudo-experiment generation. By this choice, “true” values of top quark parameters are chosen for the considered fit scenario. Selected template is used to generate a set of data corresponding to the expected scan result, so called pseudo-experiment data (or pseudo-data). For each scan point, cross section value taken from the base template is varied according to the expected statistical fluctuations (from Poisson distribution), taking selection efficiency and background contribution into account. Parameter fit procedure is then applied to the generated pseudo-data set. The values of the top-quark mass and other model parameters can then be extracted from the fit of the polynomial χ^2 dependence on the parameter values. For details of the fit procedure please refer to [4].

3. Baseline threshold scan results

Previous studies [1, 7, 8] considered at most two-parameter fits to the threshold scan data. The approach presented in this contribution, thanks to its simple, semi-analytic form, allows to perform fits with more parameters. Moreover, it is possible to add additional constraints on the selected parameters to make the fit reflect the expected experimental situation better. The constraint that clearly influences the fit results is the assumed uncertainty in the data normalisation,[1] see Fig. 1. Four different fit configurations are considered: two-dimensional fit of mass and width (2D), fit of mass, width and strong coupling constant (3D alpha), fit of mass, width and Yukawa coupling (3D Yukawa), and the simultaneous fit of the top-quark mass, width, Yukawa coupling and the strong coupling constant (4D).[2] As mentioned above, model parameters will be measured by many experiments preceding CLIC, so the fit should not assume they are “free”. Assuming that the

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[1] This also includes systematic uncertainties of the event selection procedure and of the theoretical predictions.

[2] Normalisation scaling factor α is always considered as an additional fit parameter.

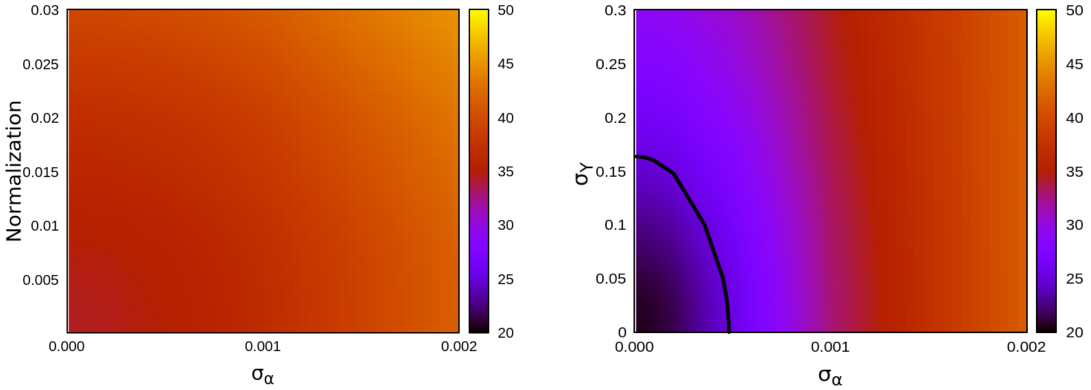

Figure 2: Statistical uncertainty in the top-quark mass expected from the fit involving all considered model parameters (4D). Left: as a function of the strong coupling constant and normalisation uncertainties, assuming no constraints on the top Yukawa coupling. Right: as a function of the strong coupling constant and the Yukawa coupling uncertainties assuming normalisation uncertainty $\Delta = 10^{-3}$. Black line indicates the uncertainty of 25 MeV.

selected parameters are known with given uncertainty before the threshold scan measurement makes the analysis closer to the situation expected in an actual experiment. The statistical uncertainties of the fit are significantly reduced, as shown in Fig. 1 (right), where the top-quark mass uncertainty from the 4D fit is plotted as a function of the normalisation uncertainty for different sets of constrains on the the Yukawa coupling and the strong coupling constant.

As shown in Fig. 2 (left), if no constraints are imposed on the top Yukawa coupling, the top-quark mass can not be extracted with statistical precision better than 34 MeV, even for negligible uncertainties in normalisation and strong coupling (refer also to results in Fig. 1). The estimated top-quark mass uncertainty decreases significantly, if external constraints on the Yukawa coupling are imposed, as shown in Fig. 2 (right), for normalisation uncertainty $\Delta = 10^{-3}$. To be able to extract the top-quark mass with precision of the order of 25 MeV, top Yukawa coupling has to be constrained from earlier measurement to about 10% and the strong coupling constant has to be known to better than 0.0005.

4. Optimisation

Genetic algorithms are widely used in many objective optimisation problems. Non dominated sorting genetic algorithm II [9] was chosen for the presented study for its high efficiency and elasticity. Scan measurement scenario (set of energy points with total integrated luminosity of 100 fb $^{-1}$) is considered a genotype and results of the fit procedure constitute a phenotype. In order to study how different model parameters influence each other in the optimisation procedure, multiple objective optimisation was considered, focusing on pairs of top-quark parameters. In the evolution of the large set of possible measurement scenarios, next generation of scenarios was chosen by sorting the so called Pareto frontiers [10]. To efficiently perform sorting calculations the Jensen algorithm as used [11].

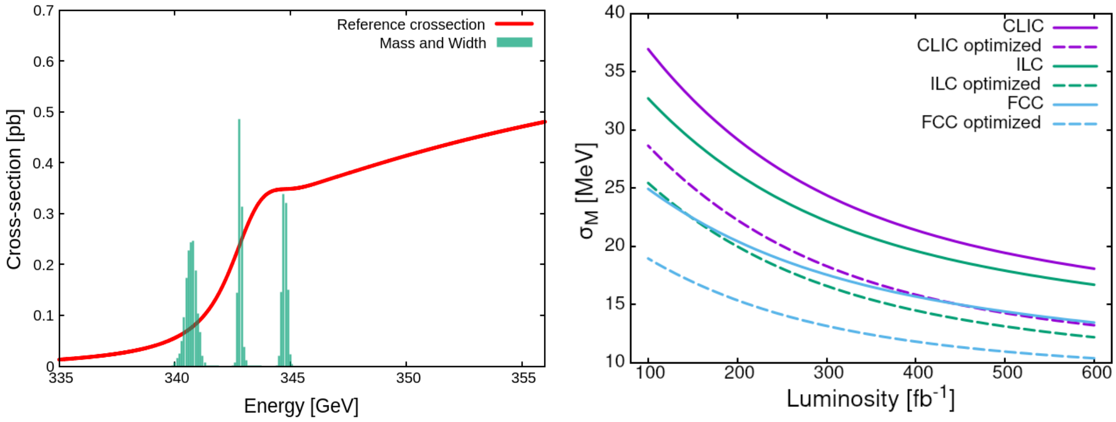

Figure 3: Left: distribution of the energy points selected by the genetic algorithm for the best measurement of the top-quark mass and width (arbitrary scale) compared with the reference cross section template. Right: expected statistical uncertainty in the top-quark mass from the baseline (solid lines) and optimised (dashed lines) scan scenarios, as a function of the total scan luminosity, for different collider projects.

Results of the mass and width measurement optimisation are shown in Fig. 3. For best statistical precision, the scan should focus in three energy regions: just below the threshold, in the middle of the threshold, where the cross section slope is highest and at the plateau just above the threshold. Improvement of about 25% can be achieved for both mass and width statistical uncertainty.

One scenario from the last optimisation step was selected for detailed comparison with the baseline reference scenario, based on the analysis of 20 000 pseudo-experiments. While the baseline scenario assumes 100 fb^{-1} of data collected during the top threshold scan at CLIC, we also considered larger values of integrated luminosity, allowing to reach statistical uncertainty below 20 MeV. To simplify the comparison, the normalisation uncertainty of 1% is assumed, strong coupling uncertainty of 0.001 and, to make comparison even more realistic, top quark mass uncertainty of 200 MeV is assumed in the pseudo-experiments generation.

Expected dependence of the statistical mass uncertainty on the total integrated luminosity, $\mathcal{L}$, is shown in Fig. 3 (right), for three e^+e^- collider projects. Two running scenarios are considered for each project: reference 10 point scenario and 6 point scan scenario optimised for mass and width measurement. Due to additional constraints imposed on the normalisation and the strong coupling constant, the uncertainties decrease more slowly than with $\sqrt{\mathcal{L}}$. For each collider, statistical uncertainty in the top quark mass can be reduced by around 25 – 30% when using the optimised scenario. This corresponds to the same precision as the reference scenario with the luminosity increased by a factor of 2.

5. Summary

Complementary fit and optimisation procedures have been developed for the top-quark threshold scan analysis at CLIC. The new fit procedure is more flexible that the one used in the previous studies [1, 7, 8] and allows to include other relevant model parameters in the fit, as well as additional constraints coming e.g. from earlier measurement and constraints on data normalisation. For the baseline scan scenario assumed at CLIC, with 100 fb^{-1} of integrated data luminosity, top quark mass can be measured with statistical uncertainty below 25 MeV only if the normalisation of the data and theory predictions is known to better than 0.1%, strong coupling constant with uncertainty below 0.0005 and Yukawa coupling with relative uncertainty below 0.10.

Optimisation procedure based on non dominated sorting genetic algorithm II was used to propose different running scenarios. It is possible to improve statistical precision of top-quark mass determination by about 25-30%, also improving the measurement of the top-quark width. With optimised running scenario, the statistical uncertainties on mass an width are similar to the uncertainties expected for the reference scenario with doubled integrated luminosity (200 fb^{-1}).

Acknowledgments

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