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Optimising top-quark threshold scan at CLIC using genetic algorithm

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Summary

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. In this thesis, the study of the expected precision of the top-quark mass determination from the threshold scan at CLIC is presented. The most general fit approach is used with all relevant model parameters and expected constraints from earlier measurements taken into account. It is demonstrated that the top-quark mass can be extracted with statistical precision of the order of 30 to 40 MeV and additional improvement is possible if the running scenario is optimized. With the optimisation procedure based on the genetic algorithm the statistical uncertainty of the mass measurement can be reduced by about 25%.

Keywords

top quark, linear accelerators, electron-positron colliders, genetic algorithms, measurement optimisation, artificial intelligence, CLIC, CERN

Title of the diploma thesis in Polish

Wykorzystanie algorytmu genetycznego do optymalizacji pomiaru progu na produkcję kwarku top w akceleratorze CLIC.

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Chapter 1

Introduction

1.1. Top quark

Top quark is the heaviest currently observed elementary particle. Its mass of $172.9 \pm 0.4 \text{ GeV}$ [1] is about the same as for the atom of rhenium [2]. It was first observed in 1995 by the CDF and DØ experiments at Fermilab [3, 4]. As a fermion it has spin $\frac{1}{2}$ and an electric charge of $+\frac{2}{3}e$ as an up-type quark. Top quark takes part in all fundamental interactions: strong, weak, electromagnetic and gravitational. So far it has only been produced (and observed) in hadron colliders, Tevatron and LHC. With the estimated mean lifetime of around $5 \times 10^{-25} \text{ s}$ [5], the top quark decays before it can form any hadronic bound state, as the hadronisation timescale (time scale for strong interaction) is about twenty times larger. This property gives an unique opportunity to study "bare" quark interactions. Top quark decays only through the weak interactions, as only the $W^\pm$ boson exchange allows for the change of quark flavour. Most likely is its decay to a W boson and a bottom quark, but decays to a strange quark or, least probable, a down quark, as expected from the quark mixing, described by Cabibbo–Kobayashi–Maskawa matrix. Production of the top-quark pairs at the high energy e^+e^- colliders will open unique opportunities to test predictions of the Standard Model (SM) and quantum chromodynamics (QCD) in clean environment, for quasi-free quarks (before hadronisation). Precise measurement of the top-quark mass is of particular importance, as it is essential for the understanding of the Higgs mechanism, electroweak symmetry breaking and for constraining many "new physics" scenarios.

1.2. The Compact Linear Collider

The Compact Linear Collider (CLIC) is a linear e^+e^- collider project, that is now being considered as a possible next large infrastructure at CERN [6, 7]. CLIC is proposed as a staged machine running at energies from 380 GeV up to 3 TeV. The physics program of CLIC focuses on three main research areas: precise measurements of the Higgs boson properties including its couplings to other SM particles and its selfcoupling, study of top-quark production and decays, as well as direct and indirect searches for "new physics".

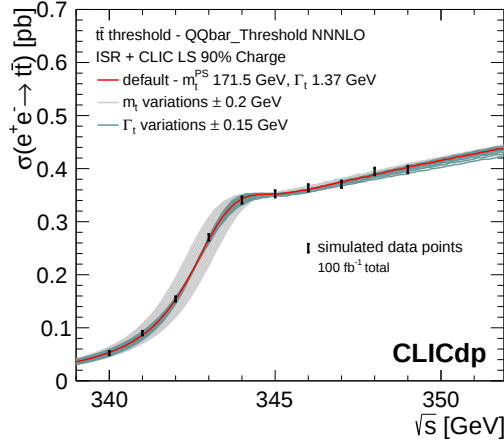


Figure 1.1: Top quark threshold scan at CLIC with a total luminosity of 100 fb^{-1} [8].

Production of top quark pairs is possible already at the first CLIC stage. Scanning the threshold for top-quark pair production, $e^+e^- \rightarrow t\bar{t}$, is assumed to be the most precise method for top-quark mass determination and least sensitive to theoretical uncertainties. Precise determination of the top-quark mass is crucial for the validation of the SM predictions. The higher-energy stages of CLIC will enlarge data-sets from the first stage with additional samples of $t\bar{t}$ pairs produced above the threshold, increasing the possibility to detect phenomena beyond the Standard Model.

1.3. Motivation

The threshold scan is expected to be the most precise way to measure top-quark mass. Scan scenario with ten energy points separated by 1 GeV, with 10 fb^{-1} of data collected at each energy is considered as a baseline scenario for CLIC, as shown in Fig. 1.1. Recent study [8] showed that expected statistical uncertainty on the mass is around 21 MeV and on the top-quark width - 51 MeV. However the analysis took only the two model parameters, top-quark mass and width, into account. Yet, threshold cross-section shape depends also on other parameters, as the top Yukawa coupling and the strong coupling constant.

The main goal of the presented study was to quantify the influence of additional model parameters, and related uncertainties, on the statistical precision of top-quark mass determination at CLIC. Also, as the baseline running scenario seems to be conservative, the additional objective was to investigate to what extent the optimised running scenario can result in reduction of the statistical uncertainties.

This work was carried out in the framework of the CLIC detector and physics (CLICdp) collaboration. All presented results, unless indicated otherwise, were obtained by the author of the thesis. Results included in this thesis supersede results presented in [9, 10].

Chapter 2

The Fit

Described in this chapter is the procedure developed to model the top-quark pair production cross section measurements in a threshold scan at CLIC. Two kinds of input data are required in this procedure: theoretical predictions given in terms of the cross section templates and the expected luminosity spectra for CLIC.

2.1. Input data

2.1.1. Cross-section templates

Considered cross section templates were generated using `QQbar_threshold` software [11, 12, 13], assuming different values of top quark parameters, as a part of an earlier study [14]. Six model parameters described below have to be set as an input to `QQbar_threshold`. Nominal cross section template was first generated for nominal values of all parameters. Parameters considered in the study were then varied in small steps, corresponding to the expected experimental sensitivities, from their nominal values, resulting in additional cross section templates. Following values of parameters were used:

- top-quark mass, m_t :
nominal value of 171.5 GeV, varied from 171.4 to 171.6 with step of 25 MeV
- strong coupling constant α_s :
nominal value 0.1185, varied from 0.1145 to 0.1225, step 0.001
- overall renormalisation scale, μ :
nominal value 80 GeV, values of 60 and 100 GeV considered for systematic check
- energy scale for nonresonant contributions, μ_w :
nominal value of 350 GeV used for all templates (fixed)
- top-quark width, Γ_t :
nominal value 1.37 GeV, varied from 1.17 to 1.57 GeV, step 0.05 GeV

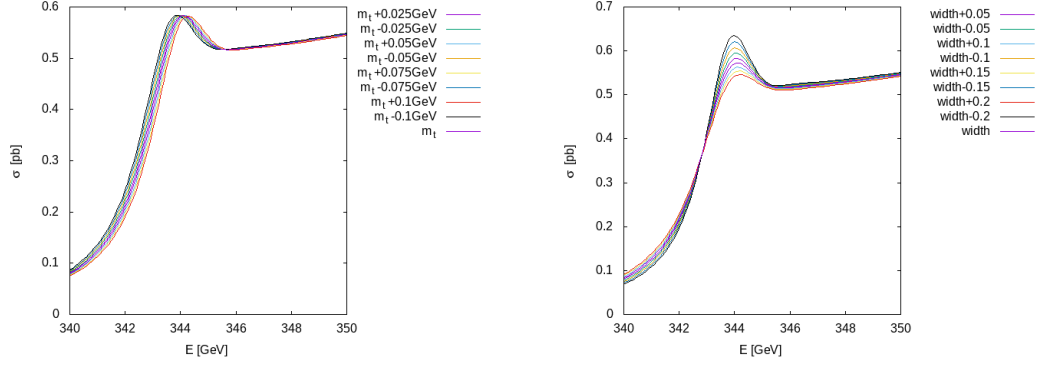


Figure 2.1: Examples of cross-section templates generated using QQbar_threshold software for different values of top-quark mass (left) and width (right) [14].

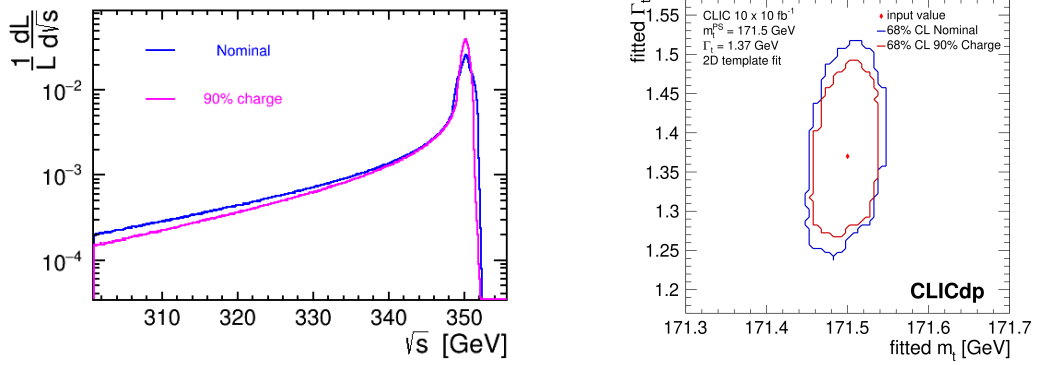


Figure 2.2: Comparison between luminosity spectra with nominal and reduced charge. On the right side contours of statistical uncertainties from CLIC study [8].

- top-quark Yukawa coupling (relative to SM prediction), y_t :
nominal value 1, varied from 0.6 to 1.4, step 0.1

Total of 274 templates were generated for different variations of model parameters. Each of those templates consists of 300 points representing cross-section for energy in range from 330 to 360 GeV. Examples of cross-section templates are shown in Fig. 2.1. Initial state radiation was included in the template cross section calculations.

2.1.2. Luminosity spectra

In order to take into account the experiment environment, theoretical cross section templates, $\sigma^{th}(\sqrt{s})$, as generated with the QQbar_threshold, were convoluted with the expected CLIC luminosity spectra, $\frac{1}{L} \frac{dL}{d\sqrt{s}}$, to obtain final cross-section templates used in the analysis. Two luminosity spectra were considered for the threshold scan: the nominal spectra expected for the first stage of CLIC, and the spectra with reduced bunch

charge (90% charge), which allows to obtain narrower energy spectra at the cost of reduced instantaneous luminosity. A dedicated study [8] showed that the reduced charge option results in smaller statistical uncertainties of the threshold fit, see Fig. 2.2, and this spectra was therefor used for the presented study.

2.2. Reference scenario

The first stage of CLIC will allow an energy of 380 GeV to be reached, giving access to most Higgs boson and top quark measurements. With 1 ab^{-1} of total integrated luminosity at this stage, a dedicated scan of 100 fb^{-1} is planned at the $t\bar{t}$ threshold. As already mentioned above, the baseline scenario of the threshold scan assumes running at 10 equidistant energy points taking 10 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 [15]. Reconstruction efficiency is assumed to be independent on the collision energy (in the considered energy range) and on the model parameters.

2.3. Method

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. Unless specified otherwise, nominal parameter values (and nominal template) were used in all calculations.

Selected template is used to generate a set of data corresponding to the expected scan results at CLIC, 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. Example of the generated pseudo-data set is shown in Fig. 2.3.

Parameter fit procedure is then applied to the generated pseudo-data set. For each considered cross section template the χ^2 value is calculated from the formula

$$\chi^2(\vec{p}, \alpha) = \sum_i \left(\frac{m_i - \alpha \cdot \mu_i(\vec{p})}{\sigma_i} \right)^2 + \left(\frac{\alpha - 1}{\Delta} \right)^2 + \sum_j \left(\frac{p_j - \tilde{p}_j}{\sigma_{p_j}} \right)^2 \quad (2.1)$$

where m_i and σ_i are the measured cross section values with their statistical uncertainties (pseudo-data set), $\mu_i(\vec{p})$ denotes the template cross section values for corresponding collision energies and given parameter set $\vec{p} = (m_t, \Gamma_t, \alpha_s, y_t^2)$, and α is the template normalisation factor. The second term in the χ^2 formula corresponds to the normalisation constraint, where different values of the relative normalisation uncertainty Δ are considered. The normalisation factor α can be evaluated analytically separately for each

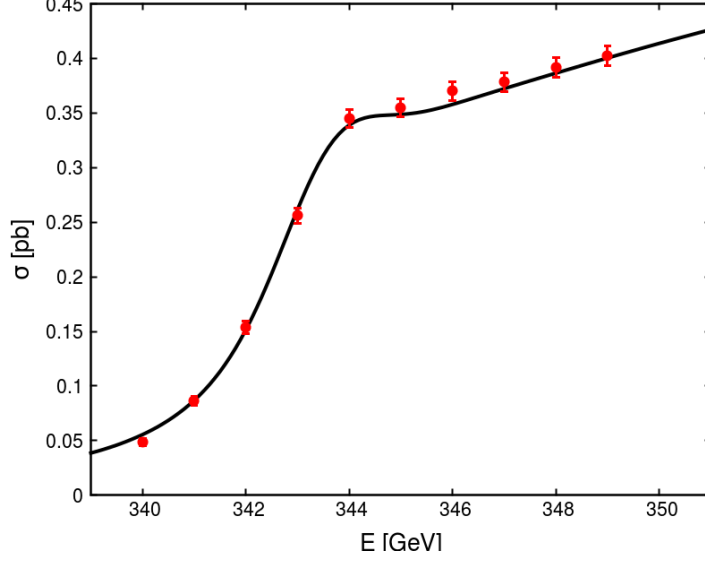


Figure 2.3: Reference scenario for the top-quark threshold scan. The error bars on the simulated data points show the expected statistical uncertainties of the cross section measurements assuming total integrated luminosity of 10 fb^{-1} per measurement and event selection efficiency of 70.2%.

template by solving the minimisation condition $\frac{\partial \chi^2}{\partial \alpha} = 0$. The third term represents possible constraints on the model parameters p_j resulting from the earlier, independent measurements with uncertainty σ_{p_j} . In this study, external constraints are only considered for α_s and y_t .

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 components of $\vec{p}$

$$\chi_\alpha^2(\vec{p}) = \sum_{i=0}^N \sum_{j=0}^N A_{i,j} p_i p_j \quad (2.2)$$

where χ_α^2 is the χ^2 value minimised w.r.t. normalisation factor α , N is the number of considered model parameters and i, j are parameter indexes ($i, j = 1 \dots N$). $A_{i,j}$ is the symmetric matrix of coefficients of N-dimensional parabola. To simplify the formula, $p_0 \equiv 1$ was defined (the linear part is thus given by $2A_{0,j}p_j$ and the constant part is $A_{0,0}$). The values of parameters $A_{0,0}, \dots, A_{n,n}$ are found by solving a set of linear equations, where χ_α^2 values calculated for different parameter sets $\vec{p}$ are used as input. The fitted values of $A_{0,0}, \dots, A_{n,n}$ are then used to extract the parameter values minimising the $\chi_\alpha^2(\vec{p})$, which constitute the fit result. Statistical uncertainties of the fitted parameter values, $\vec{\sigma} = (\sigma_{m_t}, \sigma_{\Gamma_t}, \sigma_{\alpha_s}, \sigma_{y_t^2})$, and their correlation coefficients, $r_{i,j}$, are extracted from the fit covariance matrix V , calculated by numerical inversion of the χ^2 second derivative

matrix ($i, j = 1 \dots N$):

$$V = \sigma^T \begin{pmatrix} 1 & \dots & r_{N,1} \\ \vdots & \ddots & \vdots \\ r_{1,N} & \dots & 1 \end{pmatrix} \sigma = \left(\frac{1}{2} \frac{\partial^2 \chi_\alpha^2}{\partial p_i \partial p_j} \right)^{-1} = \begin{pmatrix} A_{1,1} & \dots & A_{1,N} \\ \vdots & \ddots & \vdots \\ A_{N,1} & \dots & A_{N,N} \end{pmatrix}^{-1} \quad (2.3)$$

2.4. Validation

To validate the parameter fitting procedure and the error calculation algorithm 4000 pseudo-data sets were generated for the reference scan scenario (see Fig. 2.3) and nominal parameter values. The fitting procedure was applied taking only mass and width into account as free model parameters. Fitted values of mass and width were then used to fill a 2D histogram shown in Fig. 2.4. The distribution of the fit results is well described by the 2-D Gaussian profile; results of the profile fit to the data are indicated by the one, two and five sigma contours indicated in the plot.

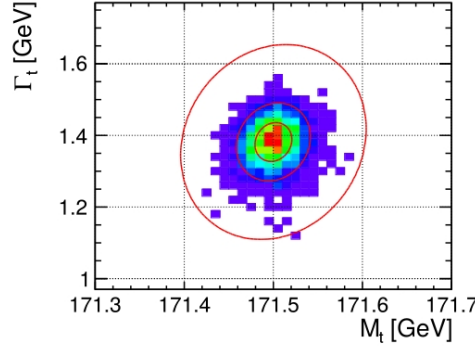


Figure 2.4: Results of the two-parameter fits to the top threshold scan, for sets of pseudo-data generated for nominal parameter values, $\tilde{m}_t = 171.5$ GeV and $\tilde{\Gamma}_t = 1.37$ GeV. One, two and five sigma contours represent the 2-D Gaussian distribution fitted to the presented results.

For the considered 2-D fit configuration (top-quark mass vs top-quark width), fits to the marginalized parameter distributions result in $\sigma_{m_t} = 21$ MeV and $\sigma_{\Gamma_t} = 54$ MeV. These uncertainties are in a very good agreement with results of the previous study [8], see Fig. 2.2 (right).

Shown in Fig. 2.5 are the distributions of the top-quark mass uncertainty and the top-quark width uncertainty, resulting from the two-parameter fits presented in Fig. 2.4.

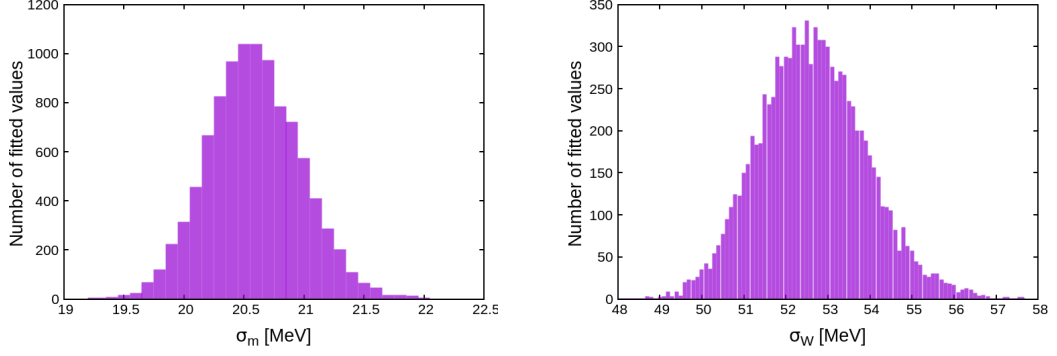


Figure 2.5: Distributions of the top-quark mass uncertainty (left) and the top-quark width uncertainty (right), from the two-parameter fit to a set of pseudo-data generated from the nominal template.

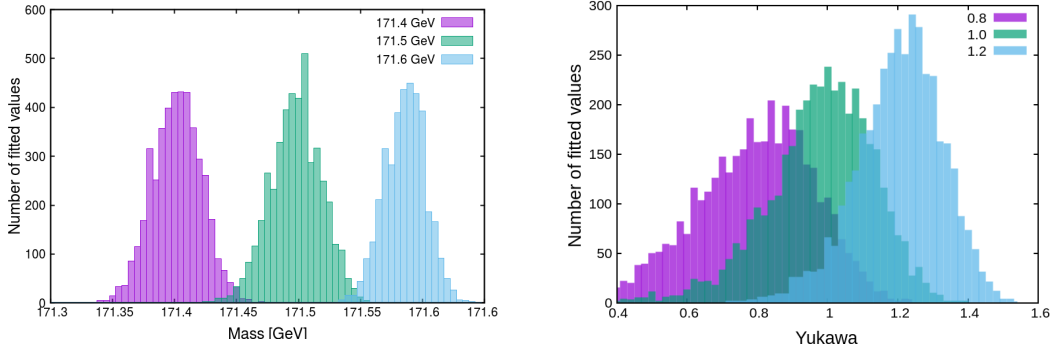


Figure 2.6: Histograms of fitted values for the top-quark mass (left) and top Yukawa coupling (right). Different histograms corresponds to the pseudo-data sets generated using cross-section templates with different values of the corresponding model parameter, as indicated in the plot.

These uncertainties are calculated from the parameter covariance matrix, as described by Eq. 2.3. The uncertainties estimated from the covariance matrix of the fit are in very good agreement with those obtained from the distributions of parameter fit results. This confirms the validity of the parameter uncertainty evaluation method.

To further confirm validity of the fit approach the fit procedure was repeated for sets of pseudo-data generated with non-standard model templates. Shown in Fig 2.6 are the distributions of the fitted top-quark mass from the two-parameter fit (2D) and the fitted top Yukawa coupling parameter from the four-parameter fit (4D), for the pseudo-data sets generated using cross-section templates with different values of these parameters. For both the top-quark mass and Yukawa coupling variations, fit results follow very closely the input parameter values.

Chapter 3

Baseline threshold scan results

3.1. Configuration

As mentioned above, studies presented so far [8, 15, 16] considered at most two-parameter fits to the threshold scan data. Presented approach, thanks to its simple, semi-analytical form, allows to perform fits with more free model parameters. Moreover, it is possible 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 on the data normalisation¹, Δ (see Eq. 2.1). The effect is clearly visible in Fig. 3.1 showing the expected statistical precision of the top-quark mass as a function of the assumed normalisation uncertainty. 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). Please note that the normalisation scaling factor α is always considered as an additional fit parameter (refer Eq. 2.1). For results shown in Fig. 3.1, no constraints are imposed on other model parameters.

¹This uncertainty also includes the possible overall normalisation uncertainty of the theoretical prediction.

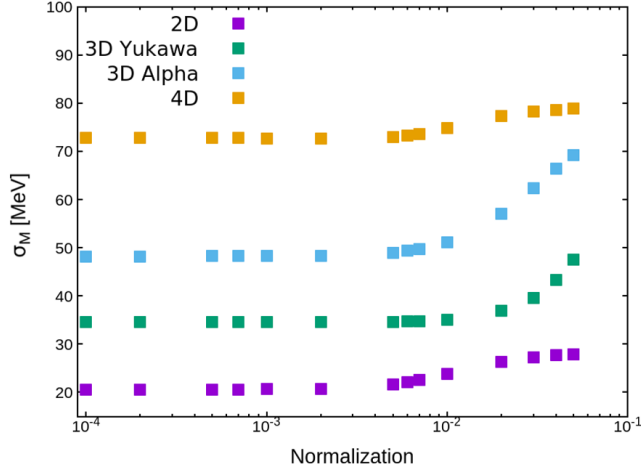


Figure 3.1: Statistical uncertainty on the top-quark mass as a function of the normalisation uncertainty. Four fit configurations are considered, see text for details.

Presented results demonstrate that, to allow for the most precise top-quark mass determination, the overall normalisation of the data (and theory expectations) has to be known on sub-percent level. Also visible in Fig. 3.1 is the effect of adding more model parameters to the fit. While the statistical uncertainty on the top-quark mass around 20 MeV can be achieved when the 2D fit procedure is used (i.e. mass and width fit only), the uncertainty increases substantially when other parameters (strong coupling or Yukawa coupling) are added to the fit. However, the strong coupling constant is not a "free" parameter, and it has to be taken into account that it can be measured to high accuracy in independent experiments.[17] Also the top Yukawa coupling can be constrained from other studies at CLIC or by other experiments [18].

3.2. Constrains

As mentioned above, assuming that all parameters in the fit are "free" is unrealistic, as model parameters will be measured by many experiments preceding CLIC, including top quark parameters. Constraining the fit algorithm by assuming parameter value is known with some uncertainty before the measurement makes the analysis closer to the situation expected in an actual experiment. It also mitigates statistical uncertainties. This is shown in Fig. 3.2, where the top-quark mass uncertainty from the 3D fit (with mass, width and strong coupling as free parameters, as well as normalisation) is plotted as a function of the assumed strong coupling and normalisation uncertainties. To be able to extract the top-quark mass with 25 MeV precision, the strong coupling constant has to be known to better than 0.0005 and the uncertainty of 0.001 (current world average [19]) would only allow to reach the precision of the order of 30 MeV.

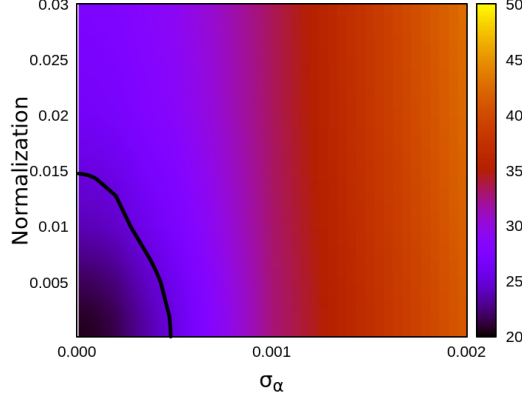


Figure 3.2: Expected statistical uncertainty on the top-quark mass as a function of the uncertainty of strong coupling constant and normalisation. Results from the fit of mass, width and the strong coupling (3D). Colour maps are obtained using a linear interpolation algorithm. Black line corresponds to the uncertainty of 25 MeV.

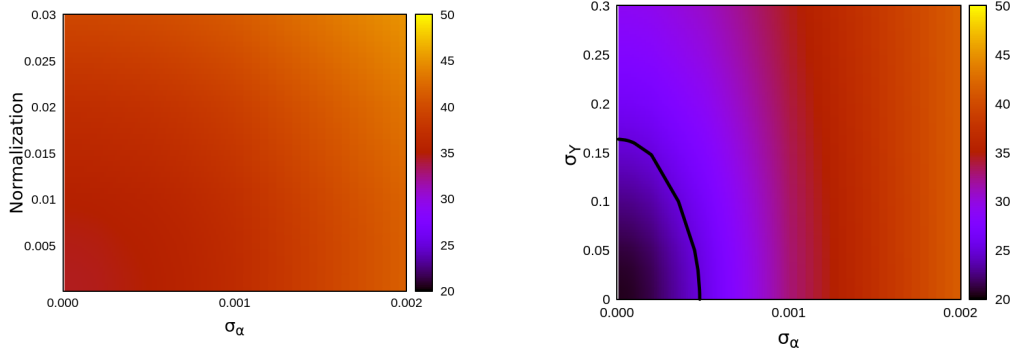


Figure 3.3: Expected statistical uncertainty on the top-quark mass from the fit involving all considered model parameters (4D). Left: as a function of the strong coupling constant and normalisation uncertainties, assuming no constraints on the Yukawa coupling. Right: as a function of the strong coupling constant and Yukawa coupling uncertainties assuming normalisation uncertainty, $\Delta = 10^{-3}$. Black line represents uncertainty of 25 MeV.

The conclusions change significantly, if one includes Yukawa coupling as an additional parameter in the fit. As shown in Fig. 3.3 (left), if no constraints are imposed on the 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 ‘3D Yukawa’ results in Fig. 3.1). The estimated top-quark mass uncertainty decreases significantly, if external constraints on the Yukawa coupling are imposed, as shown in Fig. 3.3 (right), for normalisation uncertainty $\Delta = 10^{-3}$. To be able to extract

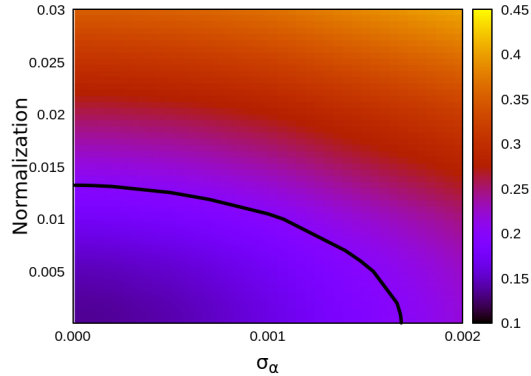


Figure 3.4: Expected statistical uncertainty on the top Yukawa coupling from the fit involving all considered model parameters (4D), as a function of the strong coupling constant and normalisation uncertainties. The black line indicates the parameter range where 5σ significance can be expected.

the top-quark mass with precision of the order of 25 MeV, top Yukawa coupling has to be constrained from other measurement to about 5% and the strong coupling constant has to be known to better than 0.0005.

As the top-quark pair-production cross section depends on the top Yukawa coupling, the threshold scan data can also be used to constrain its value. The statistical precision of the Yukawa coupling determination from the 4D fit was investigated as a function of the assumed normalisation and strong coupling uncertainties. Results presented in Fig. 3.4 indicate that contribution from the Yukawa coupling can be observed with high significance (above 5σ , i.e. with statistical precision below 0.2). Assuming the normalisation is known at per-mille level and the strong coupling is independently measured to better than 0.0003, statistical precision on the Yukawa coupling of the order of 15% should be feasible.

3.3. Systematic effects

The systematic uncertainties of the threshold cross section measurements are likely to limit the ultimate precision of the top-quark mass determination. Various sources of uncertainties have been investigated in [8] and the combined systematic uncertainty on the top-quark mass is expected to be in the range 30 MeV to 50 MeV, which however includes uncertainty related to the value of the strong coupling constant (which is included in the fit in our framework). Here, the size of systematic effects is investigated in the top mass and Yukawa coupling determination from the proposed threshold scan fit procedure.

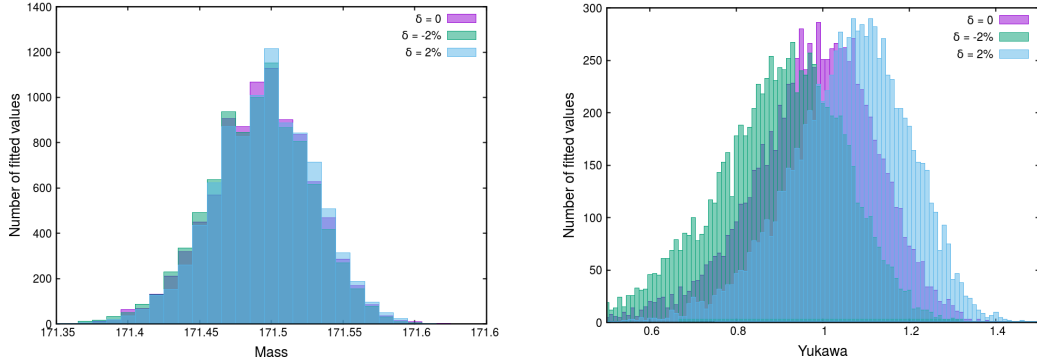


Figure 3.5: Distributions of the top-quark mass (left) and top Yukawa coupling (right) values resulting from the fits to the pseudo-data sets generated with the nominal background level as well as for the $\pm 2\%$ variations in the background contribution, as indicated in the plots.

3.3.1. Background uncertainty

Standard pseudo-data generation and scan fit procedures assume background contribution corresponding to 73 fb [15]. Figure 3.5 presents histograms of the fitted top quark mass and top Yukawa coupling values from the modified 4-D fit procedure, when the background level was changed by $\pm 2\%$ in the pseudo-data generation (and not changed in the data analysis procedure resulting in background over- or underestimate). Systematic uncertainty resulting from the background normalisation is negligible for the top-quark mass determination, but it becomes significant for the Yukawa coupling determination. Assumed 2% background variation results in about 10% shift in the extracted value of the Yukawa coupling.

3.3.2. Renormalisation scale variation

Figure 3.6 shows distributions of the fitted top-quark mass and Yukawa coupling values from 4-D procedure, when assuming different values of the renormalisation scale μ ($\mu = 60, 80$ and 120 GeV) in the pseudo-data generation (nominal value of μ was still used in the fit procedure to model the possible shift in the theoretical predictions). The corresponding systematic uncertainty for mass and Yukawa coupling determination turns out to be negligible. Assumed default value of $\mu = 80$ GeV corresponds to minimal cross section value on the threshold, which reduces sensitivity of the fit procedure to small changes of this parameter.

3.4. Initial mass uncertainty

The nominal pseudo-experiment procedure starts from selecting the 'true' model parameters, including the true value of the top-quark mass. It will be known with limited precision in the actual experiment, so the position of the scan energy points w.r.t. the

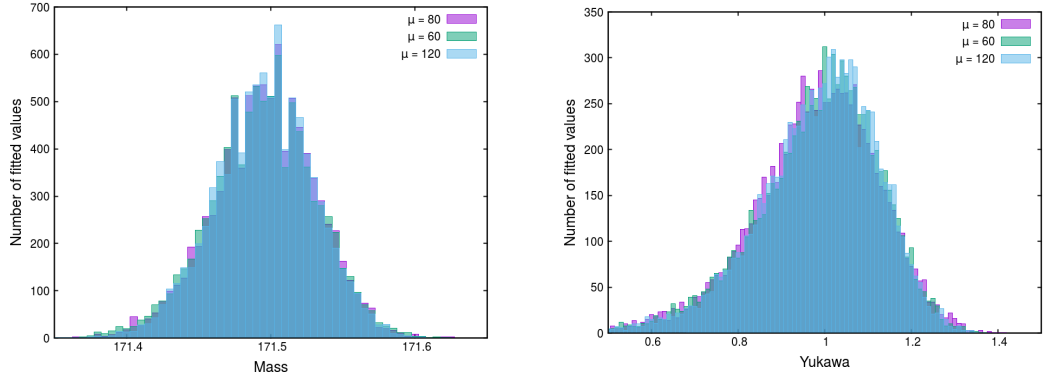


Figure 3.6: Distributions of the top-quark mass (left) and top Yukawa coupling (right) values resulting from the fits to the pseudo-data sets generated for the nominal value of the renormalisation scale, $\mu = 80$ GeV as well as for the ± 20 GeV scale variations, as indicated in the plots.

true mass will not be known. To verify if this affects the expected scan results, the fit procedure was repeated multiple times assuming top-quark mass is known with given uncertainty. For each set of pseudo-experimental data true mass value was drawn from normal distribution with given spread, σ . After extracting mass value from the fit, the difference between the nominal mass value (171.5 GeV) and the assumed true mass value for particular data-set was subtracted. In this way, the initial mass shift is corrected when investigating the mass fit precision. By creating large sets of pseudo-data with different initial mass spread, it is possible study how the mass uncertainty influences results of our algorithm.

Figure 3.7 presents histograms of the fitted top-quark mass values from 4-D procedure assuming different initial top-quark mass spread: $\sigma = 0$, 200 and 1000 MeV. The

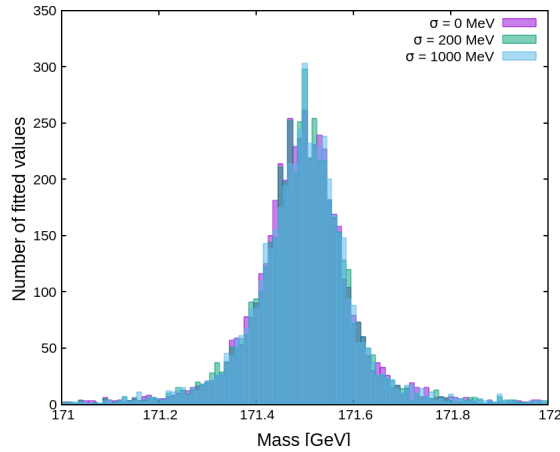


Figure 3.7: Histograms of fitted values for the top-quark mass, assuming drawing true mass value from Gaussian distribution of different width.

lack of sensitivity to the assumed initial uncertainty of the top-quark mass seems counter intuitive, but this is the feature of the reference scan scenario, with equidistant energy points. Shifting the assumed true mass by ± 1 GeV is equivalent to changing one measurement point only (at lowest or highest energy). Thanks to wide energy range and equal separation between points the loss in precision is negligible even in the case of significant change in the initial top-quark mass value.

Chapter 4

Optimisation

4.1. Multi-objective optimisation

When looking for the best scenario of the top-quark threshold scan at CLIC (or at any other future e^+e^- collider) one needs to consider different aspects of the measurement. The top quark mass is not the only parameter that needs to be extracted (with the best possible statistical uncertainty). There are other model parameters, measurement of which need to be optimised at the same time. Multi-objective optimisation problems are likely to be complex and must be approached differently, depending on the specific case. When looking for the best optimisation approach it is necessary to take into account, for example, how easy it is to find solution to the considered problem and how many solutions are expected. It could be that there are so many possible solutions that all of them cannot be analyzed.

The easiest case is when one can propose a set of equations describing the problem, defining the variables to be optimised. These equations can be then solved analytical or numerically, to find the optimum. Yet, it is rarely the case when the problem can be reduced to such a set of equations.

In most real-world problems, heuristic procedures are being used to find optimal solutions. They include Genetic algorithms, that are inspired by biological evolution processes, such as reproduction, mutation, recombination, and selection [20]. In a Genetic algorithm, a set of proposed solutions to an optimization problem, called **Individuals**, is evolved towards better solutions. Each Individual has a defined set of properties, called **genotype**, which can be mutated and altered, and set of measurable traits, called **phenotype**, that are determined by the genotype. Phenotype consists of traits that are used to evaluate their performance and choose the best Individuals to the next generation. During consecutive iterations of the algorithm population evolves towards better solutions. Ultimately, after a finite number of iterations, population should converge to the optimal solution.

4.2. Non dominated sorting genetic algorithm II

From many available Genetic algorithms it was decided to use Non dominated sorting genetic algorithm II, proposed by Kalyanmoy Deb in 2002 [21]. It was chosen for its high efficiency and elasticity. Each iteration of the algorithm is divided into three steps:

- Creating Children and adding them into population
- Non dominated sorting of the population (with Jensen algorithm [22])
- Choosing the best Individuals for the next generation

Each one of those steps is highly customizable, so it is possible to adjust the implementation in order to achieve best results. Thanks to use of efficient non dominated sorting algorithm it was possible to lower time complexity from original $O(MN^2)$ [21] to $O(MN \log^{M-1} N)$ [22], where M is number of objectives and N is the size of the population.

4.3. Implementation

4.3.1. Creating Individuals and First Generation

First it was required to translate our measurement procedure into Genetic algorithm language. One measurement scenario was assumed as an Individual, which genotype is represented by a scan sequence, set of centre-of-mass energy points (scan points make a multiset, as they can repeat, but their order is irrelevant). In this way each scan point can be considered a chromosome. Constant total integrated luminosity of 100 fb^{-1} was assumed and its equal sharing among all scan points. This might seem restrictive, but scan points with higher luminosity are actually allowed by allowing energy points to repeat in the scan sequence. This way it is also possible to optimise luminosity distribution. The measurement procedure described in previous chapters translates scan sequence (genotype) into measured top quark parameters with their uncertainties (phenotype). Yet, this process is non-deterministic, as statistical fluctuations were drawn from Poisson distribution separately for each generated pseudo-data set. To take statistical fluctuations into account pseudo-experiment procedure is always repeated three times and the worst result for each objective is taken.¹ The First Generation is seeded by creating 2000 identical Individuals using baseline scenario. Results presented in Chapter 3 show that it provides good fit results for all parameters.

4.3.2. Pairing and breeding Individuals

There are many proposed strategies to find the best pair of parents, but they are computationally costly. In order to ensure diversity in population, each Individual has three

¹The number of pseudo-experiments run for each Individual is limited by the processing time. However, already with three experiments the possible bias of the optimisation due to statistical fluctuations is basically excluded.

children, one with each of three other, randomly chosen Individuals. This method was used because of computational efficiency and for maximizing diversity in population. After obtaining two parent genotypes, it is necessary to ensure they are of the same length before making a new one (a child). It was done by inserting empty chromosomes into a shorter one, to match their sizes. While iterating over parental genotypes, parent chromosome to insert into child's genotype is chosen randomly. To allow changing genotype length, 5% chance to drop any of the chromosomes was added. To avoid systematic loss of chromosomes, additional random chromosome was added at the end of the genotype with a 10% probability. It was always required that the length of the resulting genotype is not shorter than 2, as shorter ones can not be used for the phenotype evaluation (threshold fit procedure). When copying parent chromosome, it is also shifted by a random mutation in a given range. At the beginning of the evolution, the mutation range is ± 0.5 GeV, but it shrinks geometrically in each iteration by factor of 0.9. In this way, it was possible to quickly mutate the initial baseline scenario without losing the ability to converge around the best solution after a larger number of iterations. After creating all children in the generation their phenotypes were computed and they were inserted into the population.

4.3.3. Performance evaluation and selecting the next Generation

When considering more than one objective in the scan optimization, one cannot simply compare (and sort) Individuals by their phenotype (parameter uncertainties from the fit). Instead, desired configuration is Pareto optimality, which is defined as a configuration that cannot be modified so as to improve any objective without making at least one other objective worsen [23]. In order to find optimal solution Individuals must be compared with each other. To find which one is better, their Pareto dominance must be checked, which is the situation when one Individual is better in at least one objective, and not worse in all other [23]. The condition for Individual x dominating Individual y , $x \succ y$, can be described by the formula:

$$x \succ y \iff \forall_i : f_i(x) \geq f_i(y) \wedge \exists_j : f_j(x) > f_j(y) \quad (4.1)$$

where $f_i(x)$ denotes objective i calculated for Individual x . When neither of them dominates the other, then the two Individuals are Pareto optimal. Individuals were grouped based on this criteria and such groups are called Pareto Frontiers [23]. They can be described by the formula:

$$P(Y) = \{y' \in Y : \{y'' \in Y : y'' \succ y'\} = \emptyset\} \quad (4.2)$$

Individuals were chosen for the next generation by sorting Pareto frontiers. It is based on criteria that a solution in $Front_{k+1}$ must be dominated by at least one solution in $Front_k$ and may or may not dominate solutions in $Front_{k+2}$ [24]. To efficiently perform those calculations Jensen algorithm as used [22]. After sorting Pareto frontiers the next generations consists of 2000 Individuals from frontiers with lowest ranks.

4.4. Results

4.4.1. Single objective

The performance of the optimisation procedure based on the Genetic algorithm is first studied for the measurement of one model parameter only: top-quark mass, top-quark width or top Yukawa coupling. The objective is to minimize the statistical uncertainty resulting from the fit of the given parameter in a fit procedure with four free model parameters (4D). Population size is set to 2000 and number of generations to 30. All results presented in this section were calculated assuming normalisation uncertainty of 1% and strong coupling constant uncertainty of 0.001. Results of the optimization procedure for the three considered model parameters are summarised in Figs. 4.1, 4.2 and 4.3.

When optimizing scan procedure for the top-quark mass measurement, it is possible to reduce the expected statistical uncertainty on the top-quark mass by about 35%, from about 37 MeV expected for the ten-point baseline scan scenario to 24 MeV (see left plot in Fig. 4.1). The optimised scan is focused in three energy regions, with most of the luminosity taken in the middle of the threshold, where the cross section slope is highest and at the plateau just above the threshold (see right plot in Fig. 4.1). At the same time precision of the width determination decreases by up to 25% for such a running scenario.

When optimizing for the top-quark width precision, see Fig. 4.2, even larger relative improvement can be obtained. The statistical uncertainty on the width is reduced by about 40%, from about 66 MeV for the baseline scenario to around 40 MeV for the optimal scenarios. The three energy regions selected for the optimal scenarios are basically the same as for the mass measurement optimisation. However, when optimizing for the width measurement, much larger fraction of the luminosity has to be taken just below the threshold, at about 340 GeV. Because of that, the precision of the top-quark mass determination decreases by about 30%. One can also notice that the mass fit becomes much more sensitive to scan details and statistical fluctuations.

In the case of the top Yukawa coupling measurement, see Fig. 4.3, there is very little room for improvement and the statistical uncertainty can be reduced by about 10% only. As shown in the measurement points distribution, significant fraction of the luminosity has to be taken in a wide region above the threshold. As the reference scenario has half of its points above the threshold (see Fig. 2.3), where the cross section is most sensitive to the top Yukawa coupling, this explains also why only limited improvement can be obtained.

Looking at the measurement points distributions in Figs. 4.1, 4.2 and 4.3 one can clearly see that four energy regions are relevant in the scan optimisation: energies just below the threshold (around 340 GeV), in the middle of the threshold (around 343 GeV), on the plateau just above the threshold (around 345 GeV) and further above the threshold (around 348-350 GeV). However, different regions are sensitive to different parameters. For the mass measurements the regions in the middle and just above the threshold are most relevant, for the width measurement additional measurement below the threshold is crucial, whereas the Yukawa coupling determination depends on the amount of luminosity which can be devoted to running few GeV above the threshold. This comparison

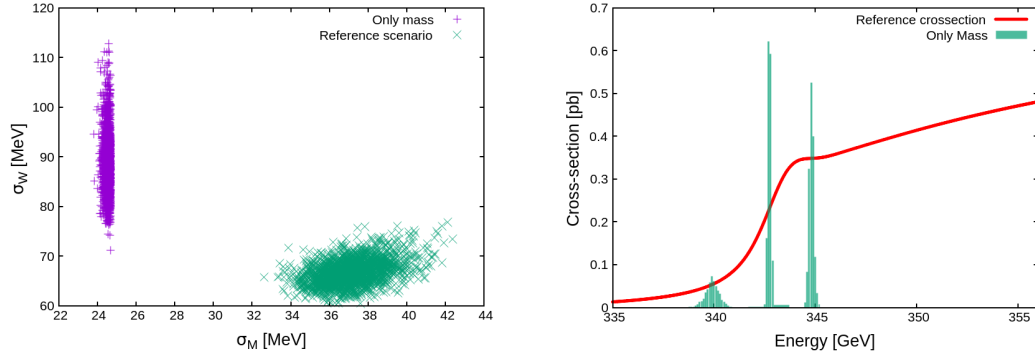


Figure 4.1: Left: mass and width uncertainty distribution in the first (green) and the last (blue) generation for scan optimized for mass determination precision only. Right: distribution of the measurement points from last generation (arbitrary scale) compared with the reference cross section template.

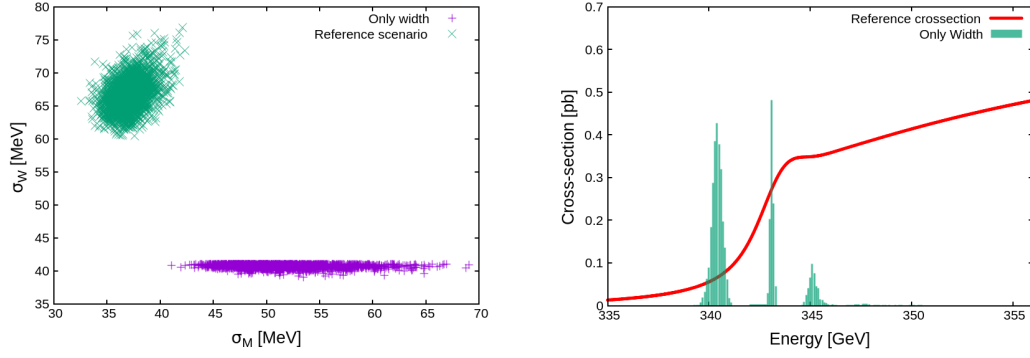


Figure 4.2: As in Fig. 4.1, but for scan optimized for width determination precision only.

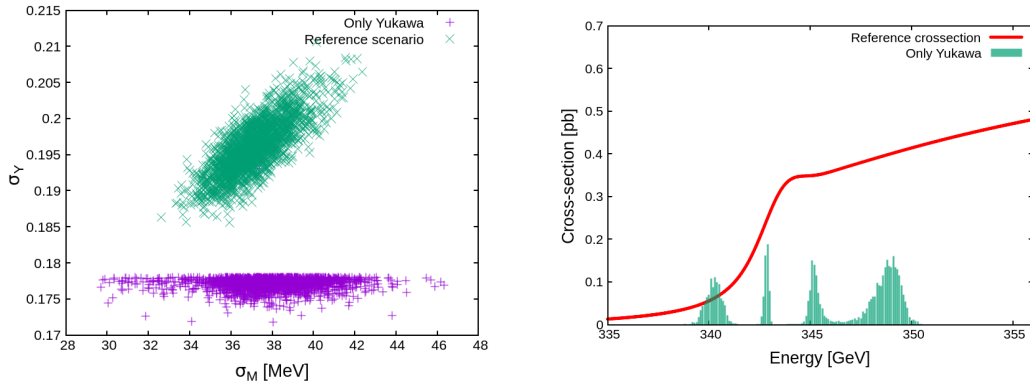


Figure 4.3: As in Fig. 4.1, but for scan optimized for Yukawa coupling determination precision only.

shows that the same choice of energy points can be optimal (or close to optimal) for all considered parameters. However, sharing of the luminosity between four energy regions depends on the optimization goal.

4.4.2. Multiple objectives

When considering multiple objectives, it was decided to focus on pairs of top-quark parameters, in order to study how they influence each other in the optimization procedure.

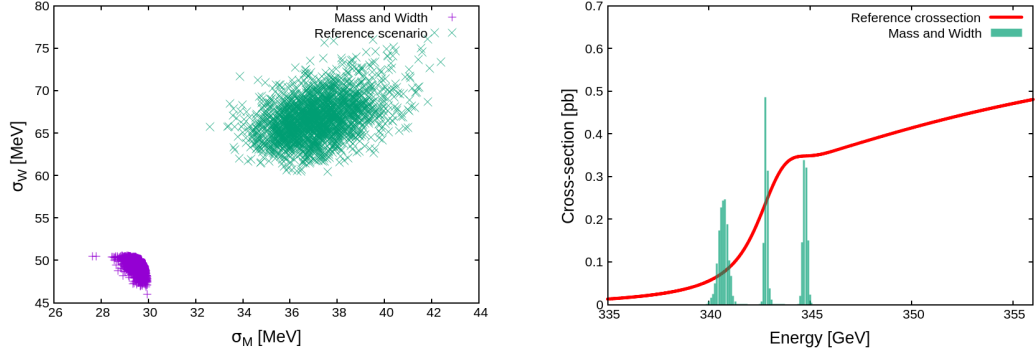


Figure 4.4: Left: mass and width uncertainty distribution in the first (green) and the last (blue) generation for scan optimized for both mass and width determination precision. Right: distribution of the measurement points from the last generation (arbitrary scale) compared with the reference cross section template.

Shown in Fig. 4.4 are the results of mass and width measurement optimization. For both parameters, improvement of about 22% can be achieved: mass uncertainty is reduced by about 8 MeV, from 37 MeV to 29 MeV, while the width uncertainty is reduced by about 16 MeV, from 66 MeV to 50 MeV. The uncertainties increase, when compared to single objective optimisation, but only by 10-15% (about 5 MeV for mass and 10 MeV for width uncertainty). As expected, the optimized measurement point distribution shows clear similarities with results obtained for one parameter optimisation (see Figs. 4.1 and 4.2).

When optimising the scan procedure for simultaneous top-quark mass and top Yukawa coupling measurement, see Fig. 4.5, results are again very similar to those obtained for one objective optimisation. Improvement of about 25% can be expected for the mass measurement, from 37 MeV to 28 MeV, but only about 7% improvement in the Yukawa coupling uncertainty. Interesting conclusions can be drawn from the measurement point distribution. There are two main peaks in the middle and just above the threshold, similar to the case of mass only optimisation (see Fig. 4.1), as well as region further above the threshold, corresponding again to the Yukawa only optimisation (see Fig. 4.3). Yet, there is also a peak below the threshold, in a region most sensitive to the top-quark width. This shows that for precise determination of the Yukawa coupling and top-quark mass at least decent precision in the top-quark width determination is required.

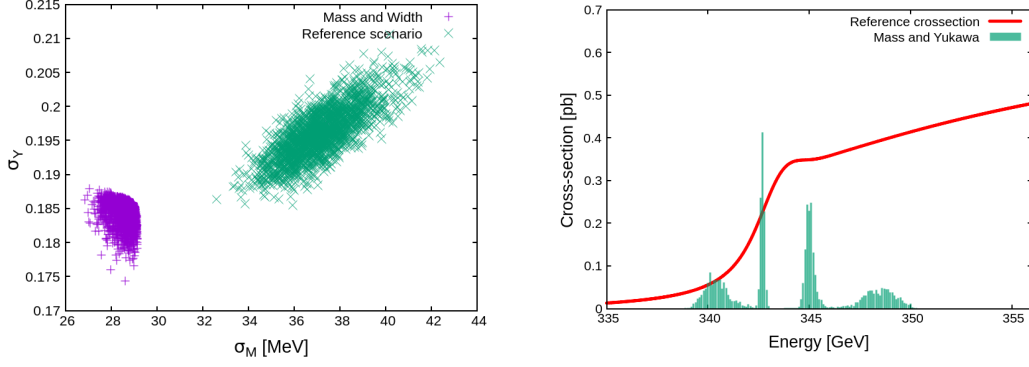


Figure 4.5: As in Fig. 4.4 but for scan optimized for mass and Yukawa coupling determination precision.

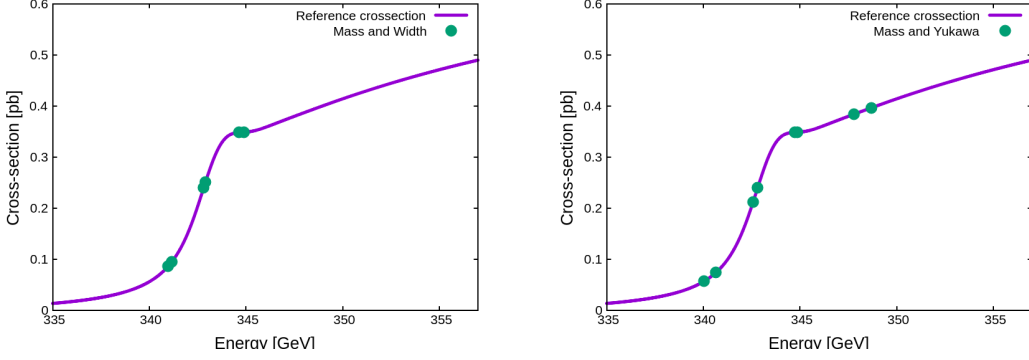


Figure 4.6: Scan energy points for the “best scenarios” taken from the last generation compared with the reference cross section template: (left) 6 point scenario optimised for mass and width determination precision and (right) 8 point scenario optimised for mass and Yukawa coupling determination precision.

For detailed comparison of the optimised scenario with the baseline threshold scan configuration, one scenario was selected from the last generation for each of the aforementioned multi objective optimisations. These “best scenarios” were compared with the reference scenario based on results coming from 20 000 pseudo-experiments. As before, normalisation uncertainty is 1%, strong coupling uncertainty is 0.001 and, to make comparison even more realistic, initial top quark mass uncertainty of 200 MeV is assumed. Two selected scenarios are presented in Fig. 4.6: six-point scenario optimised for mass and width measurement and eight-point one, optimised for mass and Yukawa coupling. In both scenarios points group in pairs, in places where peaks were observed in measurement point distributions. This indicates that equal luminosity distribution is preferred.

Results of the comparison for the six-point scenario are presented in Fig. 4.7. Shown are the distributions of the fit uncertainties, based on the sample of 20 000 pseudo-experiments. For the optimised scenario most probable value of expected mass uncer-

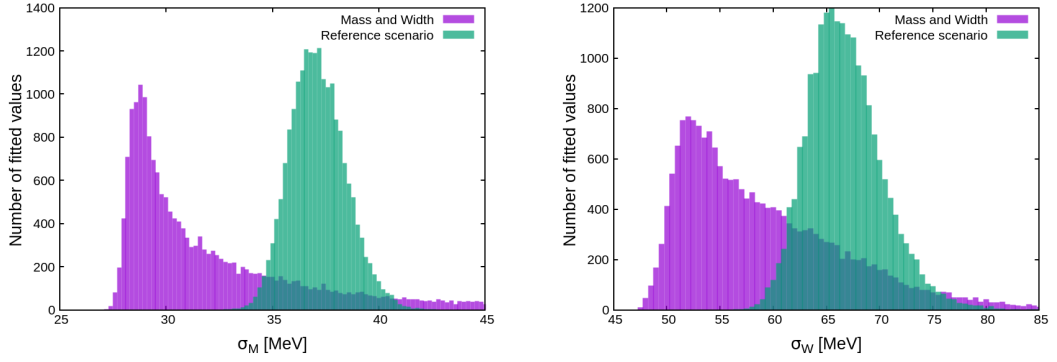


Figure 4.7: Uncertainty distribution for mass (left) and width (right) measurement, for 6 point scan scenario optimized for mass and width measurement (see Fig. 4.6), compared with the distributions for the reference scenario.

tainty is around 29 MeV, while for width it is around 52-54 MeV. Those values are consistent with results presented above, but looking just at the most probable or expected value is not enough. The shape and width of the distribution are also very important, showing the sensitivity of the scenario to statistical fluctuations in the experimental data and to the uncertainty of the initial top-quark mass. For the mass measurement, one can be almost sure that the optimised scenario will give better results than the reference one. However, for the width measurement uncertainty distribution is much wider for optimised scenario than for the reference one. In case of significant fluctuations or significant shift in the initial top-quark mass, the optimised measurement can result in the uncertainty similar to that expected from the reference scenario. This comparison shows that thanks to our optimisation procedure one cannot lose, but only gain precision for mass and width determination. It is also worth noticing that it is possible to achieve using just 6 measurement points instead of 10 (although with the same total integrated luminosity).

Results for scenario optimised for mass and Yukawa coupling are shown in Fig. 4.8. Uncertainty distribution for the mass measurement is very similar to the one obtained for mass and width optimised scenario (Fig. 4.7). However, for the Yukawa coupling uncertainty, the most probable value of uncertainty is only about 3% smaller than for the reference scenario. Moreover, for optimised scenario the distribution is wider and more asymmetric, so there is a significant chance of getting worse measurement than in the reference scenario. Nevertheless, probability of observing Yukawa coupling contribution to the pair-production cross section with statistical significance higher than 5σ (corresponding to the statistical uncertainty below 0.2) is still very high.

All results presented so far were obtained assuming 100 fb^{-1} of data collected during the top threshold scan at CLIC (baseline scenario). This luminosity is not sufficient to reach statistical uncertainty below 20 MeV, which was considered a goal in the previous study [8]. However, statistical uncertainties can be significantly reduced, if more luminosity is collected at the threshold.

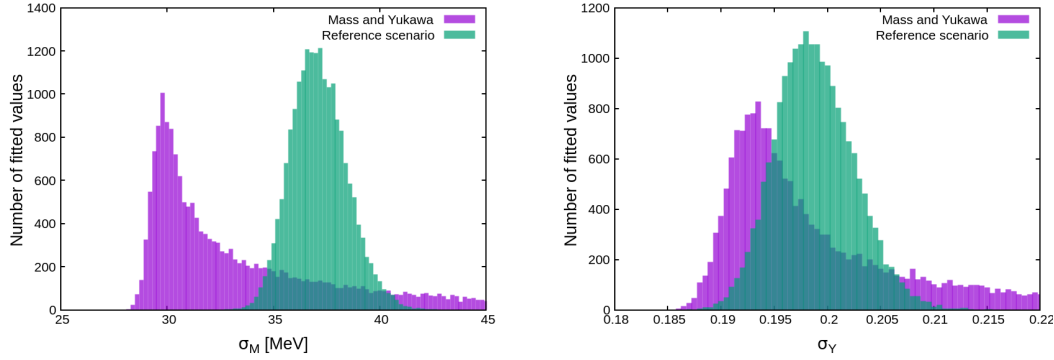


Figure 4.8: Uncertainty distribution for mass (left) and Yukawa coupling (right) measurement, for 8 point scan scenario optimized for mass and Yukawa coupling measurement (see Fig. 4.6), compared with the distributions for the reference scenario.

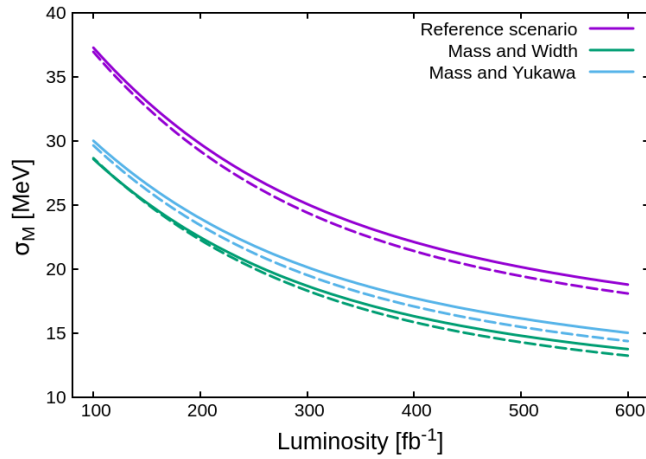


Figure 4.9: Comparison between reference and optimised scenarios assuming different total luminosity. Continuous lines represents results calculated assuming normalisation uncertainty of 1%, while dashed lines of 0.1%. Each point was computed based on average uncertainty from 1000 pseudo-experiments.

Expected dependence of the statistical mass uncertainty on the integrated threshold scan data luminosity is shown in Fig. 4.9. Three running scenarios are considered: reference 10 point scenario, 6 point scan scenario optimized for mass and width measurement and 8 point scan scenario optimized for mass and Yukawa coupling measurement. Due to additional constraints imposed on normalisation and the strong coupling constant, the uncertainties decrease slower than with $\sqrt{\mathcal{L}}$. In order to achieve 20 MeV mass uncertainty with reference running scenario at least 500 fb^{-1} of data is required, assuming normalisation uncertainty of 1%. The optimised scenarios can reach this level of precision already with 250 fb^{-1} . This shows clear advantage of optimised scenarios, as they can provide same precision as the reference scenario with the luminosity lower by a factor of 2.

Presented results confirm that the optimisation procedure based on Genetic algorithm can be 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 or top Yukawa coupling at the same time. With optimised running scenario, the statistical uncertainties on mass and width are similar to the uncertainties expected for the reference scenario with doubled integrated luminosity (200 fb^{-1}).

Chapter 5

Conclusions

Complementary fit and optimisation procedures have been developed for the top-quark threshold scan analysis at CLIC. The new fit procedure is more flexible than the one used in the previous study [8] and allows to include all relevant model parameters as well as additional constraints on model parameters, coming eg. 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 0.05. At the same time, cross section contribution from the top Yukawa coupling can be confirmed with statistical significance higher than 5σ (with normalisation uncertainty below 1% and strong coupling constant uncertainty below 0.001). Stability of fit results has also been studied for different systematic effects: background normalisation, initial mass shift and renormalisation scale variations. Mass fit results are hardly sensitive to systematic effects, they can however be very important for the Yukawa coupling determination.

Optimisation procedure based on non dominated sorting genetic algorithm II has been proposed. Each measurement scenario (set of energy points with total equally distributed luminosity of 100 fb^{-1}) is considered a genotype and results of the fit procedure constitute a phenotype. Implementation of the genetic evolution, starting from the baseline scenario, includes random mutations: mixing of parent genotypes, possibility to drop or gain a new (random) chromosome (scan point). Stable optimisation results are obtained for population size of 2000 and number of generation of 30. Using single and multi objective optimisation, it was shown that optimisation procedure can reduce the mass uncertainty by 20-25%. Those results show that by applying optimisation procedure it should be possible to lower statistical uncertainties of the top threshold fit corresponding to factor of 2 increase in the integrated luminosity. For the optimised running scenario statistical uncertainty on the top-quark mass of 20 MeV can be reached with 250 fb^{-1} .

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