Measurement of the top quark mass using lepton distributions only

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1 Introduction

The top quark mass (m_t) is a parameter which plays a fundamental role in the Standard Model of Particle Physics. The radiative corrections to SM observables like the Higgs boson mass are dominated by the large top quark mass. Thus a precise measurement of m_t provides a cross check of the internal consistency of SM and could help to place constraints to physics Beyond the Standard Model.

Since the discovery of the top quark by the CDF and D0 experiments at the $p\bar{p}$ Tevatron collider in 1995 [1, 2] its mass has been measured with high accuracy in different top decay channels using several extraction techniques. The combination of different measurements at CDF and D0 experiments yields 173.20 ± 0.87 GeV which has a precision of ± 0.5 [3]. Most of these measurements are based on a full reconstruction of the top quark decay products which envolves leptons, jets and missing transverse energy.

At the LHC, top quarks are predominantly produced in quark–antiquark pairs, and the experimental signature is characterized by the subsequent decays of the daughter W bosons and fragmentation and hadronization of bottom quarks into jets. We select $t\bar{t}$ events, where both W bosons decay leptonically, one to an electron and a neutrino and the other to a muon and a neutrino. We obtain a final state consisting of two b jets, an electron, and a muon.

This analysis aims to extract the mass of the top quark using observables based solely on lepton kinematic distributions. This has the advantage that in our detector leptons are easier to identify and their momentum and energy can be measured with great precision. With this approach we expect to have minimal sensitivity to the modelling of both perturbative and non-perturbative QCD effects.

2 Simulation and Event selection

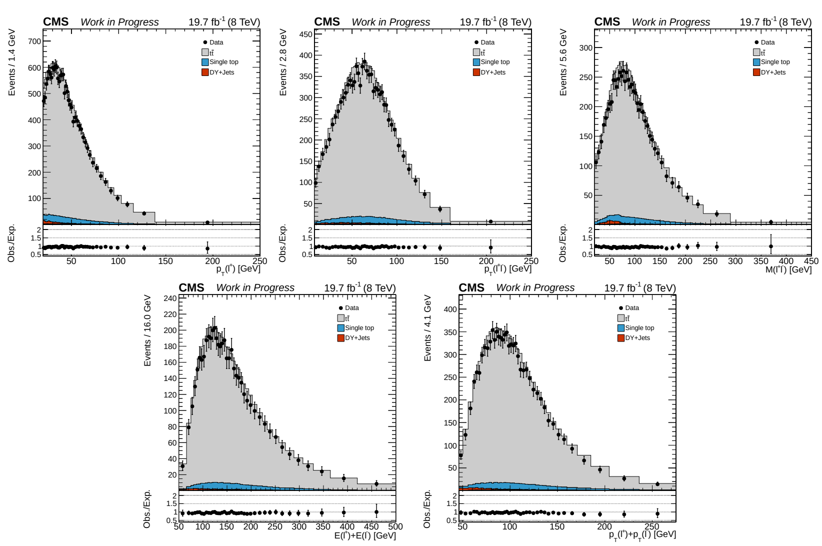

Figure 1: Data-MC Comparison plot of all observables: p_T. MC is normalized by the cross section and the integrated luminosity. The hatched bands show the ratio between data and MC.

The MC samples for various backgrounds (Drell-Yan, single top, W+jets) and signal ($t\bar{t}$) processes relevant to this analysis were generated using the MADGRAPH [4], PYTHIA [5] or POWHEG [6] generators and a full simulation of the CMS detector based on Geant4 [7]. For the purpose of evaluating systematic uncertainties dedicated samples are used.

The channel is determined by both the trigger and the offline reconstructed final state. We followed the general recommendations for event selection in the dilepton channel of the CMS TOP group.

For offline selection we require at least one charged lepton. We require two leptons with $p_T > 20$ GeV, $|\eta| < 2.5$ and $m_{ll} > 12$GeV. In this analysis jets are only used to select $t\bar{t}$ events, we require at least two AK5 PF-reconstructed jets with $p_T > 20$ GeV and $|\eta| < 2.5$. And for same-flavour dilepton events we require further that $E_T^{miss} > 40$ GeV.

3 Measuring the top quark mass using leptons only

Given the current precision in the measurement of m_t it is important to compare the results obtained from different methods, with different sensitivities to the modelling of the kinematics of observed final states. With this in mind, kinematic distributions of leptons in dileptonic events can be studied, as recently proposed in [9]. In order to study the feasibility of a top quark mass measurement using this approach we made a blinded study of the performance of this method. The method is in itself simple as no full reconstruction of the top quark takes place, instead, only final state particles are used.

The set of observables considered in this analysis are the same as the one considered in the theoretical study from which this analysis is based on [9] and their labeling conventions are given in Table 1: $p_T(l+)$ is the single-inclusive transverse momentum of the positively-charged lepton; $p_T(l+l-)$ and $M(l+l-)$ are the transverse momentum and the invariant mass, respectively, of the charged-lepton pair; finally, $E(l+)$ + $E(l-)$ and $p_T(l+)$ + $p_T(l-)$ are the scalar sums of the energies and transverse momenta of the two charged leptons, respectively.

Label	Kinematic Distribution
1	$p_T(l+)$
2	$p_T(l+l-)$
3	$M(l+l-)$
4	$E(l+)$ + $E(l-)$
5	$p_T(l+)$ + $p_T(l-)$

Table 1: Set of kinematic leptonic observables used in this analysis.

The extraction of the top quark mass utilizes the sensitivity of the shapes of kinematic distributions to the value of m_t. We work with their lower Mellin moments, as suggested in [9]. Given an observable O they are defined as:

$$\mu_O^{(1)} = <O> \; (Mean), \qquad \mu_O^{(2)} = <O^2> = \sigma^2 + <O>^2 \tag{1}$$

Before performing the extraction of the top quark mass we have followed a procedure that allows us to correct the binned kinematic distributions for experimental effects, such as limited detector resolution and detection inefficiencies. This effects cause a bin-to-bin smearing effect on the measured distributions and a distortion of them from the true underlying distributions for which we have to correct.

3.1 Choice of bins for our measurement

Due to the bin-to-bin smearing effect it becomes necessary to choose a correct binning for our measurement. While using a larger number of bins allows precision in understanding of smearing, it would result in large bin-to-bin oscillations caused by statistical fluctuations. But using very few bins is also sub-optimal due to reduced information about the smearing.

The bin-to-bin migration effect means that the measured number of events in the reconstructed distribution of an observable will change: events that are generated in bin k of an observable will not always end up in the same bin after reconstruction but will migrate into the neighboring bins and similarly events from neighboring bins can migrate into bin k. This effect can be studied for each observable in terms of the purity and stability in each bin: purity p quantifies the migration of events from the neighboring bins into bin k while stability describes the migration out of bin k (see Fig. 2). They are defined as:

$$p^k = \frac{N^k_{rec\&gen}}{N^k_{rec}} \qquad s^k = \frac{N^k_{rec\&gen}}{N^k_{gen}} \tag{2}$$

(a) Stability (b) Purity

Figure 2: Stability (left) is quantifying the migration of events out of a bin while purity is quantifying the migration of events into a bin. Both quantities compare events generated in a certain variable range (bin) to where they are reconstructed.

where $\mathrm{N}^k_{rec\&gen}$ is the number of events both generated (true) and correctly reconstructed in a given bin k and $\mathrm{N}^k_{rec}(\mathrm{N}^k_{gen})$is the number of events reconstructed (generated) within bin k but generated (reconstructed) anywhere. The binning is then chosen such that p_k and s_k stay above 0.5. This means that, at most, 50 % of all

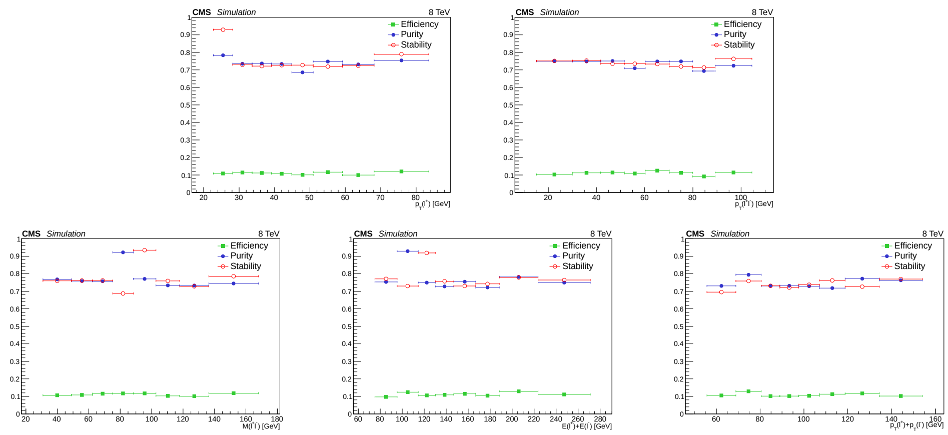

Figure 3: Each plot shows the stability, purity and efficiency for each of the kinematic distributions. The horizontal bars indicate the size of the bin. We define efficiency as the number of events reconstructed in a given bin which are matched at generator level divided by the total number of events which have been matched at generator level.

events generated in bin k will stay in bin k after reconstruction and that no more than 50 % of all reconstructed events in bin k come from other bins in the generated distribution. To achieve this we use quantiles to choose the bins in such a way that all bins in the histograms contain the same number of events. This will increase the stability of the method as we obtain a flat truth spectrum. Then we merge the bins of generated events until they satisfy the requirements of p and s greater than 0.5.

3.2 Unfolding procedure

In general, after backgrounds are subtracted, the measured distribution b is related to the underlying parton-level distribution x by the matrix equation: $b = SAx$, where A is a diagonal matrix describing the acceptance in each bin of the measured distribution, and S is a non-diagonal smearing matrix describing the migration of events between bins due to the detector resolution and reconstruction techniques. The binned data is multiplied by the inverse matrices to recover the true parton-level distributions from the background subtracted distributions in data: $x = A^{-1}S^{-1}b$.

Additionally, if statistical errors of the measurement are substantial, it can result in amplification of essentially random components in the solution. These issues can be resolved by implementing a regularization parameter τ in the unfolding procedure. Larger values of τ mean the unfolded output will be more strongly constrained by the supplied bias distribution, and smaller values of τ mean the output will be less strongly constrained. We perform our unfolding using the TUnfoldSys [8] package which has implemented a regularization parameter and background subtraction. We chose the value of τ by minimizing the mean of the global correlation between the bins as shown in Fig. 5.

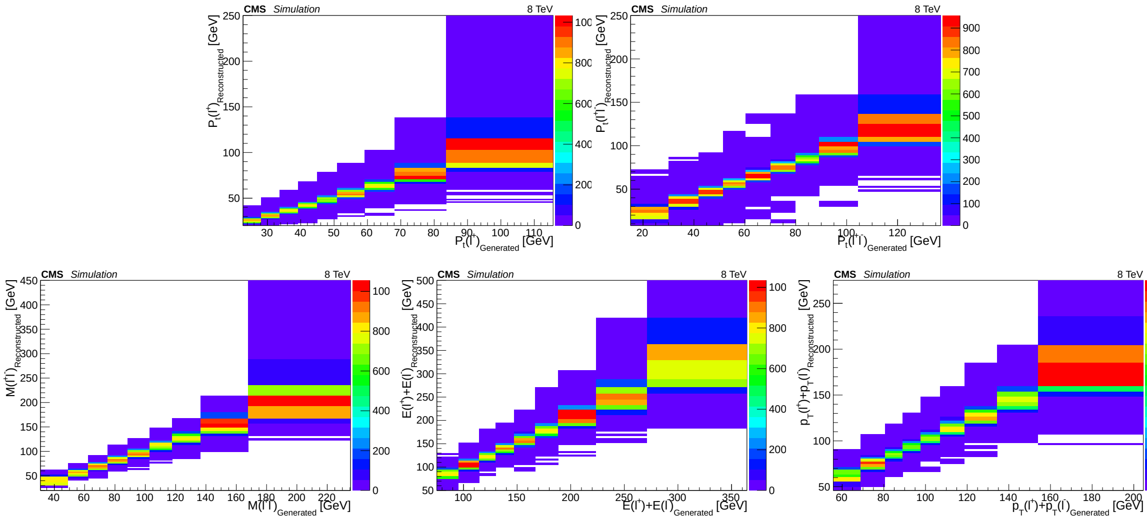

Figure 4: Two dimensional distributions (smearing matrices), generated versus reconstructed observable, and the bin choices for the different kinematic variables.

3.3 m$_t$ extraction procedure

We tested the procedure for the m$_t$ extraction in a blinded way using only MC samples. We obtained the unfolded distributions for each of the kinematic variables, using the new binning and the optimized unfolding procedure, which are shown in Fig. 6.

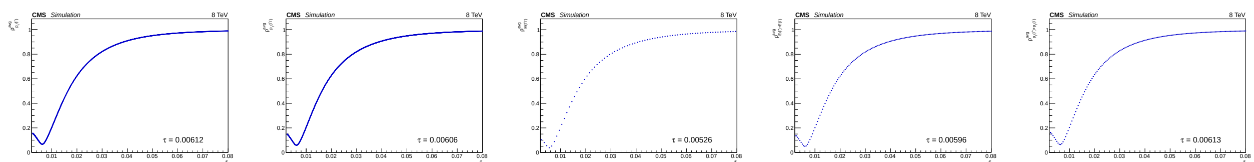

Figure 5: Average global correlation between the bins in the measurement for each variable. The minimum of each curve indicates the optimal regularization τ value for each observable

We first calibrate the measurement by using signals generated with different MC mass samples. For each of them we obtained an unfolded distribution (a comparison between the different distributions for each of the mass samples is shown in Fig. 7) and extracted the first Mellin moments from them. We compared the measured moments from each sample with the top mass, and obtained a calibration curve for each of the kinematic observables, which is shown in Fig. 8.

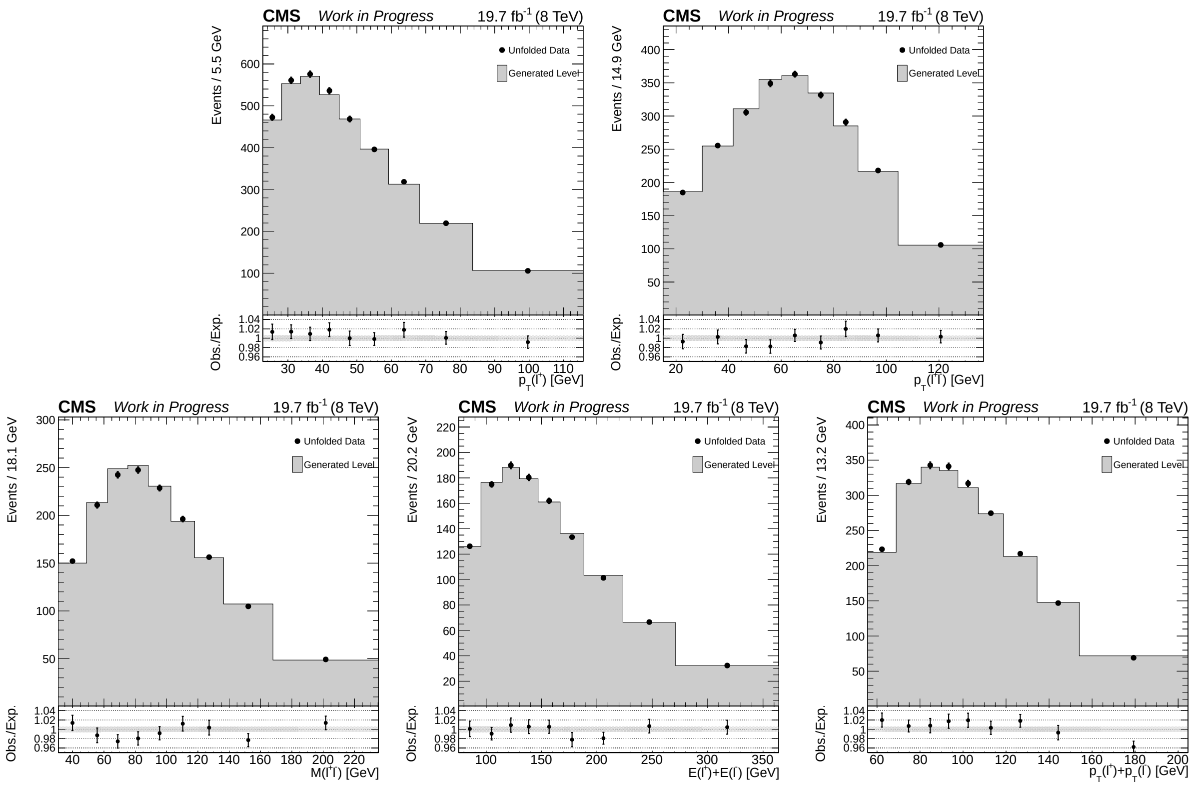

Figure 6: Unfolded distributions for each of the kinematic lepton variables of interest. A good agreement is shown between the unfolded data distributions and the distributions at generated level.

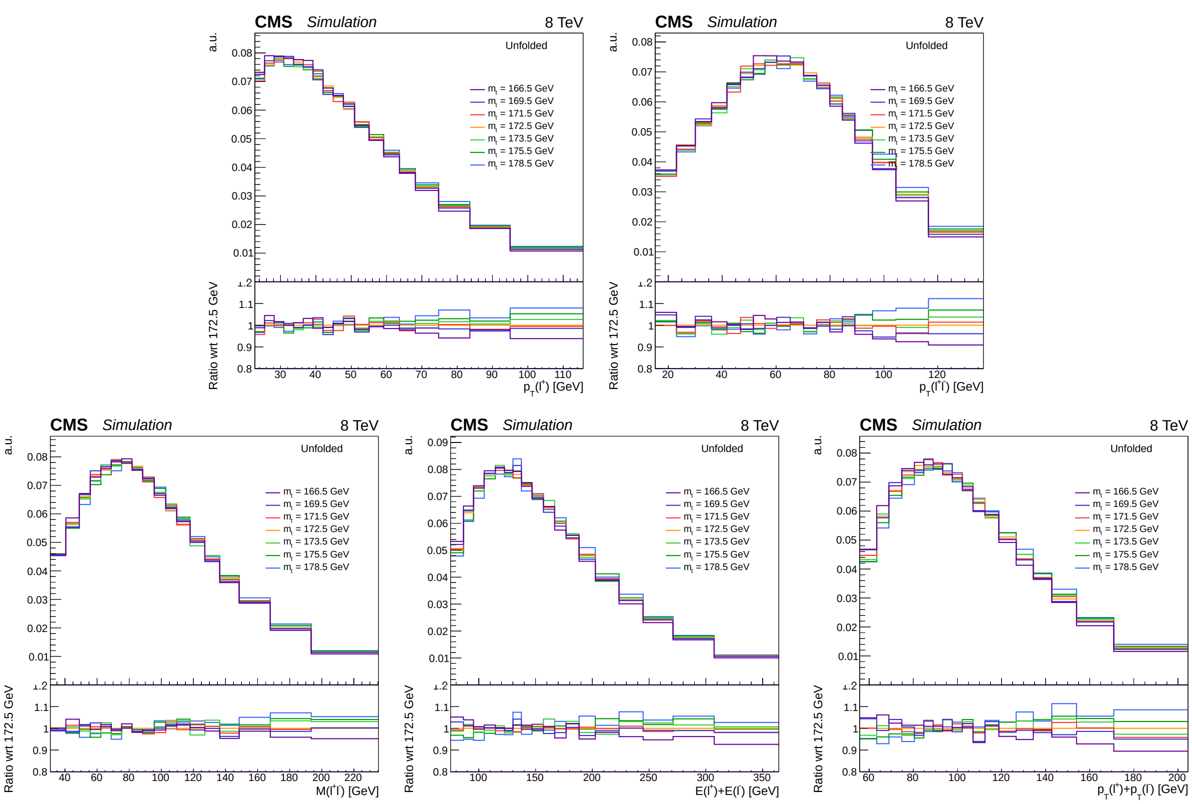

Figure 7: Comparison plot of the unfolded distributions for each of the kinematic lepton variables of interest varying the MC mass sample. A dependency on the value of the top mass is observed specially in the last bins.

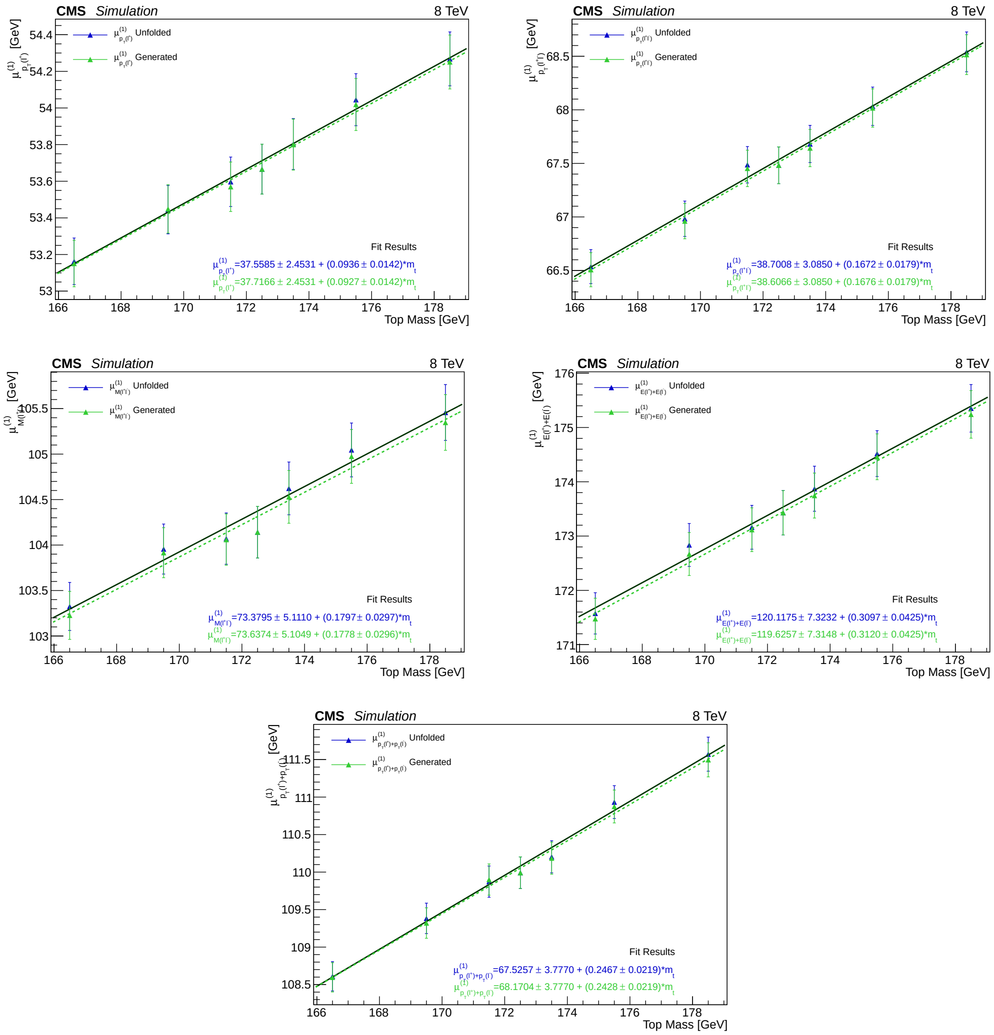

Figure 8: Calibration curves for the first Mellin moment, for each of the kinematic distributions. The calibration is observed to be linear with respect to the top mass with a small bias. The fit results for the unfolded distribution are shown in blue.

4 Systematic Uncertainties

We used alternative samples or re-weighted nominal samples to evaluate shifts in m_t. From this we calculated the main systematic uncertainties, theoretical and experimental for each of the kinematic observables, these are shown in Table 2.

	δ m_t [GeV]				
	$P_t(l^+)$	$P_t(l^+l^-)$	$M(l^+l^-)$	$E(l^+)+E(l^-)$	$P_t(l^+)+P_t(l^-)$
QCD Scale Up	-1.05 ± 0.54	-1.70 ± 0.42	-0.44 ± 0.77	-0.35 ± 0.74	-1.14 ± 0.37
Down	1.09 ± 0.58	2.85 ± 0.24	2.82 ± 1.68	2.29 ± 2.02	1.35 ± 0.37
ME/PS Up	0.55 ± 0.66	-0.87 ± 0.6	0.81 ± 1.06	0.22 ± 0.68	-0.94 ± 0.47
Down	2.01 ± 1.02	2.26 ± 0.96	3.32 ± 1.16	2.42 ± 2.71	1.98 ± 1.03
Pile Up	0.30	0.14	0.35	0.15	0.26
Down	-0.23	-0.14	-0.32	-0.18	-0.23
Lepton Sel. Up	-0.04	-0.02	-0.05	-0.33	-0.03
Down	0.04	0.03	0.05	0.34	0.04
Top Pt	-5.09	-0.67	-8.53	-5.55	-4.79
LES Up	0.12	0.47	0.70	0.54	0.39
Down	-0.21	-0.45	-0.71	-0.55	-0.38
Total syst.	+2.37	+3.67	+5.60	+3.40	+2.44
	−5.21	−2.08	−4.50	−8.57	−5.03

Table 2: Expected systematic uncertainties for the Top Mass extraction based on the first Mellin moment of the distributions.

For most of the variables, the uncertainty stemming from the mismodelling of the Top quark P_t dominates, followed by the QCD scale choice and choice of matrix element/parton shower thresholds. In the latter case the statistics of the MC samples used for the systematics may have a non-negligible impact.

If instead a full shape analysis is performed (using a parametrization of the χ^2 evolution as function of the top quark mass) we expect to decrease effectively some of the low-statistics related effects and some of the systematic uncertainties as well. As an example, Table 3 compares the systematic uncertainties for the $P_t(l^+l^-)$ where the first Mellin moments or the shape analysis are used. A final systematic uncertainty $\approx$ 2 GeV is expected from the shape analysis.

$P_t(l^+l^-)$	δ m_t [GeV]	
Source	Mellin moments	Full shape analysis
QCD Scale Up	-1.70 ± 0.42	-1.21 ± 0.09
QCD Scale Down	2.85 ± 0.24	1.55 ± 0.10
ME/PS Up	-0.87 ± 0.60	-0.73 ± 0.01
ME/PS Down	2.26 ± 0.96	1.38 ± 0.03
Pile Up Up	0.14	0.09
Pile Up Down	-0.14	-0.10
Lepton Sel. Up	-0.02	-0.02
Lepton Sel. Down	0.03	0.01
Top Pt	-0.67	-0.60
LES Up	0.47	0.31
LES Down	-0.45	-0.31
Total syst. uncert.	$+3.67/-2.08$	$+2.10/-1.57$

Table 3: Expected systematic uncertainties for the Top Mass extraction based on a shape analysis and $\mu^(1)$.

5 Conclusions and Outlook

In this project we have fully implemented the analysis proposed by theorists at [9] and have shown that is feasible to measure m_t using lepton distributions only. We observed that the kinematic variables have lower sensitivity to m_t than the ones quoted in [1]. And based on our results from the calibration curves we can see the slope differ from the theoretical prediction making the shapes less sensitive to the m_t.

We found larger uncertainties than expected but some of them may be affected by the statistical fluctuation of the samples used in the calculation. We studied how to improve the matching and scale uncertainties using shape analysis and we proved that we may mitigate some of them related to the statistics of the MC. The expected systematic uncertainty for the shape analysis is: $+2.1/-1.6$ GeV.

Our next step will be to optimize the unfolding procedure and understand the systematic uncertainties, specially the significant ones. We would like to compare more carefully the current calibration with the one found on [9]. And we could also study the combination of measurements from different variables using different Mellin moments. As we observed some improvement of the systematics performing a shape analysis on one of the variables we would study the behavior of a full shape analysis. In the future, once the procedure is fairly well established and is approved by the CMS TOP group we could make the measurement using real data.

References

[1] CDF Collaboration, F. Abe et al., Phys. Rev. Lett. 74, 2626 (1995), [arXiv:hep-ex/9503002 [hep-ex]].

[2] D0 Collaboration, S. Abachi et al., Phys. Rev. Lett. 74, 2632 (1995),[arXiv:hep-ex/9503003 [hep-ex]].

[3] Tevatron Electroweak Working Group, "Combination of CDF and D0 results on the mass of the top quark using up to 8.7 fb$^-1$ of $p\bar{p}$ collisions." , Conference Note 10976, Fermilab, 2013.

[4] J. Alwall et al., "MadGraph 5 : Going Beyond", JHEP 1106 (2011) 128, doi:10.1007/JHEP06(2011)128, arXiv:1106.0522.

[5] T. Sjostrand, S. Mrenna, and P. Z. Skands, "PYTHIA 6.4 Physics and Manual", JHEP 05 (2006) 026, doi:10.1088/1126-6708/2006/05/026, arXiv:hep-ph/0603175.

[6] S. Alioli, P. Nason, C. Oleari, and E. Re, "A general framework for implementing NLO calculations in shower Monte Carlo programs: the POWHEG BOX", JHEP 1006 (2010) 043, doi:10.1007/JHEP06(2010)043, arXiv:1002.2581.

[7] GEANT4 Collaboration, "GEANT4: A simulation toolkit", Nucl. Instrum. Meth. A506 (2003) 250–303, doi:10.1016/S0168-9002(03)01368-8.

[8] Schimitt S., "TUnfold, an algorithm for correcting migration effects in high energy physics", Journal of Instrumentation 10003 (2012), arXiv:1205.6201, doi:10.1088/1748-0221/7/10/T10003.

[9] Frixione, Stefano and Mitov, Alexander, "Determination of the top quark mass from leptonic observables" JHEP **1409**, 012 (2014) [arXiv:1407.2763 [hep-ph]].