Fe6preting CMS data in the phenomenological MSSM

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Abstract

We in15rpret the data taken with the CMS detector during the 7 TeV LHC run within the phenomenological MSSM (pMSSM). The pMSSM is a 19-dimensional parametrization of the general MSSM, that captures most of the phenomenological features of the MSSM. It encompasses, and goes beyond, a broad range of more constrained SUSY models (such as the CMSSM). Using profile likelihoods, we

1 Introduction

After the successful operation of the Large Hadron Collider (LHC) and the CMS detector in 2010, and with good prospects for the future, the LHC is now ready to shed light on a number of open questions in Particle Physics, such as the mechanism of electroweak (EW) symmetry breaking, or the nature of the new physics Beyond the Standard Model (BSM) that stabilizes the EW scale.

A wealth of theories that extend the Standard Model have been put forth during the past decades. Supersymmetry (SUSY) is arguably the best motivated BSM theory — and certainly the most thoroughly studied. Indeed, searches

group equations to derive model-specific testable predictions. It is expected that once SUSY particles are discov-

For each of the 6K pMSSM points we generate 10K events.

We perform three blessed CMS analyses, namely the “di-jet $_T$” (Had), “opposite-sign di-lepton” (OS) and “same-sign di-lepton” (SS) analyses on each of the 6K pMSSM samples.

5 Results

We present the results obtained by following the analysis path in Section 4, in terms of plots of likelihood ratios L_p/L_{max} as a function of each parameter of interest. Further details on this ratio as a measure can be found in the Appendix.

Plots of the likelihood ratio L_p/L_{max} are shown for the 19 input pMSSM parameters in Figures 1 to 5. Similarly Figures 6 to 11 show the likelihood ratio for the physical sparticle masses. The relationships between the scalar

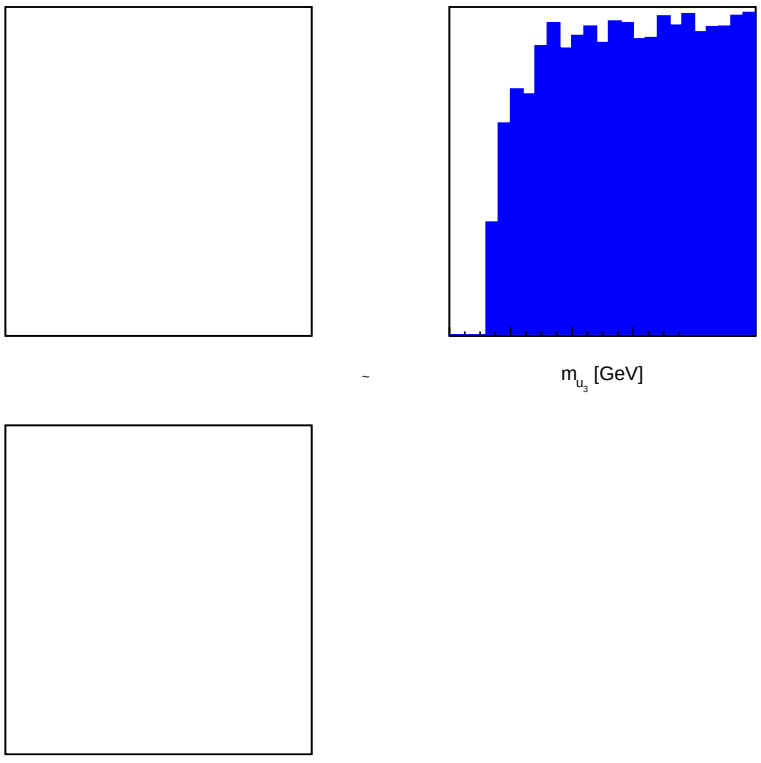


Figure 1: Ratios of profile likelihood L_p to maximum likelihood L_{max} shown for the squark mass parameters at SUSY scale. The colored and shaded histograms show the utions before and after the inclusion of the CMS results.

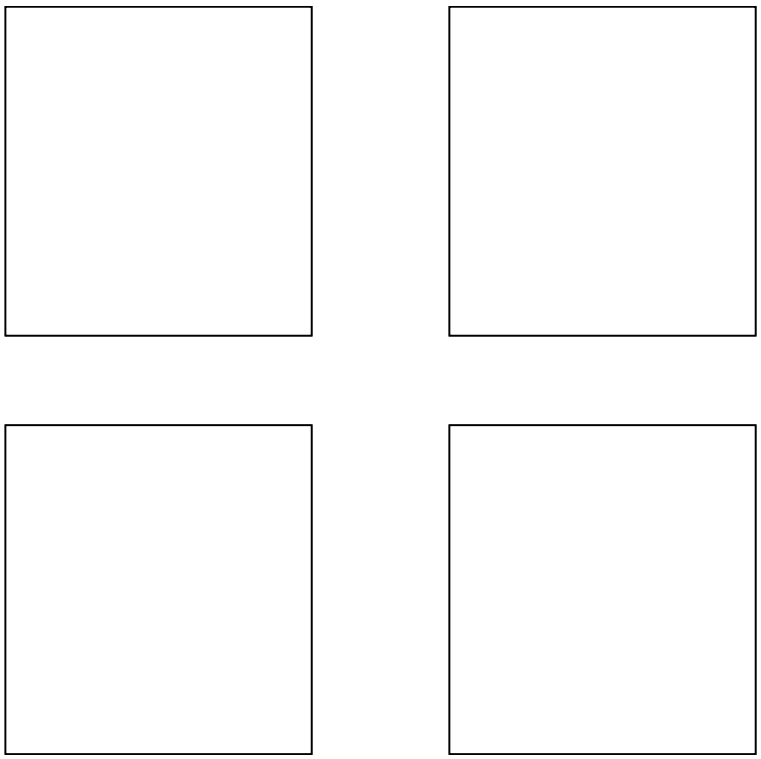


Figure 2: Ratios of profile likelihood L_p

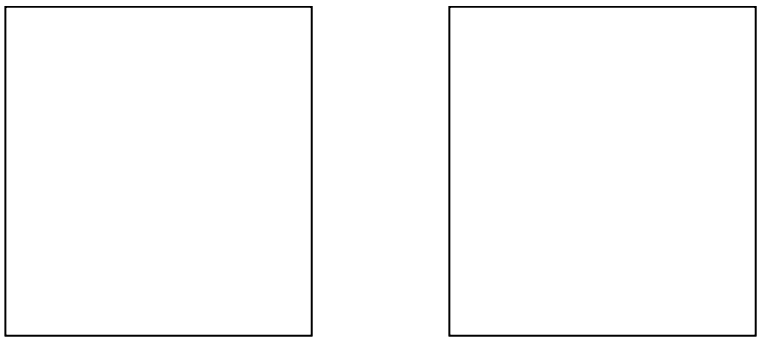


Figure 3: Ratios of profile likelihood L_p μ

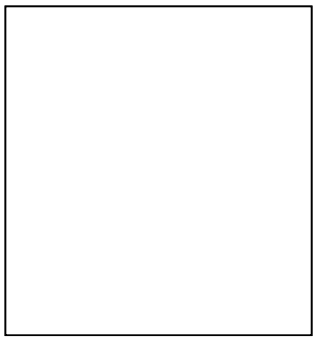


Figure 4: Ratios of profile likelihood L_p to maximum likelihood L_{max} shown for trilinear couplings at SUSY scale. The colored and shaded histograms show the distributions before and after the inclusion of the CMS results.

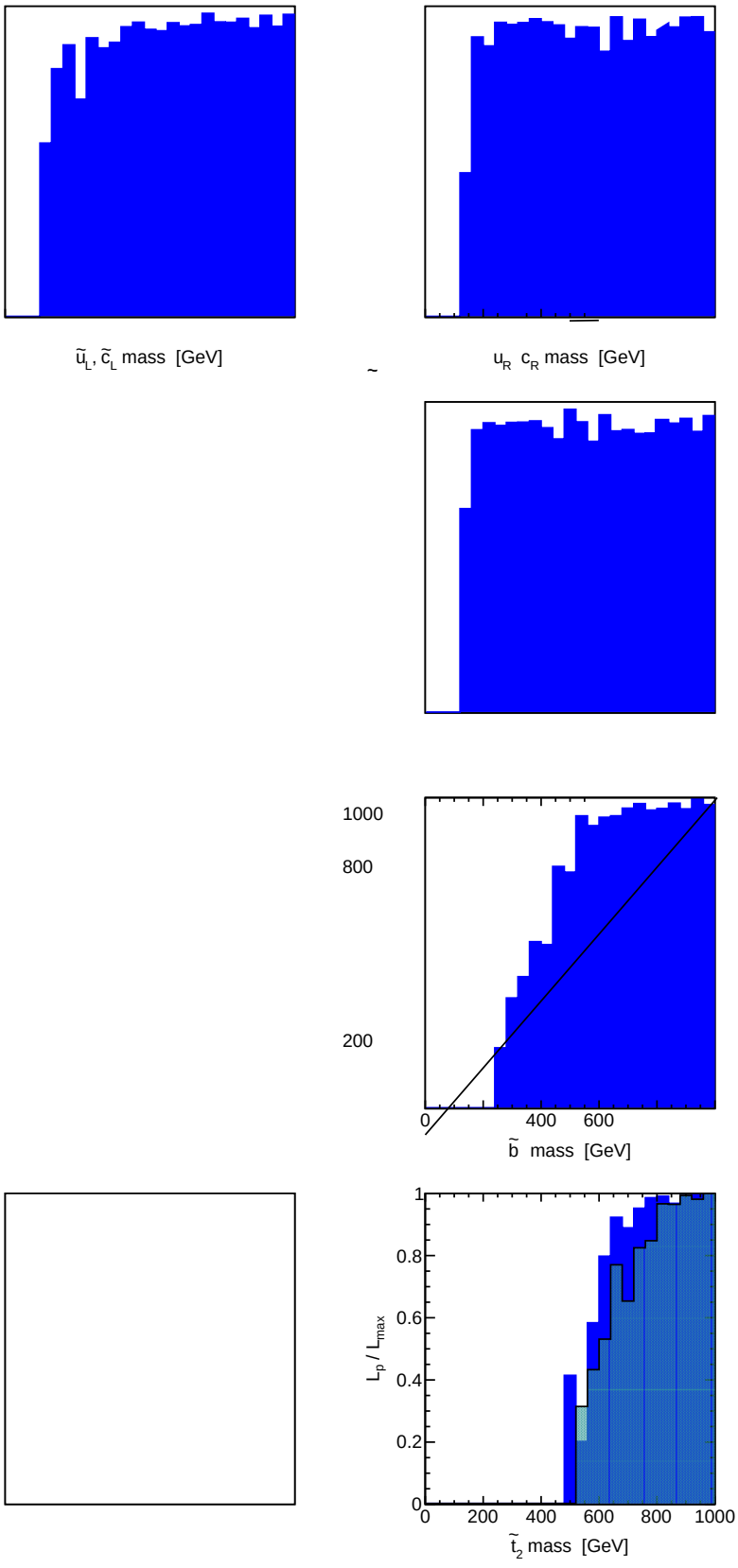
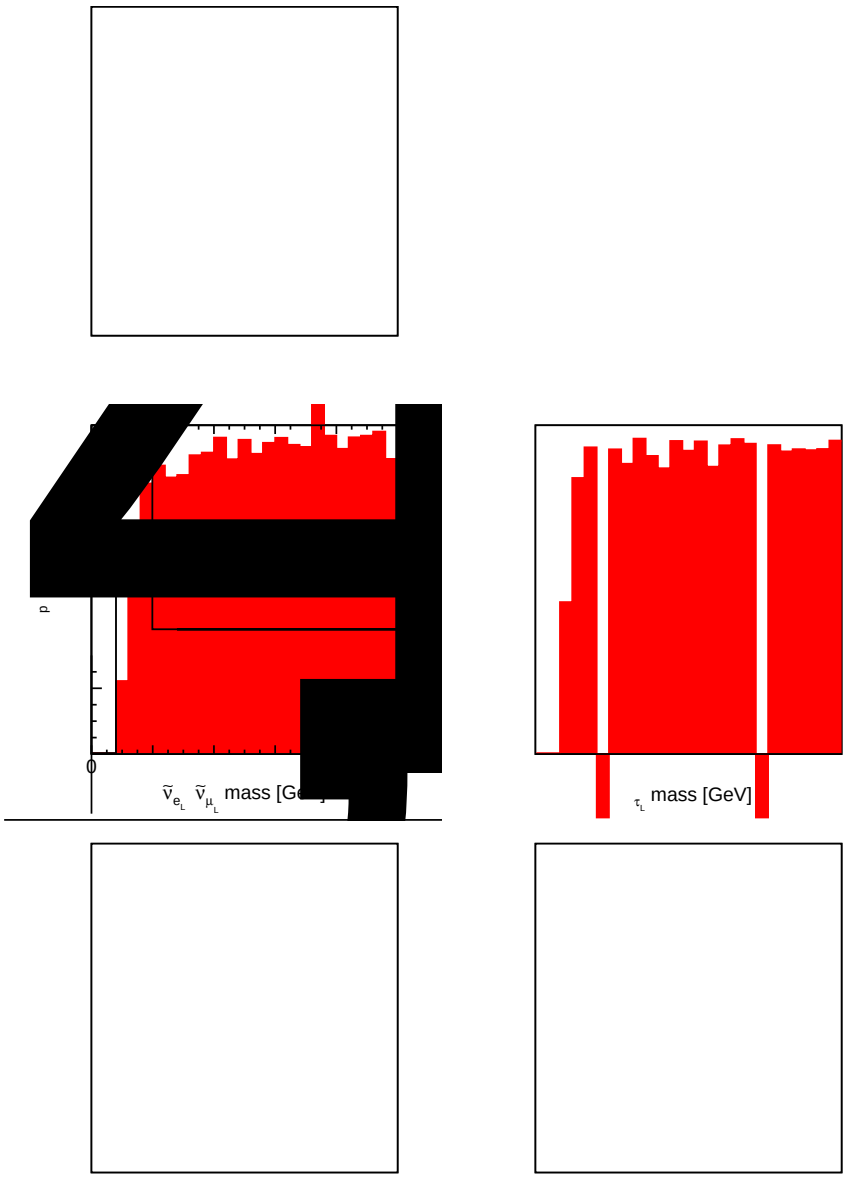


Figure 6: Ratios of profile likelihood L_p to maximum likelihood L



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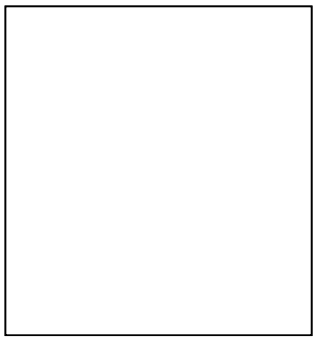

Figure 10: Ratios of profile likelihood L_p to maximum likelihood L_{max} shown for chargino masses. The colored and shaded histograms show the distributions before and after the inclusion of the CMS results.

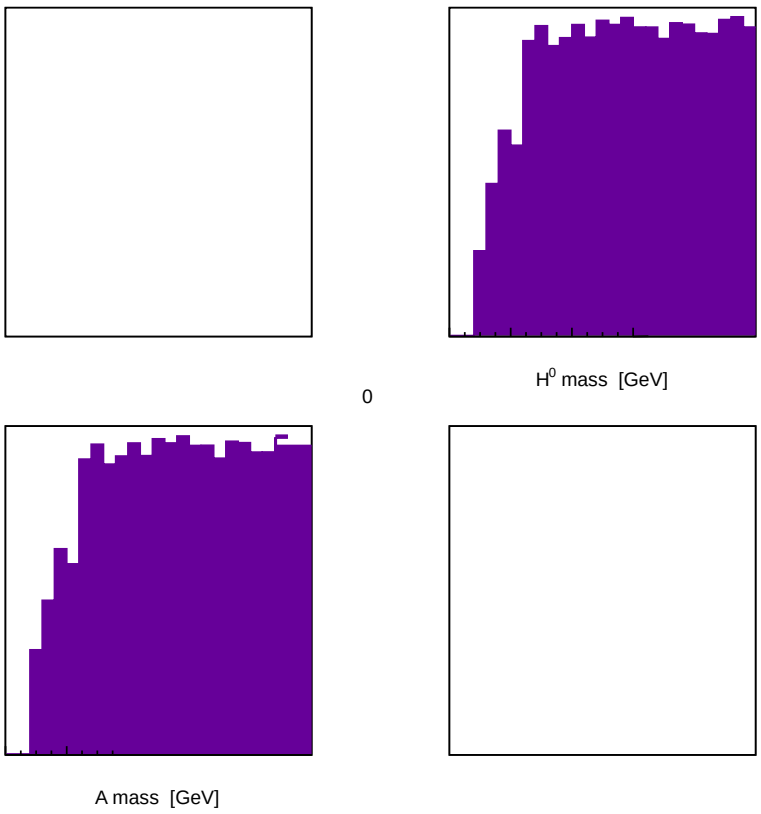

Figure 11: Ratios of profile likelihood L_p to maximum likelihood L_{max} shown for the Higgs masses. The colored and shaded histograms show the distributions before and after the inclusion of the CMS results.

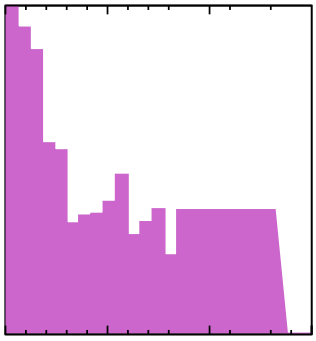

Figure 12: Ratio of profile likelihood L_p to maximum likelihood L_{max} shown for lightest neutralino dark matter relic density. The colored and shaded histograms show the distributions before and after the inclusion of the CMS results.

demonstrated that interpretation of CMS data in terms of broad classes of multi-parameter SUSY models is feasible with the currently available statistical tools, and that it is indeed possible to make meaningful statements on the natures of such models.

References

[1] K. Choi and H. P. Nilles, JHEP **04**, 006 (2007), hep-ph/0702146.

[2] S. P. Martin, Phys. Rev. **D79**

Appendices

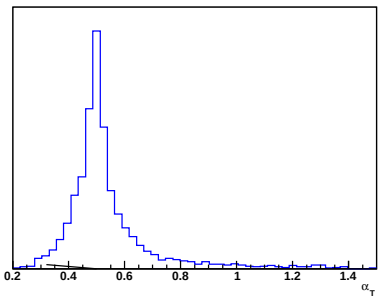

Figure 17: Distributions using the CMSSW full simulation and Delphes for the LM1 benchmark point as a function of $_T$ (top left), (top right) and MHT/MET (bottom)

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10,11 Find largest density $DMAX$ so far.

12–14 Return average of estimates of profile likelihood.

The above algorithm is implemented in a class we developed called `KDTProfileLikelihood`, which makes use of the multi-dimensional histogrammer `TKDTreeBinning` in Root. The d-dimensional histogram is created through recursive binary partitioning of the parameter space in such a way that bins have equal counts. The underlying data structure is a kd-tree [31].