



A profile likelihood analysis of the **CMSSM** with Genetic Algorithms

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mSUGRA/CMSSM

- **Weak-scale supersymmetry** provides a well-known solution to the technical **hierarchy** problem.
- Specializing to a **minimal** extension of the **Standard Model**, the **MSSM**, one can provide a weakly interacting massive particle (**WIMP**) **dark matter** candidate, provided **R-parity** is respected by the model.
- The general MSSM is rather complicated and suffers from the lack of predictiveness due to a **large number of free parameters** (over 120), most of which arise from the **SUSY breaking sector**.
- The observed rareness of flavour changing neutral currents (**FCNCs**) and **CP-violation** restrictions suggest that the vast majority of the parameter space for general SUSY breaking terms is ruled out.
- One highly studied and theoretically well motivated subset of such terms is that of **Minimal Supergravity (mSUGRA)**, often called the **Constrained MSSM (CMSSM)** (with minor differences).
- This is a **four** parameter model, with one **sign** that must be chosen.

Model parameters

- In the CMSSM, at some high energy scale, typically taken to be the scale of unification of electroweak gauge couplings (**GUT scale**), all of the SUSY breaking **scalar mass** terms are assumed to be equal to m_0 , the **scalar trilinear** terms are set to A_0 and the **gaugino masses** are set equal to $m_{1/2}$.
- Aside from the **universal soft terms** m_0 , $m_{1/2}$ and A_0 , other non-standard model CMSSM input parameters are taken to be $\tan\beta$, the ratio of the two **Higgs vacuum expectation values**, and the **sign** of μ (the **Higgs/higgsino mass parameter** in the MSSM).
- If we fix $\text{sign}(\mu) = +1$, the remaining four free CMSSM parameters are therefore:

$$m_0, m_{1/2}, A_0, \tan\beta$$

The goal is to constrain these parameters as much as possible using different experimental data: **SUSY Global Fit**

+ Nuisance parameters

- The statistical uncertainty associated with our **imperfect knowledge** of the values of **relevant SM parameters** must be taken into account in order to obtain correct statistical conclusions on the regions of high probability for the CMSSM parameters.
- This can easily be done by introducing a set of so-called **nuisance parameters**.
- The most relevant ones are:

$$m_t, m_b(m_b), \alpha_{em}(m_Z), \alpha_s(m_Z)$$

where m_t is the pole **top quark mass**, $m_b(m_b)$ is the **bottom quark mass** at m_b , while $\alpha_{em}(m_Z)$ and $\alpha_s(m_Z)$ are the **electromagnetic** and the **strong coupling constants** at the Z pole mass m_Z .

Both sets of the CMSSM parameters and nuisance parameters altogether form the **basis parameters**:

$$\Theta = (m_0, m_{1/2}, A_0, \tan \beta, m_t, m_b(m_b))^{\overline{MS}}, \alpha_{em}(m_Z)^{\overline{MS}}, \alpha_s(m_Z)^{\overline{MS}})$$

Statistical framework

Two different approaches for statistical analysis of a model:

- **Bayesian statistics:** ———— | **prior dependent**

We are interested in the **marginal posterior** of the parameters:

$$p(\theta_i|D) = \int p(\Theta|D)d\theta_1\dots d\theta_{i-1}d\theta_{i+1}\dots d\theta_m$$

- **Frequentist statistics:** ———— | **in principle independent of the prior**

We are interested in the **profile likelihood** of the parameters:

$$\mathbb{L}(\theta_i) \equiv \max_{\theta_1, \dots, \theta_{i-1}, \theta_{i+1}, \dots, \theta_m} L(\Theta)$$

Thus in the profile likelihood one maximizes the value of the likelihood along the hidden dimensions, rather than integrating it out as in the marginal posterior.

Statistical framework

Bayes' theorem:

$$p(\Theta|D) = \frac{p(D|\Theta)p(\Theta)}{p(D)}$$

The diagram shows the equation $p(\Theta|D) = \frac{p(D|\Theta)p(\Theta)}{p(D)}$ with four red boxes pointing to its components: *likelihood* points to $p(D|\Theta)$, *prior probability density function* points to $p(\Theta)$, *evidence or model likelihood* (with a sub-note) points to $p(D)$, and *posterior probability density function* points to $p(\Theta|D)$.

- One practically interesting consequence of Bayesian inference is that it gives a powerful way of estimating **how robust a fit is**, i.e., if the **posterior** is strongly **dependent** on the **different priors**, this actually means that **the data** are **not sufficient or accurate enough** to constrain the model parameters.
- If a fit is robust, the Bayesian and frequentist methods should result in similar confidence regions of the parameter space. This is **NOT** the case for the CMSSM.

SuperBayes

(www.superbayes.org)

- Developed by **Roberto Ruiz de Austri, Roberto Trotta, Farhan Feroz, Leszek Roszkowski, and Mike Hobson.**
- It is a package for **fast** and **efficient** sampling of the CMSSM.
- Compares SUSY predictions with observable quantities, including **sparticle masses, collider observables, B-factory data, dark matter relic abundance, direct detection cross sections, indirect detection quantities** etc.
- The package combines **SoftSusy, DarkSusy, FeynHiggs, Bdecay** and **MicrOMEGAs.**
- It uses **Bayesian** techniques to explore multidimensional SUSY parameter spaces. Scanning can be performed using **Markov Chain Monte Carlo (MCMC)** technology or more efficiently by employing the new scanning technique called **Nested Sampling (MultiNest algorithm).**
- Although these methods have been used for the **profile likelihood** analysis of the model, they are essentially **optimized for the marginal posterior analysis** of the model.

Genetic Algorithms (GAs)

In order to make a profile likelihood analysis of a model correctly, it is extremely important to know, with enough accuracy, the highest value of the likelihood function in the parameter space of the model. Otherwise, the calculated confidence regions might be very far from the real ones.

GAs seem to be helpful, because:

- The actual use of these algorithms is to **maximize/minimize** a specific function; this is exactly what we need in the case of a profile likelihood scan.
- GAs are usually considered as **powerful methods** in probing the global extrema when the parameter space is **very large, too complex** or **not enough understood**; these are precisely what we have in the case of the supersymmetric models including the CMSSM.

Genetic Algorithms (GAs)

GAs are a class of **adaptive heuristic search techniques** that incorporate the **evolutionary ideas of natural selection and survival of the fittest** in biology, the very mechanisms that led in particular to our own existence. As such, they represent an intelligent random search within a defined search space to solve a complex problem.

General structure:

```
 $P^0 := \{\Theta_i^0\}, \quad i = 1, \dots, I$  [initialization]  
 $f_i^0 := f(\Theta_i^0), \quad i = 1, \dots, I$  [computing initial individual's fitness values]  
 $k := 0$   
do while  $|f(\Theta) - T| \leq \varepsilon$  (or  $k < N$ ) [reproduction loop]  
   $k := k + 1$   
   $P^k := \mathbb{G}(P^{k-1})$  [generating new population through genetic operators]  
   $f_i^k := f(\Theta_i^k), \quad i = 1, \dots, I$  [computing individual's fitness values in current generation]  
end do  
 $\Theta_{max} := \Theta_j^k$  if  $f_j^k = \max \{f_i^k\}, \quad i = 1, \dots, I$  [reading the best-fit point]
```

SuperBayes v1.35



PIKAIA 1.2*

* Developed by P. Charbonneau *et. al.*, can be downloaded from <http://www.hao.ucar.edu/modeling/pikaia/pikaia.php>

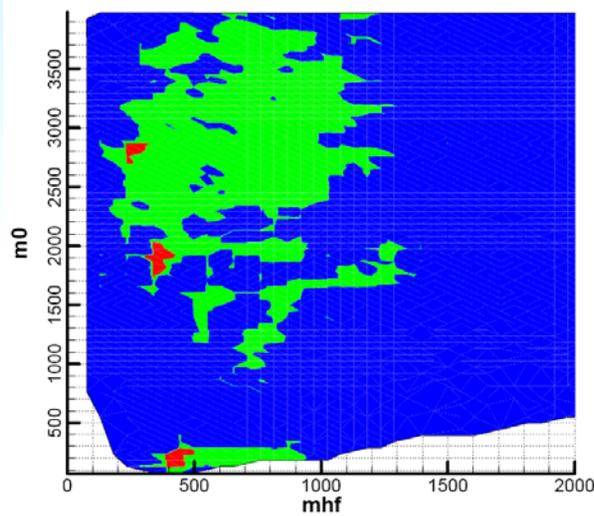
Observables and constraints

Observable	Mean value	Uncertainties (variances)	
		experimental	theoretical
SM (nuisance) parameters			
m_t	172.6 GeV	1.4 GeV	-
$m_b(m_b)^{\overline{MS}}$	4.20 GeV	0.07 GeV	-
$\alpha_s(m_Z)^{\overline{MS}}$	0.1176	0.002	-
$1/\alpha_{em}(m_Z)^{\overline{MS}}$	127.955	0.03	-
measured			
m_W	80.398 GeV	25 MeV	15 MeV
$\sin^2 \theta_{eff}$	0.23153	16×10^{-5}	15×10^{-5}
$\delta a_\mu^{SUSY} \times 10^{10}$	29.5	8.8	1.0
$BR(\overline{B} \rightarrow X_s \gamma) \times 10^4$	3.55	0.26	0.21
ΔM_{B_s}	17.77 ps^{-1}	0.12 ps^{-1}	2.4 ps^{-1}
$BR(\overline{B}_u \rightarrow \tau \nu) \times 10^4$	1.32	0.49	0.38
$\Omega_\chi h^2$	0.1099	0.0062	$0.1 \Omega_\chi h^2$
limits only (95% CL)			
$BR(\overline{B}_s \rightarrow \mu^+ \mu^-)$	$< 5.8 \times 10^{-8}$		14%
m_h	$> 114.4 \text{ GeV}$ (SM-like Higgs)		3 GeV
ζ_h^2	$f(m_h)$ (see ref. [16])		negligible
m_χ	$> 50 \text{ GeV}$		5%
$m_{\chi_1^\pm}$	$> 103.5 \text{ GeV}$ ($> 92.4 \text{ GeV}$)		5%
$m_{\tilde{e}_R}$	$> 100 \text{ GeV}$ ($> 73 \text{ GeV}$)		5%
$m_{\tilde{\mu}_R}$	$> 95 \text{ GeV}$ ($> 73 \text{ GeV}$)		5%
$m_{\tilde{\tau}_1}$	$> 87 \text{ GeV}$ ($> 73 \text{ GeV}$)		5%
$m_{\tilde{\nu}}$	$> 94 \text{ GeV}$ ($> 43 \text{ GeV}$)		5%
$m_{\tilde{t}_1}$	$> 95 \text{ GeV}$ ($> 65 \text{ GeV}$)		5%
$m_{\tilde{b}_1}$	$> 95 \text{ GeV}$ ($> 59 \text{ GeV}$)		5%
$m_{\tilde{q}}$	$> 375 \text{ GeV}$		5%
$m_{\tilde{g}}$	$> 289 \text{ GeV}$		5%

Results: m_0 vs $m_{1/2}$

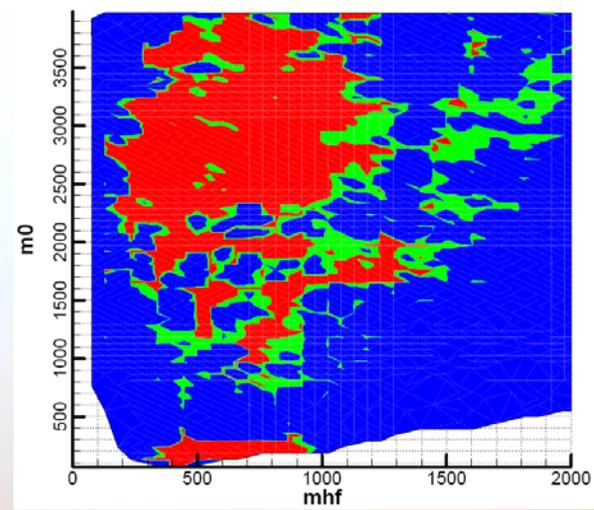
1σ and 2σ CR
based on GA best-fit point
($\chi^2 = 9.3367$)

GA
points:

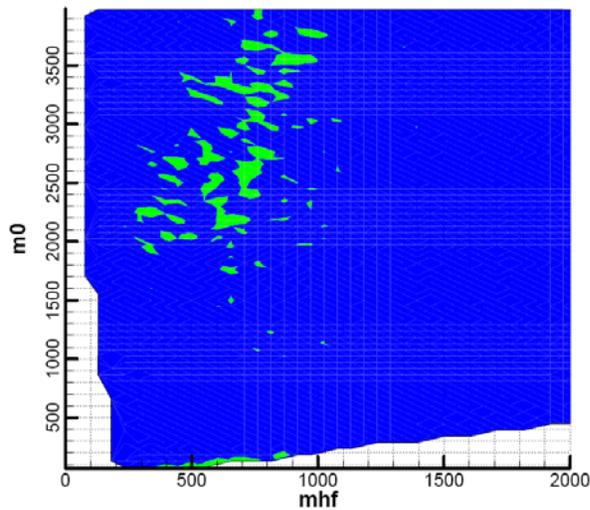


1σ and 2σ CR
based on MN best-fit point
($\chi^2 = 13.511$)

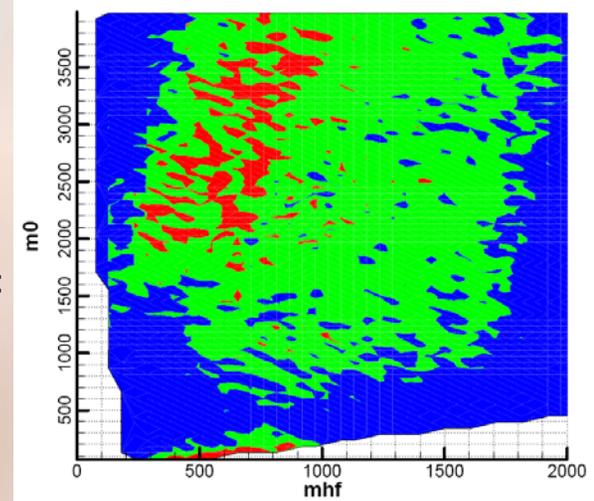
GA
points:



MN
points:



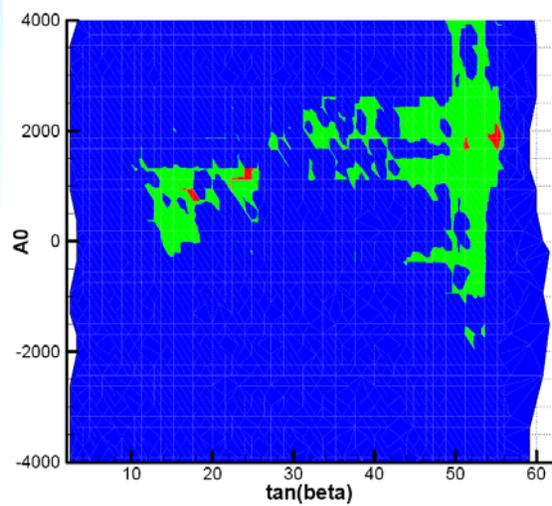
MN
points:



Results: A_0 vs $\tan\beta$

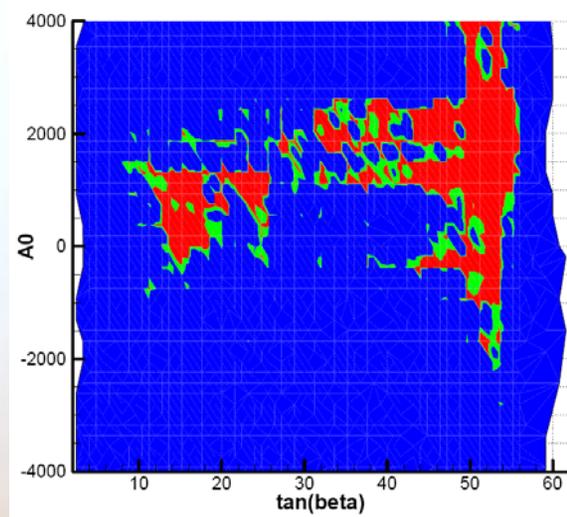
1σ and 2σ CR
based on GA best-fit point
($\chi^2 = 9.3367$)

GA
points:

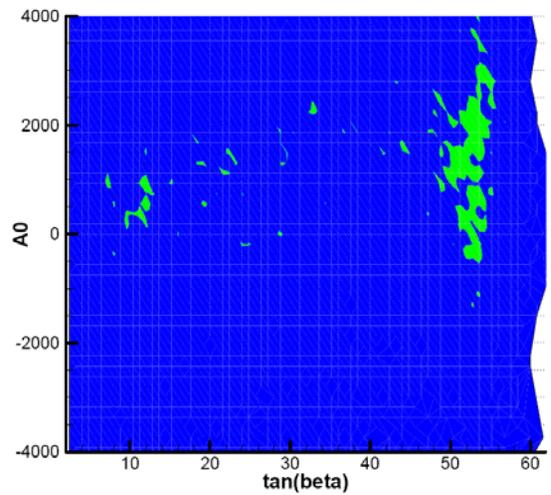


1σ and 2σ CR
based on MN best-fit point
($\chi^2 = 13.511$)

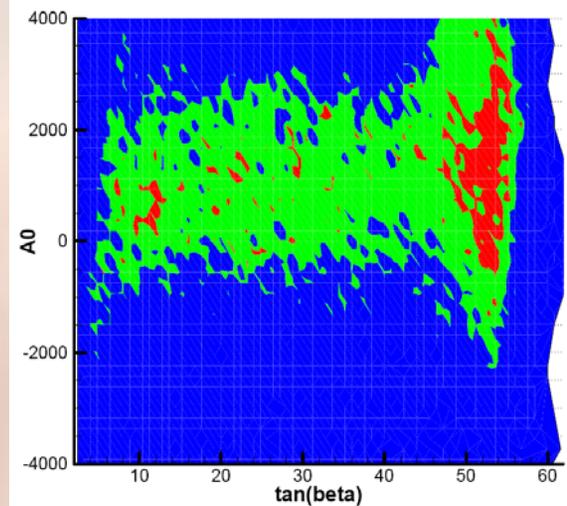
GA
points:



MN
points:



MN
points:



Summary

- The CMSSM, as perhaps the simplest, most popular and widely studied supersymmetric extension to the Standard Model of particle physics offers at the same time a viable and interesting dark matter candidate.
- CMSSM parameter space is very complex and not very well-understood.
- Currently available data do not sufficiently constrain the model parameters in a way completely independent of the priors and statistical measures. Therefore, the Bayesian and frequentist approaches give different results.
- The popular Bayesian scanning techniques (i.e. MCMC and MultiNest) are not good enough for the profile likelihood analysis of the CMSSM.
- Genetic Algorithms seem to offer a new powerful method for this types of analysis with much better outcomes.
- These methods can be used for even more complicated models and/or adding more observables and constraints (such as the Fermi data - [see Pat Scott's presentation tomorrow](#)).

The background of the image shows a close-up of a glass filled with beer, with a white rectangular overlay in the center. The glass is partially filled with a golden beer, and the background is a soft, out-of-focus gradient of light blue and white. The text "Thank You" is written in a white, italicized, sans-serif font with a thin black outline, centered within the white overlay.

Thank You