Sampling of SUSY Models, Statistical Coverage and Genetic Algorithms

or How Darwin Makes Life Easier for SUSY scanners

OKC PROSPECTS Workshop, AlbaNova/ September 16, 2010

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In collaboration with:

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JHEP 04, 057 (2010) [arXiv:0910.3950]

&

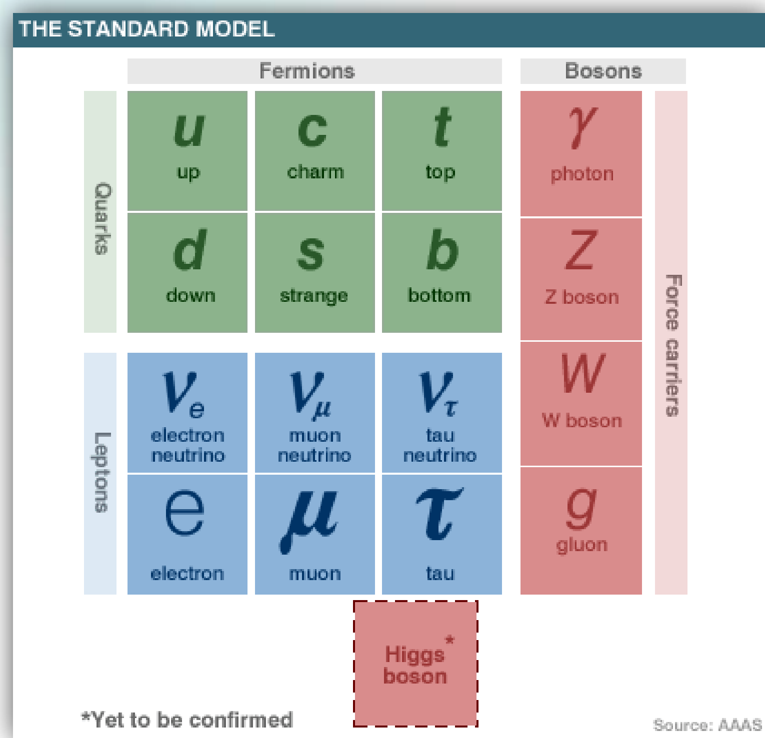
Statistical coverage of Bayesian posterior and profile likelihood methods for supersymmetric parameter estimation, in preparation

Stockholm University

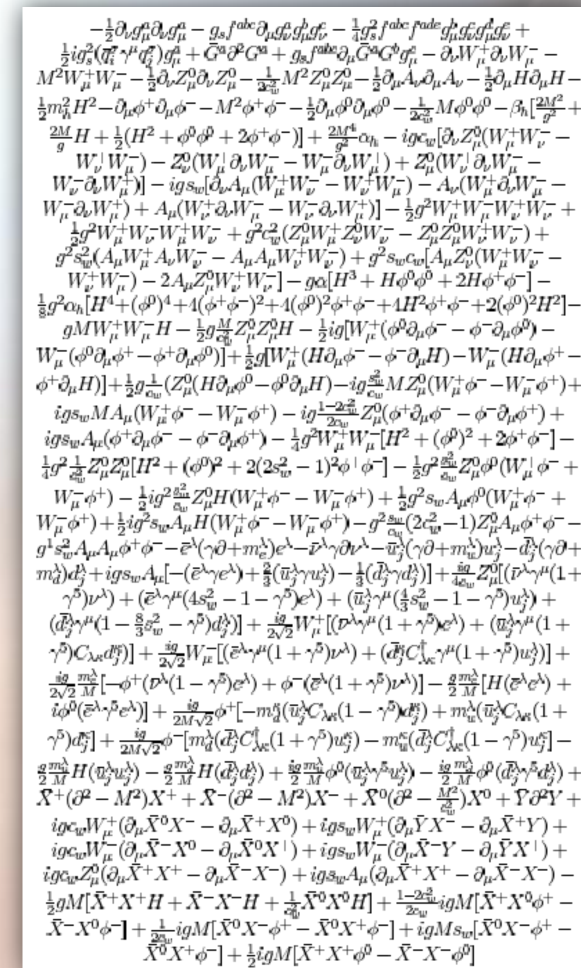
Oskar Klein centre

Oskar Klein Center for Cosmoparticle Physics (OKC)

Standard Model of Particle Physics [SU(3)xSU(2)xU(1)]



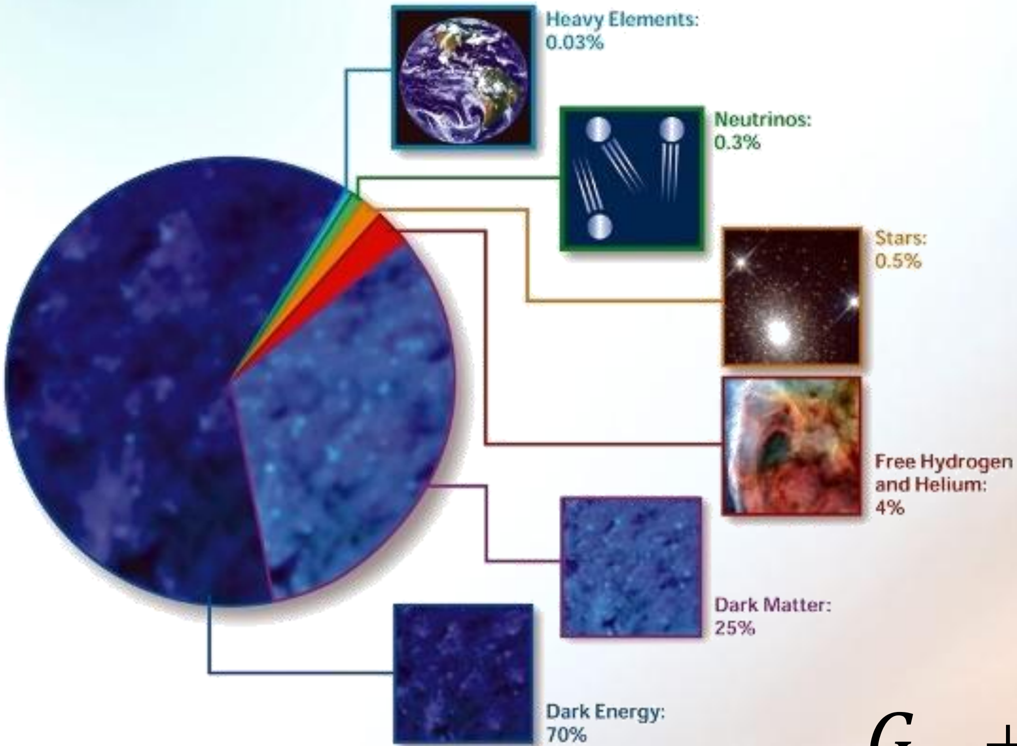
$\mathcal{L} =$



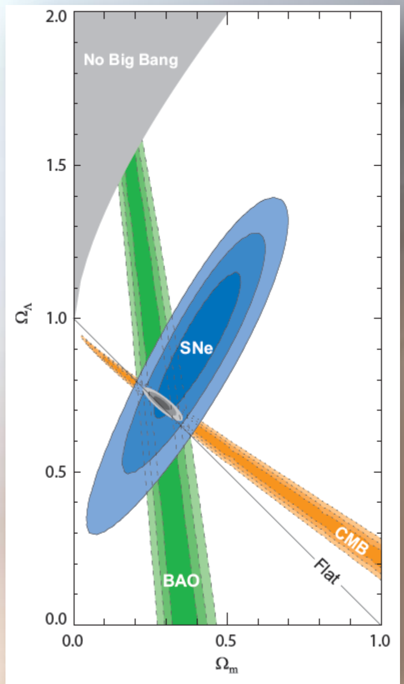
19 Free Parameters

- Consistent with all existing laboratory experimental data

Standard Model of Cosmology [ΛCDM]



Credit: P. Scott (Ph.D. Thesis)



$$G_{\mu\nu} + \Lambda g_{\mu\nu} = 8\pi G T_{\mu\nu}$$

+ FRW metric + perfect fluid

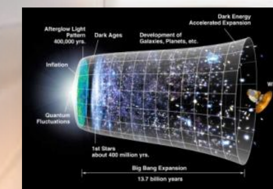
O(20) Free Parameters

- Consistent with all existing astrophysics data

Demands for New Physics Beyond the SM

Problems introduced/highlighted by the SM of Cosmology:

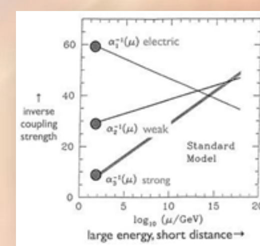
Quantum Gravity: Need a physics that reconciles **Einstein's classical theory of gravity** with the **quantum-field-theoretical nature of the SM** (required to describe **very early moments of the Universe** and very properties of **extreme astrophysical objects**)



Dark Matter (DM)

Dark Energy (DE) & the related **Cosmological Constant Problem** (CCP)

Problems of the SM on its own:



- Particular **gauge symmetric structure** of the SM
- Large differences in **strengths of the gauge interactions**
- Specific **number of generations** for quarks and leptons
- Peculiar **cancellation of anomalies** from the quark and lepton sectors
- Origin of the **fermion masses**
- Specific scale of **EW symmetry breaking** (and the underlying breaking mechanism)
- **Gauge hierarchy problem**: absence of any SM mechanism for protecting the Higgs mass against radiative corrections (fine-tuning)

$$\Delta m_h^2 \sim \frac{\lambda^2}{16\pi^2}\int^{\Lambda}\frac{d^4p}{p^2} \sim \frac{\lambda^2}{16\pi^2}\Lambda^2$$

- **Strong CP** problem
- **Neutrino masses** and mixings

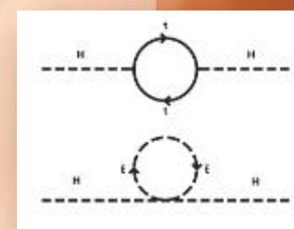
Going beyond the SM seems entirely unavoidable.

New Physics at TeV Scales: Supersymmetry (SUSY)

Arguably the most favoured theory beyond the SM is:

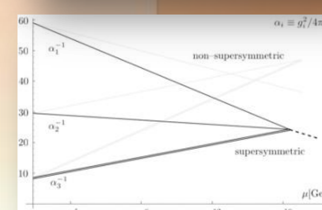
Weak-Scale SUSY

It solves many problems, and paves the way for many others to be solved in broader theoretical frameworks, by providing:



- Natural solution to the **hierarchy problem** **(by eliminating the quadratic divergences in the Higgs mass via the cancellation of the contributions from SM particles and corresponding superpartners)**
- Mechanism for **EW symmetry breaking** **(via renormalisation group evolutions)**
- Viable **DM candidates** **(such as the lightest neutralino, gravitino, sneutrino and axino)**

- **Gauge-coupling unification**
- Answers to many of the questions about the **mathematical structure** of the SM **(if connected to grand unified theories (GUTs) above the unifcation scale)**
- Extensive scope for unifying **gravity** and other fundamental interactions **(either in the framework of supergravity (SUGRA) theories or as the essential ingredient of most versions of string theory)**
- Shedding light on the physics of **very early Universe** and its **late-time behaviour (DE and CCP)**.



Minimal Supersymmetric Standard Model

Field Content:

slightly more than a doubling of the SM particle content

$\Big($ SM fermions and gauge bosons

+

$h, H, A, H^{\pm}$ [Higgs Bosons (Spin 0)]

[after EW Symmetry Breaking] $\Big)$ +

$\tilde{e}_{L,R}, \tilde{\mu}_{L,R}, \tilde{\tau}_{L,R}$	[Sleptons (Spin 0)]
$\tilde{\nu}_e, \tilde{\nu}_\mu, \tilde{\nu}_\tau$	
$\tilde{u}_{L,R}, \tilde{c}_{L,R}, \tilde{t}_{L,R}$	[Squarks (Spin 0)]
$\tilde{d}_{L,R}, \tilde{s}_{L,R}, \tilde{b}_{L,R}$	
$\tilde{B}, \tilde{W}^0, \tilde{H}_u^0, \tilde{H}_d^0$	[Neutralinos (Spin 1/2)]
$\tilde{W}^+, \tilde{H}_u^+$	[Charginos (Spin 1/2)]
$\tilde{W}^-, \tilde{H}_d^-$	
$\tilde{g}$	[Gluinos (Spin 1/2)]
$\tilde{G}$	[Gravitino (Spin 3/2)]

partner of Graviton (G)
(not necessarily included)

If SUSY is an exact symmetry of Nature:

$$m_p = m_{\tilde{p}}$$

SUSY has to be broken at low energies

Minimal Supersymmetric Standard Model

Free Parameters:

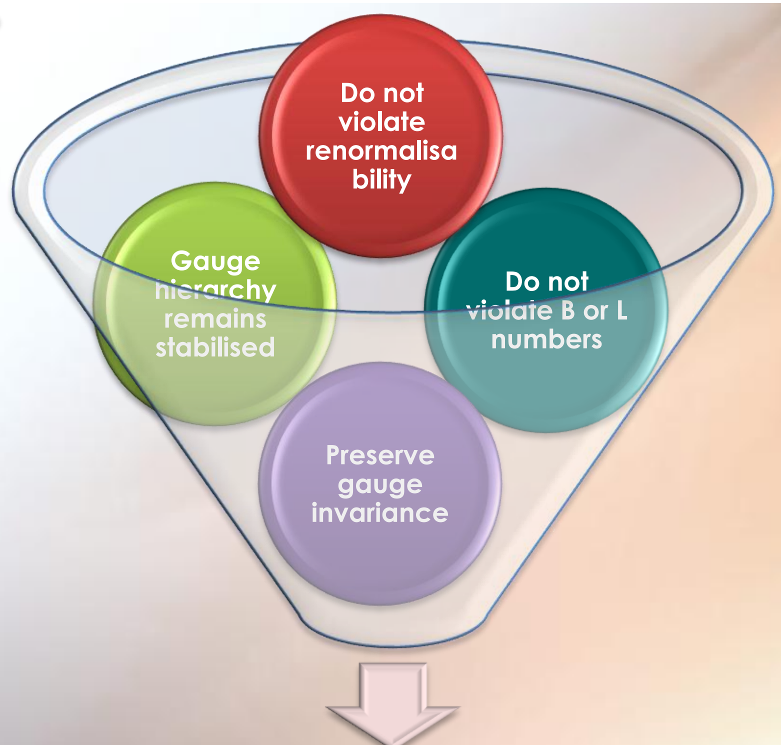
MSSM Lagrangian contains two parts: SUSY'ic terms + SUSY-breaking terms

- **SUSY'ic part in terms of superpotential:**

$$\hat{W} = \mu \hat{H}_u^a \hat{H}_{da} + \sum_{i,j=1,3} \left[(\mathbf{Y}_u)_{ij} \epsilon_{ab} \hat{Q}_i^a \hat{H}_u^b \hat{U}_j^c + (\mathbf{Y}_d)_{ij} \hat{Q}_i^a \hat{H}_{da} \hat{D}_j^c + (\mathbf{Y}_e)_{ij} \hat{L}_i^a \hat{H}_{da} \hat{E}_j^c \right]$$

NEW

- **SUSY-breaking part:**



Soft SUSY-breaking terms

Minimal Supersymmetric Standard Model

Soft SUSY-breaking terms:

$$\mathcal{L}_{\rm soft} = -\frac{1}{2}\left[M_1\bar{\tilde{B}}^0\tilde{B}^0 + M_2\bar{\tilde{W}}_A\tilde{W}_A + M_3\bar{\tilde{g}}_B\tilde{g}_B\right]$$
$$-\frac{i}{2}\left[M_1'\bar{\tilde{B}}^0\gamma_5\tilde{B}^0 + M_2'\bar{\tilde{W}}_A\gamma_5\tilde{W}_A + M_3'\bar{\tilde{g}}_B\gamma_5\tilde{g}_B\right]$$
$$+\left[bH_u^aH_{da} + \text{h.c.}\right] + m_{H_u}^2|H_u|^2 + m_{H_d}^2|H_d|^2$$
$$+\sum_{i,j=1,3}\Big\{-\Big[\tilde{Q}_i^\dagger(\mathbf{m_Q^2})_{ij}\tilde{Q}_j + \tilde{d}_{\mathrm{R}i}^\dagger(\mathbf{m_d^2})_{ij}\tilde{d}_{\mathrm{R}j}$$
$$+\tilde{u}_{\mathrm{R}i}^\dagger(\mathbf{m_u^2})_{ij}\tilde{u}_{\mathrm{R}j} + \tilde{L}_i^\dagger(\mathbf{m_L^2})_{ij}\tilde{L}_j + \tilde{e}_{\mathrm{R}i}^\dagger(\mathbf{m_e^2})_{ij}\tilde{e}_{\mathrm{R}j}\Big]$$
$$+\Big[(\mathbf{A}_u)_{ij}\epsilon_{ab}\tilde{Q}_i^aH_u^b\tilde{u}_{\mathrm{R}j}^\dagger + (\mathbf{A}_d)_{ij}\tilde{Q}_i^aH_{da}\tilde{d}_{\mathrm{R}j}^\dagger$$
$$+(\mathbf{A}_e)_{ij}\tilde{L}_i^aH_{da}\tilde{e}_{\mathrm{R}j}^\dagger + \text{h.c.}\Big]$$
$$+\Big[(\mathbf{C}_u)_{ij}\epsilon_{ab}\tilde{Q}_i^aH_d^{*b}\tilde{u}_{\mathrm{R}j}^\dagger + (\mathbf{C}_d)_{ij}\tilde{Q}_i^aH_{ua}^*\tilde{d}_{\mathrm{R}j}^\dagger$$
$$+(\mathbf{C}_e)_{ij}\tilde{L}_i^aH_{ua}^*\tilde{e}_{\mathrm{R}j}^\dagger + \text{h.c.}\Big]\Big\}$$

violates CP

suppressed in many SUSY-breaking schemes

With:

$$R = (-1)^{3(B-L)+2s}$$

R-parity is conserved in MSSM. } **LSP is absolutely stable.**

$\Longrightarrow$ **Lightest Neutralino (if LSP) is a WIMP DM candidate.**

Phenomenologically very rich, but any comparison of the model with real data becomes highly challenging

Full MSSM Lagrangian:

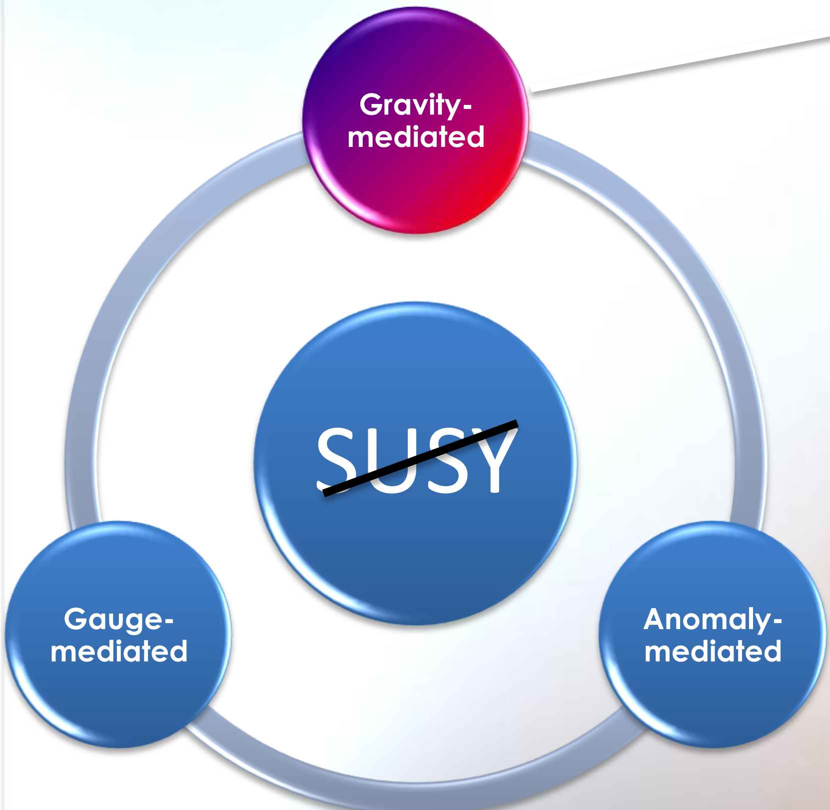
at least 105 new parameters

159 if 'C-terms' are retained

Constraints on flavour-changing neutral currents (FCNCs) and CP-violation can help

Minimal Supersymmetric Standard Model

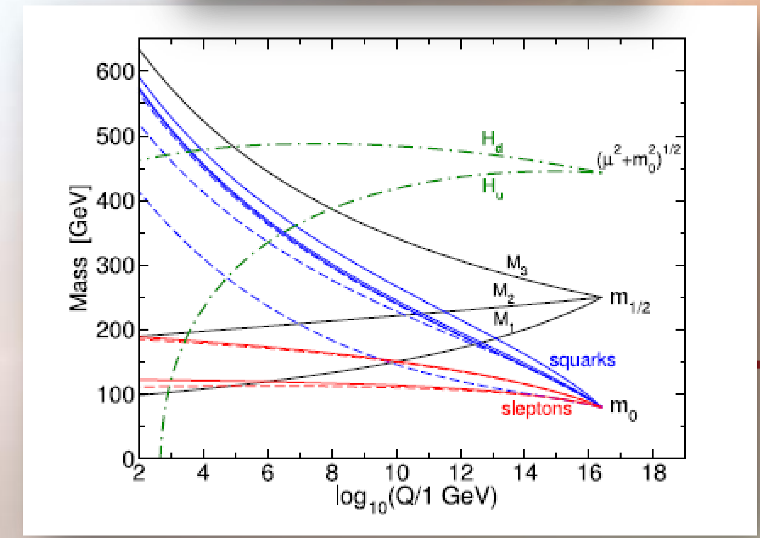
- impose rather experimentally motivated relations directly to the low-energy parameters (e.g. MSSM-7, 8, 10, 11, 18, 24)
- select a particular SUSY-breaking mechanism which relates or even unifies many of the model parameters at certain energies



mSUGRA/CMSSM

unified at GUT Scale

$$\underbrace{\{m_0, m_{1/2}, A_0}_{}, \tan\beta, \mathrm{sign}(\mu)\}$$



S. P. Martin [arXiv:hep-ph/9709356]

Still too complex!

at EW scale: $M_1 : M_2 : M_3 \simeq 1 : 2 : 7$

Renormalisation Group Equations (RGEs)

Scanning Supersymmetric Parameter Spaces

Goal: given a particular version of SUSY, determine **which** parameter combinations fit all experiments, and **how well**

SUSY Global Fit

Issue 1: Combining fits to different experiments

Easy – composite likelihood $(L_1 \times L_2 \equiv \chi_1^2 + \chi_2^2)$

- Dark matter relic density from WMAP
- Precision electroweak tests at LEP
- LEP limits on Higgs and sparticle masses
- B-factory data (rare decays, $b \to s\gamma$)
- Muon anomalous magnetic moment (*g*-2)
- Dark matter direct detection (DD)
- Dark matter indirect detection (ID) (gamma rays, neutrinos, etc.)

Issue 2: Finding the points with the best likelihoods

Tough – grid scans, MCMCs, nested sampling or **GENETIC ALGORITHMS**

Public codes: **SuperBayeS, SFitter, Fittino**

Statistical Framework(s)

Bayes' Theorem:

likelihood

$$p(D|\Theta)p(\Theta)$$

- 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 **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 **SUSY models**.

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

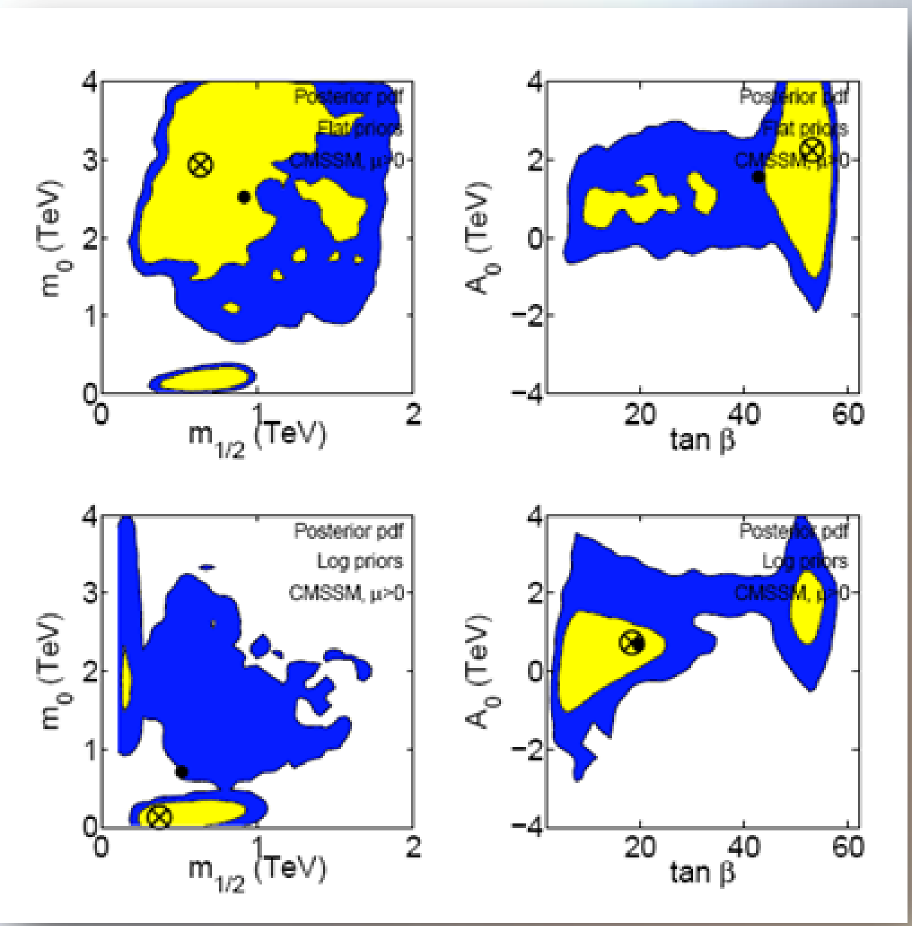
Thus in the profile likelihood one maximizes the value of the likelihood along the hidden dimensions, rather than integrating it out as in the marginal posterior.

CMSSM + SuperBayeS (with MultiNest)

Some CMSSM Scans with SuperBayeS:

Flat Prior:

Log Prior:



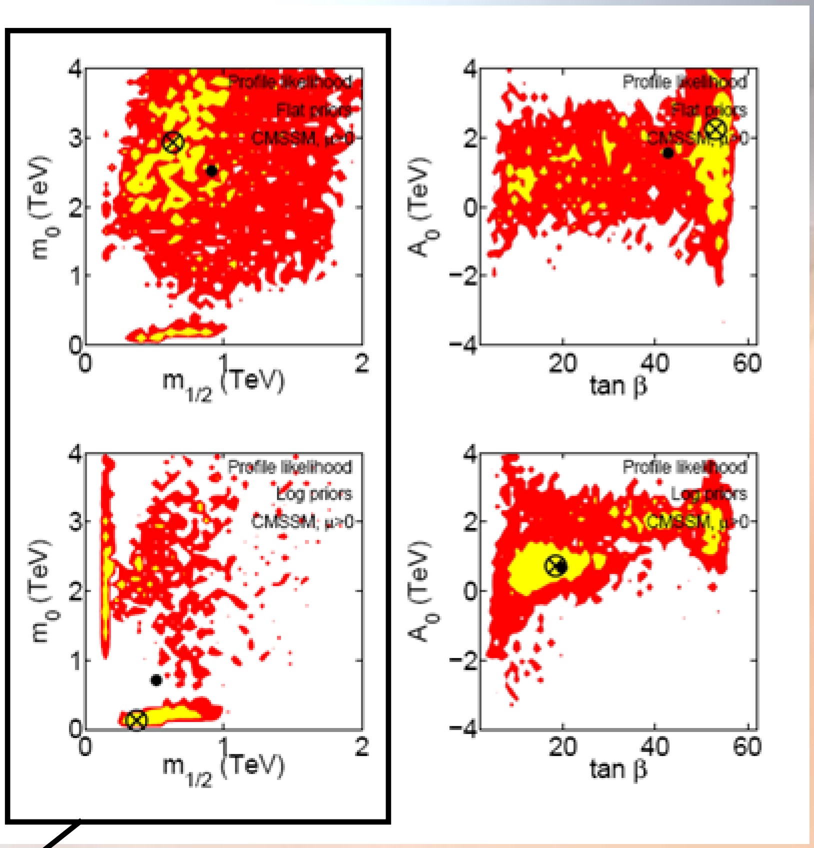
R. Trotta, F. Feroz, M.P. Hobson, L. Roszkowski and R. Ruiz de Austri, *The impact of priors and observables on parameter inferences in the Constrained MSSM*, JHEP 12 (2008) 024 [arXiv:0809.3792]

CMSSM + SuperBayeS (with MultiNest)

Profile Likelihoods:

Flat Prior:

Log Prior:



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Look very different: **prior dependent ?!!**

Not a very interesting technique for profile likelihood approach

According to the SB people, MCMC scans give similar results up to some statistical noise

Complex/Fine-tuned Parameter Spaces

Marginal Posterior vs. Profile Likelihood:

Spike-like best-fit region (problematic)

- Posterior Mass
- Highest Likelihood

In thermodynamic language:

- Thermal Energy
- Temperature

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.

Fine-tuned regions are very important!

Genetic Algorithms (GAs)

GAs can 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 global extrema when the parameter space is **very large**, **complex** or **poorly understood**; **these are precisely what we have in the case of the supersymmetric models including the CMSSM.**

Statistical Coverage

PHYSICAL REVIEW D VOLUME 57, NUMBER 7 1 APRIL 1998

Unified approach to the classical statistical analysis of small signals

Gary J. Feldman*
Department of Physics, Harvard University, Cambridge, Massachusetts 02138

Robert D. Cousins†
Department of Physics and Astronomy, University of California, Los Angeles, California 90095

(Received 21 November 1997; published 6 March 1998)

We give a classical confidence belt construction which unifies the treatment of upper confidence limits for null results and two-sided confidence intervals for non-null results. The unified treatment solves a problem (apparently not previously recognized) that the choice of upper limit or two-sided intervals leads to intervals

G. J. Feldman, R. D. Cousins, Phys. Rev. D 57 (1998) 3873 [physics/9711021]

[...

$$P(\mu \in [\mu_1, \mu_2]) = \alpha. \tag{2.3}$$

...

If Eq. (2.3) is satisfied, then one says that the intervals "cover" μ at the stated confidence, or equivalently, that the set of intervals has the correct "coverage". If there is any value of μ for which $P(\mu \in [\mu_1, \mu_2]) < \alpha$, then we say that the intervals "undercover" for that μ. Significant undercoverage for any μ is a serious flaw. If there is any value of μ for which $P(\mu \in [\mu_1, \mu_2]) > \alpha$, then we say that the intervals "overcover" for that μ. A set of intervals is called "conservative" if it overcovers for some values of μ while undercovering for no values of μ. Conservatism, while not generally considered to be as serious a flaw as undercoverage, comes with a price: loss of power in rejecting false hypotheses.

...]

Likelihood for Coverage Studies

Xe
XENON
Dark Matter Project

Direct Detection with XENON10

- 13 events, no background

rather high statistics

The likelihood is based on the expected number of WIMP-nucleon scattering events **dN** per nuclear recoil energy window **dE_r** which is given by:

$$\frac{dN}{dE_r} = \frac{\sigma\rho}{2\mu^2 m_\chi} F^2 \int_{v_{\min}(E_r)}^{v_{esc}} \frac{f(v)}{v} dv$$

with:

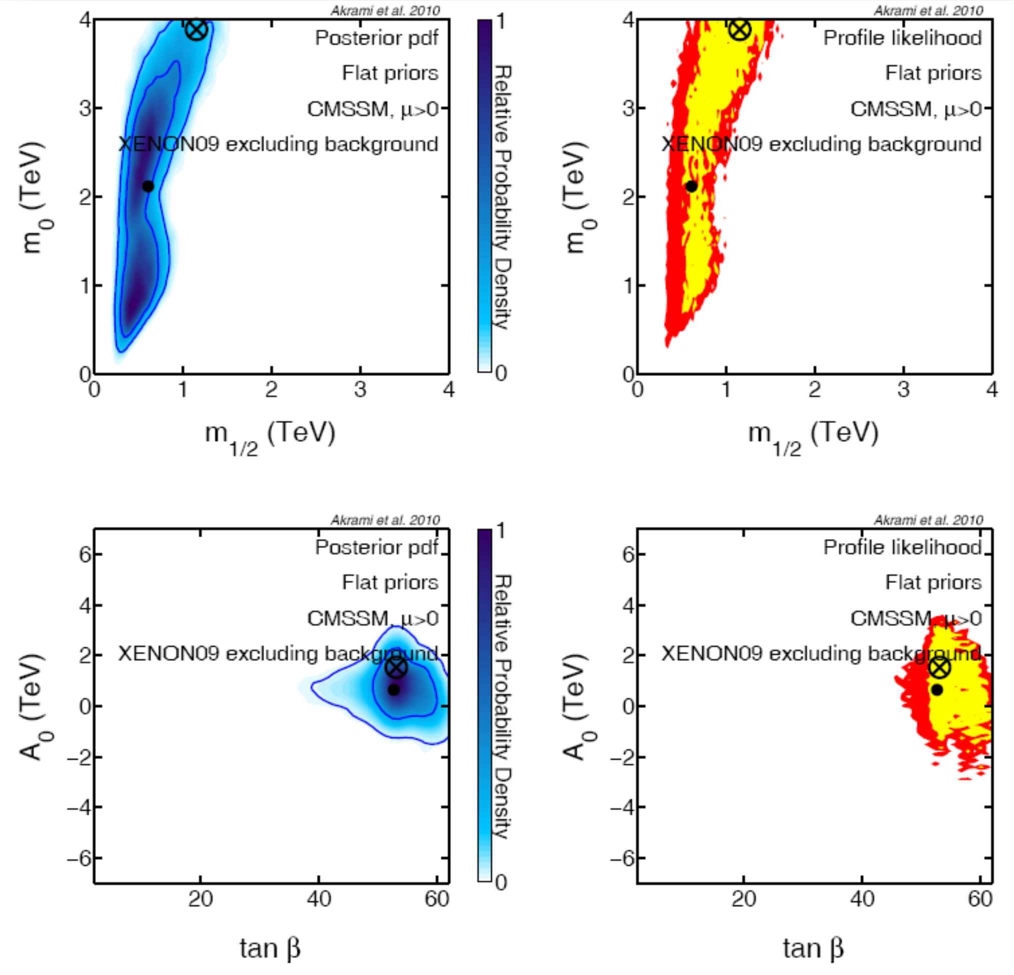
σ: WIMP-nucleus cross-section, **ρ**: local WIMP density, **m_X**: WIMP mass, **F**: nuclear form factor, **$\mu \equiv (m_X m_{nuc})/(m_X + m_{nuc})$**: WIMP-nucleus reduced mass, **f(v)**: distribution of WIMPs in the halo with velocities **v**, **$v_{min}(E_r)$**: minimum velocity required to produce a recoil of energy **E_r**, **v_{esc}**: halo escape velocity.

We assume the standard halo model (i.e. a Maxwellian velocity distribution with **$v_{RMS} \approx 220$ km s^{-1}** and a local density of **0.3 GeV cm^{-3}**) and calculate **dN/dE_r** for each CMSSM point using **DarkSUSY 5.04**.

Listen to Chris Savage's talk tomorrow

Benchmarks for Coverage Studies

CMSSM Parameter:



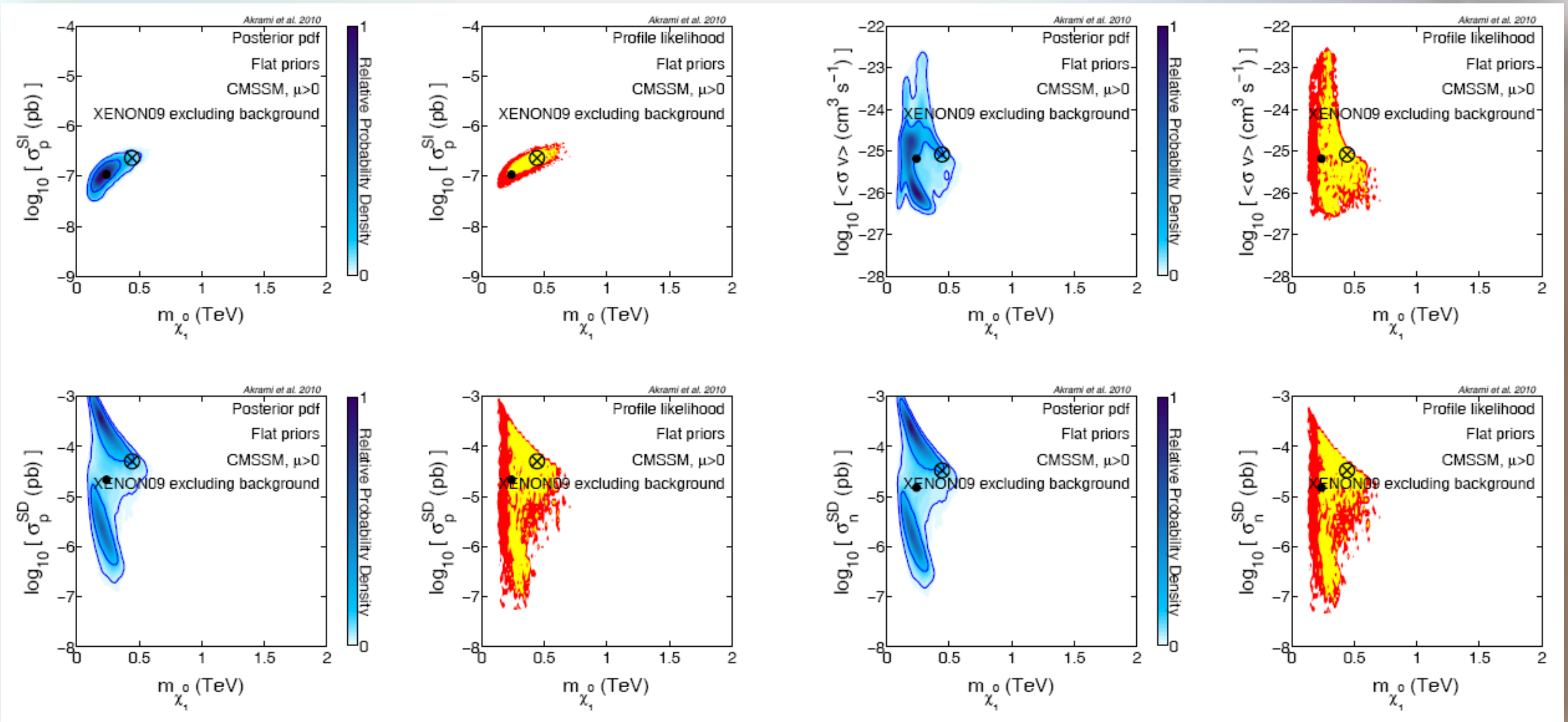
Strategy:

1. Two points are selected (PMean & BFP)
2. New data are generated (100 times)
3. Scans are performed for each set of data (with both flat and log priors)
4. Coverage is verified for 1D marginal PDFs and profile likelihoods

- Cross: Best-fit Point
- Dot: Posterior Mean

Benchmarks for Coverage Studies

Scattering and Annihilation Cross-sections vs Neutralino Mass:



- Cross: Best-fit Point
- Dot: Posterior Mean

UNDERCOVERAGE:

Statistical Coverage (Results)

PRELIMINARY

Flat Prior:

	Posterior Mean: Marginal PDF		Posterior Mean: Profile Likelihood		Best-fit Point: Marginal PDF		Best-fit Point: Profile Likelihood	
	1σ (68%)	2σ (95%)	1σ (68%)	2σ (95%)	1σ (68%)	2σ (95%)	1σ (68%)	2σ (95%)
m_0	98	100	96	100	0	1	62	93
$m_{1/2}$	45	97	78	97	0	0	39	89
A_0	91	100	100	100	0	95	96	100
$\tan\beta$	19					100	99	100
m_χ	53					22	51	87
σ_p^{SI}	18					0	45	93
$\langle\sigma v\rangle$	98					100	95	98

Log Prior:

	Posterior Mean: Marginal PDF		Posterior Mean: Profile Likelihood		Best-fit Point: Marginal PDF		Best-fit Point: Profile Likelihood	
	1σ (68%)	2σ (95%)	1σ (68%)	2σ (95%)	1σ (68%)	2σ (95%)	1σ (68%)	2σ (95%)
m_0	15					0	17	47
$m_{1/2}$	2	30	67	92	0	0	1	17
A_0	43	91	99	100	0	24	91	100
$\tan\beta$	16	91	93	100	38	99	99	100
m_χ	22	65	71	97	0	1	15	59
σ_p^{SI}	17	37	57	88	23	23	2	15
$\langle\sigma v\rangle$	57	98	84	100	21	94	83	98

Posterior Mean | **Best-fit Point**

There is certainly a problem,

- either in choosing **statistical measures/priors**
- or **scanning technique**

(or both)

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. As such, they represent an intelligent random search within a defined search space to solve a complex problem.

- **Selection**
- **Crossov**
- **M**

NNUGA

Neural Network Using Genetic Algorithms

and's Schema Theorem

(early 1970s)

Generation 1 **Generation 2** **Generation N**

Average fitness of the whole population increases. (Survival of the Fittest)

EXAMPLE

Genetic Algorithms (GAs)

Encoding:

a. Binary Encoding

➤Binary encoding is the most common one, mainly because the first research of GA used this type of encoding and because of its relative simplicity.

➤In binary encoding, every **chromosome** is a string of bits - 0 or 1, for example:

chromosome A: **101100101100101011100101**
chromosome B: **111111100000110000011111**

b. Permutation Encoding

➤Every chromosome is a string of numbers that represent a position in a sequence, for example:

chromosome A: **(1 5 3 2 6 4 7 9 8)**
chromosome B: **(8 5 6 7 2 3 1 4 9)**

c. Value Encoding

➤Every chromosome is a sequence of some values. Values can be anything connected to the problem, such as integers, real numbers, characters or any objects.

1.2324 5.3243 0.4556 2.3293 2.4545
ABDJEIFJDHDIERJFDLDFLFEGT
(back), (back), (right), (forward), (left)

Genetic Algorithms (GAs)

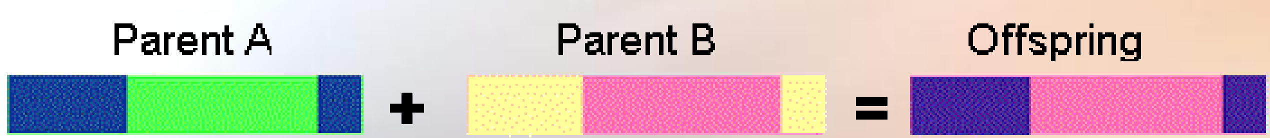
Crossover:

Binary-encoding Crossover

❖**Single point crossover** - one crossover point is selected, binary string from the beginning of the chromosome to the crossover point is copied from the first parent, the rest is copied from the other parent:

11001 | 011 + 11011 | 111 = 11001 | 111

❖**Two point crossover** - two crossover points are selected, binary string from the beginning of the chromosome to the first crossover point is copied from the first parent, the part from the first to the second crossover point is copied from the other parent and the rest is copied from the first parent again:



10 | 0010 | 11 + 11 | 0111 | 01 = 10 | 0111 | 11

Genetic Algorithms (GAs)

Crossover:

❖**Uniform crossover** - bits are randomly copied from the first or from the second parent:

0 | 10 | 010 | 11 + 1 | 00 | 111 | 01 = 1 | 10 | 111 | 11

❖**Arithmetic crossover** - some arithmetic operation is performed to make new offspring:

11001011 + 11011111 = 11001001 (AND)

Permutation-encoding Crossover:

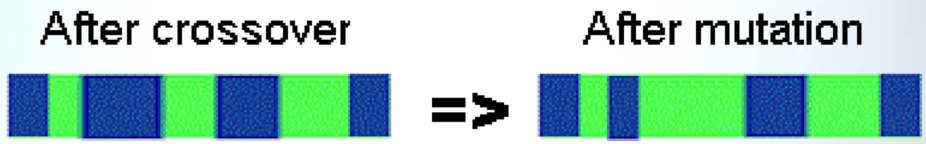
❖**Single point crossover** - one crossover point is selected, the permutation is copied from the first parent till the crossover point, then the other parent is scanned and if the number is not yet in the offspring, it is added:

(1 2 3 4 5 | 6 7 8 9) + (4 5 3 6 8 9 7 2 1) = (1 2 3 4 5 6 8 9 7)

Value-encoding Crossover: All crossovers from binary-encoding crossover can be used.

Genetic Algorithms (GAs)

Mutation:



Binary-encoding Mutation

❖ **Bit inversion** - selected bits are inverted:

1 **1** 0 0 1 0 0 1 → 1 **0** 0 0 1 0 0 1

Permutation-encoding Mutation

❖ **Order changing** - two numbers are selected and exchanged:

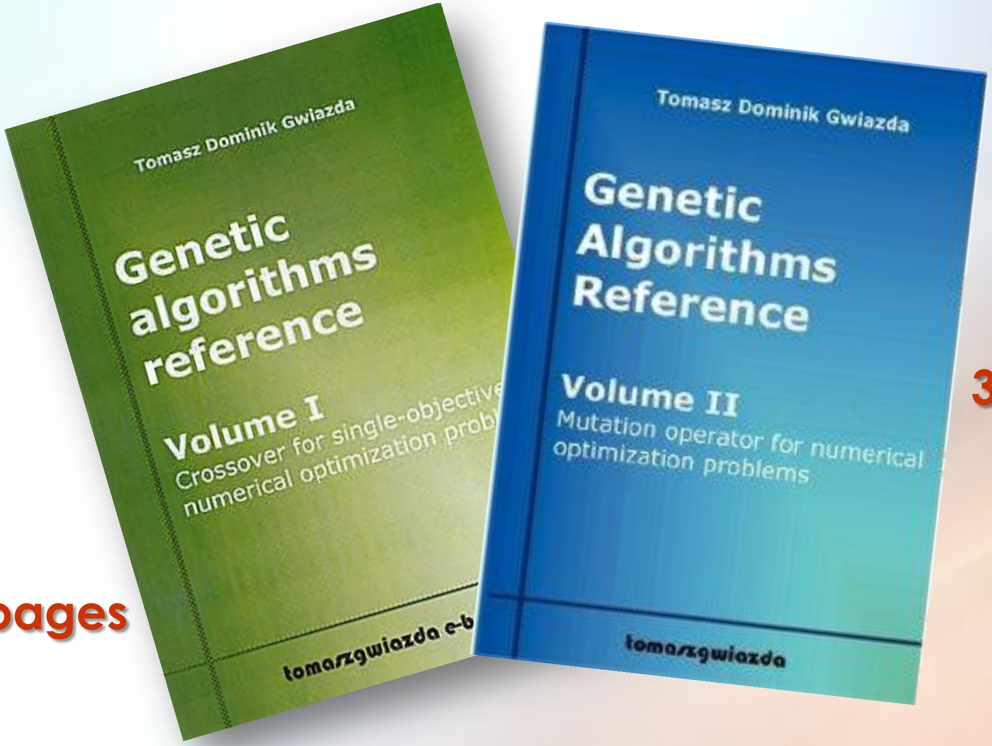
(1 **2** 3 4 5 6 **8** 9 7) → (1 **8** 3 4 5 6 **2** 9 7)

Value-encoding Mutation:

❖ **Adding** a small number (for real value encoding) - a small number is added to (or subtracted from) selected values:

(1.29 5.68 **2.86** **4.11** 5.55) → (1.29 5.68 **2.73** **4.22** 5.55)

Genetic Algorithms (GAs)



412 pages

300 pages

Our implementation: Model/Nuisance Parameters

- **CMSSM:** GUT-scale parameterisation

m_0: scalar mass parameter
$m_{1/2}$: gaugino mass parameter
tanβ: ratio of Higgs VEVs
A_0: trilinear coupling
sgn μ: Higgs mass parameter (+ve in our scans)

Just a testbed – techniques are applicable to any MSSM parameterisation

- **SM nuisances:** reflecting our imperfect knowledge of the values of relevant SM parameters

m_t: pole top quark mass
m_b: bottom quark mass
a_{em}: EM coupling constant
a_s: strong coupling constant

Our implementation: Data/Constraints

Observable	Mean value	Uncertainties (standard deviations) 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	-
$1/\alpha_{\text{em}}(m_Z)^{\overline{MS}}$	127.955	0.03	-
	measured		
m_W	80.398 GeV	25 MeV	15 MeV
$\sin^2\theta_{\text{eff}}$	0.23153	16×10^{-5}	15×10^{-5}
$\delta a_\mu^{\text{SUSY}} \times 10^{10}$	29.5	8.8	1.0
$BR(\overline{B} \to X_s\gamma) \times 10^4$	3.55	0.26	0.21
ΔM_{B_s}	17.77 ps^{-1}	0.12 ps^{-1}	2.4 ps^{-1}
$BR(\overline{B}_u \to \tau\nu) \times 10^4$	1.32	0.49	0.38
$\Omega_\chi h^2$	0.1099	0.0062	$0.1\,\Omega_\chi h^2$
	limits only (95% CL)		
$BR(\overline{B}_s \to \mu^+\mu^-)$	$< 5.8 \times 10^{-8}$		14%
m_h	$>$ 114.4 GeV (SM-like Higgs)		3 GeV
ζ_h^2	$f(m_h)$ (see Ref. 21)		negligible
$m_{\tilde{\chi}_1^0}$	$>$ 50 GeV		5%
$m_{\tilde{\chi}_1^\pm}$	$>$ 103.5 GeV ($>$ 92.4 GeV)		5%
$m_{\tilde{e}_R}$	$>$ 100 GeV ($>$ 73 GeV)		5%
$m_{\tilde{\mu}_R}$	$>$ 95 GeV ($>$ 73 GeV)		5%
$m_{\tilde{\tau}_1}$	$>$ 87 GeV ($>$ 73 GeV)		5%
$m_{\tilde{\nu}}$	$>$ 94 GeV ($>$ 43 GeV)		5%
$m_{\tilde{t}_1}$	$>$ 95 GeV ($>$ 65 GeV)		5%
$m_{\tilde{b}_1}$	$>$ 95 GeV ($>$ 59 GeV)		5%
$m_{\tilde{q}}$	$>$ 375 GeV		5%
$m_{\tilde{g}}$	$>$ 289 GeV		5%

+

- **Physicality**
  - self-consistent solutions to the RGEs exist
  - conditions of EW symmetry breaking are satisfied
  - no masses become tachyonic)
- **Neutralino is the LSP**

Our implementation: Scanning Algorithm

General Structure:

Genetic Operator: $\mathbb{G} = \mathbb{RMCS}$

- **R**eproduction
- **M**utation
- **C**rossover
- **S**election

initialisation:

$P^0 := \{\Theta_i^0\}, \ \forall i \in [1, I]$

$k := 0$

reproduction loop:

do while not $\mathbb{T}$

$k := k + 1$

generating new population through genetic operators:

$P^k := \mathbb{G} P^{k-1}$

end do

reading the best-fit point:

$\Theta_{max} := \Theta_l^m \text{ where } \mathcal{L}(\Theta_l^m) = \max\{\mathcal{L}(\Theta_i^k)\}, \ \forall i \in [1, I], \ \forall k \in [1, K]$

We keep all generated points to map confidence regions.

SuperBayes v1.35 + PIKAIA 1.2*

Huge potential for parallelisation

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

SuperBayes
(www.superbayes.org)

New version v1.5 now available (June 2010)

- Developed by **R. Ruiz de Austri**, **R. Trotta**, **F. Feroz**, **L. Roszkowski**, and **M. 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**, **MicrOMEGAs**, **FeynHiggs**, and **Bdecay**.
- 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 also been used for **profile likelihood** analyses of the model, they are essentially **optimised for marginal posterior analyses** only.

Partly added by our group for DD, Hess, Fremi, etc.

~~200~~ 50 times faster

Listen to R. Ruiz's talk after lunch

Our implementation: Scanning Algorithm

Fitness function: $1/\chi^2$ (**positive**, to be **maximised**)

Encoding: decimal alphabet (a string of **base 10** integers, every normalised parameter θ_i (i=1…8)is encoded into a string $\mathbf{d_1 d_2 \ldots d_{n_d}}$, where the ($d_i > 0$) ϵ [0; 9]. $\mathbf{n_d=5}$, i.e. every individual chromosome's length is $m \times n_d$ = 8x5 = 40.

Initialisation and population size: completely **random** points in the parameter space for initial population; population size of $\mathbf{n_p = 100}$ – fixed.

Selection: (**Roulette Wheel Algorithm**) a stochastic mechanism; probability of an individual to be selected for breeding is based on its fitness:

- assign to each individual $\boldsymbol{\theta_i}$ a rank $\mathbf{r_i}$ based on its fitness $\mathbf{f_i}$ (**r=1** corresponds to the fittest individual and $\mathbf{r=n_p}$ to the most unfit)
- a ranking fitness $\mathbf{f'_i}$ is defined in terms of this rank:

$$f'_i = n_p - r_i + 1$$

- the sum of all ranking fitness values in the population is computed and $\mathbf{n_p}$ running sums are defined as:

$$F = \sum_{i=1}^{n_p} f'_i \qquad S_j = \sum_{i=1}^{j} f'_i,\ j = 1, \ldots, n_p$$

Obviously: $\mathbf{S_{j+1} \geq S_j}$ and $\mathbf{S_{n_p} = F}$.

Our implementation: Scanning Algorithm

- a random number **R ϵ [0; F]** is generated and the element **S_j** is located for which **$S_{j-1} \leq R < S_j$**. The corresponding individual is one of the parents selected for breeding; the other one is also chosen in the same manner.

Other selection methods exist: **Boltzman selection, Tournament selection**, **Rank selection**, **Steady-State selection**, etc.

Crossover: combination of **one-point** and **two-point** crossover (to avoid "**end-point bias problem**") - crossover operation is applied only with a preset probability (**85%**)

uniform one-point crossover		
initial parent chromosomes	6739...8451	4394...0570
selecting a random cutting point	6739...84|51	4394...05|70
swapping the sub-strings	6739...84|70	4394...05|51
final offspring	6739...8470	4394...0551
uniform two-point crossover		
initial parent chromosomes	6739...8451	4394...0570
selecting two random cutting points	67|39...845|1	43|94...057|0
swapping the sub-strings	67|94...057|1	43|39...845|0
final offspring	6794...0571	4339...8450

Our implementation: Scanning Algorithm

Mutation: **uniform one-point mutation** operator. Different genes in the offspring's chromosomes (i.e. decimal digits in the 40-digit strings) are replaced with a predefined probability (the '**mutation rate**'), by a **random** integer in the interval [0; 9].

Local Maxima – Randomness

instead of using a fixed mutation rate we allow it to **vary dynamically** throughout the run, such that the degree of '**biodiversity**' is monitored and the mutation rate is **adjusted** accordingly.

Degree of clustering is assessed based on the difference between the actual fitness values of the **best** and **median** points:

$$\Delta f = (f_{r=1} - f_{r=n_p/2})/(f_{r=1} + f_{r=n_p/2})$$

(with lower and upper **critical** values of **0.05** and **0.25**, multiplicative factor of **1.5**, mutation **limits** of **0.0005** and **0.25**, and **initial** value of **0.005)**.

Elitism: To guarantee survival of this individual, we use an elitism feature in our reproduction plan.

Termination and number of generations: **fixed** and predetermined number of generations (~3000)

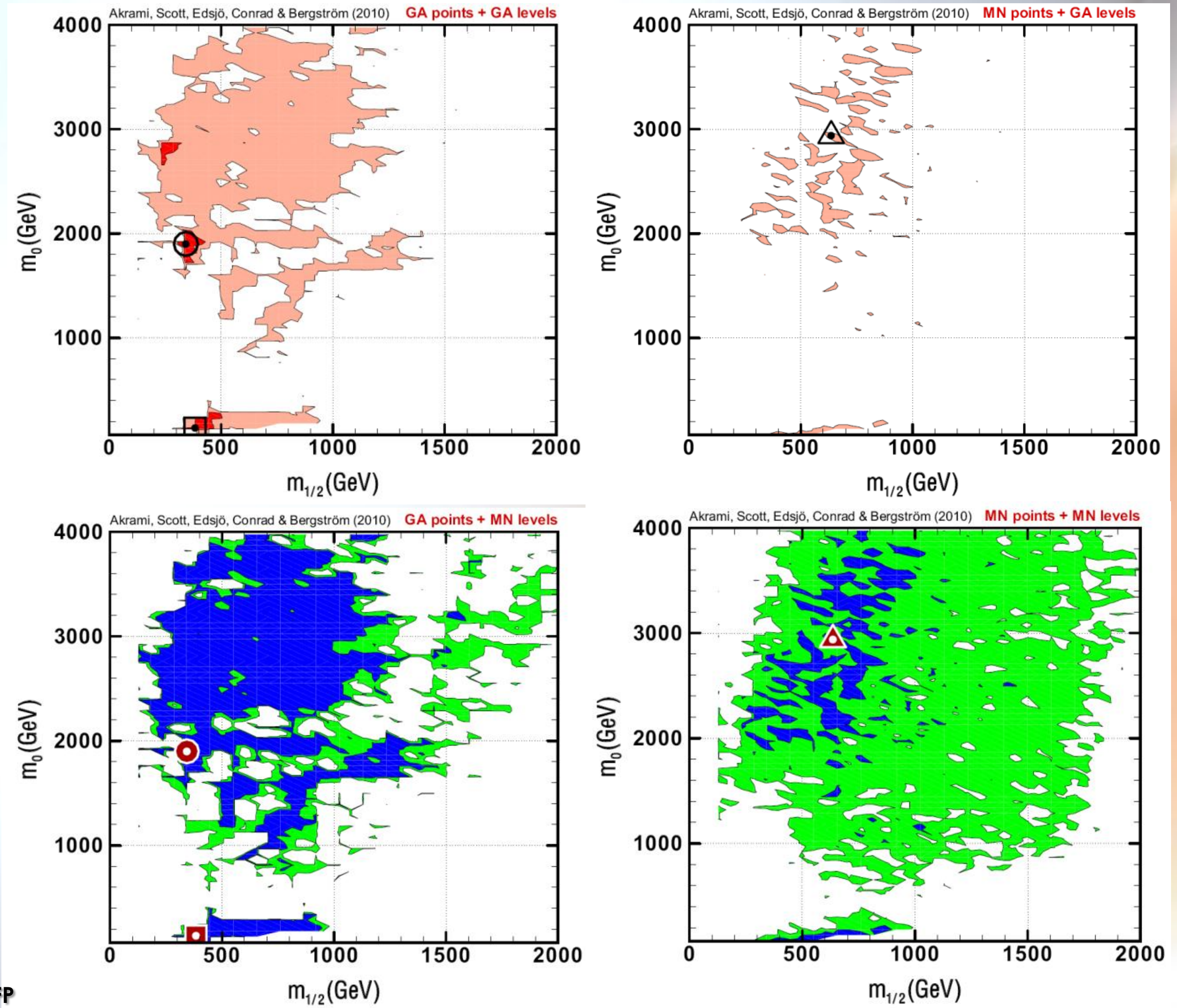
Results: 2D Profile Likelihoods in m_0-$m_{1/2}$ Plane

GAs find better fits than nested sampling (X^2 = 9.35 vs. X^2 = 13.51).

3x10[6] points in total

Contours based on GA best-fit point:

Contours based on MN best-fit point:

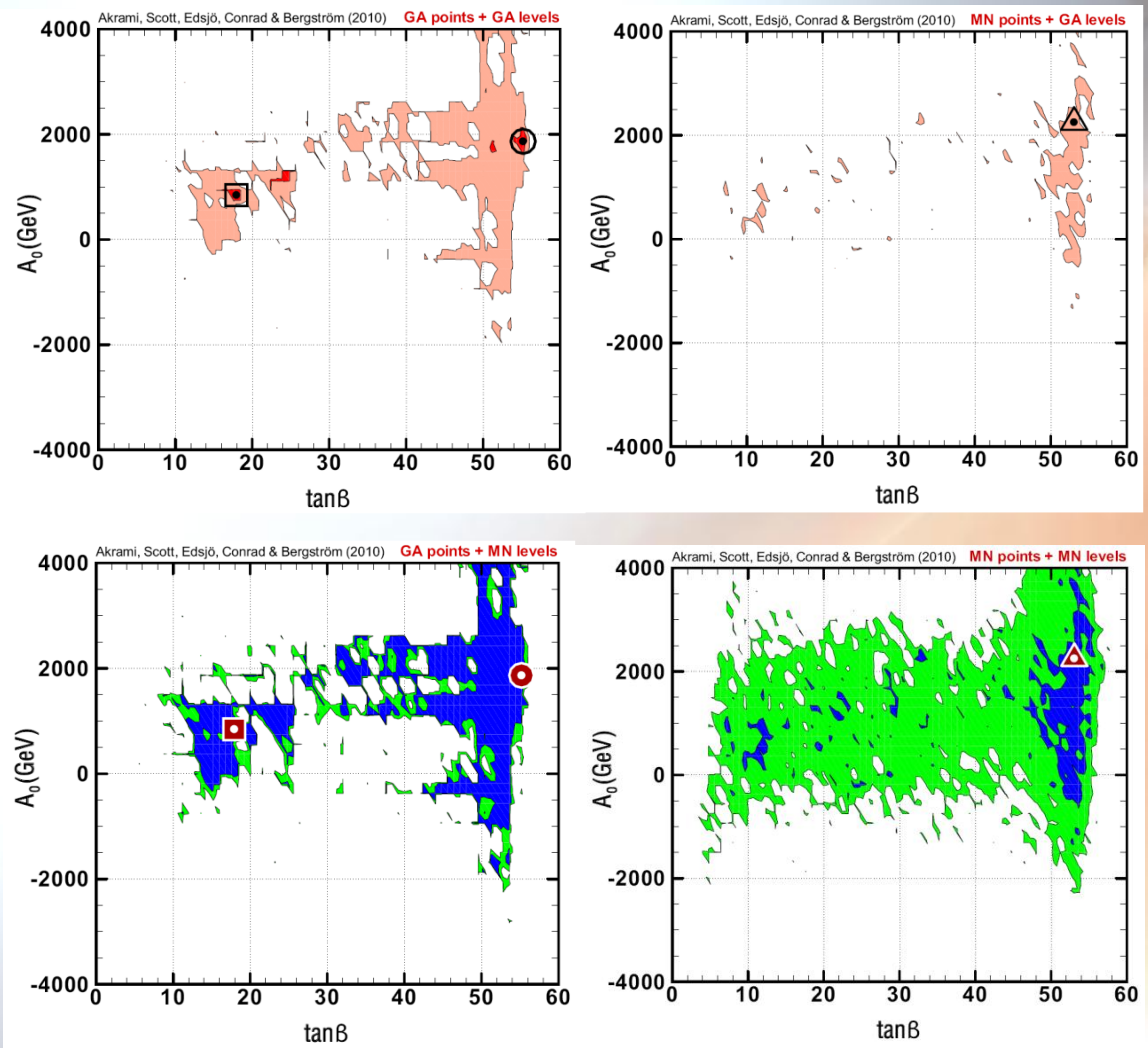


- Dotted circle: GA global BFP
- Dotted square: GA COA BFP
- Dotted triangle: MN global BFP

Results: 2D Profile Likelihoods in A_0-tanβ Plane

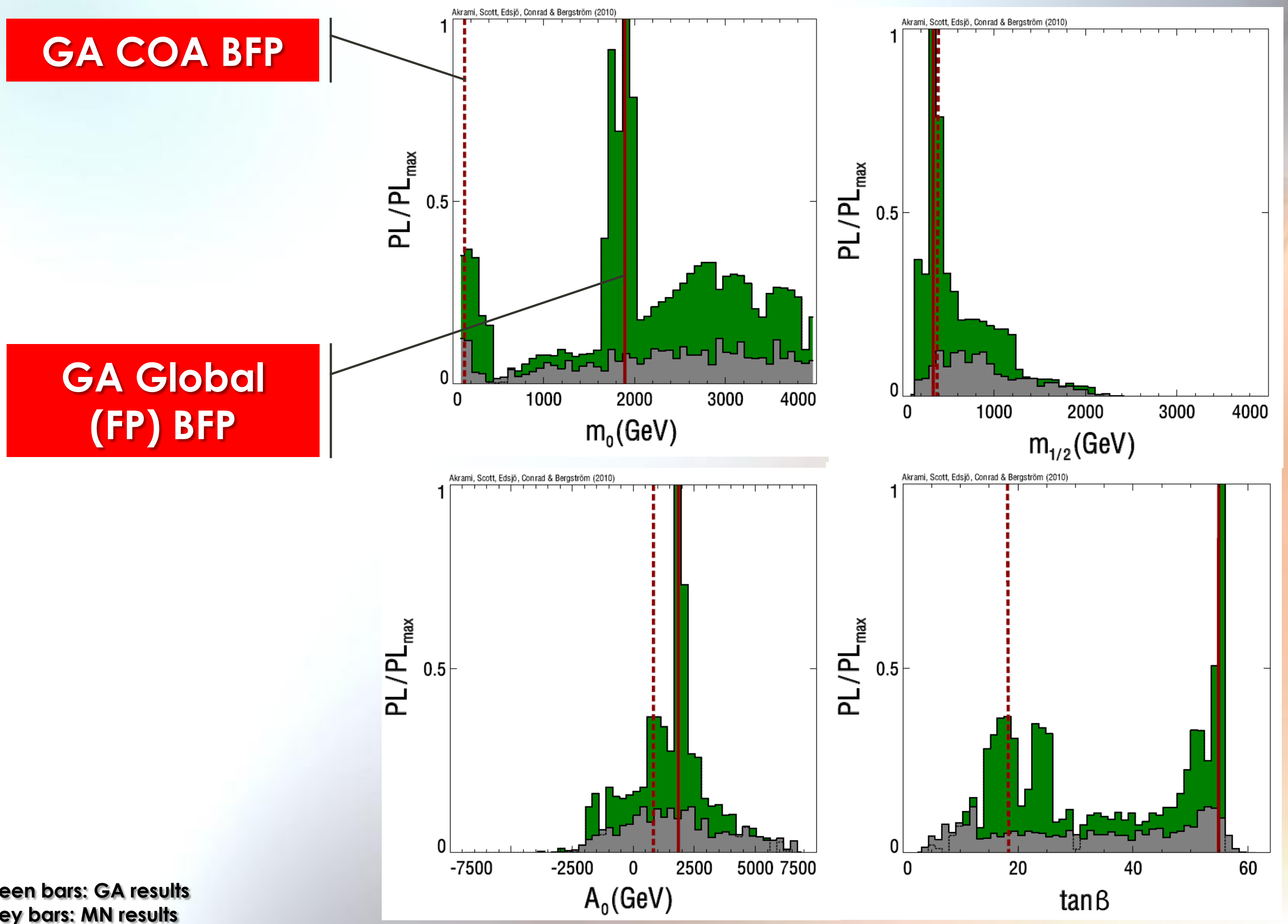
Contours based on GA best-fit point:

Contours based on MN best-fit point:



- Dotted circle: GA global BFP
- Dotted square: GA COA BFP
- Dotted triangle: MN global BFP

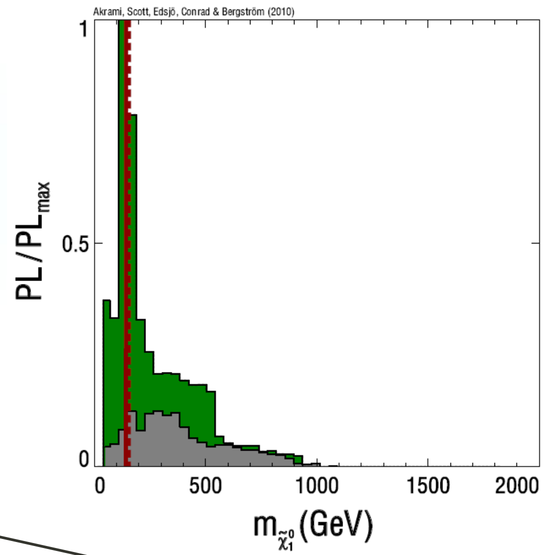
Results: 1D Profile Likelihoods for CMSSM Parameters

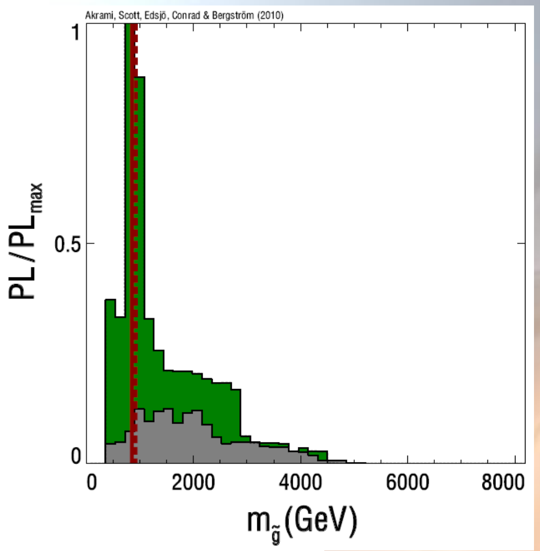


- Green bars: GA results
- Grey bars: MN results

Results: 1D Profile Likelihoods for Some Observables

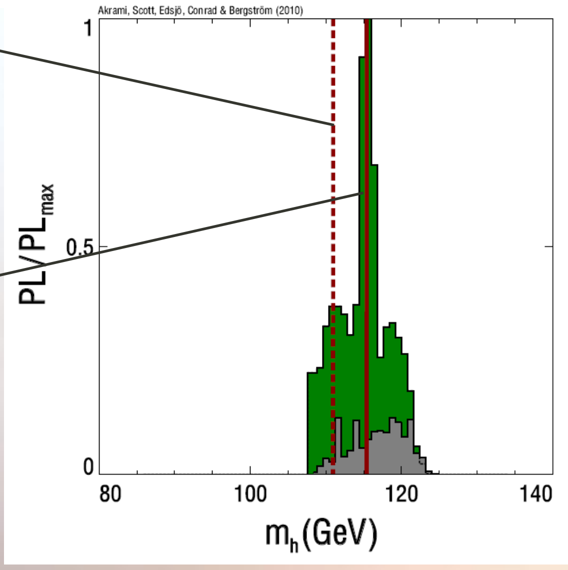
- Green bars: GA results
- Grey bars: MN results





GA COA BFP

GA Global (FP) BFP

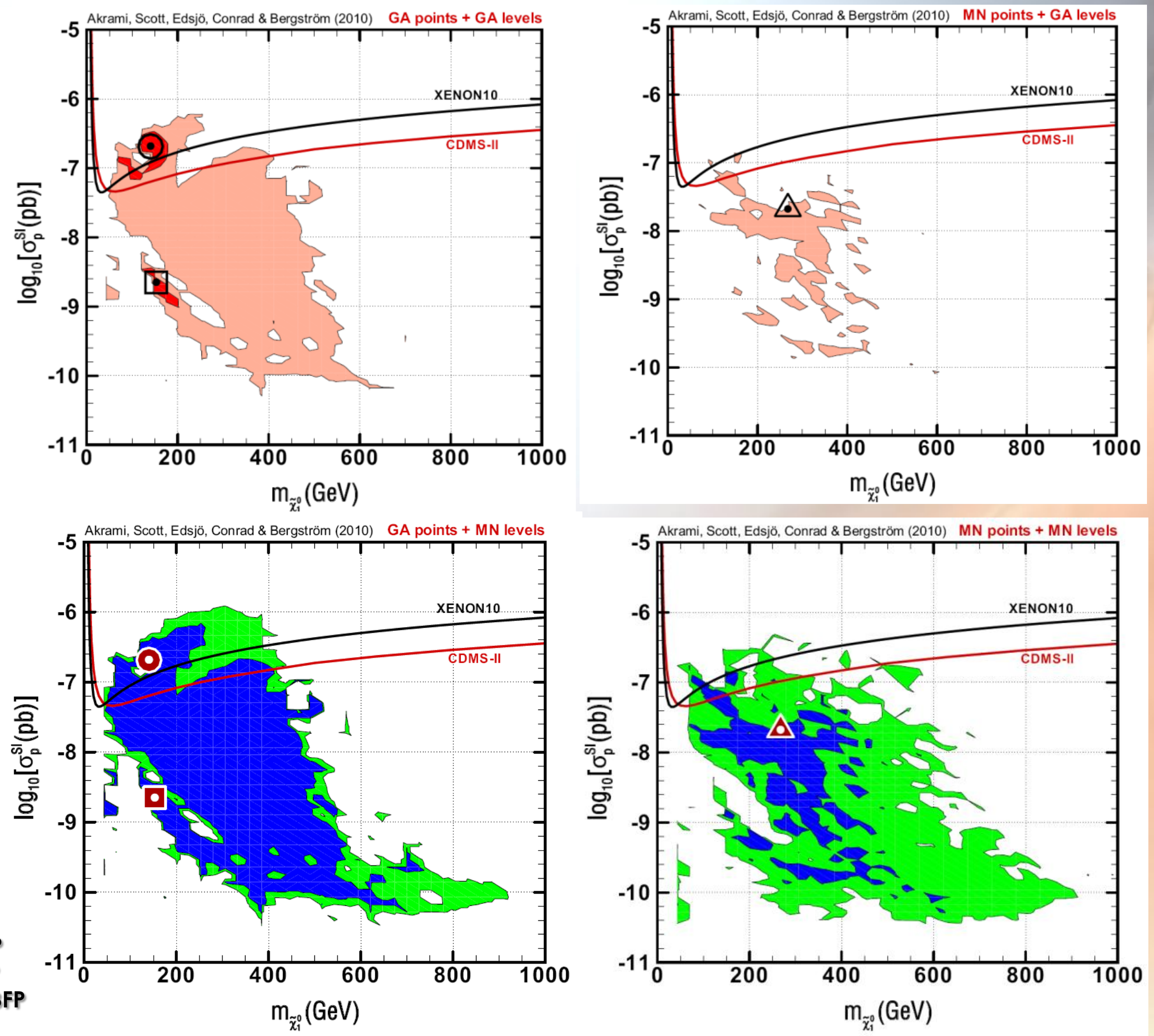


- The LHC is in principle able to investigate a large fraction of the high-likelihood points in the CMSSM parameter space if it explores sparticle masses up to around 3 TeV.

Results: 2D Profile Likelihoods in DM DD Plane (SI)

Contours based on GA best-fit point:

Contours based on MN best-fit point:



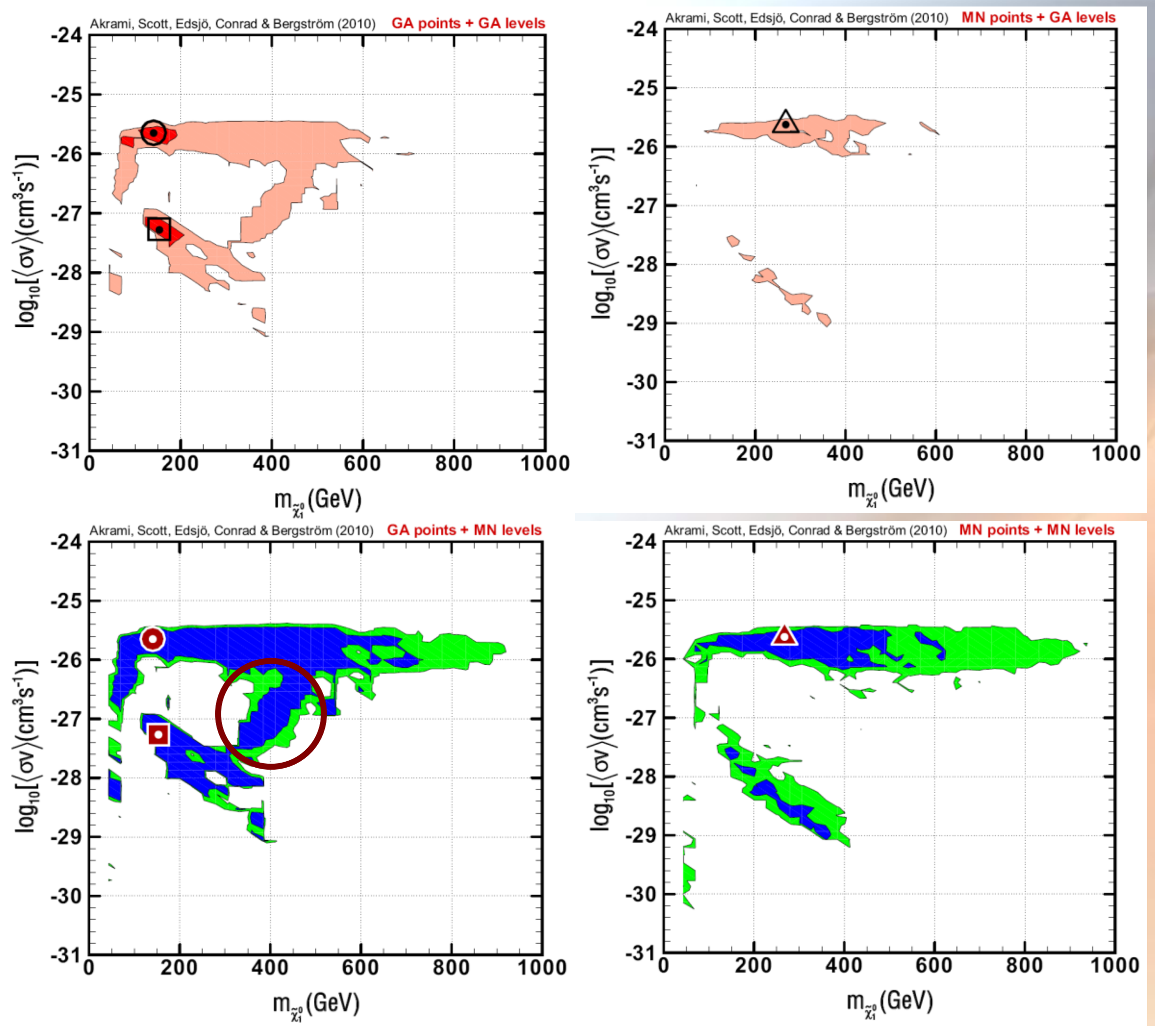
- Dotted circle: GA global BFP
- Dotted square: GA COA BFP
- Dotted triangle: MN global BFP

- Best-fit point is actually ruled out by direct detection (under standard halo assumptions).
- Secondary maximum still OK.

Results: 2D Profile Likelihoods in DM ID Plane

Contours based on GA best-fit point:

Contours based on MN best-fit point:



- **Dotted circle: GA global BFP**
- **Dotted square: GA COA BFP**
- **Dotted triangle: MN global BFP**

- **Global best-fit point should be probed soon by *Fermi* (**See e.g. P. Scott, J. Conrad, J. Edsjö, L. Bergström, C. Farnier & **YA**. *Direct Constraints on Minimal Supersymmetry from Fermi-LAT Observations of the Dwarf Galaxy Segue 1*, JCAP 01, 031 (2010) [arXiv:0909.3300]**)**
- **The GA turns up a 'new' region at moderate <σv>, around 400 GeV. This region is a high-m_0 stau coannihilation region, apparently missed in other scans.**

Conclusions

- SUSY parameter spaces are complex
- Statistical inference strongly depends on statistical measures/priors and scanning techniques
- GAs help for profile likelihood studies
- Still far from being “The Algorithm”

A Quotation by the Inventor

Living organisms are consummate problem solvers. They exhibit a versatility that puts the best computer programs to shame. This observation is especially galling for computer scientists, who may spend months or years of intellectual effort on an algorithm, whereas organisms come by their abilities through the apparently undirected mechanism of evolution and natural selection.

John Holland

Thank You

for your attention

Results: Best-fit Parameter Values

model (+nuisance) parameters		
	GA global BFP (located in FP region)	GA COA BFP
m_0	1900.5 GeV	133.9 GeV
$m_{1/2}$	342.8 GeV	383.1 GeV
A_0	1873.9 GeV	840.6 GeV
$\tan\beta$	55.0	17.9
m_t	172.9 GeV	173.3 GeV
$m_b(m_b)^{\overline{MS}}$	4.19 GeV	4.20 GeV
$\alpha_s(m_Z)^{\overline{MS}}$	0.1172	0.1183
$1/\alpha_{\rm em}(m_Z)^{\overline{MS}}$	127.955	127.955

observables		
	GA global BFP (located in FP region)	GA COA BFP
m_W	80.366 GeV	80.371 GeV
$\sin^2\theta_{\rm eff}$	0.23156	0.23153
$\delta a_\mu^{\rm SUSY} \times 10^{10}$	5.9	14.5
$BR(\overline{B} \to X_s\gamma) \times 10^4$	3.58	2.97
ΔM_{B_s}	17.37 ps^{-1}	19.0 ps^{-1}
$BR(\overline{B}_u \to \tau\nu) \times 10^4$	1.32	1.46
$\Omega_\chi h^2$	0.10949	0.10985
$BR(\overline{B}_s \to \mu^+\mu^-)$	4.34×10^{-8}	3.87×10^{-8}

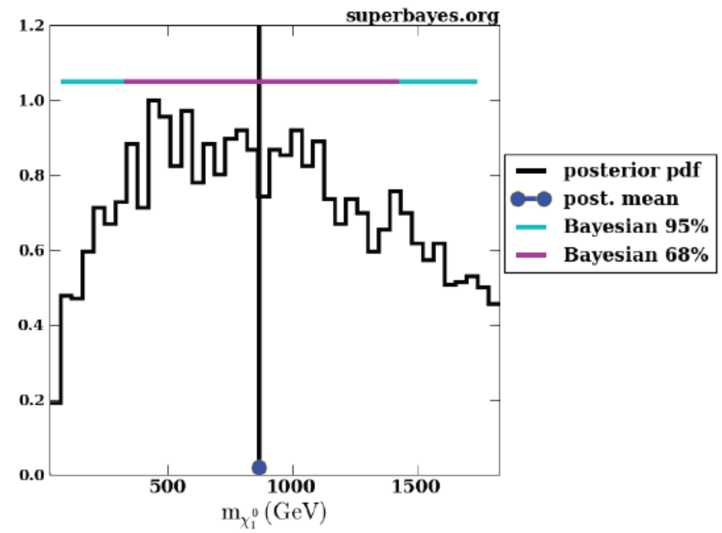
Results: Best-fit Parameter Values

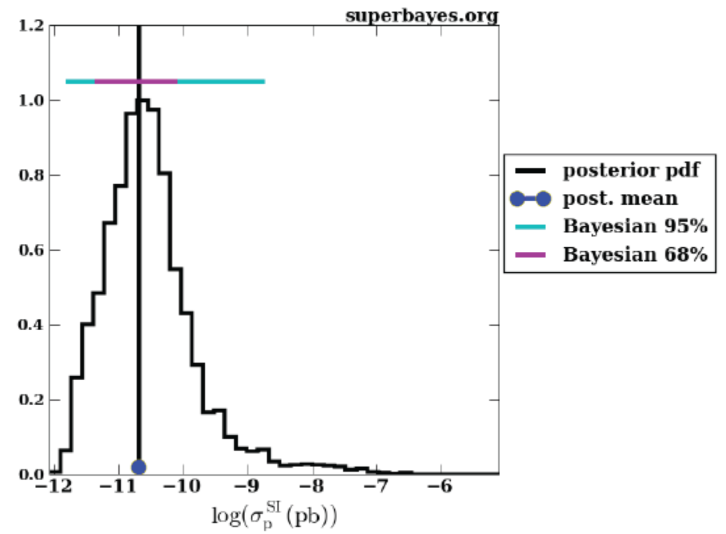
observable	partial χ^2 (fractional contribution to the total χ^2 in %)			
	GA global BFP located in FP region	GA COA BFP	MN global BFP with flat priors	MN global BFP with log priors
nuisance parameters	0.12 (1.27%)	0.35 (3.10%)	0.48 (3.56%)	0.81 (6.78%)
mw	1.21 (12.95%)	0.83 (7.29%)	1.48 (10.92%)	0.69 (5.83%)
$\sin^2\theta_{\text{eff}}$	0.024 (0.26%)	$\sim 10^{-4}$ (0.001%)	0.07 (0.49%)	0.0040 (0.034%)
$\delta a_\mu^{\text{SUSY}}$	7.09 (75.79%)	2.86 (25.21%)	9.21 (68.20%)	2.40 (20.18%)
$BR(\overline{B} \to X_s\gamma)$	0.010 (0.11%)	3.03 (26.76%)	0.10 (0.74%)	3.83 (32.20%)
ΔM_{B_s}	0.028 (0.30%)	0.26 (2.31%)	0.09 (0.66%)	0.29 (2.41%)
$BR(\overline{B}_u \to \tau\nu)$	$\sim 10^{-5}$ (10^{-4}%)	0.050 (0.44%)	1.91 (14.14%)	0.043 (0.36%)
$\Omega_\chi h^2$	0.0011 (0.012%)	$\sim 10^{-5}$ (10^{-4}%)	0.03 (0.2%)	0.13 (1.07%)
$BR(\overline{B}_s \to \mu^+\mu^-)$	0.016 (0.17%)	0.00 (0.00%)	0.00 (0.00%)	0.00 (0.00%)
m_h	0.85 (9.14%)	3.96 (34.88%)	0.15 (1.09%)	3.70 (31.13%)
sparticles	0.00 (0.00%)	0.00 (0.00%)	0.00 (0.00%)	0.00 (0.00%)
all	**9.35 (100 %)**	**11.34 (100 %)**	**13.51 (100 %)**	**11.90 (100 %)**

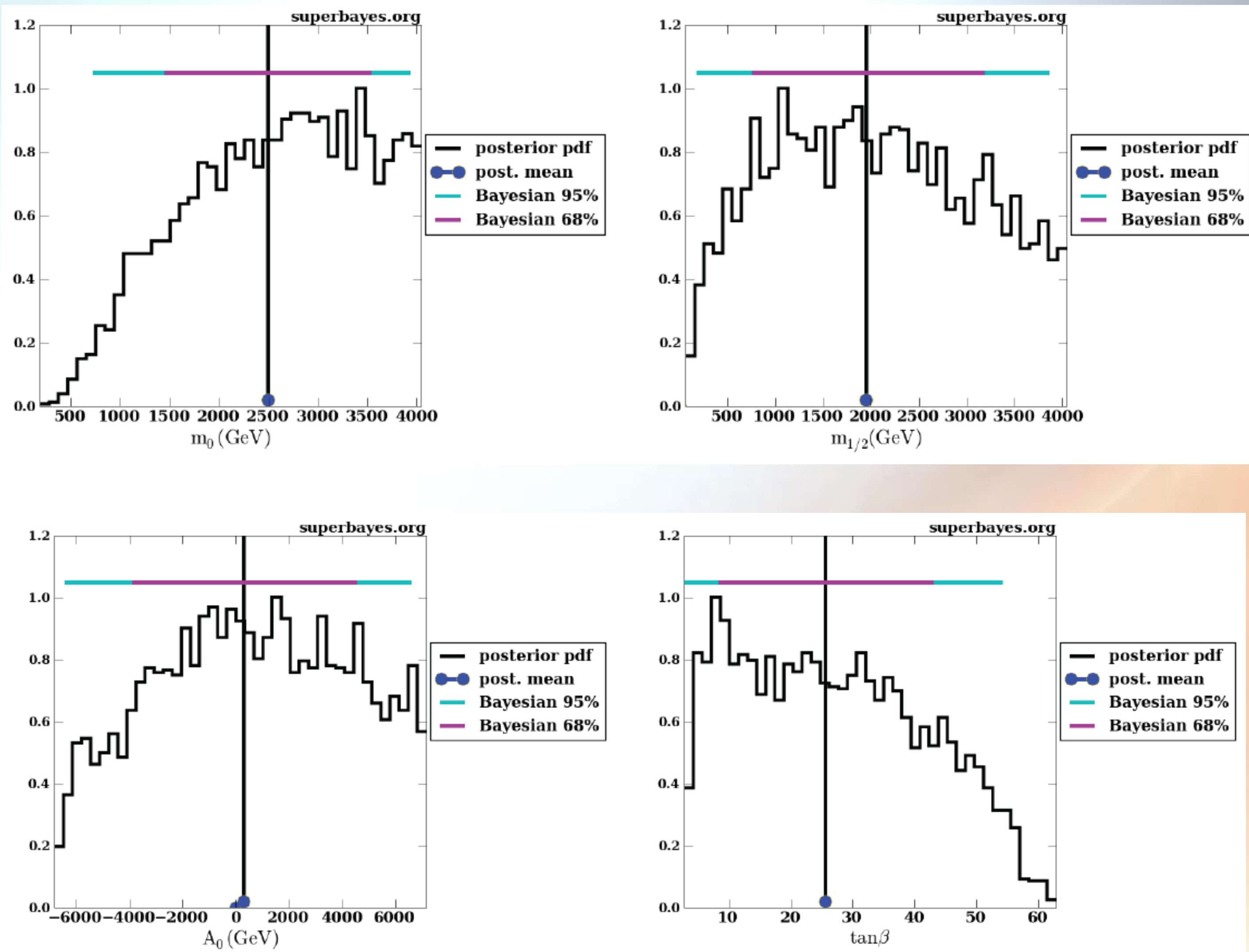
Results: Mass Spectrum at Best-fit Points

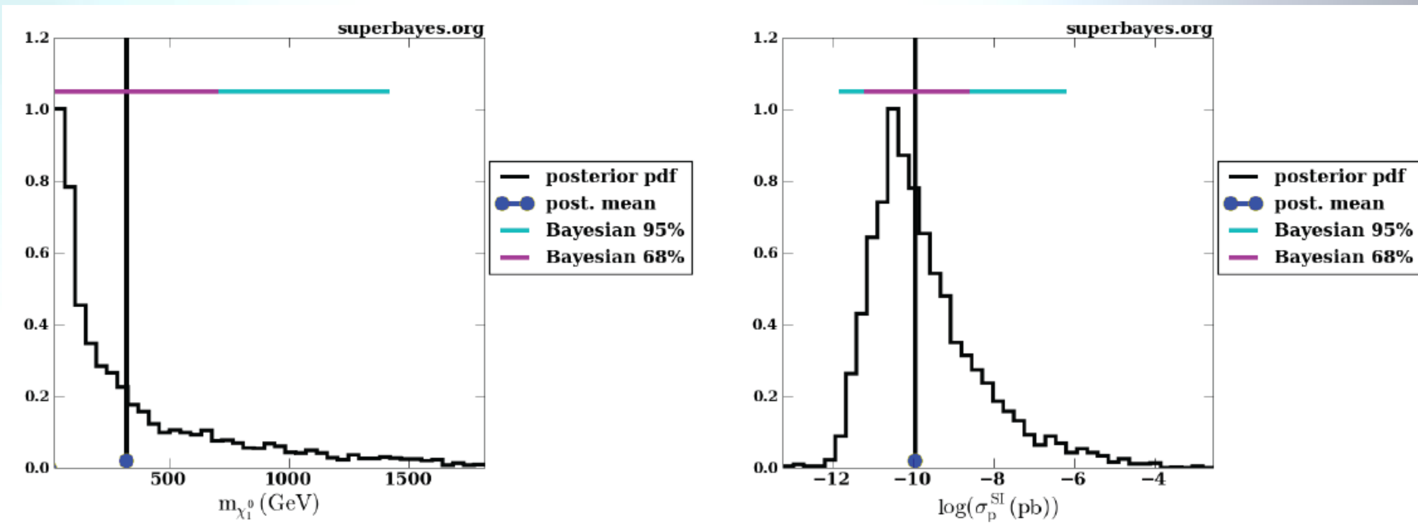
(GeV)	GA global BFP located in FP region	GA COA BFP
$m_{\tilde{e}_L}$	1908	294.1
$m_{\tilde{e}_R}$	1903	202
$m_{\tilde{\mu}_L}$	1907	294.1
$m_{\tilde{\mu}_R}$	1901	201.9
$m_{\tilde{\tau}_1}$	1100	160.1
$m_{\tilde{\tau}_2}$	1560	289.2
$m_{\tilde{\nu}_e}$	1906	283.3
$m_{\tilde{\nu}_\mu}$	1905	283.3
$m_{\tilde{\nu}_\tau}$	1560	272.5
$m_{\tilde{u}_L}$	1998	826.1
$m_{\tilde{u}_R}$	1996	805.4
$m_{\tilde{c}_L}$	1998	826.1
$m_{\tilde{c}_R}$	1996	805.4
$m_{\tilde{t}_1}$	1194	672.8
$m_{\tilde{t}_2}$	1364	803
$m_{\tilde{d}_L}$	2001	832.4

(GeV)	GA global BFP located in FP region	GA COA BFP
$m_{\tilde{d}_R}$	1994	798.1
$m_{\tilde{s}_L}$	2000	832.4
$m_{\tilde{s}_R}$	1994	798.1
$m_{\tilde{b}_1}$	1354	765
$m_{\tilde{b}_2}$	1492	793.4
$m_{\tilde{\chi}_1^0}$	140.4	152.6
$m_{\tilde{\chi}_2^0}$	269.9	285.4
$m_{\tilde{\chi}_3^0}$	519.7	451.1
$m_{\tilde{\chi}_4^0}$	529.7	469.6
$m_{\tilde{\chi}_1^\pm}$	270.4	286.9
$m_{\tilde{\chi}_2^\pm}$	530.3	468.5
m_h	115.55	111.11
m_H	179.93	504.24
m_A	179.83	504.04
$m_{H^\pm}$	201.14	510.67
$m_{\tilde{g}}$	877.1	898.8

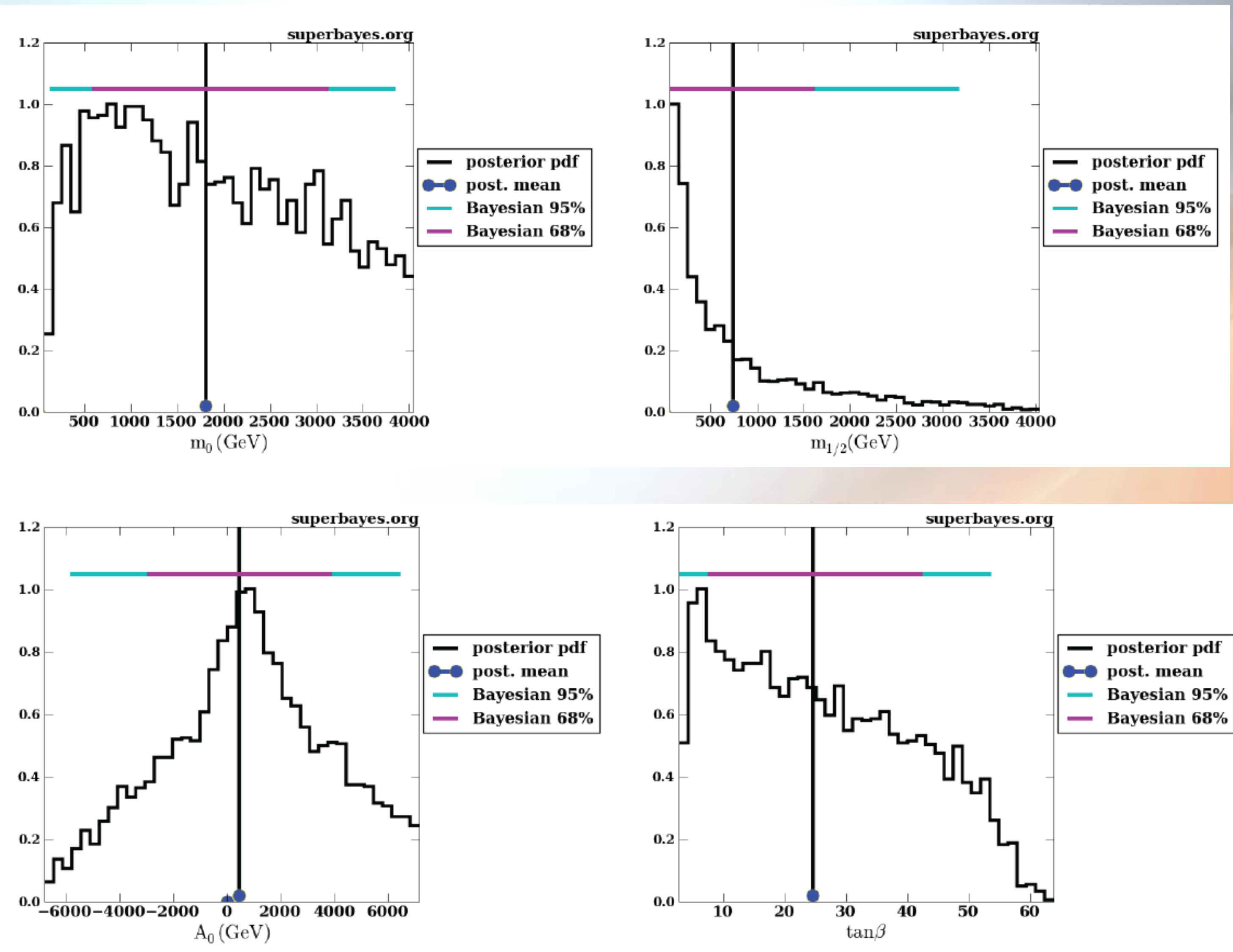

superbayes.org
posterior pdf
post. mean
Bayesian 95%
Bayesian 68%
$m_{\chi_1^0}$ (GeV)


superbayes.org
posterior pdf
post. mean
Bayesian 95%
Bayesian 68%
$\log(\sigma_p^{SI}\,(pb))$

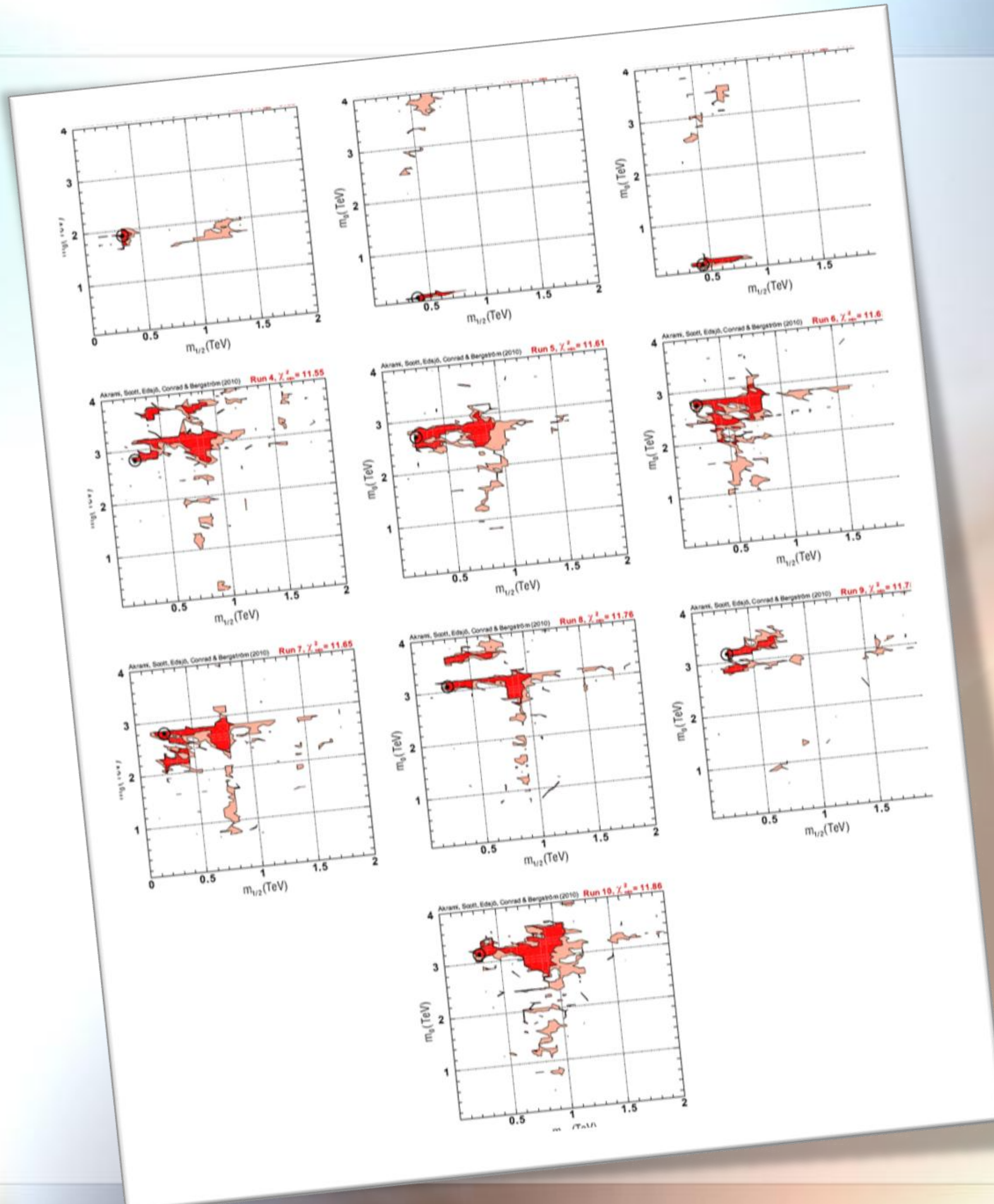

superbayes.org
posterior pdf
post. mean
Bayesian 95%
Bayesian 68%
m_0 (GeV)
$m_{1/2}$(GeV)
A_0 (GeV)
$\tan\beta$



superbayes.org
posterior pdf
post. mean
Bayesian 95%
Bayesian 68%
$m_{\chi_1^0}$ (GeV)
$\log(\sigma_p^{SI}\,(pb))$


superbayes.org
posterior pdf
post. mean
Bayesian 95%
Bayesian 68%
m0 (GeV)
superbayes.org
posterior pdf
post. mean
Bayesian 95%
Bayesian 68%
m1/2(GeV)
superbayes.org
posterior pdf
post. mean
Bayesian 95%
Bayesian 68%
A0 (GeV)
superbayes.org
posterior pdf
post. mean
Bayesian 95%
Bayesian 68%
tanβ

direct detection		
	GA global BFP	GA BFP in COA region
σ_p^{SI}	2.057×10^{-7} pb	2.236×10^{-9} pb
σ_p^{SD}	2.435×10^{-6} pb	4.231×10^{-6} pb
σ_n^{SD}	1.644×10^{-6} pb	3.142×10^{-6} pb
indirect detection		
	GA global BFP	GA BFP in COA region
$\langle \sigma v \rangle$	$2.260 \times 10^{-26} \mathrm{cm}^3 \mathrm{s}^{-1}$	$5.385 \times 10^{-28} \mathrm{cm}^3 \mathrm{s}^{-1}$



Akrami, Scott, Edsjö, Conrad & Bergström (2010)
Run 4, χ^2_{min} = 11.55
Run 5, χ^2_{min} = 11.61
Run 7, χ^2_{min} = 11.65
Run 8, χ^2_{min} = 11.76
Run 10, χ^2_{min} = 11.86
m_0(TeV)
$m_{1/2}$(TeV)

Summary and Conclusions

1. Constraining the parameter space of the MSSM using existing data is under no circumstances an easy or straightforward task. **Even in the case of the CMSSM, a highly simplified and economical version of the model, the present data are not sufficient to constrain the parameters in a way completely independent of computational and statistical techniques.**

1. Many recent activities in this field have used scanning methods optimised for calculating the Bayesian evidence and posterior PDF. **Highly successful in revealing the complex structure of SUSY models, demonstrating that some patience will be required before we can place any strong constraints on their parameters.**

2. Bayesian scanning methods have also been employed for frequentist analyses of the problem, particularly in the framework of the profile likelihood. **These methods are not optimised for such frequentist analyses, so care should be taken in applying them to such tasks.**

3. We have employed a completely new scanning algorithm, based on GAs. **They seem to be a powerful tool for frequentist approaches to the problem of scanning the CMSSM parameter space. We compared the outcomes of GA scans directly with those of the state-of-the-art Bayesian algorithm MultiNest, in the framework of the CMSSM.**

4. We found many new high-likelihood CMSSM points, which have a strong impact on the final statistical conclusions of the study. **These not only influence considerably the inferred high-likelihood regions and confidence levels on the parameter values, but also indicate that the applicability of the conventional Bayesian scanning techniques is highly questionable in a frequentist context.**

Summary and Conclusions

5. Although our initial motivation in using GAs was to gain a correct estimate of the likelihood at the global best-fit point, which is crucial in a profile likelihood analysis, we also realised that they can find many new and interesting points in almost all the relevant regions of parameter space. **These points strongly affect the inferred confidence regions around the best-t point. Even though we cannot be confident of exactly how completely our algorithm is really mapping these high-likelihood regions, it has certainly covered large parts of them better than any previous algorithm.**

6. By improving the different ingredients of GAs, such as the crossover and mutation schemes, this ability might even be enhanced further. **We largely employed the standard, simplest versions of the genetic operators in our analysis, as well as very typical genetic parameters. These turned out to work sufficiently well for our purposes. Although we believe that tuning the algorithm might produce even more interesting results, it is good news that satisfactory results can be produced even with a very generic version. This likely means that one can apply the method to more complicated SUSY models without extensive ne-tuning.**

7. We have also compared our algorithm with MultiNest in terms of speed and convergence, and argued that GAs are no worse than MultiNest in this respect. **GAs have a large potential for parallelisation, reducing considerably the time required for a typical run. This property, as well as the fact that the computational eort scales linearly (i.e. as kN for an N-dimensional parameter space), also makes GAs an excellent method for the frequentist exploration of higher-dimensional SUSY parameter spaces.**

Summary and Conclusions

8. The focus point region is favoured in our analysis over the co-annihilation region, in contrast to findings from some other MCMC studies, where the opposite is claimed. We also found a rather large part of the stau co-annihilation region, consistent with all experimental data, located at high m_0. **That is, at least in our particular setup, high masses, corresponding either to the FP or the COA regions, are by no means disfavoured by current data (except perhaps direct detection of dark matter). The discrepancy might originate in the different scanning algorithms employed, or in the different physics and likelihood calculations performed in each analysis. We have however shown, by comparing our results with others produced using exactly the same setup except for the scanning algorithm, that one should not be at all confident that all the relevant points for a frequentist analysis can be found by scanning techniques optimised for Bayesian statistics, such as nested sampling and MCMCs.**

Summary and Conclusions

The **bottom line** of our work is that:

We once again see that even the CMSSM, despite its simplicity, possesses a highly complex and poorly-understood structure, with many small, fine-tuned regions. This makes investigation of the model parameter space very difficult and still very challenging for modern statistical scanning techniques. Although the method proposed in this paper seems to outperform the usual Bayesian techniques in a frequentist analysis, it is important to remember that it may by no means be the final word in this direction. Dependence of the results on the chosen statistical framework, measure and method calls for caution in drawing strong conclusions based on such scans. The situation will of course improve significantly with additional constraints provided by forthcoming data.

	m_0 (GeV)	$m_{1/2}$ (GeV)	A_0 (GeV)	$\tan\beta$	m_t (GeV)	$m_b(m_b)^{\overline{MS}}$ (GeV)	$\alpha_s(m_Z)^{\overline{MS}}$	$1/\alpha_{\mathrm{em}}(m_Z)^{\overline{MS}}$	χ^2_{min}
Run 1	1900.5	342.8	1873.9	55.0	172.9	4.20	0.1172	127.955	**9.35**
Run 2	133.9	383.1	840.6	17.9	173.3	4.20	0.1183	127.955	**11.34**
Run 3	198.8	426.3	1059.4	22.6	173.3	4.20	0.1183	127.955	**11.45**
Run 4	2817.3	244.6	1712.9	51.2	172.9	4.20	0.1179	127.954	**11.55**
Run 5	2693.1	240.0	1706.0	51.0	172.6	4.20	0.1179	127.954	**11.61**
Run 6	2737.8	238.7	1692.6	51.0	172.6	4.20	0.1176	127.954	**11.63**
Run 7	2775.1	248.2	1780.2	51.1	172.6	4.20	0.1179	127.954	**11.65**
Run 8	3102.3	287.3	1976.8	51.2	172.8	4.20	0.1176	127.954	**11.76**
Run 9	3158.9	276.6	1901.2	51.1	173.1	4.21	0.1174	127.955	**11.78**
Run 10	3159.3	317.0	2136.8	51.2	172.7	4.20	0.1180	127.955	**11.86**

OKC PROSPECTS WORKSHOP

(http://agenda.albanova.se/conferenceDisplay.py?confId=1983)

AlbaNova

OKC PROSPECTS Workshop

15-17 September 2010

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PROSPECTS - PROblems in Statistical Parameter Estimation and ConsTraints for Supersymmetry

With a new energy frontier opening up we all want to be ready to set out on the road to discoveries. We know that along the way we will face hordes of data, the constraining shackles of statistical error bar and the nefarious plotting of systematic errors, we know we must endure the hardships of complicated parameter interdependencies. All this to perhaps, finally, reach the undiscovered country of New Physics

The aim of this workshop is to investigate approaches to constraining the parameters of New Physics models with data from current collider and astrophysics experiments, with some emphasis on models with Supersymmetry. This is a field which has seen a lot of activity over the past few years, and our goal is to gather experts to discuss some of the issues involved in interpreting data and applying statistical methods. Furthermore, we want to have brief reviews of current methods and the tools available, and finally some PROSPECTS for the future.

Topics:

- Statistics & Algorithms (Talks on statistical methods and scanning algorithms)
- Packages & Codes (Presentations of available tools and recent tool developments)
- Experimental Constraints (Summaries of current and expected near-future experimental results)
- Phenomenology/Results (Updates on current parameter scans and their phenomenological consequences)

List of Invited Speakers:

- Ben Allanach (DAMTP, Cambridge)
- Geneviéve Bélanger (LAPTH, Annecy)
- Kyle Cranmer (New York University)
- Klaus Desch (Bonn)
- Joakim Edsjö (Stockholm)
- John Ellis (CERN)
- Michael Hobson (Cavendish, Cambridge)
- Tilman Plehn (Heidelberg)
- Roberto Ruiz de Austri (IFIC, Valencia)
- Roberto Trotta (Imperial College)
- Martin White (University of Melbourne)

The workshop will be a small-scale event with ample time for discussions. Note that there is no registration fee for the workshop, but there is a fee for those who wish to participate at the workshop dinner on Thursday the 16th of September.

Local Organizing Committee

A. Raklev (co-chair, Stockholm University), P. Scott (co-chair, Stockholm University), Y. Akrami (Stockholm University), J. Edsjö (Stockholm University), J. Conrad (Stockholm University), A. Putze (Stockholm University/KTH), J. Ripken (Stockholm University), C. Savage (Stockholm University).