

# **The Bayesian Analysis Toolkit**

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#### BAT → Software package for solving of statistical problems using Bayesian approach

Bayes' formula for parameter estimation

$$p(\vec{\lambda} \mid \vec{D}) = \frac{p(\vec{D} \mid \vec{\lambda}) p_0(\vec{\lambda})}{\int p(\vec{D} \mid \vec{\lambda}) p_0(\vec{\lambda}) d\vec{\lambda}}$$

#### Motivation:

- many of us have done Bayesian analyses in HEP always having to implement the numerical
  algorithms and tools by ourselves → generally non-trivial
- create a package/toolkit to take care of that

### The idea behind BAT

- Merge common parts of every Bayesian analysis into a software package
- Provide flexible environment to phrase arbitrary problems
- Provide a set of well tested/tuned numerical algorithms and tools
- C++ based framework (flexible, modular)
- Interfaces to ROOT, Cuba, Minuit, user defined, ...

# The idea



$$p(\vec{\lambda} \mid \vec{D}) = \frac{p(\vec{D} \mid \vec{\lambda}) p_0(\vec{\lambda})}{\int p(\vec{D} \mid \vec{\lambda}) p_0(\vec{\lambda}) d\vec{\lambda}}$$

#### USER DEFINED

- create model
- read-in data

## MODEL INDEPENDENT (common tools)

- normalize
- find mode / fit
- test the fit
- marginalize wrt. one or two parameters
- compare models
- provide nice output

#### Define MODEL

- define parameters  $\vec{\lambda}$
- define likelihood  $p(\vec{D} \mid \vec{\lambda})$
- define priors  $\rho_0(\vec{\lambda})$

#### Read DATA

• from text file, ROOT tree, user defined





- - Markov Chain Monte Carlo (MCMC)
    - key tool in the package
    - lot of emphasis put on efficiency, performance and validation
- Integration
  - Monte Carlo (sampled mean), Cuba (Vegas, ...)
- Maximization
  - Monte Carlo, MCMC, Minuit, Simulated Annealing
- Model testing
  - Posterior comparison, K-factors, p-value calculation
- User interface
  - simple model definition
  - standard output: text output, plots, ROOT histograms and trees, ...





f(y)

- In BAT implemented Metropolis algorithm
- Map positive function f(x) by random walk towards higher probabilities
- Algorithm:
  - Start at some randomly chosen  $x_i$
  - Randomly generate y
  - If  $f(y) \ge f(x_i)$ , set  $x_{i+1} = y$
  - If  $f(y) < f(x_i)$ , set  $x_{i+1} = y$  with probability  $p = \frac{f(y)}{f(x_i)}$
  - If y not accepted, stay where you are, i.e. set  $x_{i+1} = x_i$
  - Start over

 $f(x_i) = \frac{1}{y} + \frac{1}{x_i} + \frac{1}{y} + \frac{1$ 

• Sampling is enhanced in regions with higher values of f(x)





- In BAT, use MCMC to scan parameter space  $f(\vec{\lambda}) = \rho(\vec{D} \mid \vec{\lambda}) \rho_0(\vec{\lambda})$
- MCMC converges towards underlying distribution
  - Determining of the overall probability distribution of the parameters  $p(\vec{\lambda} \mid \vec{D})$
- Marginalize wrt. individual parameters while walking  $\rightarrow$  obtain  $p(\lambda_i | \vec{D}) = \int p(\vec{D} | \vec{\lambda}) p_0(\vec{\lambda}) d\vec{\lambda}_{i\neq i}$
- Find maximum (mode)
- Uncertainty propagation
  - calculate and store value of any function of parameters  $\boldsymbol{\lambda}$

$$p(\vec{\lambda} \mid \vec{D}) = \frac{p(\vec{D} \mid \vec{\lambda}) p_0(\vec{\lambda})}{\int p(\vec{D} \mid \vec{\lambda}) p_0(\vec{\lambda}) d\vec{\lambda}}$$







Running several chains in parallel (default is 5)

- Start at random locations in allowed parameter space
- Iniitialize chains by doing a pre-run to achieve convergence
  - Convergence defined using r-value (Gelman & Rubin, StatSci 7, 1992)
    - Ratio of the mean of the RMS values of the probability and the RMS of the mean values
    - Convergence criterion |r-1| < 0.1
- Steps in parameter space done consecutively for each parameter and chain
- Proposal function for new steps is chosen flat with varying ranges
- The efficiency for accepting new point is evaluated for each parameter and chain over last (npar+1)\*1000 iterations and the step size is adjusted to increase the performance
  - If efficiency > 50%, increase the step size
  - If efficiency < 15%, decrease the step size
- use MCMC only after pre-run has ended, convergence was reached and all parameter step-sizes have been adjusted

#### Most parameters can be set by the user



- Danger of non-convergence still remains  $\bullet$
- the full chain(s) can be stored for further analysis and parameter tuning
- available formats: text file, ROOT Tree  $\bullet$ 
  - allows direct usage of standard ROOT tools for analysis
  - e.g. fast access to marginalized distributions root[1] chain0 -> Draw("p0") root[2] chain0 -> Draw("p1:p2")
- Markov Chain contains the complete information about the ightarrowposterior probability (except for the normalization)









- download from http://www.mppmu.mpg.de/bat
- comes in the form of shared library (plus a .rootmap file for interactive ROOT session)
- depends on ROOT I/O and drawing functionality
  - can in principle be removed if there's need
- can be compiled with Cuba support
- BAT contains 15 classes at the moment which provide:
  - main infrastructure
  - algorithms
  - output and logging
  - extension classes to solve specific (frequent) fitting problems







#### Define a model class inheriting from a base model class **BCModel**:

- add parameters:
- implement likelihood:
- implement prior:

# AddParameter("p0",-4,4); double LogLikelihood(vector<double> params) double LogAPrioriProbability(vector<double> params)

#### Main program/macro:

- create instance of the model:
- read data:
- assign data to the model:
- do the analysis:

```
MyModel * mm = new MyModel("Model 0");
BCDataSet * data = new BCDataSet();
data->ReadFromFileTxt("file.txt",4);
mm->SetDataSet(data);
mm->Normalize();
mm->MarginalizeAll();
mm->FindModeMinuit( mm->GetBestFitParameters() );
mm->PrintAllMarginalized("distributions.ps");
etc.
```





Output

- marginalized distributions 1D and 2D
  - probability intervals, contours
  - probability limits
  - mode, mean, median, rms





#### • uncertainty bands



- MCMC itself
- information about local maxima and uncertainty intervals/probability limits in text file or ROOT file



Three BCModel extensions for standard fitting problems: (using flat priors)

- **BCGraphFitter** fits graph (TGraphErrors) assuming Gaussian uncertainties
- **BCHistogramFitter** fits histogram (TH1D) assuming poissonian uncertainties
- BCEfficiencyFitter
  - fits efficiency a ratio of two histograms (TH1D) where numerator is a subset of denominator – assuming binomial uncertainties

#### Simple use:

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Since all three fitters inherit from **BCModel** all other standard class methods can be used, e.g normalization, model comparison, pretty printing etc.



- development version 0.2 of BAT was released in January
  - received a lot of important feedback from first users
  - next release with few small updates coming soon
- since no detailed manual available yet, mostly oriented to experts at the moment
- lot of things to be added
  - standard predefined priors
  - MCMC diagnostics and checks
  - performance tuning
  - other algorithms for integration, MCMC, maximization, ...
  - library of other standard problems
- interfacing BAT with RooStats
  - BCRooStatsInterface class implemented by RooStats team
  - validation ongoing
- current BAT code structure has historical origin far from being optimal, hard to extend
  - restructuring is on the way while having in mind the interactions with RooStats
  - looking into possibility to include BAT into ROOT



- BAT allows to solve simple statistical problems like function fitting as well as complex Data vs. Theory comparisons and parameter estimation
- BAT collects common tools used in Bayesian analyses in a single modular framework
- Markov Chain Monte Carlo is the key tool
- Even though Bayesian, not rejecting non-Bayes algorithms and tools
  - e.g. p-value
  - ready to add more useful tools
- Still, the main responsibility for meaningful results is on users, since they have to define the model, we only provide the tools (and some suggestions)
- BAT attempts to fill the gap on the market with statistical tools
  - clearly a challenge to convince the users
- Also the manpower situation is not optimal but should improve in near future
- we have started discussions with other teams doing Bayesian analyses and got positive feedback and eventually they would also like to contribute