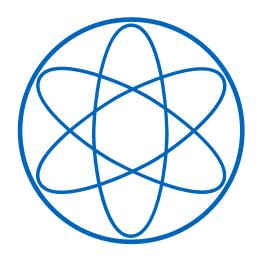


# Development and Benchmarking of a Bayesian Inference Pipeline for LHC Physics



Scientific Thesis for the procurance of the degree

BACHELOR OF SCIENCE

from the Physics Department at the Technical University of Munich.

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Abstract

TODO

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Abbreviations

# Abbreviations

**BAT** Bayesian Analysis Toolkit.

**GC** garbage collector.

**HEP** High Energy Physics.

**HF** HistFactory.

**HMC** Hamiltonian Monte Carlo.

**LHC** Large Hadron Collider.

MC Monte Carlo.

**MH** Metropolis-Hastings.

**pdfs** probability density functions.

**POI** parameter of interest.

vi Abbreviations

# Introduction

Large Hadron Collider (LHC) Luminosity LHC  $2.1 \cdot 10^3 4 cm^{-2} s^- 1$ 

# **Mathematical Preliminaries**

# 2.1 Frequentist versus Bayesian Inference

Given observed data, the likelihood  $\mathcal{L}(\boldsymbol{\theta})$  then serves as the basis to test hypotheses on the parameters  $\boldsymbol{\theta}$ .

# 2.2 MCMC Sampling

Monte Carlo (MC)
Markov chain Monte Carlo (MCMC)

#### 2.2.1 Markov Chains

#### 2.2.2 Metropolis Hastings

Metropolis-Hastings (MH)

#### 2.2.3 Hamiltonian Monte Carlo

Hamiltonian Monte Carlo (HMC)

# **HistFactory**

HistFactory (HF) is a tool for binned statistical analysis which is widely used in LHC physics to measure the consistency of collision events with theoretical predictions. It has been employed for the discovery of the Higgs Boson [1] and is used in searches for new physics [2] by research groups around the planet. The relationship between theoretical predictions and collision events is formalized as statistical model  $p(x | \theta)$ . It describes the probability of observing data x given the model parameters  $\theta$ . Typically, models in High Energy Physics (HEP) are complex with hundreds of parameters. HF enables a standardized way to build parametrized probability density functions (pdfs) and infer parameter properties from it.

#### 3.1 Formalism

Statistical models in HistFactory describe simultaneous measurements of disjoint channels c (binned distributions as subspace of all collision events), where we observe the event counts n. In a particle detector several physical processes produce particles in the selected channels. Hence, the total number of expected events<sup>1</sup> is the sum of all involved processes – the so called samples. This sample rates underlie variations and can be modified by the parameters  $\theta$ . It is distinguished between free parameters  $\eta$  (e.g. the luminosity) and constrained parameters  $\chi$  that account for systematic uncertainties. In a frequentist setting, these constrained terms can be viewed as auxiliary measurements a which result together with the channel events a in the observations a (a). Equation (3.1) illustrates this parametrization

$$p(\boldsymbol{x} \mid \boldsymbol{\theta}) = p(\boldsymbol{n}, \boldsymbol{a} \mid \boldsymbol{\eta}, \boldsymbol{\chi}) \tag{3.1}$$

<sup>&</sup>lt;sup>1</sup>this is often denoted as *event rate* since it used as input parameter to a Poisson distribution

The statistical model in HF consists of two parts – the *main model* of simultaneous measurements over multiple channels, and a *constrained term* that takes into account auxiliary measurements.

$$p(\boldsymbol{n}, \boldsymbol{a} \mid \boldsymbol{\eta}, \boldsymbol{\chi}) = \prod_{\substack{c \in \text{channels } b \in \text{bins}_c}} \text{Pois}(n_{cb} \mid \nu_{cb}(\boldsymbol{\eta}, \boldsymbol{\chi})) \qquad \prod_{\substack{\chi \in \boldsymbol{\chi} \\ \text{simultaneous measurement}}} c_{\chi}(a_{\chi} \mid \boldsymbol{\chi}) \qquad (3.2)$$
simultaneous measurement
of multiple channels
for "auxiliary measurements"

For each bin b and channel c, the total event rate  $\nu_{cb}$  is is the sum over sample rates  $\nu_{scb}$ .

$$u_{cb}(oldsymbol{\eta}, oldsymbol{\chi}) = \sum_{s \, \in \, ext{samples}} 
u_{scb}(oldsymbol{\eta}, oldsymbol{\chi})$$

The sample event rates  $\nu_{scb}$  are determined by a nominal rate  $\nu_{scb}^0$  and a set of multiplicative and additive rate modifiers  $\kappa(\theta)$  and  $\Delta(\theta)$ , which are controlled by the model parameters  $\theta = (\eta, \chi)$ .

$$\nu_{cb}(\boldsymbol{\eta}, \boldsymbol{\chi}) = \sum_{s \in \text{ samples}} \underbrace{\left(\prod_{\kappa \in \boldsymbol{\kappa}} \kappa_{scb}(\boldsymbol{\eta}, \boldsymbol{\chi})\right)}_{\text{multiplicative modifiers}} \left(\nu_{scb}^{0}(\boldsymbol{\eta}, \boldsymbol{\chi}) + \underbrace{\sum_{\Delta \in \boldsymbol{\Delta}} \Delta_{scb}(\boldsymbol{\eta}, \boldsymbol{\chi})}_{\text{additive modifiers}}\right)$$
(3.3)

The available modifiers in HistFactory are summarized in Table 3.1. Each modifier is defined for bin b, sample s and channel c and is controlled by at least one parameter  $\theta \in \{\gamma, \alpha, \lambda, \mu\}$ . By convention, bin-wise modifiers are denoted by  $\gamma$  and interpolation parameters with  $\alpha$ . In contrast, luminosity  $\lambda$  and scale factors  $\mu$  affect all bins equally.

Table 3.1: HistFactory modifiers and constraints [3]

Description	Modification	Constraint Term $c_\chi$	Input
Uncorrelated Shape shapesys	$\kappa_{scb}(\gamma_b) = \gamma_b$	$\prod_{b} \operatorname{Pois} \left( r_{b} = \sigma_{b}^{-2}     \rho_{b} = \sigma_{b}^{-2} \gamma_{b} \right)$	$\sigma_b$
Correlated Shape histosys	$\Delta_{scb}(\alpha) = f_p(\alpha \mid \Delta_{scb,\alpha=\pm 1})$	Normal $(a = 0 \mid \alpha, \sigma = 1)$	$\Delta_{scb,\alpha=\pm 1}$
Normalisation Uncert.	$ \kappa_{scb}(\alpha) = g_p\left(\alpha   \kappa_{scb,\alpha\pm 1}\right) $	Normal $(a = 0 \mid \alpha, \sigma = 1)$	$\kappa_{scb,lpha\pm1}$
MC Stat. Uncertainty staterror	$\kappa_{scb}(\gamma_b) = \gamma_b$	$\prod_{b} \operatorname{Normal} \left( a_{\gamma_b} = 1   \gamma_b, \delta_b \right)$	$\delta_b^2 = \sum_s \delta_{sb}^2$
Luminosity lumi	$\kappa_{scb}(\lambda) = \lambda$	Normal $(l = \lambda_0 \mid \lambda, \sigma_{\lambda})$	$\lambda_0,\sigma_\lambda$
Normalisation normfactor	$\kappa_{scb}(\mu_b) = \mu_b$		
Data-driven Shape shapefactor	$\kappa_{scb}(\gamma_b) = \gamma_b$		

3.1. FORMALISM 7

The first five entries in Table 3.1 are constrained modifiers that are defined by a constraint term  $c_{\chi}$  (right part in (3.2)) and an input parameter (auxdata).

- Uncorrelated shape modifiers affect each bin individually and are constrained by a Poisson. They are applied to model uncorrelated background, with rate uncertainties  $\delta_b$  for each bin.  $\sigma_b = \delta_b/\nu_b$  is the *relative* uncertainty of the expected total event rate  $\nu_b$  and serves as input for the constraint term.
- Correlated shape modifiers are additive modifiers and controlled by a single parameter.

#### 3.2 Workspaces

Statistical models in HF are described in plain-text JSON format. This scheme fully specifies the model structure as well as necessary constrained data in a single document, and hence is implementation independent. This JSON files represent a *workspace* which consists of *channels*, *measurements* and *observations*.

- Channels are certain regions in the space of collision events, each described by a statistical model. The regions are chosen to be disjoint and typically contain signal regions (SR) and control regions (CR) for a certain particle decay of interest.
  - The statistical model for a channel is constructed by a list of *samples* (models of involved physical processes) which consists of the predicted event rates and a set of modifiers (see Table 3.1).
- Measurements are a small subset of all model parameters the parameter of interest (POI). The measurement scheme in the JSON file can be configured with the initial value, interval bounds or auxdata for the parameter.
- Observations are the actual observed events for each bin in all channels.

For a detailed description of the HF JSON format, the reader is referred to the pyhf documentation [3].

Models in this thesis. Since real world examples are too complex to benchmark in acceptable time, this work mainly uses "toy" workspaces with a single channel. All model specifications utilized in this work are listed in Appendix A.

# 3.3 HistFactory Implementations

Currently, HistFactory is available in three different programming languages

- a C++ implementation, (cite?)
- a Python version pyhf [4], and
- a Julia implementation LiteHF [5]

In chapter 5, this work employs pyhf and LiteHF for run-time benchmarks. To verify the equivalence of pyhf and LiteHF, the log posterior measure is evaluated for both implementations. The log likelihood in Python for a parameter vector  $\theta$  is computed by the logpdf of the main\_model, i.e.

```
def llh(param: np.ndarray) -> float
    """pyhf log likelihood from the main_model."""
    return model.main_model.logpdf(main_data, param)
```

In LiteHF one can access the log likelihood function by

For visualization purposes, the verification step is illustrated for the 2D 2\_bin\_corr model in section A.2. The prior vector is chosen to be

$$p(\boldsymbol{\theta}) = \begin{bmatrix} \text{Uniform}(0, 5) \\ \text{Normal}(0, 1) \end{bmatrix}$$
(3.4)

and the log posterior measure is evaluated for  $10^5$  points  $x \sim p(\theta)$  with equal initial seed. The samples coincidence for both implementations up to numerical precision. In Figure 3.1 1000 randomly chosen data points are picked out and illustrated for pyhf (blue) and LiteHF (orange).

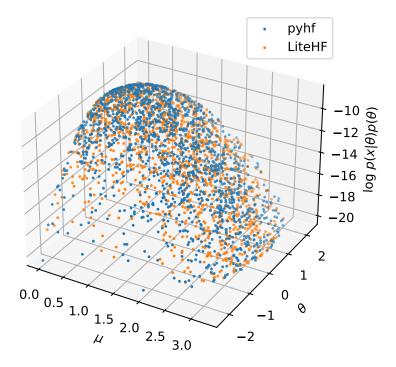


Figure 3.1: Verify the equivalence of the pyhf and LiteHF implementation by evaluating the log posterior measure  $\log (p(\boldsymbol{x} | \boldsymbol{\theta}) p(\boldsymbol{\theta}))$  at 1000 random points  $\boldsymbol{x} \sim p(\boldsymbol{\theta})$  for the 2\_bin\_corr model (see section A.2). The 2D prior vector is set to  $p(\boldsymbol{\theta}) = [\text{Uniform}(0,5), \text{Normal}(0,1)]^T$ .

# Bayesian Inference with HistFactory

While the majority of statistical results in LHC physics are obtained by a frequentist setting, this chapter formalizes a Bayesian approach for parameter inference with HistFactory. First, it introduces the Bayesian Analysis Toolkit (BAT) which is used for MCMC sampling. Second, it derives a formalism to obtain prior distributions from HF models. Third, it discusses implementation details of batty — a Python-Julia interface to execute BAT code (written in Julia) in Python in order to perform Bayesian inference on pyhf models. The chapter closes with ... TODO

#### 4.1 BAT

Bayesian Analysis Toolkit (BAT) [6]

#### 4.2 Priors from auxdata

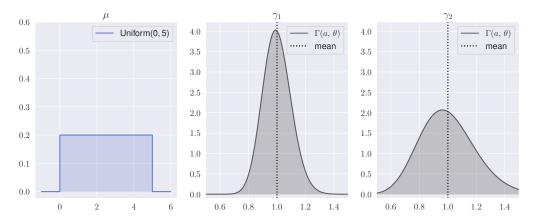
#### 4.2.1 Conjugate Priors

#### 4.2.2 Implementation

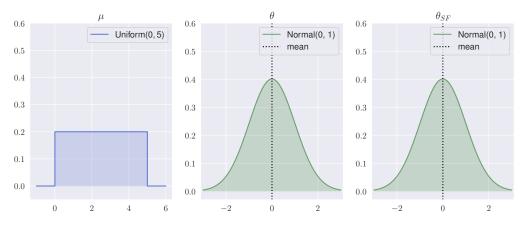
Generating priors  $p(\theta)$  from auxdata in HF models is summarized in the Python package priorhf which was implemented during this work.

model.config.par\_map is a ordered mapping from the parameter name to the slice in the parameter vector.

[7]



(a) Prior distributions for the 2\_bin\_uncorr model (section A.1) parameters



(b) Prior distributions for the 4\_bin model (section A.3) parameters

Figure 4.1: Conjugate prior for the 2\_bin\_uncorr model and 4\_bin model. The signal strength parameter  $\mu$  is uniformly distributed for both models. The dashed line represents the mean the of Gamma and Normal distribution. Priors for the 2D 2\_bin\_corr model (section A.2) are equal to the first two distributions for the 4\_bin model.

## 4.3 batty – BAT to Python Interface

The complete pipeline for calling BAT code from Python is fully implemented in batty, the BAT to Python Interface, developed here [8]. During this work, batty was steadily tested an updated with several contributions. An old version of batty used PyCall.jl [9] to access Julia code from Python, which had one major drawback: The complete Python environment needed to be compiled each time batty was imported, which takes about 2 minutes. The current version of batty employs PythonCall.jl [10]

#### 4.3.1 Gradients for HMC

In order to run HMC in

- use median instead mean
- $\bullet$  use bar + box plot

# 4.3.2 pyhf Backends

• jax jitted log likelihood is 4 times faster with numpy backend

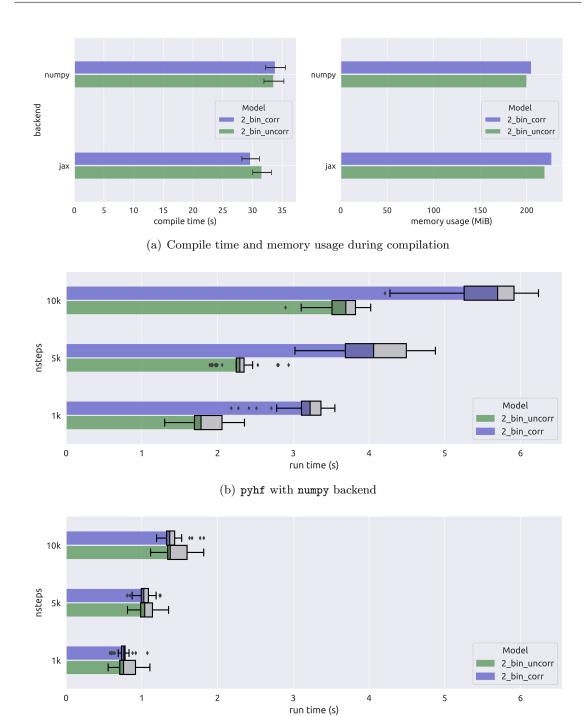


Figure 4.2: Compile time and run-time performance of bat\_sample() once using the numpy backend and once with jax backend of pyhf. The run-time is evaluated for two different models 2\_bin\_corr and 2\_bin\_uncorr.

(c) pyhf with jax backend

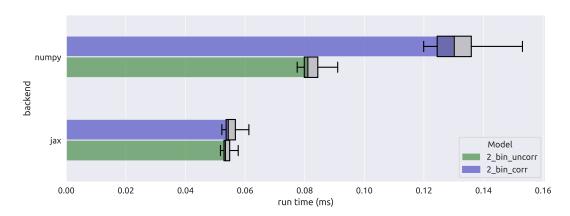
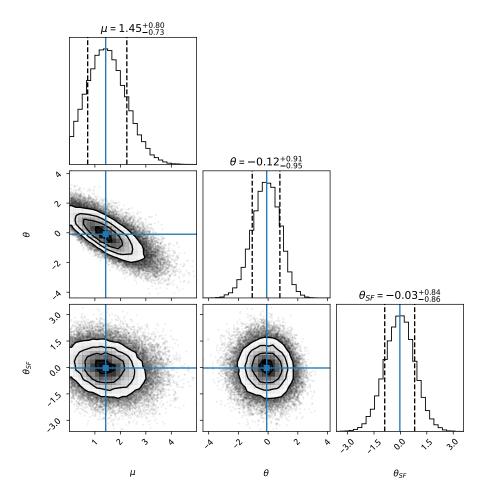


Figure 4.3: Benchmarking the likelihood for the numpy and jax pyhf backend based on two HF models.

# 4.4 Bayesian Inference Examples



**Figure 4.4:** Corner plot for the  $4\_bin$  Model (section A.3) for 100k samples. (dashed line 0.16, 0.84 quantile, blue lines mode) XX

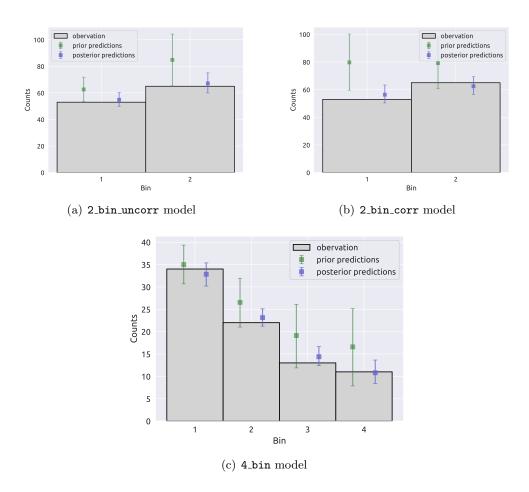


Figure 4.5: Prior and posterior predictive checks for all used models. The dot represents the median for expected output and the error bars indicate the  $1\sigma$  quantile.

# Benchmarking the Python-Julia Pipeline against the Julia Implementation

This chapter compares the run-time performance of batty (section 4.3) with a pure-Julia implementation of Bayesian inference with LiteHF [5]. More specific, the following three implementations are evaluated

- Python + BAT (visualized in blue)
   Uses the Python-Julia bridge batty for Bayesian inference on HF models in Python.
- Julia + LiteHF (visualized in green)

  The complete inference chain is written and executed in Julia by using LiteHF [5], the Julia implementation of HF.
- Julia + pyhf (visualized in red)

The whole code runs in Julia but uses the Python likelihood from pyhf for inference. Executing Python code from Julia is accomplished by the PythonCall.jl module [10]. The pyhf likelihood are outsourced in a module pyhf\_llh that can be embedded in Julia by

```
11h = pyimport("pyhf_11h")
11h_func, 11h_with_grad = 11h.pyhf_11h_with_grad("path/to/model")
```

Run-times benchmarks are measured for both, MH and HMC based on two different HF models.

### 5.1 Benchmark Setup

For each implementation run-time of the bat\_sample() method is measured. For that, it takes two arguments, the posterior measure to be sampled and the MCMC method to be used.

```
# Metropolis Hastings
method = BAT.MCMCSampling(mcalg=BAT.MetropolisHastings(), nsteps=nsteps, nchains=2)
# or HamiltonianMC
method = BAT.MCMCSampling(mcalg=BAT.HamiltonianMC(), nsteps=nsteps, nchains=2)
samples = bat_sample(posterior, method).result
```

The number of chains nchains is set to 2 for all benchmarks, and the run-time is measured for different numbers of steps nsteps.

To ensure reproducible benchmarks the following steps are taken into account

- Code that is executed by bat\_sample() like computing the log likelihood does not use global variables. Accessing global variables inside a function increases the run-time in Julia and Python.
- Since Julia code is pre-compiled before execution, a distinction is made between the compile time and run-time of bat\_sample(). The proportion of both times is illustrated in Figure 5.1 for the 2\_bin\_corr model for sampling 10k steps. The compile time accounts for more than 90% of the total execution time in all implementation and has a uncertainty of ±4%. Compiling bat\_sample() in Python takes about twice as long as in Julia (see Figure 5.1 left).
- Benchmarks in Julia are obtained using the BenchmarkTools.jl module [11]. To measure "long" run-times sufficiently, the @benchmarkable maken is configured as

```
b = @benchmarkable bat_sample(posterior, mcalg) setup=(mcalg=$method)
sec = bootstrap_sec()
res = run(b, samples=samples, seconds=maximum([sec, 40]))
```

where the required time sec is bootstrapped from previous run-times.

- All run-time benchmarks are written in Python or Julia scripts, since Jupyter Notebooks have lots of overhead.
- All benchmarks are carried out on a Linux computer with a Intel(R) Core(TM) i7-7700HQ CPU.

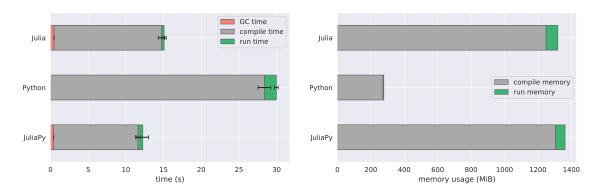


Figure 5.1: Total execution time and memory usage of bat\_sample() for the 2\_bin\_corr model with 10k steps. The red, grey and green portion is the garbage collector (GC) time, the compile time and run time respectively. Compiling bat\_sample() in Python takes about twice as long as in Julia. In contrast, the memory usage during compilation in Python is only one sixth of the memory usage in Julia. (The run-time memory usage in Python can't be measured sufficiently and hence is neglected in the right plot. Moreover, the GC time can not be evaluated in Python.)

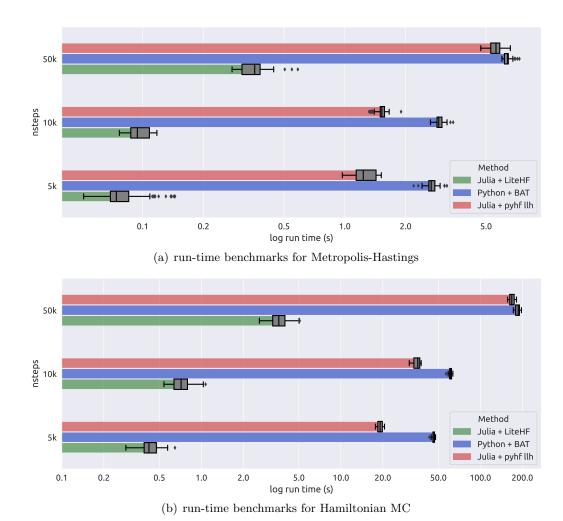
#### 5.2 Benchmarks

#### 5.2.1 2\_bin\_corr Model

First, the run-time of the 2\_bin\_corr model is evaluated for different values of nsteps. The results are visualized in Figure 5.2a) for Metropolis Hastings and in Figure 5.2b) for Hamiltonian MC. The run-time on the x-axis is plotted logarithmically and the numerical values are summarized Table 5.1.

**Table 5.1:** Summary of run-time benchmarks in Figure 5.2. The values represent the median run-time with  $1\sigma$  standard deviation without outliers for 5k, 10k and 50k nsteps.

		5k	10k	50k
Method	Implementation	$\mathbf{run\text{-}time}\ (\mathrm{s})$		
	$\mathrm{Julia} + \mathtt{LiteHF}$	$0.07 \pm 0.01$	$0.09 \pm 0.01$	$0.35 \pm 0.04$
$\mathbf{MH}$	Python + pyhf	$2.67 \pm 0.20$	$2.91 \pm 0.15$	$6.39 \pm 0.30$
	Julia + pyhf	$1.23 \pm 0.16$	$1.52 \pm 0.10$	$5.59 \pm 0.43$
	$\mathrm{Julia} + \mathtt{LiteHF}$	$0.42 \pm 0.07$	$0.71 \pm 0.10$	$3.59 \pm 0.50$
$\mathbf{HMC}$	Python + pyhf	$45.9 \pm 1.3$	$61.2 \pm 1.9$	$186\pm 8$
	Julia + pyhf	$19.1 \pm 2.0$	$35.6 \pm 2.3$	$168 \pm 9$



**Figure 5.2:** Run-time benchmark of the 2\_bin\_corr model for different values of nsteps with logarithmic time axis. Uncertainties are visualized as box-plot as illustrated in Figure B.1. The run-time in Julia is averaged over 100 runs, for the other two implementations over 40 runs for MH and 10 runs for HMC.

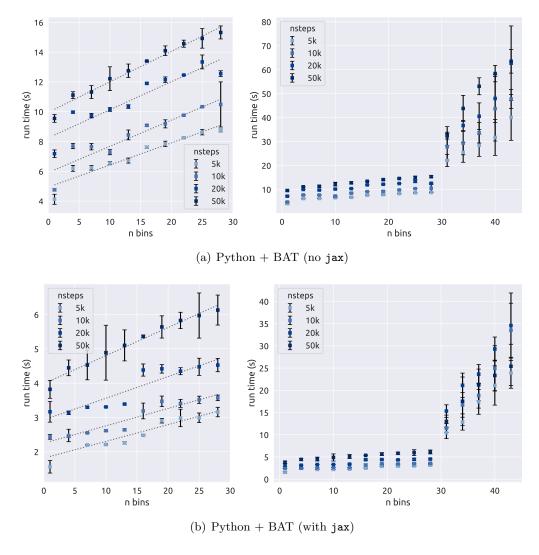
Metropolis Hastings. The run-time of the pure-Julia implementation (green) is about 20 times faster than the Python-Julia pipeline (blue) for all steps. Executing the pyhf likelihood from Julia (red) is about 12 times slower that the pure-Julia implementation. For an increasing number of samples (nsteps) the run-time of Julia + pyhf approaches the execution time of batty (Python + pyhf).

Hamiltonian MC. Executing HMC in Python is about 100 times slower than the pure-Julia implementation for 5k and 10k steps, and about 50 times slower for 50k steps. Again, calling the pyhf likelihood from Julia (red) outperforms the batty implementation (blue). For a small number of nsteps=[5k, 10k] the Julia version (Julia + pyhf) is about two times faster than batty, for 50k steps both implementations require almost the same time. 5.2. BENCHMARKS 23

#### 5.2.2 n-Bin-Model

The runtime measurements in this section examine how the dimensionality of the parameter space affects the run-time. The n-bin model is implemented as simplemodel with uncorrelated background according to the 2\_bin\_uncorr model in section A.1. Repeatedly appending bins to the histogram is used as a simple method to increase the dimensionality of the inference problem (n bins corresponds to a (n+1)-dimensional parameter vector).

#### Metropolis-Hastings (MH)



**Figure 5.3:** Run-time benchmark of the n-bin model in Python using Metropolis Hastings. A model with n bins represents a (n+1)-dimensional parameter vector. The upper Figure uses a Float64 likelihood with no just-in-time compilation by jax, the likelihood in the lower Figure is jitted and has Float32 precision.

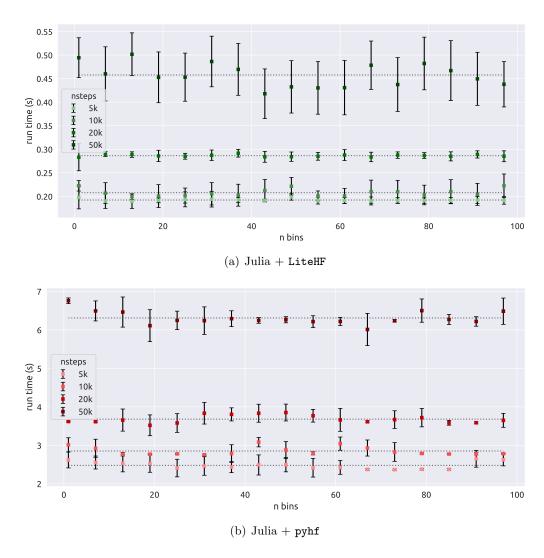


Figure 5.4: Run time benchmark of the n-bin Model in Julia using Metropolis Hastings.

Figure 5.3 shows the run-time development in Python (batty) for a likelihood with and without just-in-time compilation by  $\mathtt{jax}^1$ . In both plots the run-time slightly increases for models with less than 30 bins (left). For larger models with n > 30 bins (right), the run-time in Python increases more sharply. The run-time for a 40-bin model already takes about 5 times longer than a 30-bin model.

#### Explain?

The Julia benchmarks for the n-bin model are visualized in Figure 5.4. The pure-Julia version (green) is more than 10 times faster than the the jitted Python implementation. Moreover, run-times stay constant up to a 100 dimensional parameter vector for different

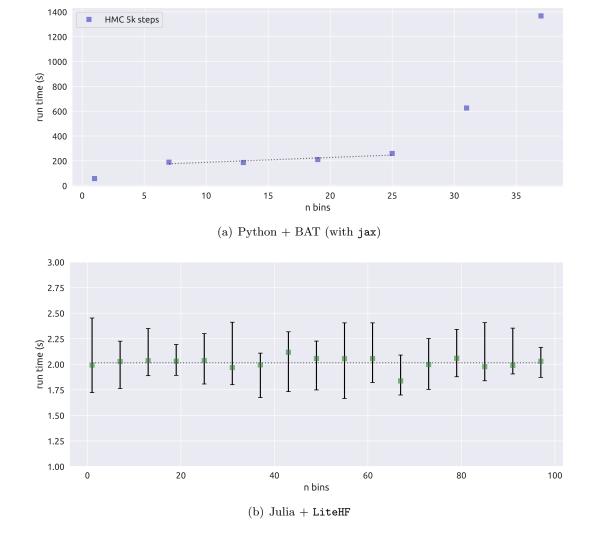
 $<sup>^{1}</sup>$ The jitted likelihood is about 2.5 times faster for the n-bin model.

5.2. BENCHMARKS 25

number of steps. The same behaviour can be observed for calling the pyhf likelihood from Julia (Figure 5.4b) while this implementation is about 12 times slower than the pure-Julia version.

#### Hamiltonian Monte Carlo (HMC)

The HMC run-times for the n-bin model are illustrated in Figure 5.5 for 5k nsteps. Similar to MH in Figure 5.3, run-times for the batty implementation only slightly increase for models with less than 30 parameters. Afterwards, the run-time significantly increases for n > 30 bins.



**Figure 5.5:** Run time benchmark of the n-bin Model in Julia using HMC for 5k steps. The Julia run-times are averaged over 100 runs, the Python run-times only represent a single run.

The run-times for the pure-Julia implementation are shown in Figure 5.5b). Again, run-

times stay constant up to a 100 bin model and are about 100 times faster the Python version.

#### 5.3 Discussion

In all considered benchmarks, the pure-Julia runs significantly faster than the other two implementations, where the <code>pyhf</code> likelihood is involved. Metropolis Hastings runs about

 $\dots$  n-bin model in python jump at 30... However, the executing time of the log likelihood only slightly decreases

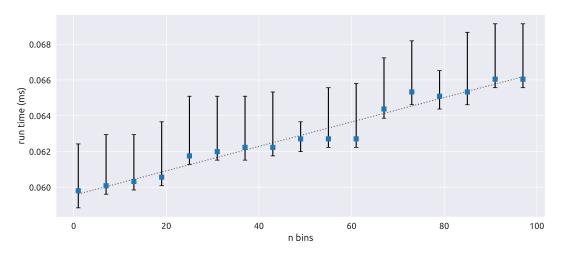


Figure 5.6: Evaluating the log likelihood for the *n*-bin model up to 100 bins.

Python Issue for large dimensions (> 30): sampler chains often do not converge, since BrooksGelmanConvergence is not achieved. MCMCMultiCycleBurnin needs to be adapted...

- Explain
- Although

# Appendix A

# HistFactory Models

#### A.1 2\_bin\_uncorr Model

```
• parameter \boldsymbol{\theta} = [\mu, \gamma_1, \gamma_2]
```

- signal model [5.0, 10.0], normfactor modifier
- bkg model [50.0, 60.0], shapesys modifier with relative uncert. [10%, 20%]

```
"channels": [
  { "name": "singlechannel",
    "samples": [
      { "name": "signal",
        "data": [5.0, 10.0],
        "modifiers": [ { "name": "mu", "type": "normfactor", "data": null} ]
      { "name": "background",
        "data": [50.0, 60.0],
        "modifiers": [
          { "name": "uncorr_bkguncrt",
            "type": "shapesys",
            "data": [5.0, 12.0] }
        ]
    ]
  }
],
"observations": [
  { "name": "singlechannel", "data": [50.0, 60.0] }
],
"measurements": [
  { "name": "Measurement", "config": {"poi": "mu", "parameters": []} }
],
"version": "1.0.0"
```

#### A.2 2\_bin\_corr Model

```
• parameter \boldsymbol{\theta} = [\mu, \, \theta]
   • signal model [12.0, 11.0], normfactor modifier
{
    "channels": [
      { "name": "singlechannel",
        "samples": [
          { "name": "signal",
            "data": [12.0,11.0],
            "modifiers": [ { "name": "mu", "type": "normfactor", "data": null } ]
          },
          { "name": "background",
            "data": [ 50.0, 52.0 ],
            "modifiers": [
              { "name": "correlated_bkg_uncertainty",
                 "type": "histosys",
                 "data": { "hi_data": [45.0, 57.0], "lo_data": [55.0, 47.0] }
              }
            ]
          }
        ٦
      }
    "observations": [
      { "name": "singlechannel", "data": [53.0, 65.0] }
    ],
    "measurements": [
        "name": "Measurement",
        "config": {
        "poi": "mu",
        "parameters": []
        }
      }
    ],
    "version": "1.0.0"
```

#### A.3 4\_bin Model

```
• parameter \boldsymbol{\theta} = [\mu, \, \theta, \, \theta_{SF}]
  "channels": [
    { "name": "singlechannel",
      "samples": [
        { "name": "signal MC",
           "data": [2, 3, 4, 5],
           "modifiers": [ { "name": "mu", "type": "normfactor", "data": null } ]
        },
           "name": "bkg MC",
           "data": [30, 19, 9, 4],
           "modifiers": [
             { "name": "theta",
               "type": "histosys",
               "data": { "hi_data": [31, 21, 12, 7], "lo_data": [29, 17, 6, 1] }
             { "name": "SF_theta",
               "type": "normsys",
               "data": {"hi": 1.1,"lo": 0.9}
             }
          ]
        }
      ]
    }
  ],
  "observations": [
    { "name": "singlechannel", "data": [34, 22, 13, 11]}
  "measurements": [
    { "name": "Measurement", "config": {"poi": "mu", "parameters": []} }
  ],
  "version": "1.0.0"
}
```

# Appendix B

# Run-time Statistics

While executing code on a PC, the execution time of a function varies due to other active processes. A typical run time statistics for 10k runs is illustrated in Figure B.1.

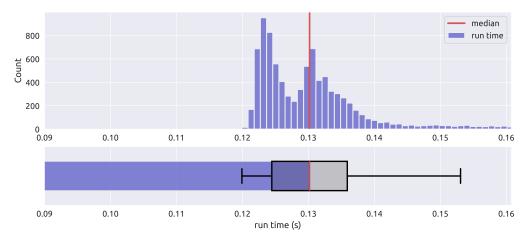


Figure B.1: Run-time statistics for evaluating the log likelihood 10k times.

In order simplify the plot while keeping track of the process statistics, run-times are visualized as bar-plot with an box-plot on top. The final value of the bar is the median run-time, which represents the red line in the box-plot. The box contains  $50\,\%$  of the data that is closed to the median and the whiskers mark the minimum and maximum value.

# Appendix C

# Additional Run-time statistics

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