# Nested sampling cross-checks using order statistics

Andrew Fowlie, Will Handley, and Liangliang Su (June 2020). In: arXiv: 2006.03371 [stat.CO]

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# Model selection

### **Model selection**

Throughout science, we have the following problem:

I have data and some models. What is the status of my models in light of the data?

# Bayesian updates

Compute the change in plausibility of a model in light of data relative to another model or set of models.

We just apply probability theory to the problem. All models treated equally.

Simple in theory; in practice there are difficulties.

# **Bayes factors**

Let's pursue the Bayesian approach (Jeffreys 1939).

The Bayes factor (Kass and Raftery 1995) relates the relative plausibility of two models after data to their relative plausibility before data;

$$Posterior\ odds = Bayes\ factor\ imes\ Prior\ odds$$

where

$$Bayes factor = \frac{p(Observed \ data \ | \ Model \ a)}{p(Observed \ data \ | \ Model \ b)}$$

A nice result — by applying laws of probability, we see that models should be compared by nothing other than their ability to predict the observed data.

# Bayesian evidence

The factors in the ratio are Bayesian evidences

$$\mathcal{Z} \equiv p(D \mid M) = \int_{\Omega_{\Theta}} \mathcal{L}(\Theta) \pi(\Theta) d\Theta,$$

where D is the observed data,  $\mathcal{L}(\Theta) = p(D \mid \Theta, M)$  is the likelihood and  $\pi(\Theta) = P(\Theta \mid M)$  is our prior, and  $\Theta$  are the model's parameters.

# Bayesian evidence

The evidence is often the single most important number in the problem and I think every effort should be devoted to calculating it

Mackay (2003)

The single most important number in inference? Let's think about how to compute it!

# It's a difficult integral

**Multi-dimensional:** Our models of physics might have many parameters. Even simple models contain  $\mathcal{O}(10)$  parameters

**Multi-modal:** We don't live in Gaussian land. In physics, the likelihoods can feature degeneracies and multiple modes

Fat-tailed: Large variance if you try Monte Carlo integration

# Nested sampling

# Algorithm

Skilling's idea (Skilling 2004; Skilling 2006). We can write

$$\mathcal{Z} = \int \mathcal{L}(X) \, \mathrm{d} X$$

where the volume variable

$$egin{aligned} X(\mathcal{L}^{\star}) &= \text{Fraction of prior volume with } \mathcal{L}(\mathbf{\Theta}) \geq \mathcal{L}^{\star} \ &= \int_{\mathcal{L}(\mathbf{\Theta}) \geq \mathcal{L}^{\star}} \pi(\mathbf{\Theta}) \, \mathrm{d}\mathbf{\Theta} \end{aligned}$$

and  $\mathcal{L}(X(\lambda))=\lambda.$  This is a one-dimensional integral. We can approximate it by a Riemann sum

$$\mathcal{Z} \approx \sum \mathcal{L}(X) \Delta X$$

We haven't achieved much yet. The trick is how to estimate X?

- 0. Draw  $n_{live}$  samples from the prior the live points
- 1. Denote the smallest likelihood amongst the live points by  $\mathcal{L}^{\star}$
- 2. Replace that live point by one drawn from the constrained prior

$$\pi^{\star}(\mathbf{\Theta}) \propto \begin{cases} \pi(\mathbf{\Theta}) & \mathcal{L}(\mathbf{\Theta}) \geq \mathcal{L}^{\star} \\ 0 & \text{otherwise} \end{cases}$$

- 3. Make a statistical estimate of  $X(\mathcal{L}^*)$  from this procedure
- 4. Increment estimate of evidence,  $\mathcal{Z} \to \mathcal{Z} + \mathcal{L}^* \Delta X$
- 5. If we have completed evidence sum to given tolerance, stop. Otherwise go to 1.

So we evolve a set of  $n_{live}$  live points to higher and higher likelihoods, replacing one live point at a time.

We know that  $X_0 = 1$ . How much do we expect X to contract when we replace the worst point?

Drawing from the constrained prior means live points are distributed uniformly in X from 0 to  $X(\mathcal{L}^*)$ .

In other words, the

$$f_i = \frac{X(\mathcal{L}_i)}{X(\mathcal{L}^*)}$$

are uniformly distributed from 0 to 1.

We know that  $X_0 = 1$ . How much do we expect X to contract when we replace the worst point?

The smallest one,  $t \equiv \min f_i$ , gives us the compression. We can write

$$p(t) = \binom{n_{\text{live}}}{1} \cdot t^{n_{\text{live}} - 1} \cdot 1 = n_{\text{live}} t^{n_{\text{live}} - 1}$$

where the factors are combinatorial, the probability of  $n_{live} - 1$  samples less than t, and lastly the probability density of a point at t.

We know that  $X_0 = 1$ . How much do we expect X to contract when we replace the worst point?

We find the expected compression:

$$\langle \log t \rangle = n_{\text{live}} \int_0^1 t^{n_{\text{live}} - 1} \log t dt = -\frac{1}{n_{\text{live}}}$$

Thus we may estimate that at iteration i

$$X_i \equiv X(\mathcal{L}_i^{\star}) \approx e^{-i/n_{live}}$$

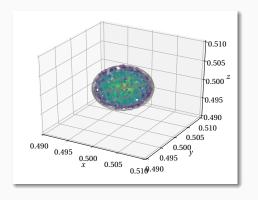
# How can we find an independent sample from the constrained prior?

This step in nested sampling was needed for our estimates of the volume, *X*.

Failure to correctly sample from the constrained prior leads to faulty estimates of the evidence.

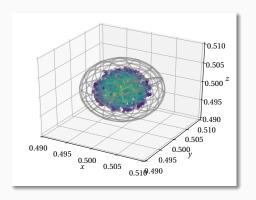
This requires an exploration strategy.

MultiNest (Feroz and Hobson 2008; Feroz, Hobson, and Bridges 2009; Feroz et al. 2013) — bound live points by ellipsoids. Use them to approximate iso-likelihood contour. Sample from the ellipsoids.



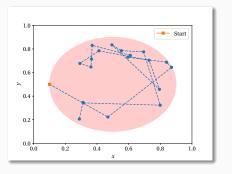
Two-dimensional Gaussian.

MultiNest (Feroz and Hobson 2008; Feroz, Hobson, and Bridges 2009; Feroz et al. 2013) — bound live points by ellipsoids. Use them to approximate iso-likelihood contour. Sample from the ellipsoids.



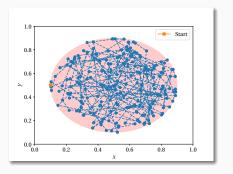
Expand to be safe — at expense of sampling efficiency.

PolyChord (Handley, Hobson, and Lasenby 2015a; Handley, Hobson, and Lasenby 2015b) — slice sampling walk, starting from a randomly chosen live point.



Two-dimensional Gaussian. 20 steps.

PolyChord (Handley, Hobson, and Lasenby 2015a; Handley, Hobson, and Lasenby 2015b) — slice sampling walk, starting from a randomly chosen live point.



200 steps. More steps to reduce correlation — at expense of sampling efficiency.

# Things can go wrong...

- What if I don't expand the ellipsoids enough?
- What if I don't use enough steps?
- What if my exploration strategy isn't actually drawing independent samples from the constrained prior?

It would violate assumption and lead to faulty estimate of evidence.

But how would I know?

A new cross-check

# What if we new the *X* of every sample?

Suppose we knew the *X* of every sample,  $X(\mathcal{L}_i)$ . We could look at

$$f_i = \frac{X(\mathcal{L}_i)}{X(\mathcal{L}^*)}$$

it should be uniformly distributed from 0 to 1 as each new  $X(\mathcal{L}_i)$  should be uniformly distributed from 0 to  $X(\mathcal{L}^*)$ .

You could test whether the f indeed followed a uniform distribution (Buchner 2016).

### What do we know?

We don't know that. We do know the likelihood of every new sample,  $\mathcal{L}_i$ , and that  $X(\mathcal{L})$  is a monotonic function.

So we can rank the  $n_{live}$  points by  $X(\mathcal{L}_i)$  by ranking them by  $\mathcal{L}_i$ .

The rank of every new sample, r, should be uniformly distributed from 1 to n<sub>live</sub>.

It's just as likely to be the worst, second worst, ..., second best, best likelihood.

We can test whether the r indeed follow a discrete uniform distribution.

### KS test

To compare the samples with the uniform distribution, we compute a *p*-value form a Kolmogorov-Smirnoff test.

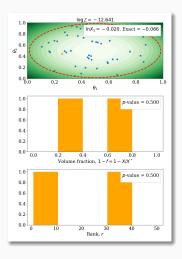
Sorry to sully a Bayesian algorithm with a p-value.

We use all the iterations and we test chunks of  $n_{live}$  iterations.

The latter stops biased periods in long runs being diluted by lots of unbiased iterations.

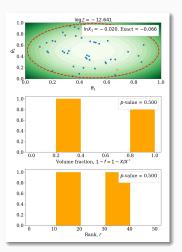
# Histogram of ranks r

Let's run a two-dimensional Gaussian nested sampling run. We will monitor the fractions and the insertion ranks, r.



# **Detecting faults**

This time, let's make the sampling biased by sampling from the wrong iso-likelihood contour — we find the correct one then contract it by a (random) factor  $0.8 \pm 0.1$ .



# **Detecting faults**

We see a tiny p-value and a biased overestimate of  $\mathcal{Z}$  — overestimated because the likelihoods that we draw are greater than they should be.

### **Correlations**

The ranks r are not, however, independent — the distribution of the live points only changes by one point every iteration.

If live points a are clustered together in X, insertion indexes in that region are unlikely.

We ignore this complication. However, if anything, correlations make the insertion ranks repel each other,



# Toy problems

In our paper, we introduce 4 toy problems. Here we discuss only one of them.

We compute the evidence using MultiNest and PolyChord, and *p*-values from our test.

We do 100 repeats. And good efr  $\ll$  1 and bad efr  $\gg$  1 exploration settings.

### Gaussian

Multi-dimensional Gaussian likelihood

$$\mathcal{L}(\mathbf{\Theta}) \propto e^{-rac{\sum (\mathbf{\Theta} - \mu)^2}{2\sigma^2}}$$

We pick a uniform prior from 0 to 1 for each dimension.

The analytic evidence is always  $\log \mathcal{Z} = 0$  since the likelihood is a pdf in  $\Theta$ , modulo small errors as the infinite domain is truncated by the prior.

We pick  $\mu=0.5$  and a diagonal covariance matrix with  $\sigma=0.001$  for each dimension.

# MultiNest. Gaussian, $\log \mathcal{Z} = 0$

Tiny *p*-values and biased results shown in red.

### Smaller efr ⇔ stricter run

efr	d	$\log \mathcal{Z}$	Inaccuracy	Bias	<i>p</i> -value	Rolling
0.10	2	$-0.00 \pm 0.10$	-0.04	-0.47	0.50	0.49
0.10	10	$0.01 \pm 0.23$	0.04	0.48	0.59	0.60
0.10	30	$0.38 \pm 0.41$	0.93	10.56	0.52	$2.7 \cdot 10^{-4}$
0.10	50	$2.08 \pm 0.52$	3.98	41.25	0.38	$4.5\cdot 10^{-24}$
1	2	$-0.00 \pm 0.10$	-0.04	-0.46	0.52	0.49
1	10	$0.57 \pm 0.23$	2.43	26.07	0.21	$1.2 \cdot 10^{-4}$
1	30	$2.35 \pm 0.40$	5.83	63.82	0.23	$2.2 \cdot 10^{-23}$
1	50	$4.06\pm0.52$	7.81	92.99	0.30	$1.3 \cdot 10^{-34}$
10	2	$-64.75 \pm 0.11$	-532.44	-6.95	$7.7\cdot 10^{-3}$	0.06
10	10	$\textbf{2.81} \pm \textbf{0.23}$	12.30	150.55	$2.1 \cdot 10^{-6}$	$1.7 \cdot 10^{-19}$
10	30	$4.30 \pm 0.40$	10.75	174.47	0.02	$3.1 \cdot 10^{-68}$
10	50	$6.04 \pm 0.52$	11.66	197.79	0.08	$1.1 \cdot 10^{-93}$

# **PolyChord. Gaussian,** $\log \mathcal{Z} = 0$

Tiny *p*-values and biased results shown in red.

### Smaller efr ⇔ stricter run

efr	d	$\log \mathcal{Z}$	Inaccuracy	Bias	<i>p</i> -value	Rolling
0.50	2	$0.01\pm0.11$	0.11	1.03	0.54	0.60
0.50	10	$-0.00\pm0.23$	-0.01	-0.10	0.48	0.52
0.50	30	$-0.06\pm0.41$	-0.15	-1.61	0.54	0.57
0.50	50	$-0.05\pm0.52$	-0.10	-0.85	0.58	0.51
1	2	$-0.02\pm0.11$	-0.19	-1.96	0.42	0.48
1	10	$-0.04\pm0.23$	-0.17	-2.20	0.55	0.59
1	30	$-0.83 \pm 0.41$	-2.06	-20.73	0.61	0.46
1	50	$-2.48\pm0.52$	-4.73	-54.22	0.49	0.59
2	2	$-0.01 \pm 0.11$	-0.12	-0.89	0.47	0.53
10	10	$\boldsymbol{2.20 \pm 0.23}$	9.50	30.29	0.13	0.22
30	30	$48.37 \pm 0.64$	112.25	70.58	$8.2 \cdot 10^{-10}$	0.02
50	50	$69.74 \pm 3.05$	23.31	106.51	$8.0 \cdot 10^{-86}$	$1.4\cdot 10^{-6}$

# Summary of toy problem

### A lot of numbers...

- Less strict exploration settings or high number of dimensions
- ... leads to a biased estimate of evidece
- ... often detected by tiny *p*-value by our test

# Example from cosmology

# Cosmology

Handley considered Bayesian evidence for a spatially closed Universe (Handley 2019a). Evidences from combinations of four datasets were computed using PolyChord for a spatially flat Universe and a curved Universe.

The Bayes factors showed that a closed Universe was favoured by odds of about 50/1 for a particular set of data.

There were 22 NS computations in total (Handley 2019b).

# Cosmology

We ran our cross-check on each of the 22 NS runs finding p-values in the range 4% to 98%.

THis does not suggest problems with the NS runs. The *p*-value of 4% is not particularly alarming, especially considering we conducted 22 tests.

	Flat		Curved	
Data	<i>p</i> -value	Rolling <i>p</i> -value	<i>p</i> -value	Rolling <i>p</i> -value
BAO	0.89	0.82	0.07	0.05
lensing+BAO	0.72	0.54	0.19	0.43
lensing	0.26	0.14	0.04	0.64
lensing+SH <sub>0</sub> ES	0.08	0.08	0.78	0.04
Planck+BAO	0.39	0.56	0.14	0.43
Planck+lensing+BAO	0.68	0.69	0.70	0.27
Planck+lensing	0.94	0.49	0.89	0.72
Planck+lensing+SH <sub>0</sub> ES	0.92	0.92	0.33	0.82
Planck	0.81	0.69	0.84	0.88
Planck+SH <sub>0</sub> ES	0.20	0.48	0.92	0.97
$SH_0ES$	0.59	0.59	0.98	0.98

29/30

# Summary

- Nested sampling is a popular algorithm for computing Bayesian evidence
- We developed the first test of single nested sampling runs
- · Appears to work nicely on toy and realistic problems
- Could become an important part of nested sampling analysis
- Could become a best practice to apply the check whenever using nested sampling

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