

NestedSamplers.jl: Composable Nested Sampling in Julia

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DOI: [DOIunavailable](#)

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Submitted: N/A

Published: N/A

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Summary

Nested sampling is a method for estimating the Bayesian evidence (Skilling, 2004). The core of the algorithm is rooted in integrating iso-likelihood “shells” in the prior space. This simultaneously produces the Bayesian evidence and weighted posterior samples. In contrast, Markov Chain Monte Carlo (MCMC) only generates samples proportional to the posterior. Nested sampling also has a variety of appealing statistical properties, which include: well-defined stopping criteria, independently generated samples, flexibility to model complex, multi-modal distributions, and direct measurements of the statistical and sampling uncertainties from a single run.

The basic algorithm can be described by the quadrature estimate of dynamically evolving points in the prior space. The Bayesian evidence is an integral, and the nested sampling algorithm estimates it with a sum of discrete measurements, represented by an array of points. The nested sampling algorithm successfully removes the point with the lowest likelihood and replaces it with a point of equal or higher likelihood. At each iteration, the full set of “live” points describes a volume, which has shrunk by the removal of the iso-likelihood shell around it. The volumes of these shells are used in the quadrature estimate of the Bayesian evidence described in Skilling (2004).

Statement of need

Nested sampling has grown immensely in popularity, due in part to its “black-box” nature, as well as the popularity of codes like MultiNest (Feroz et al., 2009; Feroz & Hobson, 2008) in the astronomical community, where high-dimensional, multi-modal problems are commonplace. Recently, dynesty (Speagle, 2020) created an API which fully separates two independent steps of the nested sampling algorithm. These steps are, first: describing the statistical distribution of the live points, then second: likelihood-constrained sampling for replacing live points. This process is shown schematically in Figure 1.

NestedSamplers.jl mimics the API of dynesty by separating the independent steps of the nested sampling algorithm. Our library heavily utilizes multiple-dispatch enabled by the Julia programming language (Bezanson et al., 2017) to enable a highly-expressive, composable, and efficient nested sampling library. Multiple-dispatch allows fully encapsulating the independent components of the algorithm, in other words, the code specific to each bounding distribution and proposal algorithm is never repeated, and it comes with no performance loss thanks to the just-in-time compilation of Julia code. In addition, NestedSamplers.jl incorporates the AbstractMCMC.jl interface, which is an extensible interface for statistical sampling which enables entry points for using our nested samplers in various programming contexts.

NestedSamplers.jl currently has three bounding distributions: NoBounds, which represents the entire prior space (Skilling, 2004), Ellipsoid, which bounds the live points in an ellipsoid (equivalent to a multivariate Gaussian) (Mukherjee et al., 2006), and MultiEllipsoid, which uses an optimal clusterign of ellipsoids, first demonstrated by MultiNest (Feroz et al., 2009; Feroz & Hobson, 2008). In the future, we plan to implement the ball and cube distributions

derived in Buchner (2014) and Buchner (2017).

NestedSamplers.jl has five restricted-likelihood sampling algorithms (proposal algorithms), using a slew of MCMC techniques. The first is the Rejection algorithm, which simply generates samples from the prior and rejects those outside the likelihood constraint (Skilling, 2004). RWalk and RStagger use a Metropolis-Hastings-like walk for evolving a sample (Skilling, 2006). RSlice and Slice use slice sampling in random (Handley et al., 2015a, 2015b) or principal directions (Neal, 2003), respectively, to evolve points. In the future, we plan to support Hamiltonian slice sampling (Speagle, 2020), which requires gradients and Jacobians.

NestedSamplers.jl currently uses a static nested sampler (integrator), where the number of live points is fixed throughout the sampling. Dynamic nested samplers allow tuning the integrator to avoid (or prefer) regions of high likelihood, which can be preferred in cases where posterior samples are more relevant than the Bayesian evidence estimate (Speagle, 2020). In the future, we plan to implement a dynamic nested sampler which can make use of the existing bounding distributions and proposal algorithms.

Comparisons to existing software

NestedSamplers.jl has many features similar to dynesty, and the predecessor code nestle. dynesty currently has more features, including a dynamic nested sampler, Hamiltonian slice sampling, and ball and cube distributions. The recent ultranest code (Buchner, 2021) has a subset of the features of dynesty. MultiNest can be reproduced by using our MultiEllipsoid bounding distribution, and the exact algorithm can be reproduced with an appropriate Rejection proposal algorithm. The Polychord algorithm can be reproduced by using the RSlice algorithm, with typically an Ellipsoid bounding distribution.

References

- Bezanson, J., Edelman, A., Karpinski, S., & Shah, V. B. (2017). Julia: A Fresh Approach to Numerical Computing. *SIAM Rev.*, 59(1), 65–98. <https://doi.org/10.1137/141000671>
- Buchner, J. (2021). Nested Sampling Methods. *arXiv e-Prints*, 2101, arXiv:2101.09675. <http://adsabs.harvard.edu/abs/2021arXiv210109675B>
- Buchner, J. (2014). *A statistical test for Nested Sampling algorithms*. <https://ui.adsabs.harvard.edu/abs/2014arXiv1407.5459B>
- Buchner, J. (2017). *Collaborative Nested Sampling: Big Data vs. Complex physical models*. <https://ui.adsabs.harvard.edu/abs/2017arXiv170704476B>
- Feroz, F., & Hobson, M. P. (2008). Multimodal nested sampling: An efficient and robust alternative to Markov Chain Monte Carlo methods for astronomical data analyses. *Monthly Notices of the Royal Astronomical Society*, 384, 449–463. <https://doi.org/10.1111/j.1365-2966.2007.12353.x>
- Feroz, F., Hobson, M. P., & Bridges, M. (2009). MULTINEST: An efficient and robust Bayesian inference tool for cosmology and particle physics. *Monthly Notices of the Royal Astronomical Society*, 398, 1601–1614. <https://doi.org/10.1111/j.1365-2966.2009.14548.x>
- Handley, W. J., Hobson, M. P., & Lasenby, A. N. (2015a). Polychord: Nested sampling for cosmology. *Monthly Notices of the Royal Astronomical Society*, 450, L61–L65. <https://doi.org/10.1093/mnras/slt047>
- Handley, W. J., Hobson, M. P., & Lasenby, A. N. (2015b). POLYCHORD: Next-generation nested sampling. *Monthly Notices of the Royal Astronomical Society*, 453, 4384–4398. <https://doi.org/10.1093/mnras/stv1911>

- Mukherjee, P., Parkinson, D., & Liddle, A. R. (2006). A Nested Sampling Algorithm for Cosmological Model Selection. *The Astrophysical Journal*, 638, L51–L54. <https://doi.org/10.1086/501068>
- Neal, R. M. (2003). Slice sampling. *The Annals of Statistics*, 31(3), 705–767. <https://doi.org/10.1214/aos/1056562461>
- Skilling, J. (2004). *Nested Sampling*. 735, 395–405. <https://doi.org/10.1063/1.1835238>
- Skilling, J. (2006). Nested sampling for general Bayesian computation. *Bayesian Analysis*, 1(4), 833–859. <https://doi.org/10.1214/06-BA127>
- Speagle, J. S. (2020). DYNESTY: A dynamic nested sampling package for estimating Bayesian posteriors and evidences. *Monthly Notices of the Royal Astronomical Society*, 493, 3132–3158. <https://doi.org/10.1093/mnras/staa278>