

# Barcode Validator: A Python toolkit for structural and taxonomic validation of DNA barcode sequences

Rutger A. Vos <sup>1</sup>✉

<sup>1</sup> Naturalis Biodiversity Center, Leiden, The Netherlands ✉ Corresponding author

DOI: [10.xxxxxx/draft](https://doi.org/10.xxxxxx/draft)

## Software

- [Review](#) ✉
- [Repository](#) ✉
- [Archive](#) ✉

Editor: [Open Journals](#) ✉

## Reviewers:

- [@openjournals](#)

Submitted: 01 January 1970

Published: unpublished

## License

Authors of papers retain copyright and release the work under a Creative Commons Attribution 4.0 International License ([CC BY 4.0](#)).

## Summary

DNA barcoding has become a cornerstone technique in molecular biodiversity research, enabling rapid species identification and discovery through standardized genetic markers. The Barcode Validator is a Python toolkit designed to ensure the quality and accuracy of DNA barcode sequences before submission to public databases such as the Barcode of Life Data System (BOLD) and institutional repositories. The software performs both structural validation (assessing sequence quality, length, ambiguous bases, and marker-specific features like stop codons) and taxonomic validation (verifying specimen identifications through reverse taxonomy using BLAST-based identification services). Developed to support large-scale biodiversity genomics initiatives, particularly the Biodiversity Genomics Europe (BGE) and ARISE projects, the toolkit provides automated workflows for processing thousands of sequences with flexible configuration options and comprehensive reporting.

## Statement of need

DNA barcoding projects generate large volumes of sequence data that must meet stringent quality standards before deposition in public databases. Manual validation of sequences is time-consuming, error-prone, and impractical for projects processing hundreds or thousands of specimens. Furthermore, the increasing adoption of genome skimming and high-throughput sequencing technologies produces multiple assembly attempts per specimen, requiring intelligent selection of the best valid sequence among alternatives.

Existing validation tools are typically limited in scope: quality control tools like FastQC ([Andrews, 2010](#)) focus on raw read quality rather than assembled barcode sequences; taxonomic identification tools like BOLD's identification engine ([Ratnasingham & Hebert, 2007](#)) or standalone BLAST ([Altschul et al., 1990](#)) provide identification but lack integration with quality metrics; and no comprehensive solution exists for the specific workflow requirements of modern barcoding projects that combine multiple assembly attempts with both structural and taxonomic validation.

The Barcode Validator addresses these gaps by providing:

1. **Integrated validation:** Combined structural and taxonomic validation in a single workflow, with support for marker-specific requirements (e.g., stop codon detection for protein-coding genes via translation, GC content assessment for non-coding markers).
2. **Assembly triage:** Automatic selection of the best valid sequence when multiple assembly attempts exist per specimen, using configurable criteria including validation results and optional assembly quality metrics.
3. **Flexible taxonomic validation:** Support for multiple identification backends (BOLD API, local BLAST, Galaxy web services) and taxonomic backbones (BOLD, NCBI, Netherlands

Species Register), enabling validation against expected specimen identifications at configurable taxonomic ranks.

4. **Batch processing:** Efficient handling of large datasets through batched API calls and parallel processing where appropriate.

5. **Workflow integration:** Command-line interface suitable for automated pipelines, with Galaxy tool integration for web-based access.

The software has been deployed in production workflows at Naturalis Biodiversity Center (the Netherlands) and the Natural History Museum (United Kingdom) for the BGE project, processing thousands of arthropod COI sequences from genome skimming experiments, and the ARISE project for validation of freshly sequenced specimens. Its design supports the quality assurance requirements of modern DNA barcoding initiatives while remaining flexible enough to accommodate diverse project-specific workflows.

## Implementation

Barcode Validator is implemented in Python (3.9+) with a modular, extensible architecture built around several key design patterns:

- **Strategy pattern** for validators: An abstract `Validator` base class defines the validation interface, with concrete implementations for structural validation (`StructuralValidator` with subclasses `ProteinCodingValidator` and `NonCodingValidator`) and taxonomic validation (`TaxonomicValidator`).
- **Factory pattern** for services: Pluggable identification services (`IDService` hierarchy supporting BOLD, BLAST, and Galaxy backends) and taxonomic resolvers (`TaxonResolver` supporting BOLD, NCBI, and NSR taxonomies) enable flexible backend selection.
- **Orchestration pattern:** A `ValidationOrchestrator` coordinates the validation pipeline, managing validator initialization, batch processing, result aggregation, and output generation.

The software integrates with established bioinformatics tools including BLAST+ (Camacho et al., 2009) for sequence similarity searches, HMMER (Eddy, 2011) for profile Hidden Markov Model-based alignment and codon phase detection, and Biopython (Cock et al., 2009) for sequence manipulation and translation. External validation is performed through REST API calls to BOLD (Ratnasingham & Hebert, 2007) and Galaxy (The Galaxy Community, 2022) identification services.

Input data can be provided as FASTA files with optional CSV metadata and BOLD Excel spreadsheets containing specimen and taxonomic information. Validation results are output in both human-readable TSV format (with detailed pass/fail status for each validation criterion) and filtered FASTA format (containing only sequences meeting all validation requirements).

## Availability

The source code is available on GitHub at [https://github.com/naturalis/barcode\\_validator](https://github.com/naturalis/barcode_validator) under the Apache License 2.0. The software can be installed via PyPI (`pip install barcode-validator`) or Bioconda (`conda install -c bioconda barcode-validator`). A Galaxy tool wrapper is available in the Galaxy ToolShed for web-based access. Documentation, including detailed usage examples for common workflows, is provided in the repository README and architecture documentation.

## Acknowledgements

This work was supported by the Biodiversity Genomics Europe (BGE) project, which has received funding from the European Union's Horizon Europe Research and Innovation Programme under grant agreement No. 101059492, and the ARISE project. We acknowledge the Naturalis Biodiversity Center for institutional support and infrastructure.

## References

- Altschul, S. F., Gish, W., Miller, W., Myers, E. W., & Lipman, D. J. (1990). Basic local alignment search tool. *Journal of Molecular Biology*, 215(3), 403–410. [https://doi.org/10.1016/S0022-2836\(05\)80360-2](https://doi.org/10.1016/S0022-2836(05)80360-2)
- Andrews, S. (2010). *FastQC: A quality control tool for high throughput sequence data*. <https://www.bioinformatics.babraham.ac.uk/projects/fastqc/>
- Camacho, C., Coulouris, G., Avagyan, V., Ma, N., Papadopoulos, J., Bealer, K., & Madden, T. L. (2009). BLAST+: Architecture and applications. *BMC Bioinformatics*, 10(1), 421. <https://doi.org/10.1186/1471-2105-10-421>
- Cock, P. J., Antao, T., Chang, J. T., Chapman, B. A., Cox, C. J., Dalke, A., Friedberg, I., Hamelryck, T., Kauff, F., Wilczynski, B., & Hoon, M. J. de. (2009). Biopython: Freely available Python tools for computational molecular biology and bioinformatics. *Bioinformatics*, 25(11), 1422–1423. <https://doi.org/10.1093/bioinformatics/btp163>
- Eddy, S. R. (2011). Accelerated profile HMM searches. *PLoS Computational Biology*, 7(10), e1002195. <https://doi.org/10.1371/journal.pcbi.1002195>
- Ratnasingham, S., & Hebert, P. D. (2007). BOLD: The barcode of life data system. *Molecular Ecology Notes*, 7(3), 355–364. <https://doi.org/10.1111/j.1471-8286.2007.01678.x>
- The Galaxy Community. (2022). The Galaxy platform for accessible, reproducible and collaborative biomedical analyses: 2022 update. *Nucleic Acids Research*, 50(W1), W345–W351. <https://doi.org/10.1093/nar/gkac247>