

InMoose: the open-source Python environment for bioinformatics

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What is InMoose?

InMoose is an open-source **bioinformatics environment in Python** designed for **omics data** analysis. It enables large-scale transcriptomic analyses such as:

- Data simulation
- Batch effect correction
- Differential expression analysis
- Meta-analysis

Why we built InMoose: closing the gap between R and Python in bioinformatics

Since the first human genome was sequenced in 2000, omic profiling technologies have seen their costs reduced by multiple orders of magnitude, and omic profiling is now performed routinely. Petabytes of omic data are generated each year, yet most of it remains largely under-used. Bridging the gap between **data science, AI, informatics and biology** remains a key challenge to enable the analysis of such massive and complex data. Overcoming this challenge requires the development of efficient, easy-to-use, and interoperable tools, to let practitioners focus on scientific questions rather than technical issues.

While R has historically dominated data analysis and visualization, Python is rapidly gaining traction in bioinformatics and biostatistics. Its rising popularity is reflected in the increasing number of **bioinformatics tools** developed in Python, such as lifelines for survival analysis and scanpy for single-cell RNA-Seq. Today, some reference tools, like those for RNA velocity analysis, are exclusively available in Python, making compatibility essential. Python's versatility, powerful data management capabilities, and seamless integration with data infrastructure APIs position it as a key language for modern bioinformatics pipelines, especially as machine learning and AI become core components of the field.

We created InMoose to ease the transition for **bioinformaticians from R to Python**, offering advanced features such as:

- Quality Control (QC) report to evaluate cohorts after batch correction
- Differential expression meta-analysis tool to aggregate results across cohorts and tools

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How does it benefit your bioinformatics analyses?

InMoose is an advanced solution that transforms **bioinformatics analysis** by seamlessly integrating key Python libraries such as NumPy, SciPy, and Pandas. Its smooth R/Python portability simplifies complex workflows and enhances the efficiency of multidimensional data analysis. By optimizing computational performance, InMoose accelerates analytical processes while ensuring accurate and reproducible results. Additionally, it powers mCUBE, Epigene Labs' intuitive web platform, making advanced bioinformatics analysis accessible to researchers of all expertise levels. Thanks to the Python infrastructure, InMoose runs on all operating systems – Windows, macOS, linux.

Real-world use cases in omics data analysis

Since its release, InMoose has been applied to various omics – transcriptomics but also proteomics, metabolomics, and single-cell – in oncology and beyond: neurology, immunology, and autoimmune diseases. Unexpectedly, it has also found uses in agronomy and studies on the biological impact of pollution.

Shaping the future of bioinformatics for precision medicine research

With InMoose, we aim to empower researchers to fully harness the potential of multi-omic datasets – from exploratory analyses to advanced statistical modeling – without being limited by technical barriers or rigid environments. By combining performance, interoperability, and usability, InMoose supports a new generation of **bioinformatic workflows** that are both reproducible and scalable. Whether you're transitioning from R, scaling up analysis pipelines, or integrating multi-modal data types, InMoose is built to adapt and evolve with your scientific needs.

Explore our scientific publications

- Differential expression analysis with InMoose, the integrated multi-omic open-source environment in Python ([BMC Bioinformatics, 2025](#))
- Bridging the gap between R and Python in bulk transcriptomic data analysis with InMoose ([Scientific Reports, 2025](#))
- pyComBat, a Python tool for batch effects correction in high-throughput molecular data using empirical Bayes methods ([BMC Bioinformatics, 2023](#))

Explore the InMoose open-source bioinformatics tool on GitHub

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