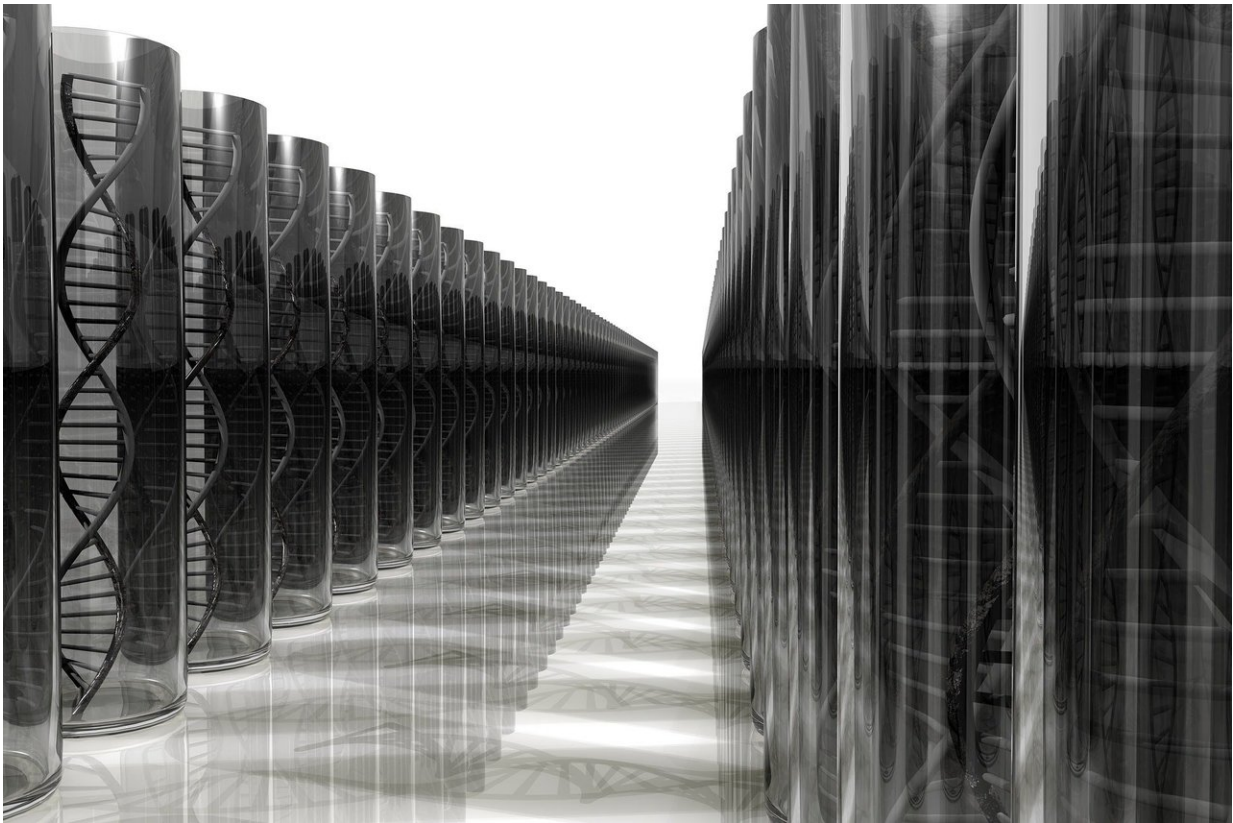


# Researchers develop tool that analyzes biomedical data within minutes

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Researchers at the Icahn School of Medicine at Mount Sinai have developed a tool that speeds up the analysis and publication of biomedical data from many months or years to mere minutes,

transforming the way researchers communicate results of their studies. Until now, the primary method available to share biomedical research data has been through print publication in scientific journals. The new tool, BioJupies, relies on cloud technologies to analyze and visualize large amounts of data, such as that acquired by genome sequencing, as described in the November 2018 issue of *Cell Systems*.

RNA sequencing is the most common experimental method used to profile cells in biomedical research. In recent years, sequencing technology has revolutionized the way scientists examine genetic data, and this advancement plays a crucial role in drug discovery and development. Traditionally, RNA sequencing analysis requires extensive computer programming skills and access to local high performance computing facilities, slowing down the speed at which biomedical data can be analyzed, shared, and published.

Through the creation of BioJupies, users can now upload and analyze their RNA sequencing data in a fraction of the time as done previously. The platform utilizes a cloud computing pipeline that reduces the cost of RNA-sequencing data processing to less than one cent per sample. BioJupies also produces a complete, open source, interactive report from the processed data allowing for 300,000 publicly available RNA sequencing datasets to be fetched, reanalyzed, and reused to bolster [biomedical research](#).

"As the amount of biomedical data generated continues to climb exponentially, so should the tools used to analyze and share them," said Avi Ma'ayan, Ph.D., Director of the Mount Sinai Center for Bioinformatics, Professor, Department of Pharmacological Sciences, faculty of Icahn Institute for Data Science, and senior author of the publication. "BioJupies not only accelerates the manner in which we analyze and interpret data, but it also provides a completely new way to share results with the global research community."

As new genomic technologies have allowed for the collection of massive amounts of biomedical information that can be harnessed for precision medicine efforts, accessibility, interoperability, and reusability of this data has become crucial to scientific research. BioJupies paves the way for researchers with no computational background to perform RNA sequencing analysis without the need to collaborate with bioinformaticians, enabling more medical and scientific advancements to flourish in our data rich world.

**More information:** Denis Torre, Alexander Lachmann, Avi Ma'ayan. "BioJupies: Automated Generation of Interactive Notebooks for RNA-seq Data Analysis in the Cloud" *Cell Systems*, [DOI: 10.1016/j.cels.2018.10.007](https://doi.org/10.1016/j.cels.2018.10.007)

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