

Tessera Therapeutics accelerates pipeline analysis and improves research productivity with the Seqera platform

CUSTOMER



<https://tesseratherapeutics.com>

LOCATION

Cambridge, MA

INDUSTRY

Biopharmaceutical research

OBJECTIVES

Tessera Therapeutics needed to obtain analysis results faster while improving research productivity, reproducibility, and auditability with a modern environment for managing data pipelines at scale.

CHALLENGES

- Need to accelerate analysis pipelines
- Make pipelines accessible to scientific users
- Improve cloud resource use efficiency
- Ensure reproducibility and auditability

SOLUTION

- Nextflow and the Seqera platform
- Seqera Labs Services
- AWS cloud environment: AWS Batch, Amazon S3
- GitLab for source code management

RESULTS

- Increased analysis capacity
- Dramatic productivity gains
- Better visibility to pipelines and data
- Reduced cloud spending

Summary

Tessera Therapeutics are pioneers in a new category of genetic medicine and rely heavily on genomic analysis pipelines to identify promising new treatments. By using the Seqera platform to manage analysis pipelines, Tessera increased its analysis throughput and research productivity, while simultaneously containing cloud spending by using resources more efficiently.

The business

Tessera Therapeutics are the innovators behind Gene Writing and Gene Rewriting, new biotechnologies designed to offer scientists and clinicians the ability to write small and large therapeutic messages into the genome, with the potential to treat and cure diseases at their source. Gene Writing holds the potential to become a new category in genetic medicine, building on recent breakthroughs in gene therapy and gene editing while eliminating important limitations in their reach, utilization, and efficacy.

The challenge

Tessera Therapeutics uses a combination of computational biology and wet-lab approaches in its research. The performance and scalability of data analysis pipelines for Next-Generation Sequencing (NGS) analysis jobs are critical to their productivity and the pace of the research.

Developing new therapeutics depends on their ability to identify and organize mobile genetic element sequences for multiple species from different genome databases and identify and prioritize promising protein and DNA signatures. Gene Writer proteins can be delivered by RNA or DNA, and research teams

extensively use RNASeq and a variety of other pipelines for analysis.

Early in their evolution, Tessera used the AWS genomics workflow reference architecture. While this served them well initially, they outgrew its capabilities. Given the importance of analysis pipelines to their business, they didn't want to rely on the open-source community for best-effort technical support.

The ease of developing, launching, and monitoring pipelines was also an issue. To improve productivity, Tessera needed a solution that would enable members of the computational biology team to work collaboratively and be self-sufficient in running and monitoring pipelines.

Ensuring traceability and repeatability was also important as research progressed to clinical trials. Understanding on-target and off-target changes are critical to evaluating therapies, and research teams need to carefully catalog all parameters, including datasets, containers, and pipeline versions.

The solution

Tessera Therapeutics began shifting to Nextflow for most of its analysis pipelines a few years ago. Today, most pipelines are implemented in Nextflow. As a next step to boost productivity, Tessera decided to deploy the Seqera platform – a management solution for Nextflow workflows designed to enable collaborative data analysis at scale.

Seqera's ability to provide technical support for Nextflow, the Seqera platform, and pipelines was important to Tessera because it meant that they were getting support directly from the source, helping avoid problems and speed time to problem resolution.

To adapt in-house developed pipelines to the Seqera environment, Tessera leveraged best practices from the nf-core community, publishing JSON schema files to make pipelines directly accessible through Seqera's web interface. Today, members of the computational biology team can easily launch pipelines directly from

Tessera's private GitLab repository using the intuitive Seqera web interface.

Results

INCREASED ANALYSIS CAPACITY

Having the capacity to run large numbers of analysis jobs quickly is a critical enabler. With faster turnaround times, researchers can analyze promising therapeutics more quickly. The mature AWS Batch integration also means that pipelines are more efficient, and reliable.

DRAMATIC PRODUCTIVITY GAINS

The Seqera interface makes pipelines exceptionally easy to launch, monitor, and study results saving time at all stages in the data analysis workflow. Yohann Potier, Director of Data Platforms at Tessera Therapeutics, observed:

"Using Seqera has helped us save time and resources. In addition to improving research productivity, our IT team's workload has been reduced considerably. This means we have more time to dedicate to more productive tasks."

BETTER VISIBILITY TO PIPELINES AND DATA

Approximately ten people regularly use Seqera to launch and manage analysis jobs at Tessera. With Seqera, users have full visibility to all pipeline runs, subject to permissions. Potier indicates:

Seqera has made it much easier to track pipeline execution and organize datasets. By maintaining a searchable run history, Seqera gives us visibility to track prior pipeline runs – a critical feature for ensuring reproducibility and auditability."

REDUCED CLOUD SPENDING

By using the AWS Batch executor, Tessera has also been able to reduce cloud spending, by maximizing their use of spot instances, packing pipeline tasks more efficiently on machine instances, and deploying cloud resources only when they are needed.

LEARN MORE

To learn more, visit www.seqera.io