ALMADEN GENOMICS

ACCELERATE DISCOVERY

Develop novel insights and deliver therapies to market faster with g.nome™, a secure and HIPAA-ready cloud-native data analysis platform from Almaden Genomics designed to bridge the gap between scientists and bioinformaticians to streamline genomic workflows.

From the detection of genetic variations to drug and therapy development, the exciting possibilities of multiomic research are as vast as they are life-changing. However, one challenge has persisted: the excessive amount of time it takes to build bioinformatic workflows. Development of these workflows can be painfully inefficient, difficult to scale and inaccessible to your broader team, slowing the iteration and analysis that leads to more effective therapeutics and drugs.

NOT ANYMORE.

g.nome™

OUR PLATFORM PROVIDES THE CAPABILITY TO BUILD STREAMLINED, SCALABLE, FLEXIBLE AND INTEROPERABLE GENOMIC WORKFLOWS, EMPOWERING YOUR TEAM TO DO WHAT THEY DO BEST:

FOCUS ON THE SCIENCE.

Have Confidence in Your Results

- Simple, visual format streamlines pipeline review and makes it easy to identify errors and inconsistencies.
- Visibility to every tool, every version and every parameter ensures detailed pipeline auditability.
- Systematic tracking assures data provenance for every pipeline run output.

Get to Market Faster

- Intuitive drag-and-drop GUI — combined with a curated library of pre-built workflows, trusted open-source tools and the ability to import custom code — makes the platform incredibly easy to use.
- Low/no-code flexibility allows contribution from users without coding expertise in addition to your advanced programmers, enabling you to iterate faster and optimize team collaboration from anyone, anywhere.
- Accelerate pipeline development with a single platform from proof of concept to production.

Scale Profitably

- Automatic scalability and proven cloud-computing architecture process large-scale datasets with great efficiency, security, and reliability.
- Stringent version control within our stable and containerized environment provides confidence that pipelines are reliable and reproducible.
- Elastic processing capabilities allow you to optimize your run and assign increased computational power to pieces of your pipeline at a granular level.

WITH g.nome™ YOUR TEAM CAN MOVE AT THE SPEED OF INNOVATION.

Accelerate Discovery

With streamlined, scalable and interoperable genomic workflows, g.nome dramatically improves the process of modifying and running bioinformatic pipelines — accelerating discovery, time to market and the ability to scale. By eliminating common frustrations and condensing pipeline builds from months to hours, g.nome is the data analysis platform scientists and bioinformaticians have been waiting for.

Optimize Your Investment

The g.nome low-code/no-code platform enables team members without coding knowledge to iterate upon pipelines from anywhere, freeing up your team to focus on discovery. This makes wider collaboration and analysis possible, including with remote teams. With g.nome, anyone who understands the science can build and participate in pipeline development, so your company can invest in its vision instead of outsourced bioinformatic services or additional staff.
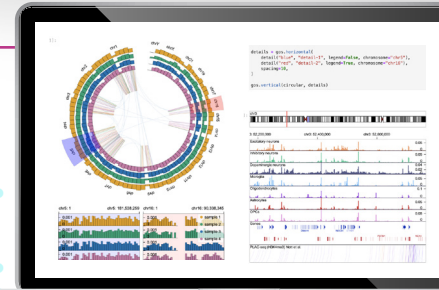
Work the Way You Want

You know what works, and g.nome makes it easy for you to leverage that for future pipeline builds. With g.nome, team members can contribute regardless of coding experience, making it easy to collaborate and analyze data. The platform incorporates existing open-source tools, as well as provides the flexibility to add custom code, easily replicate pipelines and handle big data sets reliably and efficiently.
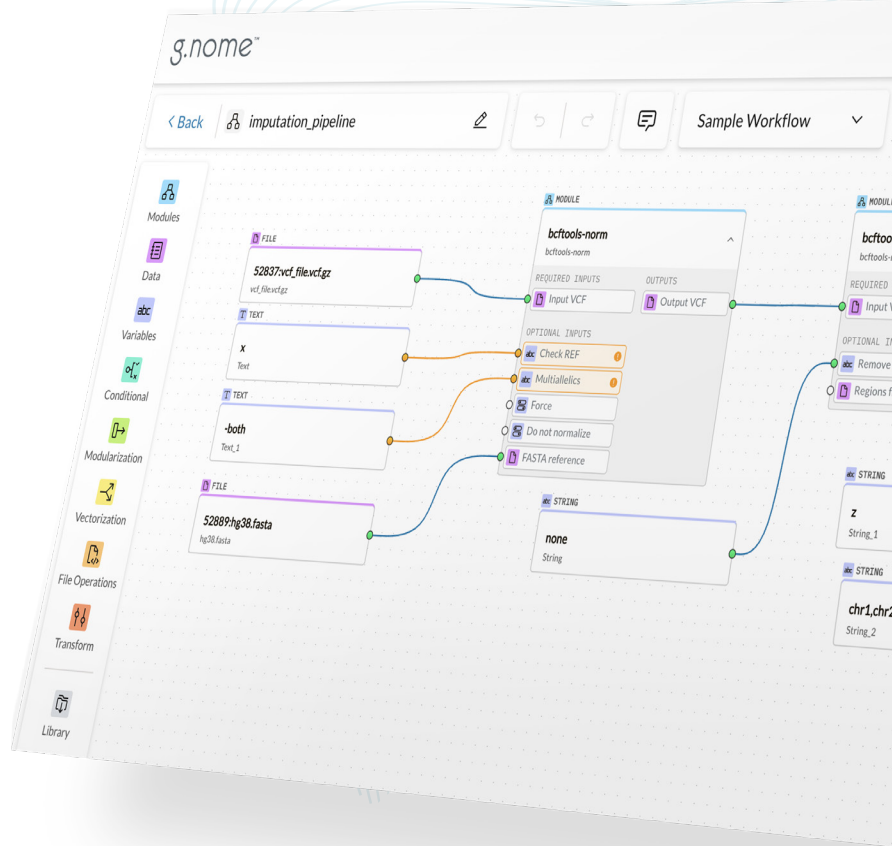
NEW

Visualization Capabilities

Integration with Jupyter Notebook allows users to visualize and interpret their data conveniently. Create heatmaps, volcano plots, or other helpful visualizations, all within the same platform.

GET A FREE TRIAL

ALMADEN GENOMICS

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