ALMADEN GENOMICS

ACCELERATE DISCOVERY

Develop novel insights and deliver assays to market faster with g.nome™, a secure and HIPAA-ready cloud-native bioinformatics platform from Almaden Genomics designed to empower your bioinformaticians and streamline genomic workflows.

From the detection of genetic diseases to drug and assay development, the exciting possibilities of genomic 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 analysis that leads to medical insights and precision medicine.

NOT ANYMORE.

g.nome™

OUR PLATFORM PROVIDES THE CAPABILITY TO BUILD STREAMLINED, SCALABLE 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 **inconsistencies and errors easy to identify.**

- ⊘ 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 **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.

- ⊘ 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:
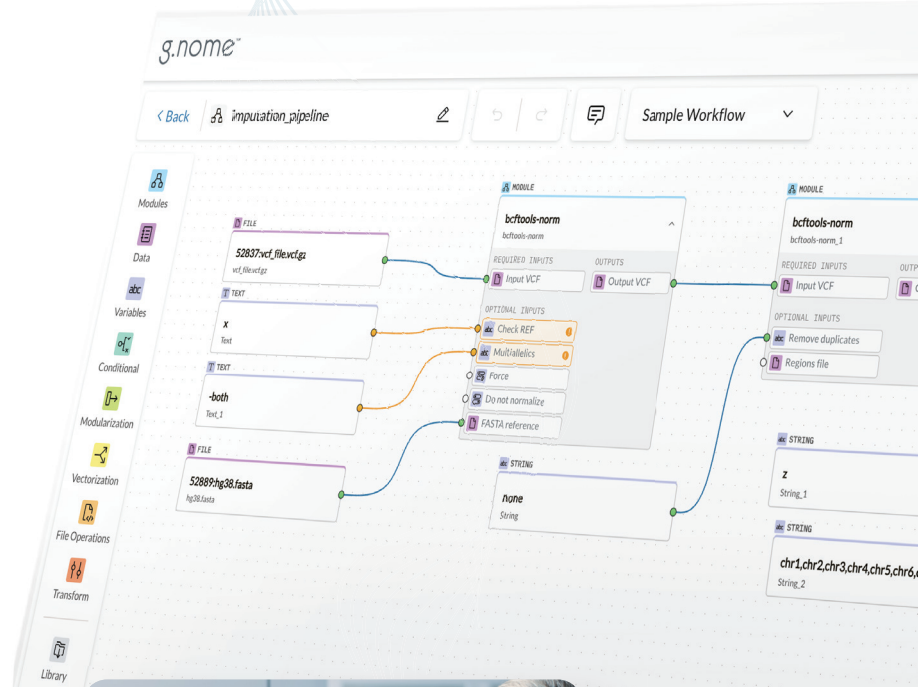
Accelerate Discovery

With streamlined, scalable and interoperable genomic workflows, g.nome dramatically improves the process of building and running bioinformatic pipelines — accelerating discovery, time to market and the ability to scale. By condensing the pipeline build from months to hours, **g.nome is the catalyst bioinformaticians have been waiting for.**

Optimize Your Talent

The g.nome low-code/no-code platform enables team members without coding knowledge to contribute to pipeline building from anywhere, freeing up your bioinformatician to focus on the science. This makes wider collaboration and analysis possible, including with remote teams. With g.nome, anyone who understands genomics can build and participate in pipeline development, so your company can invest in your vision instead of your operations.

Work the Way You Want

With g.nome, users have a path to working however the team prefers. 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. g.nome makes it easy for you to do what you know works and leverage that for future pipeline builds.

SEE THE PLATFORM

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GENOMICS

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