BIONANO GENOMICS COMPUTE SOLUTIONS
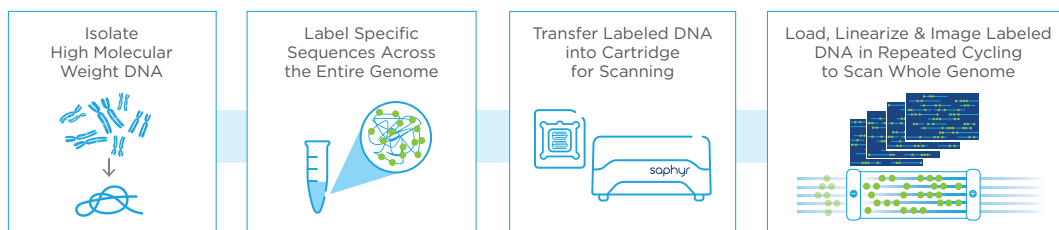
bionano®
GENOMICS

Increase Scalability and Flexibility with Bionano Compute On Demand

Bionano Compute On Demand is a pay-per-use solution accessible through Bionano Access web server for your Bionano Solve operations. Compute On Demand simplifies the way you perform genome assembly, hybrid scaffolding and structural variant analysis, without the need of any additional infrastructure, giving you the flexibility and scalability your experiment deserves.
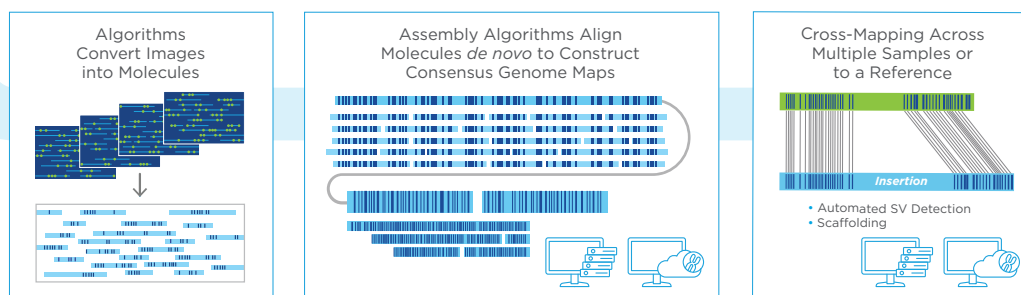
Advantages include:

- Analyze large genomes and high number of samples simultaneously
- Perform pipeline analysis operations without worrying about server capacity

- Data encrypted for secure operations
- Data centers compliant with IPAA, CSA, SOC2, ITAR regulations
- Genomic data accessible only to end users and deleted post-processing

SAPHYR® WORKFLOW

Isolate High Molecular Weight DNA

Label Specific Sequences Across the Entire Genome

Transfer Labeled DNA into Cartridge for Scanning

Load, Linearize & Image Labeled DNA in Repeated Cycling to Scan Whole Genome

High-throughput, High-resolution Imaging of Megabase Length Molecules

Algorithms Convert Images into Molecules

Assembly Algorithms Align Molecules *de novo* to Construct Consensus Genome Maps

Cross-Mapping Across Multiple Samples or to a Reference

Insertion

- Automated SV Detection
- Scaffolding

OVERVIEW OF COMPUTE OPTIONS

Choose the right option or a combination for your computing needs

COMPUTE SERVER
- Expect to run servers for >25% of the time
- Execute consistent loads
- Internet access not permitted

COMPUTE ON DEMAND
- Execute variable workloads
- No upfront server costs required
- Receive data from service providers
- Work on large genomes up to 24 Gbp genome size

Learn more at bionanogenomics.com/computeondemand

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REPRESENTATIVE RANGES FOR BIONANO SOLVE PROCESSES

	US Tokens	Europe Tokens	Time to complete
Human, 80X effective coverage* (*de novo* assembly and SV calling)	6	7**	9 hours
Human, 300X effective coverage* (rare variant pipeline, SV calling and variant annotation)	7	8	9 hours
Human, 60X coverage* (hybrid scaffolding, with DLE-1 enzyme)	1	1	6 hours
Emmer wheat, 60x effective coverage*	31	33	33 hours
Maize, 60x effective coverage*	15	16	15 hours
Hummingbird, 60x effective coverage*	5	5	5 hours

Assembly runs may vary based on quantity and quality of the input data.

Good quality data as defined as having MR > 80%, molecule N50 (>20kbp) > 180kbp.

Time to complete numbers are based on users of the current version of Bionano Access.

de novo assemblies without a reference will require more processing to first generate an automatic rough assembly.

**For human, 80X effective coverage, German-based servers are 12 tokens and take 12 hours to complete.

To get started, contact your sales representative or email orders@bionanogenomics.com

CATEGORY	Part No.	Product
COMPUTING	**80013**	**Saphyr Compute Server**
	80014	**Bionano Compute Server**
	90047	**Bionano Compute On Demand, US**
	90052	**Bionano Compute On Demand, Germany**
	90060	**Bionano Compute On Demand, Europe**

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