

Introducing novoWorx™, a Genome Data Management and Analytics platform

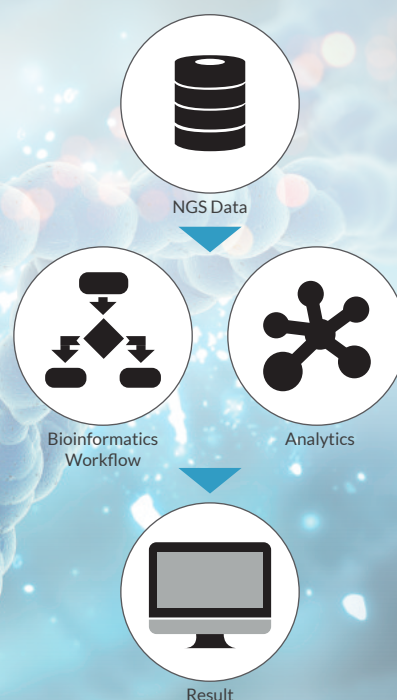
A comprehensive multi proprietary platform to accelerate your research by using sophisticated, fully automated solutions powered by the latest technologies.

Why novoWorx™?

- The only commercially available tool to offer embedded novoAlign™ and novoSort™ programs for high-throughput bioinformatics analysis.
- A modular system for delivering canned genomics pipelines.
- Process large datasets consisting of multiple samples without programming knowledge.
- Generates all the outputs in standard formats required for downstream/tertiary analysis by other systems.

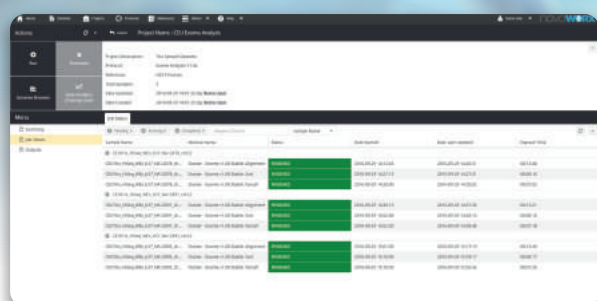
Features

- Web-enabled and secure interface with access control.
- Drag and drop files into the interface.
- Supports multiple samples run from a single click, no coding required to loop through large sample collection sets.
- Integrated genome browser.
- Cluster-aware (SGE support) and monitor all running, pending and completed jobs.
- Result file downloads.
- Browse all files as reactive tables and figures.

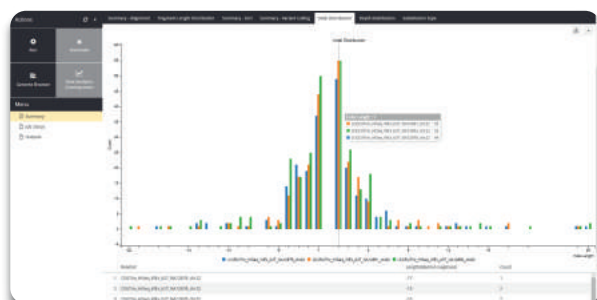


Information on pipelines and analytics tools are available on the website.

CONTACT US FOR A DEMO TODAY!



Streamlined, user-friendly interface for easy navigation



Ready to use downloadable results

Requirement	Minimum	Recommended
CPU	Dual Core 1.8 GHZ	Octa Core 3.2 GHZ
Memory	8 GB DDR2	16 GB DDR3
Storage space	5 GB for installation media 15 GB post installation* 100 GB free space**	5 GB for installation media 15 GB post installation* 100 GB free space**
Network	500Kb/s download speed	1 Mb/s download speed
Virtual Machine Environment	Any Virtual Machine Environment capable of importing OVA files	Oracle VirtualBox (recommended) or VMware
*only takes into account the OVA installation media. **post installation file size.		
	Files	Size
novoWorx™ (Required)	novoWorx Databases	2 GB
	HG19 Reference files	18 GB

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