



The BioTeam Appliance Galaxy Edition is a push-button solution that lets researchers get up and running quickly with Galaxy. The Galaxy Appliance comes preinstalled with a production instance of Galaxy, bioinformatics tools, and reference datasets. This powerful system is specifically configured for computationally intensive scientific workloads. Most importantly, the Galaxy Appliance is an open system so researchers and can install whatever tools they need and use the server as their own high-performance informatics infrastructure outside of Galaxy. BioTeam provides ongoing support for the Galaxy Appliance, enabling researchers to minimize their IT burden. The Galaxy Appliance is used by researchers around the world for metagenomic, ChIP-Seq, RNA-Seq analysis and more.

WHO IS USING THE BIOTEAM APPLIANCE GALAXY EDITION?*

University of Wisconsin – Madison University of North Carolina at Chapel Hill The University of Vermont University of California – San Francisco

University of Wisconsin – Milwaukee Texas A&M University – Corpus Christi The University of Tennessee Health Sciences Center

Queen's University Belfast Université de Genève Institute of Human Genetics

*These clients tested the early access edition of the BioTeam's product

"The [Appliance] is central to our lab's efforts to characterize the diverse microbial communities found in marine environments. While our lab members need to have some bioinformatics background to ensure they understand the nature of the programs they are using, our goal is to have a system in place that allows them to spend as much time as possible thinking about the biological implications of their data sets, not on the process of getting their data through a complex bioinformatics pipeline."

Dr. Scott Gifford, Assistant Professor, Department of Marine Sciences, University of North Carolina at Chapel Hill

"Our present workflows analyze RNA-seq datasets. We currently focus on alignments with the genome of the laboratory mouse and chicken. We aim to assemble tools that support analysis of ChIP-seq, and 4C-seq datasets as well."

Jozsef Zakany MD, Senior Research Associate

"We use our [Appliance] primarily for processing ChIP-seq and RNA-seq datasets. The Galaxy web-interface allows biologists without a computational background to process and analyze their own data. The Galaxy instance supplied by Bioteam came with a basic NGS pipeline working "out of the box" and most tools not already installed can be simply added via Galaxy's tool repository system."

Joe Boyd, Bioinformatician

IS IT RIGHT FOR ME?

As an open-source tool, there are many ways to access Galaxy. For researchers who need the flexibility of a local Galaxy instance but don't have the time or resources to devote to the initial set-up and ongoing maintenance of the hardware and software, the Galaxy Appliance is the perfect solution.

	No Wait Times	No Storage Quotas	No Job Submission Limits	No Data Transfer Bottlenecks	No Required Infrastructure	No Required Technical Experience
Galaxy Main	8	8	8	8	Ø	Ø
Local Galaxy	8	8	8	Ø	8	8
Cloud Galaxy	•	•	Ø	8	8	Ø
BioTeam Appliance	•	•	Ø	Ø	Ø	Ø

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No Required Infrastructure
No Required Technical Experience

The Galaxy Appliance has been designed to work out-of-the-box and enable computationally intensive scientific data analysis with Galaxy. The Galaxy Appliance includes the following features:

Production Galaxy Configuration

Grid Engine job scheduler FTP-enabled for large data transfers Postgres Production Database

Preinstalled Bioinformatics Tools

RNA-Seq: Bowtie, Bowtie2, BWA, Cufflinks, STAR, TopHat, TopHat2

ChIP-Seq: MACS2, SICER

NGS Tools: BEDTools, FastQC, FastX, SAMTools, BLAST

Other Tools: GNUPlot, R

Preloaded Reference Datasets

Reference Genomes
Reference genome index files for pre-packaged tools

Support

Updates to the Galaxy Instance Updates to the system configuration Support for the hardware

SPECIFICATIONS

	Base	Base+	Power	Power*
Cores	Intel E5 Xeon Processors 20 Cores			
SAS Storage	32 TB	96 TB	32 TB	96 TB
SSD Storage	2x 200 GB	2X 400 GB	2x 200 GB	2x 400 GB
RAM 386 GB		386 GB	512 GB	512 GB
Network Ports	zx 10GB Ethernet Ports	2x 10GB Ethernet Ports	2x 10GB Ethernet Ports	zx 10GB Ethernet Ports





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