

Accelerating data processing for faster diagnoses and more personalized treatments

Researchers at the Brazilian National Cancer Institute seek ways to prevent and control cancer using Dell Technologies solutions.



Customer profile

Bioinformatics and Computational
Biology Lab - Brazilian National
Cancer Institute

Life Science, Biotech and Pharma | Brazil



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Brazilian National Cancer Institute

Organization needs

The core challenge of the Bioinformatics and Computational Biology Lab in the Brazilian National Cancer Institute is to discover new cancer-causing molecular alterations by conducting faster, next-generation sequencing analysis by processing massive datasets for tumor genome analysis.

Organization results

- Accelerates genome analysis, cutting time to results from 6 days to a few hours.
- Speeds up biomarker analysis by processing more data in a shorter time frame.
- Facilitates collaboration with other researchers to identify genome mutations.
- Expedites simultaneous research projects.

Solutions at a glance

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At the Bioinformatics and Computational Biology Lab of the Brazilian National Cancer Institute (INCA) in Rio de Janeiro, researchers focus on increasing their knowledge of cancer's complex inner workings. To develop cures, they use next-generation sequencing techniques that expand the understanding of how malignant cells function.

Mariana Boroni, M.S., Ph.D., heads the Bioinformatics and Computational Biology Lab at the Brazilian National Cancer Institute. “We integrate huge amounts of data that reflect different parts of the cell, such as genomic, epigenomic, transcriptomic and proteomic data,” she says.

Managing this amount and diversity of data requires several computational approaches, including artificial intelligence and machine learning, to extract meaningful data insights.

“This helps us not only better understand cancer's complex systems but also identify biomarkers, signatures or even networks, which we can further explore as more personalized treatment protocols,” Boroni says.

Developing more assertive and effective cancer therapies

“Our group studies these biomarkers in both malignant cells and the cells they interact with, such as immune cells, especially macrophages,” Boroni adds.

INCA's researchers needed a platform that would allow them to integrate and analyze a huge amount and variety of data, aiding their integrative studies of tumors and identifying more reliable biomarkers.

“It is not easy to calculate the amount of processed data because each research group has its own data load. At this point, we have about 150 terabytes (TB) of data in our high performance computing (HPC) storage arrays, including raw and processed data,” Boroni says, noting that some datasets can be up to 10TB in size.

To achieve the computational power needed to effectively process such large and complex datasets, the INCA lab upgraded its existing HPC platform with Dell Technologies Ready Solutions for HPC Life Sciences.

“Dell Technologies is a well-established company with lots of experience in HPC technologies,” says Boroni. “They provided us with the flexible and customized HPC infrastructure we need to accomplish different types of computational requirements.”

HPC workhorse able to handle diverse projects simultaneously

The HPC system from Dell Technologies is a multi-user platform that serves all of INCA's research groups and collaborators. It has approximately 50 regular users, most of them graduate students.



Simplifies system management so researchers can focus on finding cures.



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Nicole Scherer

Ph.D., Technologist, Bioinformatics
and Computational Biology Lab,
Brazilian National Cancer Institute

Collaboration and productivity are also facilitated as researchers can access shared files with analyzed data. It also enables them to work remotely during quarantine so they can continue their cancer research as well as explore possible treatments for COVID-19.

Researchers can work simultaneously on a wide range of investigations, according to INCA technologist Nicole Scherer, Ph.D. “The shared computational environment also facilitates collaboration with other researchers.”

Scherer notes that variant annotation and differential expression analysis are the most frequently executed pipelines, followed by metagenomics studies and viral pathogen identification. “The main workload of the platform today consists of short-read sequencing analysis to identify genome mutations and patterns of gene expression in tumors. Also, we have used the platform for de novo assembly of transcriptomes and genomes,” she says.

Saving time to find cancer cures faster, saving lives

Both Boroni and Scherer agree that the researchers have vastly accelerated their investigations since the new platform’s deployment. “Processing time has been radically reduced — from as much as six days to as little as a few hours — using the upgraded Dell Technologies HPC system.” Scherer adds: “We’ve improved our ability to perform specific analyses such as transcriptomic and genomic assemblies that are very RAM-consuming.”

The platform saves time in other ways. Boroni says, “My favorite feature is the ability to expand our Dell Technologies HPC platform, making it an integrated system composed of machines designed for very specific jobs that can be combined to work together in an easy way, under the same management system.”

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