GenoLogics LIMS Accelerates NGS Research

In just a few weeks, the laboratory information management system significantly improved operations at the Illumina FastTrack Sequencing Services lab.

Introduction

Managing the pace of technological change that defines next-generation sequencing (NGS) isn't just an issue for NGS labs. It also challenges the makers of NGS instrumentation. The pressure to stay ahead of the curve is particularly felt in vendor sequencing services labs, which provide on-demand service to their instrumentation customers, as well as sequencing services to clients who outsource their sequencing projects.

"As sales increased, so did our responsibility to our customers to make sure their sequencing results were turned around as quickly as possible," said Larry DeDionisio, scientist at the Illumina FastTrack Sequencing Services lab. The lab saw such a dramatic increase in its workload that tracking and assessing its own internal performance took a back seat, as staff focused on getting high-quality sequencing data back to clients.

"We were sequencing more than ever before, which meant we were collecting more information than ever before," said Courtney McCormick, project manager for sequencing services at Illumina. "And our methods for organizing that information were still catching up. We needed a solution that would help us evaluate our processes and find ways to work more efficiently."

In May 2011, the FastTrack Sequencing Services lab opted to replace its homegrown sample tracking database with the GenoLogics LIMS, a modern laboratory information management system that provides end-to-end information management of samples, tests, and results for next-generation genomics labs. In just one week, the FastTrack Sequencing Services lab was tracking test samples in the LIMS, which is preconfigured specifically for Illumina sample preparation, cluster generation, and sequencing protocols. Even during the testing phase, the lab staff noticed significant time savings, since the LIMS automates manual tasks in the workflow. The LIMS has also been flexible enough to accommodate different types of instruments and protocol changes that pass through the lab on a near weekly basis.

"The nature of our services put us in a prime position to adopt this system," said DeDionisio. "We work with different products and methods, and we also need to track samples and keep the lab running. It's a challenging environment, but from what we've seen so far, the GenoLogics LIMS should be able to handle it."

Outgrowing Homegrown Data Management

The standard Illumina workflow (sample receipt, sample preparation, cluster generation, sequencing, analysis, and return of results to customers) can be complicated because customers often have different requirements. According to McCormick, some customers just need FASTQ output, while other customers request the raw data files so that they can run their own analysis pipeline on the data. "This means we have to provide different outputs based on who is asking for the data," she explained.

For several years, the FastTrack Sequencing Services lab used an in-house developed system to track samples as they passed through the sequencing workflow. But the system wasn't flexible enough for the lab's needs for a couple of reasons. First, according to DeDionisio, the system was not a full-featured LIMS, but rather a database. Excel spreadsheets served as the primary interface for scientists, which made data retrieval a time-consuming endeavor.

"I could probably find information about sample volume by looking at the dates on the sample manifests I'd completed over the past year, but that's an arduous process," McCormick said. "With the amount of work we had going on, we needed a better way to search data."

Second, the in-house database was not immune to the typical problems that labs encounter with homegrown systems: maintaining and updating them is difficult for labs whose first priority is doing science rather than building software.

"We needed a real LIMS—something that would map to our workflow while providing visibility into our processes so that we could get a better handle on ongoing projects and work," said DeDionisio.

Preconfigured for Fast Implementation

The FastTrack Sequencing Services lab began working with the GenoLogics LIMS in May. Impressively, the test system that was implemented was tracking the lab's sequencing runs in just one week. Many elements of GenoLogics LIMS are available preconfigured to support Illumina-specific protocols for sample preparation and cluster generation, which made the system easy to implement (Figure 1). "The preconfigured steps for sample prep were invaluable," said DeDionisio.

Figure 1: The GenoLogics LIMS is Preconfigured for the Illumina NGS Workflow

Sample preparation is generally labor intensive and manual. The former in-house system required scientists to scan barcodes for everything, even for consumable tubes that would not ultimately be stored for future use. The LIMS has completely removed unnecessary tracking steps during sample preparation, and data associated with sample transfer steps is automatically carried forward by the LIMS after an initial scan, eliminating the need for scientists to scan barcodes for every tube used for each step.

Preconfiguration in the GenoLogics LIMS also enabled the system to seamlessly interface with Illumina instruments to monitor sequencing. Once scientists have scanned the barcode and loaded the flow cell into a sequencer, the LIMS "sees" the activity, generates a sample sheet, and begins collecting data associated with the run from the appropriate sequencing server. According to DeDionisio, hardly any interaction is needed between scientists and the sequencers while runs are in progress.

"The LIMS is doing all the work, collecting data from the sequencers and loading the sample sheet in the proper place in the basecalls folder," said DeDionisio.

"The benefits of having certain things preconfigured are numerous," said DeDionisio, particularly when compared to what the lab did previously to track samples. Yet he pointed out that not everything should be preconfigured in a system. In particular, functionality that labs tend to tweak and customize themselves should not be preconfigured. DeDionisio noted that even in the sample preparation protocol, which is well specified by Illumina, labs often choose "custom" index adapters or sample placement configurations. Additionally, while it is helpful for the LIMS to handle BCL conversion after a run is finished, the LIMS should not require a particular READ length, as labs often want to select a READ length independent of the length of the run. "Choices like these really should be left to individual labs and not be dictated by the LIMS," DeDionisio explained.

Fortunately, the preconfigured Illumina package in the GenoLogics LIMS does not restrict what labs can do with the system. "GenoLogics anticipated many of the needs by preconfiguring sample prep in particular and automating the data collection off the sequencers," said DeDionisio. But in other areas, the system remains flexible enough to adapt to a range of different instruments and changing protocols. For instance, the FastTrack Sequencing Services lab recently tested a new sample prep procedure that called for the use of 48 indexes. The former in-house system could only accommodate 12 indexes, and scientists lacked the programming knowledge to change the software so that additional indexes could be added. "The GenoLogics LIMS can use any size index, which is great because our customers often have custom indexes that they provide to us with their samples," said DeDionisio.

"The flexibility is really what made this system attractive," said Christian Haudenschild, director of the FastTrack Sequencing Services lab.

Haudenschild pointed out that the lab is about to deploy a new Illumina instrument, and the instrument specifications are still evolving. "Based on our experience with the LIMS so far, we are confident that we'll be able to accommodate whatever we might run into," he said.

Saving Scientists' Time

Even before rolling out the system to production, scientists in the FastTrack Sequencing Services lab saw significant time savings. The cluster generation group used to spend about 20 hours each week collectively entering data associated with a flow cell into the in-house sample tracking system. Automation with the LIMS has cut this time in half. Hand off between the cluster group and the reader group used to create another bottleneck; now, data is transferred automatically. "I'm anticipating that some of our staff in the cluster group will be at loose ends wondering what to do once much of the manual work is eliminated," said DeDionisio. "They are figuring out that they can put more effort on checking runs in the LIMS."

Lab staff and scientists are beginning to envision other ways that the LIMS could be used to improve lab efficiency. They expect, for instance, that the LIMS will help staff with quality control. "It's all been manual, so you need eyes to look at the samples and determine what's been passed and failed and what's ready to go and what needs to stay," said McCormick. "We'd rather track this in a software program that can show us what's good to go, what needs more work, or what should be done first."

Conceivably, such visibility into the workflow should also provide some predictive control over processes. McCormick hypothesized that with data stored and searchable in a LIMS, they should be able to project how long a project will take based on the work required and the staff and instrumentation available. "Right now, we make guesses based on a general idea of past performance," she said. "Information on past runs stored in the LIMS should enable us to align our projections with actual data, which will not only help us calibrate customer expectations, but prioritize workstreams more effectively."

"Our ultimate aim is to more efficiently deliver data to customers," McCormick concluded. "The LIMS will give us better insight into all aspects of our process—what pieces of the project are finished, what has passed QC, which samples need rerunning, whether we have high enough cluster density on enough lanes to get quality output. With data easy to find, we'll be able to see where our bottlenecks are, which will make my job easier, which will make data go out faster—and faster turnaround means happier customers."

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