

KEEPING UP WITH THE SAMPLES BRAVO PLATFORM HELPS TRANSCRIPTOME LAB MEET GROWING DEMAND



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When scientists want answers, they dive into the details. Take biologists. They delve down into the very building blocks of life and study, for example, the transcriptome—the list of genes being expressed by their subjects at a given moment.

Transcriptomics (also known as expression profiling) can be very revealing. It can, for example, tell researchers whether a certain condition or treatment triggers a response from the subject's immune system.

That's one of the many reasons scientists bring blood and tissue samples to the GeT-TRiX facility in Toulouse, France. They want to see the list. They want to see which genes are switched on or off. They want to understand what biological processes are at work in their subjects.

Finding answers

GeT-TRiX, the transcriptome facility for France's highly regarded National Institute for Agricultural Research, processes samples for both academic researchers and private laboratories—and provides detailed analyses. The facility is part of the TOXALIM Research Center in Food Toxicology which contributes to the development of knowledge on the long-term effects on human and animal health of toxic compounds such as agricultural inputs, mycotoxins, packaging components, and other food contaminants.

"Demand has been growing rapidly," says Yannick Lippi, the facility's operational manager. "In 2011, the facility's first year of activity, we analyzed fewer than 100 samples. Now we analyze around 1500 samples a year."



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AGILENT BRAVO SUCCESS STORY

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YANNICK LIPPI



Projects vary, he says, from looking into the effects of food contaminants to the effects of obesity on animal or human health.

"The questions we answer depend on the samples and the biological groups," Yannick says. "Someone may bring us liver samples from healthy subjects and diabetic subjects, for example, so they want to know what genes are regulated between the two groups and what biological functions are involved in the pathology or a treatment of the pathology. Transcriptomics can also identify potential biomarkers associated with pathologies, which biomarkers can be later used for diagnostic studies."

Increasing productivity

Yannick and his colleagues at GeT-TRiX process samples using 384-well-plate qPCR and Agilent gene-expression microarrays—and they have increased productivity by adding Agilent's Bravo Automated Liquid Handling Platform.

"We have a lot of projects dealing with large amounts of samples, and we were having trouble keeping up with demand, but our throughput dramatically increased because of this solution," Yannick says. "Prior to using the Bravo, we could manually process up to 48 samples in parallel. Now we can analyze 96 samples in parallel in less time."

In this way, he was able to not only increase throughput but also reduce manipulation biases and technical variability.

Yannick notes that he was able to automate key steps in the process of RNA sample labeling, purification, and cRNA fragmentation on the Bravo platform. What's more, he developed a bioinfo/biostat pipeline for Agilent microarray data analysis using R scripts and Bioconductor packages.

"We have checked the data obtained with our pipeline, and it is comparable to data obtained with established microarray procedures and to RNA-seq data," Yannick says.

This new pipeline—able to process up to 384 samples in a week—means the lab can respond to more researchers, giving them accurate analyzed data within short time constraints.

"The Bravo is for us a good platform—very rapid, precise and robust," Yannick says. "It increased not only throughput but also reproducibility."

To learn more about the Agilent Bravo Platform and how other researchers use it, visit www.agilent.com/lifesciences/Bravo

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