



Ipsen

## Challenge

Simplify the processes involved in analyzing data to speed scientific innovation in the laboratory.

# Automated analytical applications speed up discoveries in biomarker research

Biologists at Ipsen investigate biomarkers critical to the development of new cancer therapeutics

This year, more than 14 million people throughout the world will be diagnosed with cancer. According to the World Health Organization, the disease shows no signs of slowing down, and the number of new cases is projected to increase by 70 percent over the next 20 years. Given such statistics, it goes without saying that conducting research into new ways of diagnosing and treating cancer is vitally important.

The existence of more than 100 known types of cancer necessitates diverse lines of inquiry in oncology laboratories – and pharmaceutical companies' therapy portfolios aim to improve the lives of people living with cancer in many different ways. One of the global leaders in fully integrated patient care – particularly in the fields of neuroendocrine, prostate, bladder and kidney cancer – is Ipsen, a global specialty-driven pharmaceutical group. With 13 percent of its annual revenue invested directly back into research and development, Ipsen spends more than \$200 million a year on discovery alone.

## New immunoassay profiling methods generate data sets that are useful but complex

Jean-Luc Blachon, head of statistical research in Ipsen's bioinformatics department, is one of the key people driving this innovation. He and his team collaborate with oncology researchers to help assess the effectiveness of new anti-cancer molecules, particularly through the study of biomarkers. Thanks to recent advances in clinical molecular diagnostics, biomarkers now play an essential role in helping biologists to better understand those molecular and cellular mechanisms affecting tumor provenance and progression. "Our methods involve observing a biomarker that can attach itself to cancer cells directly," Blachon says. "Increasing or reducing the presence of a biomarker in

the patient's body serves as a means of working out whether a cancer has grown or regressed."

Biomarkers have significantly improved the efficacy of available oncology therapy regimens across the board, with the standard of care for advanced-stage cancer now involving biomarker-driven treatment algorithms derived directly from a tumor's molecular characteristics. Ipsen's researchers test biomarker effectiveness through a method known as multiplex immunoassay profiling, in which biomarker proteins present in the biological fluids of malignant cells can be quickly assessed. Data generated from a series of immunoassays is compiled and handed over to Blachon's team for analysis.

"Previously, these files were processed manually," Blachon recalls. "Our biologists would collect the files, import them individually into a software program, start the processing, gather the results, collate them in an Excel file and check the whole thing. And that was on top of their work as biologists. It was a colossal and extremely repetitive task."

## JMP® customizable add-ons significantly reduce laboratory processing time

Voluminous and complex sets of data are part and parcel of the everyday lives of Ipsen's international research teams. Conducting irrelevant

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Jean-Luc Blachon, Head of Statistical Research



analyses manually, or obtaining unsatisfactory results, could harm the cutting-edge scientific research involved in the group's study of biomarkers. Blachon therefore sought to find a way of automating these processes and simplifying analytical workflows to save researchers time and avoid repetitive tasks while improving the accuracy and quality of their discoveries. For example, outliers in side effects or demographic data could bias a sample if they are not removed.

Blachon's solution? Three customizable applications that Blachon himself developed with JMP scripting language (JSL). The first application processes Excel files to gauge dose-response curves and, in so doing, enables researchers to determine the biomarker concentrations needed in a sample. The second is used to check the validity of results by calculating the limit of detection and limit of qualification within a data set. And the third application automates a series of analyses. "For any given experiment, with these three applications on hand, the time needed to process samples can be reduced from 20 or so hours to just 30 or even 15 minutes," says Blachon.

Researchers no longer need to call in third-party expertise in information technology or statistics; with their data in hand, researchers can spend more time at the lab bench and less time wrangling messy data sets in Excel. "Our aim in using JMP," Blachon says, "is to save researchers time, which they can devote instead to reflecting on the meaning of the statistical analyses they have requested, among other things. These applications free up time for thinking and carrying out more value-adding tasks. So there are gains in terms of quality too. Researchers can now explore avenues they wouldn't have even considered in the past."

## Data visualization helps biologists identify cluster points and develop new hypotheses

Customized applications aside, the highly intuitive man-machine interface in JMP makes data discovery easier. "Visualization is one of JMP's great strengths," says Blachon. "There's a deliberate emphasis on graphs, which provide a very easy starting point for proposing hypotheses." Users also have access to the powerful JMP Graph Builder, which guides them step-by-step through the graph creation process. And other visualizations help researchers easily spot outliers and cluster points in just a few clicks.

By using visualizations in JMP for data discovery, Ipsen's researchers can conduct more detailed analyses, vary hypotheses and test new ideas - while remaining the owners of their analyses. Blachon emphasizes that with the help of his JMP applications developed in JSL, "biologists can focus on their own statistics."

## By automating tasks, researchers can really focus on scientific innovation

Finally, the customizable JMP applications Ipsen has developed are compatible with the group's other IT systems, resulting in the emergence of a full-fledged statistics hub, optimized for visual exploration.

"All these advantages open up some very exciting prospects as far as research is concerned," says Blachon. "We have already entered into partnerships with a number of scientific institutes in order to work on the way in which different biomarkers interact, for example. This is a world first made possible by the tools developed in JMP."

### Solution

Use the JMP scripting language to develop automated and customizable applications that simplify data analysis and make it easier for researchers to make discoveries.

### Results

Processing time for analyzing 10 biomarkers has been reduced from 20 hours to 30 minutes, thus freeing up time for researchers to concentrate on scientific innovation.

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