

# Application Story

## University of Leipzig

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### UNIVERSITY OF LEIPZIG

German-based University of Leipzig operates a bioinformatics center that performs microarray data analysis to make important research discoveries.

#### Situation

- Needed a flexible, extensible solution to leverage microarray analyses expertise to researchers in disparate locations.

#### Insightful Solution

- S+ArrayAnalyzer™

#### Results

- Centralized, Web-based deployment solution improved collaboration and access to reliable, cutting-edge statistical methods
- A flexible, extensible platform to build customized statistically-sound solutions
- Leveraged “best practice” microarray analysis throughout their organization

### Company Overview

In 2002, the German-based University of Leipzig created an Interdisciplinary Center for Bioinformatics. At the Institute, Dr. Markus Loeffler manages a team of researchers who rely on microarray data analysis to study genetic evolution, tissue formation and cellular signal transduction. The Institute collaborates closely with researchers at the Max Planck Institutes for Evolutionary Anthropology and Mathematics in the Sciences, as well as, with the Interdisciplinary Center for Clinical Research, the Center for Biotechnology and Biomedicine and the Clinical Trials Coordinating Center.

### The Challenge

Researchers at the Institute managing high-dimensional genomic and molecular data collected from manipulated, normal and diseased tissues require software designed uniquely for microarray data analysis. Finding the right software that can meet the demands of computational biologists, statisticians and medical researchers is challenging.

### The Strategy

The Institute was interested in selecting a software solution that could provide the flexibility and extensibility it needed to deliver leading microarray analytic methods. The Institute needed a Web-based solution that would allow researchers to collaborate and share information from different research locations. Further, the solution needed to allow researchers to apply “best practices” to the collection, analysis, modeling and deployment of microarray analytics throughout the organization.

### Key Benefits

The Institute selected Insightful’s S+ArrayAnalyzer solution because it met the following stringent requirements:

- The software provided tools for accessing, analyzing and modeling research data.
- The software offered cutting-edge methods for performing microarray data analysis that produced reliable results.

- Web-based deployment of the software allowed researchers to implement “best practices” for collecting, analyzing, modeling and sharing research results.
- Insightful had more than 16 years building cutting-edge analytic software solutions for Global 1000 pharmaceutical, biotech and life science-based companies.
- A reliable, flexible and extensible platform allowed researchers to customize their microarray analysis solution to meet their unique needs.

“We selected S+ArrayAnalyzer because it offered our research team the flexibility and extensibility to customize an analytic-rich solution to meet the unique needs of our diverse research team,” said Loeffler. Insightful’s cutting-edge analytics complemented by leading BioConductor methods enhanced the analytic approaches at the Institute and provided researchers with a comprehensive microarray analysis toolkit unavailable in competitive solutions. “The solution allowed our research team to implement ‘best practices’ by deploying leading microarray analysis tools via a simple Web browser to less technical collaborators,” continued Loeffler.

Researchers adopted the solution that allowed them to choose appropriate analysis parameters interactively and study the results using links to local and public databases using simple mouse clicks. “We selected Insightful’s S+ArrayAnalyzer Solution for its flexible and easy-to-learn programming environment that allowed us to integrate the scientifically leading Bioconductor routines with our own methods. Combined with the superior memory management of S-PLUS and the easy-to-program Web interfaces, we expect the software to advance our collaborative research.”

“During an evaluation phase, we tested a number of gene expression analysis packages on the grounds of functionality and extensibility, reliability of statistical procedures, appropriateness for an interdisciplinary research environment, ability to document analyses and the security of the investment,” said Loeffler. “We found S+ArrayAnalyzer to stand out from the other solutions tested. The reasons were its large number of available statistical procedures, the ease of extending the existing code in its native S-language or via its efficient C and FORTRAN interface. Insightful’s leading position in the statistical software market gave us confidence about the reliability and accuracy of the built-in functions and the wide distribution of the S-language assured us that our development efforts will be useful for many years to come.”

### **Applications**

- Microarray Data Analysis

### **Products**

- S+ArrayAnalyzer™