

## Spotfire<sup>®</sup> Application Package for Applied Biosystems 1700 Microarray Analysis

An interactive analytical tool for quality control and differential expression analysis of microarray data.

Integromics analytical software for AB1700 microarray platform data, combines the statistical power of Bioconductor with the visual data mining of Spotfire<sup>®</sup>. This perfect synergy of two very strong applications enable users to perform easy yet powerful statistical analysis towards validating and gaining insights of AB microarray experimental results.

### Key Features

> **Microarray analysis easier than ever**

It provides one-click direct import of instrument files and guides the user throughout the analytical workflow.

> **Validate your results with state-of-the-art statistics**

Quality controls, filtering, normalization, differential expression analysis supported by most referenced algorithms in Bioconductor. As a result, the user rapidly find a statistically significant and accurate set of regulated genes from the initial gene set.

> **Advanced interactive visualization in Spotfire DecisionSite<sup>®</sup>**

Gain more insights with the powerful visualization capabilities of Spotfire. Users can benefit from the unique capabilities for browsing and inspecting gene expression data in Spotfire as well as other outstanding features like clustering methods, report generation and Gene Ontology integration.

> **Functional interpretation at hand with the PANTHER<sup>®</sup> Classification System**

The software is connected with the comprehensive database of functional annotations and references created by Applied Biosystems PANTHER<sup>®</sup> Classification System.

> **Validate results with TaqMan<sup>®</sup> and RealTime-PCR assays**

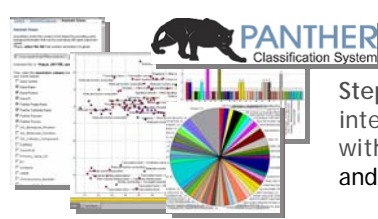
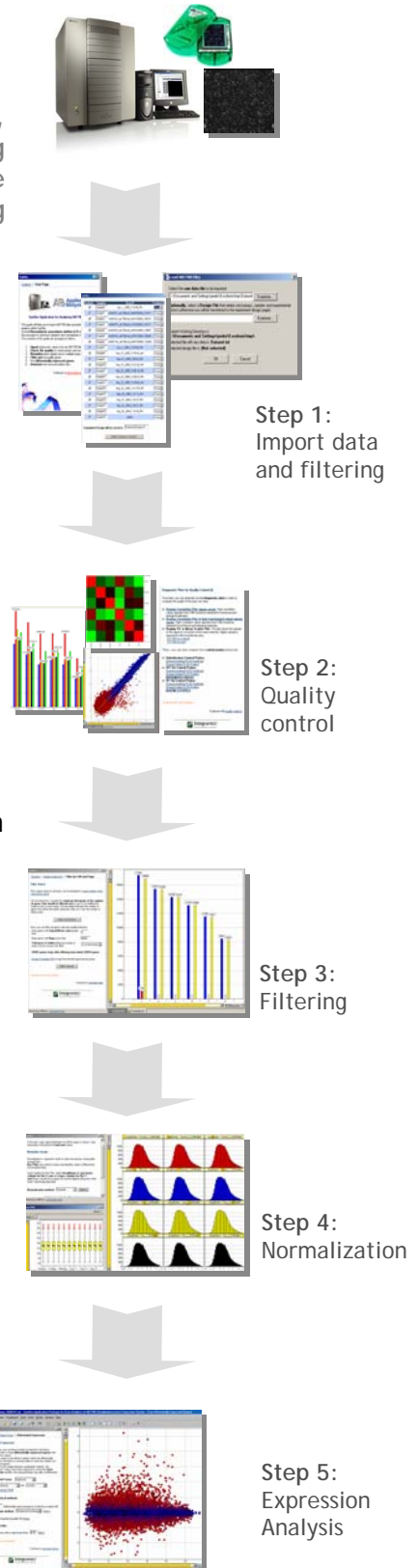
The application facilitates the integration with PCR gene quantifications in order to confirm regulated genes.

> **Customizable**

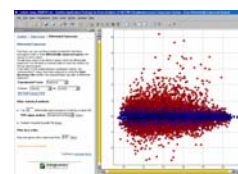
Tool totally customizable to specific researcher needs like the integration of existing R-scripts.

> **Functional interpretation**

The output can be integrated into **ArrayUnlock<sup>™</sup>** towards a better understanding of functional information. Thus, biological interpretation of results is naturally integrated into the analytical workflow.



Step 6: Functional interpretation with PANTHER<sup>®</sup> and ArrayUnlock<sup>™</sup>



Step 5: Expression Analysis

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