Kvik: Interactive Exploration of Multi-Omics Data from the NOWAC Postgenome Biobank

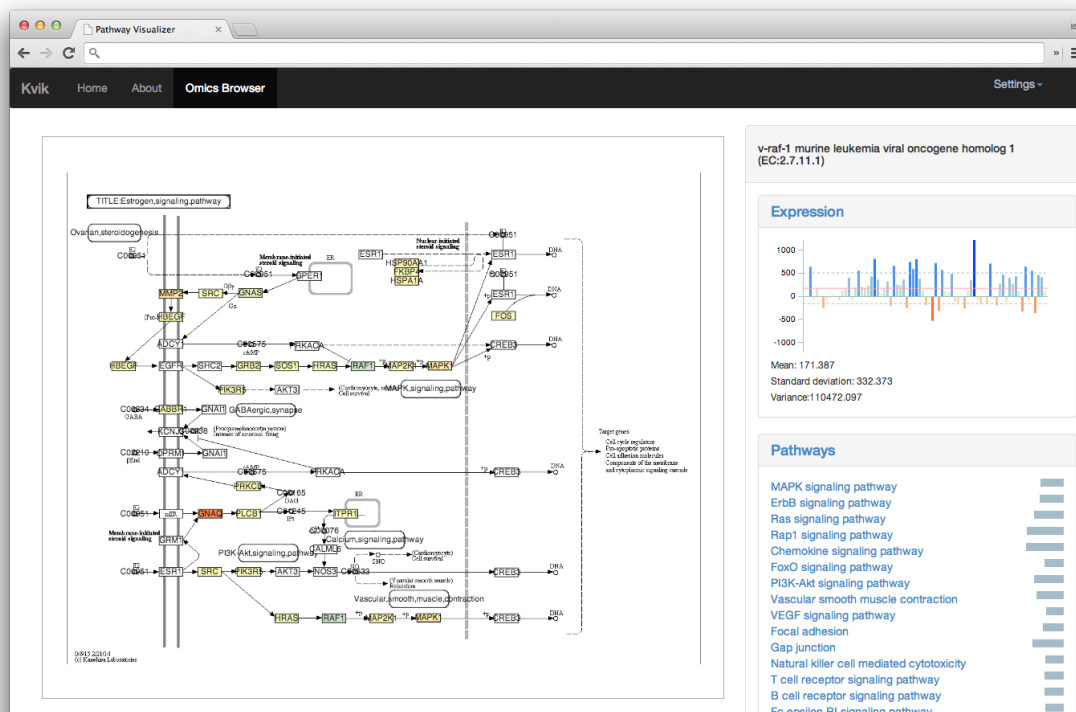Bjørn Fjukstad, Karina Standahl Olsen, Mie Jareid, Eiliv Lund and Lars Ailo Bongo

Figure 1. A screen shot of the Kvik omics browser

We have developed Kvik, a system for interactive exploration of multi-omics data from the Norwegian Women and Cancer (NOWAC) postgenome biobank. The goal of the NOWAC study is to understand the dynamics of carcinogenesis through multi-level functional analyses of transcriptomics and epigenetics using blood and tissue samples. Kvik provides a tool for exploring microarray and methylation data, incorporating both statistical analysis and interactive visualizations in a single system.

Kvik has the three-tier architecture typically used for search and exploration of large scale data. It consists of a backend for storage and computation, and a lightweight web client for exploration. The backend integrates the NOWAC databank with gene- and pathway information from publically availible databases such as KEGG. The web client builds on HTML5 and Javascript libaries, and runs in any web browser.

In this work we describe the challenges in exploring multi-omics data, and why we chose to develop a new system to manage, visualize and statistically analyze such data. We provide a requirements analysis for exploring multi-omics data, and discuss the tradeoffs in designing such systems. Kvik has already provided biological insight, and we believe it meets the storage, computation and visualization requirements of coming analysis methods for the NOWAC data.

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