



Visual Analysis of Heterogeneous Data for Molecular Biology

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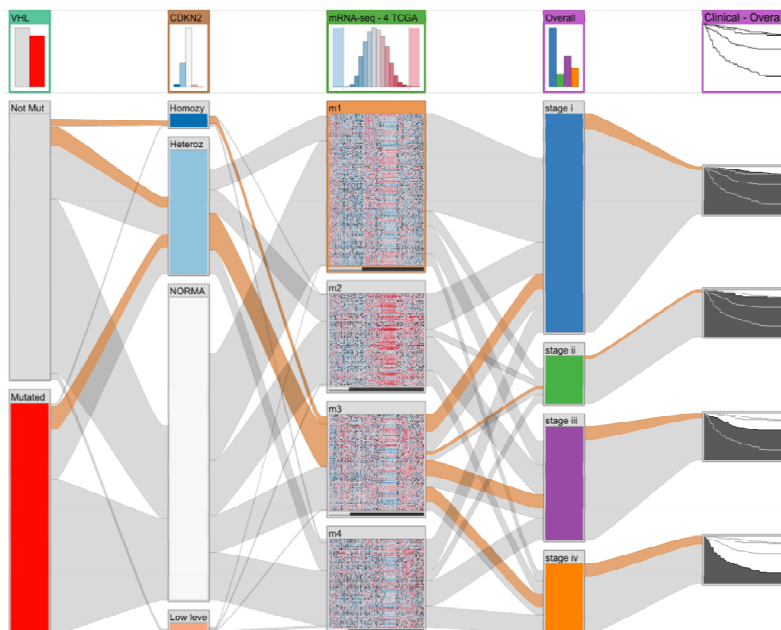
Institute of Computer Graphics
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Møllendalsbakken 7, 5th floor

Abstract

With the introduction of modern data acquisition techniques, such as next-generation sequencing, life science researchers are confronted with an exploding collection of heterogeneous data. The availability of such techniques at comparably low costs shifted the challenge from the acquisition of the data to its analysis. However, not only the sheer amount of the data but also its complexity poses a problem for making sense of the data. In this talk, I will summarize our efforts to come up with novel ways for analyzing large, heterogeneous datasets. In particular, I will discuss our work on cancer subtype analysis that allows analysts to identify and characterize tumor subtypes in large patient populations as well as techniques for investigating multi-dimensional data in the context of biological networks. The presented work is embedded in the Caleydo project (<http://www.caleydo.org>), which is a long-running collaboration between JKU Linz, TU Graz and Harvard University.



Integrating Heterogeneous Data from Cohort Studies for Multivariate Visual Analysis

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Abstract

In the context of cohort studies, usually measures are collected which relate to different and not immediately related aspects of an often large population. Such data can be large and in particular also heterogeneous by nature, amounting to substantial challenges when relating the different parts of the data to each other, in particular when multivariate analysis methods should be used. In this talk, a new conceptual model is presented which enables the visual exploration and multivariate analysis of large amounts of heterogeneous data, helping to generate and also validate hypotheses. The new model handles partially overlapping data subsets, enabling the seamless integration of the data and the linking of spatial and nonspatial views of the data.

