"Transforming Genomics Data Visualization for Cancer Research"

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Abstract: With the explosion of cancer genomics data sets, researchers need powerful tools that make it possible to identify significant events in large amounts of data and to link them with their functional implications. As a first step to address this need, we developed the Integrative Genomics Viewer (IGV), a powerful tool for biomedical researchers to examine genome-wide data sets from large next-generation sequencing and microarray studies in real time and at all genomic scales. While the IGV is already used for cancer studies, it has become clear that, faced with an increasing flood of genomic data, important work is needed to optimize IGV for today's cancer researchers. They must to be able to (a) identify patterns in or compare hundreds of datasets from many types of malignancies; (b) easily identify portions of the genome whose associated data shed light on their study; (c) examine genomic data in the context of functional or structural data that do not map to the genome but may yield new hypotheses and important directions for further study; and (d) allow groups to collaboratively annotate data views and share those insights. In the context of the Starr Cancer Consortium's wealth of creative collaborative projects, and leveraging a partnership of two strong computational labs (Mesirov and Sander) with a pre-existing SCC-funded laboratory team (Rubin and Garraway), we propose to address these challenges. We will strongly benefit from the involvement of the SCC to surface other ways in which the IGV can best serve the cancer research community. Several projects, led by SCC researchers, will provide us with an ideal user group and test bed as we make the requisite enhancements to the Integrative Genomics Viewer to further transform data visualization and accelerate the pace of cancer genomic research.