

“An Integrative Cancer Genomics Portal”

Principal Investigator:

- Jill P. Mesirov, PhD, Broad Institute of MIT and Harvard

Co-Principal Investigator:

- Cameron Brennan, MD, Memorial Sloan-Kettering Cancer Center

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Abstract: A major theme of the research supported by the Starr Cancer Consortium is the large-scale production of data to derive a molecular characterization of cancer and to gain an understanding of its molecular basis. The technologies to acquire genomic data are already generating large amounts of multimodal data. However, a significant limitation is the inability to consider results from multiple analyses in a common context to provide insights and generate new hypotheses: for example, taking the somatic mutations, segmental amplifications and deletions in one data set and linking them with clinical phenotypes, transcription profiles, effects of RNAi knock-downs, and epigenetic data in other data sets.

There is a major need in the cancer research community for a tool whereby data set descriptors and biological features derived from multiple data modalities can be jointly queried, visualized, and compared without the need for additional programming. Such a tool would allow the Starr Cancer Consortium, and the cancer research community at large, to leverage the wealth of data the community is producing.

We propose a close collaboration among Starr Consortium research scientists, computational biologists and software engineers to develop and evaluate an Integrative Cancer Genomics Portal, through which the cancer research community can access, query, and view multimodal genomic data derived from their experiments in the context of a larger repository of complementary data.