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**Title**:

An Agile Web Portal to Support Translational Neuroblastoma Research

**Abstract**:

We present a Neuroblastoma Genomics Web Portal, as a common entry point to a wide range of in-house and external resources that will help translational cancer researchers investigate and visualize genetic interactions and genotype-phenotype relationships in the context of multidimensional data. Neuroblastoma is a type of childhood cancer that accounts for 50% of all cancers in infants and is the most common extra-cranial solid tumor in children. The portal we have developed is built using Rshiny, a web powered framework that incorporates cutting edge statistical methods and data mining algorithms and allows for agile development of complex interactive visualizations. It currently harbors 9 internal and 2 external datasets, comprising of 1039 patient samples, 41 cell lines and 1803 normal samples corresponding to expression (microarray and RNAseq) data, copy number and mutation calls that have been harmonized using standard pipelines and transformations. Unlike existing resources like R2, our user interface is intuitive which makes it easier to navigate and provides both static as well as interactive visualizations. Some, among many, applications are - visualizations for gene expression across cohorts, gene-gene correlations, copy number-mRNA expression correlations, Kaplan-Meier plots and tools to compare cell lines and identify tumor vs. normal differential expression utilizing public datasets like GTEx and TARGET. By visualizing and analyzing the inter-relationships between components like DNA copy number, methylation patterns, mRNA expression and clinical parameters like age, stage and survival through this set of accessible tools, we hope to have a better understanding of the disease and thus improved patient mortality and morbidity. In future, we plan to incorporate enhancements like secured logins, usage statistics, and cloud based file systems.