

Abstract ID:- 134

Abstract Topic:- Omics technologies

Abstract Title:- SurfacOmics, an R shiny application for biomarker prioritization using Elastic-Net Regression complemented by sub-cellular localization.

Presenting author name :- Priya Kajla

Presenting author institute:- Tata Consultancy Services

Co-authors name:- Sadhana Tripathi, Bilal Abbasi, Kota Priya, Dr. Binuja Varma, Aubrey G. Bailey

Co-authors institute:-Tata Consultancy Services

Aims:-Development of an R Shiny application to aid in the prioritization of transcriptomic and proteomic biomarkers. Currently this process is a collaborative effort which involves many iterative cycles between wet and dry lab. We propose that an intuitive, guided interface will facilitate discussion about what a final analysis can achieve and suggest which candidates are most assayable.

Methods:- SurfacOmics uses the R package “glmnet” to perform penalized regression on protein/gene expression data. Surfacomics also includes a manually curated SurfacTag knowledge-base based on Gene Ontology Cellular Component data. The combination of these two is ranked for prioritizing potential biomarkers. It currently supports six model organisms (Homo sapiens, Mus musculus, Sus scrofa, Drosophila melanogaster, Macaca mulatta, and Danio rerio). It creates a comprehensive report containing interactive plots and tables in a single interface. Additionally, it provides detailed information on GO-molecular function, biological process, and antibody resources, to further assist the user.

Results:- We have tested this application on the output of a re-analyzed diabetic pig model. We performed an integrative multi-omic analysis using SurfacOmics to determine a set of previously unreported set of correlated RNA/Protein biomarkers. In co-analysis we uncovered a cascade of events which may underly weakened immune responses and delayed wound healing in this model. We used SurfacOmics to identify a single surface-expressed gene which can be used to validate this result.

Conclusions:- We demonstrated the use this tool to help to clarify the process of marker selection for further investigations.

Keywords:- Multi-omics, Biomarkers identification, Penalized Regression, Subcellular-localization