Abstract:

Gene expression survival analysis is a major research field of biomarker discovery in the war against cancer. It seeks to identify prognostic gene expression profiles which predict the probability of events such as patient relapse or survival. A number of gene signatures have been translated into the clinic to guide clinical decision making and therapy. For example Mammaprint, Oncotype DX and the Gene expression Grade Index. However, we lack of survival analysis tools that are intuitive enough to be used by clinicians and biologists and that take recently discovered molecular subtypes for different types of cancer into account.

We present a new web application that enables survival meta-analysis of single genes and gene signatures in different types of cancer, even if we only focus on breast cancer datasets in the prototype of our website. We therefore use state-of-the-art tools for survival analysis (*SurvComp*, [1]) and robust prediction of breast cancer molecular subtypes (*genefu*, [2]). This project is a collaboration with the Functional Genomics group at the European Bioinformatics Institute and their Gene Expression Atlas framework (http://www.ebi.ac.uk/gxa/).

Breast cancer is known to be a molecular heterogeneous disease with at least three clinically relevant molecular subtypes: basal-like, HER2-enriched and luminal tumors. Perou et al. (2000) [3] identified 4-6 molecular subtypes in breast cancer, each subtype having a different clinical outcome. These subtypes enable more detailed analyses of risk/survival prediction for patients and allow more effective treatment of each subgroup of patients related to a specific subtype separately.

As part of creating our background database, we performed a genome scale analysis of concordance indices from a collection of six breast cancer datasets and discovered prognostic gene signatures that are optimized for high and low risk/survival prediction of patients.

References:

[1] SurvComp, http://cran.r-project.org/package=survcomp

[2] genefu, http://cran.r-project.org/package=genefu

[3] Charles M. Perou et al., Molecular portraits of human breast tumours. *Nature*, 406 (2000): 747-752.