Institute of Computational Biotechnology

Graz University of Technology

DI Julia Feichtinger, PhD
Petersgasse 14/V
8010 Graz, Austria
Tel. +43 (316) 873-5342
julia.feichtinger@tugraz.at
http://www.tugraz.at/institute/imbt/home/

Master Thesis

Survival Analysis using Cancer Gene Expression Data

Supervisors: Julia Feichtinger, PhD & Prof. Christoph W. Sensen

Male germline genes have been reported to be activated in cancers and can encode antigens known as the cancer/testis antigens (CTAs) [1]. The expression of these genes has been linked to poor patient prognosis in a number of cancers (for example, [2]). We are interested to evaluate if certain CTAs, clusters of these CTAs or their antisense transcripts (long non-coding transcripts partially complementary to a corresponding sense transcript) exhibit potential for clinical applications.

Hence, the **overall goal** of this project is to make use of the available sequencing data and the corresponding clinical information (e.g., in TCGA [3]) and to correlate expression with patient survival. This should be established as an analysis pipeline. You will be working **with R**.

Specifically, the following **aims** should be pursued:

1. Literature research on RNA-seq data and survival analysis.
2. Getting familiar with R and the 'survival' R package [4].
3. Implementing standard survival analysis.
4. Implementing survival analysis of gene clusters (similar to [2]).
5. Implementing a Cox model to assess the association between the survival time and clinico-pathological variables (e.g., expression, cancer stage, age).
6. Visualisation of the analysis results.
7. Validation/testing using given germline genes and gene clusters.

Email: julia.feichtinger@tugraz.at

Homepage: https://www.tugraz.at/institute/icbt/home/

References

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