

Seminário

Grupo de Probabilidades e Estatística

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Via Zoom

Network-based Regularization: an application to skin diseases

Eunice Carrasquinha

Departamento de Estatística e Investigação Operacional, Faculdade de Ciências, Universidade de Lisboa, e CEAUL (Centro de Estatística e Aplicações da Universidade de Lisboa), Portugal

Abstract

Melanoma is the principal cause of death of all skin diseases, and its incidence is increasing faster than any other type of cancer. A successful treatment depends on early detection, as the metastatic form is resistant to therapies. Gene expression data are increasingly being used to establish a diagnosis and optimize treatment of oncological patients. In this work, we propose the analysis of gene expression data from metastatic melanoma as a tool to obtain potential genes that could be important targets for new therapies and treatment. However, the high-dimensionality nature of the data brings many constraints, for which several approaches have been considered, with regularization techniques in the cutting-edge research front. Additionally, the network structure of gene expression data has fostered the development of network-based regularization techniques to convey data into a low-dimensional and interpretable level. In this work, classical elastic net and two recently proposed network-based methods, HubCox and OrphanCox, are applied to high-dimensional gene expression data, to model survival data. The melanoma transcriptomic dataset obtained from The Cancer Genome Atlas (TCGA) is used, considering patients' RNA-seq measurements as covariates. The application of sparsity-inducing techniques to the skcm dataset enabled the selection of relevant genes (CIITA, HLA-DQB1, and HLA-DQA1) over a range of parameters evaluated. Comparable results were obtained for the elastic net and the network-based OrphanCox regarding model performance and genes selected.

Link para aceder ao Meeting via Zoom:

<https://videoconf-colibri.zoom.us/j/89421453444?pwd=BJkODKHt9G-8KuUyesSN1AgwixXre9.1>

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