

Regularization for sparsity, biological priors and neural networks in cancer survival models

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Survival analysis in cancer represents a classic example of application of supervised methods of machine learning to biomedical research. The general aim is to predict clinical outcome of cancer patients based on molecular and clinical data. In my talk, I will present our recent work on integrating biological prior information to increase the model accuracy and stability. I will discuss our recent models for multitask learning on cancer transcriptomics data. Moreover, I will demonstrate a simple solution for the integration of biological knowledge on cancer-related signaling pathways allowing us to drastically reduce the dimensionality of input data without compromising model accuracy.