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Machine Learning in Bioinformatics: Efficient mining of omics data and clinical documents

Tuesday 20 September 2022 18:30 (30 minutes)

Omics sciences (e.g. genomics, proteomics, and interactomics) are gaining an increasing interest in the scientific community due to the availability of novel, high throughput platforms for the investigation of the cell machinery, and have a central role in the so called P4 (predictive, preventive, personalized and participatory) medicine.

High-throughput experimental platforms and clinical diagnostic tools, such as next generation sequencing, microarray, mass spectrometry, and medical imaging, are producing overwhelming volumes of molecular and clinical data and the storage, integration, and analysis of such data is today the main bottleneck of bioinformatics pipelines.

On the other hand, textual documents, such as clinical records, Electronic Health Records, and patient's texts describing their healthcare experiences (Narrative Medicine), are more and more used in the biomedical research to extract patient's opinions and sentiments about their healthcare experience, by using NLP, Text Mining, and Sentiment Analysis methods.

Finally, networks are more and more used to model molecular interactions (e.g. biological pathways and protein-protein interaction networks), as well as brain structural and functional relationships (e.g. brain connectome), and the exploration (e.g. motif discovery) and comparison (e.g. network alignment) of such networks is gaining an increasing interest.

The talk introduces main omics data and presents some efficient bioinformatics and sentiment analysis tools and their application in biomedical research.

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Session Classification: Networks and brain segregation