BIOSTATISTICS SEMINAR

Statistical modeling for single-cell multi-omics integration: a case study in CAR-T cell immunotherapy

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CD19-directed chimeric antigen receptor (CAR)-T cell immunotherapy has been established as an effective treatment to redirect T cells' activity against tumors, yielding unprecedented response rates in patients with relapsed or refractory B cell malignancies. However, a considerable proportion of patients still do not achieve durable complete responses. Single-cell multi-omics analyses with cellular indexing of transcriptomes and epitopes by sequencing (CITE-seq) are leveraged to investigate the intrinsic genomic characteristics governing the proliferation capacity and neurotoxicity of CAR-T cell infusion products. To remove the batch effect of the CITE-seq data, a statistical normalization model, ADTnorm, is proposed, which also enables single-cell proteomics integration across studies. Moreover, to fulfill the goal of associating genomic features with patients' response to CAR-T cell therapy, a tree-based model, scanCT, is constructed to identify the associated genomic features in a highly interpretable manner. Going beyond genomic feature detection, a statistical multi-omics integration model is developed to gain further insight into the gene regulation mechanisms. Such an integration model bridges single-cell three-dimensional chromatin structure measurements with transcriptomics and epigenomics profiles. Therefore, the integration model enables the construction of a multi-modal cellular network on which the gene cis-regulations and associations with clinical outcomes can be inferred.

Thursday February 9, 2023, 3:30-4:30 PM Eastern

133 Rosenau Hall

Virtual using link and info below.

https://unc.zoom.us/j/91249030964?pwd=UXloTWlHajdQbkRqd1d5TnRaMitYdz09

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