SEMINAR

Mass spectrometry-based single-cell proteomics: challenges, opportunities and method development

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Mass spectrometry-based single-cell proteomics (SCP) has become a credible player in the single-cell omics arena thanks to substantial technical improvements that have pushed the boundaries of sensitivity and throughput. But what should one do once the precious data have been acquired, often at great cost? Reviewing the SCP literature doesn't provide much help, as every lab tends to run their own in-house, either overly complex or unrealistically trivial and undocumented analysis pipeline. When facing complex data, best is to start with simpler but principled analyses approaches to gain and understanding of the data and their peculiarities. I will describe such peculiarities in SCP data and illustrate how these have lead to the development of the scplainer approach. The goal of scplainer is to move the tension point from how to process SCP data to explain it in the light of the biological question. In this talk, I will illustrate how to approach complex data and it's underlying biological complexity, emphasising the central role of experimental designs and research software engineering.

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