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 Thursday

WEBINAR

via Webex*

45' (talk) + 30' (discussion)

11.00am - 12.15pm



Towards the molecular blood count: from small non-coding RNAs to single cell resolution immune system data

ABSTRACT

The immune system plays a dominant role for basically all human diseases. We aim to understand the specificity of molecular signatures measured from immune cells for disease classes (e.g. cancer), specific diseases (e.g. non small-cell lung carcinoma) and severity grades (e.g. stage I/II NSCLC). The original focus of our research was to understand gene regulatory patterns by identifying circulating microRNA patterns. We observed a great potential for detecting cancers such as lung cancer and neurological disorders such as Parkinson's disease. Especially the miR-34 family plays a core role in both disease classes and regulates relevant pathways such as TNF and TGF beta pathways, but also the unfolded protein response. Now, a detailed characterization of the gene expression signatures in the respective pathways becomes essential. To this end, we established a pipeline for the high-throughput measurement of single immune cells. We measured 1.1 Million blood cells of almost 400 samples, including controls, patients with mild cognitive impairment, Parkinson's disease and Alzheimer's disease. Our results pinpoint shifts in CD4 T-sub-cell clusters in mild cognitive impairment that are neither present in severe cognitive impairment nor in controls. In these and other immune cell types, hallmark pathways were affected again. As next steps we will include cancer patients in the consideration to establish an even more comprehensive single immune cell transcriptome atlas.



SPEAKER

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