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Speakers and Abstracts

Session IV: High-throughput and robotics for massive characterization

Erwin Schoof
Associate Professor
DTU Bioengineering
Technical University of Denmark

Talk ***Exploring cell heterogeneity in health and disease using single-cell proteomics and transcriptomics***

About

Erwin is a recently appointed Associate Professor in single-cell proteomics in disease biology at the Technical University of Denmark. With a background in Medicinal Chemistry (MSc. from Utrecht University) and molecular systems biology in cancer (PhD from the Technical University of Denmark), his research focuses on normal and malignant hematopoiesis. He dedicated his postdoc to the investigation of healthy and malignant blood stem cells in the lab of John Dick (Toronto, Canada) and Bo Porse (Copenhagen, Denmark), and has spent the last few years optimizing single-cell proteomics workflows to be used for deciphering cellular heterogeneity. He currently heads the Cell Diversity Lab, focusing on the development and application of high-sensitivity proteomics workflows.

Abstract

Single-cell proteomics by Mass Spectrometry (scp-MS) can provide valuable insights into distinct cell-states and signalling patterns present in a cell population. However, carrying out proteomics profiling from the limited amount of material encapsulated in an individual cell presents significant challenges. Tremendous efforts have been made to optimize all aspects of scp-MS, with the aim of minimizing losses during sample preparation and maximizing sensitivity of data acquisition.

Here, we will present recent approaches developed in the Cell Diversity Lab. We will cover key aspects of the entire workflow and showcase the application of our methods to address biological questions spanning across stem cell differentiation, and especially Acute Myeloid Leukemia. With a particular focus on the healthy and malignant human blood system, we aim to convey possible biomedical implications of scp-MS, and the joint assessment of transcriptomes and proteomes at the single-cell level. Through these examples, we provide an overview of the current technological state of the field and highlight key challenges that remain to be solved.