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MULTI-PARAMETRIC SINGLE CELL ANALYSIS USING SPECTRALLY ENCODED MICROBEADS

Researchers at Stanford and the Chan Zuckerberg Biohub have developed methods for multiple parameter single cell analysis.

Methods to analyze single cells are important for evaluating cell-to-cell variability in biological systems, especially where the characteristics of minority cell populations can be masked by bulk population. Single cell analysis methods have traditionally been limited to sequence-based biomolecule quantification (e.g., gene expression analysis via RNA-Seq). There are few technologies that can link sequence-based biomolecule quantification to phenotypic characterization (e.g., cell morphology acquired via dynamic cellular imaging). Notably, these current methods are limited in throughput and/or the number of phenotypic parameters that can be reliably measured without significantly increasing run costs.

Stage of Research
The inventors have developed a single cell analysis technology for making tandem sequence-based nucleic acid measurements and phenotypic measurements at population scale by harnessing spectrally encoded microbeads. Their system allows for the direct correlation of functional or phenotypic analyses of single cells with sequencing-based measurements by means of microbeads with a 1:1 linkage of lanthanide spectral signature and an identifier sequence attached to the bead. The inventors demonstrate the utility of their integrated platform with cellular phenotyping and transcriptomic analysis of T cell activation.

Applications

- Multiple parameter single cell analysis of heterogenous cell populations

- Precisely link tandem multi-parametric image-based cellular phenotyping (e.g., cell morphology, cytokine secretion, and calcium flux) and transcriptomic analysis (e.g., RNA-Seq)

Advantages

- Single cell analysis over multiple parameters in tandem, without sophisticated statistical or physical separation methods
- An integrated platform that employs spatial-, spectral- and sequence-encoding to perform sensitive same-cell multi-parameter analysis
- Custom algorithm to process microscopy data to sequence-based biomolecules expression data

Publications

- PCT publication WO2020243160

Patents

- Published Application: WO2020243160

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