

Enhanced Single Cell Transcriptomics for New Biomarkers and Targets in Cardiovascular Ageing

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Background

Ageing is a critical risk factor in cardiovascular disease (CVD), the greatest cause of death and economic health burden in the world.

Project Idea

We utilise novel methodology to conduct extensive RNA sequencing of young & old, healthy & diseased cardiac tissue, to identify new age-associated, disease-relevant cell types, biomarkers and drug targets.

Progress

Pilot data from sequencing 750 aged heart cells identifies all major known cell types (top-right, individual cells separated by "tSNE" mathematical plot distribution, colours distinguish cell types). Top; gene expression signatures of each cell type are identified. Gene expression may thus be correlated with age and disease status.

Direction

Sequencing 1000s of cells commenced. Data analysis, gene target identification, validation, and therapeutic evaluation to follow.

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