

Single-Cell Transcriptomic Profiling of Beta Cells in Human Pancreatic Islets: Comparative Analysis of Healthy and Type 2 Diabetic States

The production of hormones like glucagon and insulin in the pancreatic islets is very important in regulating glucose metabolism. For Type 1 and Type 2 diabetes, conditions in which genetic factors play an important role, a full understanding of the molecular mechanism underlying these cells is key. In this kind of study, RNA sequencing would be ideal since it is one of the most powerful techniques allowing the investigation of the transcriptome in high resolution.

The approach includes employing RNA sequencing data to re-analyze transcriptome profiling in human pancreatic islets. A Single-Cell Transcriptomic Profiling will be used mainly to investigate gene expression patterns, functional annotations, and differential expression in experimental contexts. This approach will be used to profile the molecular pathways controlling islet biology and possible disease states, including diabetes.

Software and Scripting Requirements

Programming Languages: Python, Bash, R.

Key Tools and Libraries:

- Python/Bash:
 - FastQC, STAR, RPKMforgenes, t-SNE, SCDE, GSEA.
 - Libraries: subprocess, os, pandas for automation and data handling.
- R:
 - Libraries: SCDE, clusterProfiler, ggplot2, DESeq2, limma, Seurat.

References

1. Research Paper:
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2. Ensembl Reference Genome and GTF File:
Ensembl. (2023). Homo sapiens GRCh38 reference genome and gene transfer format (GTF) file (Release 109) Ensembl. Retrieved from <ftp://ftp.ensembl.org/pub/release-109/>