Project Proposal Lightning Talk

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BACKGROUND/MOTIVATION

Segerstolpe Å, Palasantza A, Eliasson P, Andersson EM, Andréasson AC, Sun X, et al. Single-Cell Transcriptome Profiling of Human Pancreatic Islets in Health and Type 2 Diabetes. Cell Metabolism. 2016 Oct;24(4):593–607.

Single-Cell Transcriptome Profiling of Human Pancreatic Islets in Health and Type 2 Diabetes
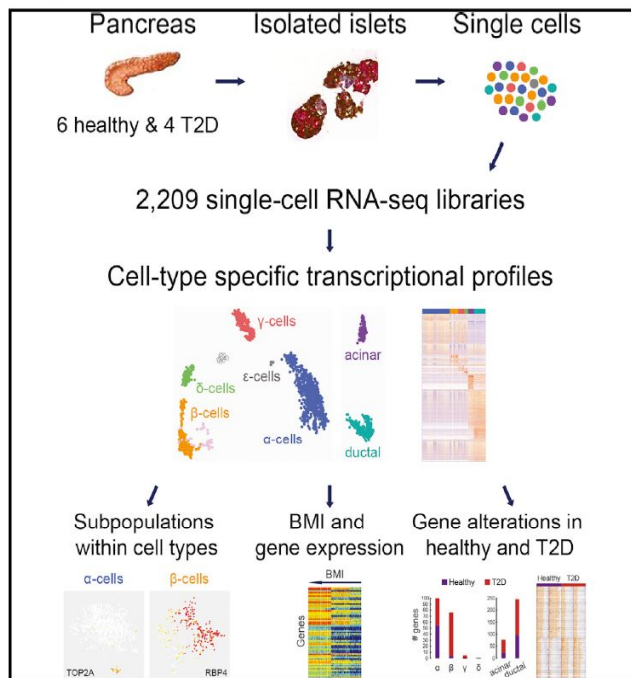
Key Findings:
- Cell-type-specific gene expression irrespective of case/control status
- Novel subpopulations
- Genes correlations to BMI
- Gene expression alterations in diabetes

HYPOTHESIS

- **Knowledge gap:** This paper used scRNA sequencing from pancreatic cells to identify the gene expression alteration with obesity (BMI > 30) and type 2 diabetes (T2D). However, the relationship between gene expressions in obesity and T2D is still unknown

- **Null Hypothesis** : The differentially expressed genes in obese cohorts are not significantly correlated with T2D

- **Expectation**: cohort with obesity has a different differential expression gene profile compared to the non-obese cohort. These differential expression genes in obese cohort are correlated with T2D development

DATA

Dataset from ArrayExpress: E-MTAB-5060 & E-MTAB-5061

Single cell RNA sequencing data measuring the RNA expression in RPKM (reads per kilobase of exon per million reads mapped) from 14 donors (2209 cells across 7 cell types) **6 healthy individuals, 8 Type 2 Diabetes**

Source Name	ENA_SAMPLE	BioSD_SAMPLE	organism	individual	organism part	disease	sex	age	time unit	Term Source REF	Term Accession Number	body mass index
HP1504101T2D_wholeislet	ERS1348457	SAMEA4437008	Homo sapiens	HP1504101T2D	islet of Langerhans	type II diabetes mellitus	male	57	year	EFO	UO_0000036	24
HP1504101T2D_wholeislet	ERS1348457	SAMEA4437008	Homo sapiens	HP1504101T2D	islet of Langerhans	type II diabetes mellitus	male	57	year	EFO	UO_0000036	24
HP1504901_wholeislet	ERS1348458	SAMEA4437009	Homo sapiens	HP1504901	islet of Langerhans	normal	male	23	year	EFO	UO_0000036	21.5
HP1504901_wholeislet	ERS1348458	SAMEA4437009	Homo sapiens	HP1504901	islet of Langerhans	normal	male	23	year	EFO	UO_0000036	21.5
HP1506401_wholeislet	ERS1348459	SAMEA4437010	Homo sapiens	HP1506401	islet of Langerhans	normal	female	48	year	EFO	UO_0000036	35
HP1506401_wholeislet	ERS1348459	SAMEA4437010	Homo sapiens	HP1506401	islet of Langerhans	normal	female	48	year	EFO	UO_0000036	35
HP1507101_wholeislet	ERS1348460	SAMEA4437011	Homo sapiens	HP1507101	islet of Langerhans	normal	male	22	year	EFO	UO_0000036	32.9
HP1507101_wholeislet	ERS1348460	SAMEA4437011	Homo sapiens	HP1507101	islet of Langerhans	normal	male	22	year	EFO	UO_0000036	32.9
HP1508501T2D_wholeislet	ERS1348461	SAMEA4437012	Homo sapiens	HP1508501T2D	islet of Langerhans	type II diabetes mellitus	female	37	year	EFO	UO_0000036	39.6
HP1508501T2D_wholeislet	ERS1348461	SAMEA4437012	Homo sapiens	HP1508501T2D	islet of Langerhans	type II diabetes mellitus	female	37	year	EFO	UO_0000036	39.6
HP1525301T2D_wholeislet	ERS1348462	SAMEA4437013	Homo sapiens	HP1525301T2D	islet of Langerhans	type II diabetes mellitus	male	52	year	EFO	UO_0000036	34.36
HP1525301T2D_wholeislet	ERS1348462	SAMEA4437013	Homo sapiens	HP1525301T2D	islet of Langerhans	type II diabetes mellitus	male	52	year	EFO	UO_0000036	34.36
HP1526901T2D_wholeislet	ERS1348463	SAMEA4437014	Homo sapiens	HP1526901T2D	islet of Langerhans	type II diabetes mellitus	female	55	year	EFO	UO_0000036	29.84
HP1526901T2D_wholeislet	ERS1348463	SAMEA4437014	Homo sapiens	HP1526901T2D	islet of Langerhans	type II diabetes mellitus	female	55	year	EFO	UO_0000036	29.84

Analysis Tools in the Prior Work

- ANOVA
  - For the cohorts of the healthy and T2D, significantly different gene expressions ($p <= 0.01$)
- Clustering (t-SNE)
  - phenotyping of cells
  - further analysis of each type for subpopulations

Figures adapted from Segerstolpe et al. (2016)
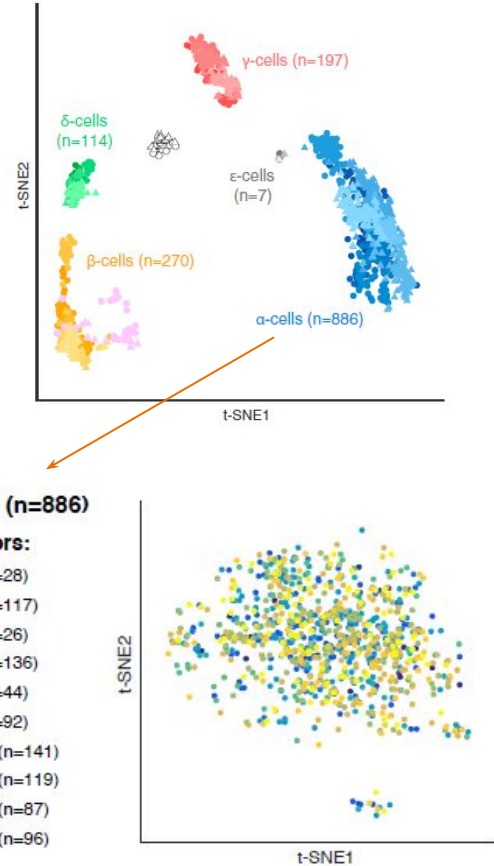
ANALYSIS PLAN

- Identify significantly differentially expressed genes for different cell types in cohorts BMI ≤ and >30
- Identify significantly differentially expressed genes for different cell types in T2D
- Examine correlation of differentially expressed genes between the obese cohort and T2D using regression analysis
- Perform 2-sample t-test on these significantly differential expressed genes in each cell type for cohorts with T2D and BMI ≤ and >30