Bioinformatics Analysis and Visualisation of Medical Genomics Data

Assignment 1 - Task 1 – Anton Hellberg

2. Answer the following questions

a. What is the medically relevant insight from the article?

Answer: That weight loss by bariatric surgery leads to a mostly normalized transcriptional change in insulin response in white adipose tissue.

b. Which genomics technology/ technologies were used?

Answer: Gene transcripits were analyzed via CAGE, a sequencing technique which specializes in sequencning only the 5´ end of cDNA (TSS or transcription start site). It is accurate in its quantative analysis, can find novel genes, does not need pre-defined probes. After this differential expression of insulin response was used for the three groups (OB, POB, NO). Next gene set enrichment analysis was performed.

3. Further related research questions

a. List and explain at least three questions/ hypotheses you can think of that extend the analysis presented in the paper.

Answer:

1. The ever-present question regarding analysis of adipose tissue is utilizing the visceral adipose tissue instead of subcutaneous, which the study focuses on. The interest being that visceral adipose tissue is the more pernicious adipose tissue of the two. So, what would be the transcriptional change in insulin response after weight loss in visceral adipose tissue instead.
2. Single-cell seq data has shown that there are different subtypes of adipocytes, and as described by Mileti *et al*. fat cell volume did not change after weight loss. Therefore analysing the same individuals under the same condition but instead to also observe if the different subtypes of adipocytes *change* would be interesting.
3. An interesting topic is to see why the genes act differently to insulin response in the three cohorts. One approach would be to analyse these gene sets with CREs (cis-regulatory elements), to determine, for example, how the CREs for insulin-resistant gene sets in the OB state differ from those in NO and POB.

b. [Optional] Devise a computational analysis strategy for (some of) the listed questions under 3a.

Answer:

1. The same computational strategy as described in Mileti *et al*.
2. The same methodology but instead change CAGE to Single-cell seq.
3. Maybe through ChIP-seq or eQTL mapping?