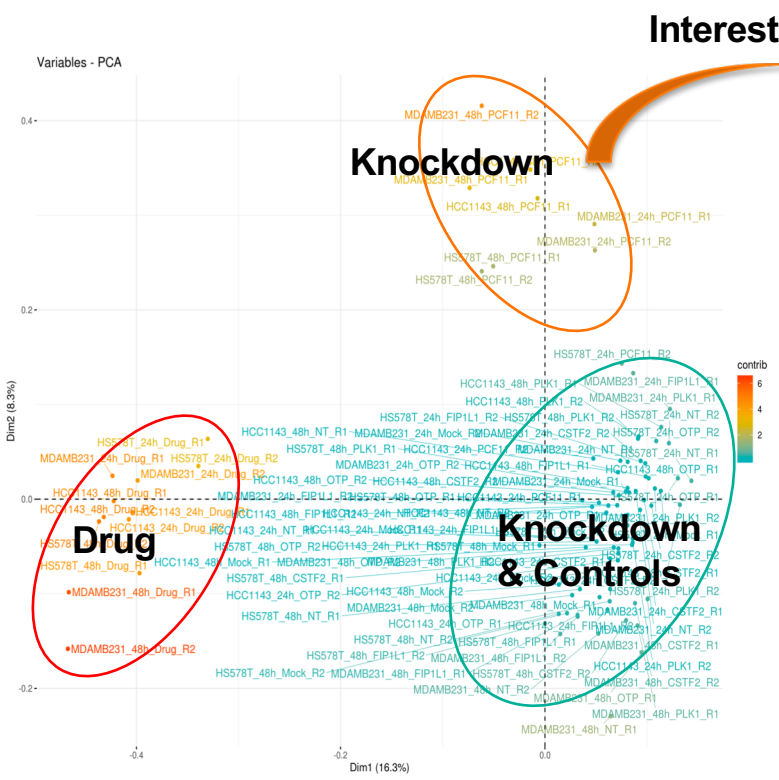
Nitika Kandhari

PhD Bioinformatics/Medicine, Nursing and Health Sciences

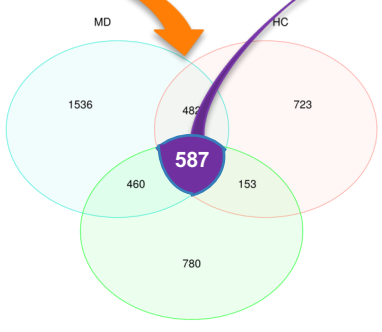
My project involves bioinformatic analyses of heaps of Cancer Patient Transcriptomic data. 3'-Untranslated Regions (UTRs) accommodate a vast array of regulatory elements that control gene expression. 70% of mammalian genes undergo Alternative Polyadenylation (APA). This changes the architecture of 3'-UnTranslated Regions (UTRs) and associated post-transcriptional regulatory control of mRNA fate. Short 3'UTRs are generally associated with de-differentiated proliferative cells (e.g. stem cells) whereas longer 3'-UTRs associate with more complex regulation and cellular specialisation. The literature suggests that ~91% APA genes switch to shorter mRNA isoforms in tumour cells. Our study aims to detect a signature of APA changes that are specific to triple negative breast cancer(TNBC) that could be applied as a novel prognostic biomarker in early-stage breast cancer.

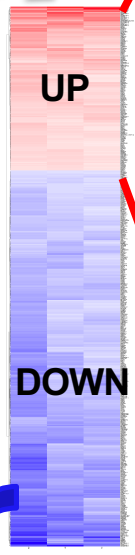
limma Glimma RStudio Shiny ggplot2 rmarkdown ade4 %>% tidyr dplyr knitr

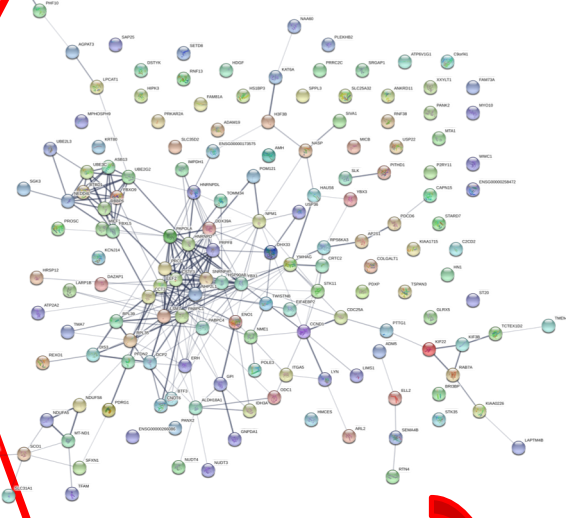
STRING



Interesting gene set

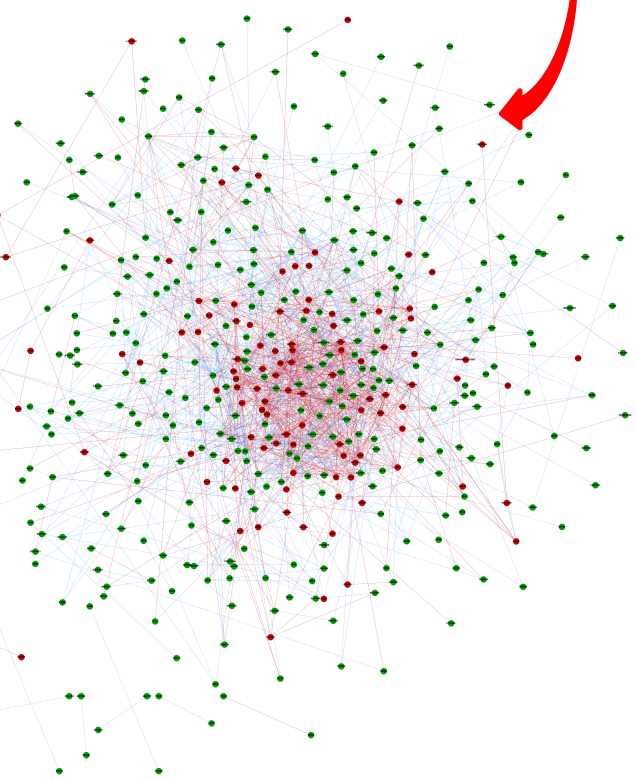




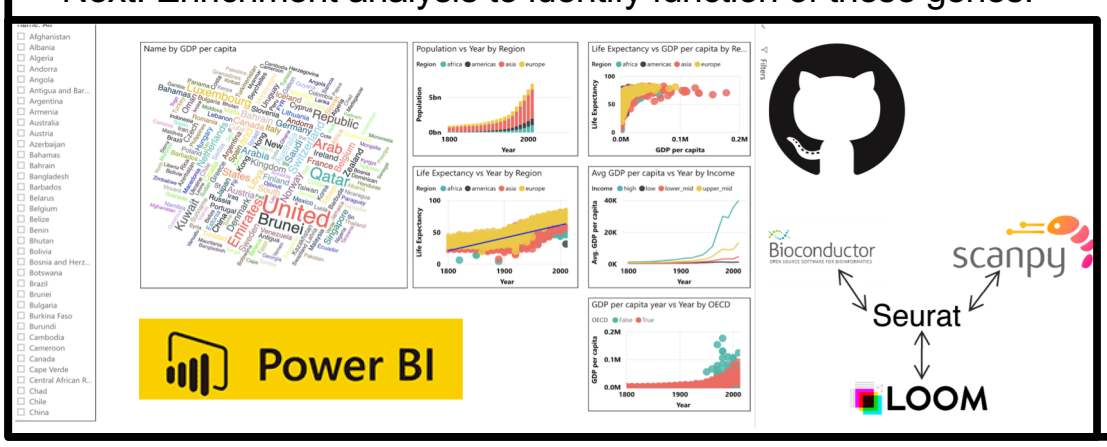


UP

DOWN



- Determine effect of gene knockdown and drug treatment across 3 TNBC cell lines.
- Identified **587 DEGs** (Up+Down regulated) in **PCF11 knockdown** treatment common to all 3 cell lines.
- **Interaction network** of these genes.
- Next: Enrichment analysis to identify function of these genes.



MONASH DATA FLUENCY

@Nitz_k92

@KandhariNitika