Kick off meeting

16/11/2023

Trajectory inference

- Infer lineages of cells
- Active area of research
- Key in understanding cellular dynamics
- Comparison of methods

Package: dynverse

- R packages: Seurat, monocle, slingshot, destiny
- Python libraries: scanpy, cellrank, PAGA

Oncogenes are turned on/off, which can upregulate, result in proliferation/apoptosis

DorothEA, package: gene regulatory network, uses footprint method
(TF activates genes. Check if it is active)

Oncogenic signalling: MYC, PD-L1, JAK-STAT, SMAD

<u>Do we see these pathways active?</u>

Goal: investigating the antitumour response phenotype following treatment with anticancer drug

Dataset: MIX-seq. Large amount of cell lines treated with different drugs, then readout of mRNA sequencing. Result: certain amounts of reads.

- What are functions of the genes?
- How effective are the drugs?

We'll be looking at **experiment 5 ,** Trametinib as drug

➔ Uses MEK pathway. Prevents downstream effects. Preferred result: less PD-L1

TO DO: create research goal and question. Discuss with Glenn before submitting

What is the problem/background? What is the challenge? Find research question

Next meeting: Tuesday 21 nov 16.00, Boaz as chair, Glenn joins

After that meetings:

Tuesdays: 14.00
Thursdays at 10.00

For next meeting:

- Read papers
- Come up with 1 research questions
- Build your story around the 4 goals

Glenn meetings, bring presentation/results