Hide&Seq Pilot Project

Pages

RareSeq Lit/ Reading

Hide&Seq Cornerstone Meeting/S

Moving Forward

Notes:

Rough outlines

1. RNA Seq Data Analysis: Collect RNASeq Data from patients, DEG with a target expression. Aim: Identity DEG from the sample, dysregulated compared to the target. Tools that can be used: edgeR, DESeq2, or limma

2. GSEA: Score and ranking of of DEG

3. Drug Target Database: Links the drugs for the dysregulated genes (Is this LINKS1K?)

- Data pre processing

- DEG

- Query DBs

- Rank

- Output

LinksCloud- best way to go.

GSEA Gene Seq Enrichment Analysis

- It helps to identify whether a pre-defined set of genes or gene sets show statistically significant differences between different experimental conditions or groups.

- Gene sets: combination of genes required or present in a particular biological pathway. Gene sets can represent biological pathways, molecular functions, cellular components, or disease-associated signatures.

- Data: RNASeq- quantification of the RNA transcription

- Ranked Gene List: Rank the most differential expressed gene, creates a set

- Enrichment Score calculation: Score of over/under expression of the ranked gene list.