Towards Integrating large-scale OMICS data to better Understand Disease Pathogenesis

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Motivation

12 tumor types
- Leukemia (LAML)
- Lung adenocarcinoma (LUAD)
- Lung squamous (LUSC)
- Kidney (KIRC)
- Bladder (BLCA)
- Endometrial (UCEC)
- Glioblastoma (GBM)
- Head and neck (HNSC)
- Breast (BRCA)
- Ovarian (OV)
- Colon (COAD)
- Rectum (READ)

Oomics characterizations
- Mutation
- Copy number
- Gene expression
- DNA methylation
- MicroRNA
- RPPA
- Clinical data

TCGA Pan-cancer project
Ellrott et al. 2013
Integrative network based approach

1. RNA expression
2. DNA methylation
3. miRNA expression
4. Somatic mutations

Differential Analysis

- Differentially expressed genes
- Differentially methylated genes
- Differentially expressed miRNAs

Proximity interactions with somatic mutations
miRNA-mRNA interactions
TF-mRNA interactions

Driver mutations
Key drivers identification
Functional enrichment and druggability analysis

Network pruning

Prior network
Bayesian Learner
TFmiR: Construction of disease-specific networks