

# Digestive tract diseases and the microbiome: How to functionally integrate host transcriptomics and metabolomics

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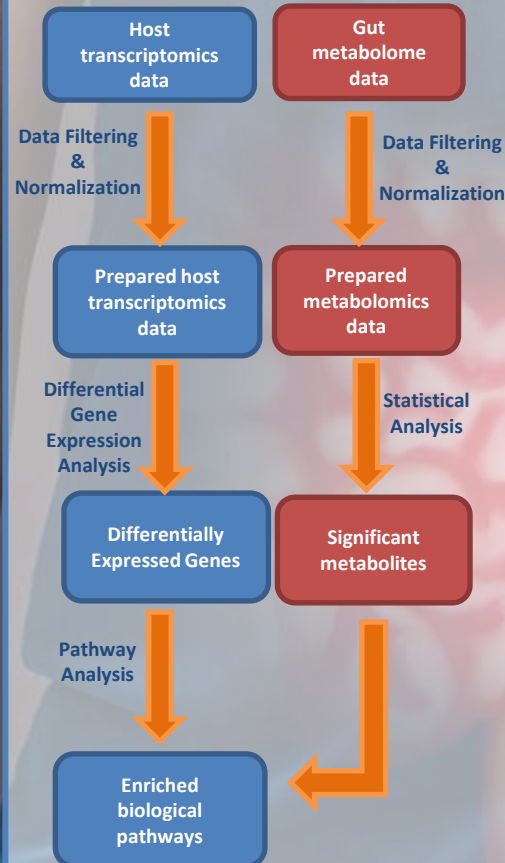
## BACKGROUND & AIM

Crohn's disease and ulcerative colitis are chronic disorders which affect millions of people worldwide. Here we provide functional integrated analysis of **host-transcriptome (RNAseq)** and **gut metabolome** of Chron's disease and ulcerative colitis disease patients from a publicly available dataset [1] which consists of longitudinal molecular profiles of host and microbial activities during disease. We are trying to develop workflows to track gut microbiota alteration in disease and how it contributes intestinal inflammation and how it affects human health.

456 metabolites      17760 transcripts



## ANALYTICAL WORKFLOW



## RESULTS

- ✓ 1896 and 1339 genes were significantly differentially expressed in the ileum and rectum for **Crohn's disease**.
- ✓ 121 and 6809 genes were significantly differentially expressed in the ileum and rectum for **ulcerative colitis** disease.
- ✓ Enrichment analysis testing for overrepresentation of WikiPathways among differentially expressed genes and altered metabolites confirmed strong representation of immune-related pathways.
- ✓ Enriched pathways include genes which are responsible for **inflammation directly** such as **IL1A** and **IL-6**.
- ✓ **Tryptophan** and **taurine** are altered metabolites during Chron's disease and ulcerative colitis disease.

Figure 1. Cytokine and Inflammatory Response pathway

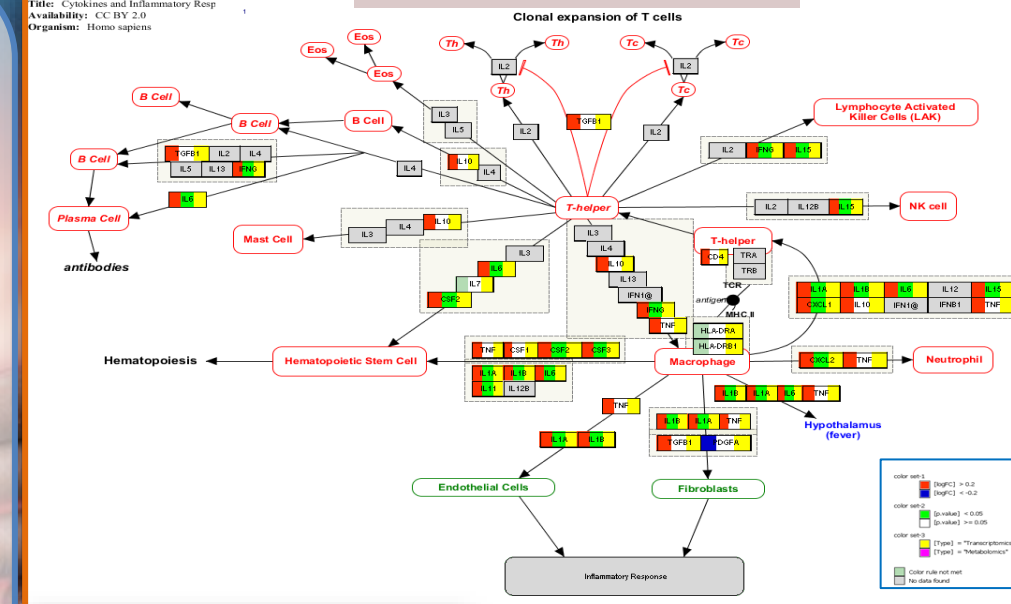
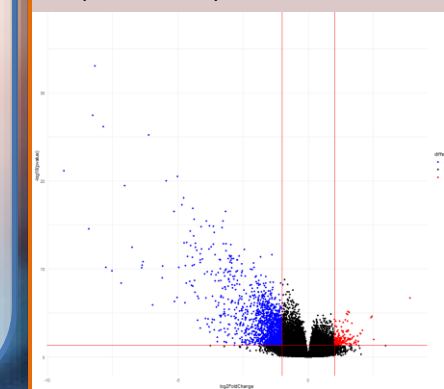


Figure 2. Volcano plot for comparison of ulcerative disease patients and healthy individuals on ileum location



## CONCLUSION

Our study uses **functional integration** of host-transcriptomics and metabolomics data, both data types confirm that **Chron's Disease** is primarily an **Inflammatory ileum** disease, but effects in rectum are visible, while the **Ulcerative Colitis** effects are smaller and **concentrate in rectum** as expected.