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2021 UC San Diego Undergraduate Library Research Prize

Title

Characterization of the age-associated intratumoral microbiome in pancreatic adenocarcinoma

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Author

Tsai, Joseph

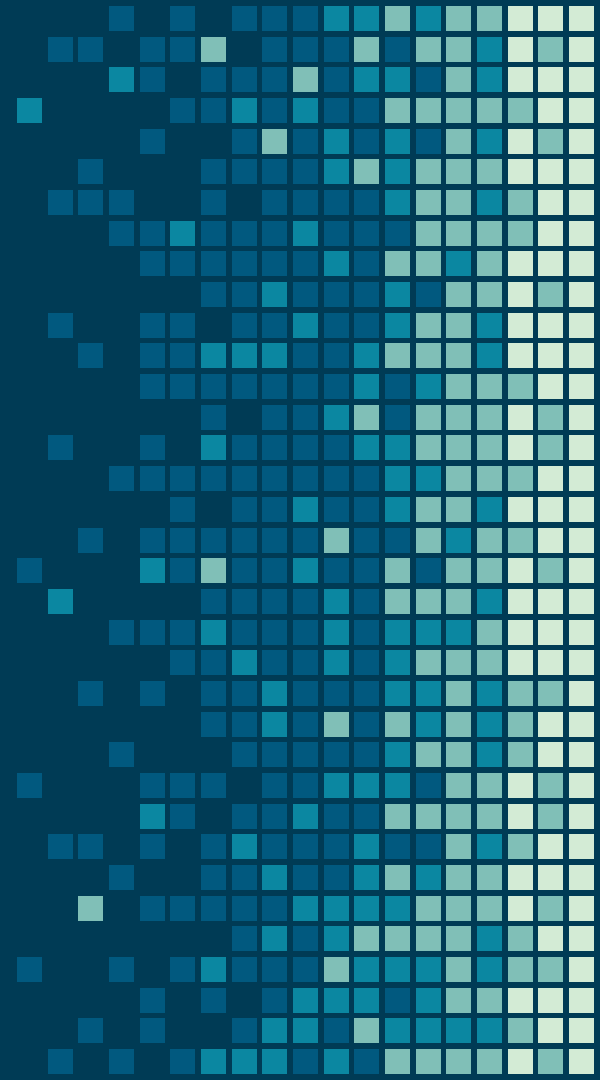
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Characterization of the age-associated intratumoral microbiome in pancreatic adenocarcinoma

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Dr. Weg Ongkeko



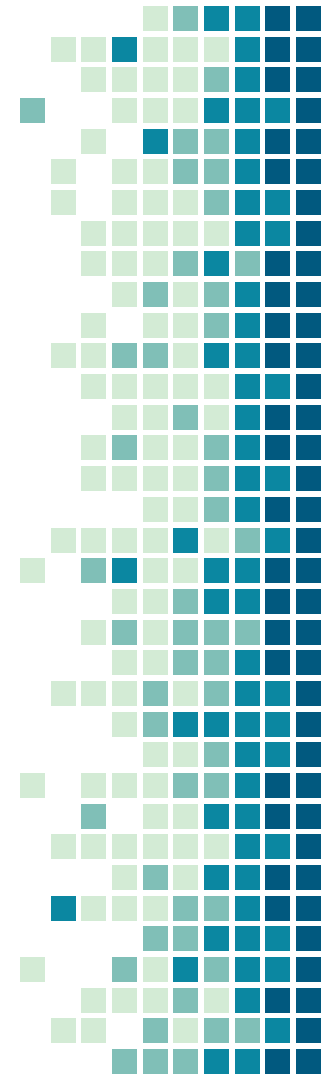
Influence of the microbiome on cancer and immunotherapy

Cancer Immunotherapy

- Early Stage Diagnosis
- Combination with current immunotherapeutic strategies to increase efficacy

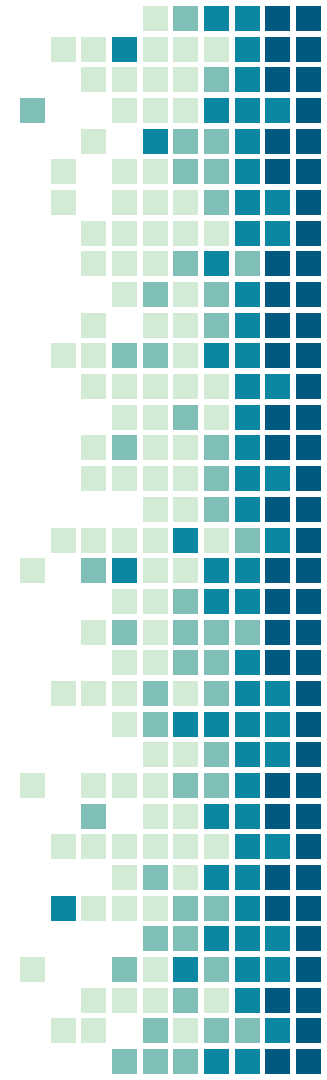
The Microbiome

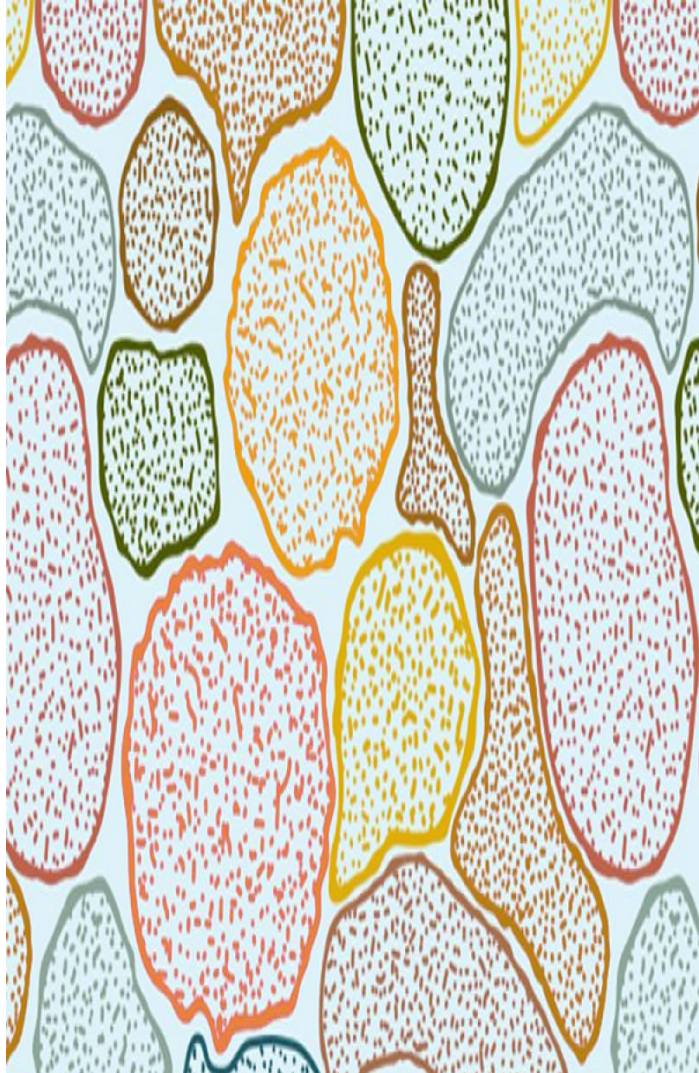
- the collective genomes of microbes within a community
- Crosstalk between the microbes and the immune system is crucial
 - Germ free mice with severe defects in immunity (Johansson et al, 2015)



Pancreatic Adenocarcinoma

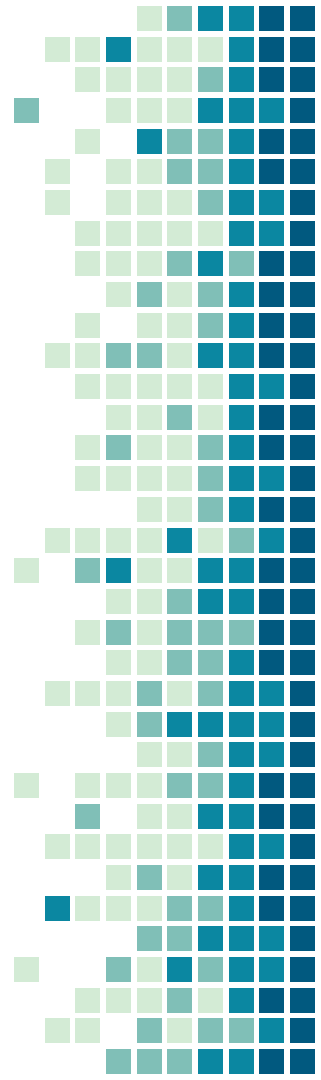
- Third most common malignancy in the USA (Rawla et al, 2016)
- Age is a big risk factor
- 5 Year survival rate is a mere 9%





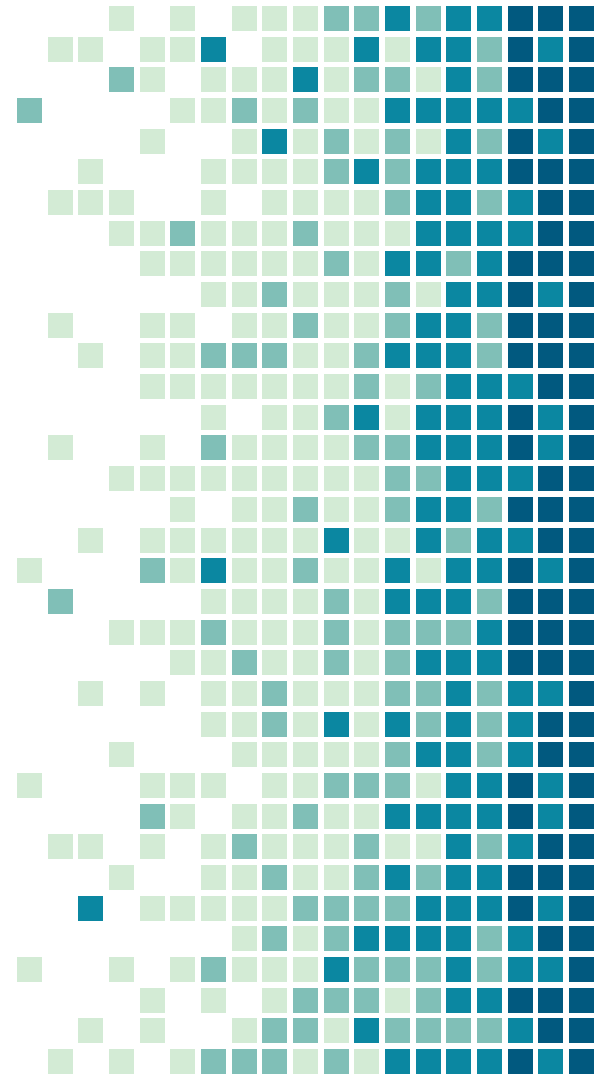
Ultimate goal

Identify and characterize the microbes contributing to PAAD progression and to elucidate why age is such a big risk factor.

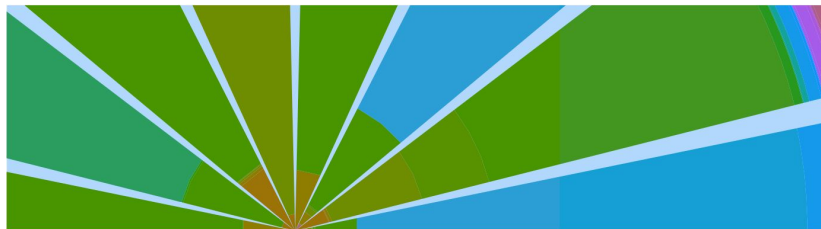


The Analyses

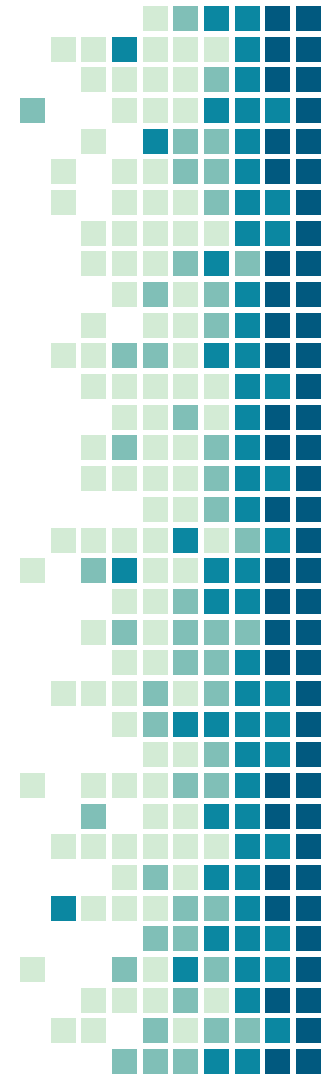
1. Pathoscope
2. Differential Expression
3. Microbe Relative Abundance
4. Survival
5. Clinical Variables
6. GSEA
7. Spearman Correlation



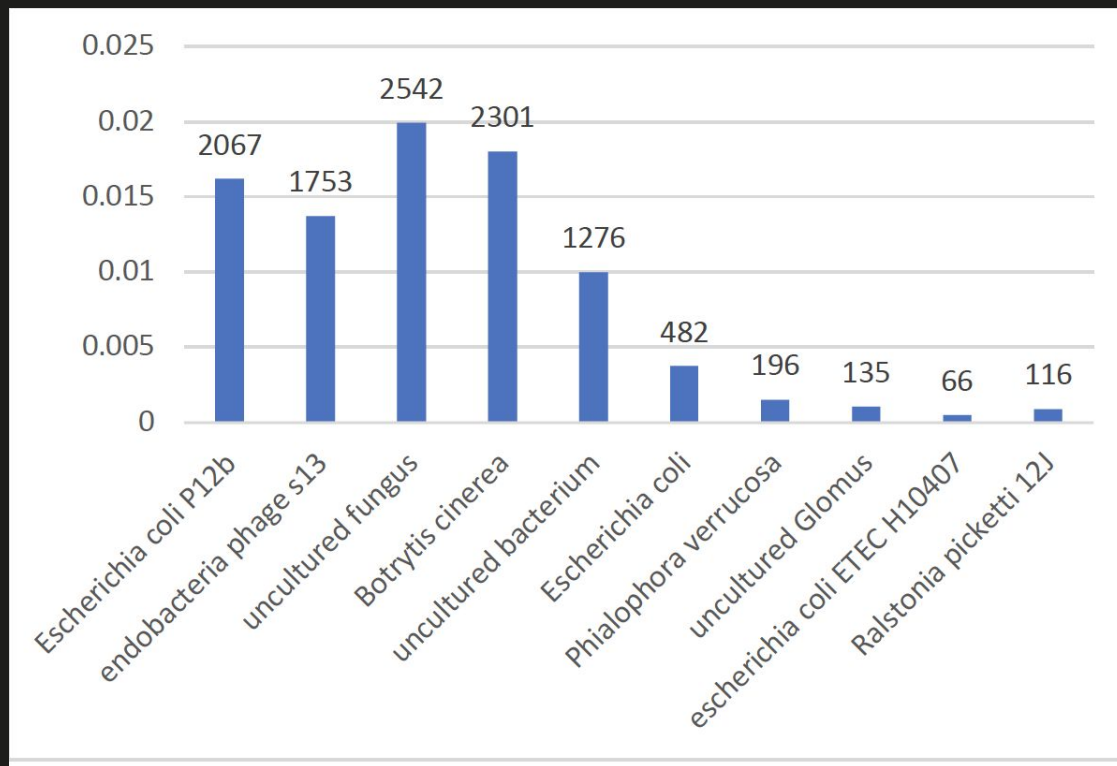
PathoScope 2.0



1. PathoLib
 - a. Generates custom genome library (from NCBI) and a filter file
2. PathoMap
 - a. Map patient reads (from TCGA) against the library created from PathoLib
3. PathoID
 - a. Identifies and employs the reads with unique alignment to guide the ambiguous alignments



Top 10 most prevalent microbes in PAAD patients



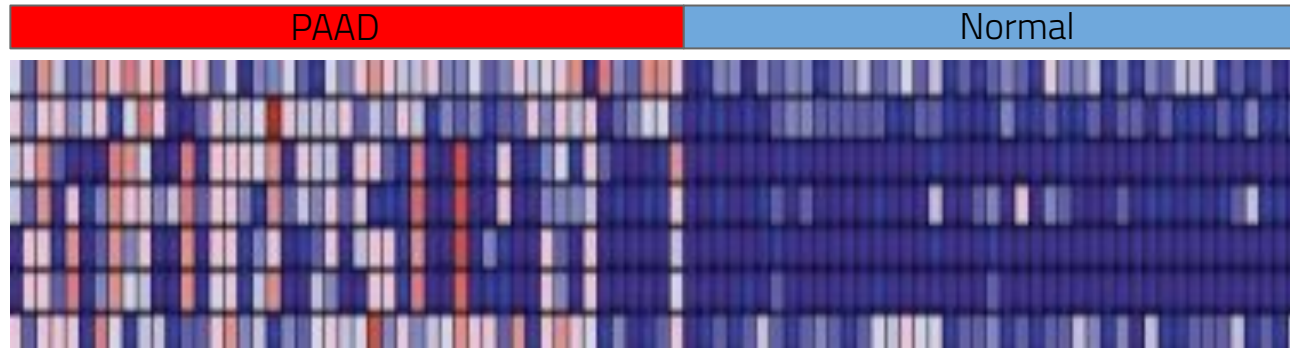
Differential Expression Analysis

Data of Pancreatic Adenocarcinoma (PAAD) patients from TCGA

- 185 PAAD patients
- 166 normal (control)
 - Compare to reveal dysregulated microbes and immune associated genes

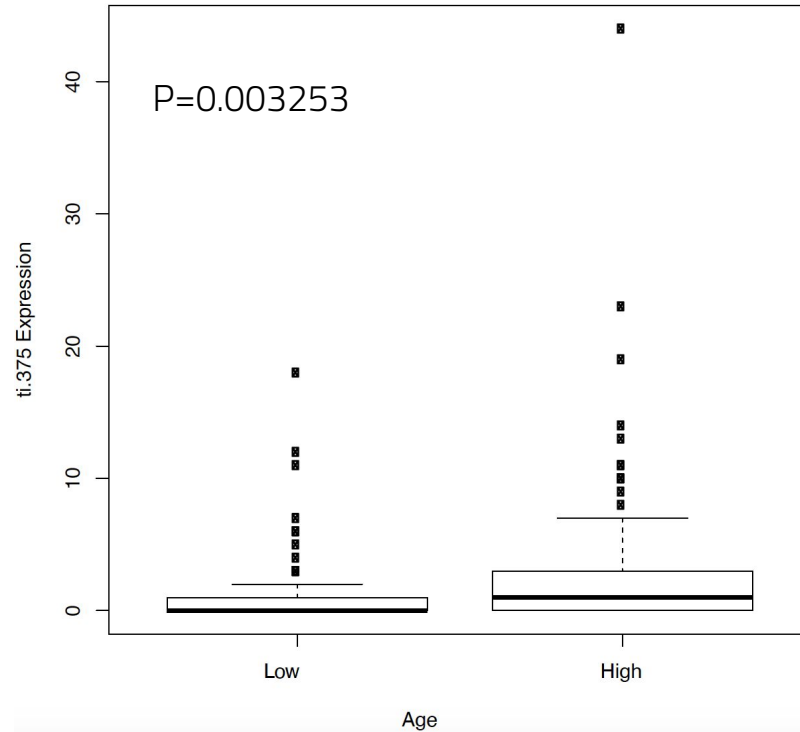


Differentially Abundant Microbes



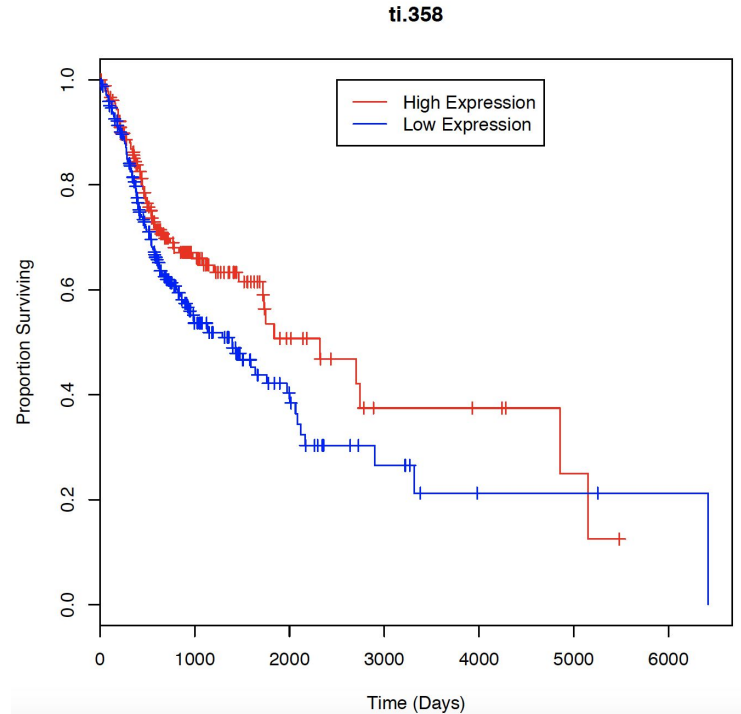
Age Correlation

Find which differentially microbes are significantly correlated with age.



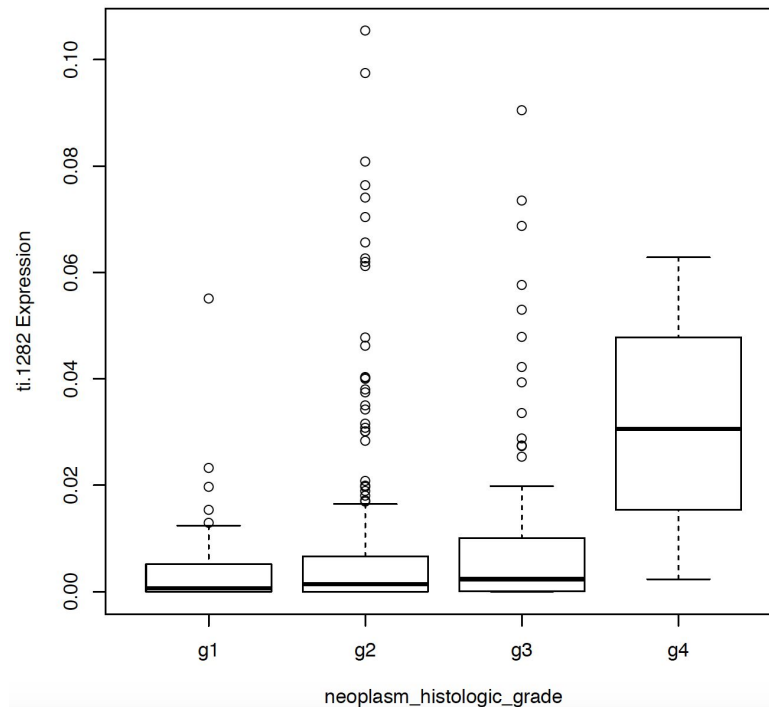
Survival

- Cox Regression analysis to produce Kaplan-Meier Graphs
- RED: high expression
- BLUE: low expression



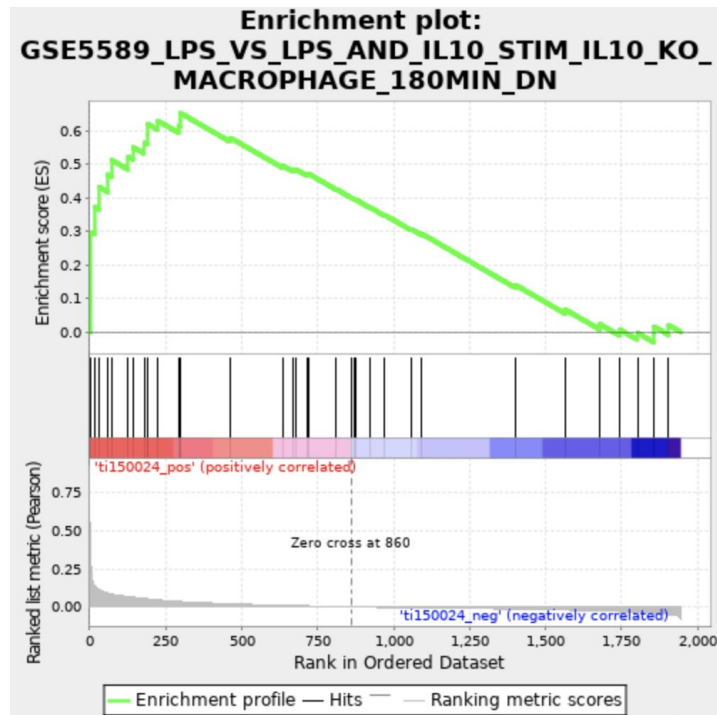
Clinical Variable Analysis

Purpose: Correlate various clinical variables to microbe expression confirm clinical relevance



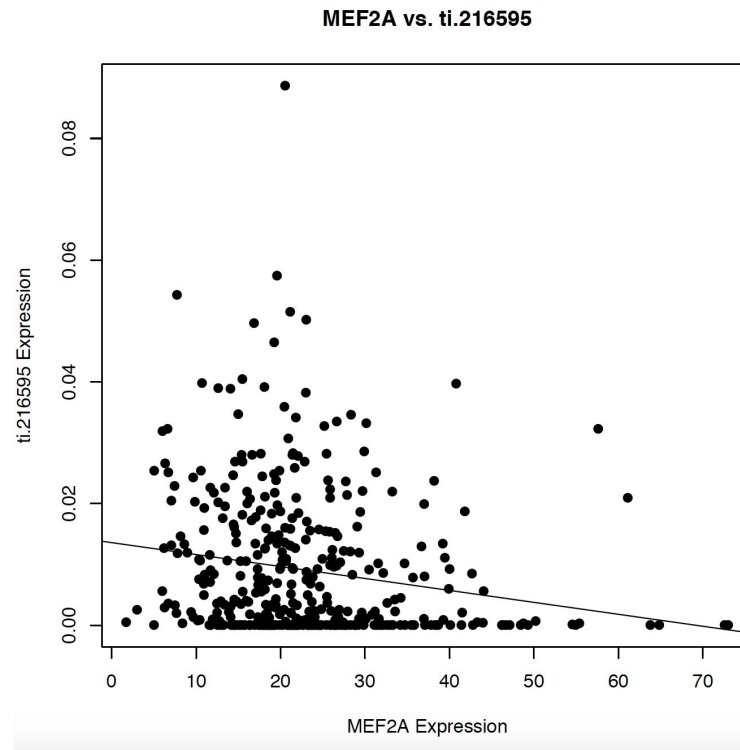
Gene Set Enrichment Analysis

- Investigates which microbes are associated with which pathways



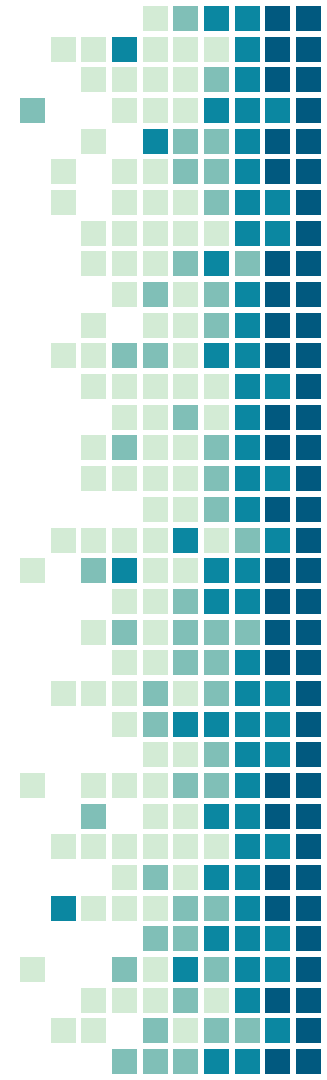
Spearman Correlation

- Elucidate the correlation between the IA genes and microbe expression



Discussion and Future Direction

- Contamination Correction
- In-vitro validation for computational analyses for potential contamination
 - Co-culture with bacterial peptides



Thank you to the URS Eureka! Scholarship and Mr. and Mrs. Lewis for their generous support



THANKS!

Any questions?

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