**Use cases of the Ontology of Host-Microbiome Interactions (OHMI)**

Meeting on: Fri 3/24/2017

Attendees: Jihad Obeid; Alexander Alekseyenko; Jie Zheng; Anna Maria Masci; Haihe Wang, Oliver He

**Use cases:**

* Oliver He and Alex: Ankylosing spondylitis: a form of arthritis and spine. Preliminary studies between arthritis and microbiome. Need to collect patient clinical data and microbiome data: 16S rRNA gene (specific to prokaryotes) – as well as preserved region (ultra-conserved because of rRNA) as well hypervariable (9) regions (v1 through v9) which provide fingerprints of the different taxa.
* Oliver: RNAseq data: overarching use case for analyzing RNAseq for host gene expression and microbiome – microbiome relation to human health, e.g. COPD and smoking and impact of microbiome.
* Alex: oral microbiota evolution over time, anatomical position, interventions.
* Alex: IgA coated bacteria: compare iga coated bacteria to everything else and what is unique about the bacteria for the host
* Alex: paraffin embedded colorectal cancers 16s rRNA genes. Looking at host immune gene expression, looking for specific immune cell types in relation to microbiota, and differences across races. (funded by pilot from COM).

Objective of Group: What does the ontology add?

* Oliver: Host microbiome is very complex, data intensive. Has a pipeline from multi-dimensional big data to small output. Includes clinical and demographic data. To analyse from multiple sources have to harmonize data from multiple sources.
* Oliver: Data sharing (MUSC, duke, Michigan) – each can analyze individually, but how can computer understand different microbiome protocols and analyses. For data integration you need an ontology.
* Anna Maria: Microbiome ontology: interaction between of host and organism depends on which part of host you are looking at. I.e. looking at analysis in context.
* Jie: The interaction part is not covered yet. Need to standardize data from different sources + how to organize the data.
* Oliver: Ontology to represent the knowledge e.g. newborn gut microbiota so terms for interactions to represent common knowledge.

Progress: (basic terms)

* Examined existing ontologies and standards (Oliver)
  + MicrO: published last year (<https://github.com/carrineblank/MicrO/>) Ontology of Prokaryotic Phenotypic and Metabolic Characters.
  + MEOWL: by: Ramona L. Walls: Microbial Environments described using OWL (MEOWL Ontology)
  + Ontology for Microbial Phenotypes (OMP), Deborah A. Siegele, Ph.D., Texas A&M University
* OHMI Statistics: Terms in OHMI: new and imported
* Links: <https://github.com/OHMI-ontology>