Discovering Patterns in Human Microbiome Data (HMD)
March 16-18, 2015

SCHEDULE

Monday March 16th

8:00-8:30   Registration

8:30-8:45   Opening Remarks: **Snehalata Huzurbazar**, University of Wyoming and
                   Paul Brooks, Virginia Commonwealth

8:45-9:15   SAMSI Working Group Summary and Workshop Introduction

9:15-10:15   **Susan Holmes**, Stanford University
                   *"Generalizing PCA to Accommodate for the Multiple Sources of Data and
                   Constraints in the Human Microbiome"*

10:15-10:30   Break

10:30-11:30   **Vanni Bucci**, University of Massachusetts Dartmouth
                    *"Predictive Models of Microbiome Dynamics: Designing Bacterial Cocktails to
                    Ameliorate Enteric Infection and to Stimulate Immune Systems"*

11:30-12:00   Breakout Meeting Discussion

12:00-1:30   Lunch (SAMSI 2nd Floor Lounge)

1:30-3:30   Breakout Research Meetings:
                   Groundtruthing 16S experiments – Room 150
                   Interaction inference in longitudinal data – Room 203
                   Predicting community state type changes – Room 259
                   Sparse multiway data integration – Room 219

3:30-4:00   Breakout Meeting Reports

4:00-5:30   Short Talk Session:
      Giseon Heo, University of Alberta
      "Comparing Clostridium Difficile Infected Patients before and after a Treatment Using Loops in DNA Sequences"

      Michelle Wright, Virginia Commonwealth University
      "Alpha Diversity of the Vaginal Microbiome Clusters within Families: a Twin Study"

      Duncan Wadsworth, Rice University
      "Bayesian Variable Selection for Multinomial-Dirichlet Regression with an Application to Microbiome Data Integration"

      Ekaterina Smirnova, University of Wyoming
      "Vaginal Microbiome: Comparison of Bacterial Vaginosis 16S rRNA Taxa Composition"

5:30-7:30   Poster Session/Reception (SAMSI, 2nd Floor Lounge)
(The board dimensions are 4 ft. wide by 3 ft. high. They are tri-fold with each side being 1 ft. wide and the center 2 ft. wide. Please make sure your poster fits the board. The boards can accommodate up to 16 pages of paper measuring 8.5 inches by 11 inches.)

Tuesday, March 17th

8:45-9:00   Registration and Announcements: **Paul Brooks**, Virginia Commonwealth

8:00-10:00   **Hector Corrada Bravo**, University of Maryland
      "Statistical and Visualization Methods for Metagenomic Analysis**"

10:00-12:00   Breakout Research Meetings
      Predicting community state type changes – Room 150
      Sparse multiway data integration – Room 259
      Additional groups – Room 219

12:00-1:30   Lunch (SAMSI 2nd Floor Lounge)

1:30-2:00   Breakout Meeting Reports

2:00-3:00   **Shanaka Wijesinghe**, Virginia Commonwealth

3:00-3:30   Break

3:30-5:00   Short Talk Session:
                   Brandie D. Wagner, University of Colorado
                   "Analysis of Longitudinal Microbiota Data"

                   Gholamali Rahnavard, Harvard School of Public Health
                   *"High-Sensitivity Pattern Discovery in High-Dimensional Heterogeneous
                   Datasets"*

                   Ayshwarya Subramanian, Harvard School of Public Health
                   *"Multivariate Association of Microbial Communities with Rich Metadata in
                   High-Dimensional Studies"*

Wednesday, March 18th

8:45-9:00   Registration and Announcements: **Paul Brooks**, Virginia Commonwealth

9:00-10:00   **Bill Shannon**, Washington University in St. Louis
                   *"Microbiome Power/Sample Size Calculations (plus a bit of formal hypothesis
                   testing)"*

10:00-12:00   Breakout Research Meetings
                   Interaction inference in longitudinal data – Room 150
                   Analyzing human microbiome data – Room 259
                   Additional groups – Room 219

12:00-1:00   Breakout Meeting Reports and Discussion

1:00   Adjourn and Box Lunch