Microbiome Measurements Workshop:
Breakout Sessions Aug.10, 2016

Details: Breakout 1

- Schedule:
    - Randomly sit 6-8 to a table
    - 18 min: Pick a note taker, discuss two questions (5 min & 2 min warnings)
    - 5 min: All but note taker move to a differently-colored table
    - 18 min: pick a note taker, discuss two questions (5 min & 2min warnings)
    - 19 min: report from each table (≈2min/table)

Reference Materials & Mock Communities

- Heritage Room
- SME: Emma Allen-Vercoe and Russ Carmical
- Moderator: Ryan Ranallo
- Note taker: Jason Kralj
- Email: NISTMicrobiome_BreakOut1@nist.gov
- **Phone: 877-972-3591**
    - **Participant: 564046582612**
- Red Questions:
    - How can mock communities improve microbiome measurements? How should they be used?
    - What microbiome reference materials currently exist? How do current options fall short?
- Blue Questions:
    - How would you build an ideal microbiome reference material?
    - Can there be a one-size-fits-all? Or how similar does a mock community need to be to the ecosystem of interest?

Bioinformatics & Analysis Pipelines

- Portrait Room
- SME: Curtis Huttenhower and Pat Schloss
- Moderator: Samantha Maragh
- Note taker: Nate Olson
- Email: NISTMicrobiome_BreakOut2@nist.gov
- **Phone: 877-934-4815**
    - **Participant: 564046582613**
- Red Questions:
    - How does pre-analytical processing of raw data (e.g., quality filtering, trimming, merging, chimera identification) impact OTU calling?
    - Reference Databases like Greengenes, etc. How can database curation be improved/accelerated?

- Blue Questions:
    - How do we assess sensitivity and specificity of bioinformatic pipelines. How are biases identified?
    - What kind of data reporting standards might be used to assess bioinformatic reproducibility

DNA Extraction

- West Square
- SME: Scott Tighe
- Moderator: Sam Forry
- Note taker: Nancy Lin
- Email: NISTMicrobiome_BreakOut3@nist.gov
- **Phone: 877-956-9484**
    - **Participant: 564046582614**
- Red Questions:
    - What are the best metrics for comparing/evaluating extraction kits and protocols?
    - How does extraction performance depend on sample type?
- Blue Questions:
    - What factors contribute measurement uncertainty to and limit comparability between extraction methods?
    - How can results acquired using different extraction protocols be compared?

Microbiome sampling and sample handling

- Green Auditorium (Note: potential swap)
- SME: Joel Dore and Jacques Ravel
- Moderator: Scott Jackson
- Note taker: Sandra Da Silva
- Email: NISTMicrobiome_BreakOut4@nist.gov
- **Phone: 866-717-9051**
    - **Participant: 564046582615**
- Red Questions:
    - What are the best metrics for comparing/evaluating sampling protocols?
    - How would a “standard” sample collection protocol be developed?
- Blue Questions:
    - What are the best procedures for sampling low-biomass microbiomes?
    - How can results acquired under different sample handling protocols be compared?

Details: Breakout 2

- Schedule:
    - Go to assigned room/table (LR B replaced by Heritage)
    - 18 min: Pick a note taker, discuss two questions (5 min & 2 min warnings)
    - 5 min: All but note taker move to a differently-colored table
    - 18 min: pick a note taker, discuss two questions (5 min & 2min warnings)
    - 19 min: report from each table (≈2min/table)

Heritage Room

- Moderator: Ryan Ranallo
- Note taker: Jason Kralj
- Email: NISTMicrobiome_BreakOut1@nist.gov
- **Phone: 877-972-3591**
    - **Participant: 564046582612**
- Red Questions:
    - How can we integrate/compare 16s data with metagenomic data?
    - What improvements to current technologies are needed to improve microbiome measurements
- Blue Questions:
    - How can the field move from correlations and relative measurements toward absolute quantitation?
    - What minimum reporting requirements would improve confidence in and comparability of microbiome measurement results?

Portrait Room

- Moderator: Samantha Maragh
- Note taker: Nate Olson
- Email: NISTMicrobiome_BreakOut2@nist.gov
- **Phone: 877-934-4815**
    - **Participant: 564046582613**
- Red Questions:
    - How can we integrate/compare 16s data with metagenomic data?
    - What improvements to current technologies are needed to improve microbiome measurements?
- Blue Questions:
    - How can the field move from correlations and relative measurements toward absolute quantitation?
    - What minimum reporting requirements would improve confidence in and comparability of microbiome measurement results?

West Square

- Moderator: Sam Forry
- Note taker: Nancy Lin
- Email: NISTMicrobiome_BreakOut3@nist.gov
- **Phone: 877-956-9484**
    - **Participant: 564046582614**
- Red Questions:
    - How can we integrate/compare 16s data with metagenomic data?
    - What improvements to current technologies are needed to improve microbiome measurements
- Blue Questions:
    - How can the field move from correlations and relative measurements toward absolute quantitation?
    - Which step in the microbiome measurement process contributes the greatest variability?