
Details: Breakout 1
- Schedule:
  o Randomly sit 6-8 to a table
  o 18 min: Pick a note taker, discuss two questions (5 min & 2 min warnings)
  o 5 min: All but note taker move to a differently-colored table
  o 18 min: pick a note taker, discuss two questions (5 min & 2 min warnings)
  o 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
  o Participant: 564046582612
- Red Questions:
  o How can mock communities improve microbiome measurements? How should they be used?
  o What microbiome reference materials currently exist? How do current options fall short?
- Blue Questions:
  o How would you build an ideal microbiome reference material?
  o 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
  o Participant: 564046582613
- Red Questions:
  o How does pre-analytical processing of raw data (e.g., quality filtering, trimming, merging, chimera identification) impact OTU calling?
  o Reference Databases like Greengenes, etc. How can database curation be improved/accelerated?
• Blue Questions:
  o How do we assess sensitivity and specificity of bioinformatic pipelines. How are biases identified?
  o 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:
  o What are the best metrics for comparing/evaluating extraction kits and protocols?
  o How does extraction performance depend on sample type?
- Blue Questions:
  o What factors contribute measurement uncertainty to and limit comparability between extraction methods?
  o 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:
  o What are the best metrics for comparing/evaluating sampling protocols?
  o How would a “standard” sample collection protocol be developed?
- Blue Questions:
  o What are the best procedures for sampling low-biomass microbiomes?
  o 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?