Friday, October 25, 2019

NIH Project Design

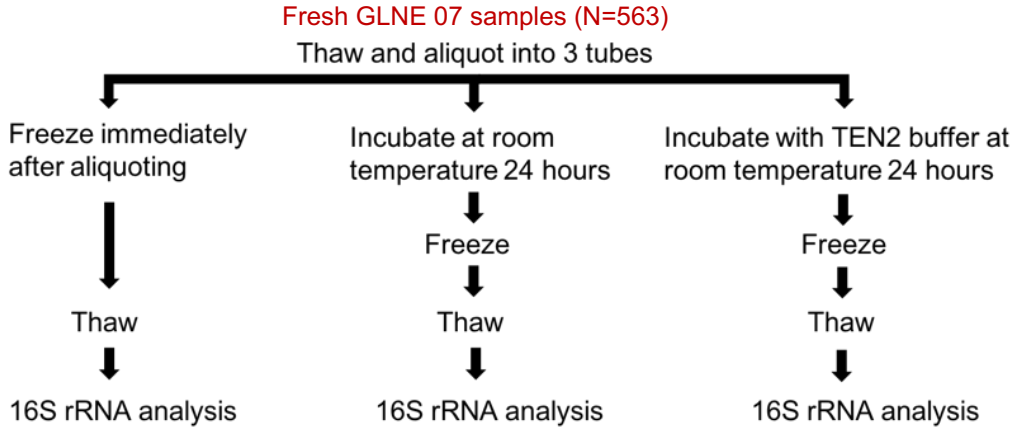
Test the biases in the microbial community due to the stool preservation buffer and incubation time at different temperatures during the transit of the sample.

- We will test this using a fresh copy of GLNE007. We have 563 GLNE007 samples. This experiment will use the full set.

1. Native stool samples:

- Thaw the samples.
- Upon thaw, an aliquot will be DNA extracted. This is our T0 community(1).
- Another aliquot will be mixed with preservation buffer using a pre-defined distribution and protocol. This will be incubated at room temp in an icebox for 24 (the appendices Pat sent me show that slurry is not stored in an icepack) and then DNA extracted. This is our Tf wet community.
- Another aliquot will be incubated at room temp in an icebox for 24h and then DNA extracted. This is our Tf dry community.
- We will compare different conditions to one another
- **(The incubations experiments are done for native samples)**

Approach



Each sequencing run has similar distribution of diagnosis, gender and sample treatment.

2. FIT samples:

- Another aliquot will be used to make 4 FIT technical replicates to be tested as shown in diagram.
- We need to decide on time and temperature conditions.