16S ribosomal RNA (rRNA) sequencing is a common amplicon sequencing method used to identify and compare bacteria present within a given sample. Next-generation sequencing enables analysis of the entire microbial community within a sample. With the ability to combine many samples in a sequencing run, researchers can use NGS-based 16S rRNA sequencing as a cost-effective technique to identify strains that may not be found using other methods.

- In collaboration with the Duke Center for Genomics of Microbial Systems (GEMS), we are providing experimental design, processing and analysis consultation

- Sample preparation from:
  - Fecal swabs or 0.1 gram of solid fecal material in 1.5 or 2ml tube
  - Watery stool samples of 750 ul in 1.5 or 2ml tube
  - Soil samples of 0.3 grams in 1.5 ml tube
  - Swabs of other sample types in 1.5 or 2ml tube

- DNA extraction, library preparation and Illumina sequencing

- Data Analysis is provided through the GEMS Bioinformatics Group

- Pricing:
  - $40 for DNA extraction and generation of library per sample
  - $1265 MiSeq 150bp PE V2 Sequencing
  - $92 data storage up to 1TB per year