Data Collection	iMAP: Integrated Microbiome Data Analysis Pipeline			
Sampling & DNA Sequencing	**Gathering materials & Profiling metadata**	**Pre-processing & Quality control**	**Sequence processing & Taxonomic classification: mothur-based*** **Alternative method also available*	**OTU clustering, Taxonomy assignment & Preliminary analysis (mothur-based)**

Demultiplexed reads

DNA sequencing

Library Preparation

DNA Extraction

Sampling & Recording

Gather required materials
- Clone iMAP repository
- Add demultiplexed reads (fq.gz)
- Add sample metadata
- Add mapping files
- Install docker
- Pull dependencies installation images

Explore the metadata
- Inspect uniformity of sample identifiers
- Review experimental variables
- Review missing data

Read inspection
- Review per sample read depth
- Review read length

Quality control of raw reads
- Review base-call quality
- Trim and filter poor reads
- Remove retained phiX reads

Merge forward & reverse Reads
- Review, screen and filter by sequence length
- Pick representative sequences

Align to reference 16S rRNA gene alignment
- Review, screen & filter by sequence length
- Remove poor alignments & chimeras

Classify sequences with reference taxonomy classifiers
- Remove non-bacterial
- Estimate error rate
- Remove mock sequences

Cluster OTUs & assign conserved taxonomy
- Phylotypes approach
- OTU clusters approach
- Phylogeny approach

Preliminary analysis
- OTU abundance
- Alpha diversity
- Beta diversity

Phylogenetic annotation
- Upload trees to iTOL viewer
- Prepare annotation files
- Add annotation files to the tree
- Manage trees interactively
- Export annotated tree

Sample metadata	**Progress Report 1** Metadata profiling	**Progress Report 2** Pre-processing	**Progress Report 3** Sequence-processing	**Progress Report 4** Preliminary analysis
Field & Wet Lab	**Review-As-You-Go (RAYG): Progress Reports Summarizing Bioinformatics Analysis and Exploratory Visualization**			