

Run CLOVR-Microbe

1. Upload data

1. On Data Sets tab: Add
2. Paste URL: <http://cb2.igs.umaryland.edu/microbe.tgz>
3. File Type: "Nucleotide FASTQ"
4. Name: e.g. "illumina_test"

Run CLOVR-Microbe

2. Configure Pipeline

1. Select from applications panel: **microbe**
2. **Select Sequencing Dataset(s)** : "illumina_test"
3. **Select a CLOVR Microbe Track:**
"Assembly+Annotation"
4. **Output prefix:** e.g. "nmen"
5. **Organism:** e.g. "Neisseria meningitidis"
7. **Database Name:** e.g. "nmen"
8. **Manatee Username:** e.g. "asmquest"
9. **Manatee Password:** e.g. "stiontio65"
10. **Pipeline Description:** e.g. "asm_microbe"
11. **Submit**