

FORAGer tutorial

FORAGer example

Set up

FORAGer_mapper.pl needs the following files & directories to begin:

- A 'query_list' file; tab-delimited; 3 columns:
 - query_organism_name
 - query_forward_read_file (or all reads file)
 - query_reverse_read_file (or blank)
- A 'subject_list' file; tab-delimited; 2 columns:
 - subject_FIG_ID
 - subject_fasta

The query list associates the query organism with the reads used for mapping and also tells FORAGer where to find the read files.

The subject list associates the subject organism FIG (needed for ITEP) with its genome sequence file.

example of a query_list file

```
Methanosarcina_mazei_S6 Msar_mazei_S6_2m_F.fq Msar_mazei_S6_2m_R.fq

Methanosarcina_mazei_SarPi Msar_mazei_SarPi_2m_F.fq Msar_mazei_SarPi_2m_R.fq

Methanosarcina_mazei_WWM610 Msar_mazei_WWM610_2m_F.fq
Msar_mazei_WWM610_2m_R.fq

Methanosarcina_mazei_LYC Msar_mazei_LYC_2m_F.fq Msar_mazei_LYC_2m_R.fq
```

example of a subject_list file

```
2209.24 Methanosarcina_mazei_C16.fna

2209.27 Methanosarcina_mazei_LYC.fna
```

213585.6 Methanosarcina_mazei_S_6.fna

2209.22 Methanosarcina_mazei_SarPi.fna

2209.25 Methanosarcina_mazei_WWM610.fna

192952.1 Methanosarcina_mazei_Go1.fna

Mapping reads

Example files for this exercise:

- qulist