

mcorr example data for <https://github.com/kussell-lab/mcorr>

The example contains two data sets from the *H. pylori* transformation experiment (20 strains, 1532 genes):

- Whole-genome alignment:

```
mcorr-xmfa TC1_genome.xmfa TC1_genome
```

```
python3 $HOME/go/src/github.com/kussell-lab/mcorr/cmd/fitting/FitP.py  
TC1_genome.csv TC1_genome --fit_bootstrap
```

- Read alignment:

```
mcorr-bam NC_018939.gff TC1_read.bam TC1_read
```

```
python3 $HOME/go/src/github.com/kussell-lab/mcorr/cmd/fitting/FitP.py  
TC1_read.csv TC1_read --fit_bootstrap
```

On a normal desktop computer, running the two data sets took about 10 min.