

Ex. 6 Recap

Q1: What is the Sequence Type of our *S. aureus* isolate?

Answer: ST243

Q2: Are any of the identified MLST alleles less than perfect matches to the MLST allele in the MLST database (for a perfect match, the %ID is 100 and the length of the alignment (HSP) equals the length of the database allele)?

Answer: No, they are all perfect matches

```
Sequence Type: ST243
MLST Scheme: saureus
*****
  GENE          % IDENTITY   HSP Length   Allele Length   GAPS   BEST MATCH
*****
  ARCC          100.00         456          456             0      ARCC_2
  AROE          100.00         456          456             0      AROE_2
  GLPF          100.00         465          465             0      GLPF_5
  GMK           100.00         417          417             0      GMK_2
  PTA           100.00         474          474             0      PTA_6
  TPI           100.00         402          402             0      TPI_3
  YQIL          100.00         516          516             0      YQIL_2
=====
```

Q3: What is the sequence type of the draft assembly generated on the basis of the untrimmed reads. Was this to be expected?

Answer: Also ST243 and all perfect matches. N50 for the draft assembly made on the basis of the untrimmed reads was only 19.000, but apparently no problem.

Q4: What would you write as MLST scheme (instead of “saureus”) in the above commands, if your draft genome was an *E. coli*?

Answer: *ecoli* or *ecoli_2* (*ecoli* = Achtman scheme, *ecoli_2* = Pasteur scheme)

