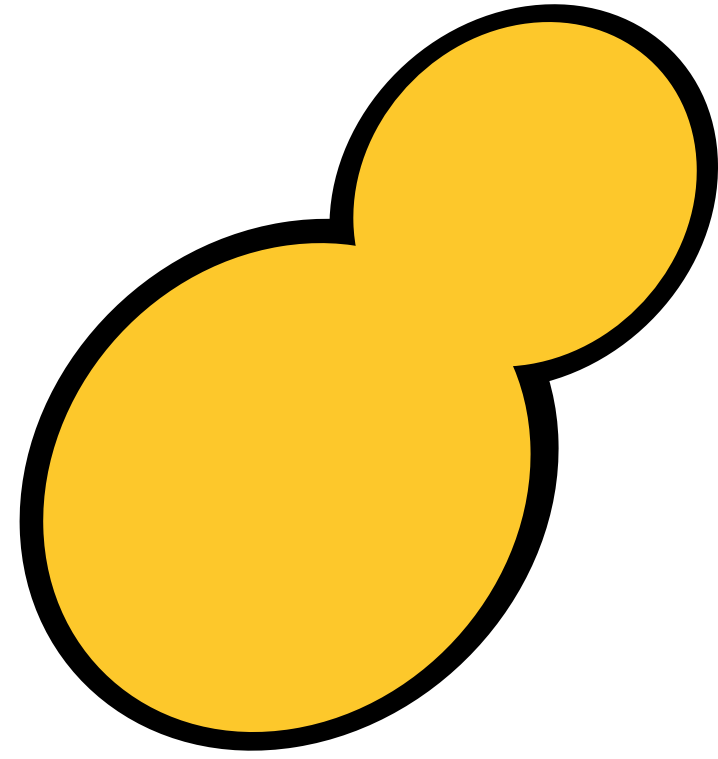


Yeast from the brewmaster

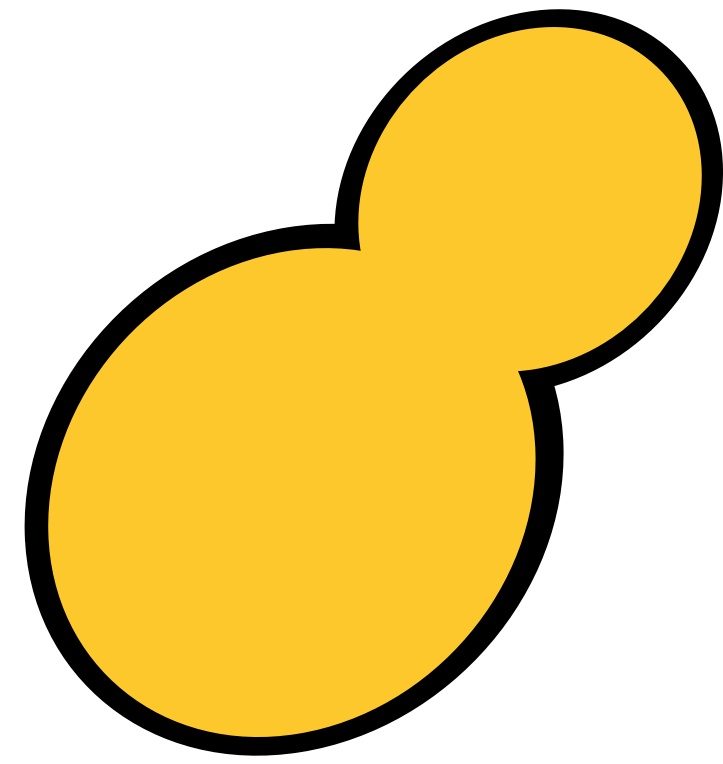


Steps taken before practical



???

Steps taken before practical

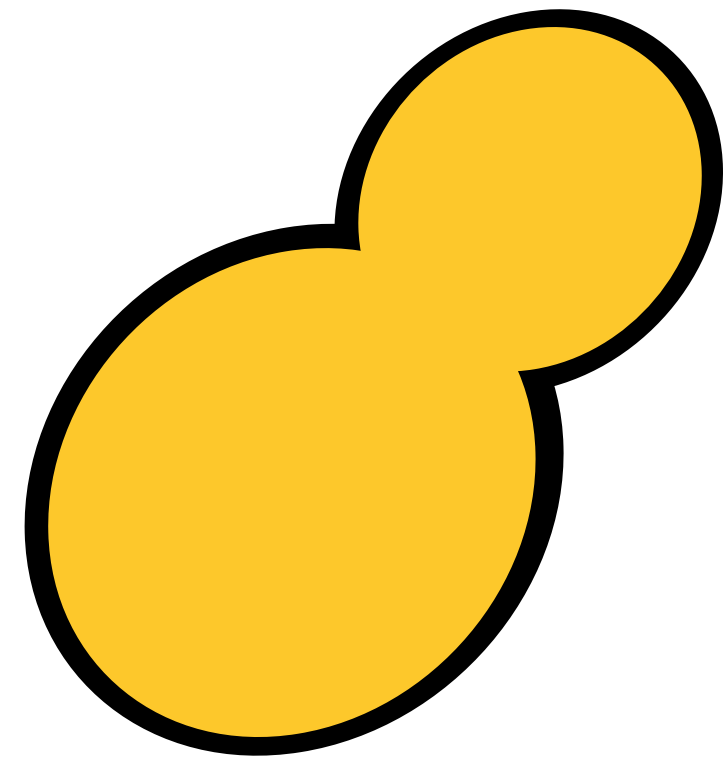


???

Sequence
Genome
→



Steps taken before practical



???

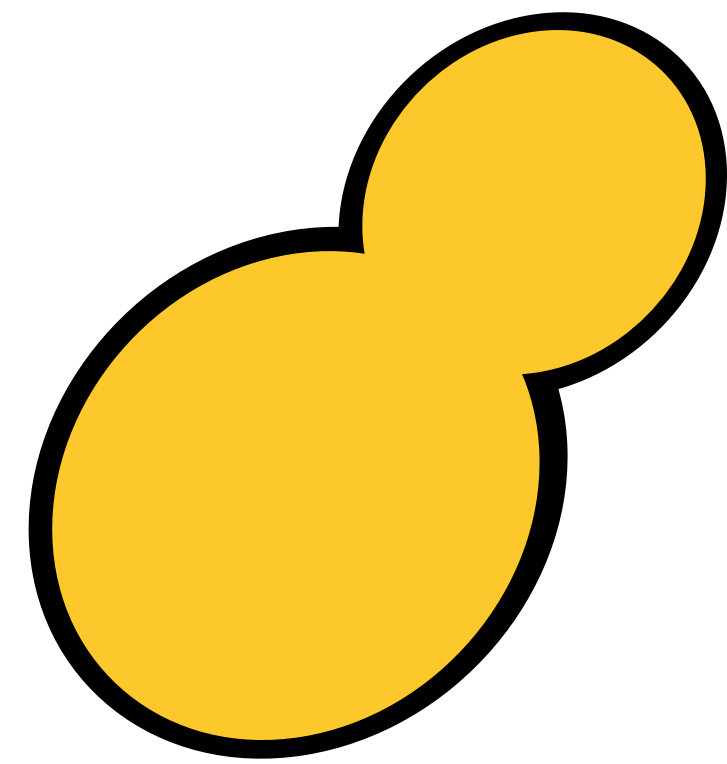
Sequence
Genome



Add other
yeast
genomes



Steps taken before practical



???

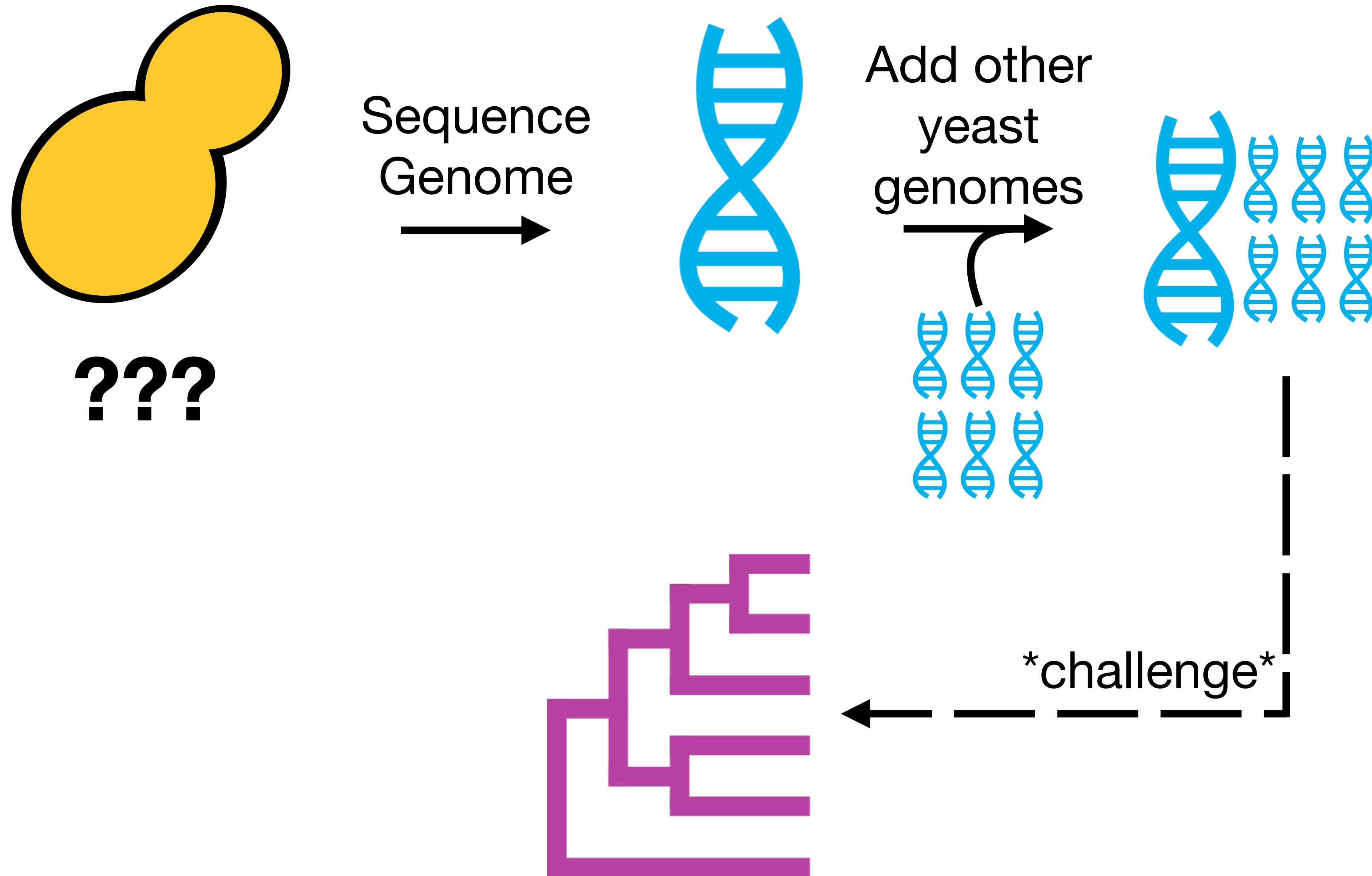
Sequence
Genome
→



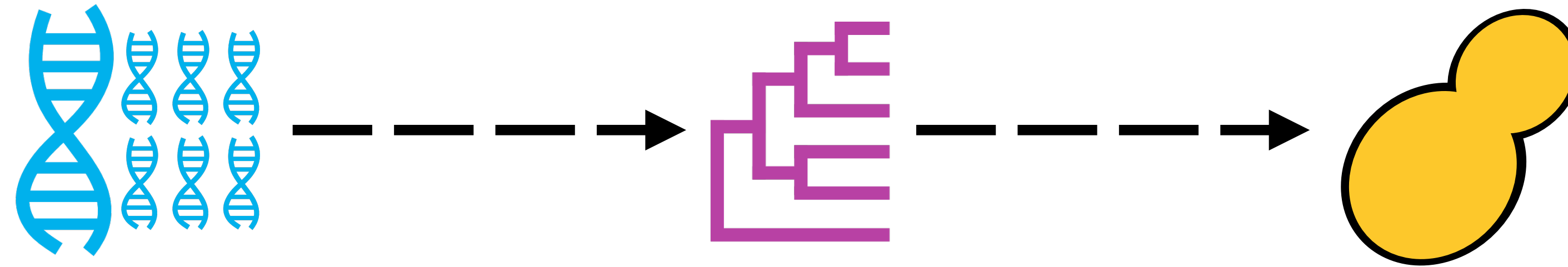
Add other
yeast
genomes
→



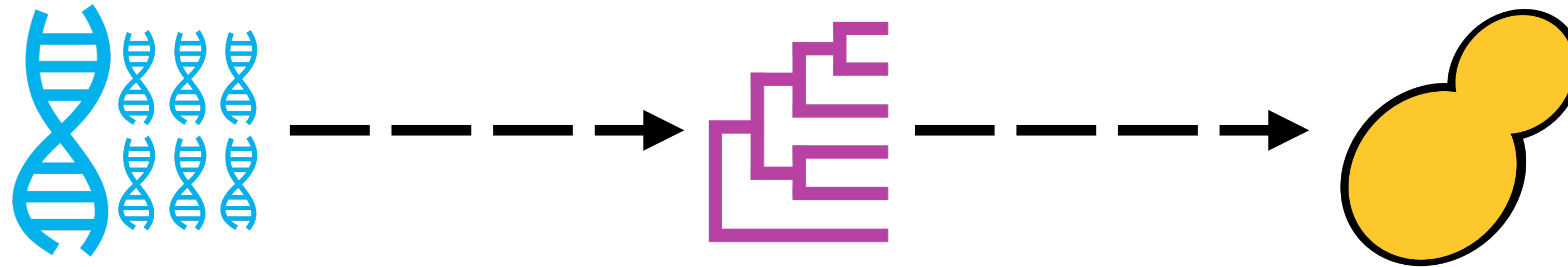
Steps taken before practical



Challenge



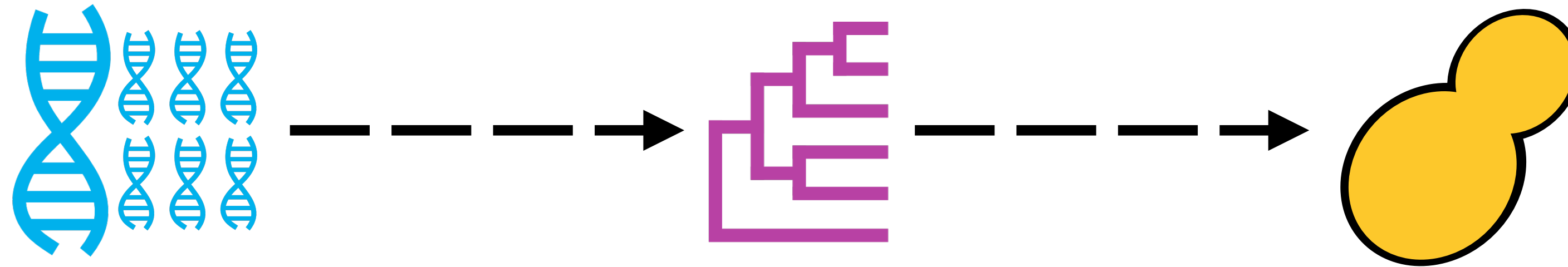
Challenge



- Using a reduced set of protein sequences in `FILES_Wed_challenge_fastas.tar.gz` to determine what the yeast is
- 1) Call orthologs
 - 2) Align and trim orthologs
 - 3) Concatenate sequences
 - 4) Infer putative species tree

Hint: outgroup taxa are
Starmerella apicola
Starmerella bombicola
Wickerhamiella versatilis

Challenge



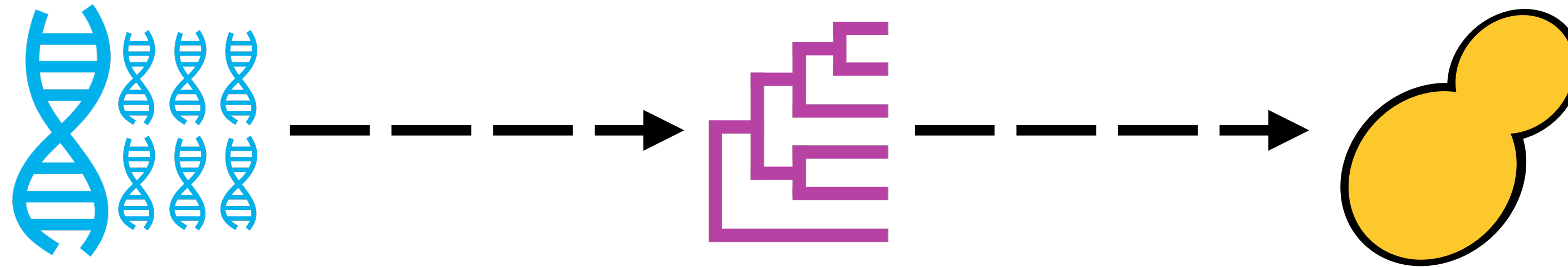
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Hint: You can extract a FASTA entry from a multi-FASTA file using samtools faidx function with the format:

```
Samtools faidx fasta.file fasta.entry
```

e.g. if I want to extract gene *Brewery_genome_1* from multi-FASTA file *Brewery_genome.fa* I would execute the command,

```
samtools faidx Brewery_genome.fa  
Brewery_genome_1
```

Yeast from the brewmaster

