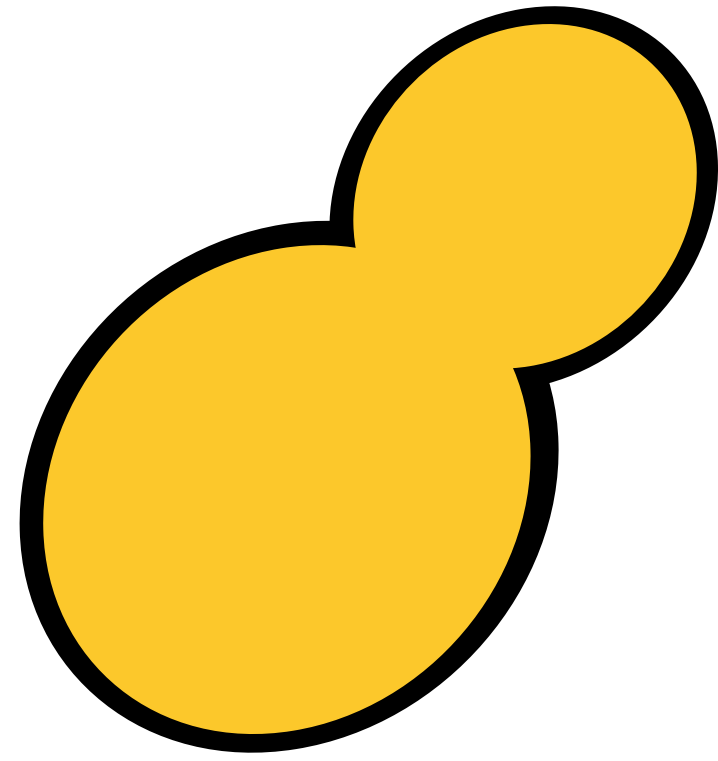


Yeast from the brewmaster

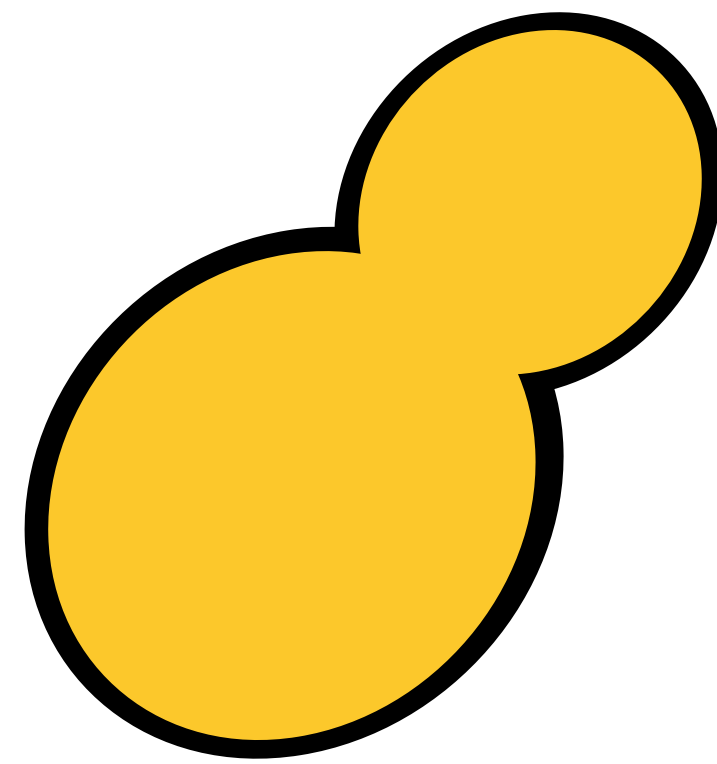


Steps taken before practical



???

Steps taken before practical

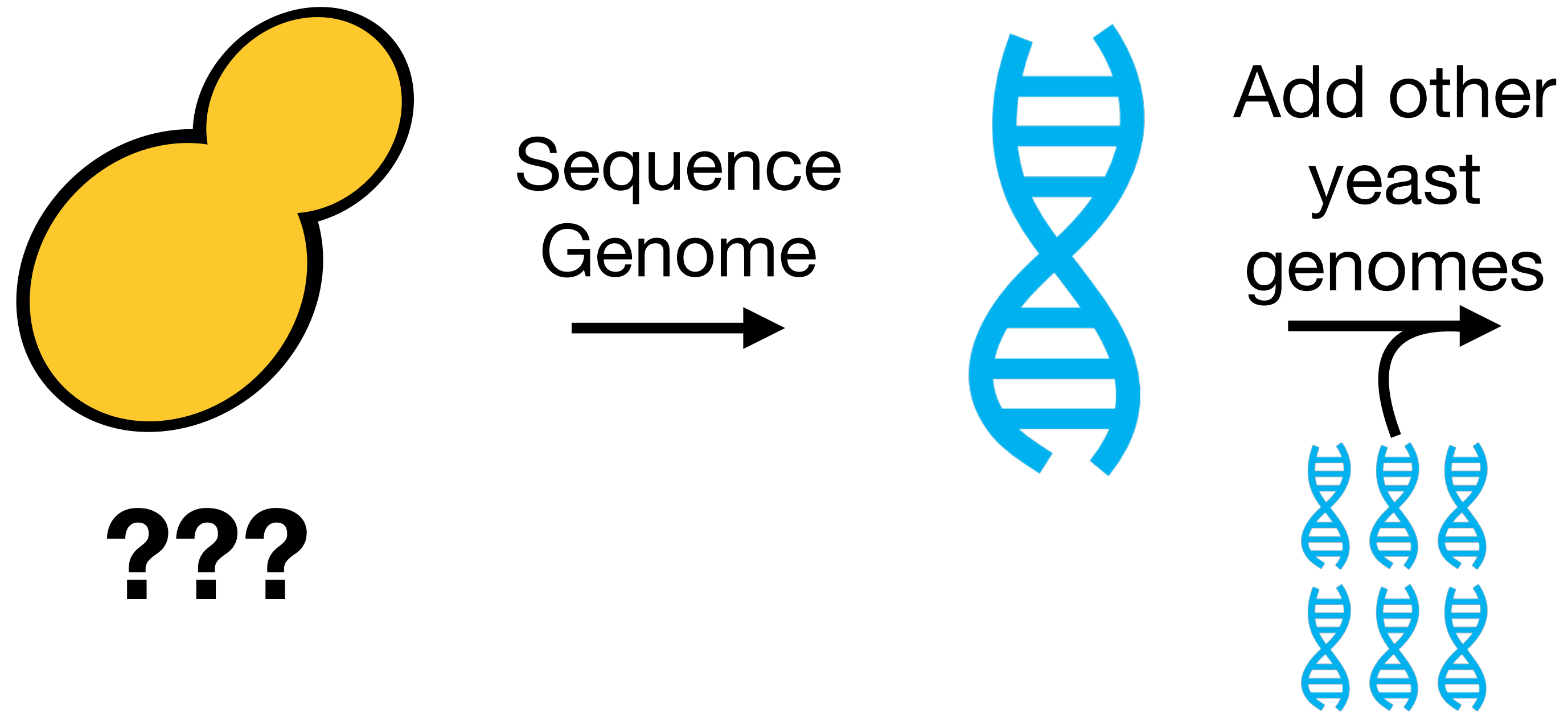


???

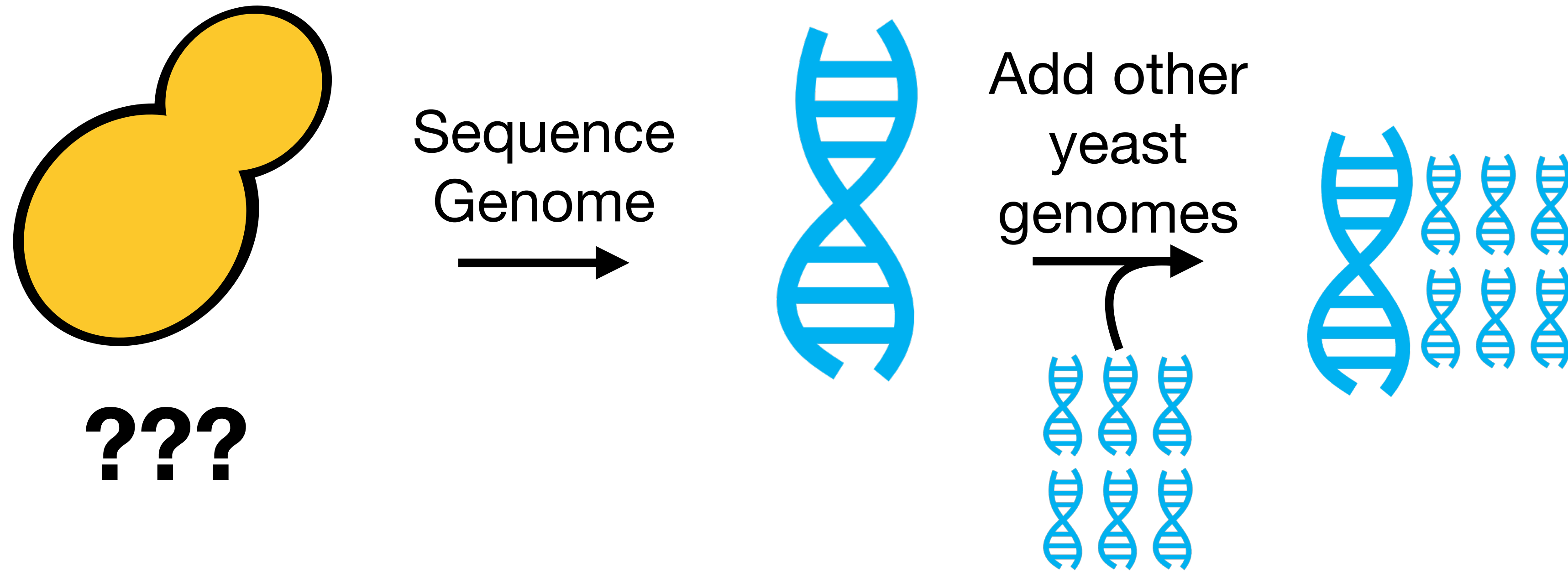
Sequence
Genome
→



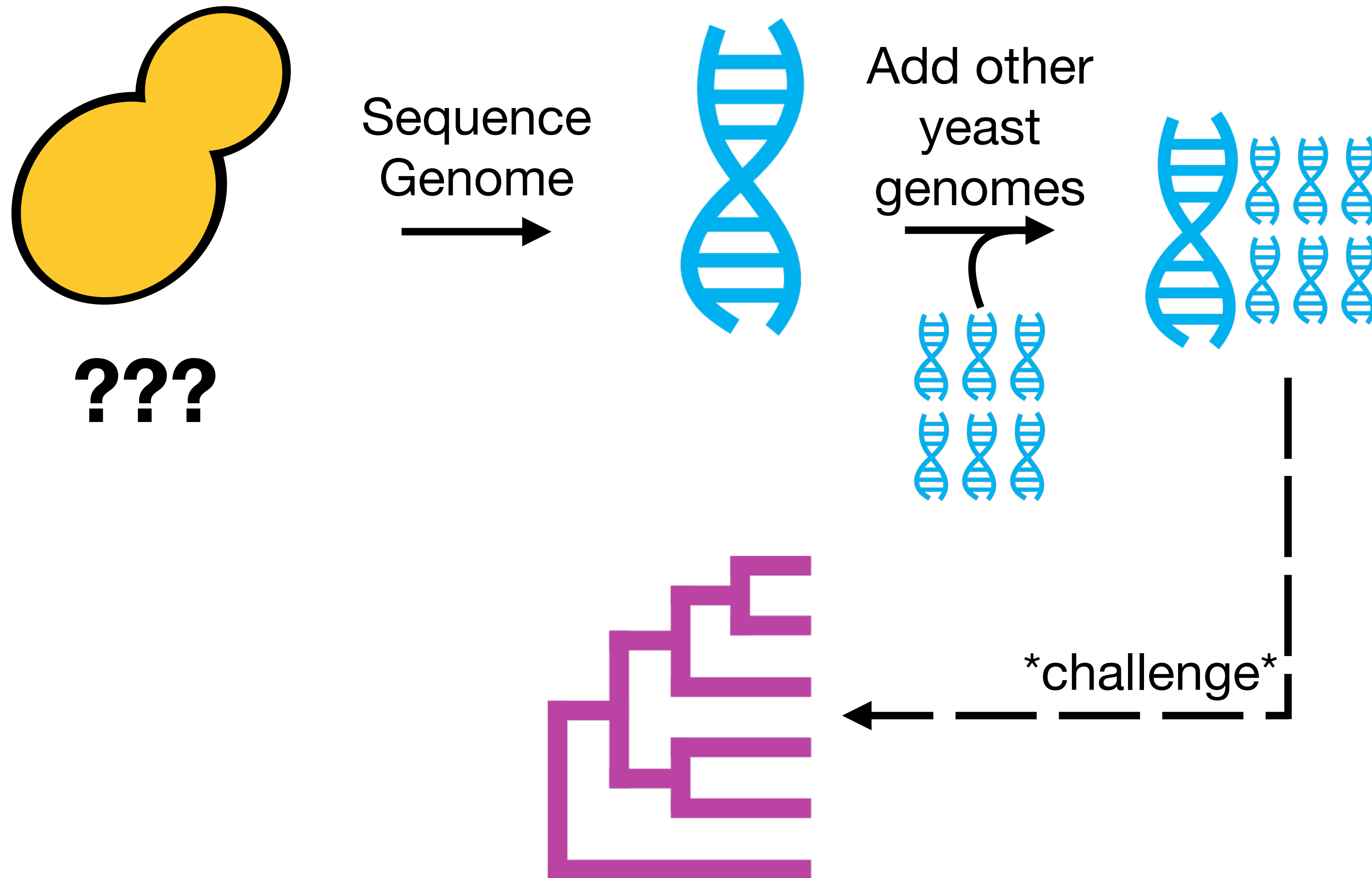
Steps taken before practical



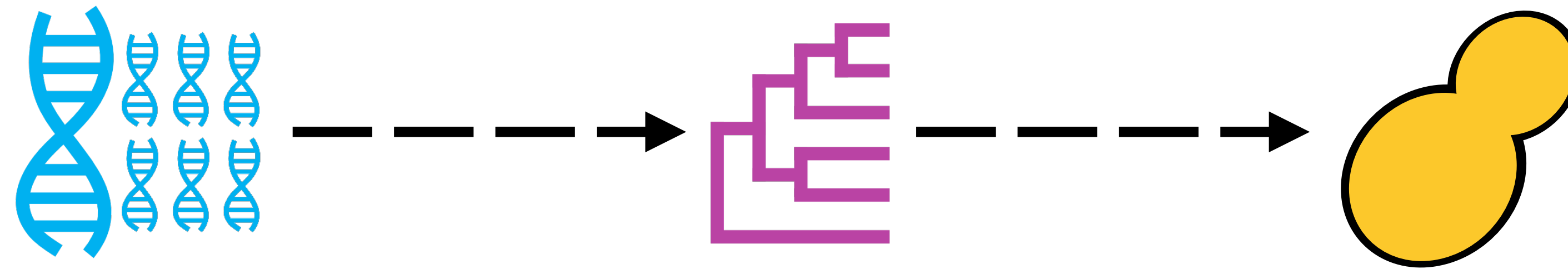
Steps taken before practical



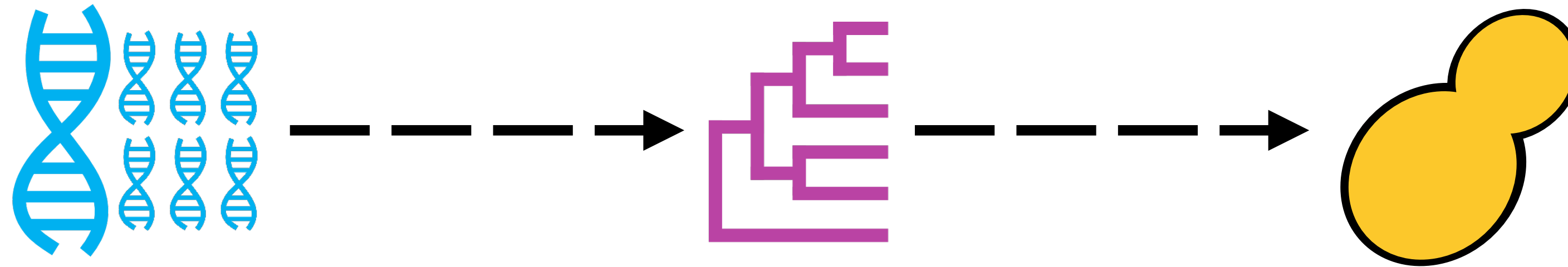
Steps taken before practical



Challenge



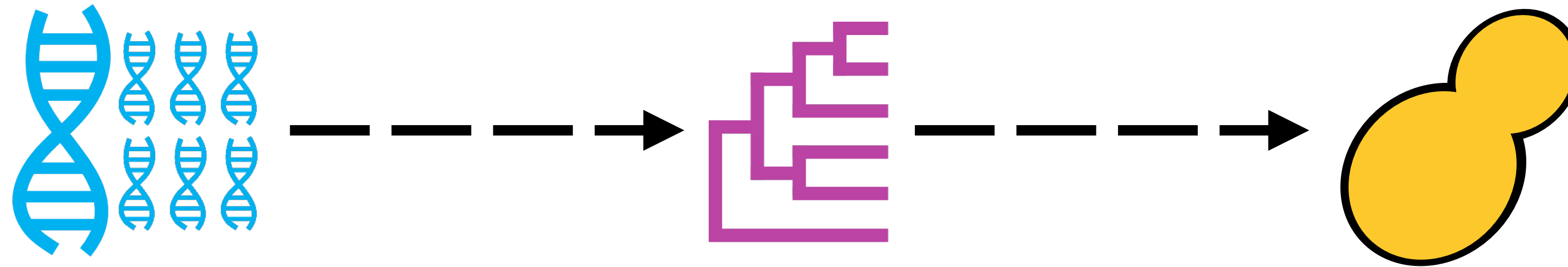
Challenge



- 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

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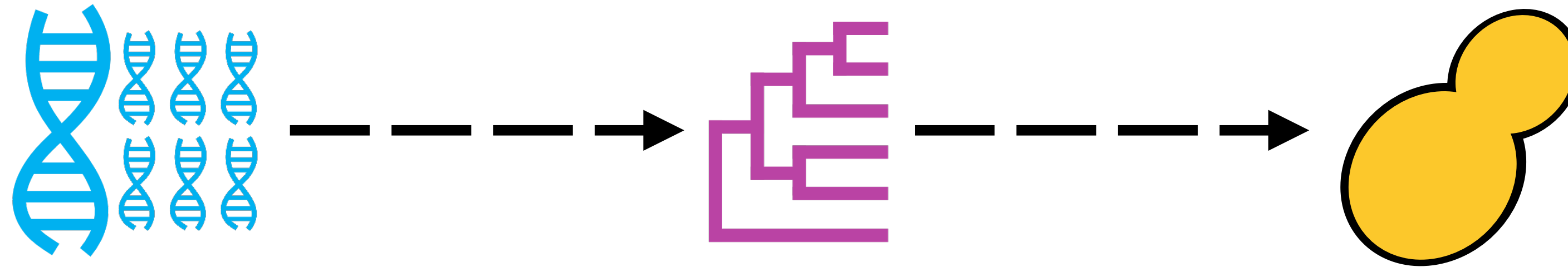
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Hint: You can extract a FASTA entry from a multi-FASTA file using samtools faidx function with the format:

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

