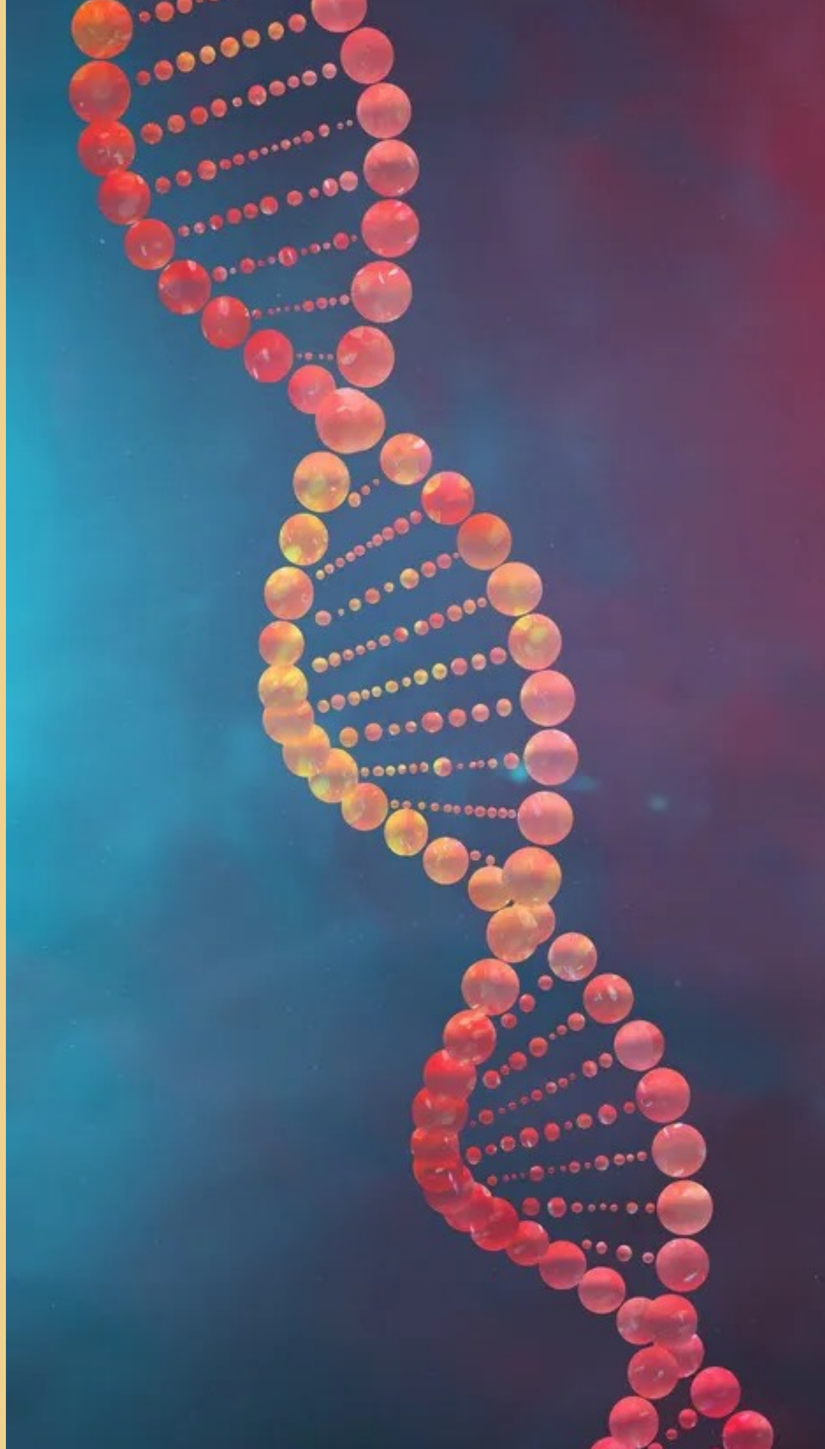
DAWG Workshop 3

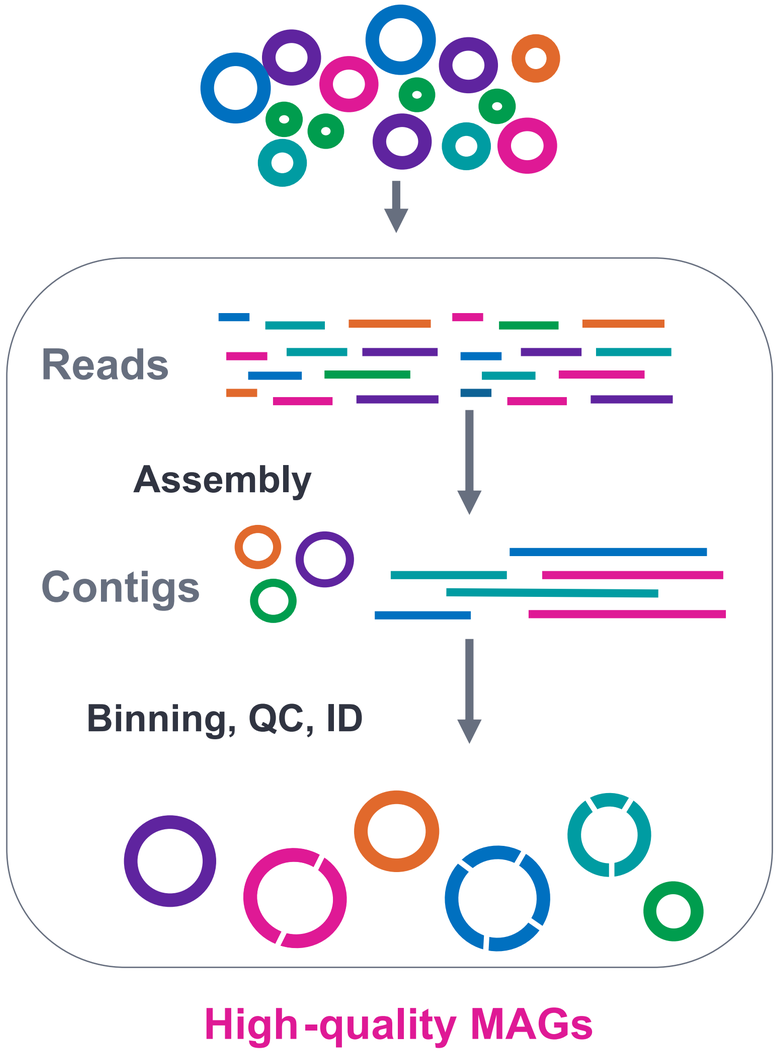
Metagenomic Sequencing
Tree of Life Workshop Series

Dec 5th, 2025



Workshop Pipeline

- QUALITY CONTROL (QC)
- ASSEMBLY
- MAPPING & COVERAGE
- BINNING
- QUALITY ASSESSMENT
- ANNOTATION & VISUALIZATION



QC

FastP

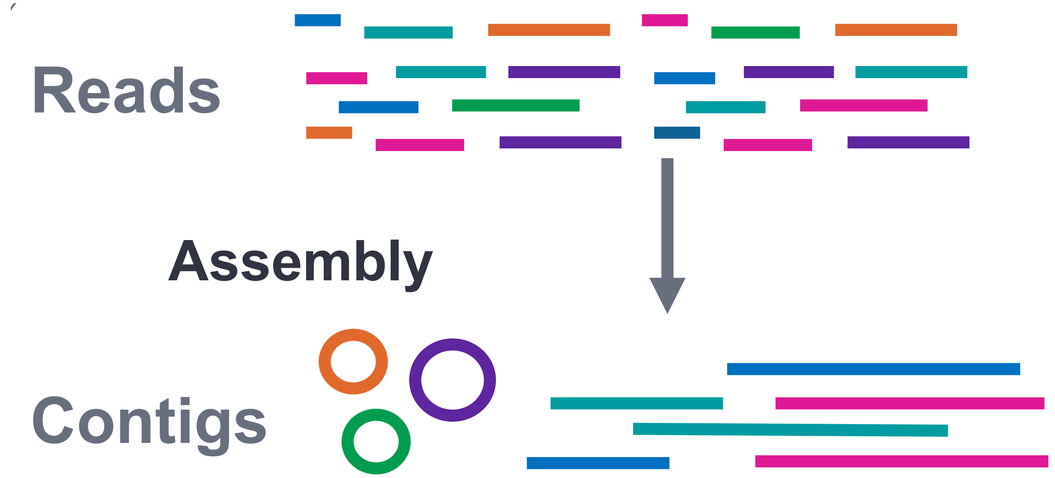
- Used for read trimming and quality control
- Removes adapter sequences
- Trims low-quality bases
- Removes reads that are too short

ASSEMBLY

MEGAHIT

INPUT: Raw reads (FastQ files)

OUTPUT: Assembled contigs (Fasta file)



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MEGAHIT

INPUT: Raw reads (FastQ files)

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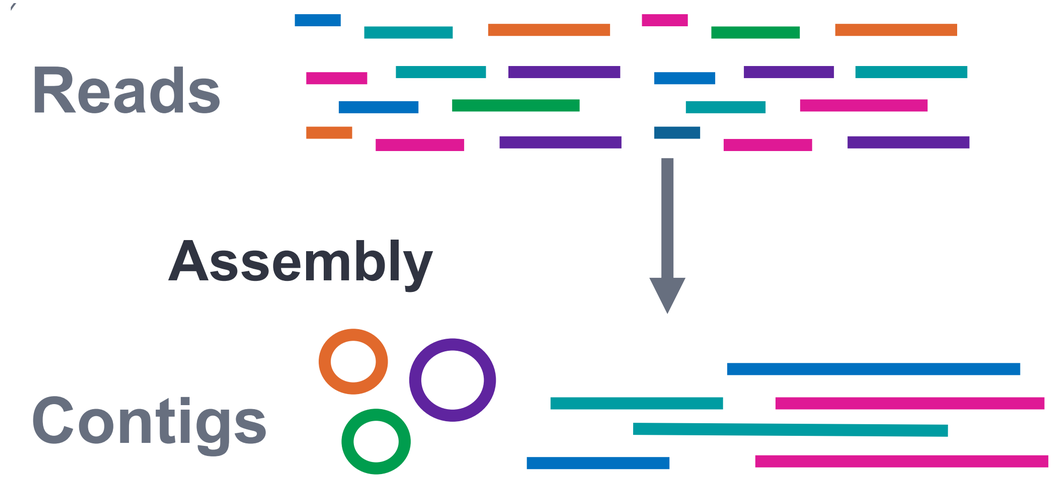
Longer contiguous sequences



MAPPING

Bowtie2

INPUT: Raw reads (FastQ files) & Assembled contigs (Fasta files)

OUTPUT: Aligned reads (BAM file) and a subsequent depth/ coverage file

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SAM file

convert to binary version using SAMTOOLS

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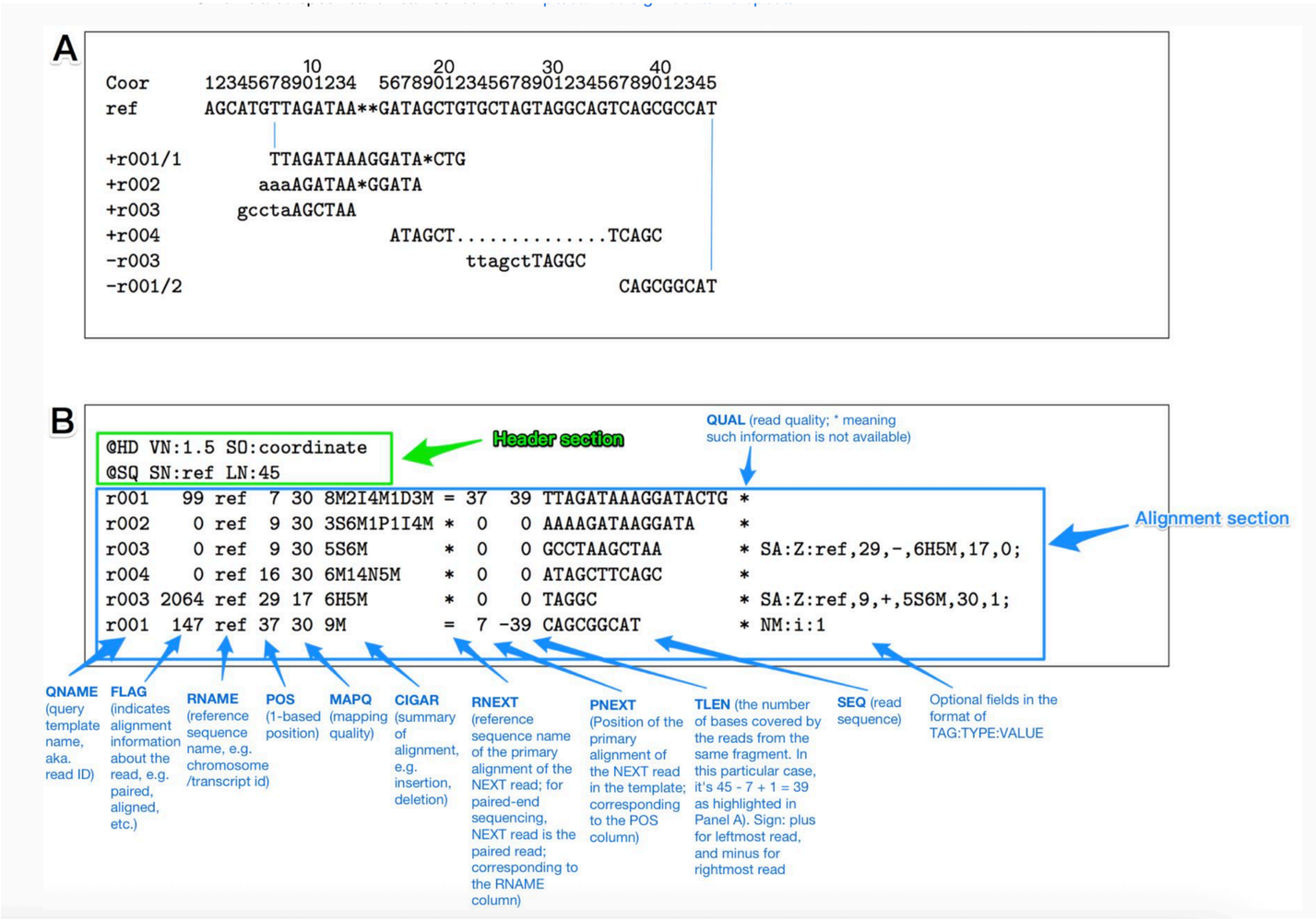

COVERAGE

jgi_summarize_bam_contig_depths

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Script used to calculate the depth of each contig across multiple BAM files.

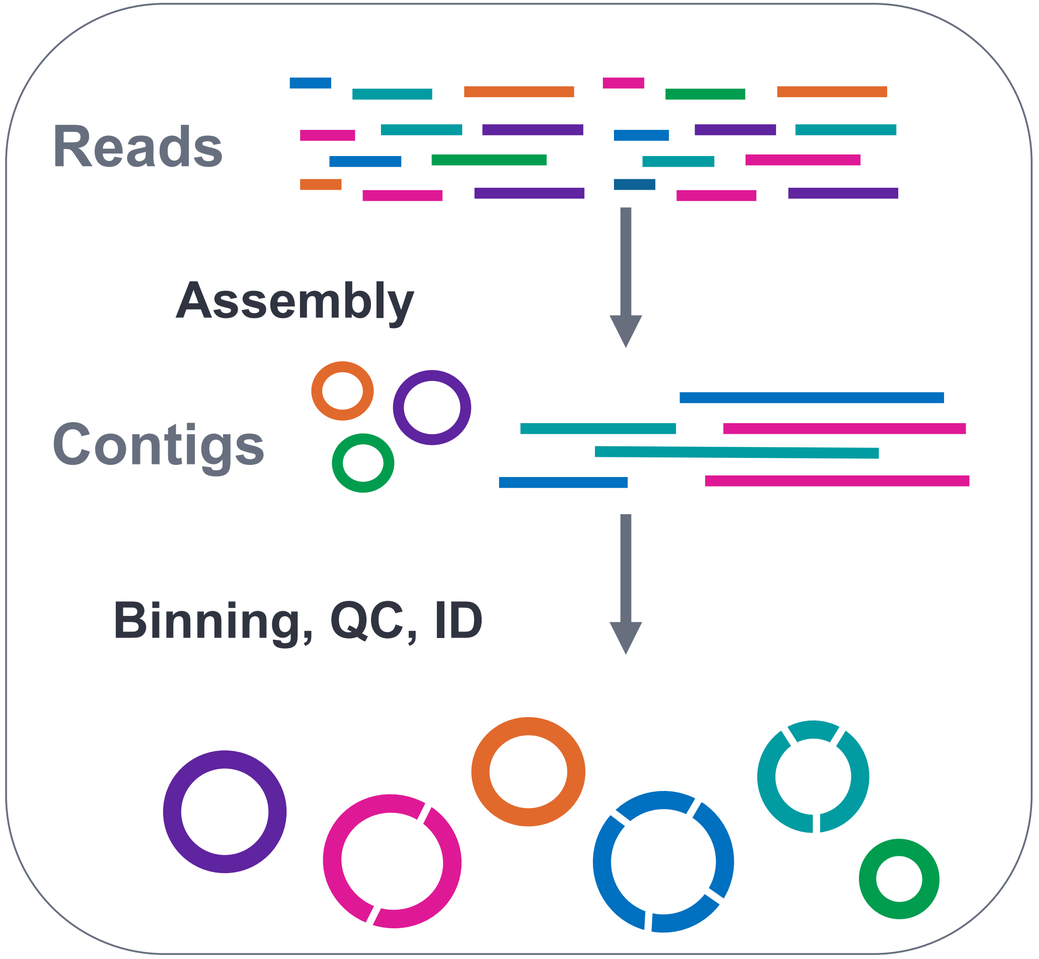
It determines the average number of reads that align to each contig.

This depth information is crucial for binning -> grouping contigs into potential genome bins based on coverage similarity. Input for **METABAT**.

BINNING

METABAT2

INPUT: Contigs (FASTA files) and coverage/depth information



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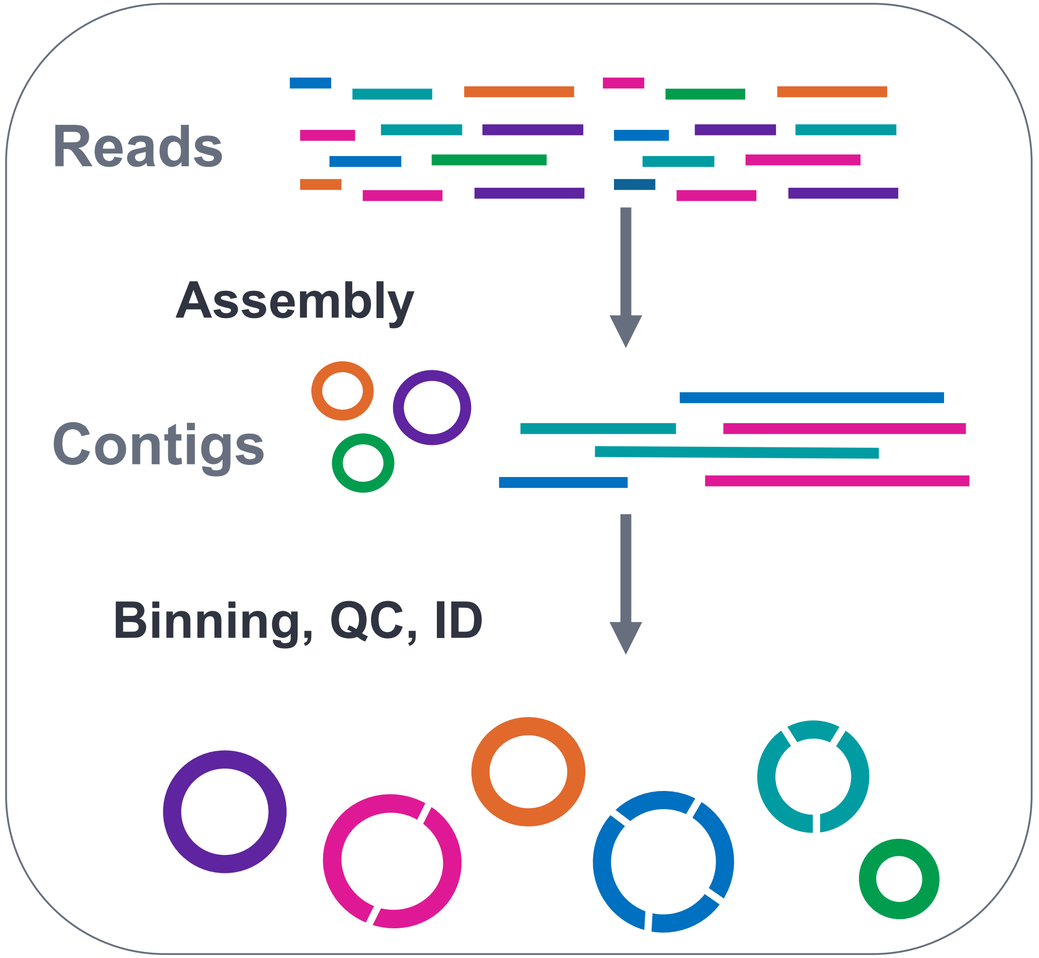
INPUT: Contigs (FASTA files) and coverage/depth information

OUTPUT: Draft MAGs (multiple FASTA files, one for each "bin")



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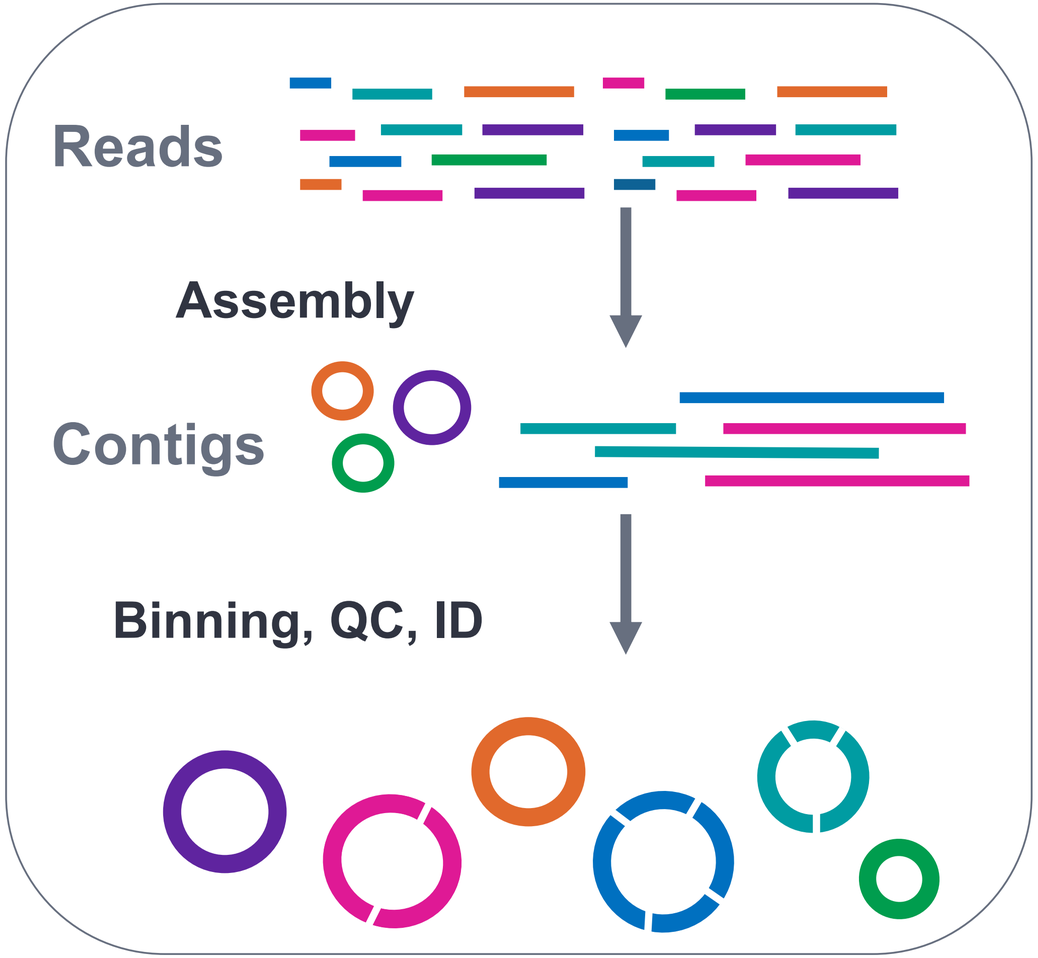
AIM: group contigs into species



QUALITY ASSESSMENT

CheckM

INPUT: Draft MAGs/bins (FASTA files)

OUTPUT: Summary table with quality scores.

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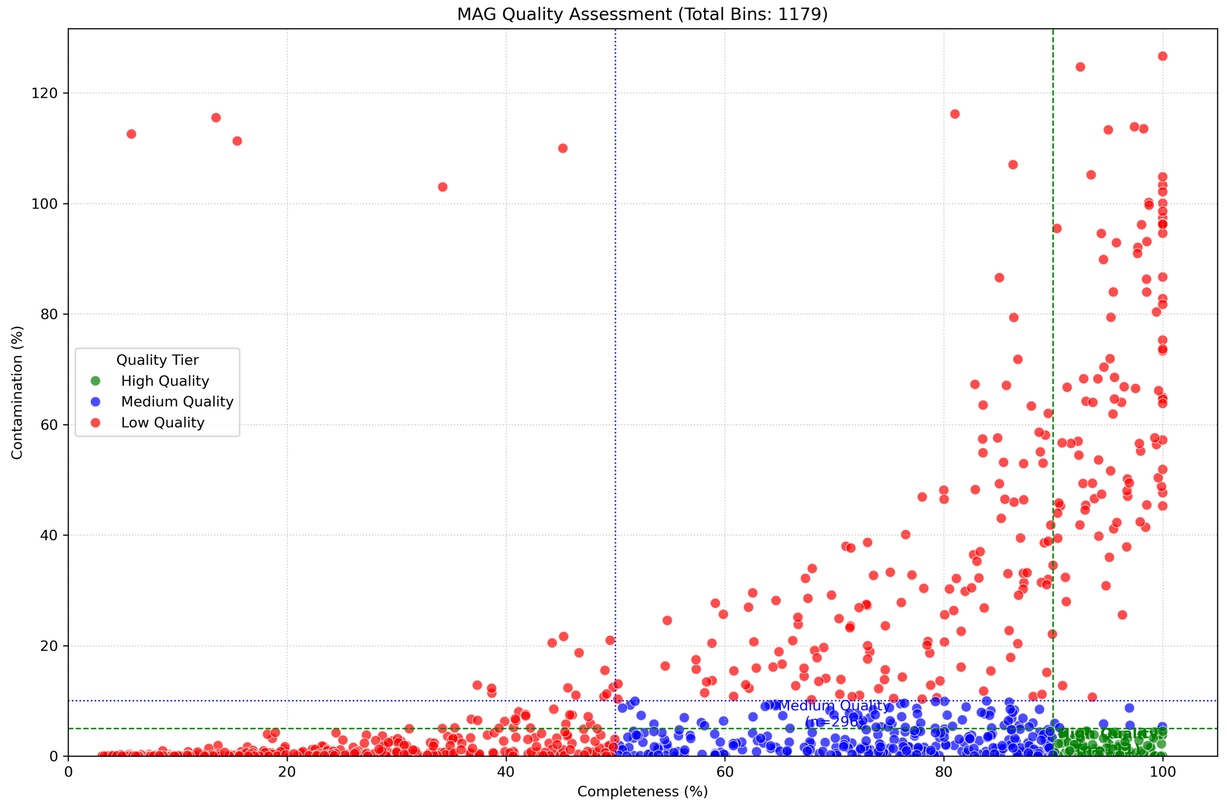

- [x] ANNOTATION and VISUALIZATION

☑ ANNOTATION and VISUALIZATION

BAKTA & Proksee

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INPUT: High-quality MAGs (FASTA files)

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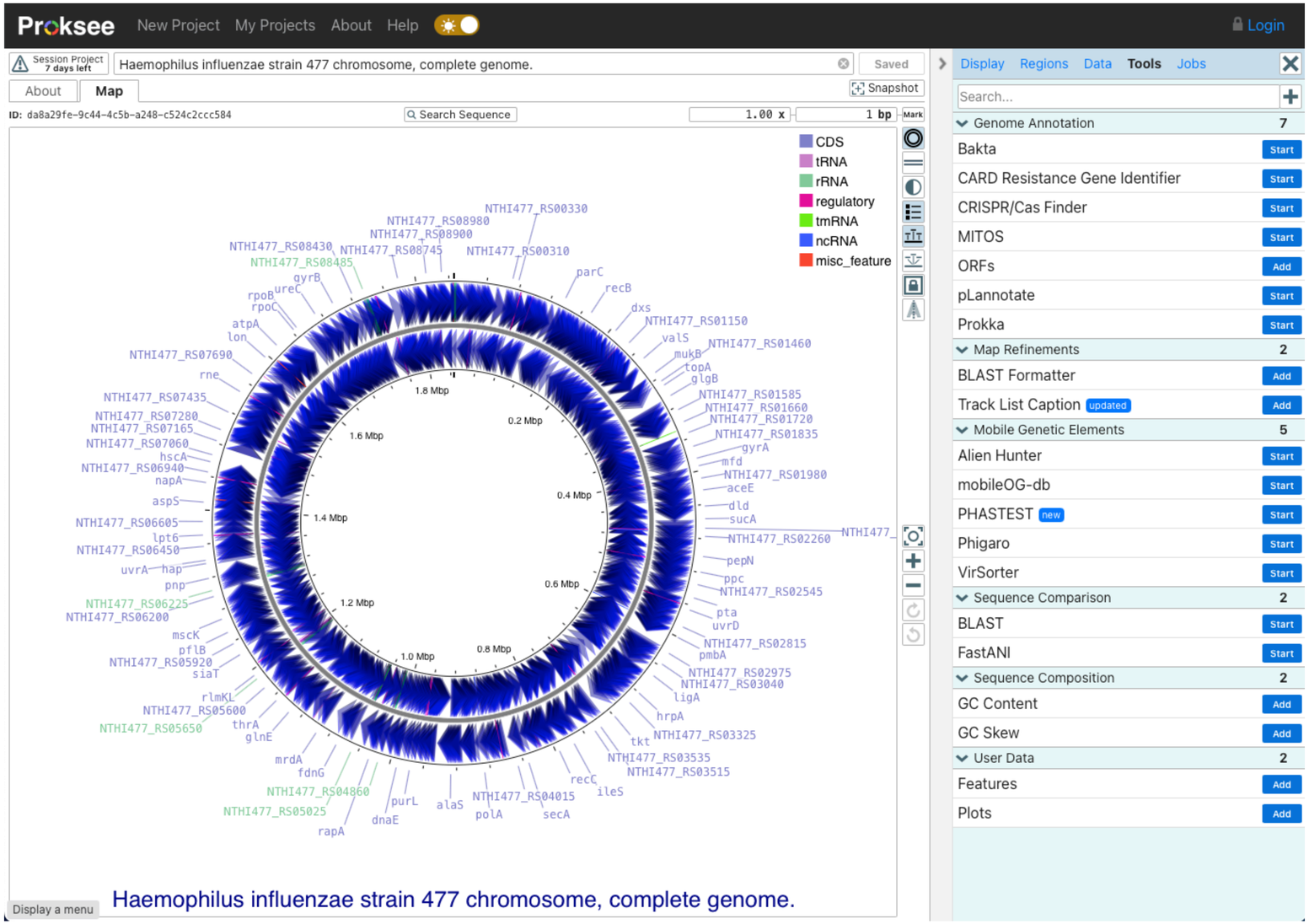

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