

Bioinformatics and metagenomics

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Report outline

Bioinformatics tasks

Alignments

Assembly

Pattern recognition

Bioinformatics tasks

Bioinformatics is the application of **computer science** and **information technology** to the field of biology and medicine. Bioinformatics deals with algorithms, databases and information systems, web technologies, artificial intelligence and soft computing, information and computation theory, software engineering, data mining, image processing, modeling and simulation, signal processing, discrete mathematics, control and system theory, circuit theory, and statistics, for generating new knowledge of biology and medicine, and improving & discovering new models of computation (e.g. DNA computing, neural computing, evolutionary computing, immuno-computing, swarm-computing, cellular-computing).

What will be used in Bioinformatics?

Statistics (The world is based on the statistics.)

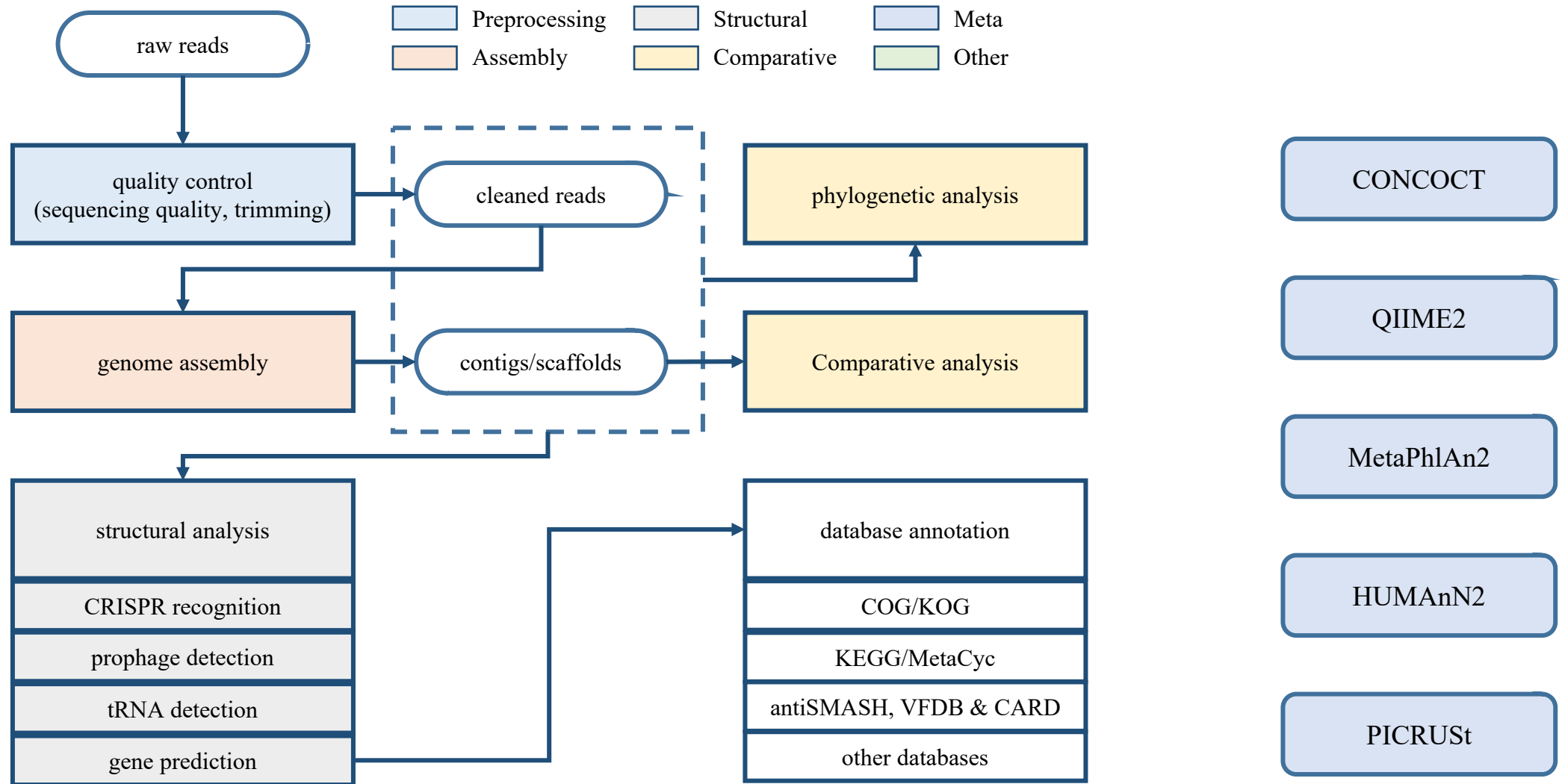
Computing Science (The biological data is in large volume.)

Database tech

Mathematics (models / algorithms)

In mathematics and computer science, an algorithm is an effective method expressed as a finite list of well-defined instructions for calculating a function. Algorithms are used for calculation, data processing, and automated reasoning. **In simple words an algorithm is a step by step procedure for calculations.**

Microbiome analysis pipeline



mainly used algorithm in Bioinformatics

- **Alignment**
- Assembly
- Pattern recognition

In bioinformatics, a sequence alignment is a way of arranging the sequences of DNA, RNA, or protein to identify regions of similarity that may be a consequence of functional, structural, or evolutionary relationships between the sequences.

- short reads – long seq
- long seq – long seq
- short reads – database
- ...

