Questions:

Quiz 1: Short Answer
What is the research question addressed in this study?

Quiz 2: Single Choice
Which algorithm is used for taxonomic annotation in MMseqs2?
A. LCA*
B. 2bLCA
C. Cactus
D. MetaPhlAn

Quiz 3: Multiple Choice
Which of the following are steps in the MMseqs2 taxonomy-assignment algorithm?
A. Translate contigs in six reading frames
B. Apply k-mer clustering
C. Use 2bLCA for annotation
D. Determine the final label by weighted voting
E. Perform whole-genome alignment

Quiz 4: Short Answer
What is the difference between the bacterial dataset from 2020 and the one from 2015?

Quiz 5: Which of the following statements about the comparison between MMseqs2 and CAT are correct? (Multiple Choice)

A. The new tool presented in this paper (MMseqs2) can be used across domains, whereas the existing tool (CAT) is limited to prokaryotes.
B. The parameter selection process of the existing tool (CAT) is automatic, whereas the new tool (MMseqs2) requires manual selection of key parameters.
C. The new tool (MMseqs2) is faster in runtime compared to the existing tool (CAT).

Quiz 6: Multiple Choice
Which fields can benefit from the application of MMseqs2?
A. Metagenomics
B. Microbial ecology
C. Quantum physics
D. Epidemiology

Quiz 7: Multiple Choice
Which of the following are application areas mentioned for MMseqs2?
A. Cancer genomics
B. Identification of pathogenic microbes
C. Antibiotic discovery in soil
D. DNA fingerprinting

Solutions:

Quiz 1: Short Answer

Correct answer: Fast and sensitive taxonomic assignment to metagenomic contigs

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Quiz 2: Single Choice

Correct answer: B

Quiz 3: Multiple Choice

Correct answers: A, C, D

Quiz 4: Short Answer

Correct answers: The 2015 dataset lacks species-level data, while the 2020 dataset includes them.

Quiz 5: Which of the following statements about the comparison between MMseqs2 and CAT are correct? (Multiple Choice)

Correct answers: A, C

Quiz 6: Multiple Choice

Correct answers: A, B, D

Quiz 7: Multiple Choice

Correct answers: B, C