P2: Informed and automated k-mer size selection for genome assembly

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Question 1:
How many datasets were used for the implementation of KMERGENIE?

A. 2
B. 5
C. 3

Question 2:
Based on what metric was the performance of KMERGENIE evaluated?

A. Number of distinct k-mers
B. Abundance histogram
C. Number of errors

Question 3:
The best value of k for assembly is the one that provides the _____ distinct genomic k-mers.

A. Maximum
B. Average
C. Minimum

Question 4:
KMERGENIE's performance was compared to other tools. Which of the following tools was one of them?

A. Pareto
B. Velvet
C. Viterbi

Question 5 (Feedback)
How would you rate the overall organization and flow of the flashtalk? 1 (very good), 2 (good) and 3 (bad)

A. 1
B. 2
C. 3

What did you like /dislike most about the flashtalk?