

# 03 Informed and automated k-mer size selection for genome assembly

Cem Bakisoglu, Kristiyana Tsenova

July 2022

## Question 1

What is the name of the presented tool?

Name:

## Question 2

Which distributions are used to model the genomic and erroneous  $k$ -mers?

Genomic  $k$ -mers:

Erroneous  $k$ -mers:

## Question 3

Fill the missing term.

In order to fit the model to the abundance histogram, the parameters of the model are estimated by a .

## Question 4

Which three measured values are taken into consideration for the assembly quality?

- 1.
- 2.
- 3.

## Question 5

Fill the missing term.

"The best choice of  $k$  provides the most  $k$ -mers to the assembler"

## Question 6

Which probability enables the estimation of the distinct genomic  $k$ -mers?

The probability of a  $k$ -mer

## Feedback

Was the research objective clearly presented (grade 1 (best) to 6)?

(1)    (2)    (3)    (4)    (5)    (6)

Were the slides appropriately designed?

1    2    3    4    5    6

General feedback: