AssemblyDenovo UML

Genome

+ sequence
+ genome_size
+ nucleotides
+ reads
+ kmers

+ __init__()
+ createRandomRead()
+ createKmers()
+ isEqual()
+ __str__()

Graph

+ list_adja
+ go_in_node
+ number_edge

+ __init__()
+ addNode()
+ addEdge()
+ isEulerian()
+ getEulerianCycle()

USE

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Main

with fasta file:

create: genome from the fasta file, reads, kmers

from kmers create a graph

from graph if it is eulerian find an eulerian cycle and retrieve the a sequence from reads.

Test the sequence founded. And write it in fasta file.

without fasta file:

create: genome, reads, kmers

from kmers create a graph

from graph if it is eulerian find an eulerian cycle and retrieve the a sequence from reads.

Test the sequence founded. And write it in fasta file.

Output:

print if a sequence is founded. If not print why no sequence is found.

write fasta file if their are sequence.