

PythoFragam: A Python-based Optimization Tool for DNA Fragment

This repository contains the code for DNA fragment assembly based on a metaheuristic Overlap Layout Consensus Approach: Restarting recentering hybrid genetic algorithm (RRHGA). Complete code is written in Python 3.

System requirements

1. Python 3.4+
2. Swalign
3. Pandas
4. Numpy

Datasets

<http://chac.sis.uia.mx/fragbench/>

1. GenFrag Instances
 2. DNAgen instances
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Main.py-This script contains the main functions for solving the problem of DNA fragment assembly. These are given below.

- **Importing the dataset-**
First, import a FASTA format file. The file is open and appends the fragments into a list name is sequences. The second is the CSV file includes the matrix, the value of the cell, is overlapping scores among the sequences.
- **Setting the parameters**
The parameters such as Population size, Mutation rate, Number of Trans, and Cutoff value, the percentage of Trans is increased or decreased in case of improvement and no improvement.
- **run_2opt**
This function takes the overlapping score matrix as an input, and find the initial Centre (optimal path-order of the fragments) for the genetic algorithm.
- **D_Rep**
This function gets the Centre as an input, and generate the populations based on directed transpositions.
- **Genetic_alg**
Once the populations are generated. The called function **genetic_alg** gets the populations, **num_parents_mating**, **n_generation**, **mutation_rate** as inputs. The **genetic_algo** import **partially_cross** function for evolutionary operators such as crossover and mutation. However, the **array_contig** function used PALS as an evolutionary operator to order the fragments while minimizing the number of contigs. The **init_pop_score** function used the local alignment algorithm for the fitness value evaluation.
- **last_fit_score**

This function gives the final output, by calculating the sum of overlap score, and the number of contigs of the best solution generated from RRHGA.

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