Extending BACTOME functionality

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1 Motivation

After the first human genome was sequenced, many genome databases and online browsers were created to study each species genomic and transcriptomic landscape. With the same goal, researchers have developed BACTOME [Hornischer et al., 2018], an interactive reference database for the opportunistic pathogen *Pseudomonas aeruginosa*.

Currently, the BACTOME web portal has three main topics: a general overview of phenotypes of the collected *P. aeruginosa* strains, interactive tools for identifying genomic variants between the strains, and similar tools to explore the variability of the transcriptomic landscape. In 2019-2020, the whole site has changed. The database was re-designed and re-populated, then the website and the phenotype view were re-designed and implemented using django and javascript.

Aiming to improve the existing new website, we seek to find motivated student assistants that will implement the genome and transcriptome views. Achieving this, the new BACTOME will be ready to be used by researchers through the web. In this effort, we will use and extend already available software packages for web interactive genome viewers. To name a few, general viewers such as the one developed by Cao et al. [2018], or existing browsers tailored for bacterial genomes like the ones by Aurisano et al. [2015], Garanina et al. [2018]. We refer to the work of Pavlopoulos et al. [2015] for a general survey of genome visualization tools. Finally, we will test the system offline and online in order to ensure its applicability.

2 Goal/Deliverables

Upon successful completion, the student assistant, based on the already implemented django framework, should:

- Implement genomic and transcriptomic views

- Design, implement and test code

- Explain her/his work in a scientific report

A supervisor will always help with major questions, testing of the code and writing of the report.

3 Prerequisites

1. Motivation & interest in the topic

2. Self-contained work in a multi-disciplinary team

3. Python (Django)

4. JavaScript

5. Experience in genomics and transcriptomics is a plus

4 Contact

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