Extending the user experience of BACTOME

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March 13, 2019

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. Aiming to improve the existing website, we will survey and extend existing methods for a better encapsulation of information by genomic viewers for general sequences [Pavlopoulos et al., 2015]. We will also explore ideas from existing browsers tailored for bacterial genomes, such as Aurisano et al. [2015], Garanina et al. [2018]. After having implemented the new user experience (interface), we will evaluate its memory and time requirements. Finally, we will test the system offline and online in order to ensure its applicability.

2 Goal/Deliverables

Upon successful completion, the master student should:

- Deliver a redesigned and efficient user experience for BACTOME

- Implement genomic and transcriptomic viewers

- Design, implement and test code

- Conduct experiments for (time and memory) performance comparison

- 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 and Java

4. JavaScript, html, CSS

5. Experience in genomics and transcriptomics is a plus

4 Contact

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