



# PROJECT PROPOSAL

## BWAW

VERSION 1

### Team members:

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## I. Overview

- Our project is a short reads aligner to a reference genome web-based application.
- Our model tool is BWA aligner.
- The main algorithm considered is Burrows-Wheeler.

## II. Problem

Due to the difficulty of using and running BWA commands and utilities through Linux command line window, we aim to develop a web application with GUI to make it easy and familiar to the user. Visualization of reference genome and reads facilitate understanding of possible alignments positions quickly.

## III. Goals and methodology

- **Input:** FASTA file containing reference genome, FASTQ file containing sample reads.
- **Output:** quick description about the alignment, SAM format represented in graphical interface, visualization of reference and reads.

## IV. Next steps

- Highlight mutations and allocate SNPs normal variations positions in reads comparing to the reference.
- Error prediction.