

Computational Pipeline for Full Plasmid Validation

Team 13: Daniel Thompson¹, Dhwanil Patel¹, Jackie Tang¹, Dr. William Dampier²

Drexel University, School of Biomedical Engineering and Health Sciences¹, College of Medicine²

Need

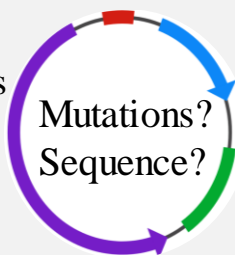
No existing software that assembles raw reads and visualize the plasmid and its mutations

Objective

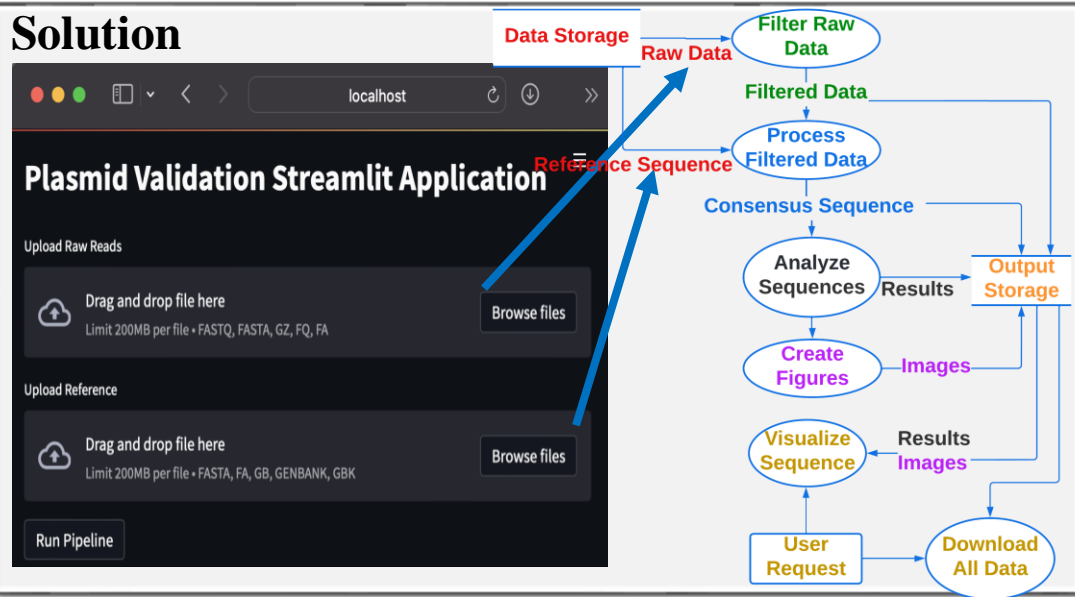
Develop an app that **analyzes plasmid sequences** and **visualizes mutations**

Requirements

- Accurate detection of features and mutations with a resolution of 1 base pair
- Visualization of results



Solution



Results

Highly accurate and fully functional web application

Original Seq.	Changed Seq.	Mutation Shown	Element	Visual
CGGCAA	GGTTC A	GGTTC ▶ CGGCA	Plasmid Map	Yes
TGCCATT CGAC	CCGAGAACT TAA	10 mutations	Features List	Yes
			INDEL	Yes

Future

Impact – Simplify plasmid validation by encapsulating all the steps into one application

Revisions – Include de novo assembly and a suite of synthetic biology computational tools