COMPREHENSIVE GENOME BROWSER FOR GENOME ANALYSIS

Brendon Cara, Daniel Groves, Jasmyn Pellebon,
Michael Pham, Ojas Rade, Varsha Srinivasan

SUMMARY

We aim to develop a user-friendly genome browser that extends the capabilities of similar software and incorporates current state-of-the-art downstream analyses and plugins for a cohesive, integrative experience. Our proposed tool will offer a much more intuitive user experience, plug-ins for the integration of several types of large biological datasets, and an all-in-one type approach to the standard practice, aligning with the principles of human-computer interaction.

WHAT IS A GENOME?

A genome refers to the complete set of genetic material or DNA present in an organism. It contains all the instructions necessary for an organism's growth, development, functioning, and reproduction.

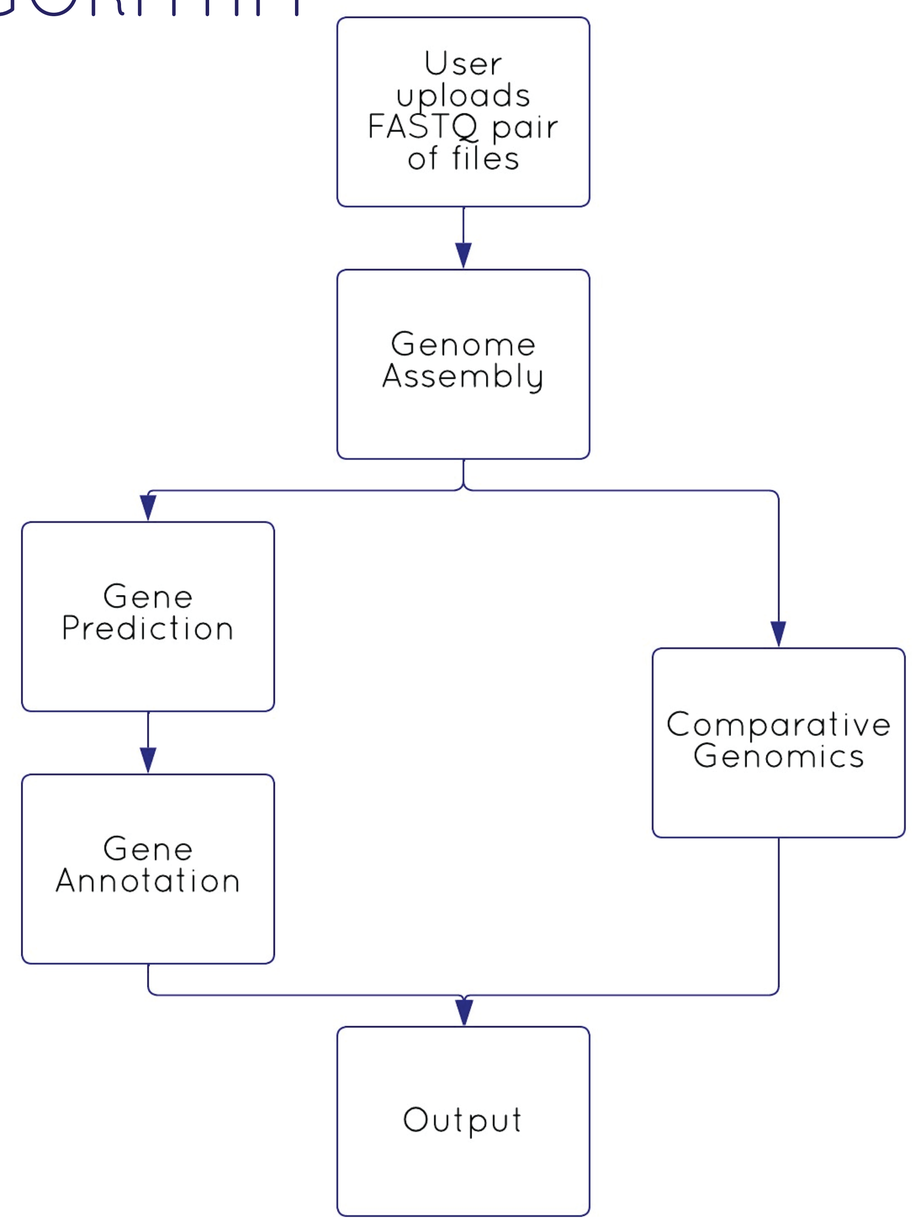
WHY IS THIS IMPORTANT?

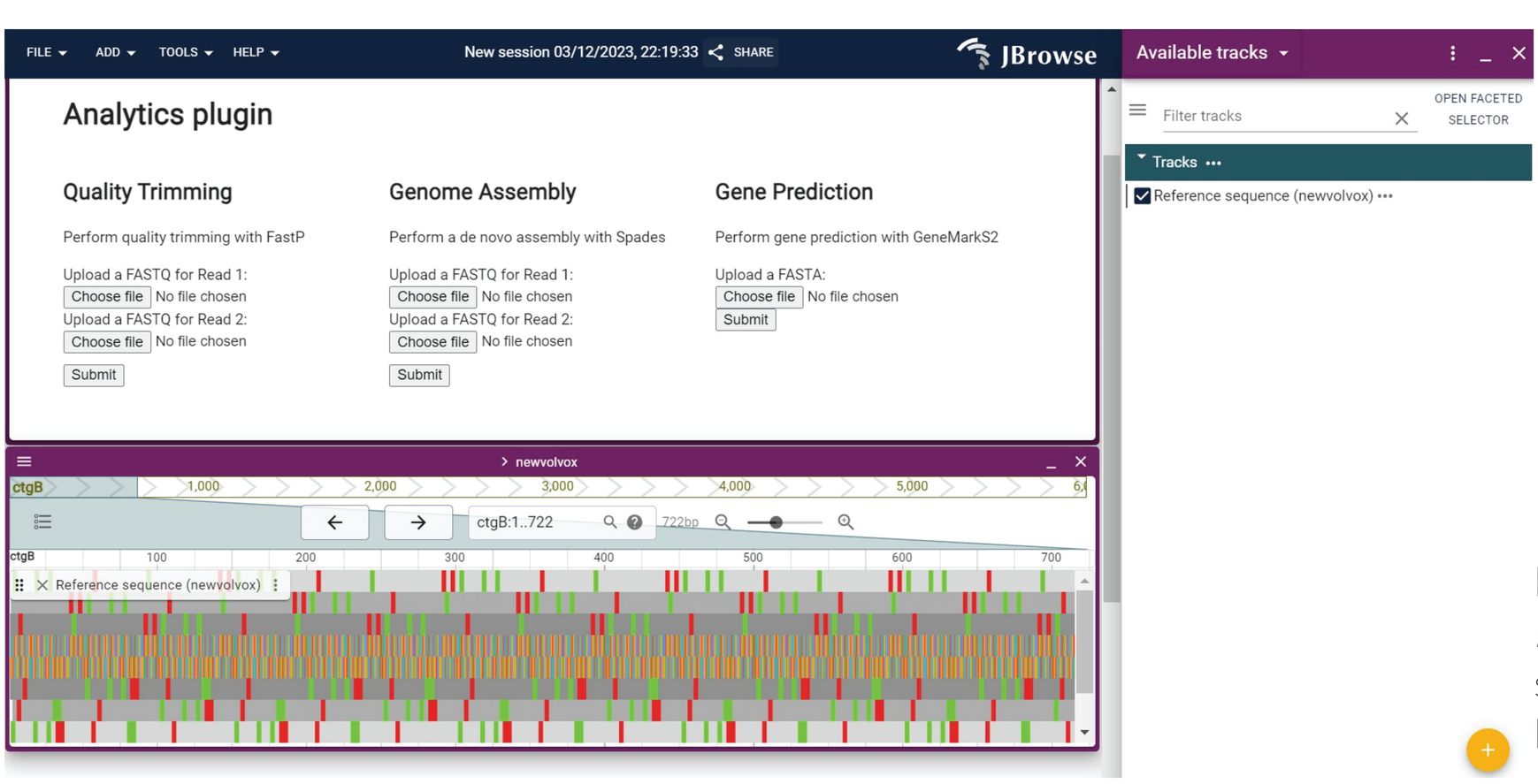
Organizations such as the CDC often have to deal with sudden outbreaks of food-borne illnesses, often caused by unknown bacteria. The first step to tackling it is to identify the pathogen, pinpointing the origin and source of the outbreak and characterizing the functional profile of the virulent isolates (i.e. virulence factors and antimicrobial profile) to understand how the pathogen works. Following this, specific recommendations are made to respond to the outbreak and treat the affected.

DATASET

We used 50 randomly chosen datasets (28 GB total) in the European Nucleotide Archive from a 2017 outbreak of *Salmonella enterica* in Denmark. This study evaluates core-genome single nucleotide polymorphism (SNP) analysis for outbreak detection and linking of sources of subspecies *serovar typhimurium* and its variants in a 7-month surveillance period in Denmark.

ALGORITHM





Plug-in view of the *Salmonella typhimurium* reference sequence before file uploads