ViralWasm: a client-side user-friendly web application suite for viral genomics

Daniel Ji, Robert Aboukhalil, Niema Moshiri

BioSys Workshop 2024

Computational Tools in Epidemiology: Problem Statement

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- Goal: Fast and accurate diagnosis of patient viral sequences
  - Take raw sequence data and perform viral diagnosis and mutation evolution
- Learning Curve
  - Requirement: Computer-science background
  - Technical know-how: Software installation, terminal usage

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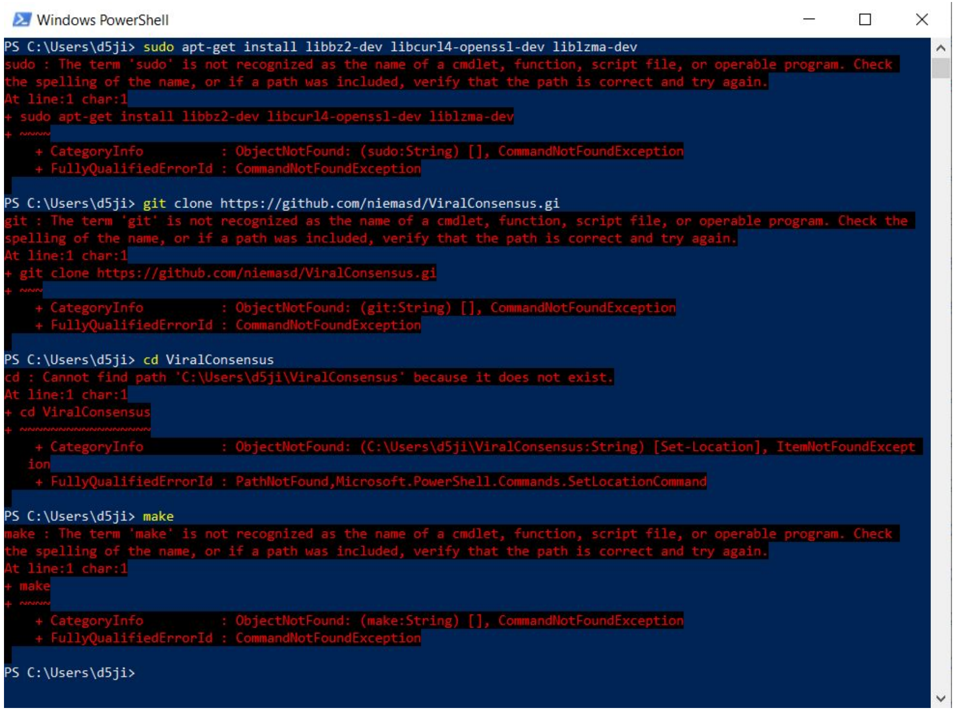

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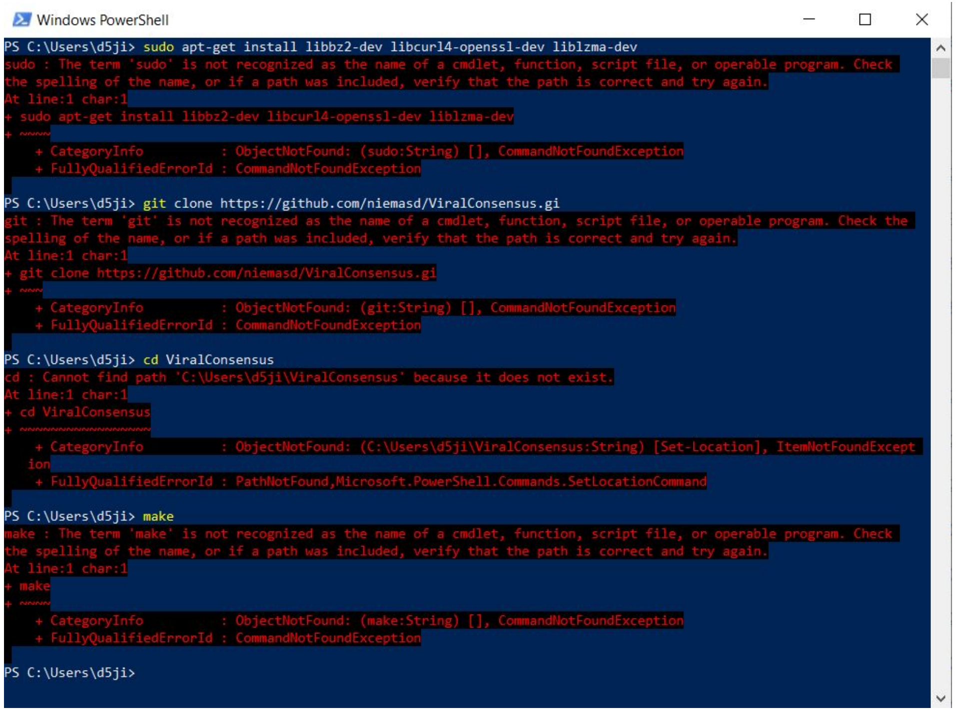

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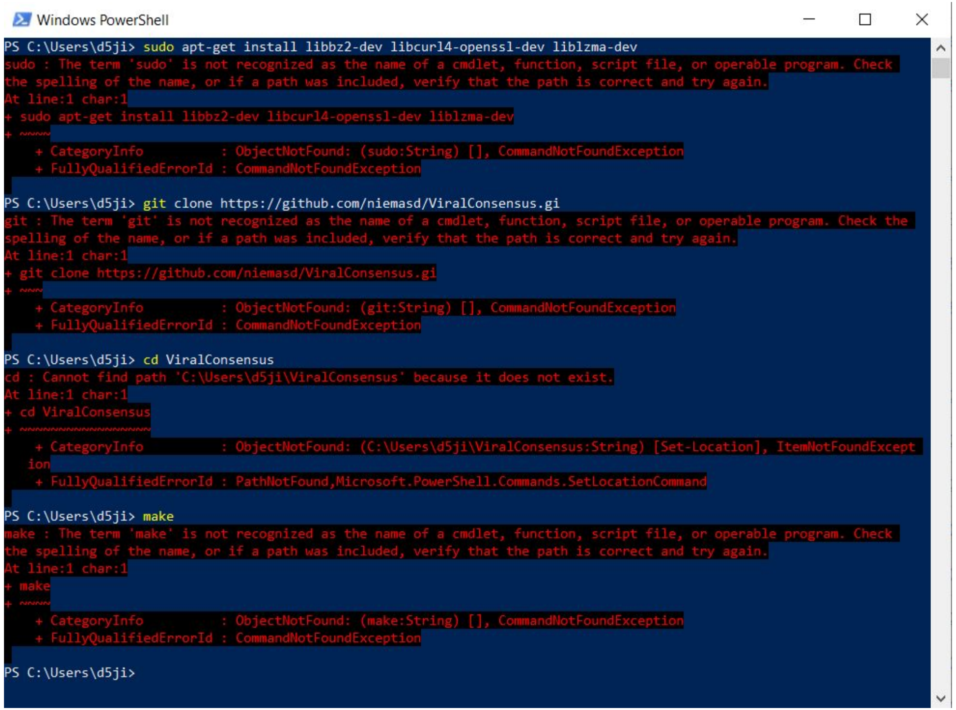

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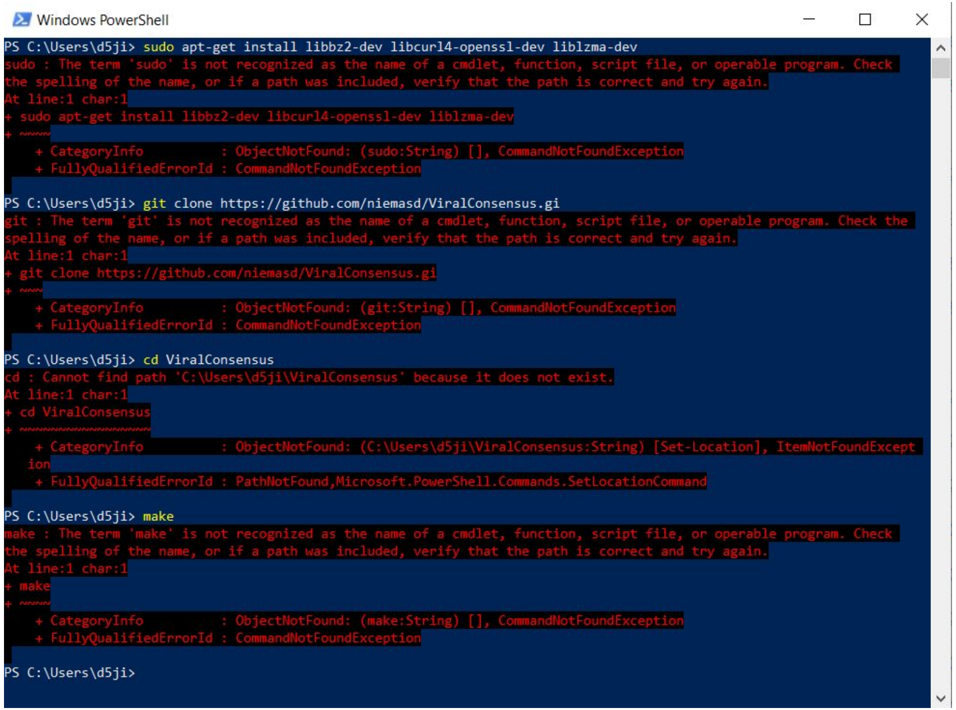

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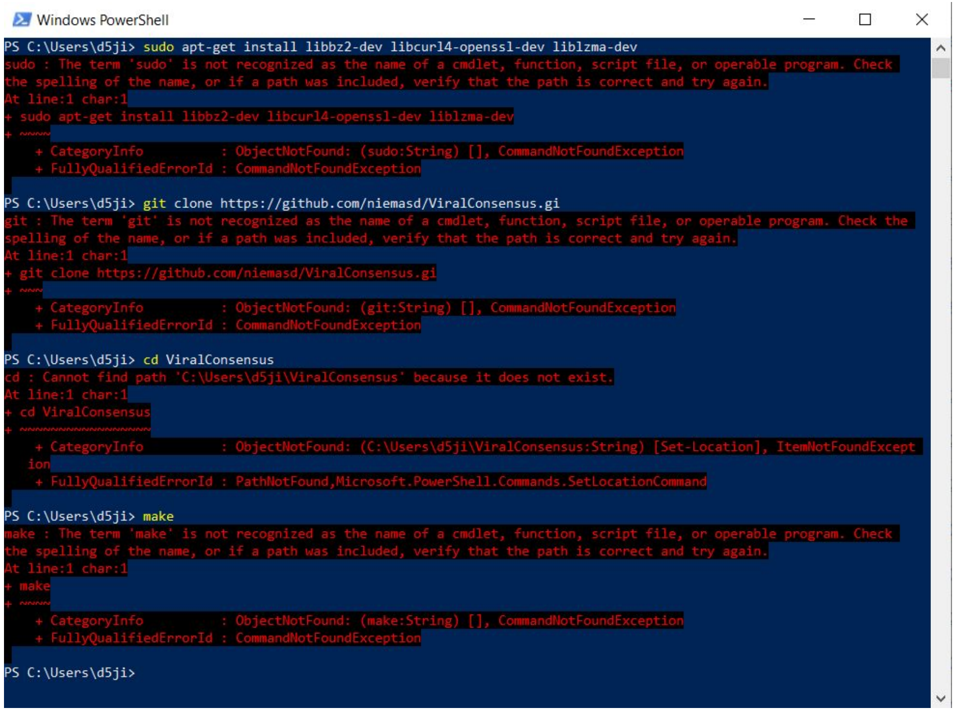

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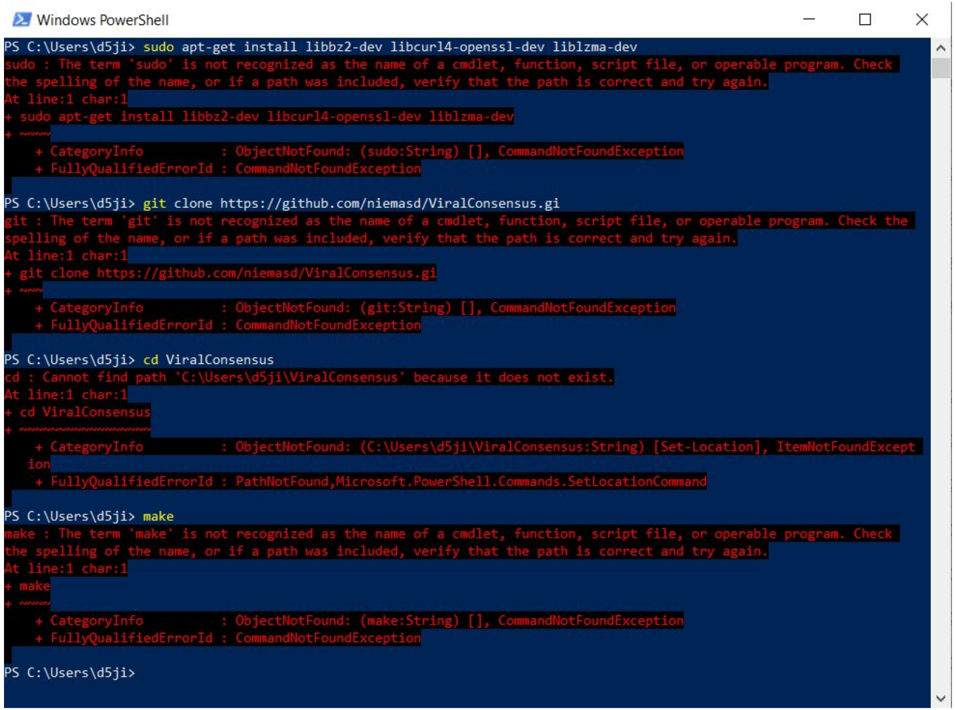

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Offline Capabilities
- Entire website + tool downloadable for offline use, just through a few clicks.

Technical Approach

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Two primary pipelines

- ViralWasm-Epi: multi-sequence alignment, molecular clustering, phylogenetic tree inference, and tree rooting and dating
    - Pipeline software: ViralMSA, minimap2, tn93, FastTree 2, Seqtk, LSD2

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Web technologies used: Emscripten, Biowasm, Pyodide, React.js, and Bootstrap

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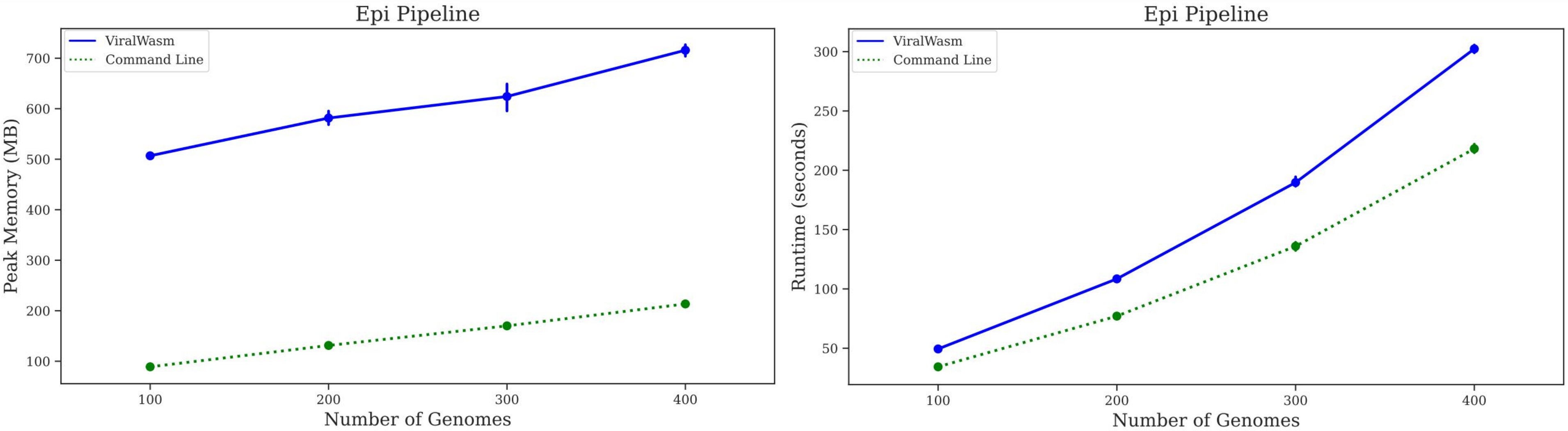
- Web vs. CLI benchmarks (full-pipeline runs): web scale reasonably in terms of memory and runtime

Benchmarks: ViralWasm-Epi



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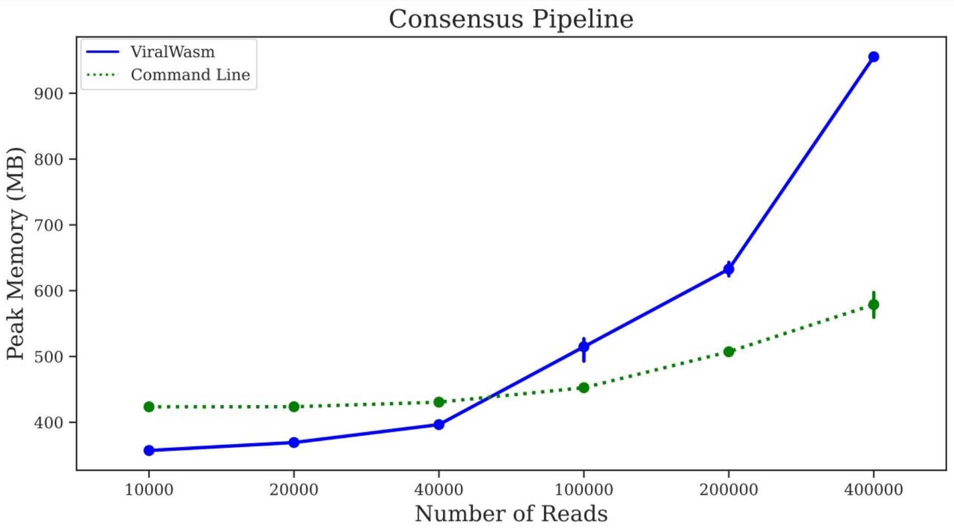

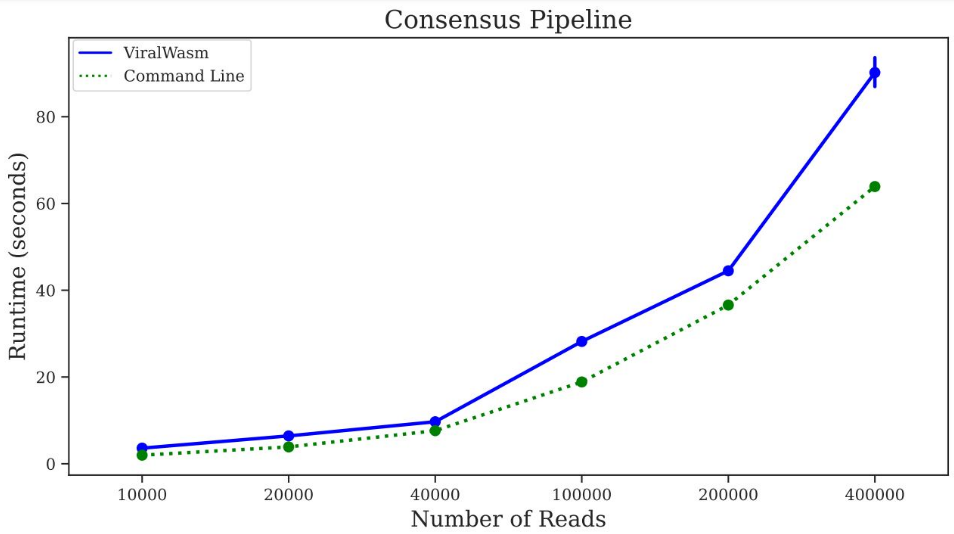

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  - Automating custom tool Wasm web app creation

Live Demo

niema-lab.github.io/ViralWasm

Thank You! Questions?

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