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Ziplign: a simple-to-use interactive tool to compare bacterial genomes

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Software

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Summary

Ziplign is a user-friendly interactive application to visually compare two bacterial genome sequences and their annotation. It requires no command-line use, and is intended to make genome comparison easily accessible to the biologist. Genome files can be directly drag-and-dropped into Ziplign, or will be automatically downloaded when an accession is provided. All commonly-used file formats and compression are supported. The comparison between genomes is generated using NCBI BLAST+ (Camacho et al., 2009), which is run for the user, and then the two genomes, their annotation, and sequence matches are displayed by Ziplign. A screenshot of Ziplign is shown in Figure 1.

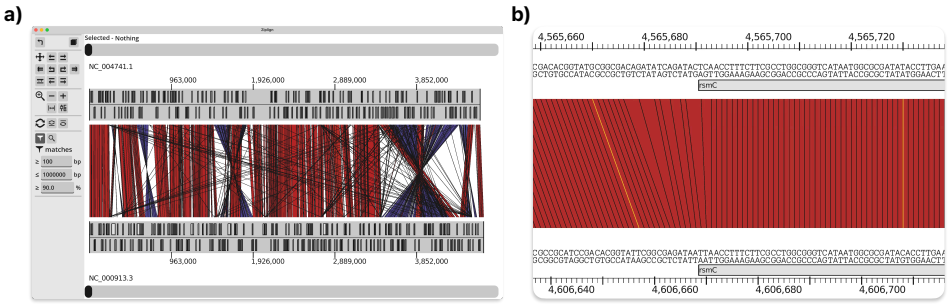

Figure 1: Screenshots of Ziplign comparing the Shigella flexneri 2a genome GCF_000007405.1 (Wei et al., 2003) - shown at the top - with the Escherichia coli K-12 substr. MG1655 GCF_000005845.2 (Riley, 2006) - shown at the bottom. BLAST matches are shown in red when the direction of the match is the same in both genomes, and in blue when they are in opposite directions. To reduce noise in the screenshot, only matches of at least 2000bp and 95% identity are shown (configurable by the user via the panel on the left). Annotation features on the forward/reverse strand are shown in the top/bottom of each contig. a) Default view, showing the complete genomes and their overall structural similarities. b) Zoomed to the base-pair level, matching nucleotides marked with black lines, SNPs are in orange, and non-parallel black lines denote indels in the alignment.

Statement of need

Comparing two bacterial genome sequences is a fundamental task in genomics, used in numerous scenarios: comparing closely related strains to discern differences such as the overall structure and any rearrangements, the presence or absence of important features such as virulence factors or anti-microbial genes, or to identify horizontal gene transfer. Genome assemblies can be compared to each other or against a reference genome for debugging or determining the most accurate assembly. Whilst many command line tools are available for processing samples at scale and report statistics, it is invaluable to visually and interactively compare two genomes. This is often the simplest way to truly understand the differences between two sequences.

To our knowledge ACT (T. J. Carver et al., 2005) and Mauve (Darling et al., 2004) are the only existing tools for displaying genomes and matches between them in an interactive manner - however both tools are no longer supported. Since ACT is based on Artemis (T. Carver et al., 2012), it incorporates the extensive feature set implemented in Artemis. However, ACT has a number of limitations. It can be difficult for non-technical users to install and use, Java must be installed, the user must provide (most likely via running command line tools) a genome comparison file, multi-sequence genomes are not supported out of the box, and alignment details including SNPs and small insertions and deletions are not shown. Mauve is simple to run but it displays global alignments of locally collinear blocks shared between genomes, meaning that repeats may not be shown. We tested this using a 1000bp randomly generated sequence sampled uniformly from A, C, G, T characters, comparing it to a second contig comprising two identical copies of the first 1000bp sequence, and Mauve showed no matches (also tested again using a 10,000bp sequence).

Here we introduce Ziplign, which fills the need for an easy-to-install and simple-to-use genome comparison tool. It is heavily inspired by ACT, with a very similar user interface, but is significantly easier to install and use.

Usage and availability

Ziplign is intended for microbiologists with no command line experience. As such, no use of a terminal is required. First, two genomes must be provided, either with an NCBI accession or by dragging-and-dropping local files. FASTA, FASTQ, GFF3, EMBL, and GenBank file formats are supported, optionally with gzip, bzip2 or xz compression. Genome sequences and annotation are automatically downloaded when an accession is used. Ziplign runs BLASTN from the NCBI BLAST+ suite to generate the matches between the two genomes. The BLASTN options are configurable by the user.

Genomes are displayed at the top and bottom of the window, with BLAST matches shown between them (Figure 1). The view can be zoomed and panned using mouse, trackpad or keyboard controls, or with buttons in the control panel on the left. Features include searching by nucleotide sequence or annotation, contig reordering, and reverse complementing contigs. Ziplign can save and load an entire "project" - the genomes, annotations, and BLAST matches - using a single binary file, removing the need to store the original files.

Ziplign is available for Windows 11, macOS, and Linux operating systems from GitHub https://github.com/martinghunt/ziplign, under the MIT license. Comprehensive documentation is hosted on ReadTheDocs https://ziplign.readthedocs.io/en/.

Implementation

Ziplign is primarily written in GDScript, the scripting language of the free, open-source, MIT-licensed, game engine Godot (https://godotengine.org, https://github.com/godotengine/godot). This handles the graphical user interface (GUI), and displaying and interacting with

all the genome and comparison data. Bioinformatics tasks such as parsing sequence/BLAST files and downloading genomes are processed using a separate command line program called zlhelper https://github.com/martinghunt/zlhelper, also with the MIT license, written in the Go programming language. All command line programs are hidden from the user, so that the only interaction is simply with the GUI.

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