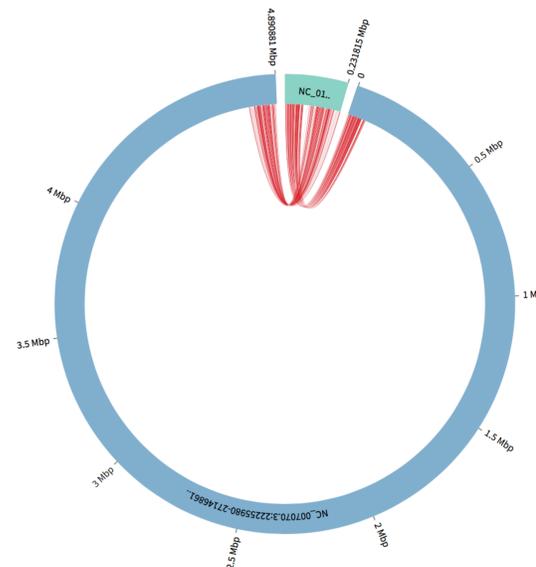


Background

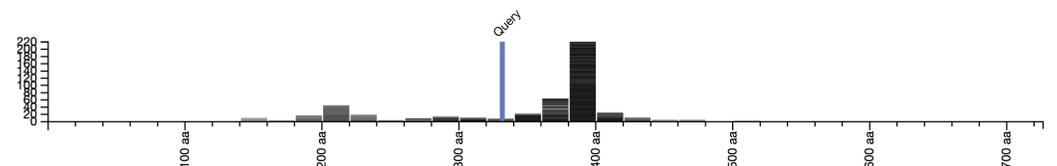
SequenceServer enables users to rapidly setup a BLAST server on custom datasets, and presents an interface that is modern looking and intuitive to use. In version 2.0 (currently in beta), we have rearchitected the software to enable visualisation of BLAST results and much more!

Key features (2.0 beta)

1. Supports BLAST 2.9.0 and the new v5 BLAST database
2. Ability to import and visualise BLAST XML, including from DIAMOND
3. Summary overview of top hits in a circos plot
4. Length distribution of hits per query
5. Relative length and position of matching regions for each query-hit pair (Kablammo)
6. Ability to bookmark and share results



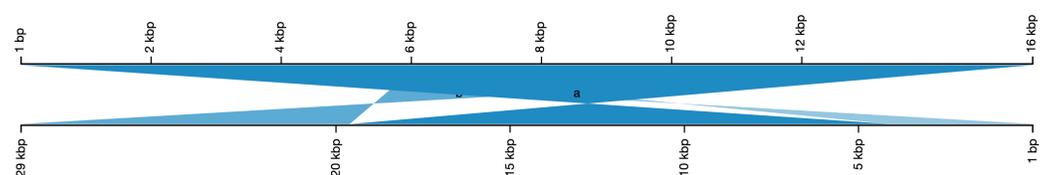
Genomic region compared to another species, showing a rearrangement.



A predicted protein sequence compared to the NR database: the predicted sequence is shorter compared to the most similar hits suggesting an issue with the prediction (likely a frameshift).

Beta to stable

1. Publication ready visualisations
2. Performance optimisation
3. User reported bug fixes



Genomic region compared to a new assembly of the same species, showing a tandem duplication, or an assembly artefact.

Outlook (beyond 2.0)

1. Results data available in browser
 - i. Any JS visualisation library can be integrated
 - ii. Interactive filtering of results e.g., by evaluate
2. Equipped to run and visualise large BLAST searches, at scale
 - i. Async job submission architecture (easy to integrate with grid engines)
 - ii. Built-in thread-pool to control number of concurrent jobs
 - iii. Load and render only what's in viewport

References

1. Camacho C et al. (2009). BLAST+: Architecture and applications. BMC Bioinformatics 10:421
2. Cui Y, Chen X, Luo H, Fan Z, Luo J, He S, Yue H, Zhang P, and Chen R (2016). BioCircos.js: an interactive Circos JavaScript library for biological data visualization on web applications. Bioinformatics 32:1740-1742.
3. Wintersinger JA and Wasmuth JD (2015). Kablammo: An interactive, web-based blast results visualizer. Bioinformatics 31:1305-1306

