

Viewing and using

Dan Jones



The Bioinformatics Institute



THE UNIVERSITY
OF AUCKLAND

NEW ZEALAND

Te Whare Wānanga o Tāmaki Makaurau

Outputs of a well-designed *de novo* genomics program

- An assembled genome, with an appropriate level of coverage (at least 30x)
- Metrics to assess the assembly quality
- Predicted genes, repeats (low-complexity regions, transposable elements)
- Annotation of the annotations: what are my predicted genes most similar to?
- Mitochondrial and (Chloroplast) genomes
 - Depending on your tissue of origin, organelle genomes will often have a much higher level of coverage than the nuclear genome
- All of the above, in a searchable form, and visualised in a genome browser

Browsers

Free: **IGV**

Tablet (but only for mapped reads)

Gbrowse (not simple to setup, but useful, fast and can be web-facing)

ENSEMBL browser (they do workshops on it!)

ARGO (Broad institute)

Commercial: **Geneious**

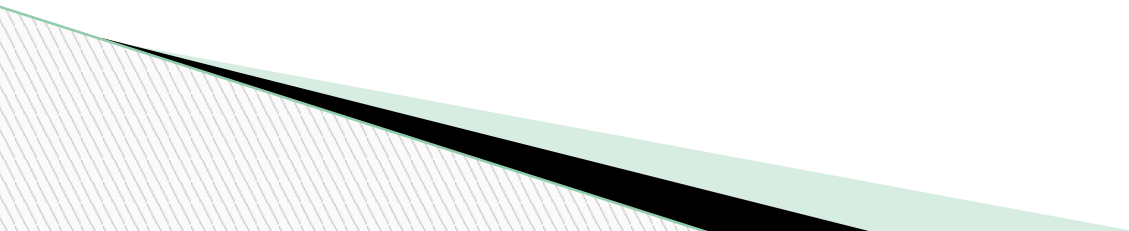
CLC Bio



Making your genome searchable

You can (and should) make your genome into a BLAST database to enable searching against this

- ☐ Easy to do on command-line (see exercise)
- ☐ Many programs like Geneious can do this for you

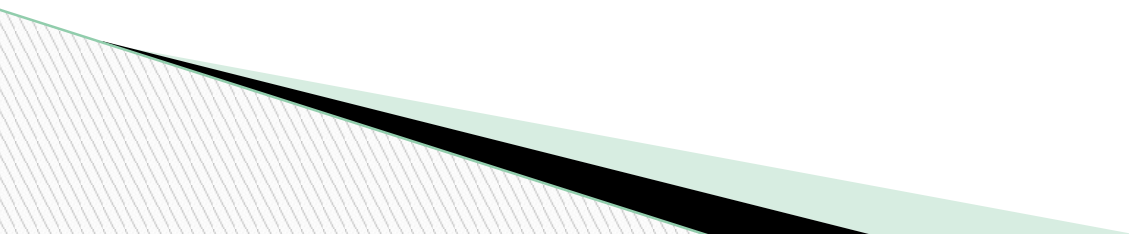


Collaboration

- ☐ Many organisations offering to host your genome in their browser
 - ☐ IGV hosts several genomes
 - ☐ 1000 fungal genomes

..although microbial genomes + annotations are probably small enough to email around!

- ☐ Web-facing browsers like Gbrowse enable you to setup your own website/browser
 - ☐ PFR Strawberry genome is a good example



Where to go for help

☐ SeqAnswers!

www.seqanswers.com

