Companion
Reference Based Genome Annotation and analysis of parasite genomes

https://companion.sanger.ac.uk/
https://doi.org/10.1093/nar/gkw292

- Web service pre-loaded with EuPathDB and GeneDB genomes
- Produces an annotation of your assembled genome
  - Gene models (protein coding, ncRNA)
- Performs some analyses between your genome and reference
  - Visualization
  - Species tree
  - synteny
• **INPUT** – assembled genome (contigs, scaffolds or chromosomes)

• Pseudochromosome contiguation – Orient genomic sequences to match chromosome structure of the reference

• Structural annotation – produced gene models (homology and ab initio)

• Functional annotation – info about the activity/purpose/activity of the gene product (OrthoMCL and PfamHMMER)

• **OUTPUT** – files in yellow
• VISUALIZATION and ANALYSES
  • Circos Synteny plots between your genome and reference
  • Species tree
  • Venn diagram of shared and species specific genes.
Upload genomic sequences in Fasta format
Choose params for the annotation run
Start the run
Look at results tomorrow