

Practical Session: Pairwise Genome Alignments using minimap2

Let's get familiar with doing whole genome alignments using minimap2 and interpreting the results in PAF and BAM format.

1. Install minimap2 using bioconda: `conda install -c bioconda`
2. Download the five mitochondrial genomes inside the folder to your computer
3. Have a look at the description of the pairwise alignments (PAF format):
<https://dgenies.toulouse.inra.fr/documentation/formats>
4. Obtain all the pairwise alignments against the other mitogenomes using the `unknown_MT.fasta`
5. How would you compute the identity among two sequences?
6. Obtain a table with the divergence between species
7. Could you identify the closest species?
8. Do all the mitogenomes align entirely (end to end)?
7. Look at the alignments in SAM/BAM format. How do they look compared to the PAF format

Web Links

Minimap2 <https://github.com/lh3/minimap2>

PAF format <https://dgenies.toulouse.inra.fr/documentation/formats>