**The Darwin Tree of Life project**

The advent of high-throughput long-read sequencing and genome mapping technologies \cite{}, improvements in base accuracy of long reads \cite{} and development of algorithms that take advantage of the longer read length and long-range genomic interactions \cite{} has brought new enthusiasm to sequence and assemble high-quality reference genomes \cite {}.

The Darwin Tree of Life (DToL) project is an ambitious project that aspires to construct chromosome-length scaffolds for 70, 000 eukaryotic species in Britain and Ireland \cite{}. In parallel, other international consortiums has initiated projects with similar aspirations for insects \cite{}, vertebrates \cite{}, invertebrates \cite{} and all of life \cite{}. The DToL project, currently, uses CCS reads for contig generation, Hi-C reads to order and orient contigs, and Hi-C contact matrix to manually inspect and correct chromosome-length scaffolds. We would like to highlight that the DToL project regularly updates their primary sequencing and mapping technologies and assembly, purging and scaffolding algorithms to reflect the advancements in the field. At the time of writing, the DToL project has sequenced approximately 800 species, completed the assemblies of approximately 500 species, and raw data and reference genomes have been made available to the public \cite{}.