



Bioinformatic aspects of the GAP reference genome project.

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The Genomics for Australian Plants (GAP) project is undertaking the large scale genome sequencing of key Australian plant species to provide reference genomes in taxonomic groups where no other genomes are available. As a final stage of this project, ~20 plant species have been selected for simultaneous DNA isolation, long-read sequencing, and assembly. In this presentation we will give an overview of the chosen bioinformatic pipelines for this work and their pros and cons.

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