Phylogenies derived from somatic mutations agree with physical topologies in *Eucalyptus*

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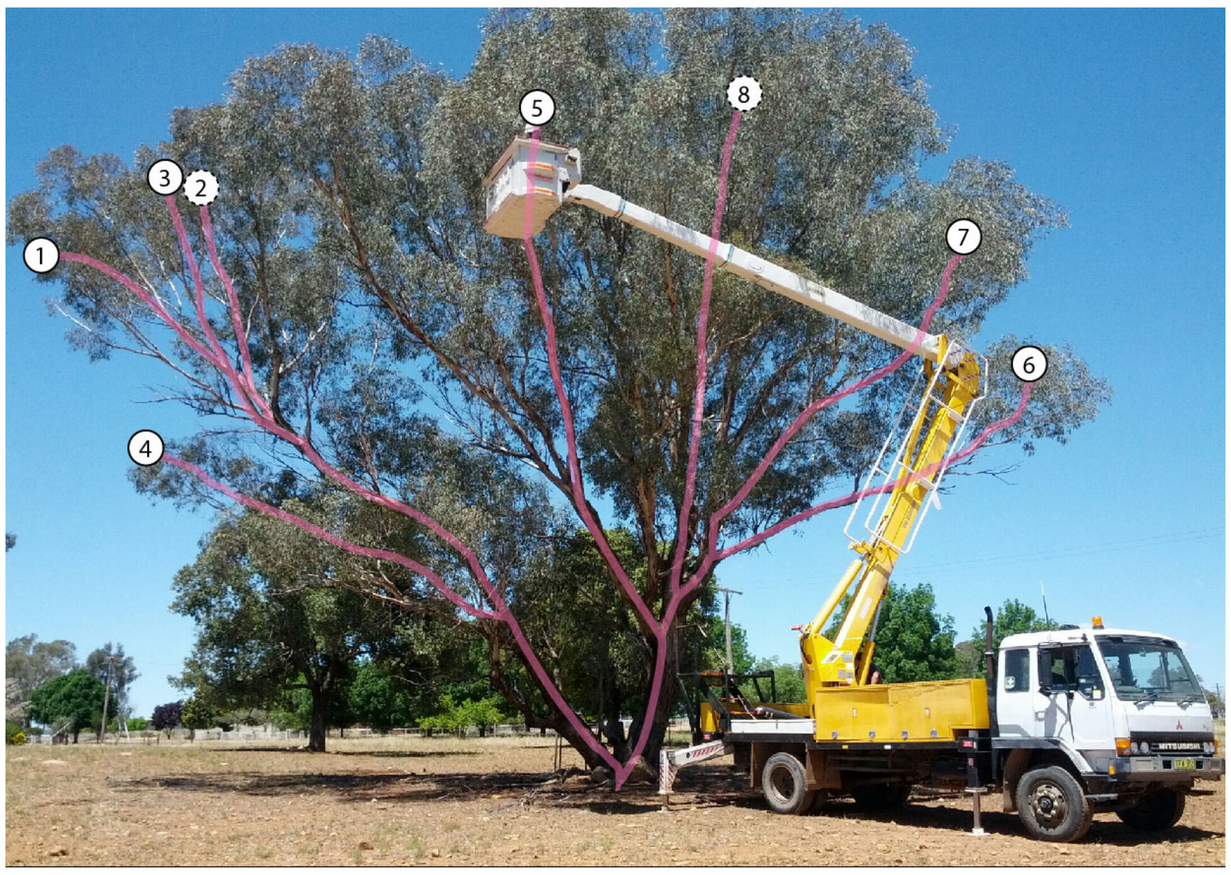
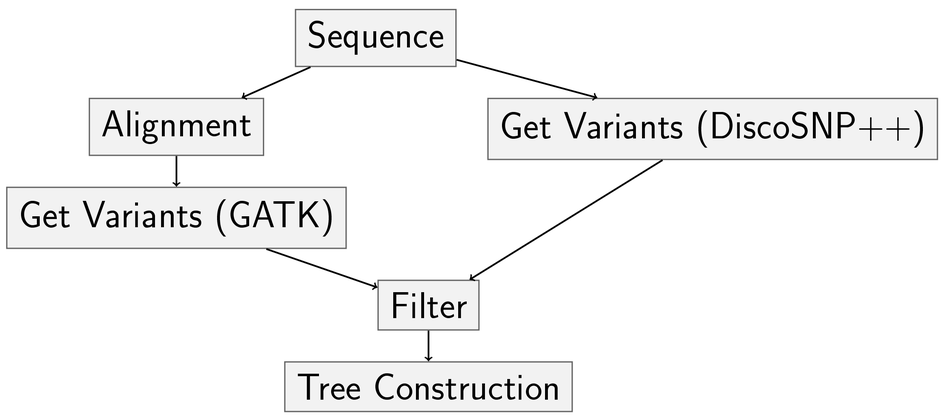
Introduction

- Somatic mutations are rare but sequencing errors are common, making somatic mutations difficult to detect.
- Little is known about the spread of somatic mutations, despite the key role they play in cancer development.
- If the pattern of mutations in the phylogeny matches the branching pattern of the plant, then plants can be used to easily validate somatic mutations.

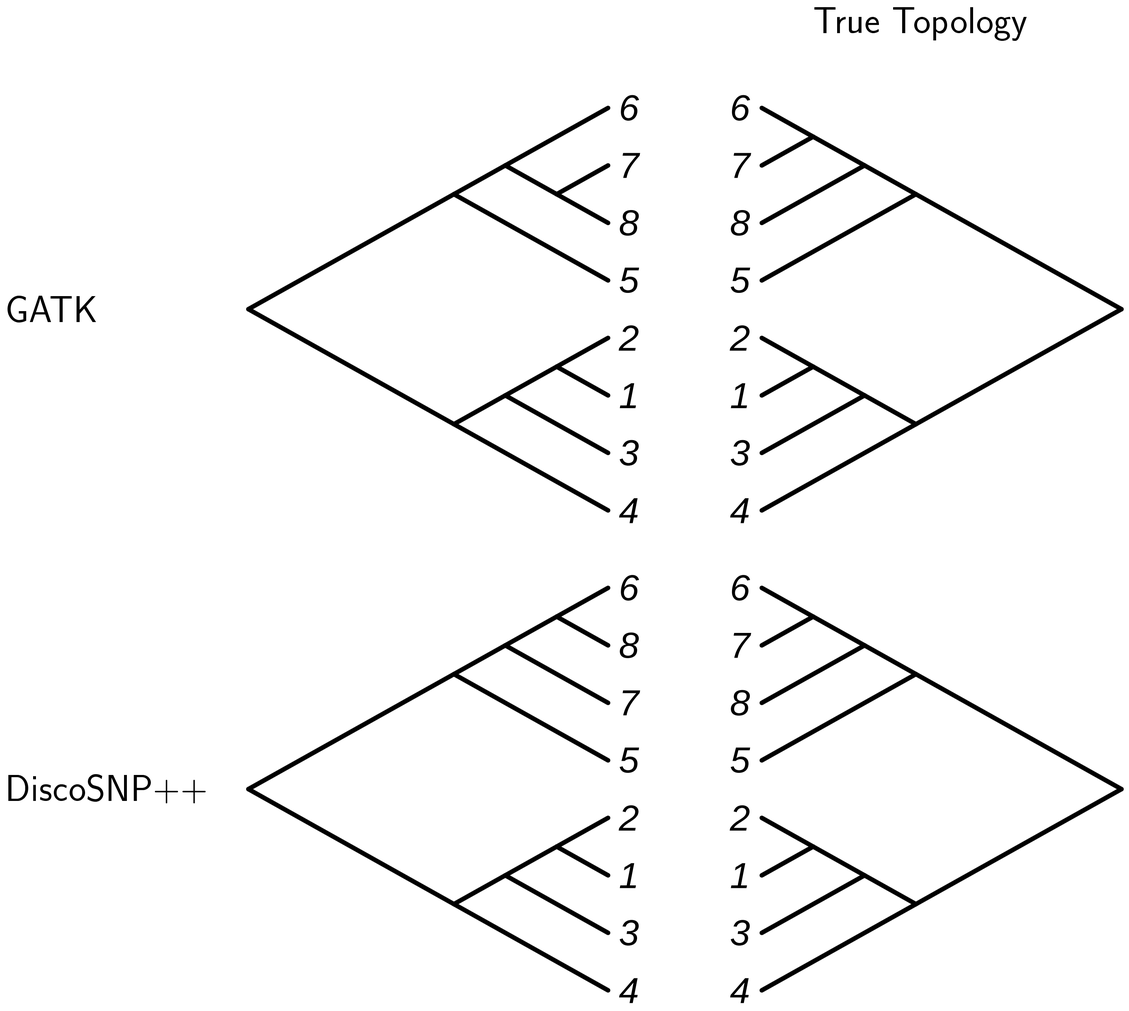
Methods: Variant Detection



- 8 samples collected in triplicate
- Variants were removed if the genotypes of all replicates of a sample were not identical



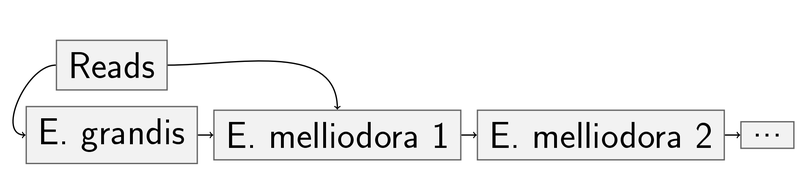
Results: Variant Detection



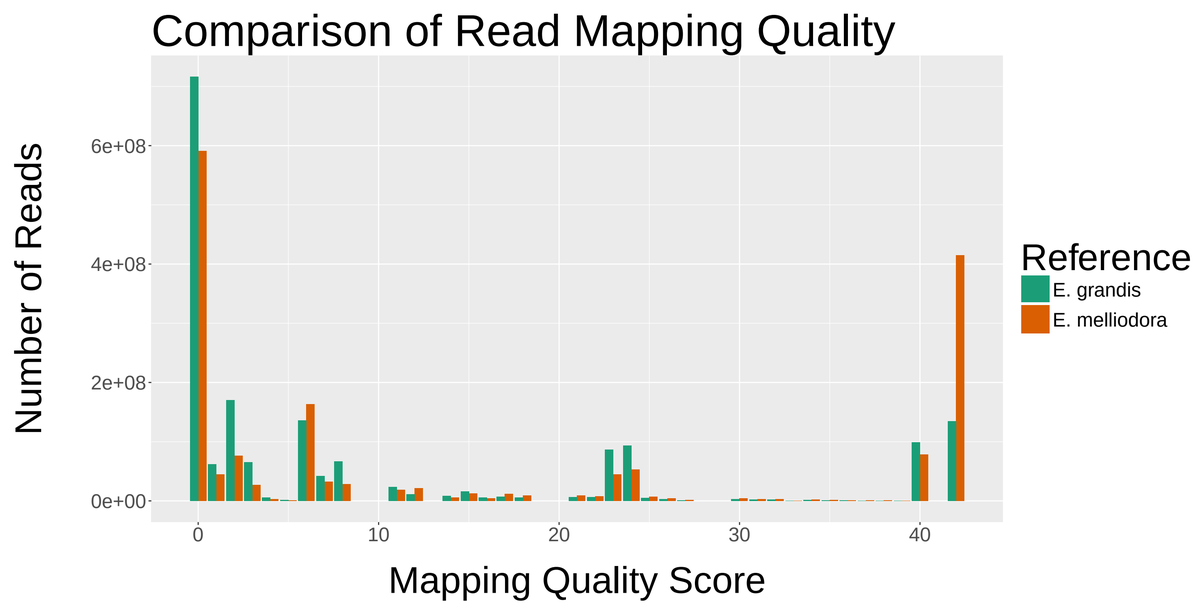
Next steps: Reference Improvement

To improve resolution of short internodes, we attempt to modify the *E. grandis* genome to make it more suitable for *E. melliodora* by:

- Aligning the reads to the *E. grandis* genome
- Creating a consensus sequence from this alignment
- Aligning the reads to this consensus to create a draft *E. melliodora* genome



Results: Reference Improvement



Alignment to the consensus sequence produces an alignment with higher overall quality scores than alignment to the *Eucalyptus grandis* reference.

The Choice of Mapper Affects Generated Reference Quality

Conclusions

- Phylogenies of somatic mutations within a *Eucalyptus* tree match the branching patterns of the tree using both a reference-based and a reference-free variant caller.
- Aligning reads to a close relative, obtaining a consensus sequence, then realigning to that consensus seems to improve alignment quality.
- The choice of aligner makes a difference.

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