Navigating phylogenetic conflict and evolutionary inference in plants with target capture data

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Abstract

Target capture has quickly become a preferred approach for plant systematic and evolutionary research, marking a step-change in the generation of data for phylogenetic inference. While this advancement has facilitated the resolution of many relationships, phylogenetic conflict continues to be reported, and often attributed to genome duplication, reticulation, incomplete lineage sorting or rapid speciation – common processes in plant evolution. The proliferation of methods for analysing target capture data in the presence of these processes can be overwhelming for many researchers, especially students. In this review, we break down the causes of conflict and guide researchers through a target capture bioinformatic workflow, with a particular focus on robust phylogenetic inference in the presence of conflict. Through the workflow, we highlight key considerations for reducing artefactual conflict, managing paralogs, and assessing conflict, and discuss current methods for investigating causes of conflict. While we draw from examples in the Australian flora, this review is broadly relevant for any researcher working with target capture data. We conclude that conflict is often inherent in plant phylogenetic research, and that although further methodological development is needed, target capture data can still provide unprecedented insight into the extraordinary evolutionary histories of plants when carefully analysed.

Keywords: paralogy, polytomy, discordance, incongruence, incomplete lineage sorting, deep coalescence, hybridisation, polyploidy, HybSeq, target enrichment, Genomics for Australian Plants, PAFTOL, GAP, Angiosperms353

Introduction

Target capture sequencing (also referred to as target enrichment and HybSeq) has rapidly become a preferred approach for phylogenetic inquiry. In Australian plant systematics, a multitude of data types are used (Nauheimer *et al.* 2019; Fowler *et al.* 2020; Gunn *et al.* 2020, 2024; Orel *et al.* 2023, 2024), but the ongoing trend points to a greater adoption of target capture sequencing (Fig. 1). Briefly, target capture sequencing works by breaking genomic DNA into short fragments, capturing fragments that belong to loci of interest ('target loci') by binding ('hybridising') them to pre-designed baits (also referred to as 'probes'), and then amplifying those fragments while washing away most fragments that are not of interest. The remaining DNA fragments of targeted loci (often called 'enriched' or 'hybridised' libraries) are then

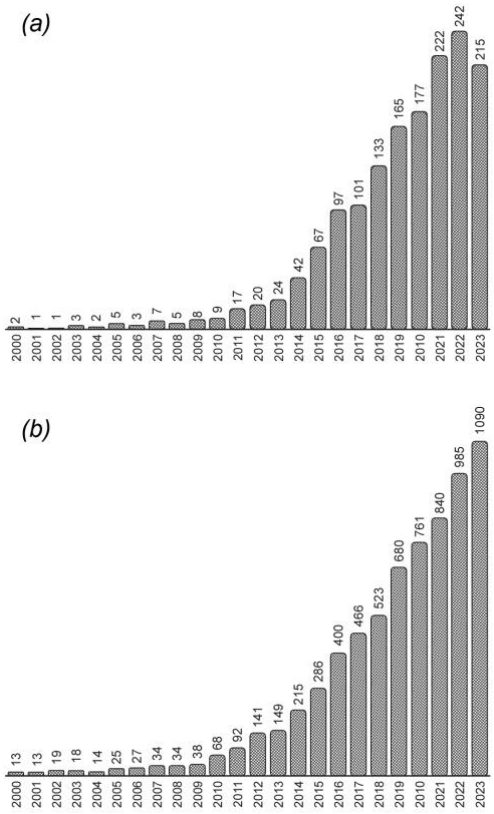

Fig. 1. Number of academic papers in Google Scholar published each year from 2000–2023 matching the search terms '"target capture" OR "target enrichment" OR "Hyb-Seq" AND "DNA" AND "plant"': *(a)* matches also including the search term 'Australia', *(b)* matches not including the search term 'Australia'. Obtained using the Python script of Strobel (2018).

sequenced, and these short sequences ('reads') are reassembled through a bioinformatic pipeline to reconstruct the sequences of the targeted loci (for more detail see e.g. Andermann *et al.* 2020). The rapid uptake of this technique in phylogenetic research is due to the many advantages that target capture data offers, including the ability to sequence a high number of loci with large amounts of phylogenetic information, compatibility across datasets using the same baits, and the ability to obtain targeted loci from degraded material such as herbarium specimens (Hart *et al.* 2016; Shee *et al.* 2020). It has been further expedited through the establishment of initiatives such as Plant and Fungal Trees of Life (PAFTOL) in 2016 (Baker *et al.* (2021); https://www.kew.org/science/our-science/projects/plant-and-fungal-trees-of-life) and Genomics for Australian Plants (GAP; https://www.genomicsforaustralianplants.com) in 2017. These ventures coordinated efforts of researchers and institutions to use the Angiosperms353 (A353) bait kit (Johnson *et al.* 2019) to sequence 353 single- or low-copy nuclear loci conserved in angiosperms, facilitating the generation of the most densely-sampled and data-rich nuclear phylogeny of angiosperms to date (Zuntini *et al.* 2024). Other universal bait kits have also been developed in the past five years, such as the GoFlag bait kit for flagellate plants (Breinholt *et al.* 2021) and the OzBaits kit for Australian plants (Waycott *et al.* 2021), and custom bait kits for particular groups are now commonplace for finer-scale phylogenetic investigation (e.g. Compositae1061, Siniscalchi *et al.* (2021); Vatanparast *et al.* (2018)) or when groups have proven challenging to investigate with Angiosperms353. This has culminated in the production of an unprecedented volume of data for plant phylogenomic research across taxonomic levels within the Australian flora, as detailed in Table 1.

Although target capture has aided the resolution of many previously elusive plant relationships (e.g. Larridon *et al.* 2021; Pillon *et al.* 2021; Schmidt-Lebuhn and Grealy 2024), it has proved not to be the 'silver bullet' for resolving the evolutionary history of many plant groups as well supported bifurcating

Table 1 List of studies using target capture sequencing that have included members of the Australian flora. Ongoing work on several other Australian plant groups as part of GAP Stage 2 using Angiosperms353 baits can be found here: https://www.genomicsforaustralianplants.com/phylogenomics/. 'Nuclear' is abbreviated as 'nuc'; 'chloroplast' is abbreviated as 'cp'.

Plant group	Baits kit	Assembly method	Tree inference method	Authors	DOI
Caladenia and Diurideae (Orchidaceae)	Custom baits (up to 1000+ loci)	Custom pipeline, Hybpiper	Both	Peakall *et al.* (2021)	10.1111/1755-0998.13327
Eucalypts (Myrtaceae)	Custom baits (101 nuc exons)	Custom pipeline	Both	Crisp *et al.* (2024)	10.1111/jse.13047
Eucalyptus (Myrtaceae)	Custom baits (568 nuc genes, including Angiosperms353 & OzBaits)	Hybpiper-nf, HybPhaser	Both	McLay *et al.* (2023)	10.1016/j.ympev.2023.107869
Calandrinia (Montiaceae)	Custom baits for Caryophyllales	Custom pipeline	Both	Hancock *et al.* (2018)	10.1002/ajb2.1110
Cryptandra (Rhamnaceae)	OzBaits	Custom pipeline	Concatenated	Nge *et al.* (2024)	10.1093/botlinnean/boad051
Pomaderris (Rhamnaceae)	OzBaits	Custom pipeline	Concatenated	Nge *et al.* (2021)	10.1016/j.ympev.2021.107085
Calytrix (Myrtaceae)	OzBaits	Custom pipeline	Both	Nge *et al.* (2022)	10.1002/ajb2.1790
Adenanthos (Proteaceae)	OzBaits	Custom pipeline	Both	Nge *et al.* (2021)	10.3389/fevo.2020.616741
Crinum (Amaryllidaceae)	OzBaits	Custom pipeline	Concatenated	Simpson *et al.* (2022)	10.1071/SB21038
Halophila (Hydrocharitaceae)	OzBaits	Custom pipeline	Concatenated	Van Dijk *et al.* (2023)	10.3390/d15010111
Pogonolepis (Asteraceae)	Angiosperms353	Hybpiper	Concatenated	Schmidt-Lebuhn (2022)	10.1071/SB22010
Anthemideae tribe	Angiosperms353	Hybpiper-nf	Concatenated	Schmidt-Lebuhn & Grealy	10.1071/SB23012
Gnaphalieae tribe	Custom baits (Compositae 1061)	Hybpiper	Both	Schmidt-Lebuhn & Bovill	10.1002/tax.12510
Hakea (Proteaceae)	Custom bait kit (450 nuc loci)	Custom pipeline	Both	Cardillo *et al.* (2017)	10.1111/evo.13276
Thelypteridaceae	GoFlag (451 nuc loci)	Hybpiper,	Both	Bloesch *et al.* (2022)	10.1016/j.ympev.2022.107526
Cunoniaceae	Angiosperms353	Hybpiper	Coalescent	Pillon *et al.* (2021)	10.1002/ajb2.1688
Zanthoxyloideae subfamily	Angiosperms353	Hybpiper,	Both	Joyce *et al.* (2023)	10.3389/fpls.2023.1063174
Eriostemon group (Rutaceae)	Angiosperms353	Hybpiper-nf,	Both	Orel *et al.* (2025)	10.1002/tax.13308
Aglaia (Meliaceae)	Angiosperms353	Hybpiper,	Concatenated	Cooper *et al.* (2023)	10.54102/ajt.p8to6
Celmisiinae	Angiosperms353	Hybpiper-nf	Both	Nicol *et al.* (2024)	10.1016/j.ympev.2024.108064
Hibbertia (Dilleniaceae)*	Angiosperms353, OzBaits (nuc & cp)	CAPTUS	Both	Hammer *et al.*	
Drosera (Droseraceae)	Angiosperms353, OzBaits (nuc & cp)	CAPTUS	Both	Williamson *et al.*	
Alismatales	Angiosperms353, OzBaits (nuc & cp)	CAPTUS	Both	Waycott *et al.*	
Chamelaucieae tribe	Angiosperms353	SECAPR	Both	Nge *et al.* (2025)	https://doi.org/10.1071/SB24014
Minuria (Asteraceae)	Angiosperms353	HybPiper-nf	Both	Schmidt-Lebuhn *et al.* (2025)	

trees, with ‘conflict’ continuing to be reported. Conflict, also often referred to as ‘discordance’ or ‘incongruence’, refers to when phylogenies of individual loci do not share the same topology with either the species tree or with each other. Such conflict can be the result of contamination during lab work, data artefacts introduced by researchers during analysis, or inherent biases in target capture data (Steenwyk *et al.* 2023; Frost *et al.* 2024). Alternatively, conflict can be the product of real biological processes that cause evolutionary histories of genes and lineages to deviate from each other or from a bifurcating tree. Such processes, like whole-genome duplication (WGD) events, reticulation, and incomplete lineage sorting (ILS) have long been known to be common and important events in the evolution of plants but were difficult to detect in phylogenetic studies prior to the broad adoption of high-throughput sequencing techniques. Now, the findings of a growing number of target capture datasets demonstrate that these processes are pervasive in plants, manifesting as conflict. For example, in the Australian flora, conflict has been attributed to likely WGD events in target capture datasets of *Adenanthos* (Nge, Biffin, *et al.* 2021), *Pomaderris* (Nge, Kellermann, *et al.* 2021), *Calytrix* (Nge *et al.* 2022), *Cryptandra* (Nge *et al.* 2024), *Senecio* (Schmidt-Lebuhn *et al.* 2024), *Celmisiinae* (Nicol *et al.* 2024) and many lineages in Sapindales (Joyce *et al.* 2023). Conflict due to reticulation has been detected in *Adansonia* (Karimi *et al.* 2020) and Thelypteridaceae (Bloesch *et al.* 2022), and reticulation in concert with deep coalescence in *Adenanthos* (Nge, Biffin, *et al.* 2021) and *Eucalyptus* (McLay *et al.* 2023).

As illustrated by the above examples, conflict in target capture data, if handled carefully, can give insight into key biological processes in the evolutionary history of plants. However, the recent and rapid proliferation of software and pipelines for target capture analysis can be confusing for those new to the field, especially students. Faced with this abundance of methods, it can be unclear how to design a bioinformatic pipeline for analysing target capture data in a way that reduces artefactual conflict introduced by the researcher and enables the researcher to test for any biological processes that might underlie any remaining conflict. In this review, we explain what phylogenetic conflict is and the causes of it, and go on to describe the key steps in a target capture bioinformatic pipeline that should be considered in the face of phylogenetic conflict. While not an exhaustive review of all software available, we highlight key practical considerations for reconstructing and interpreting a phylogeny from the starting point of having raw reads to: 1. Loci extraction, 2. Paralogy reconciliation, 3. Phylogenomic reconstruction of gene trees and species trees, 4. Conflict assessment, and 5. Investigating patterns and underlying causes of conflict. Through the steps of the pipeline we explore what conflict actually is and how to measure it, draw attention to steps where conflict can be introduced, make recommendations on how to minimise artefactual conflict, and summarise current approaches for testing for the biological processes of WGD, reticulation, deep coalescence and simultaneous/rapid speciation that may underlie any remaining phylogenetic conflict. We then go on to highlight remaining issues with current methods and areas in need of further research.

What is phylogenetic conflict, and what causes it?

Phylogenetic conflict, also often referred to as ‘discordance’ or ‘incongruence’, refers to when subsets of phylogenetic data (such as gene trees, quartets or sites) do not share the same topology with either the species tree or with each other (Lanfear and Hahn 2024). This often leads to species trees being ‘unresolved’ with poorly supported topologies, and is commonly viewed as a hindrance to conclusive evolutionary inference (see ‘Conflict assessment’ for more detail). However, when properly understood, and providing that data is correctly handled, conflict can present an opportunity to gain new insight into the evolutionary history of a lineage. Conflict in a phylogenetic dataset can be attributed to two main sources: biological processes that cause individual loci to have topologies that are different from each other and the species tree, or that cause the lineage’s evolutionary history to deviate from a bifurcating pattern (‘Biological sources of conflict’), and errors introduced into the dataset by the researcher through the analytical pipeline (‘Artefactual conflict’).

Biological sources of conflict

There are four main issues that can cause conflict in a phylogenetic dataset, that are the result of real, biological processes: (1) paralogy, (2) reticulation, (3) deep coalescence and ILS, and (4) simultaneous speciation or rapid radiation (Fig. 2). The processes that can lead to each issue are summarised below. Most are common in evolution, particularly in plants, and therefore care should be taken to design an analytical pipeline that has the best chance of being able to detect them. Detecting biological conflict can give valuable insight into the evolutionary history of a lineage and can enrich the inferences made during scientific enquiry.

Paralogy

Generally in phylogenomics, single-copy loci are targeted to ensure homologous sequences ('orthologs') that share a common ancestor are analysed. However, even when attempting to target single-copy loci paralogy is commonly encountered, whereby multiple copies of the same locus are present in a phylogenetic dataset. Paralogy is caused either by gene duplication or whole genome duplication (WGD) followed by lineage diversification. WGD events involve the doubling of an organism's entire genetic material within the same species (autopolyploidy), or after inter-species hybridisation (allopolyploidy, see also below) (del Pozo and Ramirez-Parra 2015). They are known to be common and important sources of diversity in the evolution of land plants but present challenges for phylogenomic analysis (Clark and Donoghue 2018; Morales-Briones *et al.* 2021).

Divergent evolution of the resulting gene copies will lead to differences that are inherited by descendent species and can cause retained gene copies in the same individual to group in separate clades in phylogenetic analyses. Copies from the same clade (or ortholog group) of the resulting gene family phylogeny represent orthologs (descendants of the same copy), but copies in separate clades are paralogs (descendants of different copies). Treating paralogs as orthologs can mislead phylogenetic analysis (Struck 2013), and therefore it is important to handle paralogs in an appropriate way (see '2. Paralog reconciliation'). In an ideal case, paralogy would be easily recognised by observing sister clades in a gene tree that both contain the same complement of samples (Fig. 2b), and for WGD, this pattern would be replicated across all genes. In these cases, WGD is easily detected in a phylogenetic dataset if paralogs are appropriately handled. However, while duplicated gene copies can be retained (and often specialise in function — a major source of evolutionary novelty (Flagel and Wendel 2009)), more often the locus will re-diploidise over time (lose one or more of the copies), leading to a more ambiguous pattern of gene duplications and losses (Fig. 2c) (Mason and Wendel 2020; Bomblies 2020). This means that some loci (although the exact proportion in plants is unknown, in yeasts it is estimated to be *c*. 10% of loci; Scannel *et al*. (2006)) will be present as single-copy loci, but they are in fact 'hidden paralogs' (also referred to as pseudo-orthologs) rather than orthologs. Therefore, even with careful handling of paralogs in a target-capture dataset, hidden paralogy may be an unavoidable and undetectable source of conflict in a dataset, especially in smaller datasets (Xiong *et al.* 2022). In contrast, however, some theoretical models suggest that hidden paralogs have negligible impact on phylogenetic inference in specific biological scenarios (Smith and Hahn 2022). More studies are needed to understand the impact of hidden paralogs in phylogenetic inference in plants.

Reticulation

Reticulation is caused by a variety of processes such as introgression and allopolyploid speciation that are often colloquially lumped together as 'hybridisation'. Introgression at the same ploidy level occurs when partially fertile hybrids between two species back-cross with parental species, leading to the movement of genetic material between the parents, and is increasingly recognised as a major driver of plant evolution. It can act as a source of additional genetic variation in species, and potentially even facilitate adaptation to novel stresses or habitats (Suarez-Gonzalez *et al.* 2018; Edelman and Mallet 2021). Conversely, introgression of maladaptive alleles during incipient speciation can lead to strong selective pressure towards

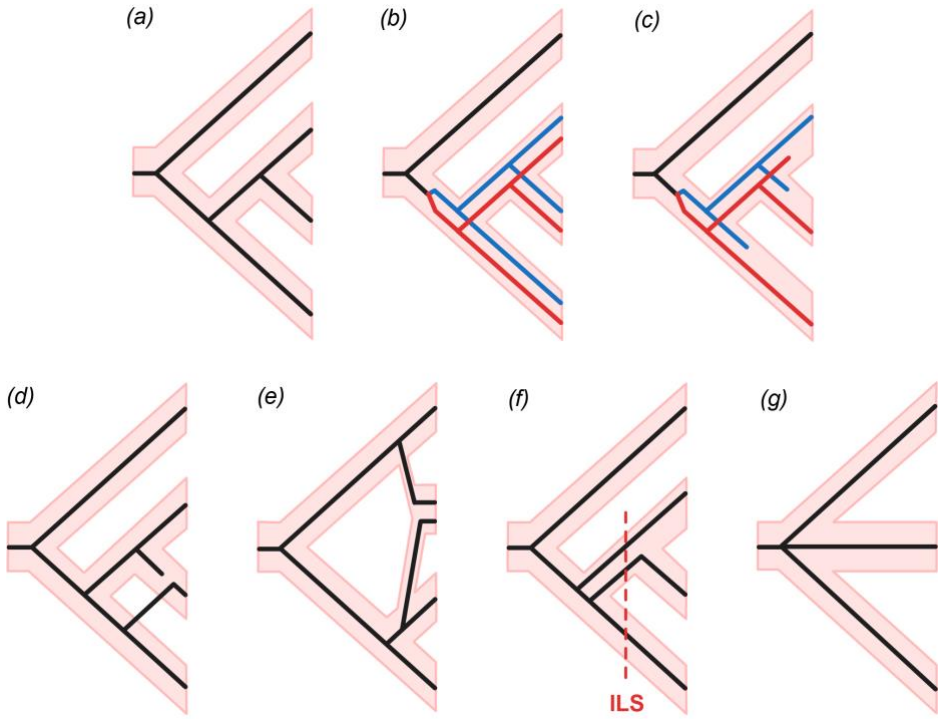

Fig. 2. Possible scenarios for gene evolution during species diversification. (*a*) Congruence between the species tree (pink bars) and gene tree (narrow lines). (*b*) Paralogy with one gene duplication and no gene losses. Red and blue indicate two ortholog groups. (*c*) Paralogy with one gene duplication followed by gene losses (or failure to capture or assemble gene copies) that left no evidence of paralogy. (*d*) Introgression (reticulation). (*e*) Allopolyploid hybridogenic speciation (reticulation). (*f*) Deep coalescence. The dotted line marked 'ILS' indicates transient incomplete lineage sorting in an ancestral lineage, i.e., the two alleles present in the middle lineage (large population) are not monophyletic (one is more closely related to an allele in the sister lineage). *(g)* True multifurcation due to simultaneous speciation.

reproductive isolation (Ostevik *et al.* 2016). In a phylogenetic context, introgression leads to incongruence between gene tree and species tree, because the transfer of alleles between species follows a reticulate rather than a bifurcating pattern (Fig. 2d).

A special case of introgression is organelle capture, with chloroplast capture particularly relevant to plant phylogenetics because of the field's traditional reliance on chloroplast loci. Evidence across many taxa indicates that organelles are more easily transferred across lineages than nuclear genes (Stegemann *et al.* 2012), resulting in cases where plastid phylogenies are incongruent with morphological, nuclear ribosomal, and low copy nuclear data (e.g., Schmidt-Lebuhn and Bovill 2021). Perhaps the best-known Australian example where phylogenetic inference has been confounded by frequent chloroplast capture is in the eucalypts (McKinnon *et al.* 1999; Nevill *et al.* 2014). Organelle capture can sometimes be inferred from conflict in the topology of species trees generated with plastid, morphological and nuclear data, in combination with tests for introgression in the nuclear dataset (e.g. Nge *et al.* 2021, McLay *et al.* 2023).

Allopolyploid speciation occurs when a hybrid between two species that is normally sterile due to an inability to produce functional gametes undergoes WGD, often through the production of unreduced gametes (Fig. 2e). This allows meiosis to be successful in their offspring, as the chromosomes can now pair with their duplicates. Allopolyploid speciation is a major factor in plant evolution (Soltis *et al.* 2009; Aïnouche and Wendel 2014; Alix *et al.* 2017; Clark and Donoghue 2018). Allopolyploid speciation produces phylogenetic conflict in a dataset in two ways: it results in a non-bifurcating pattern of gene inheritance due to the crossing of two species, and it doubles gene copies (paralogy). As in WGD or gene

duplication without hybridisation, allopolyploidy results in paralogs in a phylogenomic dataset, and the resulting copies can specialise or, more frequently, re-diploidise through gene losses (Bomblies 2020).

Deep coalescence and ILS

Under coalescent theory, incongruence between gene trees and between an individual gene tree and the species tree is expected even in the absence of paralogy or reticulation. The underlying process is referred to as either 'deep coalescence' or 'incomplete lineage sorting' (ILS), and has been understood for decades (Pamilo and Nei 1988; Maddison 1997). Ancestral species with large effective population sizes are able to maintain a high diversity of alleles. At a lineage split in an ancestral species, both daughter species inherit a random sample of this diversity. If a gene lineage splits simultaneously with the species split, over time genetic drift will lead to the extinction of relictual ancestral alleles, and the remaining alleles in each species will be monophyletic (i.e. completely sorted), and the gene tree will be concordant with the species tree. However, if effective population sizes remain large, and species lineage splits follow quickly upon each other, then ancestral alleles that diverged prior to the species splits will not yet have been lost (i.e. they are incompletely sorted), and may be inherited. In this case, the gene tree will not reflect the species phylogeny (Fig. 2f). This pattern is referred to as deep coalescence when looking deeper in the tree (Rannala *et al.* 2020), because the gene lineages coalesce deeper in the phylogeny than the species lineages they are evolving in. The same pattern is called ILS when looking towards the tips of the tree, because persistent ancestral alleles are stochastically inherited (i.e. incompletely sorted into species; Rannala *et al.* 2020). It is a common cause of phylogenetic conflict, though its detection is dependent on the lineages sampled.

Simultaneous speciation and rapid radiations

Simultaneous speciation, whereby multiple species evolve at the same time rather than in a bifurcating manner, can also be a source of conflict in a phylogenetic tree. Simultaneous speciation is thought to occur rarely, but most commonly through allopatric, non-adaptive speciation, whereby a population is separated into more than two isolated geographic areas (e.g. through vicariance, mountain building or glaciation), and the individuals in each area evolve into separate lineages (Matsubayashi and Yamaguchi 2022, e.g. Dillenberger and Kadereit 2017); however, it is also theoretically possible for multiple species to evolve simultaneously through sympatric adaptive radiation events (Bolnick 2006), and combinatorial mechanisms (Marques *et al.* 2019). In phylogenetic terms, the simultaneous evolution of multiple lineages is a 'hard polytomy', with multifurcating branches, rather than bifurcating branches (Maddison 1989; Hoelzer and Meinick 1994). When forced to be represented as bifurcations, each gene tree may have random, conflicting topologies between lineages originating by simultaneous speciation simply because the pattern of mutation does not comply with a bifurcating pattern. However, the challenge with inferring simultaneous speciation is differentiating it from cases of rapid radiations that do follow a bifurcating pattern of evolution. In these cases, little time and few mutations may separate divergent lineages, and the lack of information makes these relationships particularly difficult to reconstruct. These are often referred to as 'soft polytomies' (Maddison 1989), where it is unclear if conflict is a result of a lack of information to resolve the true, bifurcating relationships of a rapid radiation, or a genuine case of simultaneous speciation (DeSalle *et al.* 1994; Whitfield and Lockhart 2007; Orel *et al.* 2023; Zhang *et al.* 2023).

Artefactual conflict

Artefactual conflict is discordance between subsets of phylogenetic data that arises from inappropriate bioinformatic choices, leading to errors, anomalies, biases and/or noise in phylogenetic results (e.g. Frost et al. (2024)). Artefactual conflict can be introduced at any step of the bioinformatic pipeline, but is especially common during locus extraction, paralog reconciliation and phylogenetic tree inference. For example, if loci are not assembled from the raw reads with stringent enough parameters, incorrect sequences can be assembled for some loci, leading to the inference of an incorrect evolutionary history for those loci that are in conflict with other loci. Such conflict is artificial, and may lead to inaccurate results and noise

that reduces phylogenetic resolution and also prevents the detection of real biological conflict. As such, it is important that the parameters and assumptions underlying each step in the analytical pipeline are carefully considered, and that the output (especially alignments, homolog trees, and gene trees) are checked and cleaned (see also the quality control steps marked with an asterisk in Fig. 3). Below, we set out the major steps in a phylogenomic analytical workflow: 1. Locus extraction; 2. Paralogy reconciliation; 3. Phylogenomic reconstruction of gene trees and species trees; 4. Conflict assessment, and 5. Investigating patterns and underlying causes of conflict (Fig. 3), and highlight key considerations at each step for reducing artefactual conflict.

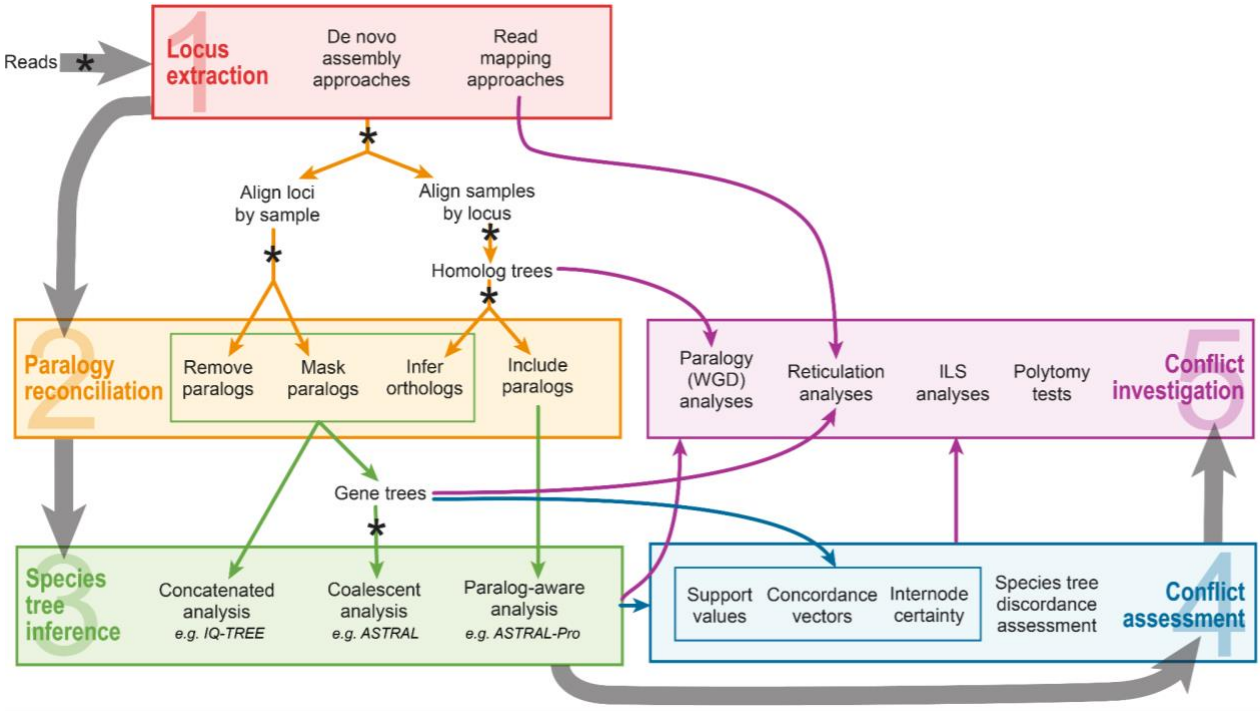

Fig. 3. Overview of the five major steps for a phylogenomic workflow with target capture data outlined in this review, from raw reads to 1) Locus extraction, 2) Paralogy reconciliation, 3) Species tree inference, 4) Conflict assessment and 5) Conflict investigation. Thick grey arrows indicate the general direction of the workflow. Within each step of the workflow, the main approaches are summarised, and coloured arrows indicate which approaches are compatible from each step. Circles with asterisks (*) indicate particularly important points where quality control should be conducted on the output of the previous step to avoid the introduction of artefactual conflict (e.g. by checking and cleaning alignments and gene tree topologies). For more details on each step, see the relevant section of this review.

Key steps for evolutionary inference in the face of phylogenetic conflict

1. Locus extraction

Following the sequencing of enriched libraries and quality control, the targeted loci must be assembled and extracted from the reads (Fig. 3). Many methods are now available for this purpose. One of the oldest and most commonly used locus extraction pipelines in plant phylogenomics is HybPiper (Johnson *et al.* 2016), which was developed specifically for the retrieval and assembly of target capture data using Angiosperms353, and is currently version 2.3.2 (see Table 2). HybPiper uses a read-mapping approach to align raw sequencing reads to reference gene sequences and then assembles those reads into contigs for both exons and their flanking intron regions (Johnson *et al.* 2016). HybPiper was greatly improved through the course of the GAP project, and version 2.0 is much easier to use as either a Python package or container,

with improvements in read-mapping, locus assembly, and recovery reporting (Jackson *et al.* 2023). Another program that implements a read-mapping approach is HybPhyloMaker (Fér and Schmickl 2018), which was also written for target capture recovery in plant phylogenomics, but in addition implements phylogenetic reconstruction. An alternative set of methods instead begins by *de novo* assembling all sequencing reads and then retrieving the target loci using reference gene sequences. Such software includes SECAPR (Andermann *et al.* 2020), PHYLUCE (which is more frequently used in animal phylogenomics with ultra-conserved elements; Faircloth 2016), and the recently developed CAPTUS (Ortiz *et al.* 2023). Assembly-first methods have the advantage of being able to cluster and extract many off-target loci without a reference target file, facilitating the extraction of additional nuclear and plastid loci for phylogenetic analysis (e.g. Ortiz *et al.* 2023). Both read-mapping and assembly-first assembly methods require a well-designed reference gene sequence file that includes sufficient coverage of the target genes across the phylogenetic scale of interest. For Angiosperms353, recovery can be improved by expanding the default target file to encompass more phylogenetic breadth (McLay *et al.* 2021). Although comparisons of some locus extraction pipelines have been published (e.g. Zhang *et al.* 2022; Raza *et al.* 2023), a comprehensive comparison of the performance of these methods across lineages and data qualities has not been conducted; as such, multiple methods could be tested on datasets to determine the most optimal and practical pipeline.

Ultimately, the choice of extraction pipeline will depend on the performance (locus recovery), computational efficiency, bait design and access to computational resources, as well as the research question. Some questions may require certain downstream analyses that are dependent on the output of particular locus extraction pipelines. For example, if one wants to use HybPhaser (Nauheimer *et al.* 2021) or Paragone (Jackson *et al*. 2023) for paralogy reconciliation (see next section "2. Paralogy reconciliation" for more detail), the output format of HybPiper is required. As such, planning the workflow ahead and checking whether output formats are compatible for downstream analyses (or can be manually altered to be compatible with downstream analyses) can help to inform which locus extraction method should be used. In some cases, using multiple locus extraction methods could be warranted. Careful attention should also be paid to matching the most appropriate extraction method to the way the baits have been designed. All baits are designed differently; not only do they target different loci, but they might target different regions of the targeted loci. Some of the first target capture methods used highly conserved regions as anchors to target highly variable regions around them, which may or may not be protein-coding (e.g. Lemmon *et al.*, 2012). In bait kits that explicitly target protein-coding regions, a 'locus' might comprise a single exon, while in other bait kits a locus may be multiple exons, introns, or the whole gene comprising exons and introns. Each locus extraction method will handle each scenario slightly differently. For example, SECAPR is designed for single-exon targets, and so portions of the pipeline must be adapted if one wants to use it to assemble loci such as the Angiosperms353 loci, which target multiple exons per locus. Because of the differences in the way assembly methods work, the methods also define and extract different regions of the targeted loci differently and care should be taken to make sure this is understood. Take, for example, a scenario where a multi-exon locus like an Angiosperms353 locus is being targeted. If HybPiper is being used, when reads are mapped to the exons some reads overhang the exon edge and represent partial sequences of the introns between exons. HybPiper calls these partial intron sequences 'flanking regions', and there is the option of concatenating these with all other exons and their flanking regions to produce a 'supercontig' for the locus. However, if CAPTUS is used, the entire gene, including full introns and exons might be able to be assembled (because *de novo* assembly of contigs occurs before extracting the targeted sequences), and the 'flanking regions' refer to the DNA sequences on either side of the whole gene. Therefore, care should be taken to understand how each assembly program will handle and define the structure of the targeted loci, and whether it will yield the desired output (exons *vs* introns *vs* genes). Finally, some locus extraction pipelines offer a workflow for additional steps beyond locus extraction, through to sequence alignment and even tree-estimation (Fér and Schmickl 2018; Ortiz *et al.* 2023). Although these pipelines are user-friendly, we caution against following these workflows without careful consideration and inspection of each step.

Artefactual conflict can be introduced by researchers at the locus extraction step in a number of ways. One cause of artefactual conflict is sequence errors introduced through misassembly; inclusion of misassembled, erroneous sequences for targeted loci (called 'contigs') can lead to the estimation of incorrect gene tree topologies that differ from the 'true' topology in other gene trees and the species tree. Therefore, misassembly issues need to be assessed and cleaned at this step of the bioinformatic pipeline to minimise artefactual phylogenetic conflict. Misassemblies can occur either through inappropriate settings for the short-read assembler program used in the locus extraction pipeline, or because of poor quality data. Different assembly pipelines use different short-read assemblers; for example, HybPiper and SECAPR use SPAdes (Bankevich *et al.* 2012), while CAPTUS uses MEGAHIT (Li *et al.* 2015). Each short-read assembler performs differently depending on the pattern of coverage, the presence of highly repetitive regions, GC and AT content, and the structural variation in each dataset (Liao *et al.* 2019). Using a suboptimal short-read assembler through the assembly pipeline can contribute to misassemblies and errors in the resulting sequences. Poor quality data can also cause misassemblies. In cases where samples have low DNA concentration or sequencing depth, read coverage (i.e. the number of reads mapping to any given section of the reference sequence for the targeted locus) may be low or uneven. The lower the read coverage, the higher chance of an erroneous base call in the contig by the short-read assembler because of a lack of information (Liao *et al.* 2019). Therefore, if loci have low coverage throughout, there is a higher chance of misassembly. Most short-read assemblers assume that there is an even coverage of reads, and use an average coverage cutoff threshold for contigs (Liao *et al.* 2019). While this means low coverage regions will be pruned out, it also can result in the assembly of contigs with a high proportion of missing data. Further, loci with low complexity or many repeated regions are also notoriously difficult to correctly assemble with short-read assemblers (Liao *et al.* 2019). Misassemblies can be detected by stringently checking the output sequences and alignments. The quality of the assemblies can be observed by manually remapping the reads to the reference sequences and checking the coverage. While time consuming and not always possible for all loci, this process can inform the researcher about whether there are issues with low or uneven read coverage, low complexity regions, or inappropriate short-read assembler settings (e.g. pruning thresholds). Misassemblies can also be detected by manually inspecting the resulting sequence alignments for each locus, paying special attention to misaligned or gappy areas of the sequence output for each locus alignment, although the judgement of the researcher of what is 'gappy' or 'well-aligned' can also introduce biases and errors. Therefore alignment summary tools can be used to rapidly and objectively summarise the alignment quality and gappiness, and a variety of programs such as AMAS (Borowiec 2016) or SEGUL (Handika and Esselstyn 2022) can be used for this. When misassemblies have been identified through these measures, a researcher can try to ameliorate these errors by remapping the reads to identify the problem causing the misassembly (as described above), adjusting the short-read assembler settings, trying another locus assembly pipeline with a different short-read assembler, manually deleting sequences with assembly errors (although this has rarely been done in the literature), or automatically deleting sequences with errors. Automatic deletion of erroneous sequences can be done at the alignment step, and after phylogenetic trees for each locus have been generated. Deletion of erroneous sequences or erroneous parts of sequences from alignments (i.e. alignment 'cleaning') can be achieved using tools such as TrimAl (Capella-Gutiérrez *et al.* 2009), ClipKIT (Steenwyk *et al.* 2020) and CIAlign (Tumescheit *et al.* 2022). Erroneous sequences can also be removed once phylogenetic trees for each locus have been generated; these sequences are likely to result in spuriously long branches, and can be detected and trimmed with tools like TreeShrink (Mai and Mirarab 2018). Once spurious tips have been deleted, the 'clean' sequences should be realigned prior to estimation of final trees. Determining the threshold for parameters for all of these tools requires comprehensive data exploration and trial and error.

Missing data can also introduce artefactual conflict. Low quality samples (for example samples with low DNA or library concentrations) may yield poor coverage or biased sequence files that can result in uneven recovery across samples or loci. This can produce extremely short sequences or loci represented by very few samples that result in alignments with substantial missing data, which is problematic for phylogenetic inference (Nute *et al.* 2018, Smirnov and Warnov 2021). While there may be a desire to keep all samples

and loci in a dataset, samples or loci with missing data can mislead phylogenetic inference through a lack of information (e.g. Smith *et al.* 2020), thereby resulting in discordant topologies for those samples or loci, and ultimately phylogenetic conflict. There is some evidence that the impact of missing data is particularly amplified in datasets with high levels of ILS (Xi *et al.* 2016; Nute *et al.* 2018). To avoid potential biases, sample removal thresholds should be high, and inspections of sequences to check for coverage (as well as the percentage of recovered length) should also be conducted. Inspection and cleaning of alignments can be achieved using the same methods for inspecting and cleaning alignments for errors as described above. Additionally, the first steps of HybPhaser (e.g. the script 1b_assess_dataset.R) and CAPTUS are useful for summarising assembly quality, missingness, and information content of the loci.

A third source of phylogenetic conflict at the locus extraction step is in the assembly of chimeric contigs. Chimeric contigs are sequences for a targeted locus that are formed from parts of different alleles or copies that have been stitched together (Nauheimer *et al.* 2021). Chimeric contigs can introduce phylogenetic conflict as they combine the phylogenetic signals of gene copies that are not homologous, and can therefore result in incorrect gene or species tree topologies that are in conflict with each other and the 'true' evolutionary history. Read-mapping methods such as HybPiper may be more prone to assembling chimeric contigs, because reads are mapped to each exon separately and then subsequently stitched together. HybPiper now has a number of options to reduce the likelihood of assembling chimeric contigs, and these should be carefully explored, particularly in cases where paralogy is an issue, and when multi-exon targets are used. Assembly-first methods such as CAPTUS may do a better job at avoiding the assembly of chimeric contigs, but are not necessarily immune to this problem, so output should still be carefully examined. As with assessing the output of locus extraction for short-read assembler errors and missing data, chimeric contigs can be detected through inspection and cleaning of alignments, spuriously long branches in gene trees and remapping reads.

2. Paralogy reconciliation

After loci have been extracted, dealing with paralogs is one of the most important parts of a phylogenomic workflow with target capture data (Fig. 3; Smith and Hahn 2021). It is particularly important for plant phylogenomics, as gene or genome duplications are common, and can produce paralogs in datasets even when using bait kits targeting 'single-copy' loci (De Bodt *et al.* 2005; Panchy *et al.* 2016; Ren *et al.* 2018; Landis *et al.* 2018; Almeida-Silva and Van de Peer 2023). There are an increasing number of workflows to handle paralogs in phylogenomic datasets that can be categorised into four main approaches: 1) remove paralogs (or paralogous loci); 2) mask the effects of paralogs; 3) infer orthologs, and 4) estimate species trees directly with a paralog-aware method (Fig. 3&4). Each approach has a different philosophy and set of underlying assumptions, which affects not only species tree estimation, but also the downstream analyses that can be applied to investigate biological processes such as ILS, hybridisation, and WGD events. The choice of approach should therefore be based on the philosophy that is most suitable for the analytical workflow the researcher wants to apply, as well as the biological system and questions at hand.

In the first approach, there are two options for removing paralogs: by filtering paralogs from paralogous loci so that only one copy is retained, or by excluding all paralogous loci detected (Fig. 4a). In the first option, paralogs are filtered based on a criterion such as similarity to a reference sequence, pairwise similarity, or length, for example, as implemented in PPD (Zhou *et al.* 2022), ParalogWizard (Ufimov *et al.* 2022) or the filtering steps of CAPTUS (Ortiz *et al.* 2023). As a result, copies of paralogous loci are removed, and only the sequence that is the longest or most similar is retained for each locus. This option may be suitable for some lineages where minimal paralogy is evident, in extremely large datasets, or for handling plastid loci, where few to no paralogs are expected to be present. However, it should be clear that this approach makes no attempt to infer orthology. As such, analysis of the remaining loci not only violates the assumptions of homology in phylogenetic inference but also runs the risk of estimating erroneous topologies and introducing artefactual conflict into phylogenetic trees, because each retained copy may not

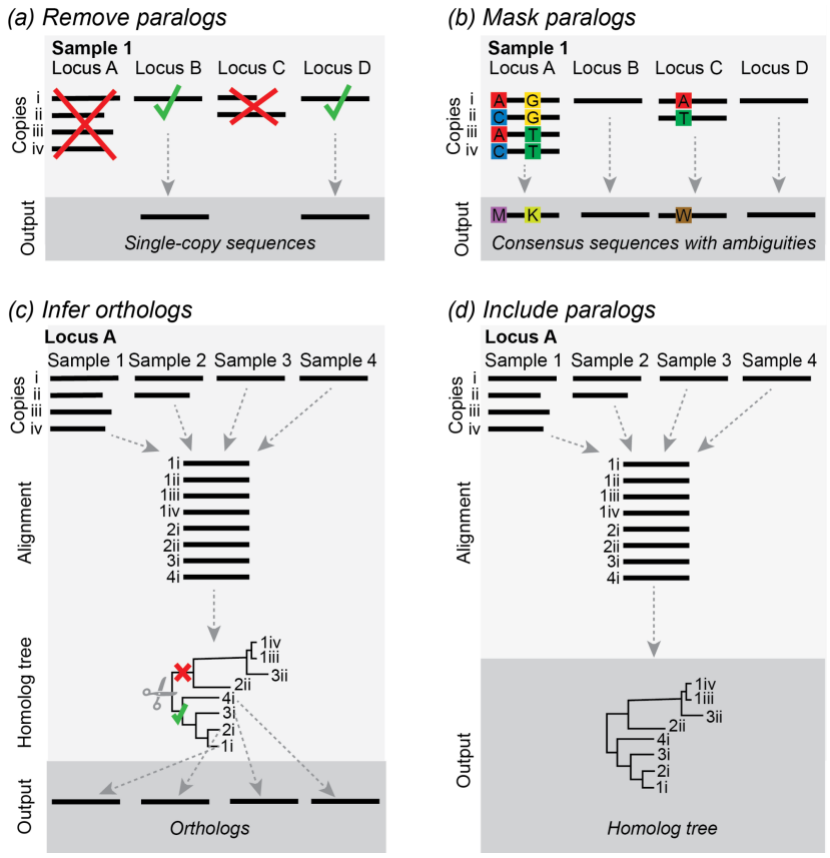

Fig. 4. Schematic diagram illustrating the four main approaches used for paralog reconciliation with target capture data in hypothetical scenarios with four samples (Samples 1–4) and four loci (Locus A–D). Locus A and C are paralogous, having multiple copies of the same locus (Copies i–iv). (a) Illustrates the removal of paralogs for a sample, whereby paralogous loci A and C are removed from the analysis and only single-copy loci B and D are retained for phylogenetic inference. This process would be repeated for each sample to obtain the final dataset for phylogenetic inference. (b) Shows paralog masking for a sample, whereby SNPs across aligned gene copies for paralogous loci A and C are coded with ambiguity characters in the consensus sequences for each locus used for phylogenetic inference. This process would be repeated for each sample to obtain the final dataset for phylogenetic inference. (c) Depicts tree-based ortholog inference, whereby all gene copies are aligned for each locus to infer homolog trees. These homolog trees are pruned (denoted by the scissors) to an ortholog sub-tree (denoted by the green tick) to identify orthologous sequences to then use in phylogenetic inference. In this scenario, the sequences in the clade of copies denoted by the red cross are discarded from the analysis. (d) Illustrates a scenario where all paralogs are used in phylogenetic inference. As in (c), homolog trees are estimated for each locus using an alignment of all gene copies, and these homolog trees are then directly used in species tree-estimation software such as ASTRAL-Pro.

share the same evolutionary history. This is especially problematic for smaller datasets, and when using concatenated methods of species tree inference (Yan et al. 2022). There is some evidence to suggest coalescent species-tree inference methods are somewhat robust to using randomly filtered paralogs for analysis in large datasets (Yan *et al.* 2022); however, this evidence is based on simulated data in specific biological scenarios and one empirical dataset. Further, this approach limits the potential for downstream investigation of conflict and gaining insight into any biological causes of conflict, as homology and paralogy is essentially ignored. Therefore, in practice for target capture studies on plants, we advise caution is taken if using this approach. The second option for removing paralogs (completely removing any paralogous locus; Fig 4a) is scientifically defensible, but also has limitations. By removing paralogous loci, researchers only include single-copy loci, which are more likely to be orthologous. In effect, this is an attempt to only include orthologs, which then satisfies the assumptions of homology in phylogenetic inference and can be justifiably used for tree inference. The downside of this method, however, is that it can substantially reduce the number of loci and therefore the amount of information for phylogenetic

inference (Yan *et al.* 2022), potentially leading to poor resolution in estimated trees in smaller bait kits such as Angiosperms353, or in lineages that have recent WGD and so all or nearly all loci would be determined to have paralogy. It may also remove signals of biological processes such as hybridisation and WGD events that might be in the evolutionary history of the lineage, and still cannot avoid the issue that some single copy loci might be hidden paralogs rather than orthologs. If identifying the presence and nature of such processes is of interest to the scientific study, then a different paralog handling approach that uses the information in paralogs is likely to be more appropriate (see paralog reconciliation approaches 2–4 below).

The second approach for dealing with paralogs in target capture datasets is by masking the paralogs with consensus sequences coded with ambiguity codes (Figs. 3 & 4b). This approach, which can be implemented in pipelines such as HybPhaser (Nauheimer *et al.* 2021) and that of Kates *et al.* (2018), aims to mitigate the effects of paralogs by encoding single nucleotide polymorphisms (SNPs) from different paralogs (and alleles) as ambiguous characters. In theory, this captures uncertain homology of the base at those sites, and therefore less weight is placed on these sites when inferring species tree topology. In doing so, it reduces the phylogenetic conflict caused by these sites across paralogs. Additionally, characterisation of the percentage of SNPs and allele divergence between paralogs through HybPhaser has been shown to be a good indication of ploidy within the phylogenetic tree (Hendriks *et al.* 2023) and can be used to phase paralogs and identify hybridisation events (Nauheimer *et al.* 2021; see section '5. Investigating patterns and underlying causes of tree conflict'). One potential pitfall of this approach is that the introduction of ambiguities into the dataset may eliminate potentially important phylogenetic signal at those sites, which can theoretically decrease the resolution of the tree. Potts *et al.* (2014) found this to be true for a series of short (< c. 1100 bp) single-gene datasets, but Kates *et al.* (2018) did not find the same for target capture data; further research is needed to test the effects of this approach on phylogenetic informativeness.

The third approach involves the inference of orthologous sequences from all sequences based on gene tree topologies (Figs. 3 & 4c). This approach, summarised by Yang and Smith (2014), takes gene trees with paralogs (herein referred to as 'homolog trees') and identifies sub-trees that only contain nodes representing speciation events (herein referred to as 'ortholog sub-trees'), rather than nodes that may be a result of gene duplication. These sub-trees include sequences for each gene that are orthologous (i.e., share a common ancestor), which can then be extracted from the original dataset, aligned, and used for species tree estimation. There are several algorithms for pruning homolog trees to ortholog sub-trees. Choice of algorithm depends on the availability and quality of outgroup sequences (which the Maximum Inclusion (MI) algorithm doesn't require) and on the trade-off between retrieving few ortholog sub-trees with good sampling (Monophyletic Outgroups (MO) algorithm) *versus* many ortholog sub-trees with many missing samples (Rooted subTrees (RT) algorithm) (Yang and Smith 2014). For reliable ortholog identification, it is important to carefully clean the initial, raw homolog trees by removing any spurious sequences (e.g. by pruning especially long branches), and reduce any monophyletic tips of the same species (that could represent alleles or neopolyploids) to one representative sequence in order to produce clean homolog trees. Orthology inference (and other downstream analyses such as WGD mapping, GRAMPA and ASTRAL-Pro — see the section '5. Investigating patterns and underlying causes of tree conflict') can then be performed on the clean homolog trees (also often referred to as 'multi-labelled trees'). Tree-based ortholog inference can be implemented through the scripts developed by Morales-Briones *et al.* (2021), or through the software Paragone (Jackson *et al.* 2023). By identifying orthologous sequences, the underlying assumption of homology in evolutionary models is maintained, and the conflicting signal of paralogs is eliminated, resulting in robust phylogenomic inferences. This approach of generating homolog trees and ortholog sub-trees also has the advantage of facilitating many options in downstream analyses for meaningful conflict investigation and inferring its underlying biological processes.

The fourth approach to dealing with paralogs entails the estimation of species trees using methods explicitly designed to accommodate paralogs (Figs. 3 & 4d), as summarised in Smith and Hahn (2021). Rather than

building homolog trees only to prune out all paralogs and only use orthologs for species tree inference (as in the previous orthology inference approach), paralog-aware methods use all paralogs from the homolog trees to infer the species tree topology. Instead of assuming a single gene tree topology across all loci, paralog-aware methods explicitly model and account for gene duplication and loss events in the estimation of species trees, though the method of doing so varies between programs. Programs such as ASTRAL-Pro (Zhang *et al.* 2020; Zhang and Mirarab 2022), FastMulRFS (Molloy and Warnow 2020), SpeciesRax (Morel *et al.* 2022), and iGTP (Chaudhary *et al.* 2010) use homolog trees and model gene evolution, duplication and loss events using two-step coalescent or parsimony-style approaches. Decomposition methods such as DISCO (Willson *et al.* 2022) apply a tree-pruning algorithm to the homolog trees (similar to the third paralog-reconciliation approach), splitting homolog trees into ortholog sub-trees (also known as 'orthogroups') prior to species-tree estimation, usually under the coalescent. As with the orthology-inference approach to paralogs, optimal implementation of these methods is dependent on the use of clean homolog trees, rather than the raw homolog trees. By integrating information across paralogous loci while accommodating gene tree discordance, these methods offer a sound option for accurate species tree estimation in complex evolutionary scenarios. However, two-step coalescent-based methods such as ASTRAL-Pro come with some drawbacks, such as treating gene tree topology as fixed even where nodes may be poorly supported because of short individual gene alignments. This potentially misleads species tree inference, and results in undefined branch lengths on the phylogeny (Mirarab *et al.* 2016; Simmons and Gatesy 2021). These issues may be mitigated with the development of new paralog-aware species tree estimation methods such as AleRax (Morel *et al.* 2024), which uses the distribution of homolog tree topologies to inform species tree inference; however, this method is yet to be applied in a plant phylogenetic context. Nevertheless, resolving paralogy *before* phylogenetic analysis gives the researcher more methodological and software options for the latter.

Each of these approaches is based on a distinct philosophy and set of underlying assumptions, influencing not only species tree estimation but also the possibilities for downstream analyses, and their interpretability and robustness. In some cases, taking multiple complementary approaches to dealing with paralogs may give additional insight into any conflict present in the dataset and help to answer research questions pertaining to underlying biological sources of conflict.

3. Phylogenomic reconstruction of gene trees and species trees

Following the first three paralogy reconciliation approaches (i.e. once a sequence copy from each locus has been chosen), there are multiple methods available for species tree inference (Fig. 3). Tree-inference methods have been reviewed comprehensively (see e.g. Leache & Rannala (2011); Simmons and Gatesy (2015); Mirarab *et al.* (2016)), so we will not review these in-depth in this paper. Briefly, the two main methods currently used to infer species trees from target capture data are Maximum Likelihood analyses conducted on concatenated sequence alignments (such as with IQ-TREE (Nguyen *et al.* 2015; Minh, Schmidt, *et al.* 2020) and RAxML (Stamatakis 2014; Kozlov *et al.* 2019), and two-step coalescent approaches based on gene tree topologies (such as with ASTRAL (Mirarab *et al.* 2014)). Bayesian analysis of phylogenomic datasets can also be performed using ExaBayes (Aberer *et al.* 2014), and for smaller datasets of fewer than a hundred terminals, Bayesian inference under the multispecies coalescent (e.g. with StarBEAST (Douglas *et al.* 2022)) is another computationally feasible option. Each method comes with its own set of assumptions that may be more or less suitable depending on the scale of taxonomic sampling, size of study group, and lineage. By using methods that rely on a concatenated sequence alignment, it is assumed that the evolutionary history of all loci is congruent with the evolutionary history of the species, but since this is not true, phylogenetic conflict can manifest as poorly supported nodes or erroneous yet strongly supported relationships if the strongest signal is incongruent with the species history. Using a two-step approach enables the estimation of independent evolutionary histories of each gene, but is dependent on the use of loci with adequate phylogenetic information to produce well-supported gene trees. Furthermore, the degree of gene-tree topology error and ILS present in a dataset can also influence the

choice of tree-inference method, as conflict can increase the computational effort required (e.g. Tea *et al.* (2022)). We recommend using multiple tree-estimation methods for target capture datasets, especially because any conflict may give insight into artefactual issues or biological processes (see section '5. Investigating patterns and underlying causes of tree conflict').

It is important to note that artefactual conflict can arise during phylogenetic tree reconstruction through inappropriate choice of evolutionary models (such as substitution model), and gene tree estimation error (Cai *et al.* 2021). As such, it is good practice to conduct phylogenetic tree reconstruction with multiple approaches, carefully consider the assumptions of all choices made in the tree estimation models used, and to inspect gene trees for signs of error. Error in gene tree topologies can be caused by a number of factors, such as the inclusion of erroneous sequences, uninformative loci (due to slow mutation rates or short loci), or loci (or sites within loci) with extremely high rates of mutation prone to saturation and homoplasy. Filtering gene trees, or phylogenomic subsampling, can reduce artefactual conflict by selecting of a subset of genes that are considered reliable. Tools such as GeneSortR (Mongiardino Koch 2021) and PhylteR (Comte *et al.* 2023) perform comparative analyses to identify a set of gene trees that have higher phylogenetic utility and accuracy, as well as removing potential outlier gene trees. GeneSortR is particularly extensive in the comparisons it performs, including average pairwise distance, compositional heterogeneity, level of saturation, root-to-tip variance, Robinson-Foulds distance to a reference topology, average bootstrap support, and proportion of variable sites. It also has the added benefit of producing easy to interpret and publication-ready images of the summarised outputs. TreeShrink (Mai and Mirarab 2018) is another useful tool to reduce artefactual gene tree conflict, by identifying and pruning outlier long branches, thereby removing spurious samples. In combination with locus assembly and alignment assessment, gene tree assessment and phylogenomic subsampling can reduce the impact of non-biological conflict in the dataset and allow for more clear inferences of the true biological cause of conflict (see section '5. Investigating patterns and underlying causes of tree conflict').

Should a researcher want to go on to produce a dated phylogeny with node-dating, special considerations need to be made to deal with target capture datasets. Bayesian approaches to obtaining a dated phylogeny (e.g. BEAST (Bouckaert *et al.* 2014), MCMCTree in PAML (Yang 2007)) are computationally demanding, and with large datasets become intractable (Barba-Montoya *et al.* 2021). This can be solved by subsampling genes to choose the most clocklike and similar to the species tree, as implemented in SortaDate (Smith *et al.* 2018), or by using more computationally efficient phylogenetic dating methods such as penalised likelihood (Sanderson 2002), as implemented in TreePL (Smith and O'Meara 2012), the R package ape (chronos) (Paradis 2013; Paradis and Schliep 2019), and r8s (Sanderson 2003), or the relative rate framework (RRF) as implemented in RelTime (Tamura *et al.* 2012, 2018). However, in cases where extensive phylogenetic conflict is present and caused by biological processes like reticulation, deep coalescence/ILS or simultaneous speciation, extreme caution should be used in dating analyses. Currently, there is no method that can date a phylogeny that deviates from a bifurcating tree, and as such, trying to apply a molecular clock that assumes a bifurcating birth-death process of species evolution to such a phylogenetic tree could lead to erroneous results (see section 'Conclusions and future perspectives').

4. Conflict assessment

Before being able to identify the cause of phylogenetic conflict, one must first be able to pinpoint where the conflict occurs, and to what degree. Conflict may manifest as discordance between the topologies of species trees estimated with different methods or different data types, or between gene trees. Conflict in topology across species trees inferred with different data types or methods (e.g. discrepancies in the topologies of plastid and nuclear phylogenies, or discordance between coalescent and concatenated phylogenies) is usually identified visually and qualitatively described (Fig. 3). Conflict between the topologies of gene trees can be quantified on the resulting species tree in three main ways: through support

values, through concordance vectors (*sensu* Lanfear and Hahn (2024)), and through internode certainty (IC) (Fig. 3).

Support values, such as bootstrap values or posterior probabilities, are statistical measures of confidence for the existence of any given branch, akin to standard errors (Lanfear and Hahn 2024). While important measures, the increasing amount of data from high-throughput sequencing datasets means that support values tend towards their maximum, often giving inflated measures of confidence (Kumar *et al.* 2012; Thomson and Brown 2022). Concordance vectors, on the other hand, are statistical measures of the variation in the relationships of any given branch, analogous to standard deviation. Unlike support values, they are more robust to the effects of larger datasets, giving an informative summary of the variation in the topology of the taxa or clades at each node independent of the size of the dataset. Concordance vectors can be calculated in three ways: as gene concordance factors, as quartet concordance factors, and as site concordance factors. These are reviewed in depth in Lanfear and Hahn (2024), and here we provide only a brief summary of the major differences between the three measures.

In short, gene concordance factors (gCFs) compare the topology for each node of each gene tree to the topology of the species tree, and summarise the proportion of gene trees that have a topology concordant with the species tree (Ané *et al.* 2007; Baum 2007; Smith *et al.* 2015; Lanfear and Hahn 2024). gCFs can be calculated in a number of ways, and the exact measures of concordance differ slightly depending on the method used. The most computationally feasible and popular methods for large datasets are implemented in IQ-TREE2 (Minh, Hahn, *et al.* 2020), BUCKy (Larget *et al.* 2010), and PhyParts (Smith *et al.* 2015), which can also calculate concordance based on homolog trees (i.e. can account for duplications).

Quartet concordance factors (qCFs) are estimated by subsampling all (or many) sets of four taxa for each locus ('quartets'), estimating the unrooted topology for each quartet, and then counting the proportion of quartets that are congruent with the species tree. Tools available to calculate qCFs include the program ASTRAL and its subsequent versions (e.g. (Mirarab *et al.* 2014; Sayyari and Mirarab 2016) and Quartet Sampling (Pease *et al.* 2018).

Site concordance factors (sCFs) sample quartets of taxa for each node of the species tree, and use parsimony or maximum likelihood to count the number of informative sites (of a single locus or concatenated loci) that support each of three possible topologies for those taxa (Minh, Hahn, *et al.* 2020). Currently, this method is only implemented in IQ-TREE2 (Minh, Hahn, *et al.* 2020; Mo *et al.* 2023); however, sCFs are more susceptible to the effects of homoplasy than other concordance vectors, and so may overestimate discordance (Kück *et al.* 2022).

Another way to measure conflict within a species tree is by calculating internode certainty, which can be seen as a summary of the aforementioned concordance vectors that compares the support for a given branch to the support for the best-supported alternative resolution of that branch (Salichos and Rokas 2013; Zhou *et al.* 2020). Internode certainty can also be compared to branch length to gain an indication of potential factors that may be causing conflict. Visualising these quantified conflicts and the relative frequencies of different topological combinations can also be conducted through DiscoVista (Sayyari *et al.* 2018). Each measure of conflict has nuanced meaning, interpretation, and pitfalls (Lanfear and Hahn 2024), so it is always good practice to characterise conflict through a number of methods.

5. Investigating underlying causes of conflict

If care has been taken to reduce artefactual conflict, it is likely that the remaining conflict measured in phylogenetic trees is largely due to biological sources of conflict. As described above, the four main biological sources of conflict are (1) paralogy, (2) reticulation, (3) deep coalescence and ILS, and (4) simultaneous speciation or rapid radiation (Fig. 2). Given 'ideal' data, it would be possible to differentiate

between these patterns and to reliably infer the underlying evolutionary process in each case; however, sufficiently clear evidence may be unavailable with reduced-representation sequencing methods such as target-capture sequencing, because of secondary loss of gene copies (hidden paralogy) or failure to capture or assemble all existing copies. Further complicating matters is that there is no one method that can satisfactorily model and test for paralogy, reticulation and deep coalescence/ILS simultaneously. Therefore it is important to carefully select a suite of methods to test for and tease apart the effect of each of these processes if conflict is detected.

Paralogy

As previously explained, paralogy is caused either by gene duplication or whole genome duplication (WGD) followed by lineage diversification. WGD events can be identified through target enrichment data in a number of ways. Locus extraction software such as HybPiper and CAPTUS may be able to infer the presence and number of paralogs for each locus (Johnson *et al.* 2016; Ortiz *et al.* 2023), depending on data quality and sequencing depth. These are useful for extracting all sequence copies, and for gaining an indication of the amount of paralogy present in a dataset; however, these detected 'paralogs' are also likely to comprise divergent alleles and contigs with sequencing errors, and so further processing is required to identify paralogs that are the result of gene/genome duplication events. One method to more accurately characterise the degree of paralogy is through HybPhaser (Nauheimer *et al.* 2021). HybPhaser enables the user to define the threshold of heterozygosity that most likely represents true paralogs (rather than sequencing errors or alleles) so that they can be quantified. Further, heterozygosity has been shown to be correlated with ploidy level, and can therefore be used to characterise lineages that have a history of genome duplication (Hendriks *et al.* 2023). Alternatively, the paralog output of locus extraction software can be processed by first building clean homolog trees from all paralogs, extracting orthogroups from each homolog tree, and mapping those to the species tree to count the number of gene duplication events that occurred at each node (e.g. Yang *et al.* (2018); Morales-Briones *et al.* (2021)). While these gene duplication mapping approaches have been shown to be useful for large (transcriptomic and genomic) datasets, their application in smaller target capture datasets (particularly Angiosperms353 datasets) has not been extensively tested. Homolog trees can also be reconciled with species trees using programs such as GRAMPA (Thomas *et al.* 2017). GRAMPA uses a modified duplication-loss (DL) reconciliation algorithm (e.g. Goodman *et al.* 1979; Page 1994) to determine whether hypothesised genome duplication events are best explained by allo- or autopolyploidisation events. However, like any DL-based method, GRAMPA does not account for deep coalescence/ILS, and can only investigate genome duplication at one node at a time; therefore use of such methods requires careful consideration and interpretation of results. The development of new reconciliation algorithms that can account for the coalescent process are an important area of future research to disentangle WGD and ILS in phylogenomic datasets (Boussau and Scornavacca 2020; Mishra *et al.* 2023). When possible, any of these analyses can be combined with additional sources of evidence, such as Ks plots from transcriptomic and genomic data or karyological data, to pinpoint WGD events in a species tree (e.g. Yang *et al.* 2018).

Dealing with hidden paralogy remains an area in need of further research in phylogenomics. The extent of hidden paralogy in plant evolution is yet to be quantified, and as yet, there are no formal methods available to handle hidden paralogs. Use of appropriate and well-designed bait kits may minimise this issue, and careful inspection of sequence alignments and homolog trees may enable a researcher to infer loci where hidden paralogy is an issue. However, at this point, hidden paralogy continues to be an unavoidable source of phylogenetic conflict.

Reticulation

There are a number of approaches available for testing the presence of reticulation, and several comprehensive reviews already widely address the issue of hybridisation and introgression in

phylogenomic datasets (e.g. Hibbins and Hahn 2022; Stull *et al.* 2023; Steenwyk *et al.* 2023). Here we focus on methods that are applicable to target capture data.

Introgression can be difficult to separate from deep coalescence/ILS due to the similar signature that they leave in the data. Many methods for the detection of introgression work by comparing the depth of coalescence between estimated gene trees and the species tree, and infer introgression if the coalescence of gene lineages is too recent to be plausibly explained by deep coalescence (e.g. Joly *et al*. (2009); see 'Deep coalescence and ILS' below). Programs such as JML (Joly *et al*. 2012), QuIBL (Edelman *et al.* 2019) and Aphid (Galtier 2024) compare branch lengths of taxon triplets from ortholog gene trees, and by examining differences in branch lengths — shorter for gene flow and longer for deep coalescence — provide estimates of speciation times, ancestral population sizes, and quantify the impact of each process on phylogenetic conflict.

In cases of allopolyploid speciation, reticulation can be difficult to distinguish from autopolyploidisation, because phylogenetic conflict is caused by both a non-bifurcating pattern of gene inheritance due to the crossing of two species, and paralogy. In these cases, WGD mapping approaches such as GRAMPA (Thomas *et al.* 2017) are useful for inferring allopolyploid events from autopolyploid events (see previous section 'Paralogy'), and inferring putative parental lineages.

Further approaches available for detection of reticulation (with and without polyploidisation) in target-capture datasets include phasing methods, whereby reads of a putative hybrids are phased into subgenomes and placed separately into the species tree to identify putative parental lineages. This is commonly achieved in target-capture data through HybPhaser (Nauheimer *et al.* 2021), and has been shown to be highly effective in cases of neoallopolyploidy (e.g. Bloesch *et al.* 2022; Bradican *et al.* 2023); however the method requires careful selection of the presence of diploid references for putative parental clades, and is often unsuitable for groups with complex or ancient reticulation (e.g. McLay *et al.* 2023). The need for a diploid reference is overcome through the Bayesian implementation of phasing in homologizer (Freyman *et al.* 2023), but may require subsampling of target-capture datasets to reduce computational demands.

Other available methods derive from population genetics ABBA-BABA (or 'D-statistic') tests, whereby any deviation in site pattern probabilities from what would be expected in a bifurcating tree indicates reticulation or deep coalescence/ILS. Such tests can be implemented in programs such as HyDe (Blischak *et al.* 2018). However, the site pattern probabilities expected in ABBA-BABA methods are calculated under a suite of assumptions, including symmetrical gene-flow between populations and constant substitution rate across lineages and genes, which may be unrealistic, and could lead to inaccurate results (Frankel and Ané 2023). Therefore, these methods should be applied and interpreted with care.

Finally, network-based methods can be used to explore and depict reticulate evolutionary relationships, but these methods are still in their infancy and present a much-needed area for development. Distance-based methods such as Neighbor-Net (Bryant and Moulton 2004) and split decomposition methods such as SplitsTree (Huson 1998) are computationally feasible for phylogenomic datasets, but do not explicitly incorporate models of evolution, nor do they account for biological processes such as deep coalescence/ILS. Other phylogenetic network packages can implement more complex models, including the likelihood methods used in PhyloNet (Than *et al.* 2008) and more recently-developed Bayesian and coalescent methods (e.g. Yu and Nakhleh 2015; Solís-Lemus and Ané 2016; Wen *et al.* 2016; Zhang *et al.* 2018), such as those applied in PhyloNetworks (Solıs-Lemus *et al.* 2017). These can give robust estimations of phylogenetic networks but remain computationally intensive (often prohibitively so), restricting analysis to datasets of very few terminals. As phylogenetic network methods develop, they will be powerful tools to model and understand evolution in the presence of reticulation. However, networks are models that are more parameter-rich than bifurcating trees, so complex, reticulate scenarios will tend to be more statistically probable, even when they may not be true (Blair and Ané 2020). Therefore, results of phylogenetic network

analyses should be evaluated critically, and they are usually most useful as a complement to bifurcating trees, rather than as a replacement for them.

Deep coalescence and ILS

Despite the expected incongruence between gene trees due to deep coalescence, the underlying species tree can still generally be reliably inferred under the assumption that ILS is the process causing the incongruence, i.e. under the multispecies coalescent. While there are multiple methods for estimating the species tree, the most relevant to target capture data that accounts for deep coalescence are summary approaches like ASTRAL that take gene trees as input. If deep coalescence is the main cause of conflict in the data, target capture data are particularly promising for resolving the species tree because individual loci may be long enough to produce relatively resolved gene trees and there are many loci. However, depending on the biological system and bait set, if most loci have little phylogenetic signal, this can mislead methods like ASTRAL and make it harder to estimate the species tree (Molloy and Warnow 2018), underscoring the importance of evaluating phylogenetic signal and gene trees earlier.

Given that deep coalescence can leave a genetic signature similar to that of reticulation, most tests of deep coalescence also test for reticulation to differentiate the effect of these processes. Such tests include ABBA-BABA tests, and branch-length based methods like Aphid (Galtier 2024) and QuIBL (Edelman *et al.* 2019).

Simultaneous speciation and rapid radiations

As simultaneous speciation is best represented as a polytomy in a phylogenetic tree, most methods available to test for simultaneous speciation and rapid radiations are statistical 'polytomy tests'. These tests treat a polytomy as the null hypothesis (whereby the branch length is zero), and reject the null hypothesis based on data (Swofford *et al.* 1996; Anisimova and Gascuel 2006). Some versions also incorporate a power test to facilitate the differentiation of soft and hard polytomies (Walsh *et al.* 1999). Alternative Bayesian approaches such as that described by Lewis *et al.* (2005) are also available. However, these methods can only be applied to single-locus data. As such, the most popular method currently used for phylogenomic data is the polytomy test available through ASTRAL (Sayyari and Mirarab 2018). This method is also based on the concept of rejecting the null hypothesis of zero-branch-length polytomies in the tree, can test across multiple gene trees, and also accounts for ILS, but by nature is sensitive to errors in gene tree topology (Sayyari and Mirarab 2018). Regardless of the analysis conducted, conclusively inferring simultaneous speciation, and differentiating it from a rapid radiation or a deficit of data is usually very difficult unless the study is conducted with large amounts of phylogenetic data, at a shallow phylogenetic scale, and in conjunction with a great deal of ecological and biological knowledge of the group in question. Realistically, the exact mode of evolution in most cases of rapid radiation and simultaneous speciation is therefore unknowable.

Conclusions and future perspectives

Given the recent and rapid advancement of target capture data for plant phylogenetic studies, there are many areas of the bioinformatic workflow that need improvement and research to further reduce artefactual conflict. One important area is locus extraction and assembly; the accurate and complete detection of paralogs resulting from gene duplication remains a challenge for plant phylogenomics, especially in groups currently without reference genomes. Aside from the unavoidable issue of hidden paralogy (see 'Biological sources of conflict – Paralogy'), and misassembly issues that can arise from short-read assembler errors (see '1. Locus extraction'), there are indications that current assembly approaches may be underestimating real paralogy in Angiosperms353 datasets based on comparisons with reference genomes (Theodore Allnut, pers. comm.). While the extent of such issues are unknown at present, further refinement of locus extraction and assembly programs, along with more affordable reference genomes, and target capture sequence from

Table 2 Summary of software and tools mentioned in this paper.

Tool	Use	Output	Citation and URL
1. Locus extraction			
HybPiper	Locus assembly and extraction	Sequence files for each locus, assembly reporting, paralogy reporting, exons and intron sequences	Johnson *et al.* 2016, Jackson *et al.* 2023; https://github.com/mossmatters/HybPiper; https://github.com/chrisjackson-pellicle/hybpiper-nf
HybPhyloMaker	Locus assembly and extraction, plus alignment, trees	Sequence files for each locus, assembly reporting, paralogy reporting, exons and intron sequences, alignments, gene trees, species trees	Fér and Schmickl 2018; https://github.com/tomas-fer/HybPhyloMaker
SECAPR	Locus assembly and extraction	Sequence files for each locus, assembly reporting, paralogy reporting, exons and intron sequences, phased loci	Andermann *et al.* 2018; https://github.com/AntonelliLab/seqcap_processor
PHYLUCE	Locus assembly and extraction, typically UCE's	Sequence files for each locus, assembly reporting, alignments	Faircloth 2016; https://github.com/faircloth-lab/phyluce
CAPTUS	Locus assembly and extraction	Sequence files for each locus, assembly reporting, paralogy reporting, exons and intron sequences, plus organellar sequences, alignments	Ortiz *et al.* 2023; https://github.com/edgardomortiz/Captus
NewTargets	Expanding target file phylogenetic breadth using available genomic resources	An expanded target file, curated to end-user needs for improved recovery.	McLay *et al.* 2021; https://github.com/chrisjackson-pellicle/NewTargets
1.1 Locus extraction: Post-assembly assessment and alignment filtering			
AMAS	Alignment assessment and manipulation (e.g. sample removal)	Various alignment formats, individual locus or concatenated alignments plus partition files	Borowiec 2016; https://github.com/marekborowiec/AMAS/
TrimAL	Alignment trimming based on several parameters (e.g. gappiness, informativeness, overlap)	Trimmed alignments in user specified format	Capella-Gutierrez *et al.* 2009; https://vicfero.github.io/trimal/
ClipKit	Alignment trimming based on several parameters (e.g. gappiness, informativeness, codon position)	Trimmed alignments in user specified format	Steenwyk 2020; https://github.com/JLSteenwyk/ClipKIT
CIAlign	Alignment trimming based on several parameters (e.g. gappiness, informativeness, length, alignment quality)	Trimmed alignments in user specified format	Tumescheit *et al.* 2022; https://github.com/KatyBrown/CIAlign
opTrimal	Assessment of optimal alignment trimming thresholds	Untrimmed alignments in user specified format	Shee *et al.* 2020; https://github.com/keblat/bioinfo-utils/blob/master/docs/advice/scripts/optrimAl.txt
TAPER	Identification of alignment errors	Trimmed or untrimmed alignmments in user specified format	Zhang *et al.* 2021
2. Paralogy reconciliation			

PPD	Uses sequence identity and heterozygous sites to identify and remove paralogs	Alignments with detected paralogs removed	Zhou *et al.* 2022; https://github.com/Bean061/putative_paralog
ParalogWizard	Refined reassembly of loci to identifiy divergent sequences (i.e. paralogs or alleles) and perform orthology inference	Alignments sorted into orthologous groups	Ufimov *et al.* 2022; https://github.com/rufimov/ParalogWizard
CAPTUS	Identification of paralogous sequences during pipeline by comparing to a reference sequence	Paralogous sequences can be sorted into different alignments with user-defined parameters, including 'best' and 'similarity', or all copies can be kept, or removed	Ortiz *et al.* 2023; https://github.com/edgardomortiz/Captus
HybPhaser	Infer parental lineages of putatively hybridogenic lineages	Phased alignments with paralogs removed	Nauheimer *et al.* 2021; https://github.com/LarsNauheimer/HybPhaser
ParaGone	Implements Yang and Smith's (2014) collection of methods for resolving paralogy using gene tree topologies	Paralogy resolved alignments and gene trees from each Y&S algorithm	Jackson *et al.* 2023; https://github.com/chrisjackson-pellicle/paragone-nf
3. Species tree inference: Paralog-aware phylogenetic tree reconstruction			
ASTRAL-PRO	Two-step coalescent phylogenetics from multi-labelled trees (i.e including paralogous sequences)	Coalescent species tree with paralogous tips reconciled to species	Zhang and Mirarab 2022; https://github.com/chaoszhang/ASTER; https://github.com/chaoszhang/A-pro
FastMulRFS	Two-step coalescent phylogenetics from multi-labelled trees (i.e including paralogous sequences), using Robinson-Fould's distances to summarise paralogous sequences	Coalescent species tree with paralogous tips reconciled to species	Molloy and Warnow 2020; https://github.com/ekmolloy/fastmulrfs
SpeciesRax	Likelihood inference of species tree from gene alignments or gene family trees	Species tree, and gene trees if starting with alignments	Morel *et al.* 2022; https://github.com/BenoitMorel/GeneRax
DISCO	Performs orthology inference of each gene tree to preserve orthologous sequences and discard paralogs	Coalescent species tree with paralogous tips reconciled to species	Willson *et al.* 2022; https://github.com/JSdoubleL/DISCO
AleRax	Likelihood inference of species tree from samples of estimated gene family trees	Species tree, reconciled and consensus gene trees, number of events	Morel *et al.* 2024; https://github.com/BenoitMorel/AleRax
3. Species tree inference: Phylogenetic tree reconstruction on single-sequence-per-species alignments			
IQ-TREE	Likelihood phylogenetics on concatenated data	Phylogenetic tree (and other outputs depending on analysis)	Minh *et al.* 2020; http://www.iqtree.org
RAxML	Likelihood phylogenetics on concatenated data	Phylogenetic tree (and other outputs depending on analysis)	Stamatakis 2014,, Kozlov *et al.* 2019; https://github.com/stamatak/standard-RAxML; https://github.com/amkozlov/raxml-ng

ASTRAL	Two-step coalescent phylogenetics	Species tree	Mirarab *et al.* 2014, Zhang *et al.* 2018b; https://github.com/smirarab/ASTRAL
SplitsTree	Implements a range of network analyses, including the popular NeighbourNet and Consensus Network algorithms	Phylogenetic network	Huson and Bryant 2006; https://uni-tuebingen.de/en/fakultaeten/mathematisch-naturwissenschaftliche-fakultaet/fachbereiche/informatik/lehrstuehle/algorithms-in-bioinformatics/software/splitstree/; https://github.com/husonlab/splitstree6
ExaBayes	Bayesian phylogenetics on concatenated data	Phylogenetic tree (and other outputs depending on analysis)	Aberer *et al.* 2014; https://cme.h-its.org/exelixis/web/software/exabayes/
StarBeast	Bayesian inference of gene trees and species tree under the multispecies coalescent.	Posterior distribution and summary tree for species tree and gene trees	Douglas *et al.* 2022; https://github.com/rbouckaert/starbeast3
3.1 Species tree inference: Gene tree assessment and phylogenomic subsampling			
GeneSortR	Sorting and subsampling phylogenomic datasets to quantify phylogenetic usefulness	Sorted alignment, partition file, gene tree file and a plot of sorted genes by estimated properties, graphical summary of metrics employed to subsample	Mongiardino Koch 2021; https://github.com/mongiardino/genesortR
PhylteR	Identify outlier loci in phylogenomic datasets	Visualised output of outlier loci for removal	Comte *et al.* 2023; https://github.com/damiendevienne/phylter
TreeShrink	Pruning long, likely erroneous branches from sets of phylogenetic trees	Pruned phylogenetic trees and corresponding alignments	Mai and Mirarab 2018; https://github.com/uym2/TreeShrink
SortaDate	Phylogenomic subsampling to choose genes for phylogenetic dating	List of locus alignments of genes	Smith *et al.* 2018; https://github.com/FePhyFoFum/sortadate
4. Conflict assessment			
IQ-TREE	Likelihood phylogenetics on concatenated data and locus alignments or partition file	Gene concordance factors (gCFs) and site concordance factors (sCFs) on phylogeny as branch labels	Minh *et al.* 2020; http://www.iqtree.org
PhyParts	Identification of concordant and conflicting bipartitions	Species phylogeny with concordance and conflict as branch labels	Smith *et al.* 2015; https://bitbucket.org/blackrim/phyparts/src/master/
ASTRAL	Measuring concordance/discordance by percentages of supporting quartets used to produce species tree	Species phylogeny with quartet concordance and conflict as branch labels	Mirarab *et al.* 2014; https://github.com/smirarab/ASTRAL

BUCKy	Estimating concordance factors from Bayesian MCMC trees of many loci	Species phylogeny with concordance and discordance scores as branch labels	Larget *et al.* 2010; https://pages.stat.wisc.edu/~ane/bucky/
Quartet Sampling	Repeated sampling of quartets to analyze branch support on molecular phylogenies	Newick tree files of various scores, a FigTree file containing all scores, and statistics files	Pease *et al.* 2018; https://github.com/FePhyFoFum/quartetsampling
5. Conflict investigation			
HyDe	Detects hybridization in phylogenomic data sets	Values including identification of species and population level hybrids with ABBA-BABA tests	Blischak *et al.* 2018; https://github.com/pblischak/HyDe
JML	Detects hybridisation on time-calibrated trees, with information about population sizes	Distances between sequences for species pairs with *P*-values for hybridisation according to the posterior predictive distributions	Joly *et al*. 2012; https://github.com/simjoly/jml
Aphid	Estimating the contributions of gene flow and incomplete lineage sorting to phylogenetic conflict	Per gene tree output of conflict and the estimated cause (e.g. ILS or gene flow) in a csv file	Galtier 2024; https://gitlab.mbb.cnrs.fr/ibonnici/aphid
GRAMPA	Use homolog gene tree topologies (i..e. MULtrees) to identify placement and types of WGD	Tree and txt files detailing the estimated ploidy placement and type of polyploid	Thomas *et al.* 2017; https://github.com/gwct/grampa
QuIBL	Uses gene tree internal branch lengths to distinguish between hybridisation and deep coalescence	For each triplet in the species tree, an estimate of the relative contribution of the locus set to ILS or gene flow	Edelman *et al.* 2019; https://github.com/miriammiyagi/QuIBL
PhyloNet	Infer phylogenetic networks from sets of loci while accounting for both reticulation and ILS, using mostly maximum likelihood-based algorithms	Networks as Nexus files	Than *et al.* 2008, Wen *et al.* 2018; https://phylogenomics.rice.edu/html/phylonet.html
PhyloNetworks	Infer phylogenetic networks from sets of loci while accounting for both reticulation and ILS, under a coalescent model	Networks as Newick files	Solís-Lemus *et al.* 2017; https://github.com/crsl4/PhyloNetworks.jl
DiscoVista	Quantify and visualise a range of phylogenomic metrics including species tree and gene tree compatibility, branch quartet frequencies and GC content.	Figures showing gene tree discordance and relative frequency of different topologies, species tree discordance and taxon occupancy	Sayyari *et al.* 2018; https://github.com/esayyari/DiscoVista
ASTRAL	Perform a polytomy test to determine if the polyomy is ‘hard’ or ‘soft’	Species phylogeny with significance values that indicate the presence of a hard polytomy	Mirarab *et al.* 2014; Sayyari and Mirarab 2018; https://github.com/smirarab/ASTRAL

those same references, will greatly assist future studies. Further, a better understanding of hidden paralogy in plants, and how different bait sets and different targeted loci (e.g. introns *vs.* exons) perform is needed to further develop best practices for reducing artefactual noise and investigating the causes of conflict.

Even when phylogenomic analysis is carefully conducted so that data artefacts are minimised, phylogenetic conflict is often inevitable and expected given underlying biological processes. Although this conflict can often be carefully investigated to identify processes such as reticulation, paralogy, deep coalescence or polytomies as its cause, many methods to detect these processes are still being developed. The inability of many conflict interrogation analyses to account for more than two processes at once can make it difficult to differentiate their effects on phylogenetic conflict, and their influence on evolution. Phylogenetic network methods also have much need for improvement so that they can be applied meaningfully to large datasets. Currently, one of the main hindrances to the further development of these analyses is modelling the complex interactions between ILS, reticulation, paralogy and polytomies in such large datasets. It is likely that machine learning will play a large role in overcoming these obstacles in the future, although this would also come with its own set of caveats and limitations (Mo *et al.* 2024). In the meantime, the limitations of the data and assumptions of models used should always be acknowledged and taken into consideration while these methods develop. The biological conclusions we make need to carefully consider and include the inherent (and real) uncertainty in our study systems.

Although identification of conflict and its underlying biological processes offers interesting insights into the mode of plant evolution, it also presents challenges for downstream evolutionary analyses such as dating, diversification analyses, ancestral area reconstruction and ancestral trait reconstruction. In cases where conflict is caused by noise from paralogs or deep coalescence, researchers may opt for downstream analyses that can account for the topological uncertainty at nodes with high degrees of conflict. In cases of reticulation and simultaneous speciation, however, it is more difficult to reasonably conduct these analyses, as most cannot yet account for evolution that is not modelled by a bifurcating tree. In these cases, we encourage researchers to be realistic about what analyses can be justifiably conducted, and when they are conducted, to be transparent about assumption violations and uncertainty in results. It is possible that creative solutions can be found in these scenarios by, for example, conducting analyses on subsets of taxa or trees. On the whole though, development of dating, diversification and ancestral state reconstruction models that can account for these processes is another area of much needed research, especially for plant evolutionary research.

We have long known that plant evolution is complex, with reticulation, whole genome duplication events, ILS and rapid radiations commonly reported, and so it should be unsurprising that phylogenetic conflict is inherent within many plant lineages. Although target capture has made conflict more obvious, in some cases it can also give unprecedented capacity to empirically test for the underlying biological processes causing it, giving new insights into the extraordinary complexities of plant evolution. For the Australian flora, this has meant shedding light on long-standing questions previously unanswerable due to a 'lack of resolution' intractable from previously available technologies. To date, target capture studies have greatly enhanced our understanding of the timing and tempo of radiations (Joyce *et al.* 2023; Nge *et al.* 2024), the role of hybridisation and introgression in evolution (Bloesch *et al.* 2022; McLay *et al.* 2023; Nge *et al.* 2021 – *Adenanthos*), polyploidy and WGD events (Nge, Kellermann, *et al.* 2021; Schmidt-Lebuhn *et al.* 2024), and the evolution of diverse and important ecological groups in Australia (Crisp *et al.* 2024; McLay *et al.* 2023; Peakall *et al.* 2021; Schmidt-Lebuhn and Bovill 2021). They have also shed light on biogeography within Australia (Nge *et al.* 2021a; 2021b – *Calytrix* and *Pomaderris*), as well as Australia's biotic connection with other land-masses (Joyce *et al.* 2023; Nge *et al.* 2021 – *Pomaderris*), demonstrating Australia's role as both a source and sink of global plant diversity (Pillon *et al.* 2021; Van Dijk *et al.* 2023). Further, they have aided in taxonomic classification and the description of new species (Cooper *et al.* 2023; Crisp *et al.* 2024; Schmidt-Lebuhn and Grealy 2024; Simpson *et al.* 2022). These studies are only scratching

the surface, but clearly have been an extraordinary advancement for our understanding of the Australian flora. We envisage that greater adoption of target capture approaches through collective (GAP and the Australian Angiosperm Tree of Life – Schmidt-Lebuhn *et al.* in prep), group-specific studies (e.g. Stage 2 GAP phylogenomics – https://www.genomicsforaustralianplants.com/phylogenomics/, accessed May 2024), will spearhead research on the evolution and systematics of the Australian flora and spotlight it on a global stage.

These Australian examples show that although much methodological development is needed, the advancement of target capture data has nonetheless facilitated a step-change in plant phylogenomic research. The difficulties of dealing with conflict within datasets and the vast array of methods involved in analysing this type of data offer new challenges to overcome and complexity to decipher. However, surmounting these challenges will ultimately provide a more comprehensive understanding and more realistic and accurate evolutionary reconstruction of plants in Australia and worldwide.

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