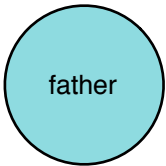
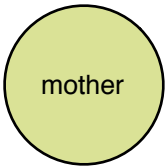
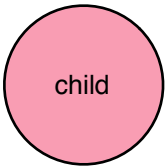
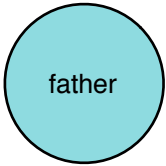
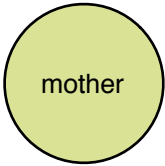
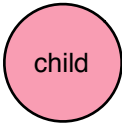


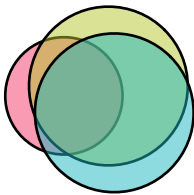
1. Construct de Bruijn graphs for child and parents (k=47)



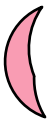
2. Remove likely sequencing errors from child's graph



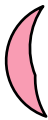
3. Combine into a multi-color "trio" graph



4. Compute initial set of novel kmers (kmers private to child)



5. Filter novel kmers



- Coverage outliers
- Contaminants
- Orphan removal
- Over-cleaning detection

=



6. Call mutations at each unutilized novel kmer in the trio graph

while in



7. Align mutations (and flanking regions) to reference

