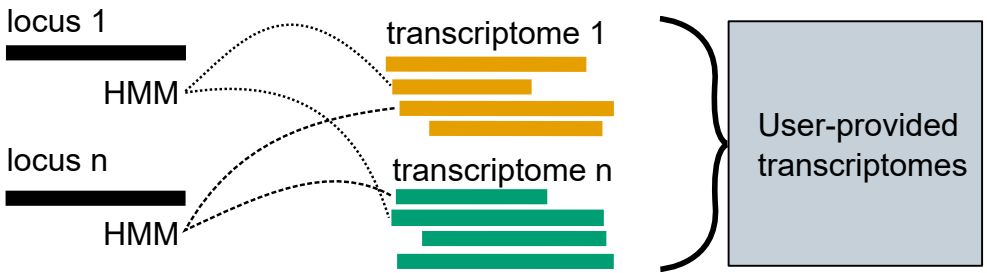


Target file (e.g. Angiosperms353)

1. Single locus alignments

2. HMM profiles produced from each alignment

3. Search user-provided transcriptomes with HMM profiles



4. Align sequences



5, 6. Trim and graft sequences



7, 8. Correct frameshifts

9. Extract sequences,
remove gap and N characters

Target file for locus assembly