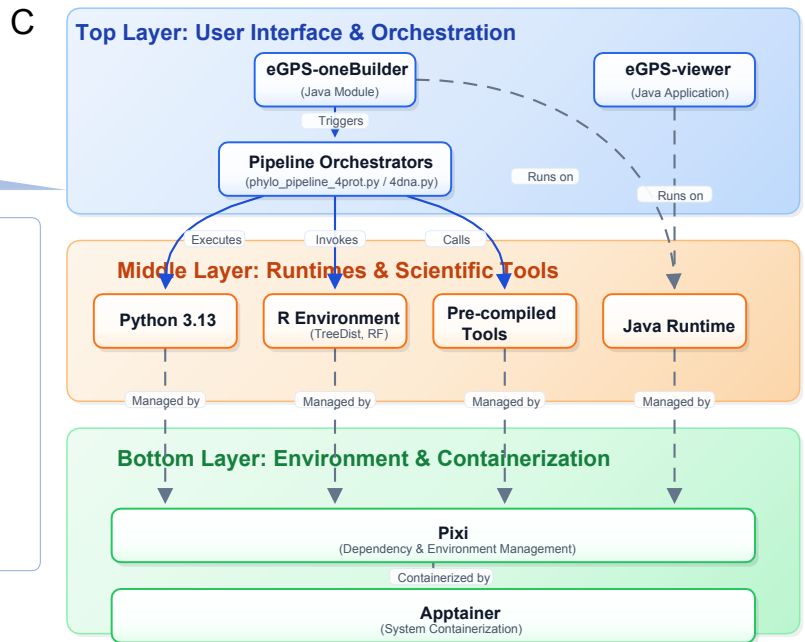
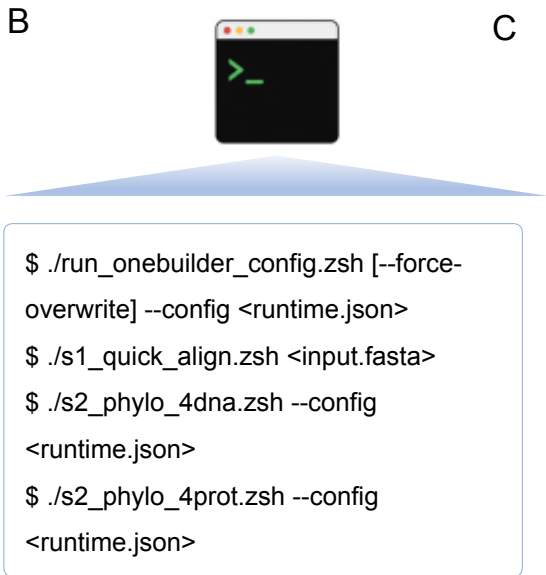
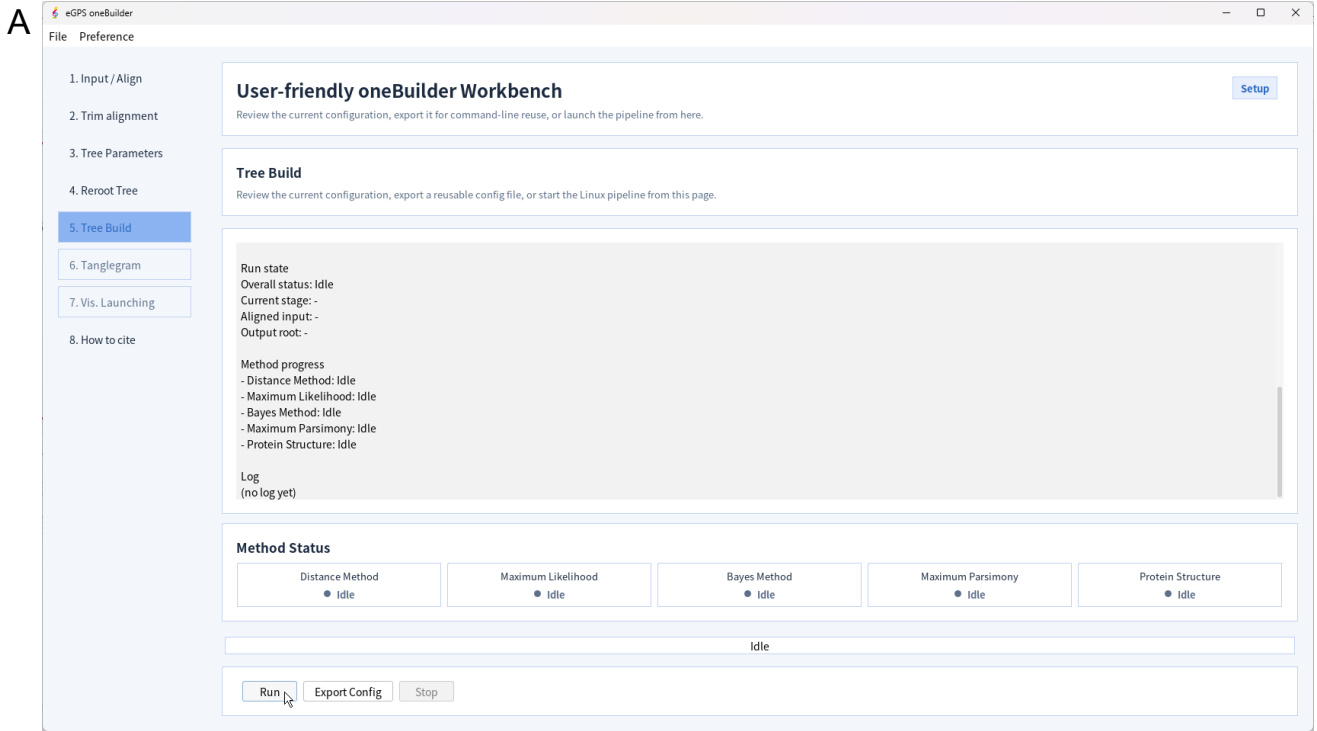
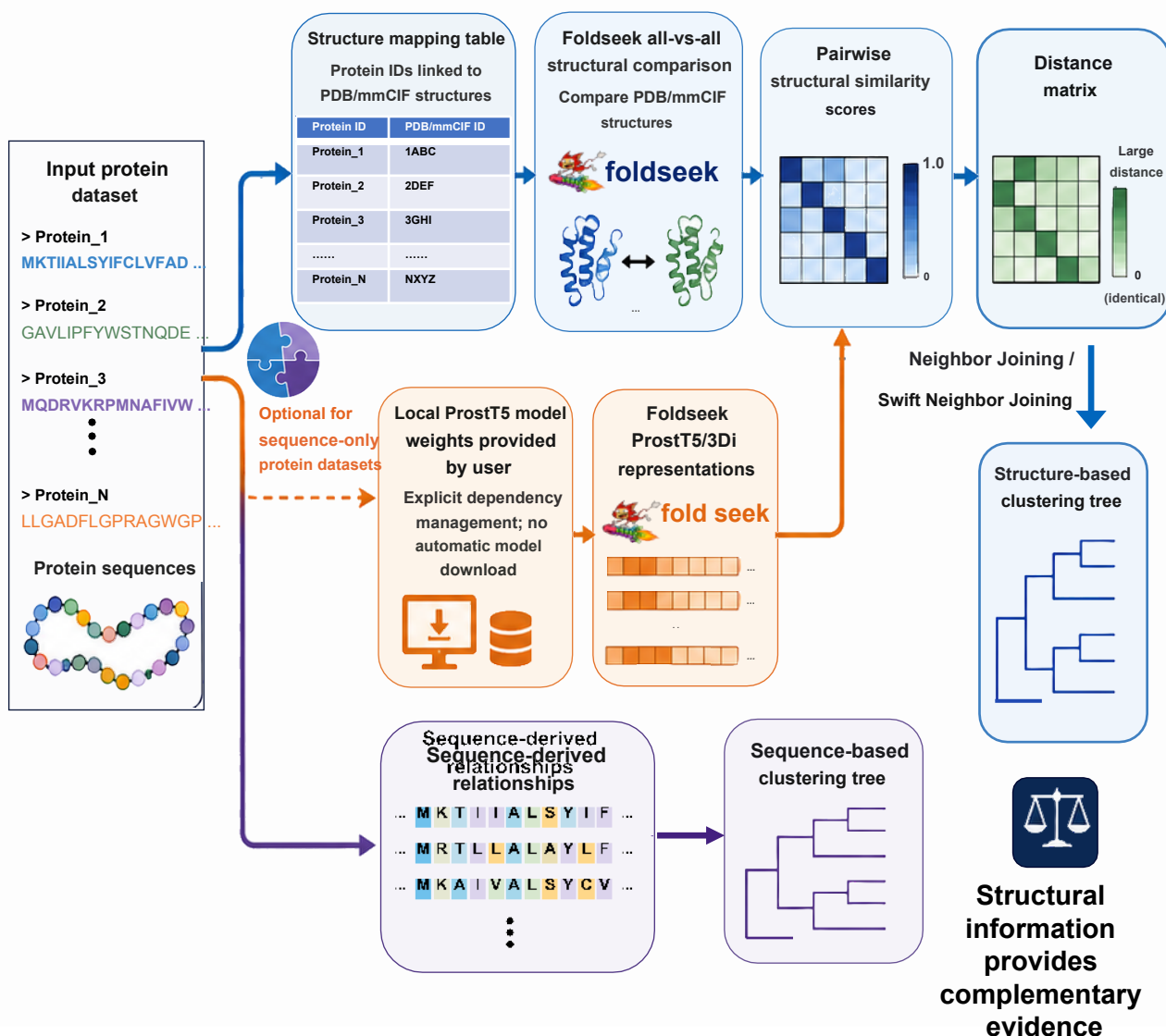
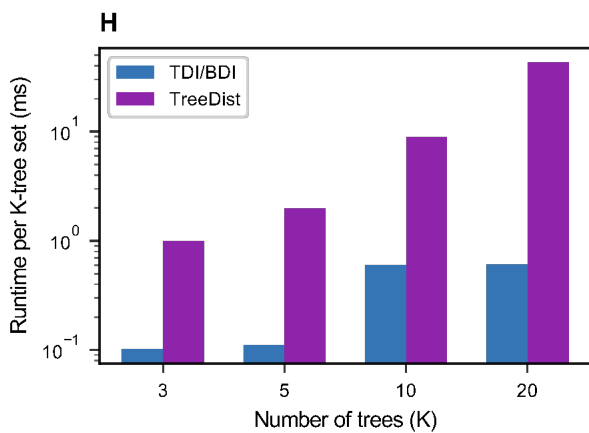
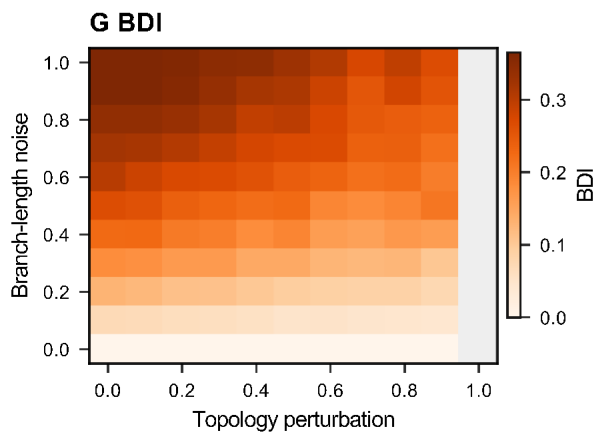
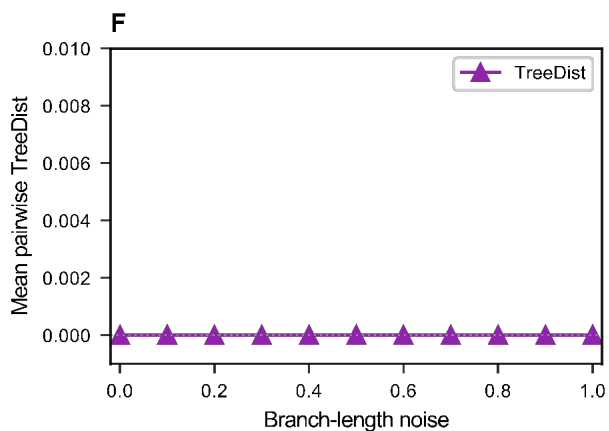
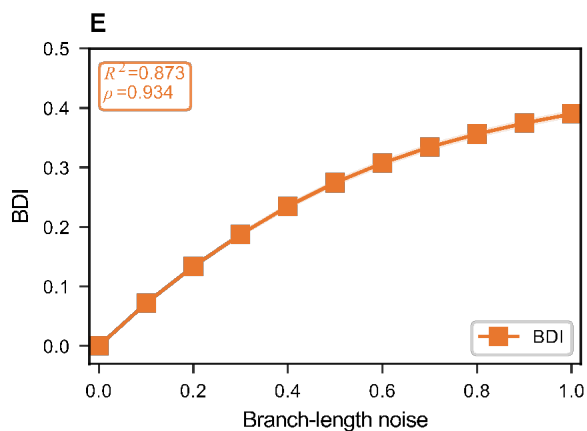
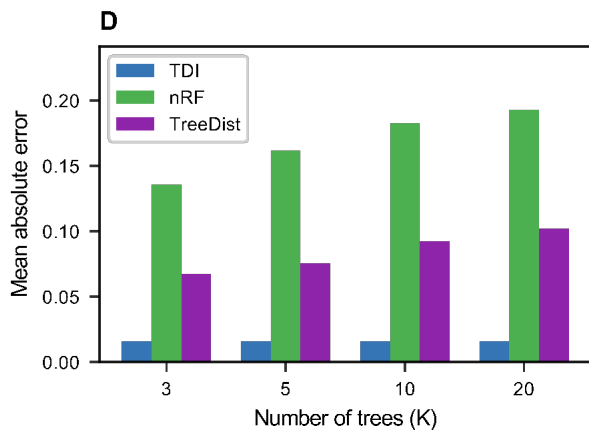
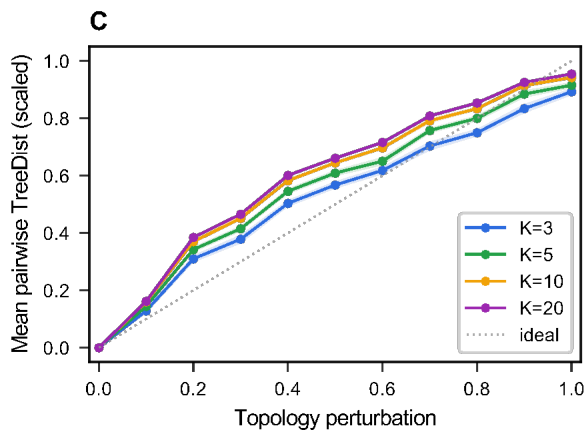
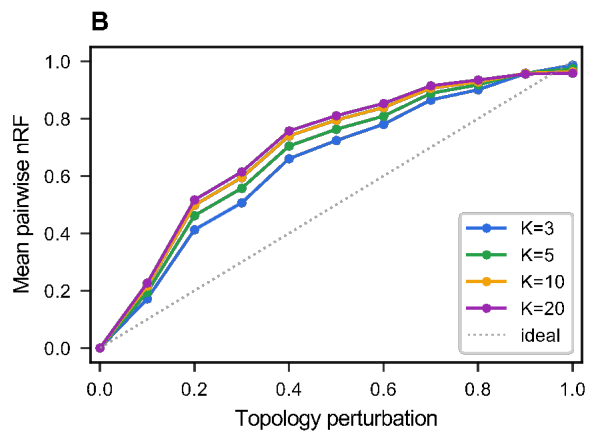
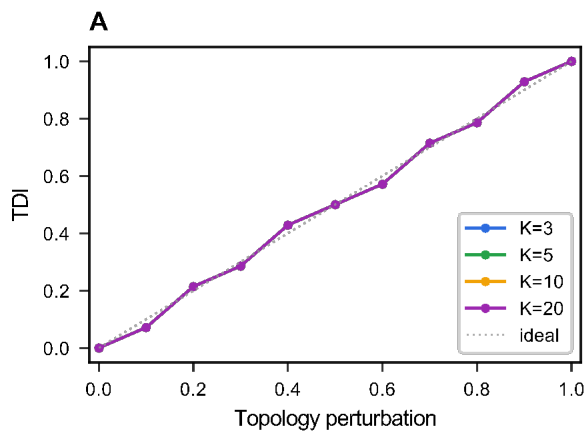


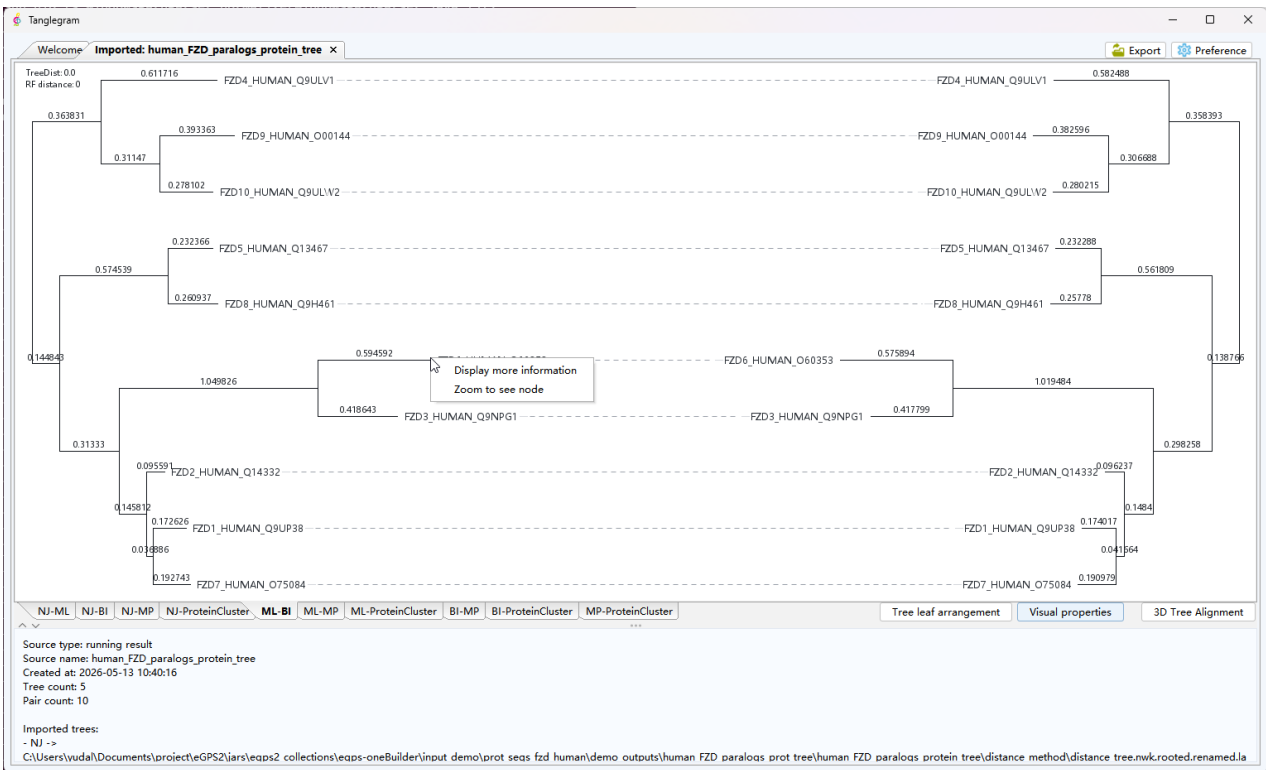


Protein Structure module

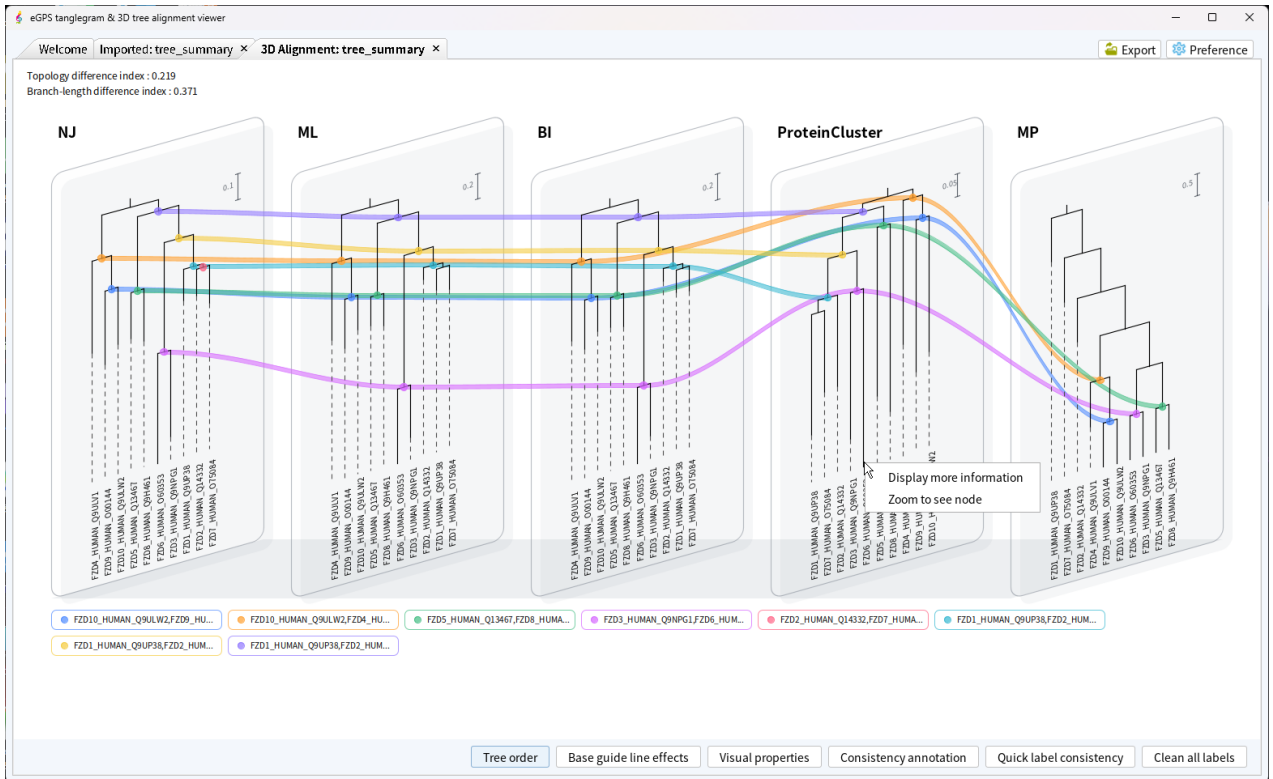


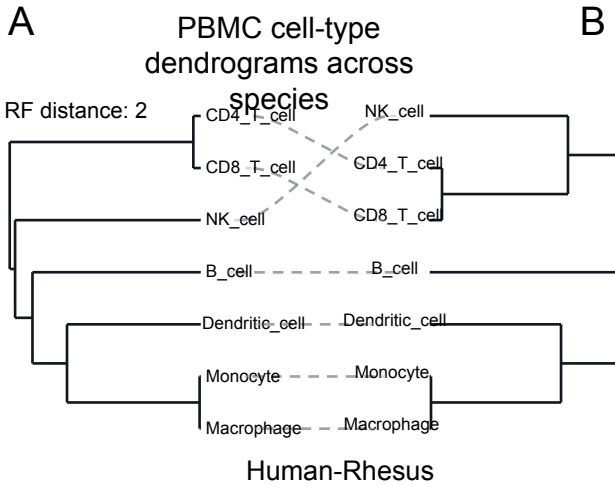


A

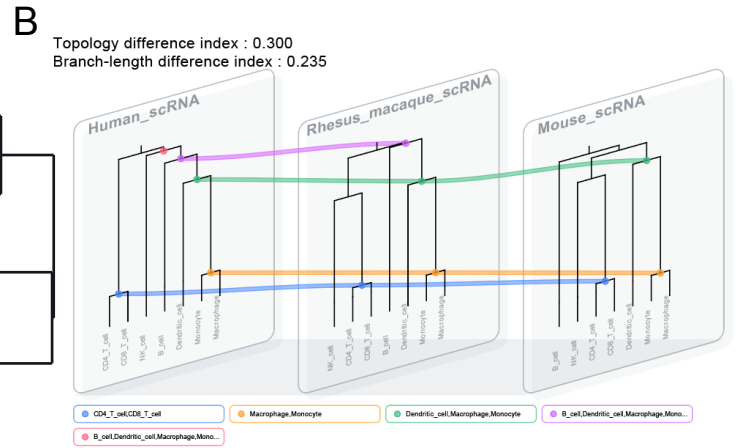


B

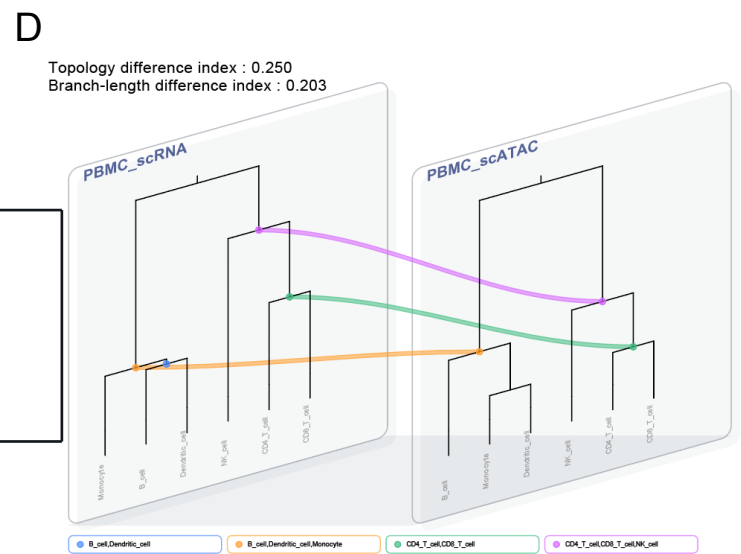
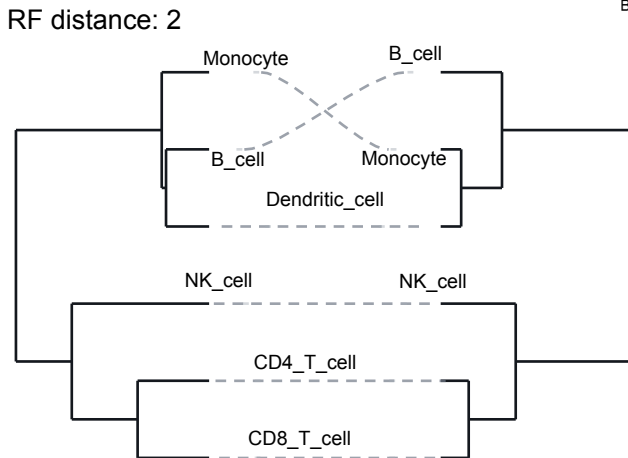




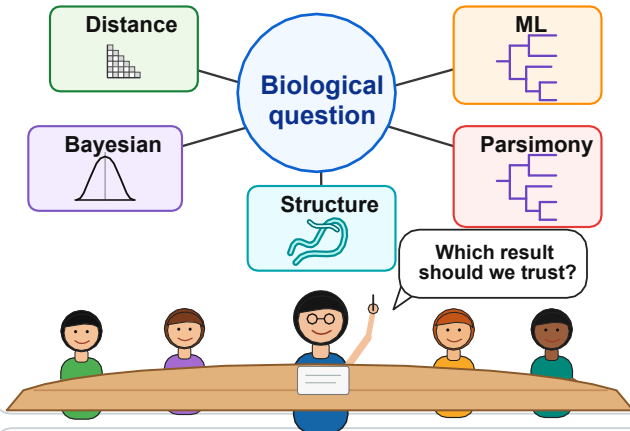
RF distance: 4 for Human-Mouse



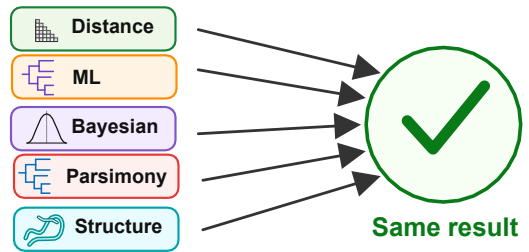
C scRNA-seq VS. scATAC-seq



A One question, many methods



B Consistency *All agree*



C Majority support

	A	B	C
Distance	☐	☒	☐
ML	☐	☒	☐
Bayesian	☐	☒	☐
Parsimony	☒	☐	☐
Structure	☐	☒	☐
	1	4	0
		↓ Winner	

D At least one support

	A	B	C
Distance	☐	☒	☐
ML	☐	☒	☐
Bayesian	☐	☒	☐
Parsimony	☒	☐	☐
Structure	☐	☒	☐
	1	4	0
	↓ Keep	↓ Keep	↓ Drop

eGPS oneBuilder

FilePreference

1. Input / Align

2. Trim alignment

3. Tree Parameters

4. Reroot Tree

5. Tree Build

6. Tanglegram

7. Vis. Launching

8. How to cite

User-friendly oneBuilder Workbench

Setup

Set input, output, and alignment behavior before moving deeper into the Linux-only pipeline.

Provide one FASTA/MSA input. On Linux, oneBuilder can run the existing MAFFT wrapper and the four-tree pipeline directly. After this page, use Tree Parameters to tune methods and Tree Build to run or export the config.

Input type

DNA/CDS

Reuse Last

Auto-detected: DNA/CDS; raw sequence lengths differ, alignment enabled.

Input FASTA/MSA

/mnt/c/Users/yudal/Documents/project/eGPS2/jars/egps2_collections/egps-oneBuilder/input_demo/prot_seqs_wnt_human/human_WNT-NDP_paralogs_cds.fasta

Browse

Output base dir

/mnt/c/Users/yudal/Documents/project/eGPS2/jars/egps2_collections/egps-oneBuilder/input_demo/prot_seqs_wnt_human/demo_outputs/protein

Browse

Output prefix

human_WNT-NDP_paralogs_cds_tree

Alignment

☒ Run multiple sequence alignment first

Turn this on when the input FASTA contains raw sequences and is not aligned yet. oneBuilder auto-enables it when multiple sequences have different lengths.

MAFFT strategy

localpair

Maxiterate

1,000

MAFFT threads

0

Alignment flags

☒ Reorder sequences

Advanced MAFFT

Advanced Parameters

☒ Export config file when running

When this option is enabled, clicking Run will also write a reusable JSON config file for the current job. That file records the selected input, alignment setup, output prefix, and all tree-method parameters so the same workflow can be rerun later from the command line on Linux, shared with collaborators, or kept as an exact record of how this analysis was configured.

Config export

Expected build input /mnt/c/Users/yudal/Documents/project/eGPS2/jars/egps2_collections/egps-oneBuilder/input_demo/prot_seqs_wnt_human/human_WNT-NDP_paralogs_cds.aligned.fasta

Next step: optionally trim the alignment, then open Tree Parameters to adjust the method tree.

Supp. Fig. S1. Input and alignment configuration page in eGPS-oneBuilder. The GUI records input type, FASTA/MSA path, output settings, MAFFT strategy, Maxiterate, thread settings, advanced MAFFT parameters, and automatic JSON config export for reproducible downstream execution.