

Supplementary Figures and Tables for CALDER: Inferring phylogenetic trees from longitudinal tumor samples

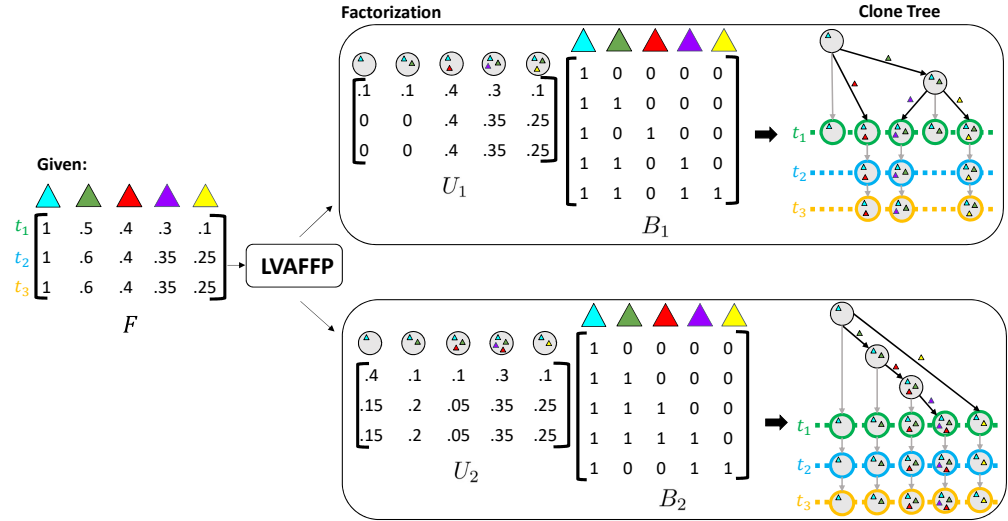


Figure S1: **Some LVAFFP solutions are trivially longitudinal, related to Figure 1.** An example of a frequency matrix F and two factorizations $F = U_1 B_1$ and $F = U_2 B_2$ that both correspond to longitudinally-observed clone trees. While U_1 (top) has some 0 entries, U_2 (bottom) does not, and thus is trivially longitudinal, with all clones present at all times.

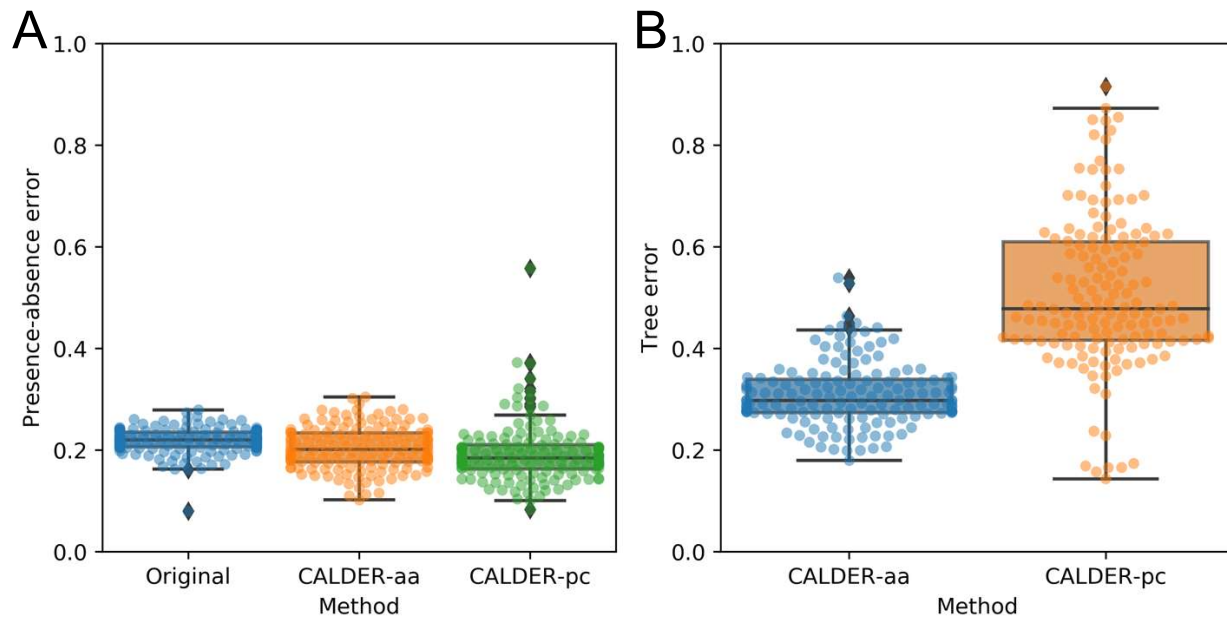


Figure S2: **Comparison of absence-aware (aa) and absence-naive PyClone (pc) clustering on simulated tumors, related to Figure 2 and STAR Methods.** CALDER-aa and CALDER-pc are the results from running CALDER on the clustered data from our absence-aware clustering method and PyClone (Roth et al., 2014), respectively. Original shows the presence-absence error between the input matrices of longitudinal samples and the ground truth. The y-axes are (A) presence-absence error and (B) tree error as described in Results.

	Average			Total		
	CALDER	PhyloWGS	CITUP	CALDER	PhyloWGS	CITUP
Wall time (min)	1.61	862	477	287	153427	84819
User time (min)	342	3024	189	60789	538300	33719
System time (min)	29	38	474	5115	6846	84437
Memory (MB)	502	51	122	504 (max)	55 (max)	127 (max)

Table S1: **Running time and space requirements for CALDER, PhyloWGS, and CITUP on simulated data, related to STAR Methods.**