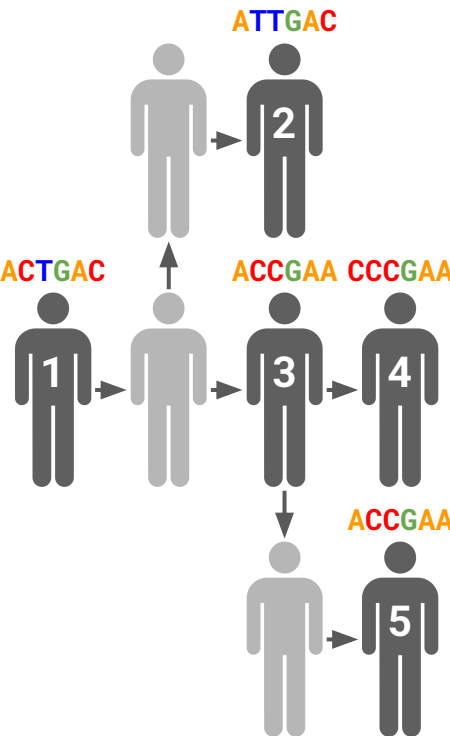


viral outbreak



intrahost variants

host	iSNV	frequency
2	C2T	60%
3	A1C	20%
5	A5G	10%
5	A6T	10%

consensus sequences

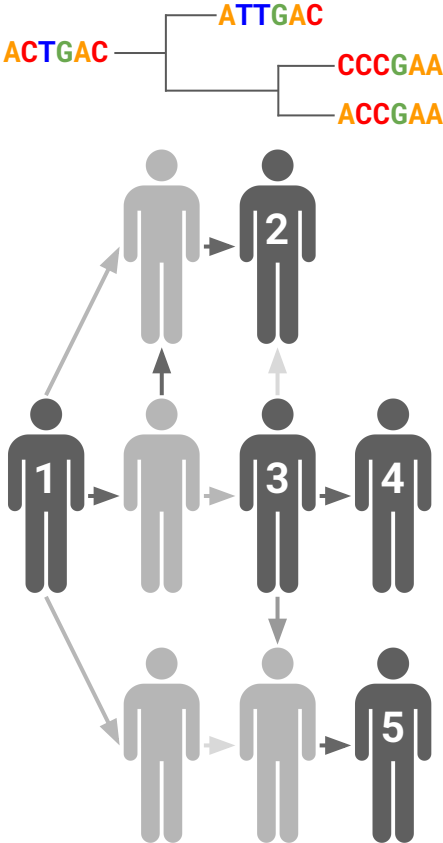
host	genome
1	ACTGAC
2	ATTGAC
3	ACCGAA
4	CCCGAA
5	ACCGAA

sample collection dates

host	date
1	2025-01-01
2	2025-01-15
3	2025-01-15
4	2025-01-22
5	2025-01-22

juniper

plausible phylogenies and transmission networks, and their probabilities



parameter estimates

