A — Within-country pairwise sequence distances
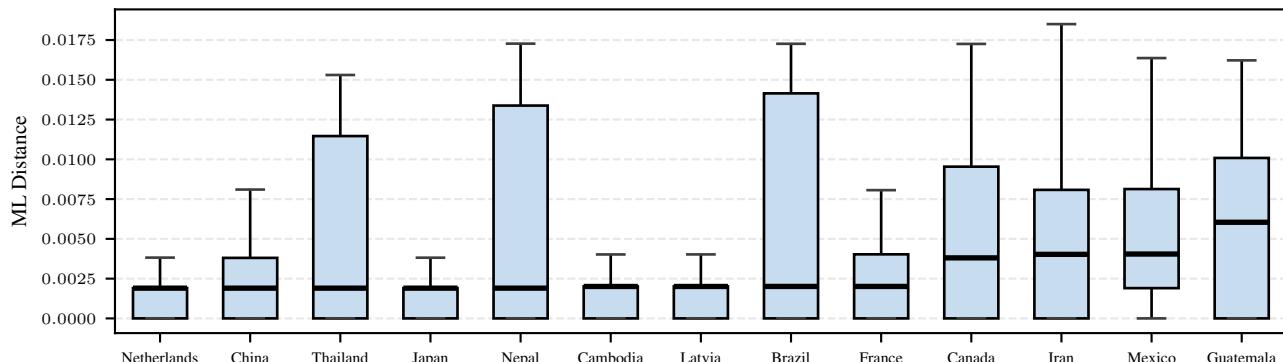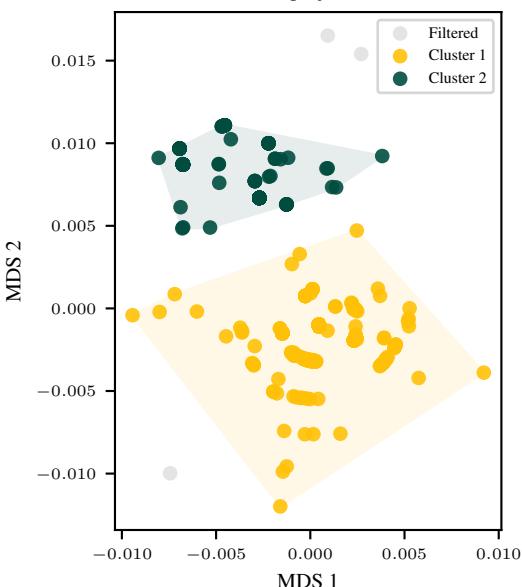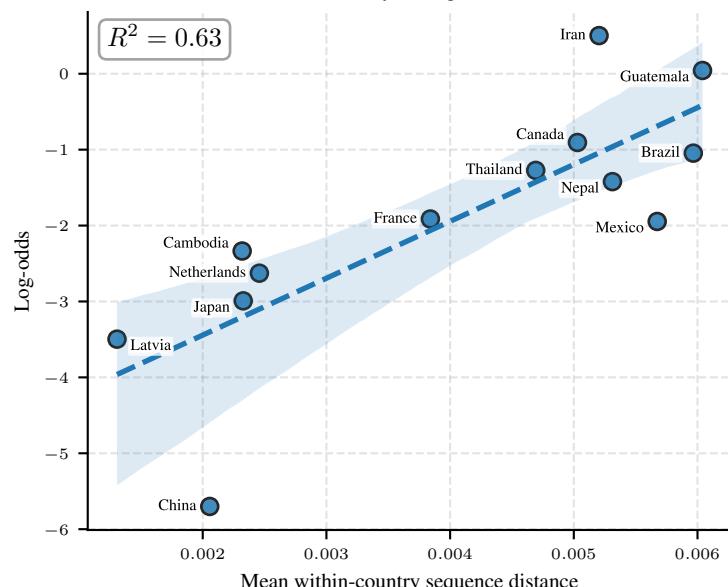
B — MDS projection

C — Diversity vs Log-odds

$R^2 = 0.63$

D — Cluster sample counts over time