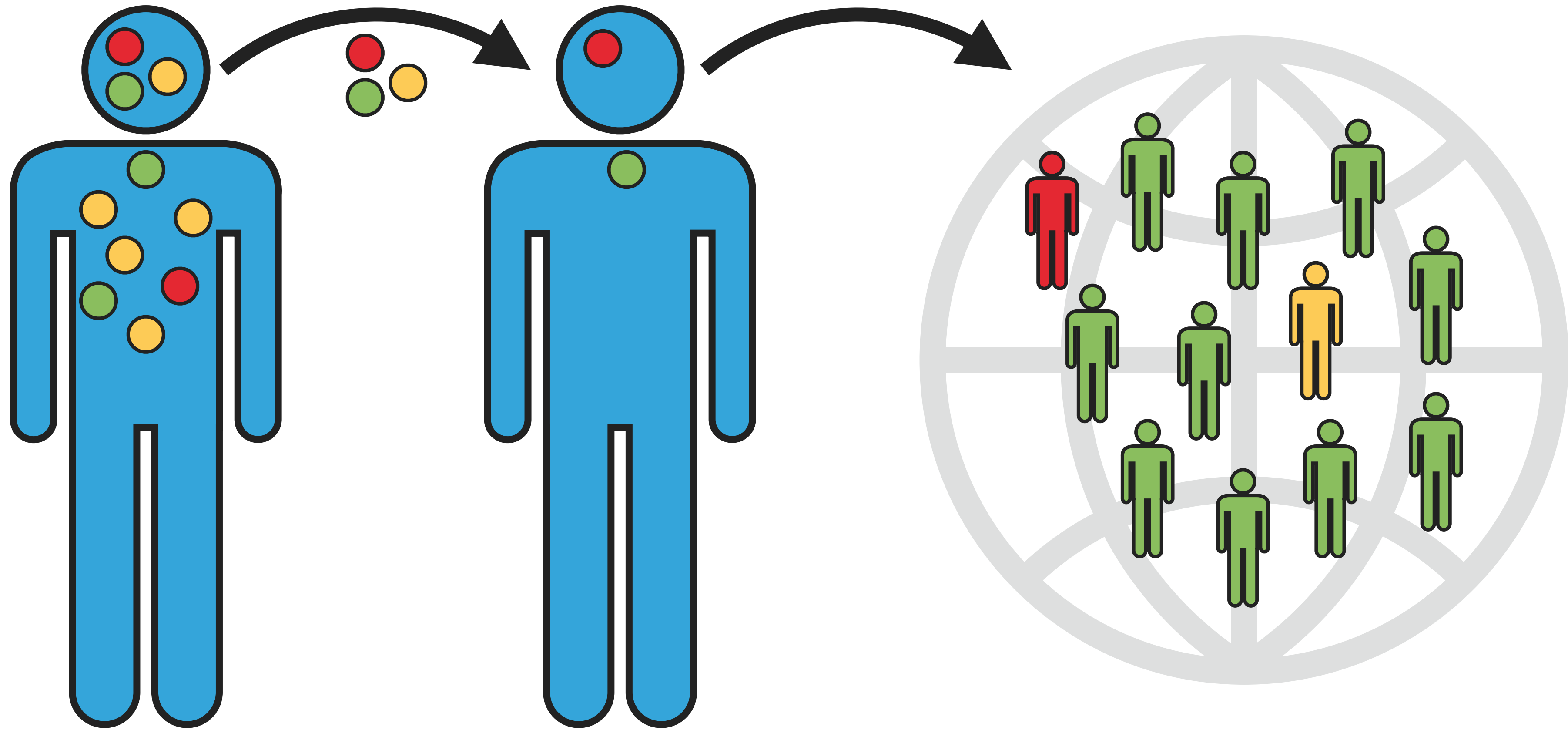


INFLUENZA VIRUS EPIDEMICS ARE LARGELY HOMOGENEOUS



How can we most effectively infer phylogenies from genetically homogenous influenza outbreaks?