Genomic insights into malaria transmission dynamics

OR How to get more information from cross-sectional samples

Benjamin Rice
Hartl Lab, OEB,
Harvard University
E2M2 2019

Cross-sectional Consistent with multiple Discriminate using genetic parameters Response prevalence estimates historical scenarios **Unstable transmission:** Few haplotypes Few polyclonal infections Stable transmission: Many haplotypes Many polyclonal infections Maroantsetra data Time Time of sampling Vs **High importation:** Many haplotypes monitor travel Many polyclonal infections **High importation** Low importation: More sensitive surveillance Few haplotypes Few polyclonal infections **Low importation**