Inferring the Mode of Selection from the Transient Response to Demographic Perturbations DANIEL BALICK, Harvard Medical School, Brigham and Women's Hospital, Broad Institute of Harvard and MIT, RON DO, Harvard Medical School, Massachusetts General Hospital, Broad Institute of Harvard and MIT, DAVID REICH, Harvard Medical School, Broad Institute of Harvard and MIT, SHAMIL SUNYAEV, Harvard Medical School, Brigham and Women's Hospital, Broad Institute of Harvard and MIT — Despite substantial recent progress in theoretical population genetics, most models work under the assumption of a constant population size. Deviations from fixed population sizes are ubiquitous in natural populations, many of which experience population bottlenecks and re-expansions. The non-equilibrium dynamics introduced by a large perturbation in population size are generally viewed as a confounding factor. In the present work, we take advantage of the transient response to a population bottleneck to infer features of the mode of selection and the distribution of selective effects. We develop an analytic framework and a corresponding statistical test that qualitatively differentiates between alleles under additive and those under recessive or more general epistatic selection. This statistic can be used to bound the joint distribution of selective effects and dominance effects in any diploid sexual organism. We apply this technique to human population genetic data, and severely restrict the space of allowed selective coefficients in humans. Additionally, one can test a set of functionally or medically relevant alleles for the primary mode of selection, or determine the local regional variation in dominance coefficients along the genome.

Daniel Balick
Harvard Medical School, Brigham and Women's Hospital