Soft Sweeps III: The Signature of Positive Selection from Recurrent Mutation (Pennings and Hermission 2006)

* If singular allele causes selective sweep 🡪 hard sweep (classical positive selection)
* If multiple alleles result in selective sweep 🡪 soft sweep
  + E.g., neutral selection and then shift in environment causes positive selection
  + Characterized by strong lD
  + Can be detected (method of paper)
* Stronger signal than hard sweeps, e.g., in LD
* Hard sweeps eliminate polymorphisms, while soft sweeps may lead to several patterns of LD due to multiple alleles 🡪 evidence of polymorphisms (this is why they’re easier to detect)
* SFS-based approach better for detecting hard sweeps, LD approach better for detecting soft sweeps

Toward an Evolutionarily Appropriate Null Model: Jointly Inferring Demography and Purifying Selection (Johri et al. 2020)

* Null model for jointly inferring jointly the effects of genetic drift and purifying selection.
* Strong background selection distorts the SFS, the neutral model is not a good null model even for neutral selection.
* Reduction of nucleotide diversity in linked neutral sites is also slow to recover
* Underlying shape of DFE determines effect of background selection on linked sites
  + Partitioned DFE inference (non-continuous) with set selective effects
  + Encompasses both neutral and non-neutral sites, synonymous and nonsynonymous
* Recapitulation of DFE is accurate, but DFE is inherently kind of wacky

The Effect of Strong Purifying Selection on Genetic Diversity (Cvijovic et al. 2018)

* Forward-in-time analysis of purifying selection and effect on reduction of genetic diversity.
  + Under strong purifying selection, neutral selection can result in sweeps (since everything else is purified)
  + Slightly deleterious mutations can reach high frequency
* Neutral alleles that are linked to mildly deleterious alleles can arise as strong purifying selection does not instantly remove deleterious alleles
* **Even with strong deleterious selection, SFS may show an excess of rare variants** compared to neutral population with reduced effective population
* These signatures in genetic diversity are qualitatively similar to those we expect from population expansions and positive selection
* Distortion in fitness of sites causes variations in background selection of neutrally selected sites
* **Strong background selection distorts the SFS**

Achtman and Zhou 2020 (Metagenomics of the modern and historical human oral microbiome with phylogenetic studies on *Streptococus mutans* and *Streptococcus sobrinus*)

Cornejo 2012 (Evolutionary and Population Genomics of the Cavity causing Bacteria *Streptococcus mutans*)

Eisenhofer 2020 (Investigating the demographic history of Japan using ancient oral microbiota)

Garud 2019 (Evolutionary dynamics of bacteria in the gut microbiome within and across hosts

Groussin 2021 (Elevated rates of horizontal gene transfer in the industrialized human microbiome

Hershberg 2008 (High Functional Diversity in *Mycobacterium tuberculosis* Driven by Genetic Drift and Human Demography)

Ostrowski 2021 (The Food Additive Xantham Gum Drives Adaptation of the Human Gut Microbiota)

Pepperell 2013 (The Role of Selection in Shaping Diversity of Natural *M. tuberculosis* Populations)

Liu (China’s tuberculosis epidemic stems from historical expansion of four strains of *Mycobacterium tuberculosis*)

Sonnenburg 2019 (Vulnerability of the industrialized microbiota)

Tett 2021 (*Prevotella* diversity, niches, and interactions with the human host)

Tett 2019 (The Prevotella copri Complex Comprises Four Distinct Clades underrepresented in Westernized Poplations)

Wibowo 2020 (Reconstruction of ancient microbial genomes form the human gut)

Schnorr 2014 (Gut microbiome of the Hadza hunter-gatheres)