Much can be learned about a species’ recent evolutionary past by fitting models to contemporary patterns of genetic variation. There are two categories of models we fit, models of demographic history and distributions of fitness effects. When we fit a demographic history model, we use synonymous mutations and infer a model to learn about things like population size, divergence time, and rates of inbreeding. A distribution of fitness effects provides information about what proportions of mutations in nonsynonymous sites are deleterious, neutral, and advantageous, which can provide key input into the evolutionary process. We aim to infer the DFE among multiple populations of wild house mice, so that the extensive knowledge of mouse molecular biology can be leveraged to understand the biological basis of the DFE. Prior to fitting a DFE, we must use synonymous mutations to infer a model of demographic history. We find the best models are those that include a distinct split between the two populations and account for inbreeding between closely related individuals. These models of demographic history are then used to set up a frequency distribution of nonsynonymous sites under a range of selection coefficients, which are used to fit the DFE. Here we present our demographic inferences along with preliminary DFEs.