Quantifying the Statistical Power in the Inference of the Evolution of the

Distribution of Fitness Effects in Canine Lineages.

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Previous work on inferring the distribution of fitness effects (DFE), or the amount of deleterious, neutral, or adaptive mutations entering a population, has shown that distantly related species have distinct DFEs. However, using genomic resequencing data from arctic wolves and breed dogs, there was no detectable difference in their inferred DFE. Here, we sought to determine if current state-of-the-art methods for DFE inference had sufficient statistical power to detect a change in the DFE between canine populations. We performed forward population genetics simulations modeling canine evolution, and compared the inferred DFE and demographic parameters of simulated and empirical data. We have modeled ancestral wolf DFEs and demographic histories and are awaiting the results of our dog DFE simulations for comparison. Understanding if we can detect a difference in DFE will provide insight towards the impact of domestication on the DFE and help confirm the results found with reported empirical data.