USC Dornsife

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Understanding the fitness effects of mutations and implications for complex traits in humans

Many mutations that occur in genomes are deleterious, resulting in a decrease in reproductive fitness. While such mutations are important for evolution and complex traits, much remains to be discovered. In this talk, I will discuss our work on estimating fitness effects of deleterious mutations using genetic variation data from natural populations. First, I will describe our computational approach, FitDadi, to estimate the distribution of fitness effects (DFE) for amino acid changing mutations in humans and other species. Analysis of how the DFE differs across species provides insights about how the DFE itself evolves. I also will show how the DFE differs for distinct types of mutations in the human genome. Next, I will describe our work on estimating another key evolutionary parameter of deleterious mutations—the degree of dominance (i.e. the relationship between the fitness effect in heterozygotes and homozygotes). Third, I provide a strategy to validate population genetic models of selection and dominance by testing whether they predict observed levels of inbreeding load and match observed genetic data. Lastly, I will discuss how the DFE and evolutionary parameters influence the architecture of complex traits in diverse human populations.

IN PERSON

HEB Seminar

February 16, 2024 | 12:00 PM – 1:00 PM Allan Hancock Foundation Building - Torrey Webb Room