Seminar/Talk

Tracking short-term evolution in a pedigreed wild population

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Host: Nick Barton

The fundamental goal of the field of population genetics is to understand the evolutionary processes that govern allele frequency change. However, the actual mechanisms causing these changes - variation in individual survival, reproductive success, and movement - are often difficult to directly measure in natural populations. Fully understanding these processes requires the population pedigree, the set of relationships among all individuals in the population through time. Here, we elucidate the relative roles of different evolutionary processes in shaping patterns of genetic variation through time using a 25-year genomic, phenotypic, and pedigree dataset in the Florida Scrub-Jay (Aphelocoma coerulescens). Using gene dropping simulations, we estimated individual long-term genetic contributions and show how they are linked to measures of individual fitness and predictions of allele frequency change. Our approach allows us to quantify the expected genetic contribution of recent immigrants and identify large allele frequency shifts due to gene flow or selection. We modeled the relative roles of different evolutionary processes in shaping patterns of genetic variation genome-wide. Finally, we modified existing selection component analysis frameworks to test for selection acting on specific life-cycle stages. We identified a number of loci that clearly exhibited male gametic selection, sexual selection, and viability selection. By combining pedigree-based models with fine-scale dissection of selection components, this work provides a one of the most complete characterizations of the roles of selection, gene flow, and drift in governing allele frequency dynamics in a natural population to date.

Monday, August 27, 2018 11:00am - 12:00pm

Meeting room 1st floor / Central Bldg. (I01.1OG - Zentralgebäude)

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