Relatedness, genealogies and DNA sharing

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Abstract

Related individuals share segments of their genome, derived from the DNA of a common ancestor in a genealogy. Variation in the DNA sequences of individuals reflects their underlying genealogical relationships and can tell us about our ancestry and origins. The implications of these relationships have many practical applications including in forensics, family identification, conservation and ecology, and tracing the history and migrations of populations (human or otherwise). They can also tell us about individual predisposition to inherited traits, and so are of use in mapping the genomic location of DNA variants that contribute to disease traits. I will provide an overview pertaining to our work in the area of trait mapping and present recent progress in exploring these ideas with real and simulated data.