

## **Genome sharing among related individuals: an approximate answer to the right question.**

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Similarities among individuals for traits determined in whole or in part by their DNA arise from their coancestry. Related individuals share segments of their genome, in the sense that these segments derive from a single DNA segment in a common ancestor. Such segments are said to be identical-by-descent or ibd and have high probability of being of the same biochemical type. While a known pedigree relationship gives a probability distribution on the marginal probability of ibd and on lengths of ibd segments, modern genomic data permits much more precise inference of shared genome. However, human individuals are diploid: even a pair of individuals have a total of four haploid genomes. Thus, at a minimum, models for sharing among four genomes are required, and these models must be such that conditional probabilities of ibd segments given dense genomic data can be computed. A new model for genome sharing along four genomes will be described, and the resulting inferences of ibd segments illustrated.