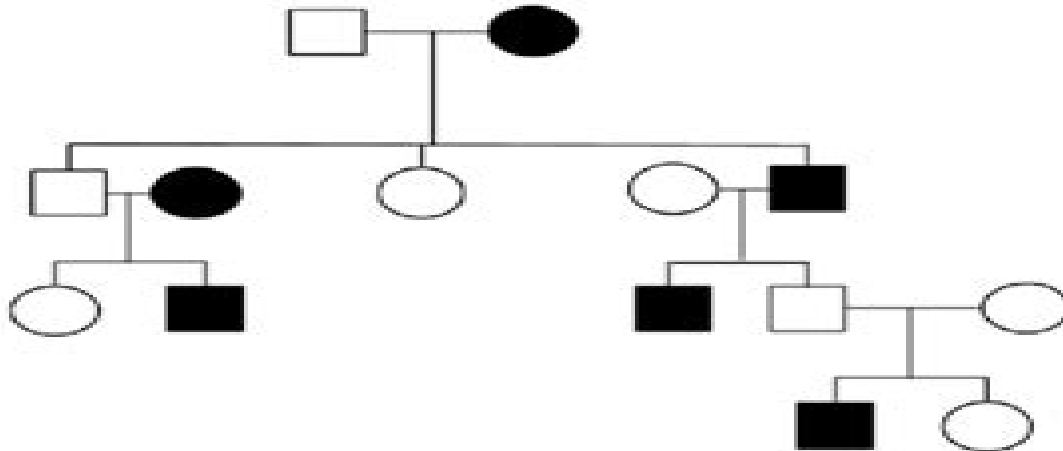


Pedigree Charts

Name: _____

A pedigree for any family, be it dogs, cats or humans, shows the pattern of inheritance in a family for a specific trait. Males are shown as squares and females are shown as circles. Each generation is shown as a Roman numeral and each person in a generation is numbered. The trait *that is being expressed* is shown as a shaded shape.



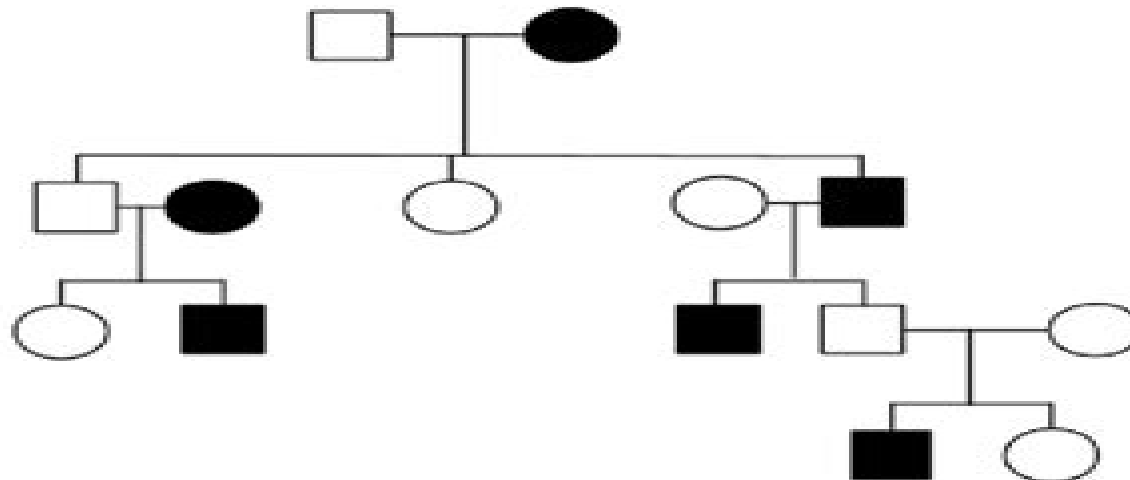
Observe the pedigree. Number the generations and each person on the pedigree.

In this family, how many individuals show the trait? _____

Which males show the trait? (generation, number)

Determining genotypes

Follow along in the [presentation](#) so you can figure this out. N = normal feet, n = webbed feet. Write down the genotypes of each individual under him/her.



Human Pedigrees Biology Lf8765

Lee Raymond Dice



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The Human Pedigree Anthony Smith, 1975 **Modern Analysis of Human Pedigrees** Laurence Hasbrouck Snyder, 1934 *The Human Pedigree* Anthony Smith, 1976 Corporate financial management is at its core a fluid and constantly challenging area Financing and Risk Management takes you inside the fundamental question of how a corporation generates capital It introduces you to the subject s often conflicting objectives and outlines ways in which you can satisfy the greatest number of those objectives while ensuring that all areas of a corporation operate and conflicts are resolved under one consistent set of financial rules **Some Extensions of the Gene Frequency Analysis of Human Pedigrees** Charles William Cotterman, 1937 **The Mendelian Collection of Human Pedigrees** George P. Mudge, 1911* **Methods for Fine Mapping Complex Traits in Human Pedigrees** Gonçalo Rocha Abecasis, William Cookson, 2001 Symbols for Human Pedigree Charts Lee Raymond Dice, 1946 The Use of Standard Nomenclature in Human Pedigrees Heidi Ann Schoenhard, 2004 Dealing with Relatives Dominic Nelson, 2021 All of humanity and indeed all living things are connected by a complex web of ancestral relationships How much of this shared pedigree is known how much can be inferred and how completely it can be described are important factors in interpreting present day genetic diversity and discovering genetic contributions to disease The challenges of using pedigree information are twofold First in human populations genealogical data is often unavailable or incomplete Second when such datasets are available there are significant computational challenges to using them In both cases the response has often been to use approximate models of pedigree structure which removes the need for complete historical data and simplifies analysis But genetic cohorts are growing and increased sample sizes necessitate more detailed models of relatedness The work presented here represents a first step in explicitly modeling the relatedness of millions of individuals and using it to understand the fine scale diversity of whole populations as well as the genetic architecture of rare diseases First we developed a software package ISGen Importance Sampling in Genealogies for inferring the ancestral origin of rare alleles in population scale pedigrees as well as their distribution among present day individuals in a fully Bayesian framework Similar analysis had never been possible before at that scale and as a proof of concept we analyzed the distribution of the allele causing Chronic Atrial and Intestinal Dysrhythmia CAID within the province of Quebec Using observations of only 11 patients and 4 heterozygous carriers of the allele we estimated the allele frequency in 26 geographic regions of the province finding the highest expected frequency in Charlevoix where no carriers had yet been observed Despite its value for supporting the design of screening programs for rare diseases ISGen is limited to rare alleles and a single locus Extending to whole genome inference is a daunting challenge and can be aided significantly by high quality data with a known transmission history Simulations are a natural source of such data yet the most efficient simulation frameworks were based on coalescent models with known biases for long genomic regions and large sample sizes We developed two tools to address this issue One is an extension to the state of the art msprime coalescent simulator which

allows simulations under a Wright Fisher model This extension makes use of the highly efficient algorithms and data structures of msprime and we showed more realistic relatedness among simulated individuals as well as improved performance over coalescent simulations at whole genome scale We then continued to develop this extension to allow simulations to be performed within a predefined pedigree and when used with the population scale genealogy of Quebec Canada we showed that simulated cohorts captured much of the structure of a real dataset from the same population and significantly more than comparable simulations of a randomly mating population To show the potential of large scale pedigree simulations more generally we further described how pedigree simulations can aid in the design of sequencing cohorts for imputation and be used to detect rare variant associations while explicitly accounting for relatedness among cohort members

Human Pedigree Studies Robert A. Peel, 1999

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