

allele frequencies in sibships

a data mishap

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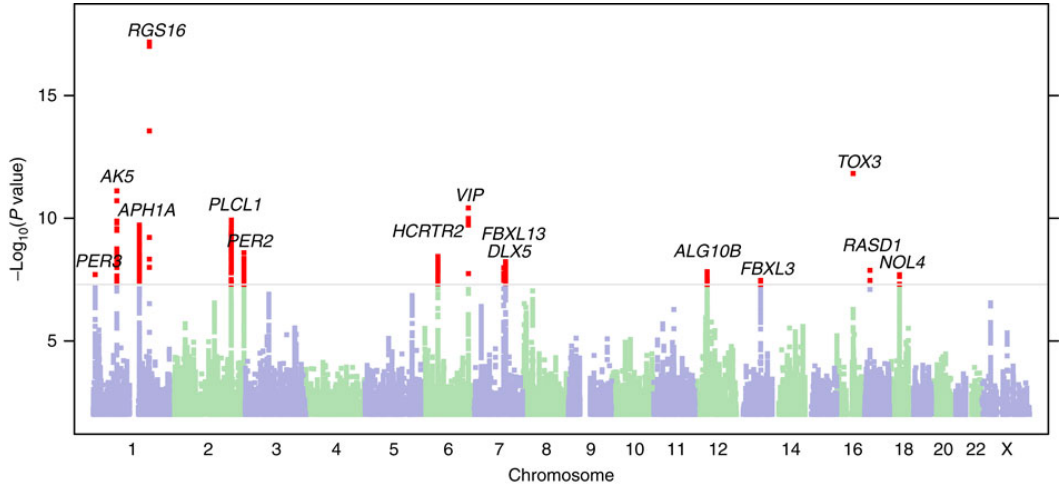
`kbroman.org`

`github.com/kbroman`

`@kwbroman`

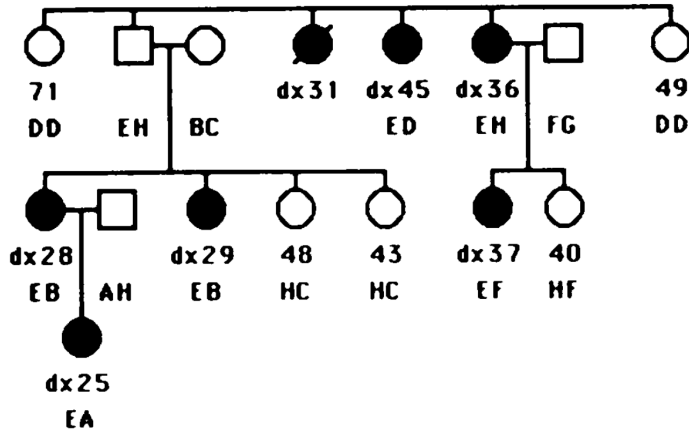
Slides: kbroman.org/Talk_DataMishap

GWAS for “morning person”



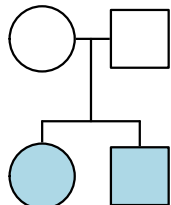
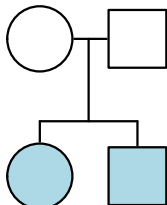
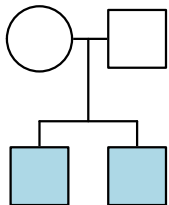
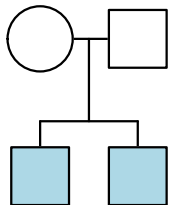
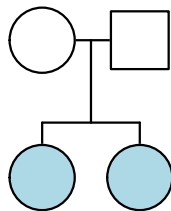
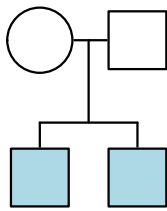
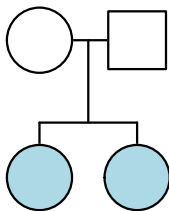
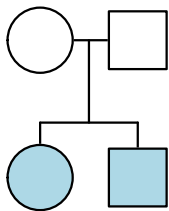
Hu et al (2016) [doi:10.1038/ncomms10448](https://doi.org/10.1038/ncomms10448)

BRCA1 pedigree

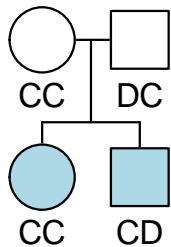
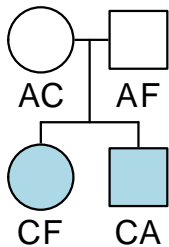
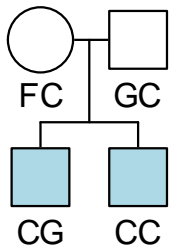
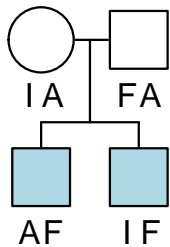
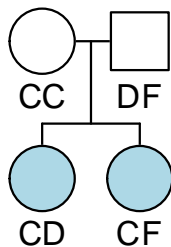
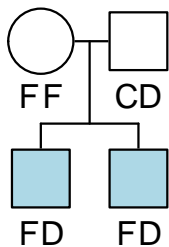
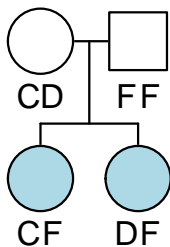
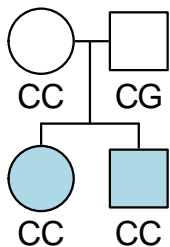


Hall et al (1990) [doi:10.1126/science.2270482](https://doi.org/10.1126/science.2270482)

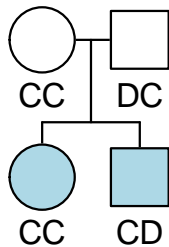
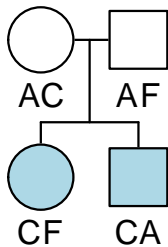
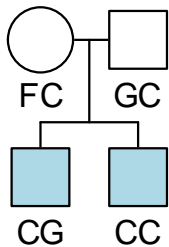
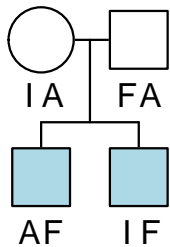
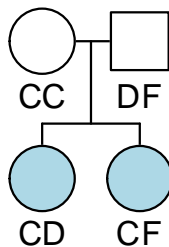
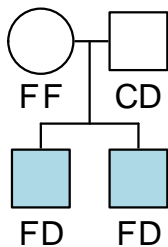
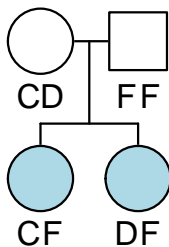
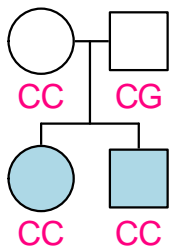
Affected sib pairs



Affected sib pairs



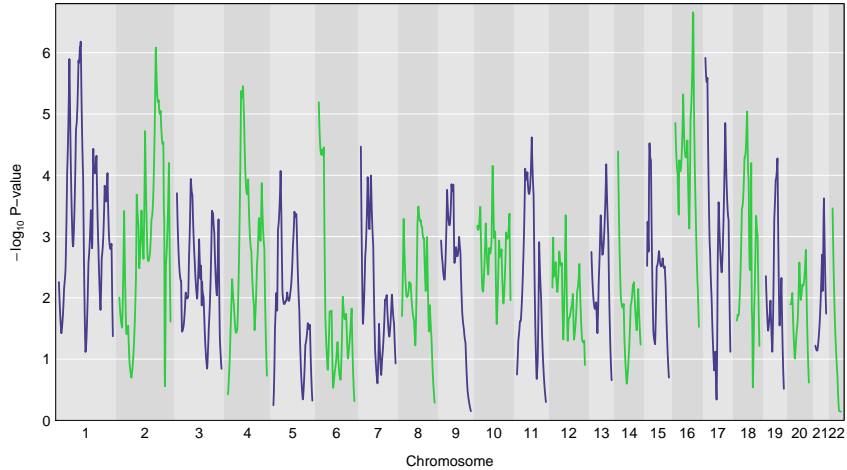
Affected sib pairs



Marshfield, Wisconsin



Prostate cancer genome scan





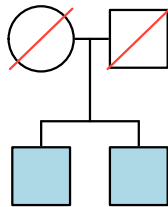
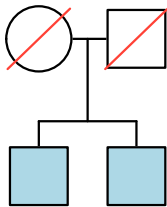
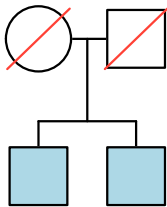
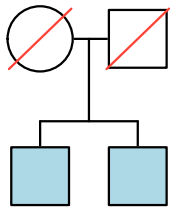
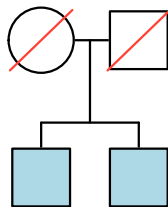
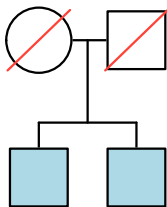
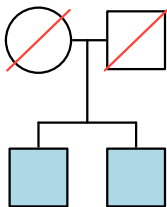
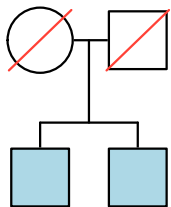
so happy



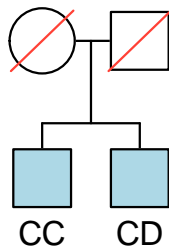
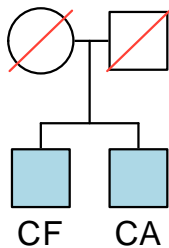
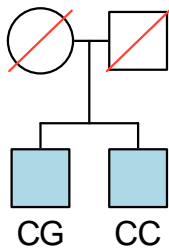
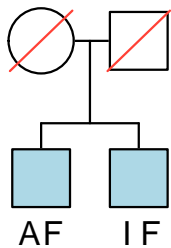
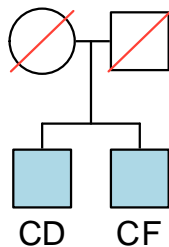
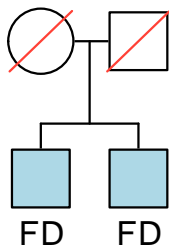
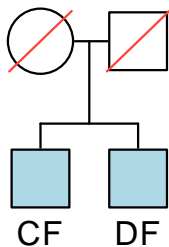
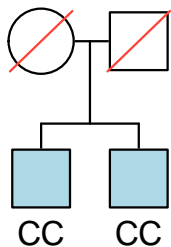
bit.ly/faxpic

If it seems too good to be true,
it probably is.

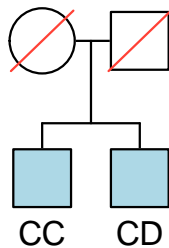
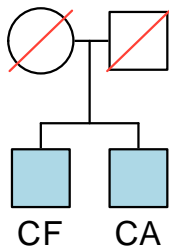
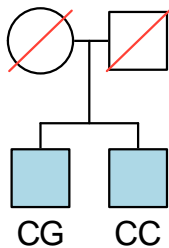
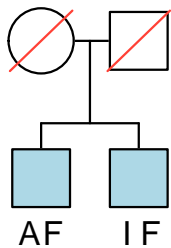
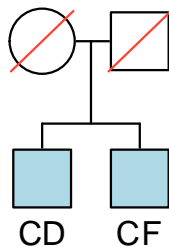
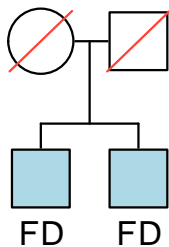
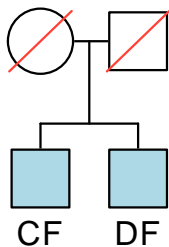
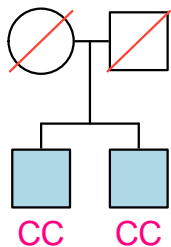
Prostate cancer pairs



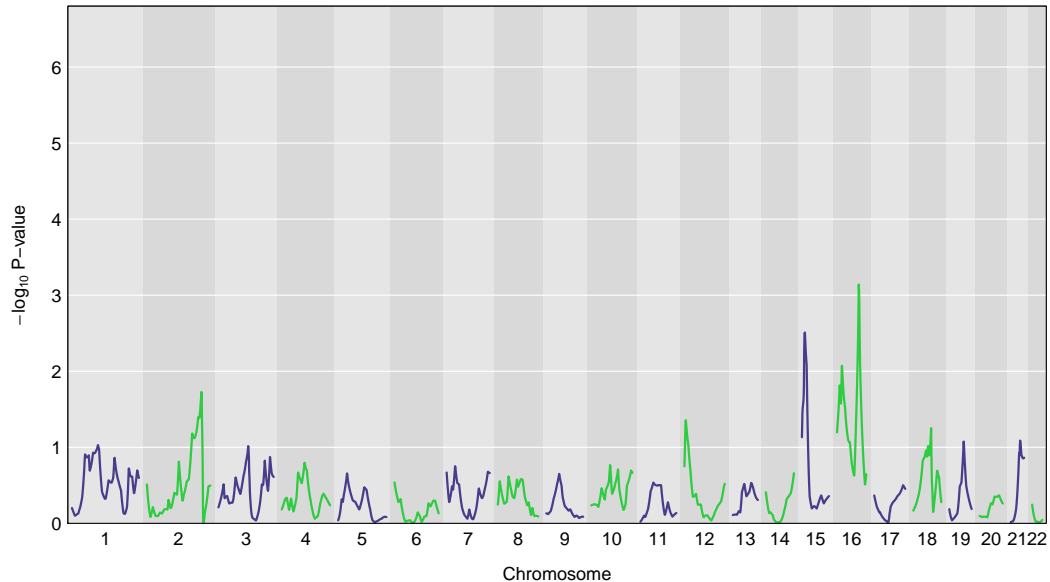
Prostate cancer pairs



Prostate cancer pairs



Prostate cancer genome scan – corrected



Estimation of Allele Frequencies With Data on Sibships

Karl W. Broman*

Department of Biostatistics, Johns Hopkins University, Baltimore, Maryland

Allele frequencies are generally estimated with data on a set of unrelated individuals. In genetic studies of late-onset diseases, the founding individuals in pedigrees are often not available, and so one is confronted with the problem of estimating allele frequencies with data on related individuals. We focus on sibpairs and sibships, and compare the efficiency of four methods for estimating allele frequencies in this situation: (1) use the data for one individual from each sibship; (2) use the data for all individuals, ignoring their relationships; (3) use the data for all individuals, taking proper account of their relationships, considering a single marker at a time; and (4) use the data for all individuals, taking proper account of their relationships, considering a set of linked markers simultaneously. We derived the variance of estimator 2, and showed that the estimator is unbiased and provides substantial improvement over method 1. We used computer simulation to study the performance of methods 3 and 4, and showed that method 3 provides some improvement over method 2, while method 4 improves little on method 3. *Genet. Epidemiol.* 20:307–315, 2001. © 2001 Wiley-Liss, Inc.

Karl W. Broman*

Department of

Allele frequencies of individuals. Individuals are grouped and estimated using the frequency and sibship; (2) data for a single account of We derived based and simulation 3 provided method 3

Erratum: Broman KW. 2001. Estimation of Allele Frequencies With Data on Sibships. Genet Epidemiol 20:307–15.

Karl W. Broman*

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In the April 2001 issue of *Genetic Epidemiology*, in the article “Estimation of Allele Frequencies With Data on Sibships,” by Broman (20:307–15), there is an error on page 310, in the second paragraph under “Method 3: Accounting for Relationships.” The stated probabilities that an allele in the second sibling is not identical by descent (IBD) with one of the first sibling’s alleles, written as $p_i/(1+p_i)$, are incorrect; we had missed two important cases. Let (g_{11}, g_{12}) denote the two alleles of the genotype of the first sibling, (g_{21}, g_{22}) denote the two alleles of the genotype of the second sibling, and $\mathbf{g} = (g_{11}, g_{12}, g_{21}, g_{22})$. Further, let \mathbf{pg} denote the genotypes for the two parents, and A denote the event “ g_{21} is not IBD with g_{11} or g_{12} .” We seek $\Pr(A|\mathbf{g})$, which we calculate by conditioning on the parents’ genotypes, as follows:

Slides: kbroman.org/Talk_DataMishap

kbroman.org

github.com/kbroman

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