

		No	
	Disease	Disease	
Exposed	15	85	100
Not	10	90	100
	25	175	

Disease Odds Ratio (DOR)

$$\begin{aligned}
 DOR &= \frac{\text{Odds of Disease given Exposure}}{\text{Odds of Disease given No Exposure}} \\
 &= \frac{O(D|E)}{O(D|\bar{E})} \\
 &= \frac{P(D|E)/[1-P(D|E)]}{P(D|\bar{E})/[1-P(D|\bar{E})]} \\
 &= \frac{15/85}{10/90} = \frac{15 \cdot 90}{10 \cdot 85} \\
 &= \frac{100}{100} = \frac{15 \cdot 90}{10 \cdot 85}
 \end{aligned}$$

		No	
	Disease	Disease	
Exposed	15	85	100
Not	10	90	100
	25	175	

Exposure Odds Ratio (EOR)

$$\begin{aligned}
 EOR &= \frac{O(E|D)}{O(E|\bar{D})} = \frac{P(E|D)/[1-P(E|D)]}{P(E|\bar{D})/[1-P(E|\bar{D})]} \\
 &= \frac{15/25}{10/175} = \frac{15 \cdot 90}{10 \cdot 85}
 \end{aligned}$$

The *Disease Odds Ratio* is equal to the *Exposure Odds Ratio* → the Odds Ratio is estimable from either type of study.

When the probability of the disease is small, the Odds Ratio (OR) approximates the Relative Risk (RR).

Sampling Distribution for $\ln(OR)$

- $\ln(\hat{OR}) = \ln\left(\frac{a \cdot d}{b \cdot c}\right)$
- Approximately normal with ...
- $SE = \sqrt{\frac{1}{a} + \frac{1}{b} + \frac{1}{c} + \frac{1}{d}}$

	Case	Control
Exposed	a	b
Not	c	d

Reasons for an observed genetic association

- The locus is a functional variant (association is causal)

Functional variant → Disease

- The locus is in linkage disequilibrium with a functional variant:

Marker locus ^{LD} → Functional variant → Disease

- The association is due to confounding by population stratification

Marker locus → Population stratification → Functional variant → Disease

Measures of Disease Association – Odds Ratios and Relative Risk

- In epidemiology, association between disease and etiological factors are usually expressed in terms of relative risk measures.

(Risk of disease in exposed subjects) / (Risk of disease in unexposed subjects)

- In genetic epidemiology, relative risks can be defined for
 - genotypes
 - alleles
 - haplotypes

Genotype Relative Risks (GRRs)

- For a diallelic locus with alleles A & a , there are three genotypes: A/A , A/a , a/a

- One is typically taken as the reference group (say a/a) and GRRs are expressed as

$$GRR_{A/A} = \frac{\text{Risk for } A/A \text{ geno}}{\text{Risk for } a/a \text{ geno}} = \phi_{A/A} \quad \& \quad GRR_{A/a} = \frac{\text{Risk for } A/a \text{ geno}}{\text{Risk for } a/a \text{ geno}} = \phi_{A/a}$$

- For a rare disease, the RRs can be estimated by odds ratios using case-control data.

	Case	Control
A/A	$D_{A/A}$	$H_{A/A}$
A/a	$D_{A/a}$	$H_{A/a}$
a/a	$D_{a/a}$	$H_{a/a}$

$$OR_{A/A} = \frac{D_{A/A} \cdot H_{a/a}}{H_{A/A} \cdot D_{a/a}}$$

$$OR_{A/a} = \frac{D_{A/a} \cdot H_{a/a}}{H_{A/a} \cdot D_{a/a}}$$

Allelic Relative Risks

- An allelic RR refers to the chromosome-level of analysis, rather than person-level.

- For a diallelic locus we have ϕ_A and ϕ_a . If allele a is the reference then $\phi_a = 1$

- They are related to Genotype RRs by a multiplicative model: $\phi_{i/j} = \phi_i \cdot \phi_j$

$$\rightarrow \phi_{A/A} = (\phi_A)^2 \quad \& \quad \phi_{A/a} = \phi_A$$

- Assuming a rare disease, the multiplicative model, and HW equilibrium in the population, the allelic RR can be estimated by an odds ratio

- The assumptions make it possible to treat chromosomes as independent and analyze the 2x2 allele-level table.

	Case	Control
Allele A	a	b
Allele a	c	d

Example: A SNP in the BRCA1 gene (Pro871Leu)

	Subjects	
	Case	Control
Leu/Leu	89	56
Leu/Pro	369	250
Pro/Pro	342	266

	Chromosomes	
	Case	Control
Leu		
Pro		

- Compute the two estimated GRRs (ORs) for the genotype table.

- Fill in the allele table.

- Compute an odds ratio estimate for the Leu/Leu genotype based on the multiplicative model.

Dominant & Recessive Models → Different 2x2 Tables

Subjects		
	Case	Control
<i>Leu/Leu</i>	89	56
<i>Leu/Pro</i>	369	250
<i>Pro/Pro</i>	342	266

Dominant		
	Case	Control
<i>Leu/*</i>	458	306
<i>Pro/Pro</i>	342	266

Recessive		
	Case	Control
<i>Leu/Leu</i>	89	56
<i>Pro/*</i>	711	516