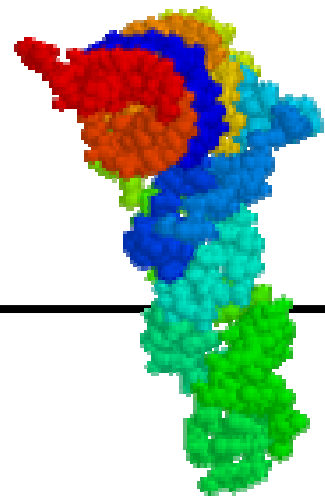


Genomics, Computing, Economics & Society



10 AM Tue 11-Oct 2005
week 4 of 14

[MIT-OCW Health Sciences & Technology 508/510](#)

[Harvard Biophysics 101](#)

Economics, Public Policy, Business, Health Policy

Class outline

- (1) **Topic priorities for homework since last class**
- (2) **Quantitative exercises: psycho-statistics, combinatorials, random/compression, exponential/logistic, bits, association & multi-hypotheses**
- (3) **Project level presentation & discussion**
- (4) **Sub-project reports & discussion:**
 - Personalized Medicine & Energy Metabolism**
- (5) **Discuss communication/presentation tools**
- (6) **Topic priorities for homework for next class**

Common Disease – Common Variant Theory. How common?

**ApoE allele $\epsilon 4$: Alzheimer's dementia,
& hypercholesterolemia**

20% in humans, >97% in chimps

HbS 17% & G6PD 40% in a Saudi sample

CCR5 Δ 32 : resistance to HIV

9% in caucasians

SNPs & Covariance in proteins

e4 20%

ApoE

e3 80%

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due to copyright
reasons.

Ancestral = Arg 112 Thr 61

One form of HIV-1 Resistance

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reasons.

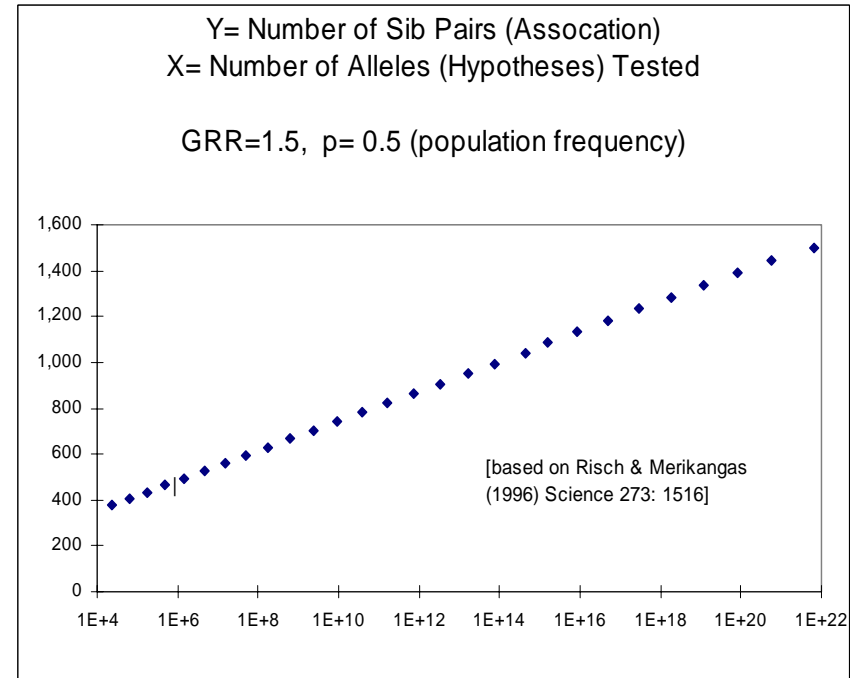
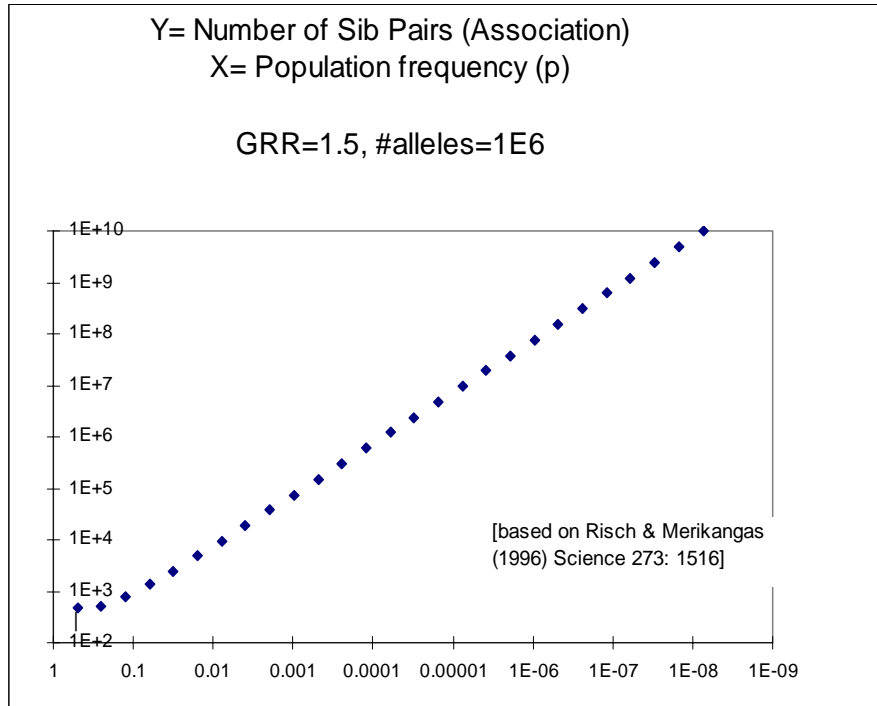
Association test for CCR-5 & HIV resistance

Alleles	Obs Neg	ObsSeroPos	total	ExpecNeg	ExpecPos
CCR-5+	1278	1368	2646	1305	1341
Δ ccr-5	130	78	208	103	105
total	1408	1446	2854		
					P
dof=(r-1)(c-1)=1		ChiSq=sum[(o-e)^2/e]=		15.6	0.00008

Figure removed due to copyright reasons.

Samson et al. [Nature 1996 382:722-5](#)

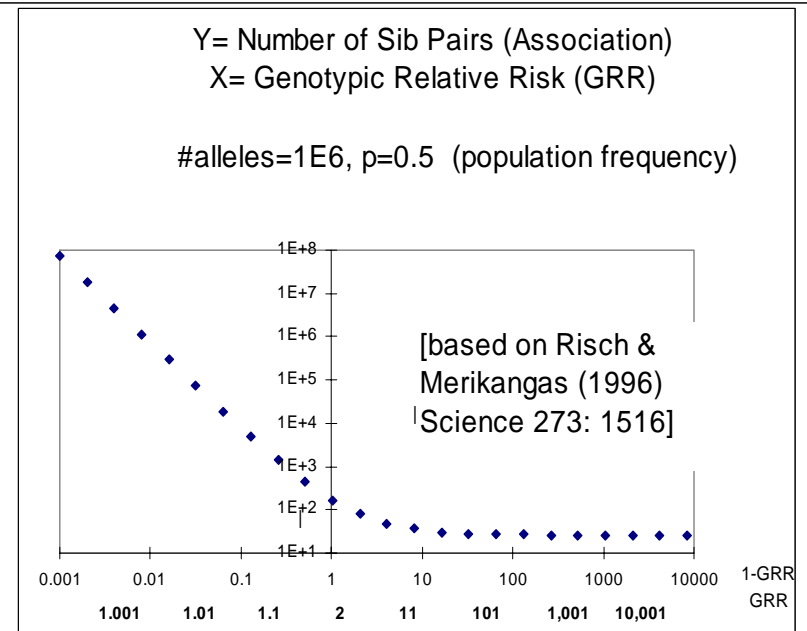
But what if we test more than one locus?



The future of genetic studies
of complex human diseases.

[Ref](#)

GRR = Genotypic relative risk



How many "new" mutations?

G= generations of exponential population growth = 5000

N'= population size = 6×10^9 now; N= 10^4 pre-G

m= mutation rate per bp per generation = 10^{-8} to 10^{-9} [\(ref\)](#)

L= diploid genome = 6×10^9 bp

$e^{kG} = N'/N$; so $k= 0.0028$

Av # new mutations $< \sum_{t=1 \text{ to } 5000} L e^{kt} m = 4 \times 10^3 \text{ to } 4 \times 10^4$
per genome

Take home: "High genomic deleterious mutation rates in hominids" accumulate over 5000 generations & confound linkage methods
And common (causative) allele assumptions.

Class outline

- (1) Topic priorities for homework since last class
- (2) Quantitative exercise
- (3) Project level presentation & discussion
- (4) Sub-project reports & discussion
- (5) Discuss communication/presentation tools
- (6) Topic priorities, homework for next class**