



## Qualitative traits

single gene

Mendelian inheritance

phenotypes in distinct  
categories

phenotype typically not  
affected by environment

ABO blood group system

Huntington disease

PKU

Duchenne muscular dystrophy

## Quantitative traits

multiple genes (**polygenic**)

no simple inheritance pattern  
but familial

phenotypes expressed on a  
continuum

phenotype influenced by  
environment

cognitive ability

late onset Alzheimer disease

schizophrenia

depression

# Schizophrenia

discontinuous trait    normal vs affected  
risk    concordance

Phenotype:    severe mental disorder

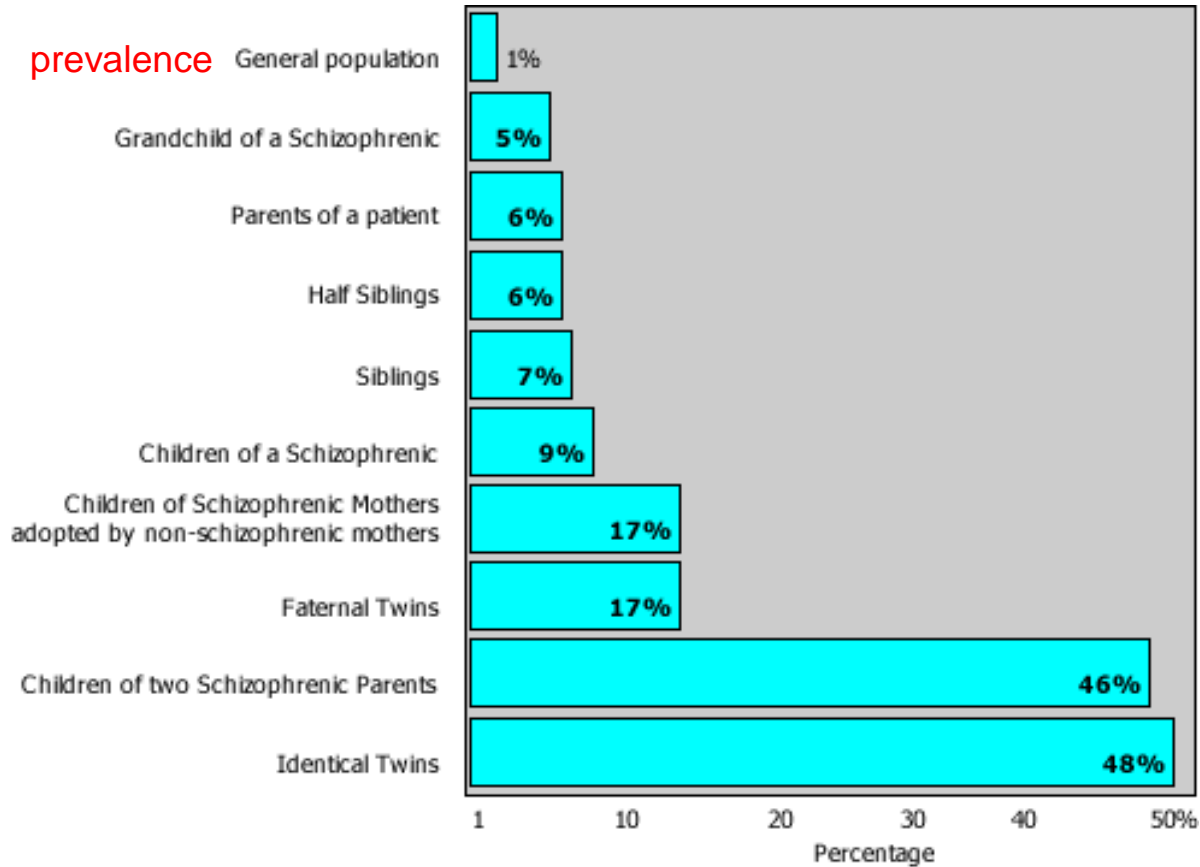
Prevalence:    1 in 100

1% worldwide

familial    pedigrees show disorder runs in families  
clearly not single gene inheritance pattern



# Risk of schizophrenia



Spousal risk = 2%

# Multifactorial **polygenic inheritance**

- multifactorial - many factors: genes, environment, interactions

- **polygenic** - influenced by many genes

combination of common mutations in same genes or result of rare genetic variants?

are sporadic cases result of new mutations or environmental factors?

low penetrance of genetic risk factors

- **genetic heterogeneity**

there are different genes associated with schizophrenia in different families

many different genotypes produce the same (or similar) phenotype

COMT gene - one allelic variant increases risk of schizophrenia by 50%  
- most schizophrenics do not have this risk allele

# General cognitive ability

- **continuous variation**

- everyone has the trait, level of the trait can be measured
- scores are adjusted to be normally distributed

can calculate **variance, covariance data**

**correlation between scores for relatives**

Phenotype: level of cognitive functioning

**familial** - ability levels do run in families, as shown by significant correlations between family members

relatives resemble each other for level of cognitive ability -  
but how much of the resemblance is due to genes  
relatives share and how much is due to the environment  
they also share?

Relationship	% genes shared	Correlation between ability scores
MZ twins	100	.85
DZ twins	50	.60
Parent/offspring	50	.45
Sibs	50	.45
½ sibs, aunts,uncles, grandparent, /child	25	.30
cousins	12.5	.15
unrelated	0	.00
spouses	0	.40

**assortative mating** spouses choose each other on basis of similar cognitive ability

**heritable** upwards of 50% of variation for cognitive ability scores is due to variation in genes

**environmental** the remaining variation is due to environmental variables

**shared (common) environment** **between family variance** - environmental effect that increases similarity within family , due to shared experiences

**non-shared (individual-specific) environment** **within family variance** – environmental effect that makes individuals differ, due to their unique experiences

## Quantitative inheritance

- many genes influence a trait
- trait shows continuous variation

- each gene still follows Mendelian inheritance laws
- most genes show **additive effects**  
all alleles contribute to the phenotype  
effects of each allele 'add up' to produce phenotype  
some alleles increase level of phenotype, some decrease it

dominant alleles produce **non-additive effects**

distribution of scores may become skewed from normal





## Problem

- what about discontinuous traits like schizophrenia
  - polygenic
  - continuous variation?

Two models used to explain this:

### Model 1 Liability-threshold model

- individuals have different **liabilities** (depending on familial factors like genes, shared environments)
- clinical disorder is not produced until certain **threshold** is exceeded

### Model 2 Continuous variation model

- term 'disorder' is an artificial construct
- there is no threshold, just a continuum from normal to abnormal
  - we just do not (or cannot) yet measure it on a continuum

