Overview/reminder of basic concepts in statistics and genetics

SISG, Visscher-Goddard Module

## Random variables, expected values and (co)variance

A discrete random variable can assume only a countable number of values
Probability mass function:

$$
p(x)=P(X=x)
$$

Expected value:

$$
\mu=E(X)=\sum x p(x)
$$

As a function of random variable:

$$
E[h(X)]=\sum h(x) p(x)
$$

Variance:

$$
\operatorname{Var}(X)=E\left[(X-\mu)^{2}\right]
$$

## Random variables, expected values and (co)variance

A discrete random variable can assume only a countable number of values
allele $x$ :

$$
\begin{aligned}
& p(x)=\left\{\begin{array}{cc}
p & x=1 \\
1-p & x=0
\end{array}\right\} \\
& E(X)=0(1-p)+1(p)=p
\end{aligned}
$$

$$
\operatorname{Var}(X)=p-p^{2}=p(1-p)
$$

## Random variables, expected values and (co)variance

A continuous random variable can be any value within a range
probability of being in shaded area
$=f_{X}(x) d x$
the interval should contribute
$=x f_{X}(x) d x$
the expected value and variance

$$
E(X)=\mu_{X}=\int_{-\infty}^{\infty} x f_{X}(x) d x \quad \operatorname{Var}(X)=E\left(\left(X-\mu_{x}\right)^{2}\right)
$$

## Random variables, expected values and (co)variance

Covariance

Let $X$ and $Y$ be a pair of continuous random variables, with respective means $\mu_{\mathrm{x}}$ and $\mu_{\mathrm{y}}$. The expected value of $\left(\mathrm{X}-\mu_{\mathrm{x}}\right)\left(\mathrm{Y}-\mu_{\mathrm{y}}\right)$ is called the covariance between X and Y .

$$
\operatorname{Cov}(X, Y)=E\left[\left(X-\mu_{x}\right)\left(Y-\mu_{y}\right)\right]
$$

If the random variables $X$ and $Y$ are independent, then the covariance between them is 0 . However, the converse is not true.

## Summary (co)variance rules

$$
\begin{aligned}
& \operatorname{Var}(x)=E[x-E(x)]^{2} \\
& \operatorname{Var}(c x)=c^{2} \operatorname{Var}(x) \\
& \operatorname{Var}(x+y)=\operatorname{Var}(x)+\operatorname{Var}(y)+2 \operatorname{Cov}(x, y) \\
& \operatorname{Var}(x+c)=\operatorname{Var}(x) \\
& \operatorname{Cov}(x, y)=E[(x-E(x)(y-E(y)] \\
& \operatorname{Cov}(c x, y)=c \operatorname{Cov}(x, y) \\
& \operatorname{Cov}(x, y+z)=\operatorname{Cov}(x, y)+\operatorname{Cov}(x, z)
\end{aligned}
$$

## Bayes' Theorem

Identify people who are liable to suffer from a genetic disease later in life.
1 in 1000 people are a carrier of the disease
No test is perfect - probability that a carrier tests negative is $1 \%$

- probability that a non-carrier tests positive is $5 \%$
$A=$ the event "the patient is a carrier"
$B=$ the event "the test result is positive"
Hence: $P(A)=0.001 ; P\left(A^{\prime}\right)=0.999 ; P(B \mid A)=0.99 ; P\left(B \mid A^{\prime}\right)=0.05$
A patient has a positive result. $\mathbf{Q}$ : What is the probability that the patient is a carrier?
Answer

$$
\begin{aligned}
P(A \mid B) & =\frac{P(B \mid A) P(A)}{P(B \mid A) P(A)+P\left(B \mid A^{\prime}\right) P\left(A^{\prime}\right)} \\
& =\frac{0.99 * 0.001}{(0.99 * 0.001)+(0.05 * 0.999)}=0.0194
\end{aligned}
$$

## Hardy-Weinberg equilibrium

Mathematical relation between allele frequencies and the genotype frequencies is:

$$
A A: p^{2} \quad A a: 2 p q \quad \text { aa: } q^{2}
$$

| Allele | A | a |
| :--- | :--- | :--- |
| Frequency | p | q |



## HWE and SNPs

If SNP genotypes are coded $X=0,1$ and 2 (alleles) and the allele frequency is $p$, then:

$$
\mathrm{E}(\mathrm{X})=(1-p)^{2 *} 0+2 p(1-p)^{*} 1+p^{2 *} 2=2 p
$$

$$
\operatorname{var}(\mathrm{X})=(1-p)^{2 *}(0-2 p)^{2}+2 p(1-p)^{*}(1-2 p)^{2}+p^{2 *}(2-2 p)^{2}=2 p(1-p)
$$

