Hardy-Weinberg Equilibrium

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Contents

Hardy-Weinberg equilibrium

- A biological population of n individuals.
- A bi-allelic genetic marker.
- One locus with alleles A and B, frequencies p and q.
- Three genotypes AA, AB, BB frequencies f_{AA}, f_{AB} and f_{BB}.

♀

			p	q
			A	B
♂	p	A	p^2	pq
	q	B	pq	q^2

f_{AA}	f_{AB}	f_{BB}
p^2	$2pq$	q^2

- Equilibrium achieved in one generation.
- Note that the allele frequency of A in the new generation is $p' = \frac{2p^2+2pq}{2} = p^2 + pq = p(p+q) = p$.

Hardy-Weinberg equilibrium: a longer derivation

- Let P, Q and R be the frequencies of genotypes AA, AB and BB, with $P + Q + R = 1$, and p, q the A and B allele frequencies.
- Note that $p = P + \frac{1}{2}Q$ and that $q = R + \frac{1}{2}Q$.

Mating	Frequency	AA	AB	BB
AA × AA	P^2	P^2	0	0
AA × AB	$2PQ$	PQ	PQ	0
AA × BB	$2PR$	0	$2PR$	0
AB × AB	Q^2	$\frac{1}{4}Q^2$	$\frac{1}{2}Q^2$	$\frac{1}{4}Q^2$
AB × BB	$2QR$	0	QR	QR
BB × BB	R^2	0	0	R^2

- In the next generation

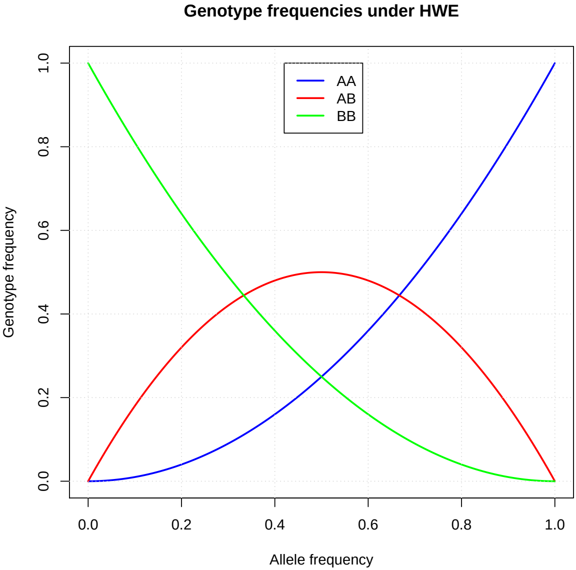
$$P' = P^2 + PQ + \frac{1}{4}Q^2 = (P + \frac{1}{2}Q)^2 = p^2$$

$$Q' = PQ + 2PR + \frac{1}{2}Q^2 + QR = 2(P + \frac{1}{2}Q)(R + \frac{1}{2}Q) = 2pq$$

$$R' = \frac{1}{4}Q^2 + QR + R^2 = (R + \frac{1}{2}Q)^2 = q^2$$

- Note we move from any arbitrary composition (P, Q, R) to $(p^2, 2pq, q^2)$ in a single generation

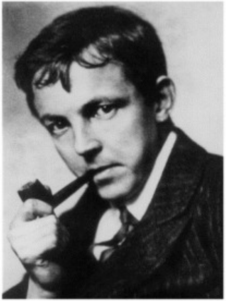
A classical genetic textbook figure



Hardy-Weinberg equilibrium

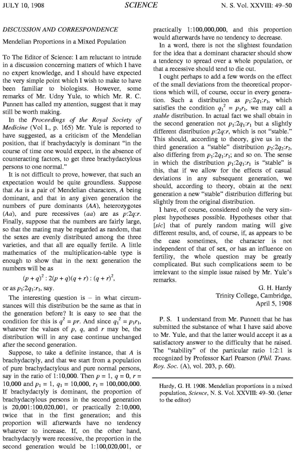
- Equilibrium refers to the fact that once the proportions $p^2, 2pq$ and q^2 are reached, allele frequencies and genotype frequencies will remain the same over the generations.
- Statistical tests for HWE test if the hypothesis $f_{AA} = p^2, f_{AB} = 2pq, f_{BB} = q^2$ is tenable.
- Strictly speaking, statistical tests for HWE do not assess equilibrium, but test for Hardy-Weinberg proportions (HWP).

The history of Hardy-Weinberg equilibrium (1/4)



Hardy, G.H. (1908) Mendelian proportions in a mixed population. *Science* 28: 49-50.

"In a word, there is not the slightest foundation for the idea that a dominant character should show a tendency to spread over the whole population, or that a recessive should tend to die out."



JULY 10, 1908 *SCIENCE* N. S. Vol. XXVIII: 49–50

DISCUSSION AND CORRESPONDENCE

Mendelian Proportions in a Mixed Population

To The Editor of Science: I am reluctant to intrude in a discussion concerning matters of which I have no expert knowledge, and I should have expected the very simple point which I wish to make to have been familiar to biologists. However, some remarks of Mr. Udny Yule, to which Mr. R. C. Punnett has called my attention, suggest that it may still be worth making.

In the *Proceedings of the Royal Society of Medicine* (Vol I., p. 165) Mr. Yule is reported to have suggested, as a criticism of the Mendelian position, that if brachydactyly is dominant "in the course of time one would expect, in the absence of counteracting factors, to get three brachydactylous persons to one normal."

It is not difficult to prove, however, that such an expectation would be quite groundless. Suppose that *Aa* is a pair of Mendelian characters, *A* being dominant, and that in any given generation the numbers of pure dominants (*AA*), heterozygotes (*Aa*), and pure recessives (*aa*) are as $p{:}2q{:}r$. Finally, suppose that the numbers are fairly large, so that the mating may be regarded as random, that the sexes are evenly distributed among the three varieties, and that all are equally fertile. A little mathematics of the multiplication-table type is enough to show that in the next generation the numbers will be as

$$(p+q)^2 : 2(p+q)(q+r) : (q+r)^2,$$

or as $p_1{:}2q_1{:}r_1$, say.

The interesting question is – in what circumstances will this distribution be the same as that in the generation before? It is easy to see that the condition for this is $q^2 = pr$. And since $q_1{}^2 = p_1r_1$, whatever the values of p, q, and r may be, the distribution will in any case continue unchanged after the second generation.

Suppose, to take a definite instance, that *A* is brachydactyly, and that we start from a population of pure brachydactylous and pure normal persons, say in the ratio of 1:10,000. Then $p = 1$, $q = 0$, $r =$ 10,000 and $p_1 = 1$, $q_1 = 10{,}000$, $r_1 = 100{,}000{,}000$. If brachydactyly is dominant, the proportion of brachydactylous persons in the second generation is 20,001:100,020,001, or practically 2:10,000, twice that in the first generation; and this proportion will afterwards have no tendency whatever to increase. If, on the other hand, brachydactyly were recessive, the proportion in the second generation would be 1:100,020,001, or practically 1:100,000,000, and this proportion would afterwards have no tendency to decrease.

In a word, there is not the slightest foundation for the idea that a dominant character should show a tendency to spread over a whole population, or that a recessive should tend to die out.

I ought perhaps to add a few words on the effect of the small deviations from the theoretical proportions which will, of course, occur in every generation. Such a distribution as $p_1{:}2q_1{:}r_1$, which satisfies the condition $q_1{}^2 = p_1r_1$, we may call a *stable* distribution. In actual fact we shall obtain in the second generation not $p_1{:}2q_1{:}r_1$ but a slightly different distribution $p{:}2q{:}r$, which is not "stable." This should, according to theory, give us in the third generation a "stable" distribution $p_2{:}2q_2{:}r_2$, also differing from $p_1{:}2q_1{:}r_1$; and so on. The sense in which the distribution $p_1{:}2q_1{:}r_1$ is "stable" is this, that if we allow for the effects of casual deviations in any subsequent generation, we should, according to theory, obtain at the next generation a new "stable" distribution differing but slightly from the original distribution.

I have, of course, considered only the very simplest hypotheses possible. Hypotheses other that [*sic*] that of purely random mating will give different results, and, of course, if, as appears to be the case sometimes, the character is not independent of that of sex, or has an influence on fertility, the whole question may be greatly complicated. But such complications seem to be irrelevant to the simple issue raised by Mr. Yule's remarks.

G. H. Hardy
Trinity College, Cambridge,
April 5, 1908

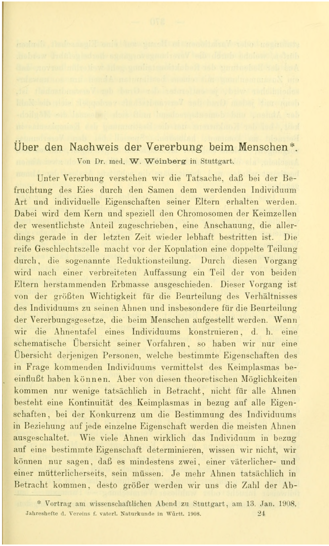
P. S. I understand from Mr. Punnett that he has submitted the substance of what I have said above to Mr. Yule, and that the latter would accept it as a satisfactory answer to the difficulty that he raised. The "stability" of the particular ratio 1:2:1 is recognized by Professor Karl Pearson (*Phil. Trans. Roy. Soc.* (A), vol. 203, p. 60).

Hardy, G. H. 1908. Mendelian proportions in a mixed population, *Science*, N. S. Vol. XXVIII: 49–50. (letter to the editor)

The history of Hardy-Weinberg equilibrium (2/4)

Weinberg, W. (1908) Über den Nachweis der Vererbung beim Menschen. Jahreshefte des Vereins für vaterländische Naturkunde in Württemberg. 64:369-382.

"Thus we obtain under the influence of panmixis in each generation the same proportion of pure and hybrid types ..."



Über den Nachweis der Vererbung beim Menschen*.

Von Dr. med. **W. Weinberg** in Stuttgart.

Unter Vererbung verstehen wir die Tatsache, daß bei der Befruchtung des Eies durch den Samen dem werdenden Individuum Art und individuelle Eigenschaften seiner Eltern erhalten werden. Dabei wird dem Kern und speziell den Chromosomen der Keimzellen der wesentlichste Anteil zugeschrieben, eine Anschauung, die allerdings gerade in der letzten Zeit wieder lebhaft bestritten ist. Die reife Geschlechtszelle macht vor der Kopulation eine doppelte Teilung durch, die sogenannte Reduktionsteilung. Durch diesen Vorgang wird nach einer verbreiteten Auffassung ein Teil der von beiden Eltern herstammenden Erbmasse ausgeschieden. Dieser Vorgang ist von der größten Wichtigkeit für die Beurteilung des Verhältnisses des Individuums zu seinen Ahnen und insbesondere für die Beurteilung der Vererbungsgesetze, die beim Menschen aufgestellt werden. Wenn wir die Ahnentafel eines Individuums konstruieren, d. h. eine schematische Übersicht seiner Vorfahren, so haben wir nur eine Übersicht derjenigen Personen, welche bestimmte Eigenschaften des in Frage kommenden Individuums vermittelst des Keimplasmas beeinflußt haben können. Aber von diesen theoretischen Möglichkeiten kommen nur wenige tatsächlich in Betracht, nicht für alle Ahnen besteht eine Kontinuität des Keimplasmas in bezug auf alle Eigenschaften, bei der Konkurrenz um die Bestimmung des Individuums in Beziehung auf jede einzelne Eigenschaft werden die meisten Ahnen ausgeschaltet. Wie viele Ahnen wirklich das Individuum in bezug auf eine bestimmte Eigenschaft determinieren, wissen wir nicht, wir können nur sagen, daß es mindestens zwei, einer väterlicher- und einer mütterlicherseits, sein müssen. Je mehr Ahnen tatsächlich in Betracht kommen, desto größer werden wir uns die Zahl der Ab-

* Vortrag am wissenschaftlichen Abend zu Stuttgart, am 13. Jan. 1908.

Jahreshefte d. Vereins f. vaterl. Naturkunde in Württ. 1908. 24

Hardy-Weinberg assumptions

- The organism under study is diploid.
- There is sexual reproduction.
- Non-overlapping generations.
- Random mating (w.r.t the trait under study).
- Population size is very large.
- Migration is negligible.
- Mutation can be ignored.
- Natural selection does not affect the trait under study.
- There is no genotyping error.

Basic law

- Genetic markers are, in general, expected to follow the HW law.
- If they do not follow the law, one (or more) of the HWE assumptions is/are violated.
- The most likely cause for disequilibrium is genotyping error.
- Markers need to be checked for HWE as part of a quality control procedure.

Hardy-Weinberg Equilibrium

$$\begin{array}{ccc} f_{AA} & f_{AB} & f_{BB} \\ p^2 & 2pq & q^2 \end{array}$$

Alternatively:

$$f_{AB}^2 = 4\ f_{AA}\ f_{BB}$$

Hardy-Weinberg for multiple alleles

If a marker has three alleles (e.g. the bloodgroup system A, B and O), with frequencies p_1, p_2 and p_3 with $p_1 + p_2 + p_3 = 1$, then under random mating we would obtain the genotype frequencies

				♀	
			p_1	p_2	p_3
			A	B	O
	p_1	A	p_1^2	$p_1 p_2$	$p_1 p_3$
♂	p_2	B	$p_2 p_1$	p_2^2	$p_2 p_3$
	p_3	O	$p_3 p_1$	$p_3 p_2$	p_3^2

In general, for a k-alleles system, homozygotes $A_i A_i$ will have frequency p_i^2, and heterozygotes $A_i A_j$ will have frequency $2 p_i p_j$.

Why is Hardy-Weinberg equilibrium important?

- It is a basic principle that, in the absence of disturbing forces, any genetic marker is expected to follow.
- Deviation from HWP is apparently most often due to genotyping error (confusion of homozygotes with heterozygotes)
- Deviation from HWP is expected (among cases) if the marker is related to disease.
- For other reasons, depending on the context of the study.
- ...

Hardy-Weinberg equilibrium and disease (numerical example)

- Let A be a rare, disease-predisposing allele with $p_A = 0.025$ (at birth, say).

	f_{AA}	f_{AB}	f_{BB}	p_A
Initial	p^2	$2pq$	q^2	
Population	0.0006	0.0488	0.9506	0.0250

- Let $P(D|AA) = 0.80$, $P(D|AB) = 0.40$ and $P(D|BB) = 0.02$
- Then, potentially after many years:

	f_{AA}	f_{AB}	f_{BB}	p_A
Diseased	0.0128	0.4998	0.4873	0.2627
Non-diseased	0.0001	0.0304	0.9694	0.0153

- Sampling from these distributions ($n = 1000$), and testing for HWP with an exact test:

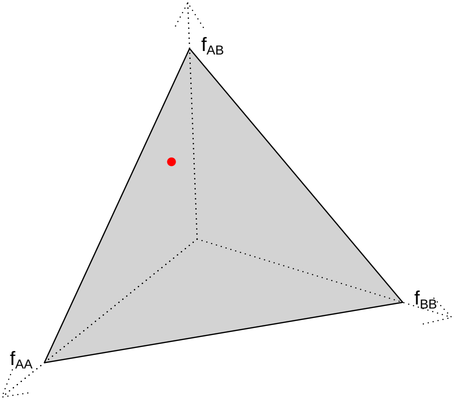
	AA	AB	BB	Exact p-value
Diseased	11	510	479	≈ 0
Non-diseased	0	19	981	≈ 1

- Disequilibrium observed in cases, but not detected in controls.

Statistical Tests for Hardy-Weinberg Equilibrium

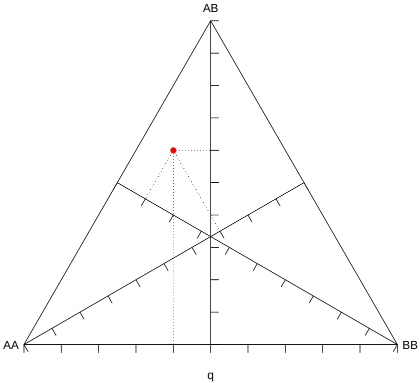
- Classical χ^2 test.
- Exact test (based on $P(N_{AB} \mid N_A)$).
- Likelihood ratio test.
- Permutation test.
- Bayesians tests.
- ...

Hardy-Weinberg Equilibrium and the Ternary Plot

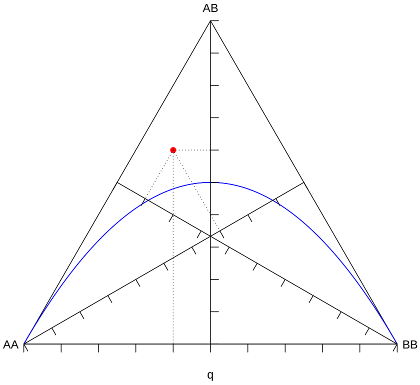


$$f_{AA} + f_{AB} + f_{BB} = 1$$

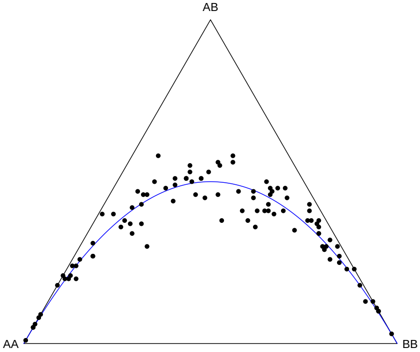
Hardy-Weinberg Equilibrium and the Ternary Plot



Hardy-Weinberg Equilibrium and the Ternary Plot



Hardy-Weinberg Equilibrium and the Ternary Plot



100 samples with n = 100, p~U(0,1), simulated under HWE

Classical χ^2 test for Hardy-Weinberg equilibrium

- The counts n_{AA}, n_{AB} and n_{BB} are regarded as a sample from a multinomial distribution.
- Expected counts under HWE are np^2, $n2p(1-p)$ and $n(1-p)^2$.
- A chi-square statistic for goodness-of-fit can be used

$$X^2 = \sum_{genotypes} \frac{(observed - expected)^2}{expected}$$

- The reference distribution is a χ^2_1 distribution.
- If we define the deviation from independence $D = \frac{1}{2}(n_{AB} - e_{AB})$, then

$$X^2 = \frac{D^2}{p^2(1-p)^2 n}$$

Example

- For an A/T polymorphism with counts AA=46, AT=39 and TT=15 we have

$$\hat{p}_A = \frac{2 \cdot 46 + 39}{200} = 0.655$$

- Expected counts under HWE

$$\begin{aligned} e_{AA} &= n\hat{p}_A^2 = 100 \cdot (0.655)^2 = 42.9025 \\ e_{AT} &= 2n\hat{p}_A(1-\hat{p}_A) = 2 \cdot 100 \cdot 0.655 \cdot 0.345 = 45.195 \\ e_{TT} &= n(1-\hat{p})^2 = 100 \cdot (0.345)^2 = 11.9025 \end{aligned}$$

- $$X^2 = \frac{(46-42.9025)^2}{42.9025} + \frac{(39-45.195)^2}{45.195} + \frac{(15-11.9025)^2}{11.9025} = 1.8789$$

- $$p - \text{value} = P\left(\chi_1^2 \geq 1.8789\right) = 0.1704601$$

Example in R

```
> library(HardyWeinberg)
> x <- c(46,39,15)
> names(x) <- c("AA","AT","TT")
> results <- HWChisq(x,cc=0,verbose=TRUE)
Chi-square test for Hardy-Weinberg equilibrium
Chi2 =  1.878892 p-value =  0.1704601 D =  -3.0975
>
```

Chi-square test with continuity correction

- If the expected counts are small, a continuity correction can be applied.
-
$$X_c = \sum_{i=1}^{3} \frac{(|n_i - e_i| - c)^2}{e_i} \qquad c = 0.5$$
- In R

```
> results <- HWChisq(x,verbose=TRUE)
Chi-square test with continuity correction for Hardy-Weinberg equilibrium
Chi2 =  1.441744 p-value =  0.2298573 D =  -3.0975
>
```

The exact test for HWE (Stevens, Levene, Haldane)

$$P\left(N_{AA}=n_{AA},N_{AB}=n_{AB},N_{BB}=n_{BB}\right)=\frac{n!}{n_{AA}!n_{AB}!n_{BB}!}\left(p_A^2\right)^{n_{AA}}\left(2p_Ap_B\right)^{n_{AB}}\left(p_B^2\right)^{n_{BB}}$$

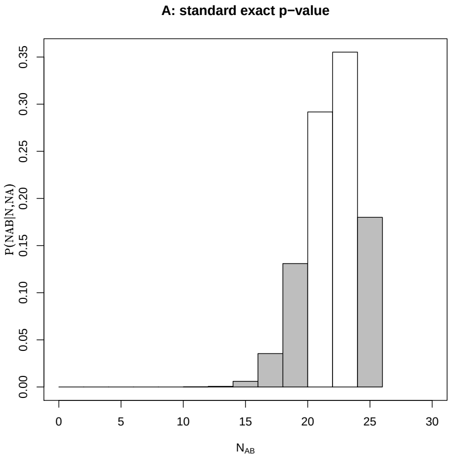
$$P\left(N_A=n_A\right)=\frac{2n!}{n_A!n_B!}\left(p_A\right)^{n_A}\left(p_B\right)^{n_{BB}}$$

$$P\left(N_{AA},N_{AB},N_{BB}|n_A,n_B\right)=\frac{n_A!n_B!n!2^{n_{AB}}}{\frac{1}{2}(n_A-n_{AB})!n_{AB}!\frac{1}{2}(n_B-n_{AB})!(2n)!}$$

Notes:

- p-value: sum all probabilities of samples as extreme or more extreme as the one you observed (there are alternatives).
- It takes much more CPU than a χ^2 test (use recursion).
- It is conservative.

The distribution for the exact test



Exact p-value calculation using Stevens' density for a sample with $n = 100$, $n_A = 25$ and $n_{AB} = 25$.

Exact test computations

Possible samples for $n = 100$ and $n_B = 14$

	AA	AB	BB	$P(n_{AB}\|n_A)$	$p-$ value	χ^2	$p-$ value	χ^2_c	$p-$ value
1	93	0	7	0.0000	0.0000	100.00	0.0000	86.17	0.0000
2	92	2	6	0.0000	0.0000	71.64	0.0000	60.01	0.0000
3	91	4	5	0.0000	0.0000	47.99	0.0000	38.58	0.0000
4	90	6	4	0.0002	0.0002	29.07	0.0000	21.86	0.0000
5	89	8	3	0.0051	0.0053	14.87	0.0001	9.86	0.0017
6	88	10	2	0.0602	0.0654	5.38	0.0204	2.58	0.1081
7	87	12	1	0.3209	0.3864	0.61	0.4334	0.02	0.8849
8	86	14	0	0.6136	1.0000	0.57	0.4516	0.02	0.8936

Example of the exact test

```
results <- HWExact(x,pvaluetype="selome",verbose=TRUE)
Haldane's Exact test for Hardy-Weinberg equilibrium
sample counts: nAA =  46 nAB =  39 nBB =  15
H0: HWE (D==0), H1: D <> 0
D =  -3.0975 p =  0.1852682
```

Permutation test (Monte Carlo scheme)

The Hardy-Weinberg law essentially states that alleles combine at random into genotypes.

- Compute a test statistic (e.g. χ^2, n_{AB}, ...) for the observed data.
- Obtain the number of A and B alleles from the observed data.
- Permute the alleles and assemble pairs of alleles into genotypes.
- Compute the test statistic for the permuted data set (pseudo-statististic)
- Repeat this N times.
- Count the number of times the pseudo-statistic is as larger or larger than the value for the observed data (C)
- Calculate the p-value as C/N.

Example permutation test

```
> x <- c(46,39,15)
> names(x) <- c("AA","AT","TT")
> HWPerm(x)
Permutation test for Hardy-Weinberg equilibrium
Observed statistic: 1.878892   17000 permutations. p-value: 0.1864706
>
```

Measures of (dis)equilibrium

Several statistics are being used as measures of the degree of disequilibrium:

- The X^2 statistic of a test for HWE
- The p-value of an exact test for HWE
- The inbreeding coefficient ($\hat{f}$)
- ...

The inbreeding coefficient (f)

$$
\begin{aligned}
P_{AA} &= p_A^2 + p_A p_B f \\
P_{AB} &= 2 p_A p_B (1 - f) \\
P_{BB} &= p_B^2 + p_A p_B f
\end{aligned}
$$

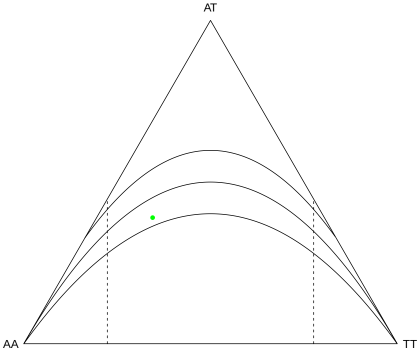
It can be shown that:

$$\frac{-p_m}{1 - p_m} \leq f \leq 1 \text{ with } p_m = min(p_A, p_B)$$

- $f = 0$: HWE
- $f = 1$: No heterozygotes
- $f < 0$: Heterozygote excess
- $f > 0$: Heterozygote dearth

For sample data, f is estimated by ML as: $\hat{f} = \frac{4 n_{AA} n_{BB} - n_{AB}^2}{n_A n_B}$.

Graphical assesment of HWE



Acceptance region for HWE: $2pq - 2pq\sqrt{\chi^2_1(\alpha)/n} \leq f_{AB} \leq 2pq + 2pq\sqrt{\chi^2_1(\alpha)/n}$

Testing Equilibrium with multiple alleles

- With many alleles, some are common and many are rare.
- Asymptotic procedures do not work well with rare alleles (small counts).
- Exact procedures and permutation tests are preferable
- Computational cost increases
- Exact density for multiple alleles:

$$P\left(N_{ij} = n_{ij} | n_1, \ldots, n_k\right) = \frac{n! 2^h \prod_{i=1}^{k} n_i!}{(2n)! \prod_{i \geq j} n_{ij}!}, \tag{1}$$

- where $h = \sum_{i>j} n_{ij}$ is the total heterozygote frequency.
- P-value: sum of all probabilities equal or smaller than the observed sample

Examples of HWE test with multiple alleles

	A	B	C
A	20		
B	31	15	
C	26	12	0

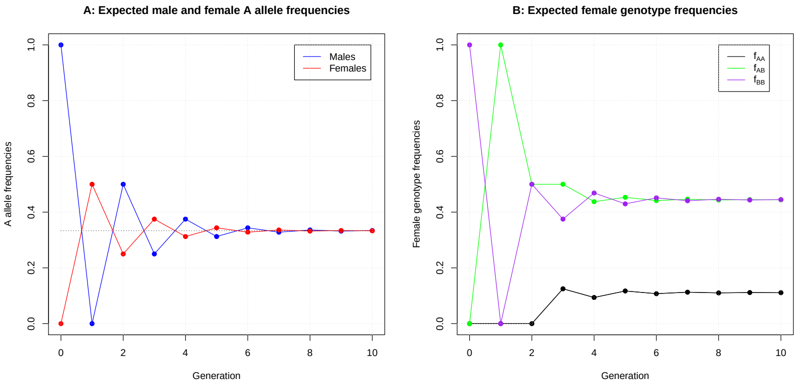
```
> x <- c(AA=20,AB=31,AC=26,BB=15,BC=12,CC=0)
> out <- HWTriExact(x)
Tri-allelic Exact test for HWE (autosomal).
Allele counts: A = 97 B = 73 C = 38
probability of the sample 0.0001122091
p-value =  0.03370688
>
> x3 <- toTriangular(x)
> out <- HWPerm.mult(x3)
Permutation test for Hardy-Weinberg equilibrium (autosomal).
3 alleles detected.
Observed statistic: 0.0001122091   17000 permutations. p-value: 0.03405882
```

Some special cases

How to test for equilibrium if...

- The variant has some recessive alleles (e.g. ABO blood groups)
- The variant is X-chromosomal
- The organism studied is tetraploid
- The variant studied has multiple copies
- ...

Hardy-Weinberg Equilibrium and the X chromosome

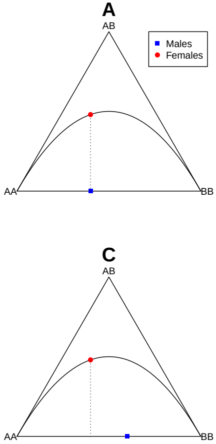


(Crow & Kimura, 1979)

Hardy-Weinberg equilibrium and the X chromosome

- For a marker on the X chromosome, it can take several generations before HWE is reached.
- A marker on the X chromosome is in HWE if and only if
  1. Females occur in the HWP proportions (AA: p^2, AB: $2pq$ BB: q^2).
  2. Male and female allele frequencies are equal.
- In practice, the second condition is ignored.
- If recognized, then four scenarios are possible.

The four scenarios in ternary plots



Graffelman & Weir (*Heredity*, 2016)

Some notation

- Let p_A be the relative frequency of the A allele.
- Let n_{AA}, n_{AB} and n_{BB} be the numbers of the three possible genotypes, if the sexes are not distinguished.
- Let m_A and m_B be the number of males carrying the A and B allele respectively,
- Let f_{AA}, f_{AB} and f_{BB} be the number of females of each of the three possible genotypes.
- Let n_m be the number of males, and n_f the number of females, and $n = n_m + n_f$ the total sample size.
- The total number of alleles is given by $n_t = 2n_f + n_m$.

Chi-square test for the X-chromosome

	Males		Females		
Genotype	A	B	AA	AB	BB
Probability	θp_A	$\theta(1-p_A)$	$(1-\theta)p_A^2$	$2(1-\theta)p_A(1-p_A)$	$(1-\theta)(1-p_A)^2$
Observed	m_A	m_B	f_{AA}	f_{AB}	f_{BB}
Expected	$n\hat{\theta}\hat{p}_A$	$n\hat{\theta}(1-\hat{p}_A)$	$n(1-\hat{\theta})\hat{p}_A^2$	$2n(1-\hat{\theta})\hat{p}_A(1-\hat{p}_A)$	$n(1-\hat{\theta})\hat{p}_A^2$

Observed and expected genotype counts for a X-chromosomal marker under Hardy-Weinberg equilibrium.

ML estimators:

$$\hat{\theta} = \frac{n_m}{n}, \qquad \hat{p}_A = \frac{n_A}{2n_f + n_m}.$$

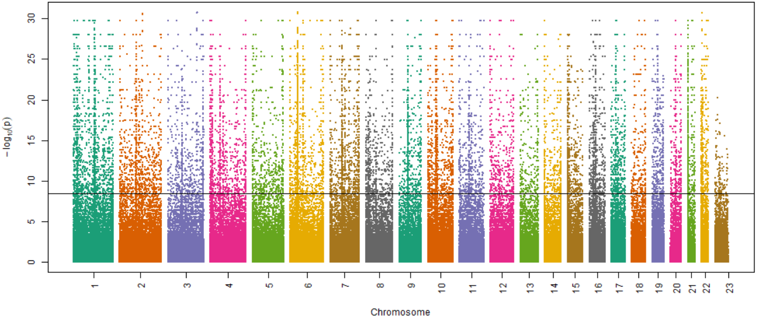
Chi-square statistic:

$$X^2 = \frac{(m_A - e_A)^2}{e_A} + \frac{(m_B - e_B)^2}{e_B} + \frac{(f_{AA} - e_{AA})^2}{e_{AA}} + \frac{(f_{AB} - e_{AB})^2}{e_{AB}} + \frac{(f_{BB} - e_{BB})^2}{e_{BB}}$$

Reference distribution:

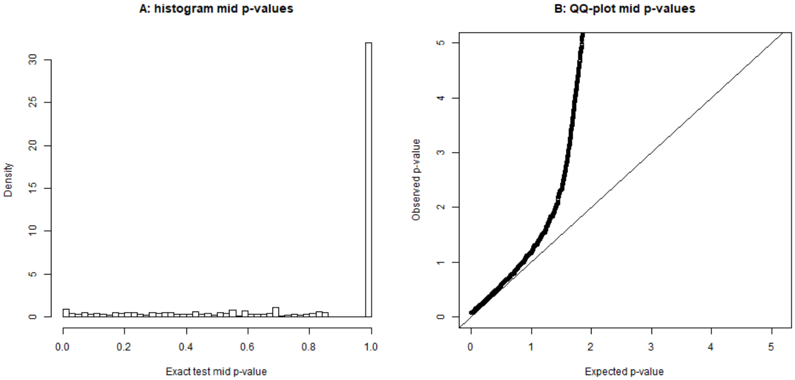
$$\chi_2^2$$

Genome-wide testing for HWE



Manhattan plot of -log10 transformed exact p-values for Hardy-Weinberg equilibrium of 13.4 million SNPs of the CHB sample. The horizontal line corresponds to the Bonferroni significance threshold

Genome-wide testing for HWE



R Software for studying HWP

- Plink (Purcell, 2007)
- R-package HWEBayes (Wakefield, 2010)
- R-package HardyWeinberg (Graffelman, 2008)
- R-package HWEintrinsic (Venturini, 2011)
- R-package hwde (Maindonald & Johnson, 2011)
- ...

References

- Graffelman, J. (2015) Exploring Diallelic Genetic Markers: The HardyWeinberg Package. *The Journal of Statistical Software* **64**(3): 1–23. http://www.jstatsoft.org/v64/i03/paper, doi: 10.18637/jss.v064.i03
- Graffelman, J. and Weir, B.S. (2016) Testing for Hardy-Weinberg equilibrium at bi-allelic genetic markers on the X chromosome. *Heredity* **116**(6) pp. 558–568. doi: 10.1038/hdy.2016.20.
- Hartl, D. L. (1980) *Principles of population genetics*, Sinauer Associates, Massachusetts,
- Weir, B.S. (1996) *Genetic Data Analysis II*, Chapter 3, Sinauer Associates, Massachusetts.

Computer exercises

- Install the package `HardyWeinberg`.
- For a certain C/G polymorphism, the genotype counts $n_{CC} = 23$, $n_{CG} = 48$ and $n_{GG} = 29$ are observed. Perform a χ^2 (without continuity correction) test for Hardy-Weinberg equilibrium. What is your conclusion? Repeat the test with continuity correction. Also perform the exact test for HWE. Are the results of the different tests consistent?
- For a certain C/T polymorphism, the genotype counts $n_{CC} = 0$, $n_{CT} = 7$ and $n_{TT} = 93$ are observed. Perform a χ^2 (without continuity correction) test for Hardy-Weinberg equilibrium. What is your conclusion? Repeat the test with continuity correction. Also perform the exact test for HWE. Are the results of the different tests consistent?
- Represent both polymorphisms in a ternary plot using the routine `HWTernaryPlot`.
- Write an R function for carrying out a permutation test for HWE.
- Apply the permutation test to the two polymorphisms studied. Are the results consistent with the tests you already performed?
- Simulate 100 SNPs with a uniform allele frequency under HWE using routine `HWData`. Depict your results in a ternary plot. How many SNPs are out of equilibrium according to a χ^2 test? How many are out of equilibrium according to an exact test?
- Collect all chi-square statistics obtained in your simulation, and make a histogram. What distribution do they follow? Repeat your simulation with 1000 or more SNPs to get a more precise idea of the distribution.