

# Testing and Modeling Genotypic Disequilibria

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## Introduction

In a diploid, sexually reproducing species, at a locus where there are two alleles  $A$  and  $a$ , the possible genotypes are  $AA$ ,  $Aa$  and  $aa$ . In a population of size  $N$ , with  $p$  the frequency of the  $A$  allele and  $q$  the frequency of the  $a$  allele, the expected numbers under Hardy-Weinberg equilibrium are  $NP_{AA} = Np^2$  for the  $AA$  genotype,  $NP_{Aa} = 2Npq$  for the  $Aa$  genotype, and  $NP_{aa} = Nq^2$  for the  $aa$  genotype. Writing  $m = \log(Np^2)$  and  $\log(p/q) = m_a$ , the logarithms of the frequencies may be written:

$$\log(Np) = m \quad (1)$$

$$\log(2Npq) = m + \log(2) + m_a \quad (2)$$

$$\log(Nq) = m + 2m_a \quad (3)$$

Thus the model is loglinear, and can be fitted as a generalized linear model with poisson error and offset  $\log(2)$  for the heterozygote. For example:

```
> obs <- c(AA = 147, Aa = 78, aa = 17)
> oset <- c(0, log(2), 0)
> ma <- c(0, 1, 2)
> hw.glm <- glm(obs ~ ma, family = poisson, offset = oset)
> summary(hw.glm)
```

Call:

```
glm(formula = obs ~ ma, family = poisson, offset = oset)
```

Deviance Residuals:

AA	Aa	aa
0.3364	-0.8854	1.0708

Coefficients:

	Estimate	Std. Error	z value	Pr(> z )
(Intercept)	4.96256	0.08137	60.99	<2e-16
ma	-1.20039	0.10778	-11.14	<2e-16

(Dispersion parameter for poisson family taken to be 1)

Null deviance: 149.3527 on 2 degrees of freedom  
Residual deviance: 2.0436 on 1 degrees of freedom  
AIC: 23.751

Number of Fisher Scoring iterations: 4

The function `hwde()` may also be used to fit this model, at the same time introducing a further “disequilibrium” term. The default output is the analysis of deviance table.

```
> hwdat <- data.frame(Observed = c(147, 78, 17), locus1 = c("AA",
+      "Aa", "aa"))
```

Now call the function.

```
> library(hwde)
> hwde(data = hwdat)

[1] "Analysis of Deviance Table"
  Resid. Df Resid. Dev Df Deviance
1         2    149.353
2         1     2.044  1  147.309
3         0 -3.553e-15  1     2.044
```

We leave till later detailed information on the use of `hwde()`, including details on how to obtain fitted values, residuals and parameter estimates. The disequilibrium term has the form

$$m_{aa} = \log \frac{4P_{AA}P_{aa}}{P_{Aa}}$$

Notice that the parameters  $m_a$  and  $m_{aa}$  have been abbreviated, in the computer output, to  $a$  and  $aa$  respectively.

If there several different populations, there must be a parameter (by default assumed to have the name `Population`), that accounts for different population sizes. In the code, this translates into a main effect `gp` in the log-linear model. Additionally, there may be different values for  $m_a$  and  $m_{aa}$  in the different populations.

A second locus requires the parameters  $m_b$  and  $m_{bb}$  for that locus. Additionally, parameters may be required that model quantities that, in the loglinear model, have the role of interactions between the two loci. Huttley and Wilson (2000) introduce the multiplicative versions of the following parameters:

$s_{ab}$ , the “sum of digenic disequilibria for the total sample”

$q_{ab}$ , the “product of digenic disequilibria for the total sample”

$m_{aab}$  and  $m_{abb}$ , which are “trigenic disequilibrium terms for the total sample”

In the usual case where phase for double heterozygotes is unknown and only nine genotypic classes can be distinguished, no degrees of freedom remain that might be used to estimate a quadrigenic disequilibrium term.

As noted above, the formulae in Huttley and Wilson (2000) give the multiplicative equivalents of these terms, using upper case letters. The additive versions used here (e.g., they have  $M_A$  where I have  $m_a = \log(M_A)$ ) use the corresponding lower case letters. Note however that in the second column on p.2131 of Huttley and Wilson, in the equations for  $\ln P_{Ab}^{AB}$  and  $\ln P_{aB}^{AB}$ ,  $\ln Q_{AB}^2$  should be, in each case,  $\ln Q_{AB}$ . The equations are given correctly in Weir and Wilson (1986), though with slight changes of notation. See also Weir (1996).

The function allows an arbitrary number of loci. Terms  $s_{ab}$ ,  $q_{ab}$ ,  $m_{abb}$  and  $m_{aab}$  are fitted for every pair of loci. Terms that correspond to second (or, with  $> 3$  loci, higher order) interactions contribute, in the present version of the code, to the residual. Try

```
> data(mendelABC)
> hwde(data = mendelABC, loci = c("seedshape", "cotylcolor", "coatcolor"))
```

## The use of `hwde()`

First recall the simple example that was described above. The data were entered, from the keyboard, into a data frame `hwdat` that had the form:

```
Observed locus1
147      AA
78       Aa
17       aa
```

The coding used in the column headed `locus1` can be varied; any two characters may be used for the alleles. With the column names that are shown, the corresponding parameter settings for the function `hwde()` can be left at their defaults.

An alternative is to enter the data, exactly as displayed above (though the spacing is immaterial), into a file. If the file is called `hw.txt` and is placed in the working directory, then it can be read in with:

```
> hwdat <- read.table("hw.txt", header = TRUE)
```

If there is a second locus, the default name is `locus2`. The default name for any third locus is `locus3`, etc. Where there is a column that has codes for different populations, the default name is `Population`.

### Example – two populations and two loci

With this introduction, we move directly to data, with two populations and two loci, that are suited to fitting all the parameters that the function currently allows. Data (Mourant et al, 1976) are:

Population	locus1	locus2	Observed
Indian	MM	SS	91
Indian	MM	Ss	147
Indian	MM	ss	85
Indian	MN	SS	32
Indian	MN	Ss	78
Indian	MN	ss	75
Indian	NN	SS	5
Indian	NN	Ss	17
Indian	NN	ss	7
Irish	MM	SS	121
Irish	MM	Ss	248
Irish	MM	ss	164
Irish	MN	SS	53
Irish	MN	Ss	422
Irish	MN	ss	375
Irish	NN	SS	9
Irish	NN	Ss	65
Irish	NN	ss	241

Assuming that this is stored in a file `IndianIrish.txt`, we can read in the data and do the analysis thus:

```
> IndianIrish <- read.table("IndianIrish.txt", header = TRUE)
> hwde(data = IndianIrish)
```

```
[1] "Analysis of Deviance Table"
      Resid. Df Resid. Dev Df Deviance
1          17    1724.07
2          16    1090.41  1    633.66
3          14     486.72  2    603.69
4          12     480.31  2      6.41
5          11     463.76  1     16.55
6          10     218.42  1    245.34
7           8     217.15  2      1.28
8           6      37.94  2    179.21
9           4      35.46  2      2.48
10          3      26.29  1      9.16
11          2       5.94  1     20.36
12          0 -5.573e-14  2      5.94
```

The above is the compact default output, in which terms that are at the same level of a hierarchy are grouped. For a first pass through the data, this may be the preferred output. A form of output in which each term corresponds to a single degree of freedom is available by using the parameter setting `group.terms=FALSE`, i.e.,

```
> hwde(data = IndianIrish, group.terms = FALSE)
```

difference from the last previous Residual Deviance term that is marked with an **r** (= reference) as the first character in the row in which it appears.

## Obtaining Additional Output

By default, the function returns (invisibly) a list with two elements. The first holds the analysis of variance table. The second holds the data and contrast terms that are required for fitting the various models. For example:

```
> hwdat.hw <- hwde(data = hwdat)

[1] "Analysis of Deviance Table"
      Resid. Df Resid. Dev Df Deviance
1           2    149.353
2           1      2.044  1    147.309
3           0 -3.553e-15  1      2.044

> names(hwdat)

[1] "Observed" "locus1"

> hwdat.hw$data.df

      obs data oset a aa
1  147   AA    1 2  1
2   78   Aa    2 1  0
3   17   aa    1 0  0
```

The following illustrates the direct use of the information in `hwdat.hw$data.df`, giving the user complete control over the models that are fitted.

```
> data.df <- hwdat.hw$data.df
> model1 <- glm(obs ~ a, family = poisson, data = data.df, offset = log(oset))
> model2 <- glm(obs ~ a + aa, family = poisson, data = data.df,
+   offset = log(oset))
> model1
```

```
Call: glm(formula = obs ~ a, family = poisson, data = data.df, offset = log(oset))
```

Coefficients:

```
(Intercept)          a
      2.562         1.200
```

Degrees of Freedom: 2 Total (i.e. Null); 1 Residual

Null Deviance: 149.4

Residual Deviance: 2.044 AIC: 23.75

Here is the output data frame for the `IndianIrish` data.

```
> II.hw <- hwde(data = IndianIrish, aovtable.print = FALSE)
> dataII.df <- II.hw$data.df
> dataII.df
```

	obs	gp	locus1	locus2	oset	a	b	aa	bb	sab	qab	abb	aab
1	91	Indian	MM	SS	1 2 2	1	1	0	2	2	2	2	
2	147	Indian	MM	Ss	2 2 1	1	0	0	1	0	1	1	
3	85	Indian	MM	ss	1 2 0	1	0	0	0	0	0	0	
4	32	Indian	MN	SS	2 1 2	0	1	0	1	1	1	0	
5	78	Indian	MN	Ss	4 1 1	0	0	1	0	0	0	0	
6	75	Indian	MN	ss	2 1 0	0	0	0	0	0	0	0	
7	5	Indian	NN	SS	1 0 2	0	1	0	0	0	0	0	
8	17	Indian	NN	Ss	2 0 1	0	0	0	0	0	0	0	
9	7	Indian	NN	ss	1 0 0	0	0	0	0	0	0	0	
10	121	Irish	MM	SS	1 2 2	1	1	0	2	2	2	2	
11	248	Irish	MM	Ss	2 2 1	1	0	0	1	0	1	1	
12	164	Irish	MM	ss	1 2 0	1	0	0	0	0	0	0	
13	53	Irish	MN	SS	2 1 2	0	1	0	1	1	1	0	
14	422	Irish	MN	Ss	4 1 1	0	0	1	0	0	0	0	
15	375	Irish	MN	ss	2 1 0	0	0	0	0	0	0	0	
16	9	Irish	NN	SS	1 0 2	0	1	0	0	0	0	0	
17	65	Irish	NN	Ss	2 0 1	0	0	0	0	0	0	0	
18	241	Irish	NN	ss	1 0 0	0	0	0	0	0	0	0	

The user can now fit any sequence of models that may be required. For example, the user may wish to a sequence of models that is different from the sequence fitted by `hwde()`.

Further control is available by supplying values for the parameters `termlist` and `refmodel`. For example, the default action with the data frame `hwdat` is equivalent to:

```
> hwde(termlist = c("+a", "+aa"), refmodel = c(1, 2), data = hwdat)
```

```
[1] "Analysis of Deviance Table"
```

	Resid. Df	Resid. Dev	Df	Deviance
1	2	149.353		
2	1	2.044	1	147.309
3	0	-3.553e-15	1	2.044

In `refmodel`, 1 refers to the model that has constant term only.

The first six models can be fitted to the data frame `IndianIrish` by setting:

```
> hwde(termlist = c("+gp", "+a", "+b", "+a+b", "+aa"), refmodel = c(1,
+ 2, 2, 2, 5), data = IndianIrish)
```

```
[1] "Analysis of Deviance Table"
      Resid. Df Resid. Dev Df Deviance
1          17    1724.07
2          16    1090.41  1    633.66
3          15     853.73  1    236.68
4          15     723.40  1    367.02
5          14     486.72  2    603.69
6          13     485.59  1         1.13
```

## Extraction of the sequence of fitted models

A further possibility, with the parameter setting `keep.models=TRUE`, is to include the full sequence of models that have been fitted in the list that is returned by the function. For example:

```
> hwdat.hw <- hwde(data = hwdat, keep.models = TRUE)
```

```
[1] "Analysis of Deviance Table"
      Resid. Df Resid. Dev Df Deviance
1           2    149.353
2           1      2.044  1   147.309
3           0 -3.553e-15  1      2.044
```

```
> hwdat.hw$models[[2]]
```

```
Call: glm(formula = obs ~ a, family = poisson, data = data.df, offset = log(oiset))
```

Coefficients:

```
(Intercept)          a
      2.562         1.200
```

Degrees of Freedom: 2 Total (i.e. Null); 1 Residual

Null Deviance: 149.4

Residual Deviance: 2.044 AIC: 23.75

```
> fitted(hwdat.hw$models[[2]])
```

```
      1      2      3
142.95868 86.08264 12.95868
```

The function `fitted()` can be replaced by any of the functions (`coef()`, `resid()`, `predict()`, etc.) that are available for use with a `glm` model object. Note that there are several different choices of residuals, with deviance residuals as the default. For the `IndianIrish` data there are, with the parameter setting `group.terms=FALSE`, 24 models from which to choose. Choose carefully!

## References

Huttley, G.A. and Wilson, S.R. 2000. Testing for concordant equilibria between population samples. *Genetics* 156: 2127-2135.

Mourant, A.E., Kopec, A.C. and Domaniewska-Sobczak, K. 1976. *The Distribution of the Human Blood Groups and Other Polymorphisms*. Oxford University Press.

Weir, B.S. 1996. *Genetic Data Analysis II*. Sinauer.

Weir, B.S. and Wilson, S.R. 1986. Log-linear models for linked loci. *Biometrics* 42:665-670.