

Goodness of fit

We observe data like that in the following table:

RR	RW	WW
35	43	22

We want to know:

Do these data correspond reasonably to the proportions 1:2:1?

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Goodness of fit

	RR	RW	WW
observed	35	43	22
expected	25	50	25

$$\begin{aligned}X^2 &= \sum \frac{(\text{observed} - \text{expected})^2}{\text{expected}} \\&= \frac{(35 - 25)^2}{25} + \frac{(43 - 50)^2}{50} + \frac{(22 - 25)^2}{25} \\&= 5.34\end{aligned}$$

$$1 - \text{pchisq}(5.34, 2) \approx 6.9\%$$

Or: `chisq.test(c(35,43,22), p=c(0.25, 0.5, 0.25))`

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Composite hypotheses

Sometimes, we ask not $p_{AA} = 0.25, p_{AB} = 0.5, p_{BB} = 0.25$

But rather something like:

$$p_{AA} = f^2, p_{AB} = 2f(1 - f), p_{BB} = (1 - f)^2 \quad \text{for some } f$$

For example: Genotypes, of a random sample of individuals, at a diallelic locus.

Question: Is the locus in Hardy-Weinberg equilibrium (as expected in the case of random mating)?

Example data:

AA	AB	BB
5	20	75

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Another example

ABO blood groups; 3 alleles A, B, O.

Phenotype A = genotype AA or AO

B = genotype BB or BO

AB = genotype AB

O = genotype OO

Allele frequencies: f_A, f_B, f_O (Note that $f_A + f_B + f_O = 1$)

Under Hardy-Weinberg equilibrium, we expect:

$$p_A = f_A^2 + 2f_Af_O$$

$$p_{AB} = 2f_Af_B$$

$$p_B = f_B^2 + 2f_Bf_O$$

$$p_O = f_O^2$$

Example data:

O	A	B	AB
104	91	36	19

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χ^2 test for these examples

- Obtain the maximum likelihood estimates (MLE) under H_0 .
- Calculate the corresponding cell probabilities.
- Turn these into (estimated) expected counts under H_0 .

- Calculate $\chi^2 = \sum \frac{(\text{observed} - \text{expected})^2}{\text{expected}}$

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Null distribution for these cases

- **Computer simulation:** (with **one wrinkle**)
 - Simulate data under H_0 (**plug in the MLEs for the observed data**)
 - Calculate the MLE with the simulated data
 - Calculate the test statistic with the simulated data
 - Repeat many times.
- **Asymptotic approximation**
 - Under H_0 , if the sample size, n , is large, the χ^2 statistic follows, approximately, a χ^2 distribution with **$k - s - 1$** degrees of freedom, where **$s = \text{no. parameters estimated under } H_0$** .
 - Note that $s = 1$ for example 1, and $s = 2$ for example 2, and so **$df = 1$** for both examples.

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Results, example 1

Example data:

AA	AB	BB
5	20	75

$$H_0: p_{AA} = f^2, p_{AB} = 2f(1-f), p_{BB} = (1-f)^2 \quad \text{for some } f$$

MLE: $\hat{f} = (5 + 20/2) / 100 = 15\%$

Expected counts:

2.25	25.5	72.25
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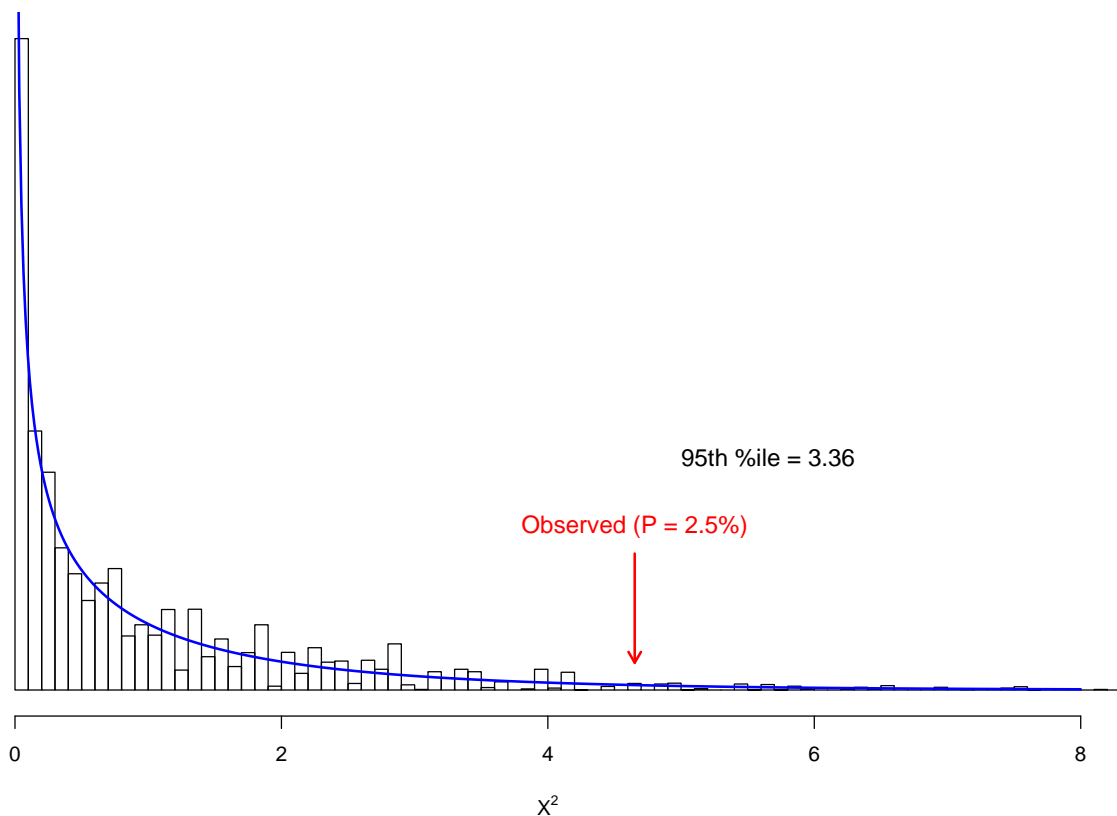
Test statistics: $X^2 = 4.65$

Asymptotic $\chi^2(df = 1)$ approx'n: $P \approx 3.1\%$

10,000 computer simulations: $P \approx 2.5\%$

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Est'd null dist'n of chi-square statistic



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Results, example 2

Example data:

O	A	B	AB
104	91	36	19

$$H_0: p_A = f_A^2 + 2f_A f_O, p_B = f_B^2 + 2f_B f_O, p_{AB} = 2f_A f_B, p_O = f_O^2, \text{ for some } f_A, f_B, f_O$$

MLE: $\hat{f}_O \approx 63.4\%$, $\hat{f}_A \approx 25.0\%$, $\hat{f}_B \approx 11.6\%$.

Expected counts:

100.5	94.9	40.1	14.5
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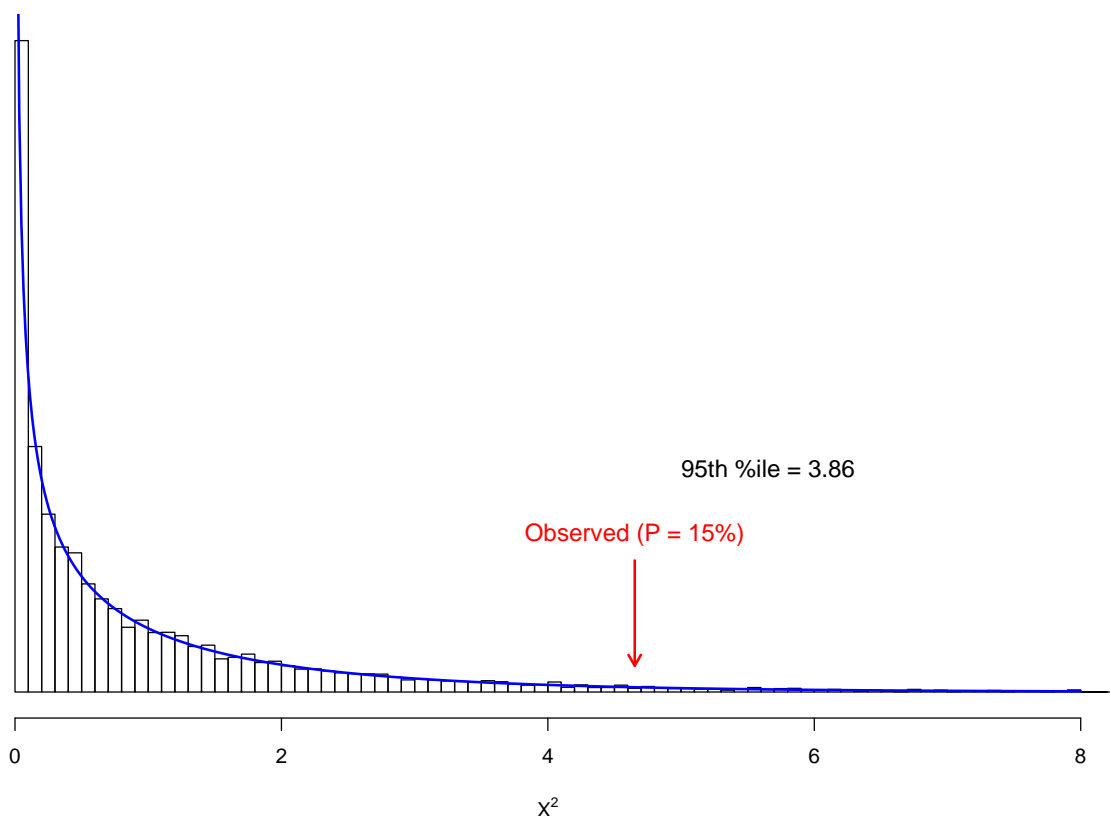
Test statistics: $\chi^2 = 2.10$

Asymptotic $\chi^2(df = 1)$ approx'n: $P \approx 15\%$

10,000 computer simulations: $P \approx 15\%$

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Est'd null dist'n of chi-square statistic



Example 3

A scientist applied a dose of DDT to groups of 10 spider mites and counted the number of mites (out of ten) that survived. A total of 50 groups of mites were considered.

	0	1	2	3	4	5	6	7	8	9	10
count	6	10	15	7	8	1	3	0	0	0	0

Q: Does this look a binomial distribution?

If $X \sim \text{binomial}(n = 10, p)$,

$$\Pr(X=k) = \binom{10}{k} p^k (1-p)^{10-k} \quad \text{for some } p.$$

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χ^2 test

MLE, $\hat{p} = (0 \times 6 + 1 \times 10 + 2 \times 15 + \dots + 10 \times 0) / (50 \times 10) = 0.232$

	0	1	2	3	4	5	6	7	8	9	10
observed	6	10	15	7	8	1	3	0	0	0	0
expected	3.6	10.8	14.7	11.8	6.2	2.3	0.6	0.1	~0.0	~0.0	~0.0

$$\chi^2 = \sum \frac{(\text{obs} - \text{exp})^2}{\text{exp}} = \frac{(6-3.6)^2}{3.6} + \frac{(10-10.8)^2}{10.8} + \frac{(15-14.7)^2}{14.7} + \dots + \frac{(0-0)^2}{0} = 15.4$$

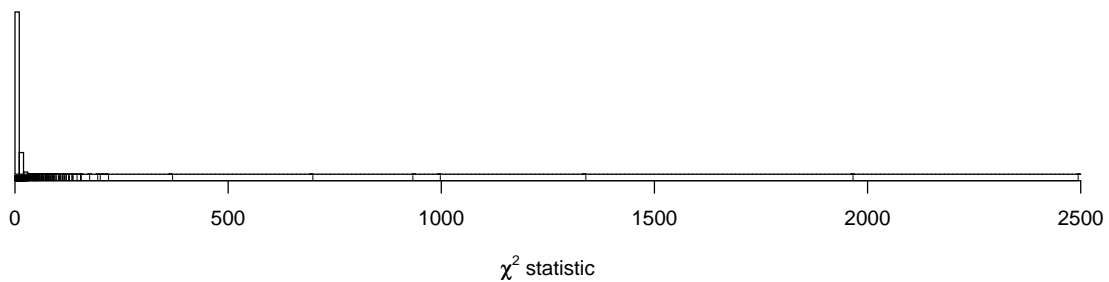
Compare to $\chi^2(\text{df} = 11 - 1 - 1 = 9) \rightarrow \text{p-value} = 0.082$.

By computer simulation: $\text{p-value} = 0.045$

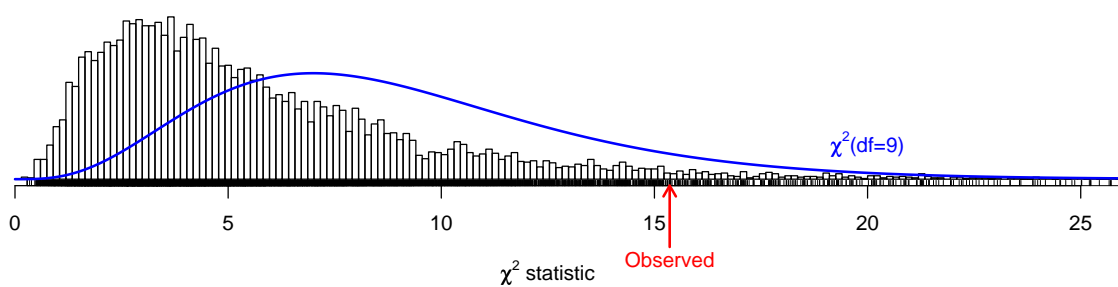
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Null simulation results

Full distribution (by simulation)



Focus on the left part



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Combine the rare bins

	0	1	2	3	4	≥ 5
observed	6	10	15	7	8	4
expected	3.6	10.8	14.7	11.8	6.2	2.9

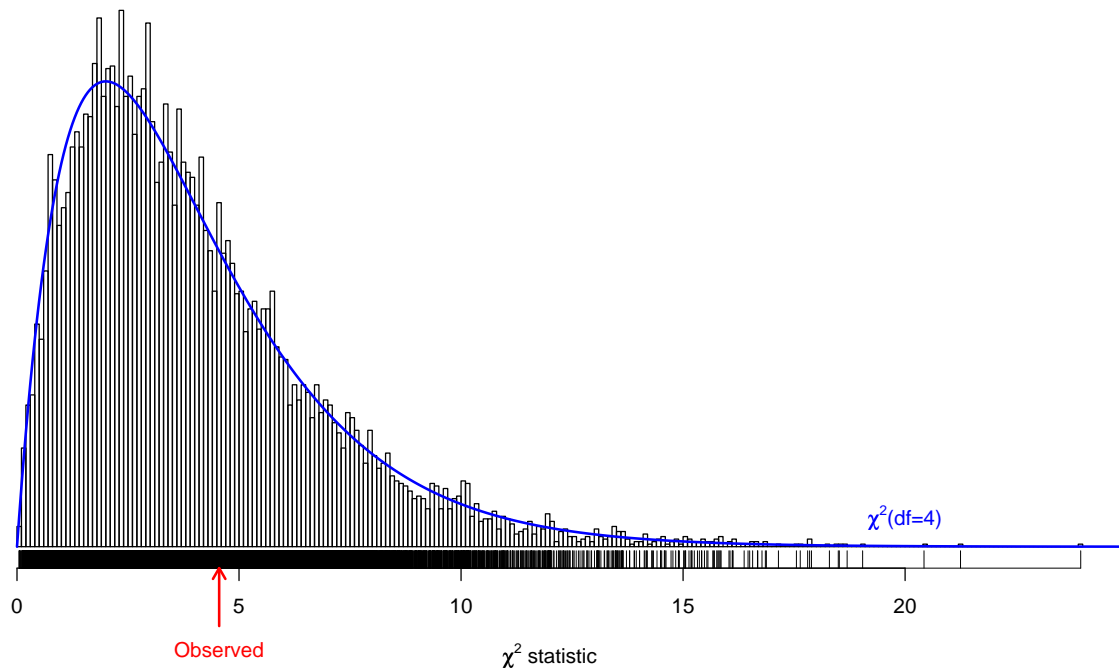
$$\chi^2 = \sum \frac{(\text{obs} - \text{exp})^2}{\text{exp}} = \frac{(6-3.6)^2}{3.6} + \frac{(10-10.8)^2}{10.8} + \frac{(15-14.7)^2}{14.7} + \dots + \frac{(4-2.9)^2}{2.9} = 4.55$$

Compare to $\chi^2(\text{df} = 6 - 1 - 1 = 4) \rightarrow \text{p-value} = 0.34$.

By computer simulation: **p-value = 0.34**

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Null simulation results (combining rare bins)



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Back to the question

A scientist applied a dose of DDT to groups of 10 spider mites and counted the number of mites (out of ten) that survived. A total of 50 groups of mites were considered.

	0	1	2	3	4	5	6	7	8	9	10
count	6	10	15	7	8	1	3	0	0	0	0

Q: Does this look a binomial distribution?

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A final note

With these sorts of goodness-of-fit tests, we are often happy when are model does fit.

In other words, we often prefer to fail to reject H_0 .

Such a conclusion, that the data fit the model reasonably well, should be phrased and considered with caution.

We should think: how much power do I have to detect, with these limited data, a reasonable deviation from H_0 ?