Goodness of Fit and Independence

STAT-S520

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General Setting

- Partition the sample space of interest, S, into k events or cells
  - $E_1 \cup E_2 \cup \cdots \cup E_k = S$
  - $E_1, \ldots, E_k$ are pairwise disjoint
- Test various hypotheses about the probabilities of those events.
- Given $E_1, \ldots, E_k$, let $p_j = P(E_j)$ and the vector of cell probabilities $\vec{p} = (p_1, \ldots, p_k)$
- Let Π be the set of all possible probability vectors $\vec{\pi} = (\pi_1, \ldots, \pi_k)$ as long as
  - $\pi_1, \ldots, \pi_k \geq 0$ and
  - $\pi_1 + \cdots + \pi_k = 1$

Hypotheses

- We test

$$H_0 : \overrightarrow{p} \in \Pi_0 \qquad \text{versus} \qquad H_1 : \overrightarrow{p} \in \Pi_1$$

where Π_0 and Π_1 are disjoint sets of probability vectors whose union is Π.

Example 1

Construct $S, E_1, \ldots, E_k$, and $\vec{p} = (p_1, \ldots, p_k)$ under the null hypothesis that a 6-sided die is fair.

$S = \{ ⚀, ⚁, ⚂, ⚃, ⚄, ⚅ \}$

$E_1 = \{ ⚀ \}, \quad E_2 = \{ ⚁ \}, \ldots, \quad E_6 = \{ ⚅ \}$

H_0: The die is fair

$\vec{p} = (p_1, p_2, \ldots, p_6) = \left(\frac{1}{6}, \frac{1}{6}, \ldots, \frac{1}{6}\right)$

$\vec{p} \in \Pi_0 \qquad \Pi_0 = \{ (1/6, 1/6, \ldots, 1/6) \}$

H_0: $p_1 = p_2 = p_3 = p_4 = p_5 = p_6 = \underline{\underline{1/6}}$

Observed and Expected Cell Counts

- The sample: repeat the experiment n times and let o_j be the number of times that E_j appears, we call this the observed cell count of cell j.
- Goodness-of-fit tests compare observed cell counts to expected cell counts.
  - Expected cell count for cell j, e_j, is obtained assuming the null hypothesis is true.
  - If p_j is the probability of observing E_j under H_0 and the total number of observed values is n, cell j's expected count is $e_j = p_j * n$.

Test Statistics

Aside
Chi-squared distribution is the sum of independent (std) normal squared random variables.

- Pearson's chi-squared statistic:

(Greek letter)
chi-squared

$$X^2 = \sum_{j=1}^{k} \frac{(o_j - e_j)^2}{e_j}$$

- The Likelihood ratio chi-squared statistic is

$$G^2 = 2 \sum_{j=1}^{k} o_j \log\left(\frac{o_j}{e_j}\right)$$

This test is slightly preferred.

- Both X^2 and G^2 statistics can be approximated by a chi-squared distribution.

Example 1: Fair Die (continued)

Let's assume we observed the following data (counts)

```
obs = c(3407, 3631, 3176, 2916, 3448, 3422)
n = sum(obs)
p = rep(1/6,6) #probabilities under the null
exp = n*p
exp
```

```
## [1] 3333.333 3333.333 3333.333 3333.333 3333.333 3333.33
```

```
X2 = sum((obs - exp)^2/exp)
X2
```

← Pearson chi-squared.

```
## [1] 94.189
```

```
G2 = sum(2*obs*log(obs/exp))
G2
```

```
## [1] 95.80227
```

Degrees of Freedom

- The correct degrees of freedom is the difference between the dimensions of the unrestricted and the restricted sets of possible $p_1, \ldots, p_k$

Under H_1

- The unrestricted set has $k - 1$ dimensions (k probabilities, but they must sum to 1)
- The restricted set has less than $k - 1$ dimensions. It is determined by how many probabilities are free to vary.

Under H_0

Example 1 (continued)

Determine whether a 6-sided die is fair. Then

$$H_0 : p_1 = p_2 = \cdots = p_6 = \frac{1}{6}$$

- The unrestricted set has $6 - 1 = 5$ probabilities that are free to vary.
- The null hypothesis specifies a single point, e.g., $p_1 = \cdots = p_6 = 1/6$,
  - No probabilities are free to vary
  - The restricted set has dimension 0.
- The degrees of freedom needed are $df = \underbrace{(6 - 1)}_{H_1} - \underbrace{0}_{H_0} = 5$

Example 1 (continued)

```r
df = (6 - 1) - 0
1 - pchisq(X2, df)
```

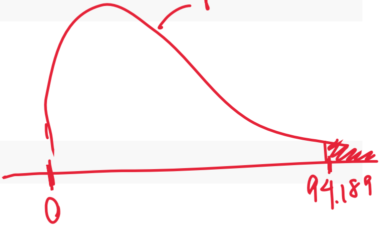
Chi-squared distribution

pdf of χ^2

```
## [1] 0
```

95

```r
1 - pchisq(G2, df)
```




```
## [1] 0
```

Reject H_0 and conclude that the die is not fair

Simulation-Based Approach

```
die= as.character(1:6)
die.vec = rep(die,obs)
df1 = data.frame(die.vec)
null_dist <- df1 %>%
  specify(response = die.vec) %>%
  hypothesize(null = "point",
              p = c("1" = 1/6, "2" = 1/6, "3" = 1/6, "4" =
  generate(reps = 1000, type = "draw") %>%
  calculate(stat = "Chisq")
null_dist %>%
  get_p_value(obs_stat = X2, direction = "greater")
```

Keep going to "6" = 1/6

Pearson chi-square.

Pearson χ^2 for original sample.

```
## Warning: Please be cautious in reporting a p-value of 0
## approximation based on the number of `reps` chosen in th
## `?get_p_value()` for more information.

## # A tibble: 1 x 1
##   p_value
```

= 0

Exercise 2 (ISI 13.4 Exercise 3)

According to Mendelian genetics, a recessive trait will appear in an offspring if and only if both parents contribute a recessive gene. If each parent has a dominant and a recessive gene, then the probability that their offspring will display the recessive trait is $1/4$.

A certain strain of tomato is either tall (dominant trait) or dwarf (recessive trait). The same strain has either cut leaves (dominant trait) or potato leaves (recessive trait). Let E_1 denote tall cut-leaf offspring, let E_2 denote tall potato-leaf offspring, let E_3 denote dwarf cut-leaf offspring, and let E_4 denote dwarf potato-leaf offspring.

$H_0: p_1 = p_2 = p_3 = p_4 = \frac{1}{4}$ → Using this (see next page)

expected count $p_j \cdot n$ $j = 1, 2, 3, 4$

Aside: This is not the only representation. For example

① $H_0: p_4 = \frac{1}{4}$ $p_1 + p_2 + p_3 = 3/4$ (but they free to change)

or ② $H_0: p_4 = \frac{1}{4}$ $p_5 = \frac{3}{4}$ where $E_5 = E_1 \cup E_2 \cup E_3$

Exercise 2 (ISI 13.4 Exercise 3 continued)

In 1931, J. W. MacArthur reported experimental results for $n = 1611$ offspring. MacArthur observed $o_1 = 926$, $o_2 = 288$, $o_3 = 293$, and $o_4 = 104$. Using this information, find:

a. $\vec{p}$, the probability of each E_j (under H_0)
b. The expected counts (under H_0)
c. The test statistic
d. The degrees of freedom
e. The conclusion to the test

(work in R) → check 04-13-23 lab

↳ p-value was close to zero → Reject H_0

Enough evidence to reject that the strain of tomato follows the Mendelian Genetics

Exercise 3: (ISI 13.4 Exercise 6: Using the Poisson Distribution)

discrete.

Let $X(S) = \{0, 1, 2, \dots\}$. The random variable X is said to have a Poisson distribution with intensity parameter $\mu \in (0, \infty)$, if X has a probability mass function (PMF)

$$f(x) = P(X = x) = \frac{\mu^x e^{-\mu}}{x!}$$

We write $X \sim Poisson(\mu)$ and it can be shown that $EX = VarX = \mu$. The Poisson distribution frequently arises when counting arrivals in a fixed time interval.

Key result

Example 3 (ISI 13.4 Exercise 6 continued)

In 1910, E. Rutherford and M. Geiger counted the numbers of alpha-particle scintillations observed in each of $n = 2608$ 72-intervals. Now we partition $X(S)$ by setting $E_j = \{j-1\}$ for $j = 1, \ldots, 10$ and $E_{11} = \{10, 11, 12, \ldots\}$. The null hypothesis states that counts of alpha-particle scintillations follow a Poisson distribution. Obtain the vector of $\vec{p}$ that represents the null hypothesis, using the proposed partition. Estimate μ, using the following counts:

E_1 E_2 E_3 E_{10} E_{11}

```
##     0   1   2   3   4   5   6   7  8  9 10 11 12 13 14
## 1  57 203 383 525 532 408 273 139 45 27 10  4  0  1  1
```

observed counts.

Rule of thumb count per cell > 5

Example 3 (ISI 13.4 Exercise 6 continued)

Using $\hat{\mu}$, find:

a. The expected counts (under H_0)
b. The test statistic
c. The degrees of freedom
d. The conclusion to the test

(work in R)

↳ check 4-13-23 lab

H_0: Count of α-particles follows a Poisson(μ)

H_1: It does not.

$df_1 = 11 - 1$

$df_0 = 1$ ← Because the param. "μ" is not fixed (estimated from data)

Update: Using $E_j = \{j-1\}$ for $j = 1, \dots, 10$

$E_{11} = \{10, 11, 12, \dots\}$

Based on the update → Fail to reject H_0