

# Lecture 25

## 25.1 Goodness-of-fit for composite hypotheses.

(Textbook, Section 9.2)

Suppose that we have a sample of random variables  $X_1, \dots, X_n$  that can take a finite number of values  $B_1, \dots, B_r$  with unknown probabilities

$$p_1 = \mathbb{P}(X = B_1), \dots, p_r = \mathbb{P}(X = B_r)$$

and suppose that we want to test the hypothesis that this distribution comes from a parameteric family  $\{\mathbb{P}_\theta : \theta \in \Theta\}$ . In other words, if we denote  $p_j(\theta) = \mathbb{P}_\theta(X = B_j)$ , we want to test:

$$\begin{cases} H_1 : p_j = p_j(\theta) \text{ for all } j \leq r \text{ for some } \theta \in \Theta \\ H_2 : \text{otherwise.} \end{cases}$$

If we wanted to test  $H_1$  for one particular fixed  $\theta$  we could use the statistic

$$T = \sum_{j=1}^r \frac{(\nu_j - np_j(\theta))^2}{np_j(\theta)},$$

and use a simple  $\chi^2$  test from last lecture. The situation now is more complicated because we want to test if  $p_j = p_j(\theta)$ ,  $j \leq r$  at least for some  $\theta \in \Theta$  which means that we have many candidates for  $\theta$ . One way to approach this problem is as follows.

(Step 1) Assuming that hypothesis  $H_1$  holds, i.e.  $\mathbb{P} = \mathbb{P}_\theta$  for some  $\theta \in \Theta$ , we can find an estimate  $\theta^*$  of this unknown  $\theta$  and then

(Step 2) try to test whether indeed the distribution  $\mathbb{P}$  is equal to  $\mathbb{P}_{\theta^*}$  by using the statistics

$$T = \sum_{j=1}^r \frac{(\nu_j - np_j(\theta^*))^2}{np_j(\theta^*)}$$

in  $\chi^2$  test.

This approach looks natural, the only question is what estimate  $\theta^*$  to use and how the fact that  $\theta^*$  also depends on the data will affect the convergence of  $T$ . It turns out that if we let  $\theta^*$  be the maximum likelihood estimate, i.e.  $\theta$  that maximizes the likelihood function

$$\varphi(\theta) = p_1(\theta)^{\nu_1} \dots p_r(\theta)^{\nu_r}$$

then the statistic

$$T = \sum_{j=1}^r \frac{(\nu_j - np_j(\theta^*))^2}{np_j(\theta^*)} \rightarrow \chi_{r-s-1}^2$$

converges to  $\chi_{r-s-1}^2$  distribution with  $r - s - 1$  degrees of freedom, where  $s$  is the dimension of the parameter set  $\Theta$ . Of course, here we assume that  $s \leq r - 2$  so that we have at least one degree of freedom. Very informally, by dimension we understand the number of free parameters that describe the set  $\Theta$ , which we illustrate by the following examples.

1. The family of Bernoulli distributions  $B(p)$  has only one free parameter  $p \in [0, 1]$  so that the set  $\Theta = [0, 1]$  has dimension  $s = 1$ .
2. The family of normal distributions  $N(\mu, \sigma^2)$  has two free parameters  $\mu \in \mathbb{R}$  and  $\sigma^2 \geq 0$  and the set  $\Theta = \mathbb{R} \times [0, \infty)$  has dimension  $s = 2$ .
3. Let us consider a family of all distributions on the set  $\{0, 1, 2\}$ . The distribution

$$\mathbb{P}(X = 0) = p_1, \mathbb{P}(X = 1) = p_2, \mathbb{P}(X = 2) = p_3$$

is described by parameters  $p_1, p_2$  and  $p_3$ . But since they are supposed to add up to 1,  $p_1 + p_2 + p_3 = 1$ , one of these parameters is not free, for example,  $p_3 = 1 - p_1 - p_2$ . The remaining two parameters belong to a set

$$p_1 \in [0, 1], \quad p_2 \in [0, 1 - p_1]$$

shown in figure 25.1, since their sum should not exceed 1 and the dimension of this set is  $s = 2$ .

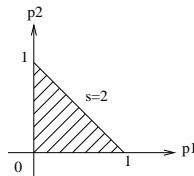


Figure 25.1: Free parameters of a three point distribution.

**Example.** (textbook, p.545) Suppose that a gene has two possible alleles  $A_1$  and  $A_2$  and the combinations of these alleles define the possible genotypes  $A_1A_1$ ,  $A_1A_2$  and  $A_2A_2$ . We want to test a theory that

$$\left. \begin{array}{l} \text{Probability to pass } A_1 \text{ to a child} = \theta : \\ \text{Probability to pass } A_2 \text{ to a child} = 1 - \theta : \end{array} \right\}$$

and the probabilities of genotypes are given by

$$\begin{aligned} p_1(\theta) &= \mathbb{P}(A_1A_1) = \theta^2 \\ p_2(\theta) &= \mathbb{P}(A_1A_2) = 2\theta(1 - \theta) \\ p_3(\theta) &= \mathbb{P}(A_2A_2) = (1 - \theta)^2 \end{aligned} \quad (25.1)$$

Suppose that given the sample  $X_1, \dots, X_n$  of the population the counts of each genotype are  $\nu_1, \nu_2$  and  $\nu_3$ . To test the theory we want to test the hypotheses

$$\left\{ \begin{array}{l} H_1 : p_1 = p_1(\theta), p_2 = p_2(\theta), p_3 = p_3(\theta) \text{ for some } \theta \in [0, 1] \\ H_2 : \text{otherwise.} \end{array} \right.$$

First of all, the dimension of the parameter set is  $s = 1$  since the family of distributions in (25.1) are described by one parameter  $\theta$ . To find the MLE  $\theta^*$  we have to maximize the likelihood function

$$p_1(\theta)^{\nu_1} p_2(\theta)^{\nu_2} p_3(\theta)^{\nu_3}$$

or, equivalently, maximize the log-likelihood

$$\begin{aligned} \log p_1(\theta)^{\nu_1} p_2(\theta)^{\nu_2} p_3(\theta)^{\nu_3} &= \nu_1 \log p_1(\theta) + \nu_2 \log p_2(\theta) + \nu_3 \log p_3(\theta) \\ &= \nu_1 \log \theta^2 + \nu_2 \log 2\theta(1 - \theta) + \nu_3 \log(1 - \theta)^2. \end{aligned}$$

To find the critical point we take the derivative, set it equal to 0 and solve for  $\theta$  which gives (we omit these simple steps):

$$\theta^* = \frac{2\nu_1 + \nu_2}{2n}.$$

Therefore, under the null hypothesis  $H_1$  the statistic

$$\begin{aligned} T &= \frac{(\nu_1 - np_1(\theta^*))^2}{np_1(\theta^*)} + \frac{(\nu_2 - np_2(\theta^*))^2}{np_2(\theta^*)} + \frac{(\nu_3 - np_3(\theta^*))^2}{np_3(\theta^*)} \\ &\rightarrow \chi_{r-s-1}^2 = \chi_{3-1-1}^2 = \chi_1^2 \end{aligned}$$

converges to  $\chi_1^2$  distribution with one degree of freedom. If we take the level of significance  $\alpha = 0.05$  and find the threshold  $c$  so that

$$0.05 = \alpha = \chi_1^2(T > c) \Rightarrow c = 3.841$$

then we can use the following decision rule:

$$\begin{cases} H_1 : T \leq c = 3.841 \\ H_2 : T > c = 3.841 \end{cases}$$

□

### General families.

We could use a similar test when the distributions  $\mathbb{P}_\theta, \theta \in \Theta$  are not necessarily supported by a finite number of points  $B_1, \dots, B_r$  (for example, continuous distributions). In this case if we want to test the hypotheses

$$\begin{cases} H_1 : \mathbb{P} = \mathbb{P}_\theta \text{ for some } \theta \in \Theta \\ H_2 : \text{otherwise} \end{cases}$$

we can discretize them as we did in the last lecture (see figure 25.2), i.e. consider a family of distributions

$$p_j(\theta) = \mathbb{P}_\theta(X \in I_j) \text{ for } j \leq r,$$

and instead consider derivative hypotheses

$$\begin{cases} H_1 : p_j = p_j(\theta) \text{ for some } \theta, j = 1, \dots, r \\ H_2 : \text{otherwise.} \end{cases}$$

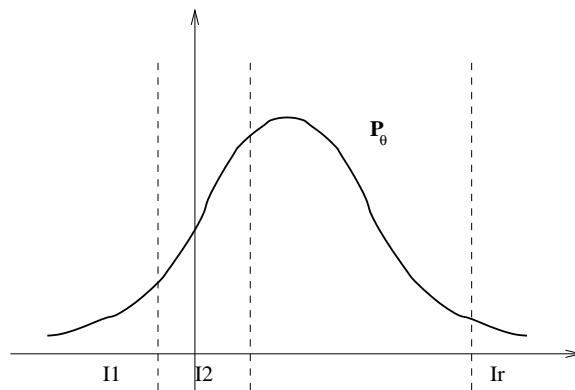


Figure 25.2: Goodness-of-fit for Composite Hypotheses.