# STATS305A - Lecture 7

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#### 1 Announcements

- Etude 1 due 5pm Thursday sharp
  - On Thursday solutions to the etude will be posted at around 5pm.
  - Students grade their own etudes.
  - Students upload a new etude with corrections made to the original submission. You must upload a revised etude. This second submission is due 5pm Friday.
- Homework 2 will be out soon.

# 2 Fisherian Testing

### 2.1 Setting

We propose a null  $H_0$ . We collect data and compute a statistic  $T_n$  which is just some function of our data. Under the null  $H_0$ ,  $T_n$  follows *some* distribution. Call this distribution T (this is not a T-distribution, just the distribution of  $T_n$  when the null holds).

We nest pick a level  $\alpha \in (0,1)$  at which to reject  $H_0$ . We choose a rejection region R where

$$\mathbb{P}_{H_0}(T \in R) \leq \alpha.$$

That is, under the null  $H_0$ ,  $T_n$  is unlikely to fall in R. We then reject if  $T_n \in R$ .

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#### 2.2 P-values

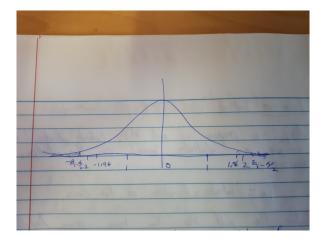
Often our rejection regions are nested. That is if  $R_{\alpha}$  denotes the rejection region at level  $\alpha$ , then

$$R_{\alpha_0} \subsetneq R_{\alpha_1}$$
, if  $\alpha_0 < \alpha_1$ .

For example if  $T \sim \mathcal{N}(0,1)$  under  $H_0$ , then we often choose

$$R_{\alpha} = (-\infty, -z_{1-\alpha/2}) \cup (z_{1+\alpha/2}, \infty),$$

where  $z_{1-\alpha}$  is the  $1-\alpha$  quantile of a standard normal  $Z \sim \mathcal{N}(0,1)$ , that is  $\mathbb{P}(Z \geq z_{1-\alpha}) = \alpha$ . See below



The *p-value* of a statistic  $T_n$  is:

- The smallest level  $\alpha$  at which we can reject the test ie  $p = \inf\{\alpha : T_n \in R_\alpha\}$ .
- Equivalently, the probability under  $H_0$  of seeing a sample as strange/extreme as what we have observed

**Example 1.** Consider the example above when  $H_0$  implies that  $T_n$  is normally distributed. Set  $t_n := T_n$  (the observed value), then our p-value is

$$p = \mathbb{P}_{H_0}(|T| \ge |T_n|).$$

**Example 2.** Assume that  $Y = X\beta + \mathbf{1}\beta_0 + \varepsilon$  where  $X \in \mathbb{R}^{n \times (d-1)}$  and Z = [1, X]. Let  $H = Z(Z^TZ)^{-1}Z = \text{projection onto full model}$ . Let  $H_0 = \frac{1}{n}\mathbf{1}\mathbf{1}^T = \text{projection onto range of the submodel}$   $Y = \mathbf{1}\beta_0 + \varepsilon$ . Our null hypothesis is that the submodel is true. Define  $S_n^2 = \frac{1}{n-d} \|(I-H)Y\|_2^2$ . Under the null hypothesis we saw that

$$T_n := \frac{\frac{1}{d-1} \| (H - H_0) Y \|_2^2}{\frac{1}{n-d} \| (I - H) Y \|_2^2} \sim F_{d-1, n-d}.$$

We reject the null if  $T_n$  is large which means the larger model explains the data better than the smaller model.

#### 2.3 Sampling/M-tests

Suppose that we decide to estimate  $\beta$  via

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$$\widehat{\beta} = \arg\min_{b} \sum_{i=1}^{n} |Y_i - X_i^T b|.$$

Where we assume  $Y = X\beta + \varepsilon$ ,  $\varepsilon \sim \mathcal{N}(0, \sigma^2 I)$  where we assume  $\sigma^2$  is known. We wish to test the null hypothesis  $\beta = 0$ .

Under the null hypothesis we can compute  $\varepsilon^{(1)}, \dots, \varepsilon^{(N)}$  independent samples from  $\mathcal{N}(0, \sigma^2 I)$  where N is big. We then define  $Y^{(i)} := \varepsilon^{(i)}$  and

$$\widehat{\beta}^{(i)} = \arg\min_{b} \sum_{i=1}^{n} \left| Y_j^{(i)} - X_j b \right|.$$

The samples  $\widehat{\beta}^{(i)}$  gives us an approximation to the distribution of  $\widehat{\beta}$  assuming that the null is true.

Abstractly all we need is some region in  $\mathbb{R}^d$  that contians a  $1 - \alpha$  fraction of all  $\widehat{\beta}^{(i)}$ . Then we reject the null if  $\widehat{\beta}$  is out of that region. Here is one way to do this.

We could compute  $q_{1-\alpha}^{sim} = 1 - \alpha$  quartile of  $\|\widehat{\beta}^{(i)}\|_2$ . Thus we have

$$\mathbb{P}_{H_0}\left(\left\|\widehat{\beta}\right\| \ge q_{1-\alpha}^{sim}\right) \le \alpha + \frac{1}{N}.$$

This is because under  $H_0$ ,  $\|\widehat{\beta}^{(i)}\|_2$  has the same distribution as  $\|\widehat{\beta}\|$ . If we define  $t_i = \|\widehat{\beta}^{(i)}\|_2$  and  $T_n = \|\widehat{\beta}\|_2$ , then  $\|\widehat{\beta}\|_2 > q_{1-\alpha}^{sim}$  if and only if  $T_n > t_i$  for a  $1-\alpha$  fraction of  $\{t_1, \ldots, t_n\}$ . And  $T_n > t_i$  for a  $1-\alpha$  fraction of  $\{t_1, \ldots, t_n\}$  occurs with probability  $\alpha \pm \frac{1}{N}$ .

The p-value in this case is

$$\inf\{\alpha: \left\|\widehat{\beta}\right\|_{2} > t_{i} \text{ for a } 1 - \alpha \text{ fraction of } \{t_{i}\}_{i=1}^{N}\}$$

$$= \inf\{\alpha: \left\|\widehat{\beta}\right\|_{2} > q_{1-\alpha}^{sim}\}$$

$$\approx \text{ the fraction of } \{t_{i}\}_{i=1}^{N} \text{ such that } \left\|\widehat{\beta}\right\|_{2} \leq t_{i}.$$

#### 2.4 Aside: power of a test

Choose an alternative  $H_1$  such as  $Y = X\beta + \varepsilon$ ,  $\|\beta\| \ge \sqrt{\frac{d}{n}}$  or  $Y = X\beta + \varepsilon$ ,  $\beta_1 > \frac{1}{\sqrt{n}}$ . The *power* of a test is also written as  $\beta$  but now  $\beta$  is a probability not a parameter in a model.

The *power* of a test is also written as  $\beta$  but now  $\beta$  is a probability not a parameter in a model. The power is defined as

$$\beta := \mathbb{P}_{H_1}(T_n \text{ rejects}).$$

Once could try to maximise the power of a test while keeping the level  $\alpha$  constant but this is subtle and complicated. The rejection region with the most power will depend on  $H_1$ . More often in practice we focus on the level and choose the rejection region in a way that reflects the null/alternative hypotheses.

# 3 ANOVA (Analysis of variance)

Suppose we have the model

$$Y_{ij} = \mu + \alpha_i + \varepsilon_{ij}$$
,

where  $i=1,\ldots,k$  are different groups and  $Y_{i,j}$  for  $j=1,\ldots,n_i$  are different samples from group i. We call  $\mu$  the population mean and  $\alpha_i$  the group effect. We are interested in testing/estimating the differences  $\alpha_i - \alpha_j$ . The structure of this model allows us to write cleaner/more direct computations and tests.

## 3.1 ANOVA Decomposition

Let  $\overline{Y}_{\bullet \bullet} = \frac{1}{N} \sum_{i=1}^{k} \sum_{j=1}^{n_i} Y_{i,j}$  be the global mean  $(N = n_1 + n_2 + \ldots + n_k)$ . Let  $\overline{Y}_{i \bullet} = \frac{1}{n_i} \sum_{j=1}^{n_i} Y_{i,j}$  be the mean for group i. Define

$$SST := \sum_{i=1}^{k} \sum_{j=1}^{n_i} (Y_{i,j} - \overline{Y}_{\bullet \bullet})^2 \quad \text{(total sum of squares.)}$$

$$SSB := \sum_{i=1}^{k} \sum_{j=1}^{n_i} (\overline{Y}_{i \bullet} - \overline{Y}_{\bullet \bullet})^2 \quad \text{(between groups sum of squares.)}$$

$$= \sum_{i=1}^{k} n_i (\overline{Y}_{i \bullet} - \overline{Y}_{\bullet \bullet})^2$$

$$SSW := \sum_{i=1}^{k} \sum_{j=1}^{n_i} (Y_{i,j} - \overline{Y}_{i \bullet})^2 \quad \text{(within groups sum of squares.)}$$

We then have

$$SST = \sum_{i=1}^{k} \sum_{j=1}^{n_i} (Y_{i,j} - \overline{Y}_{\bullet \bullet})^2$$

$$= \sum_{i=1}^{k} \sum_{j=1}^{n_i} (Y_{i,j} - \overline{Y}_{i \bullet} + \overline{Y}_{i \bullet} - \overline{Y}_{\bullet \bullet})^2$$

$$= \sum_{i=1}^{k} \sum_{j=1}^{n_i} (Y_{i,j} - \overline{Y}_{i \bullet})^2 + \sum_{i=1}^{k} \sum_{j=1}^{n_i} (\overline{Y}_{i \bullet} - \overline{Y}_{\bullet \bullet})^2$$

$$= \sum_{i=1}^{k} \sum_{j=1}^{n_i} (Y_{i,j} - \overline{Y}_{i \bullet})^2 + \sum_{i=1}^{k} \sum_{j=1}^{n_i} (\overline{Y}_{i \bullet} - \overline{Y}_{\bullet \bullet})^2$$

$$= SSW + SSB$$

This is called the ANOVA decomposition.

Suppose our null is  $H_0: \alpha_1 = \alpha_2 = \ldots = \alpha_k = 0, \ \varepsilon_{i,j} \sim \mathcal{N}(0,\sigma^2)$ . Then (exercise) under  $H_0$ :

- SSW⊥LSSB.
- $SSW \sim \sigma^2 \chi_{N-k}^2$ .
- $SSB \sim \sigma^2 \chi_{k-1}^2$ .

Thus  $\frac{1k-1SSB}{\frac{1}{N-k}SSW} \sim F_{k-1,N-k}$ .

We reject  $H_0$  when the above statistic is large which means the between group differences are large relative to the within-group differences.

### 3.2 Testing differences

Often we may care more about differences in between the mean treatments. For example we may be dosing a drug at different levels i = 1, ..., k. We care more about  $\alpha_i - \alpha_j$  more than just "is there a difference in treatment from  $\alpha_1 = \alpha_2 = ... = \alpha_k = 0$ ?"

This gives rise to testing *constrasts* which are vectors  $c \in \mathbb{R}^k$  satisfying  $c^T \mathbf{1} = 0$ . For example  $c = e_i - e_j$ . If  $\widehat{\alpha}$  is any least squares solution then  $\frac{c^T \widehat{\alpha}}{s \sqrt{c^T (X^T X)^{\dagger} c}} \sim T_{n-(d-1)}$  (*T*-distribution), where

$$S^2 = \frac{1}{n - (d - 1)} \sum_{i=1}^n (Y_i - X_i^T \widehat{\beta})^2.$$

Exercise: If  $c = e_i - e_j$  (ie  $c^T \beta = \alpha_i - \alpha_j$ ), then  $c^T (X^T X)^{\dagger} c = \frac{1}{n_i} + \frac{1}{n_j}$ .

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## 3.3 An issue

If we look at all pairs of differences  $\alpha_i - \alpha_j$  for i < j. Then we are doing  $\frac{k(k-1)}{2}$  tests. If we reject the nulls at a level  $\alpha$ , then we "expect" to have roughly  $\alpha \frac{k^2}{2}$  false rejections. Note that  $\alpha \frac{k^2}{2} >> \alpha$ . This is the issue of *multiple testing*.