

Dependent or Matched-Pairs Experimental Designs

Dependent (or matched-pairs) samples are usually more efficient and informative than are independent samples of equal size. For the dependent samples design, we try to select data in such a way as to minimize the variation contributed by extraneous variables.

Dependent samples may be used:

1. when the sample element is a member of both populations, and/or
2. when the comparison of the two populations is to be made with respect to a particular variable.

Some Examples of Dependent Samples

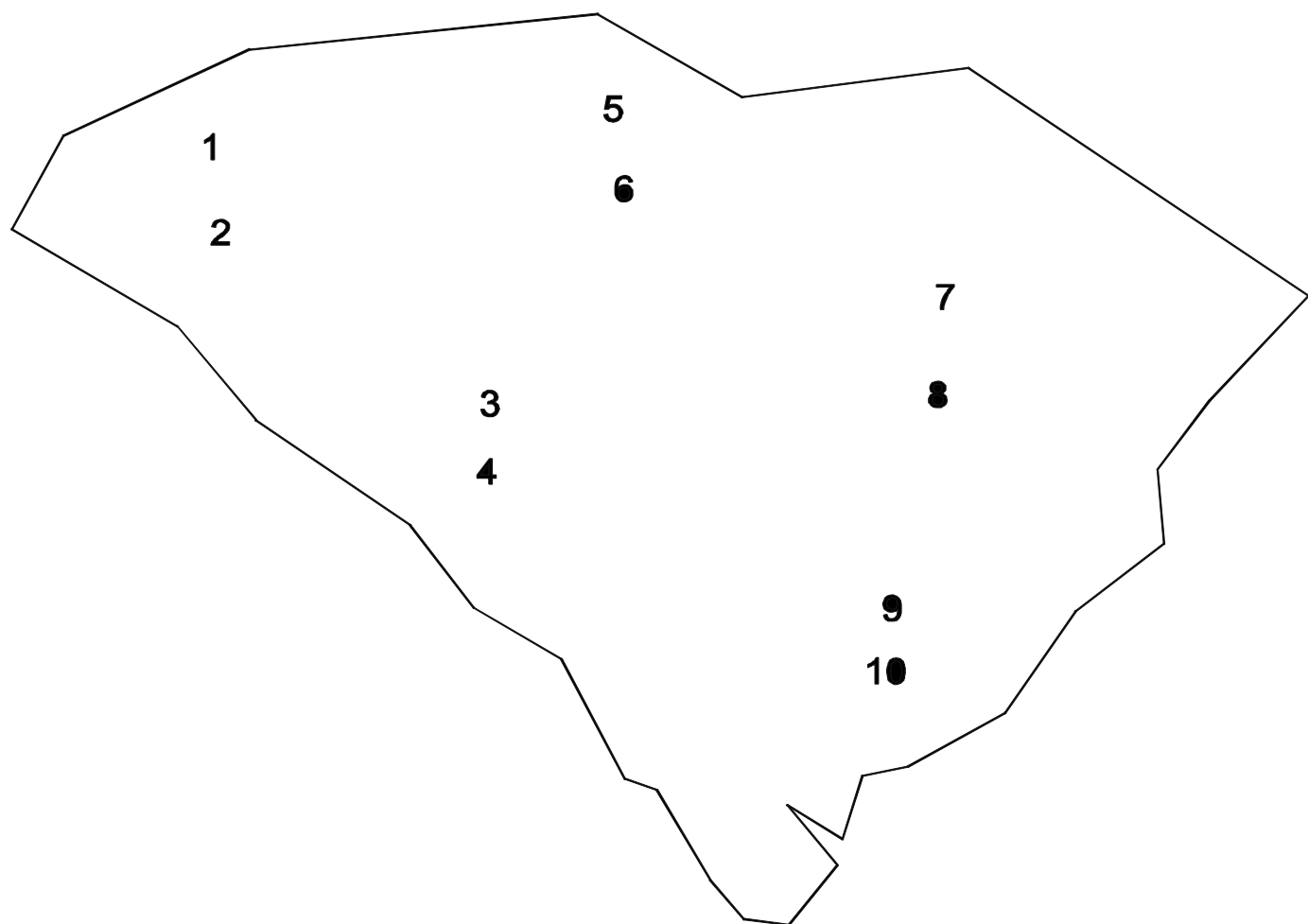
1. Testing the effects of a diet by getting before and after weights on the same people.
2. Testing the effectiveness of a teaching strategy by giving pretests and posttests to the same individuals.
3. Testing two brands of tires for tread wear by placing one brand of each tire on the rear wheels of the same car.

Example: Ten plots of land are available to determine if a new genetically-engineered variety of corn will increase the yield. The researcher plans to plant five plots with the genetically-engineered variety and five plots with the same variety which has not been genetically altered (control group). The plots of land are shown on the next page. Two plots of land are available for each of five regions of the state. The table below lists these regions and plots.

| Region | Plots |
|------------|-------|
| Clemson | 1, 2 |
| Aiken | 3, 4 |
| Rock Hill | 5, 6 |
| Florence | 7, 8 |
| Charleston | 9, 10 |

Briefly discuss how you would assign plots of land if your were conducting an independent samples experimental design. Do you see any problems with using this type of design? If so, what are they?

Do you have any suggestions on how to improve the experimental design?



A Dependent Samples Approach

We might expect that the yield would be different for the various regions of the state. In order to reduce the region-to-region variability, it seems logical to pair the plots by region. We would then plant the control group variety in one plot and the genetically-engineered variety in the other plot. Below are the results of the dependent samples experiment.

| Results from the Genetically-Engineered Corn Experiment | | |
|--|-------------------------------------|--|
| Region | Control Group (Bu./acre) | Genetically-Engineered Group (Bu./acre) |
| Clemson | 64.3 | 70.0 |
| Aiken | 101.4 | 105.6 |
| Rock Hill | 70.6 | 70.3 |
| Florence | 84.7 | 90.0 |
| Charleston | 62.6 | 65.8 |

The question now is, how do we conduct a hypothesis test for a dependent samples experimental design?

The approach used in this situation is to create new observed d_i 's that are the differences of the pairs of the original observations. We can then use the d_i 's to conduct hypothesis tests and construct confidence intervals.

Hypothesis Test for Comparing Two Population Means (Matched-Pairs Samples)

Hypotheses

$$\begin{aligned}H_0: \mu_d &= D_0 \\ H_a: \mu_d &< D_0\end{aligned}$$

$$\begin{aligned}H_0: \mu_d &= D_0 \\ H_a: \mu_d &> D_0\end{aligned}$$

$$\begin{aligned}H_0: \mu_d &= D_0 \\ H_a: \mu_d &\neq D_0\end{aligned}$$

Test Statistic:

$$t = \frac{\bar{d} - D_0}{s_d / \sqrt{n}}$$

Distribution for the Rejection Region:

The rejection is found using a t-distribution with $df=n-1$.

When is "pairing" efficient?

The larger the sample sizes the more likely we are to detect when H_0 is not true. For an independent (unpaired) sample experimental design that has the same sample size for both samples, the degrees of freedom are $n+n-2$ or $2(n-1)$. When we use a dependent (paired) sample experimental design, the degrees of freedom are $n-1$. So we see that by pairing we have lost $n-1$ degrees of freedom. Why then would we say that dependent samples are usually more efficient? Well, we hope that we will gain information by eliminating an additional source of variability (the difference between the individuals or items used in the study). If the individuals or items are homogeneous (the same) then there is no advantage to using dependent samples.

Example 3

Hypothesis Test for the Genetically Engineered Corn Experiment

| Results from the Genetically-Engineered Corn Experiment | | | |
|---|--------------------------|---|---|
| Region | Control Group (Bu./acre) | Genetically-Engineered Group (Bu./acre) | Difference (d _i) (Bu./acre) |
| Clemson | 64.3 | 70.0 | -5.7 |
| Aiken | 101.4 | 105.6 | -4.2 |
| Rock Hill | 70.6 | 70.3 | 0.3 |
| Florence | 84.7 | 90.0 | -5.3 |
| Charleston | 62.6 | 65.8 | -3.2 |

$$\bar{d} = \frac{(-5.7 - 4.2 + 0.3 - 5.3 - 3.2)}{5} = -3.62$$

$$s_d^2 = \frac{88.55 - \frac{(-18.1)^2}{5}}{4} = 5.757$$

What are the hypotheses?

$$H_0: \mu_1 - \mu_2 = 0 : \mu_d = 0$$

$$H_a: \mu_1 - \mu_2 \neq 0 : \mu_d \neq 0$$

$$C=1, G=2$$

Draw the rejection region.

$$\text{Let } \alpha = 0.05, \text{ then } t_{\text{crit}} = t_{(4, 0.025)} = \pm 2.776$$

Calculate the test statistic.

$$t_{\text{obs}} = (-3.62 - 0) / (\sqrt{5.757} / \sqrt{5}) = -3.37$$

What are your conclusions?

R H_0 ; sufficient evidence to conclude that average yield of control is less than average yield of the genetically engineered

Confidence Intervals for the Difference of Two Population Means

Independent Samples and Equal Variances

$$(\bar{y}_1 - \bar{y}_2) \pm t_{\alpha/2, (n_1+n_2-2)} s_p \sqrt{\frac{1}{n_1} + \frac{1}{n_2}}$$

$$\begin{aligned} & 5.944 \pm (2.101) (1.424) \sqrt{[(1/10) + (1/10)]} \\ & 5.944 \pm 1.338 \\ & (4.606, 7.282) \end{aligned}$$

Independent Samples and Unequal Variances

$$(\bar{y}_1 - \bar{y}_2) \pm t_{\alpha/2, df} \sqrt{\frac{s_1^2}{n_1} + \frac{s_2^2}{n_2}}$$

*where df are the degrees of freedom
found in the hypothesis testing section on page 70.*

$$\begin{aligned} & 5.944 \pm (2.131) \sqrt{[(1.194/10) + (2.862/10)]} \\ & 5.944 \pm 1.357 \\ & (4.587, 7.301) \end{aligned}$$

Dependent Samples (paired)

$$\bar{d} \pm t_{\alpha/2, (n-1)} s_d / \sqrt{n}$$

$$\begin{aligned} & -3.62 \pm (2.776) (2.399) / \sqrt{5} \\ & -3.62 \pm 2.978 \\ & (-6.598, -0.642) \end{aligned}$$

