#### Introduction to Geostatistics

9. Two-sample T-test and analysis of variance. Power and Type-II errors.

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## How large should a sample be?

Given that a 95% confidence interval, e.g. for  $\mu$  is obtained by

$$[\bar{X} - t_{df,\alpha} SE, \bar{X} + t_{df,\alpha} SE]$$

and given that  $\alpha$  is chosen and  $\sigma$  is not under our control, we can only control the width W of the interval by manipulating n:

$$W = 2t_{df,\alpha} SE = 2t_{df,\alpha} s / \sqrt{n}$$
 $n = (\frac{2t_{df,\alpha} s}{W})^2$ 

How about controlling type II errors?



### Type I and Type II errors

Of course we take a risk to wrongly rejecting a true  $H_0$ , of  $\alpha$ . There's however also a risk that we wrongly *not* reject a false  $H_0$ , which is called  $\beta$ .

	Truth	
Test result	H₀ true	$H_0$ false
Reject H <sub>0</sub>	Type I error, $\alpha$	OK, (1-β)
Do not reject $H_0$	OK (1- $\alpha$ )	Type II error, $\beta$

Next 2 slides from: Wonnacott & Wonnacott, Introductory statistics.



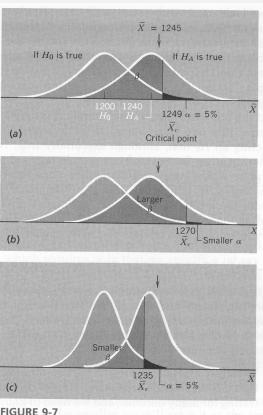
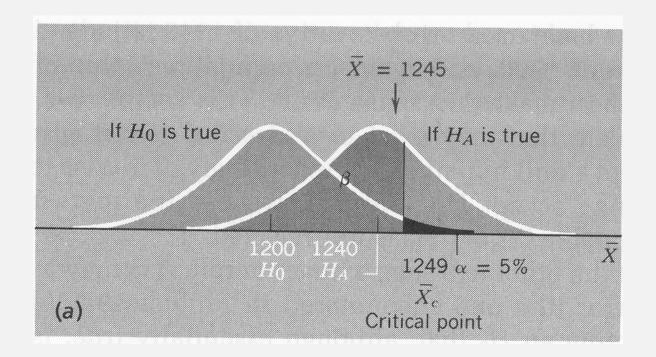


FIGURE 9-7
(a) Hypothesis test of Figure 9-6 showing  $\alpha$  and  $\beta$ . (b) How a reduction in  $\alpha$  increases  $\beta$ , other things being equal. (c) How an increase in sample size allows one error probability  $(\beta)$  to be reduced, without increasing the other  $(\alpha)$ .







## How to compute the power function?

- ▶ Given that  $H_0$  is not true, then what is true? Probabilities cannot be computed without assumptions about the population.
- ▶ Given a fixed  $H_A$ , we can compute power as in the figure in the previous slide.
- ▶ For all possible  $H_A$ 's, we obtain the *power function*.
- ▶ What determines the power?
  - ▶ The difference between the  $H_0$  and  $H_A$  means (delta)
  - ▶ The width of the curves (SE =  $\sigma/\sqrt{n}$ )

  - where is  $\alpha$ ? one-sided or two-sided
  - ▶ what is n? how is SE computed? type of test: one-sample, two-sample, paired



## Power computation using power.t.test

Description: Compute power of test, or determine parameters to obtain target power.

Details: Exactly one of the parameters n, delta, power, sd, and sig.level must be passed as NULL, and that parameter is determined from the others. Notice that the last two have non-NULL defaults so NULL must be explicitly passed if you want to compute them.



### Compute sample size

```
> power.t.test(n = NULL, delta = 1, sd = 1, sig.level = 0.05,
+ power = 0.9, type = "two.sample", alternative = "two.sided")

Two-sample t test power calculation

n = 22.02110
delta = 1
sd = 1
sd = 1
sig.level = 0.05
power = 0.9
alternative = two.sided

NOTE: n is number in *each* group
```



## Compute delta $(H_A)$

```
> power.t.test(n = 20, delta = NULL, sd = 1, sig.level = 0.05,
+ power = 0.9, type = "two.sample", alternative = "two.sided")

Two-sample t test power calculation

n = 20
delta = 1.051970
sd = 1
sig.level = 0.05
power = 0.9
alternative = two.sided

NOTE: n is number in *each* group
```



### Compute power

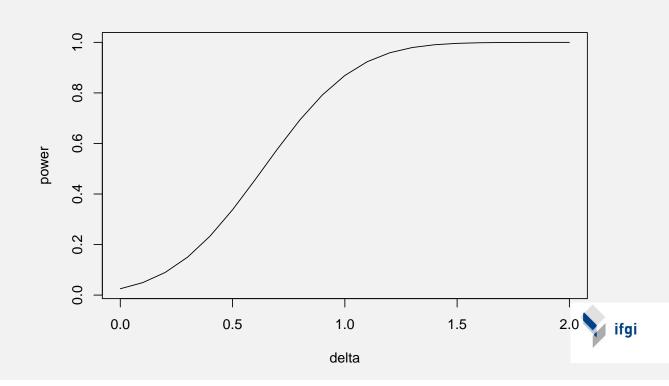


#### Compute significance level



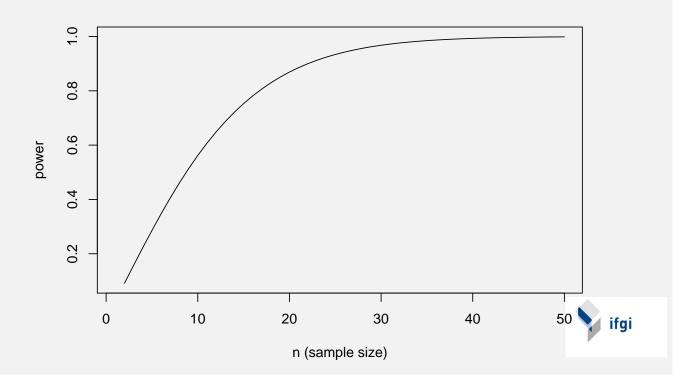
## Compute power function vs. delta, n=20

```
> plot((0:20)/10, power.t.test(power = NULL, delta = (0:20)/10,
+ n = 20)$power, type = "l", xlab = "delta", ylab = "power")
```



#### Compute power function vs. n; delta = 1

```
> plot(1:50, power.t.test(delta = 1, n = 1:50)$power, type = "l", + xlab = "n (sample size)", ylab = "power")
```



### The power concept beyond n

In a testing framework, increasing n will make every small difference in means significant, as small differences will be noted (with large power). This does not mean that the difference found is relevant.

Suppose we're studying the effect of a medication type on health, or a herbicide type on plant disease. Two large samples (with and without treatment) confirmed (showed significantly) that in the group without treatment there was 45% succes, less than in the group with treatment with 47% success.

That's OK, but should we now collectively apply the treatment? Do the effects compensate for the costs and side effects?

Significance is something else as relevance



#### The power concept beyond n

Taking a larger sample always increases power. Can we do something else to increas power? Yes: choose a more appropriate analysis. Recall the paired data of lecture 7:

obj	$t_1$	$t_2$
1	13.5	12.7
2	15.3	15.1
3	7.5	6.6
4	10.3	8.5
5	8.7	8.0

```
> x1 = c(13.5, 15.3, 7.5, 10.3, 8.7)
> x2 = c(12.7, 15.1, 6.6, 8.5, 8)
> x1 - x2
[1] 0.8 0.2 0.9 1.8 0.7
```

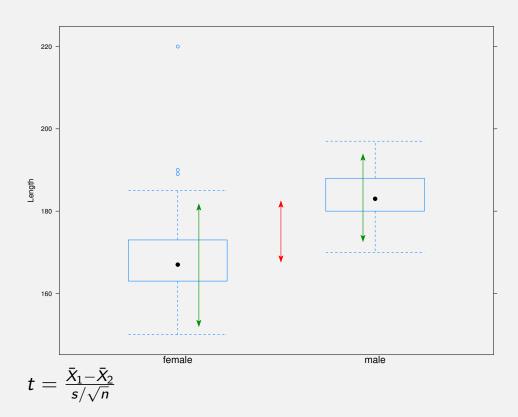


```
> t.test(x1, x2, var.equal = TRUE)
        Two Sample t-test
data: x1 and x2
t = 0.4066, df = 8, p-value = 0.695
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
 -4.111314 5.871314
sample estimates:
mean of x mean of y
    11.06
            10.18
> t.test(x1, x2, paired = TRUE)
        Paired t-test
data: x1 and x2
t = 3.3896, df = 4, p-value = 0.02754
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
 0.1591929 1.6008071
sample estimates:
mean of the differences
                   0.88
```

```
> power.t.test(delta = 0.88, n = 5, sd = sqrt((var(x1) +
      var(x2))/2))
     Two-sample t test power calculation
              n = 5
          delta = 0.88
             sd = 3.422353
      sig.level = 0.05
          power = 0.0548756
    alternative = two.sided
NOTE: n is number in *each* group
> power.t.test(delta = 0.88, n = 5, sd = sd(x1 - x2), type = "paired")
     Paired t test power calculation
              n = 5
          delta = 0.88
             sd = 0.580517
      sig.level = 0.05
          power = 0.7192318
    alternative = two.sided
                                                                 ifgi
```

NOTE: n is number of \*pairs\*, sd is std.dev. of \*differences\* within pairs

## Two-sample T-test and analysis of variance.





### Generalizing 2 to p groups: from t to F

- ▶ let  $n_1 = n_2 = \underline{n}$  and  $N = n_1 + n_2$ , and assume  $\sigma_1 = \sigma_2$
- $t = \frac{\bar{X}_1 \bar{X}_2}{s/\sqrt{n}} = \frac{(\bar{X}_1 \bar{X}_2)\sqrt{n}}{s}$
- $t^2 = \frac{(\bar{X}_1 \bar{X}_2)^2 n}{s^2} = \frac{n \text{Var}(\bar{X}_i)}{s^2}$
- ▶  $\frac{n\text{Var}(\bar{X}_i)}{s^2}$ , with  $s^2$  the pooled (averaged, joined) within-group variance
- numerator: variance, as obtained from variability between groups (group means)
- denominator: variance, as obtained from variability within groups (ignores differences between groups)
- ▶ Under the hypothesis  $H_0: \mu_1 = \mu_2 = ... = \mu_p$ ,

$$F = \frac{n \mathsf{Var}(\bar{X}_i)}{s^2}$$

follows the F distribution with p-1 (numerator) and N-p (denominator) degrees of freedom.

This idea generalizes the two-sample t-test, testing  $H_0: \mu_1 = \mu_2$  tighthe F-test, testing  $H_0: \mu_1 = \mu_2 = \dots = \mu_p$ .

## Why not use many t-tests?

Suppose we have three groups, and we can reject  $H_0: \mu_1 = \mu_2$ , we can reject  $H_0: \mu_2 = \mu_3$ , but cannot reject  $H_0: \mu_1 = \mu_3$ .

This will be clumsy to explain.

When hypothesis  $H_0$ :  $\mu_1=\mu_2=\mu_3$  can be rejected, we can continue under the model "the group means differ significantly".

Suppose we have many (10) groups with few observations (3) each. Pairwise testing has very little power (df = 4), whereas joint testing with ANOVA has (df = 20).



#### How to read ANOVA tables?

```
> summary(aov(Length ~ Gender))

Df Sum Sq Mean Sq F value Pr(>F)

Gender 1 4017.1 4017.1 45.466 1.845e-09 ***

Residuals 84 7421.8 88.4

---

Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
```

Gender: effect, explanatory variable, grouping variable, between groups

Residuals: error, within-groups, unexplained variability

Df: degrees of freedom for that row

Sum Sq: sum of squares, between or within

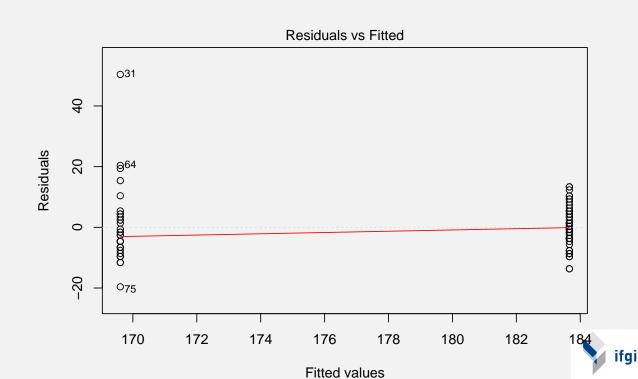
Mean Sq: mean squares: Sum Sq divided by Df

F value: Mean Sq effect divided by Mean Sq Residuals

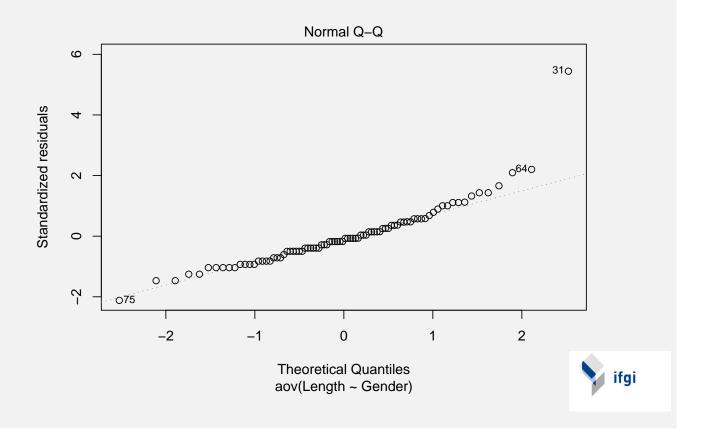
Pr(>F): significance level, p-value



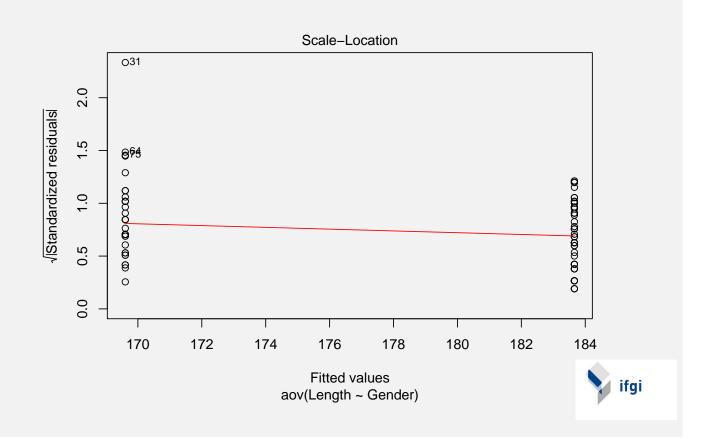
```
> plot(aov(Length ~ Gender), which = 1)
> Length[31]
[1] 220
```



aov(Length ~ Gender)







#### Two-way ANOVA; setting up data

```
The data can also be organized like this:
```

```
> x = data.frame(resp = c(x1, x2), time = rep(c("t1", "t2"),
     each = 5), obj = rep(letters[1:5], 2))
> x
  resp time obj
1 13.5
        t1
 15.3
2
        t1
            b
  7.5
3
        t1
            С
4 10.3
       t1 d
5 8.7 t1 e
6 12.7
      t2 a
7 15.1 t2 b
8 6.6
        t2 c
9 8.5 t2 d
10 8.0
        t2
```



## Two-way ANOVA

```
> summary(aov(resp ~ time, x))

Df Sum Sq Mean Sq F value Pr(>F)

time 1 1.936 1.936 0.1653 0.695

Residuals 8 93.700 11.712
```

#### Two-way ANOVA:

One-way ANOVA:



# Paired t-test vs two-way ANOVA

```
Paired t-test:
> t.test(x1, x2, paired = TRUE)
       Paired t-test
data: x1 and x2
t = 3.3896, df = 4, p-value = 0.02754
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
 0.1591929 1.6008071
sample estimates:
mean of the differences
                  0.88
Two-way ANOVA:
> summary(aov(resp ~ time + obj, x))
           Df Sum Sq Mean Sq F value Pr(>F)
time
            1 1.936 1.936 11.490 0.0275393 *
            4 93.026 23.256 138.021 0.0001545 ***
obj
           4 0.674 0.169
Residuals
                                                            ifgi
Signif. codes: 0 '*** 0.001 '** 0.01 '* 0.05 '.' 0.1 ' '
```

## Paired t-test vs. two-way ANOVA

Note: *p*-values are identical. Anova generalizes paired t-tests in the sense that e.g. time can have more than 2 levels (but is considered categorical).

Further extensions: three-way, more-way anova; interactions. Now introduce the meuse data set

