BIOE 498/598 PJ

Spring 2021

When is an effect size significant?

Linear models compute estimates of the true value of the parameters β .

The uncertainty in our estimate is quantified by the standard error.

Let's say we estimate β using n samples from a population with standard deviation σ . The standard error of our estimate is

s.e.
$$= \sigma/\sqrt{n}$$

The 95% confidence interval for a parameter is 1.96 standard errors* on each side of the estimate:

95% C.I. of
$$\beta = [\beta - 1.96$$
s.e., $\beta + 1.96$ s.e.]

* We often use 2 standard errors as a slightly conservative (and more convenient) estimate of the 95% confidence interval.

The 95% Confidence Interval

If a parameter estimate has a 95% C.I. that includes zero, we cannot be certain that the true value of the parameter is nonzero.

A parameter estimate is significant if and only if the 95% C.I. excludes zero.

The 95% C.I. depends on the number of samples (s.e. $= \sigma/\sqrt{n}$). We can narrow the 95% C.I. and improve our estimate of β by increasing n.

Example

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We always assume that the population standard deviation (σ) is independent of n. In our example, $\sigma = \sqrt{n}\,\mathrm{s.e.} = 3.8$. For our estimate to be significant, the lower end of the 95% C.I. must exclude zero, so

$$\beta - 1.96\sigma/\sqrt{n} > 0$$
 $n > (1.96\sigma/\beta)^2$
 $n > (1.96 \times 3.8/3.1)^2$
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Two more samples (n = 6) would have been sufficient for our estimate of β to be significantly nonzero.

The previous example makes two assumptions:

- ▶ The standard deviation (σ) will not change in subsequent experiments.
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The first assumption is valid since σ is a property of the underlying population. Assuming our samples are drawn from the same population, they will have the same variation.

Our assumption about β is not valid. Remember that β is only an estimate of the true parameter value. If we re-sample the population we will get a new estimate. If the new estimate of β is any lower, the confidence interval in the previous example will again include zero.

Power Analysis (continued)

We need to be more conservative in our estimate of n to account for differences in the new estimates of β . Adding another 0.84 s.e. to our bound will ensure the 95% C.I. for β excludes zero for 80% of the new estimates of β .

Power Analysis (continued)

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Our new estimate for the sample size is

$$\beta - (1.96\text{s.e.} + 0.84\text{s.e.}) > 0$$

 $\Rightarrow n > (2.80\sigma/\beta)^2$

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Our new estimate for the sample size is

$$\beta - (1.96\text{s.e.} + 0.84\text{s.e.}) > 0$$

 $\Rightarrow n > (2.80\sigma/\beta)^2$

Even with this conservative estimate, there is still a 20% chance that our estimate of β will not be significant, although this level of uncertainty seems to be acceptable to most experimenters.

Power calculations using a t-test

The significance of an effect size is determined by a t-test, which can differ from the normal distribution used on the previous slide.

Unfortunately, calculating n using a t-distribution is not simple. We use the R function power.t.test instead.

Power calculations using a t-test

The significance of an effect size is determined by a *t*-test, which can differ from the normal distribution used on the previous slide.

Unfortunately, calculating n using a t-distribution is not simple. We use the R function power.t.test instead.

- ightharpoonup delta is the effect size (β)
- sd is the standard deviation
- ▶ power is 0.8 for an 80% chance of seeing a significant result
- alternative="one.sided" assumes the effect won't change signs

Back to the farm

```
##
## Call:
## lm(formula = yield ~ ammonia + phosphate, data = fert)
##
## Residuals:
                         3
##
## -0.12172 0.03404 0.12402 0.08646 0.11808 -0.24089
##
## Coefficients:
##
             Estimate Std. Error t value Pr(>|t|)
## (Intercept) -0.1640 0.2247 -0.730 0.518
## ammonia
            0.1909 0.3152 0.606 0.588
## phosphate 0.4201
                         0.2273 1.848 0.162
##
## Residual standard error: 0.1922 on 3 degrees of freedom
## Multiple R-squared: 0.5327, Adjusted R-squared: 0.2212
## F-statistic: 1.71 on 2 and 3 DF, p-value: 0.3194
```

Power analysis for phosphate

```
## Estimate Std. Error t value Pr(>|t|)
## (Intercept) -0.1640188 0.2247293 -0.7298506 0.5183074
## ammonia 0.1908623 0.3151669 0.6055911 0.5875313
## phosphate 0.4200717 0.2273268 1.8478757 0.1617658
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   (Intercept) -0.1640188  0.2247293 -0.7298506  0.5183074
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##
## phosphate 0.4200717 0.2273268 1.8478757 0.1617658
power.t.test(n=NULL, delta=0.4201, sd=0.2273*sqrt(3),
             power=0.8, alternative="one.sided")
##
##
        Two-sample t test power calculation
##
##
                n = 11.60011
##
            delta = 0.4201
##
                sd = 0.3936951
##
        sig.level = 0.05
##
            power = 0.8
##
       alternative = one.sided
##
## NOTE: n is number in *each* group
```

Power analysis for phosphate

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                 Estimate Std. Error t value Pr(>|t|)
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##
        sig.level = 0.05
##
             power = 0.8
##
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##
## NOTE: n is number in *each* group
```

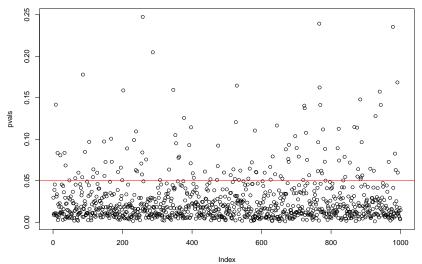
Six more runs (12 total) should be sufficient 80% of the time.

After adding six more runs...

```
##
## Call:
## lm(formula = yield ~ ammonia + phosphate, data = aug_fert)
##
## Residuals:
##
      Min 1Q Median 3Q
                                     Max
## -0.20426 -0.07663 0.05880 0.09042 0.16070
##
## Coefficients:
##
            Estimate Std. Error t value Pr(>|t|)
## ammonia 0.03634 0.11973 0.303 0.7684
## phosphate 0.29305 0.10419 2.813 0.0203 *
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ''
##
## Residual standard error: 0.1382 on 9 degrees of freedom
## Multiple R-squared: 0.4684, Adjusted R-squared: 0.3503
## F-statistic: 3.965 on 2 and 9 DF, p-value: 0.05823
```

Is six more runs always enough?

Below are the p-values for the phosphate effect from 1,000 models fit with six additional runs.



One last note

Given enough runs, any effect size — no matter how small — will become statistically significant.

Never forget that **statistical** significance does not imply **practical** significance.

Keep your focus on the effect size, not the *p*-value.