

Social Science Inquiry II

Week 8: Inference for multivariate regression, part II

Molly Offer-Westort

Department of Political Science,
University of Chicago

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Loading packages for this class

```
> set.seed(60637)
> # For plotting:
> library(ggplot2)
> # library(devtools)
> # devtools::install_github("wilkelab/ungeviz")
> library(ungeviz)
> library(ggribes)
```

► Housekeeping

P-hacking

P-values

Suppose $\hat{\theta}$ is the general form for an estimate produced by our estimator, and $\hat{\theta}^*$ is the value we have actually observed.

P-values

- ▶ A two-tailed p-value under the null hypothesis is

$$p = P_0[|\hat{\theta}| \geq |\hat{\theta}^*|]$$

i.e., the probability *under the null distribution* that we would see an estimate of $\hat{\theta}$ as or more extreme as what we saw from the data.

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- ▶ Suppose the null distribution represents the truth.
- ▶ If we test one hypothesis, what is the probability that we will find something that is statistically significant at $p \leq 0.05$?
- ▶ If we test two unrelated hypotheses, what is the probability that we will find something that is statistically significant at $p \leq 0.05$?

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- ▶ B: event we reject hypothesis 2 at $p \leq 0.05$

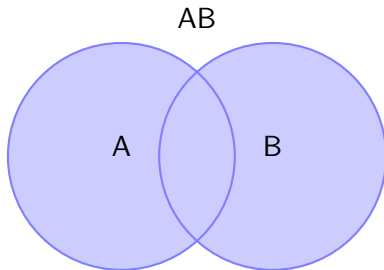
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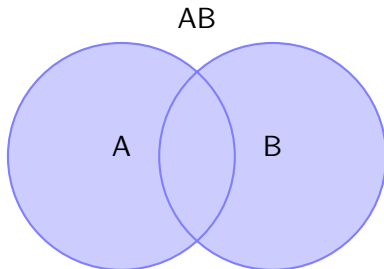
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- ▶ $A \perp\!\!\!\perp B$: the two events are independent
- ▶ $P[A] = 0.05$
- ▶ $P[B] = 0.05$
- ▶ $P[AB]$? The probability we see event A OR B?

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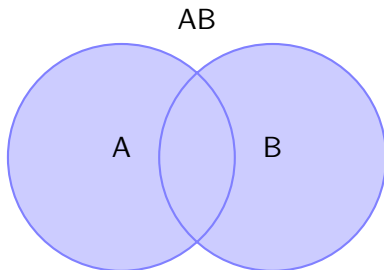
A and B are independent, so $P[B|A^C] = P[B]$



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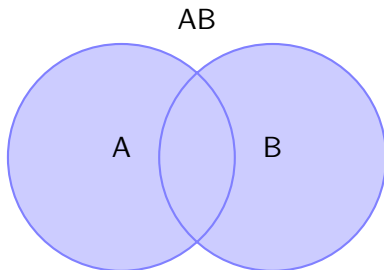


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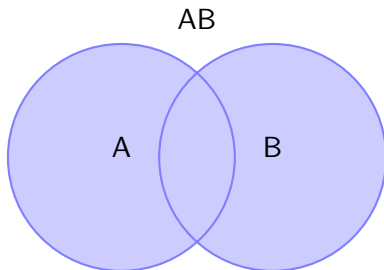
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$$P[AB] = 0.0975$$



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 $1 - 0.95^3 = 0.1426$

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This becomes a real problem when researchers run many tests in their papers!

	Fail to reject null hypothesis ($p > 0.05$)	Reject null hypothesis ($p \leq 0.05$)
Null hypothesis true	True negative	Type I error, false positive
Null hypothesis false	Type II error, false negative	True positive

- **Type I error:** (false positive) we see an effect, where one doesn't really exist

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- ▶ **Type I error:** (false positive) we see an effect, where one doesn't really exist
- ▶ **Type II error:** (false negative) we didn't see an effect, but one really does exist

Multiple testing scenarios

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These tests aren't all fully independent, but the more tests we do, the more likely we are to uncover a false positive.

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- ▶ *p-value adjustment*

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- ▶ False Discovery Rate (FDR): expected proportion of false discoveries among all discoveries; $E[\# \text{ False discoveries} / \# \text{ All discoveries}]$

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 - ▶ Bonferroni correction: for m hypotheses, for significance level α , implement α/m

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- For $\alpha = 0.05$, $1 - 0.95^4 = 0.1855$

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- With Bonferroni correction: $1 - (1 - \alpha/4)^4 = 0.0491$

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- four independent tests, the probability that *at least one of them* will be statistically significant at $p \leq \alpha$ is $1 - (1 - \alpha)^4$
- For $\alpha = 0.05$, $1 - 0.95^4 = 0.1855$
- With Bonferroni correction: $1 - (1 - \alpha/4)^4 = 0.0491$
- Ten independent tests: $1 - (1 - \alpha/10)^{10} = 0.0489$

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- ▶ Correcting FWER

- ▶ Holm correction: for m hypotheses, for significance level α :

- ▶ Order the m conventionally calculated p-values from smallest to largest

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- ▶ Correcting FDR
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 - ▶ Order the m conventionally calculated p-values from smallest to largest
 - ▶ Find the *largest* p-value indexed as k such that $p_k \leq \frac{k}{m}\alpha$
 - ▶ Reject all p-values greater than p_k , accept all p-values less than or equal to p_k

p-value adjustment

- ▶ In either case, for more complex settings, try simulation.

Multiple testing

- ▶ When can you consider tests as unrelated?

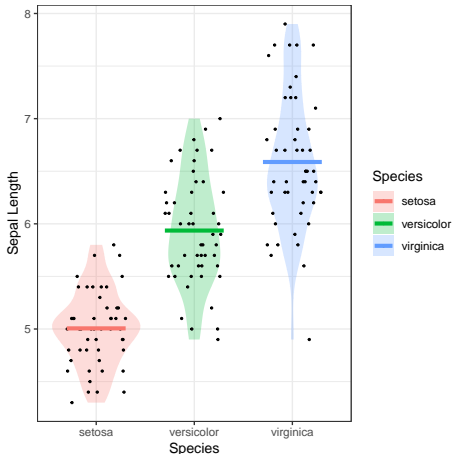
Multiple testing

- ▶ When can you consider tests as unrelated?
- ▶ Exploratory vs. confirmatory hypotheses?

Some alternatives to confidence intervals (via ungeviz)

Show the underlying data.

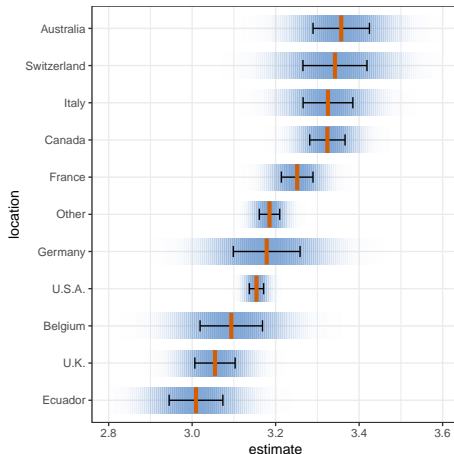
```
> ggplot(iris, aes(Species, Sepal.Length, fill = Species)) +  
+   geom_violin(alpha = 0.25, color = NA) +  
+   geom_point(position = position_jitter(width = 0.3, height = 0), size = 0.5) +  
+   geom_hline(aes(colour = Species), stat = "summary", width = 0.6, size = 1.5, fun = 'mean')
```



Some alternatives to confidence intervals (via ungeviz)

Shaded confidence strips.

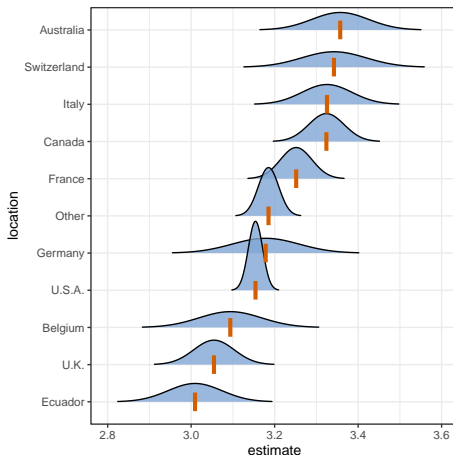
```
> ggplot(cacao_means, aes(x = estimate, y = location)) +  
+   stat_confidence_density(aes(moe = std.error), confidence = 0.68, fill = "#81A7D6", height = 0.7) +  
+   geom_errorbarh(aes(xmin = estimate - std.error, xmax = estimate + std.error), height = 0.3) +  
+   geom_vpline(aes(x = estimate), size = 1.5, height = 0.7, color = "#D55E00")
```



Some alternatives to confidence intervals (via ungeviz)

Confidence densities.

```
> ggplot(cacao_means, aes(x = estimate, y = location)) +  
+   stat_confidence_density(  
+     aes(moe = std.error, height = stat(density)), geom = "ridgeline",  
+     confidence = 0.68, fill = "#81A7D6", alpha = 0.8, scale = 0.08, min_height = 0.1) +  
+   geom_vpline(aes(x = estimate), size = 1.5, height = 0.5, color = "#D55E00")
```



References I

Clause Wilke: <https://wilkelab.org/ungeviz/index.html>