



propertee: Flexible Covariance Adjustment and Improved Standard Errors in Analyses of Intact Clusters

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It would be nice if `lm()`'s and `glm()`'s in causal analyses routinely returned estimates of marginal causal effects...

It would be nice if `lm()` and `glm()` always returned (marginal) causal estimates...

Add "experimental" somewhere in here, also because people don't only use lm() or glm() for causal reasons

- Simple to use `lm()` or `glm()` to run a regression
- Challenging to ensure the coefficient on a treatment assignment indicator has the desired interpretation *Expand with another bullet by saying "ATE" is common estimand in experiments and "ATT" is common in observational studies*
- Complicated standard error calculations may preclude more satisfying methods for covariance adjustment

Remove SE's bullet point



It would be nice if `lm()` and `glm()` always returned causal estimates...

- Simple to use `lm()` or `glm()` to run a regression
- Challenging to ensure the coefficient on a treatment assignment indicator has the desired interpretation
- Complicated standard error calculations may preclude more satisfying methods for covariance adjustment
- **propereti introduces `lmitt()`, an analog of `lm()` that:**
 - 1) Reports difference-in-means estimates (optionally, with covariance adjustment) with causal interpretations
 - 2) Returns a fitted model object equipped with special S3 methods for variance estimation



A call to `l mitt()` in the context of the Work, Family and Health Study (WFHS)¹

```
# a call to l mitt() for a difference-in-means estimate with covariance adjustment

tmod <- l mitt(
    TOPPRIORITY ~ 1,
    specification = StudySpec,
    data = RespondentData,
    absorb = FALSE,
    offset = cov_adj(logistic_mod),
    weights = "ate",
    ...
)
```



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    ...  
)
```

`StudySpec` maps cluster-level treatment assignments and cluster-level inverse propensity weights (computed based on the `weights` argument) to observations in RespondentData



A call to `lmmitt()` in the context of the Work, Family and Health Study (WFHS)¹

```
# a call to lmmitt() for a difference-in-means estimate with covariance adjustment
```

remove "with covariance
adjustment"

```
tmod <- lmmitt(  
    TOPPRIORITY ~ 1,  
    specification = StudySpec,  
    data = RespondentData,  
    absorb = FALSE,  
    offset = cov_adj(logistic_mod),  
    weights = "ate",  
    ...  
)
```

Replace studyspec
with formula,
don't name the
arg; this will show
we compute
correct IPW
weights from
RespondentData

`StudySpec` maps cluster-level treatment assignments
and cluster-level inverse propensity weights (computed
based on the `weights` argument) to observations in
RespondentData

No need to join cluster-level assignment data with
observation-level response data!

Don't need the second callout box.

Get rid of absorb and offset args here.



A call to `lImitt()` in the context of the Work, Family and Health Study (WFHS)¹

```
# a call to lImitt() for a difference-in-means estimate with covariance adjustment
```

```
tmod <- lImitt(  
    TOPPRIORITY ~ 1,  
    specification = StudySpec,  
    data = RespondentData,  
    absorb = FALSE,  
    offset = cov_adj(logistic_mod), ←  
    weights = "ate",  
    ...  
)
```

`'cov_adj()'` elicits predictions from a fitted prognostic model and stashes additional information for SE calculations in the output vector.



A call to `lImitt()` in the context of the Work, Family and Health Study (WFHS)¹

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tmod <- lImitt(  
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    data = RespondentData,  
    absorb = FALSE,  
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    weights = "ate",  
    ...  
)
```

Remove
absorb arg

`cov_adj()` elicits predictions from a fitted prognostic model and stashes additional information for SE calculations in the output vector.

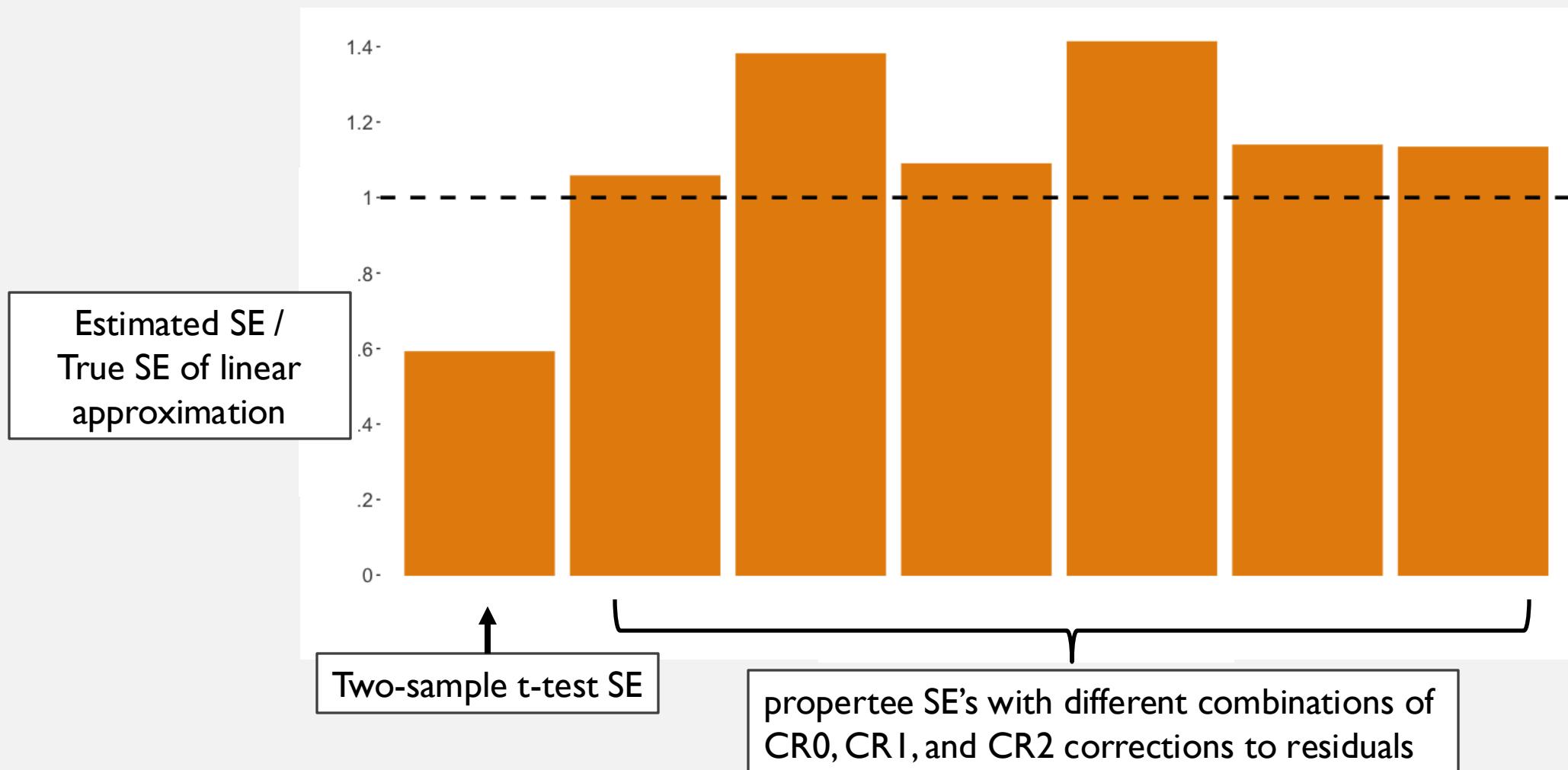
Passing prognostic scores to `offset` yields a (likely more precise) difference-in-differences type estimate, with differences of the form $Y(A) - \hat{Y}(0)$

"model predictions" in place of "prognostic scores"

cov_adj() is an analog of predict(fitted_model, type = "response")



Why should SE's incorporate information from the prognostic score model? "prognostic model"



Example output of `summary()` called on a model fit with `lmiitt()`

```
> summary(tmod, vcov.type = "CR2", cov_adj_rcorrect = "HC1", loco_residuals = TRUE)
Call:
lmiit(TOPPRIORITY ~ 1, StudySpec, RespondentData, offset = cov_adj(logistic_mod), weights = "ate")
```

Treatment Effects :

	Estimate	Std. Error	t value	Pr(> t)
CONDITION.	-0.05699	0.05499	-1.036	0.31
TOPPRIORITY:(Intercept)	0.63360	0.04209	15.052	2.24e-09 ***

Signif. codes: 0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Std. Error calculated via type "CR2"



Title: "Better SE's via lmitt(), summary() (and vcov_tee())"

Example output of `summary()` called on a model fit with `lmitt()`

```
> summary(tmod, vcov.type = "CR2", cov_adj_rcorrect = "HC1", loco_residuals = TRUE)
Call:
lmitt(TOPPRIORITY ~ 1, StudySpec, RespondentData, offset = cov_adj(logistic_mod), weights = "ate")
```

Treatment Effects :

	Estimate	Std. Error	t value	Pr(> t)
CONDITION.	-0.05699	0.05499	-1.036	0.31
TOPPRIORITY:(Intercept)	0.63360	0.04209	15.052	2.24e-09 ***

Degrees of freedom for reference t-distribution reflect clustering and known improvements for CR2 variance estimates

Signif. codes: 0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
Std. Error calculated via type "CR2"

Update the output here to reflect covariance adjustment

These are the arguments that provide the best model-based SE based on our work (Wasserman, 2025+). Design-based SE's are available in some circumstances as well.



Just get rid of this slide

Find propertee on CRAN soon and,
until then, Github!



REFERENCES

I. Work, Family and Health Network. Work, Family, and Health Study (WFHS) . Inter-university Consortium for Political and Social Research [distributor], 2018-10-03. <https://doi.org/10.3886/ICPSR36158.v2>

Add citation to my (in progress) dissertation, Github URL, Wang and Hansen (arXiv)

Wrap up with some other things propertee can do that users can look into

Add note about github here, pointing to QR

