

# Small-sample inference for linear mixed-effects models (DDF adjustments)

Xiao Yang

Senior Statistician and Software Developer  
StataCorp LP

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## Outline

- Motivation
- Currently supported methods
  - “Exact” methods
  - Approximate methods
  - Which one to use?
- Postestimation
  - Currently available commands
  - Small-sample adjustments for contrasts

The `mixed` command fits linear mixed-effects models. Mixed effects are fixed effects plus random effects. For example,

$$y_{ij} = \beta_0 + \beta_1 x_{ij1} + \cdots + \beta_p x_{ijp} + u_j + \epsilon_{ij},$$

where  $i = 1, 2, \dots, n_j$  and  $j = 1, 2, \dots, s$ .

In matrix notation,  $\mathbf{y} = \mathbf{X}\boldsymbol{\beta} + \mathbf{Z}\mathbf{u} + \boldsymbol{\epsilon}$ .

- $\beta_0, \beta_1, \dots, \beta_p$  are fixed effects
- $u_j$ 's are random effects
- $u_j \sim N(0, \sigma_u^2)$  and  $\epsilon_{ij} \sim N(0, \sigma_\epsilon^2)$
- $\mathbf{X}$  and  $\mathbf{Z}$  are design matrices

Researchers are often interested in making inferences about fixed effects.

- Large-sample approximation
  - sampling distributions of the test statistics are approximated by normal and  $\chi^2$
  - default in `mixed`
- In special cases, sampling distributions of the test statistics are known to be  $t$  or  $F$  distributions.
  - simple balanced split-plot design
  - simple balanced repeated measures
- In small samples, large-sample approximations may lead to anticonservative results.

## Introducing `mixed`, `dfmethod()` ...

- In small samples, the null sampling distributions of test statistics for fixed effects are not known in general (except for special cases).
- Sampling distributions are approximated by  $t$  and  $F$ .
- Approximations differ in how respective denominator degrees of freedom (DDF) are computed.
- Five methods for calculating DDFs.
- New in Stata 14, need to specify the `dfmethod()` option.

Choosing between DDF methods is not an easy task!

- All DDF methods are only approximations (except in some rare cases).
- The choice of DDFs is highly dependent on the models, the data structure, the size of the dataset, and the balance of the dataset.
- No single method works for all possible models.

## Example 1: Simple repeated-measures design

- From table 4.3 of Winer, Brown, and Michels<sup>1</sup>.
- The reaction time for 5 subjects each tested with 4 drugs was recorded in the variable `score`. `drug` is the repeated-measures factor.

```
. tabdisp person drug, cellvar(score)
```

| person | drug |    |    |    |
|--------|------|----|----|----|
|        | 1    | 2  | 3  | 4  |
| 1      | 30   | 28 | 16 | 34 |
| 2      | 14   | 18 | 10 | 22 |
| 3      | 24   | 20 | 18 | 30 |
| 4      | 38   | 34 | 20 | 44 |
| 5      | 26   | 28 | 14 | 30 |

---

<sup>1</sup>B. J. Winer, D. R. Brown, and K. M. Michels. *Statistical Principles in Experimental Design*. 3rd ed. New York, NY: McGraw-Hill, Inc., 1991.

- Use anova command:

```
. anova score person drug, repeated(drug)
```

```
...
```

```
Between-subjects error term:  person
                             Levels: 5          (4 df)
```

```
Lowest b.s.e. variable:  person
```

```
Repeated variable:  drug
```

```
Huynh-Feldt epsilon          = 1.0789
```

```
*Huynh-Feldt epsilon reset to 1.0000
```

```
Greenhouse-Geisser epsilon = 0.6049
```

```
Box's conservative epsilon = 0.3333
```

| Source   | df | F     | Prob > F |        |        |        |
|----------|----|-------|----------|--------|--------|--------|
|          |    |       | Regular  | H-F    | G-G    | Box    |
| drug     | 3  | 24.76 | 0.0000   | 0.0000 | 0.0006 | 0.0076 |
| Residual | 12 |       |          |        |        |        |



- Large-sample inference

```
. mixed score i.drug || person:, reml
```

```
...
```

```
Mixed-effects REML regression
```

```
Group variable: person
```

```
Number of obs      =           20
```

```
Number of groups   =            5
```

```
Obs per group:
```

```
    min =            4
```

```
    avg =            4.0
```

```
    max =            4
```

```
Wald chi2(3)       =           74.28
```

```
Prob > chi2        =           0.0000
```

```
Log restricted-likelihood = -49.640099
```

| score | Coef. | Std. Err. | z     | P> z  | [95% Conf. Interval] |           |
|-------|-------|-----------|-------|-------|----------------------|-----------|
| drug  |       |           |       |       |                      |           |
| 2     | -.8   | 1.939072  | -0.41 | 0.680 | -4.600511            | 3.000511  |
| 3     | -10.8 | 1.939072  | -5.57 | 0.000 | -14.60051            | -6.999489 |
| 4     | 5.6   | 1.939072  | 2.89  | 0.004 | 1.799489             | 9.400511  |
| _cons | 26.4  | 3.149604  | 8.38  | 0.000 | 20.22689             | 32.57311  |

```
...
```

## ● Small-sample inference

```
. mixed score i.drug || person:, reml dfmethod(repeated)
...
Mixed-effects REML regression
Group variable: person
Number of obs      =      20
Number of groups   =       5
Obs per group:
    min =          4
    avg =         4.0
    max =          4
DF method: Repeated
DF:
    min =         4.00
    avg =        10.00
    max =        12.00
F(3, 12.00) = 24.76
Prob > F      =      0.0000
Log restricted-likelihood = -49.640099
```

| score | Coef. | Std. Err. | t     | P> t  | [95% Conf. Interval] |           |
|-------|-------|-----------|-------|-------|----------------------|-----------|
| drug  |       |           |       |       |                      |           |
| 2     | -.8   | 1.939072  | -0.41 | 0.687 | -5.024874            | 3.424874  |
| 3     | -10.8 | 1.939072  | -5.57 | 0.000 | -15.02487            | -6.575126 |
| 4     | 5.6   | 1.939072  | 2.89  | 0.014 | 1.375126             | 9.824874  |
| _cons | 26.4  | 3.149604  | 8.38  | 0.001 | 17.6553              | 35.1447   |

...

- To display the DF value for each coefficient, just type

```
. mixed, dftable(pvalue)
```

| score | Coef. | Std. Err. | DF   | t     | P> t  |
|-------|-------|-----------|------|-------|-------|
| drug  |       |           |      |       |       |
| 2     | -.8   | 1.939072  | 12.0 | -0.41 | 0.687 |
| 3     | -10.8 | 1.939072  | 12.0 | -5.57 | 0.000 |
| 4     | 5.6   | 1.939072  | 12.0 | 2.89  | 0.014 |
| _cons | 26.4  | 3.149604  | 4.0  | 8.38  | 0.001 |

```
. estat df
```

```
Degrees of freedom
```

|       | Repeated |
|-------|----------|
| score |          |
| drug  |          |
| 2     | 12       |
| 3     | 12       |
| 4     | 12       |
| _cons | 4        |

## Example 2: Random-coefficient model for longitudinal data

- Simulated dataset from Kenward and Roger<sup>2</sup>.
- 24 subjects, identified by **id**, split into 3 groups of 8. The subjects of each group are being observed on the same time points. The three sets of time points are chosen to be nonoverlapping: (0, 1, 2), (3, 4, 5), and (6, 7, 8).

$$y_{ij} = \beta_0 + \beta_1 \text{time}_{ij} + u_j + \gamma_j \text{time}_{ij} + \epsilon_{ij}$$

- $\begin{bmatrix} u_j \\ \gamma_j \end{bmatrix} \sim N\left(\begin{bmatrix} b_0 \\ b_1 \end{bmatrix}, \begin{bmatrix} \sigma_0^2 & \sigma_{01} \\ \sigma_{01} & \sigma_1^2 \end{bmatrix}\right)$  and  $\epsilon_{ij} \sim N(0, \sigma_e^2)$ .
- Data are simulated from the model with  $\beta_1 = 0$ .

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<sup>2</sup>M. G. Kenward and J. H. Roger. “Small sample inference for fixed effects from restricted maximum likelihood”. In: *Biometrics* 53 (1997), pp. 983–997.

- Large-sample inference

```
. mixed y time || id: time, reml cov(unstructured)
...
Mixed-effects REML regression          Number of obs    =          72
Group variable: id                    Number of groups =          24
                                       Obs per group:
                                       min =           3
                                       avg =           3.0
                                       max =           3
                                       Wald chi2(1)      =          4.34
                                       Prob > chi2       =          0.0372

Log restricted-likelihood = -109.39153
```

| y     | Coef.    | Std. Err. | z    | P> z  | [95% Conf. Interval] |
|-------|----------|-----------|------|-------|----------------------|
| time  | .2765987 | .1327319  | 2.08 | 0.037 | .0164489 .5367485    |
| _cons | 1.045034 | .2504823  | 4.17 | 0.000 | .5540973 1.53597     |

...

- The default large-sample inference for **time** suggests that the fixed time effect is significant at a 5% level ( $p$ -value = 0.037).

- Small-sample inference with the kroger method

```
. mixed y time || id: time, reml cov(unstructured) dfmethod(kroger)
...
Mixed-effects REML regression
Group variable: id

Number of obs      =          72
Number of groups   =          24
Obs per group:
    min =            3
    avg =           3.0
    max =            3

DF method: Kenward-Roger
DF:
    min =          11.68
    avg =          17.19
    max =          22.69

F(1, 22.69) = 4.24
Prob > F    = 0.0512

Log restricted-likelihood = -109.39153
```

| y     | Coef.    | Std. Err. | t    | P> t  | [95% Conf. Interval] |          |
|-------|----------|-----------|------|-------|----------------------|----------|
| time  | .2765987 | .13434    | 2.06 | 0.051 | -.0015158            | .5547132 |
| _cons | 1.045034 | .2700712  | 3.87 | 0.002 | .4548251             | 1.635242 |

```
...
```

- After adjusting for a small sample, we do not have sufficient evidence to reject the null hypothesis of no time effect at a 5% significance level.

`mixed`, `dfmethod()` provides five DDF methods.

| Method                     | ML  | REML                                |
|----------------------------|-----|-------------------------------------|
| <code>residual</code>      | YES | YES                                 |
| <code>repeated</code>      | YES | YES                                 |
| <code>anova</code>         | YES | YES                                 |
| <code>satterthwaite</code> | NO  | <code>eim</code> , <code>oim</code> |
| <code>kröger</code>        | NO  | <code>eim</code> , <code>oim</code> |

# residual

For "exact" methods, computing DF for each coefficient is based on the single hypothesis test  $H_0 : \beta_i = 0$ , for  $i = 1, 2, \dots, p$ .

- $v_{df} = n - \text{rank}(X)$  for all tests.
- **residual provides exact degrees of freedom only in the 'iid' case.**
- **For other mixed models, provides poor approximation.**
- Available for completeness.



## repeated

- Partitions the residual degrees of freedom into the between-subject degrees of freedom and the within-subject degrees of freedom.
- Gives exact DF values for special balanced repeated-measures models with the spherical covariance structure.
- **Supported only with two-level models.**
- **Leads to poor approximations for more complex mixed-effects models or with unbalanced data.**

## anova

- Checks if the fixed effect is contained in some random-effects equations.
- If contained in some random-effects equations, then DF equals the smallest number of levels among the level variables minus one.
- If not contained in any random-effects equation, then

$$v_{df} = n - \text{rank}(X, Z)$$

- **Gives an exact sampling distribution of the test statistics only when random effects are simple and balanced and the error terms are i.i.d.**
- **Leads to poor approximations for more complex mixed-effects models or with unbalanced data.**

## Conclusion for "exact" methods

- residual, repeated, anova.
- Available for both ML and REML.
- Based on single-hypothesis tests.
- Available for multiple-hypotheses tests only if all corresponding single-hypothesis DFs are the same,  $v_{ddf} = v_{df}$ .
- If all corresponding single-hypothesis DFs are different,  $v_{ddf}$  is not defined.

## satterthwaite

- For a single-hypothesis test, Giesbrecht and Burns<sup>3</sup> developed a method of computing the DDF that is analogous to Satterthwaite's approximation of the degrees of freedom.
- For a multiple-hypotheses test, Fai and Cornelius<sup>4</sup> decomposed the contrast matrix using the spectral decomposition and repeatedly applied Giesbrecht and Burns's method to get the single-degree-of-freedom  $t$  test, then used the relationship between  $t$  and  $F$  to get the DDF.

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<sup>3</sup>F. G. Giesbrecht and J. C. Burns. "Two-stage analysis based on a mixed model: large-sample asymptotic theory and small-sample simulation results". In: *Biometrics* 41 (1985), pp. 477–486.

<sup>4</sup>A. H. Fai and P. L. Cornelius. "Approximate F-tests of multiple degree of freedom hypotheses in generalized least squares analyses of unbalanced split-plot experiments". In: *Journal of Statistical Computation and Simulation* 54 (1996), pp. 363–378.

# satterthwaite

- **Fai and Cornelius<sup>5</sup> prove that `satterthwaite` is good at approximating unbalanced split-plot designs.**
- **Schaalje, McBride, and Fellingham<sup>6</sup> recommend using the `satterthwaite` method only when the covariance structure of the data is compound symmetry and the sample size is moderately large.**

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<sup>5</sup>A. H. Fai and P. L. Cornelius. “Approximate F-tests of multiple degree of freedom hypotheses in generalized least squares analyses of unbalanced split-plot experiments”. In: *Journal of Statistical Computation and Simulation* 54 (1996), pp. 363–378.

<sup>6</sup>G. B. Schaalje, J. B. McBride, and G. W. Fellingham. “Adequacy of approximations to distributions of test statistics in complex mixed linear models”. In: *Journal of Agricultural, Biological, and Environmental Statistics* 7 (2002), pp. 512–524.

## kroger

- Kenward and Roger<sup>7</sup> proposed the scaled  $F$ -test statistic,

$$F_{KR} = \frac{\lambda}{\ell} (\mathbf{C}'\hat{\boldsymbol{\beta}} - \mathbf{b})' (\mathbf{C}'\hat{\boldsymbol{\Phi}}_A\mathbf{C})^{-1} (\mathbf{C}'\hat{\boldsymbol{\beta}} - \mathbf{b}) \sim F_{\ell, ddf_{kr}}$$

- **Accounts for the small-sample bias and the variability of the estimated random effects to obtain an adjusted estimator of the fixed-effects covariance matrix  $\hat{\boldsymbol{\Phi}}_A$ .**
- Uses a Taylor expansion for  $(\mathbf{C}'\hat{\boldsymbol{\Phi}}_A\mathbf{C})^{-1}$  and matches moments of  $F_{KR}$  with those of the approximating  $F$  distribution to obtain  $ddf_{kr}$  and  $\lambda$ .

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<sup>7</sup>M. G. Kenward and J. H. Roger. “Small sample inference for fixed effects from restricted maximum likelihood”. In: *Biometrics* 53 (1997), pp. 983–997.

# kröger

- **kröger yeilds to exact  $F$  distribution when the exact  $F$  distribution is available, and improves the approximation when the exact  $F$  distribution is not available.**
- Computing  $\widehat{\Phi}_A$  involves taking first and second derivatives of the covariance matrix of  $\mathbf{y}$  w.r.t. each random component.
- $\widehat{\Phi}_A$  is invariant under reparameterization if the covariance matrix of  $\mathbf{y}$  can be written as a linear function of random components.
- The second derivatives require more computational resources and may not be numerically stable; therefore, they are ignored.

## Conclusion for Approximate Methods

- `satterthwaite` and `kroger` are only available under REML.
- You can choose to use either `oim` or `eim` in the computation of `satterthwaite` or `kroger`; `eim` is the default.
- For a single-hypothesis test, DFs are the same between `satterthwaite` and `kroger`, but tests statistics and therefore tests are not necessarily identical.
- Suitable for complex covariance structures and unbalanced data.
- Computationally intensive.



## Which is the best `dfmethod()`?

- **[Spilke et al]** [7]: Assessed the performance of five DDF methods on RCB, split-plot, strip plots with missing data under REML. Preferred `kröger`.
- **[Alnosaier]** [1]: Assessed the performance of `satterthwaite` and `kröger` for PBIB, BIBD, and RCB with missing data designs through simulation. Preferred `kröger` method.
- **[Schaalje et al]** [6]: Assessed the performance of `kröger` and `satterthwaite` for split-plot and repeated measures designs; both methods are affected by covariance structure complexity, sample size, and imbalance. Preferred `kröger` method.
- **[Gregory]** [4]: Compared four DDF methods in the unbalanced two-way factorial design. Found no significant differences between those methods.

## Which one is the best `dfmethod()`?

- Prefer the `kröger` method when the sample size is small, the covariance structure is complicated, and/or the data is unbalanced.
- Even the `kröger` method sometimes produces inflated Type I error rates (e.g., AR(1) error covariance structure).
- The approximation methods can be computationally intensive.
- More research needs to be done to determine which method is the best for different mixed-effects models.

# Postestimation

Stata provides additional postestimation commands and options for small-sample inference after `mixed`:

- `estat df`
- `test, small`
- `testparm, small`
- `lincom, small`
- `contrast, small` (forthcoming)

## Example 3: Unbalanced split-plot design

- There are 30 observations, 8 subjects, whole plot factor  $a$  (2 levels), sub-plot factor  $b$  (4 levels), unbalanced

```
. tabdisp b s, cellvar(y) by(a) concise
```

| a and b |   | s |   |   |   |    |   |   |    |
|---------|---|---|---|---|---|----|---|---|----|
|         |   | 1 | 2 | 3 | 4 | 5  | 6 | 7 | 8  |
| 1       | 1 | 3 | 6 | 3 | 3 |    |   |   |    |
|         | 2 | 4 | 5 | 4 | 3 |    |   |   |    |
|         | 3 | 7 |   | 7 | 6 |    |   |   |    |
|         | 4 | 7 | 8 | 9 | 8 |    |   |   |    |
|         |   |   |   |   |   |    |   |   |    |
| 2       | 1 |   |   |   |   | 1  | 2 | 2 | 2  |
|         | 2 |   |   |   |   | 2  | 3 | 4 | 3  |
|         | 3 |   |   |   |   | 5  | 6 | 5 | 6  |
|         | 4 |   |   |   |   | 10 |   | 9 | 11 |
|         |   |   |   |   |   |    |   |   |    |

## estat df

estat df is a convenient tool to calculate and compare the DF's for different methods.

- Fit the model based on large-sample inference

```
. mixed y a##b || s:, reml
```

| y     | Coef.    | Std. Err. | z     | P> z  | [95% Conf. Interval] |
|-------|----------|-----------|-------|-------|----------------------|
| 2.a   | -2       | .6288677  | -3.18 | 0.001 | -3.232558 - .767442  |
| b     |          |           |       |       |                      |
| 2     | .25      | .5359916  | 0.47  | 0.641 | -.8005243 1.300524   |
| 3     | 3.108222 | .5862035  | 5.30  | 0.000 | 1.959284 4.25716     |
| 4     | 4.25     | .5359916  | 7.93  | 0.000 | 3.199476 5.300524    |
| a#b   |          |           |       |       |                      |
| 2 2   | 1        | .7580066  | 1.32  | 0.187 | -.4856656 2.485666   |
| 2 3   | .6417778 | .7943057  | 0.81  | 0.419 | -.9150328 2.198588   |
| 2 4   | 4.044205 | .7943057  | 5.09  | 0.000 | 2.487395 5.601016    |
| _cons | 3.75     | .4446766  | 8.43  | 0.000 | 2.87845 4.62155      |

## estat df

- Compare different DF methods using the method() option

```
. estat df, method(residual repeated anova satterthwaite kroger)
Degrees of freedom
```

|     | Residual | Repeated | ANOVA | Satterthwaite | Kenward-Roger |
|-----|----------|----------|-------|---------------|---------------|
| y   |          |          |       |               |               |
| a   |          |          |       |               |               |
| 1   | (empty)  |          |       |               |               |
| 2   | 22       | 6        | 16    | 18.29179      | 18.29179      |
| b   |          |          |       |               |               |
| 1   | (empty)  |          |       |               |               |
| 2   | 22       | 16       | 16    | 16.01983      | 16.01983      |
| 3   | 22       | 16       | 16    | 16.66069      | 16.66069      |
| 4   | 22       | 16       | 16    | 16.01983      | 16.01983      |
| a#b |          |          |       |               |               |
| 1 1 | (empty)  |          |       |               |               |
| ... | (empty)  |          |       |               |               |
| 2 1 | (empty)  |          |       |               |               |
| 2 2 | 22       | 16       | 16    | 16.01983      | 16.01983      |
| 2 3 | 22       | 16       | 16    | 16.36871      | 16.36871      |
| 2 4 | 22       | 16       | 16    | 16.36871      | 16.36871      |

# estat df

- Post the desired DF (kroger in our example) using the post option.

```
. estat df, method(kroger) post
```

- It is the same as refitting the model using the dfmethod() option in mixed.

```
. mixed y a##b || s:, reml dfmethod(kroger)
```

# test, small

- Obtain the large-sample inference as usual.

```
. test 2.a
( 1) [y]2.a = 0
           chi2( 1) =   10.11
           Prob > chi2 =   0.0015
```

- Use the `small` option to get small-sample adjustment.

```
. test 2.a, small
( 1) [y]2.a = 0
           F( 1, 18.29) =   10.11
           Prob > F =   0.0051
```



# testparm, small

- testparm also provides both tests, with and without small-sample adjustment.

```
. testparm a#b
( 1) [y]2.a#2.b = 0
( 2) [y]2.a#3.b = 0
( 3) [y]2.a#4.b = 0
           chi2( 3) =    29.35
           Prob > chi2 =    0.0000

. testparm a#b, small
( 1) [y]2.a#2.b = 0
( 2) [y]2.a#3.b = 0
( 3) [y]2.a#4.b = 0
           F( 3, 16.35) =    9.66
           Prob > F =    0.0007
```

# lincom, small

- lincom also provides two sets of results.

```
. lincom 2.a + 2.a#4.b
( 1) [y]2.a + [y]2.a#4.b = 0
```

| y   | Coef.    | Std. Err. | z    | P> z  | [95% Conf. Interval] |          |
|-----|----------|-----------|------|-------|----------------------|----------|
| (1) | 2.044205 | .6721771  | 3.04 | 0.002 | .7267621             | 3.361648 |

```
. lincom 2.a + 2.a#4.b, small
( 1) [y]2.a + [y]2.a#4.b = 0
```

| y   | Coef.    | Std. Err. | t    | P> t  | [95% Conf. Interval] |          |
|-----|----------|-----------|------|-------|----------------------|----------|
| (1) | 2.044205 | .6764554  | 3.02 | 0.007 | .6311736             | 3.457237 |

## contrast, small

- Suppose that we want to test the effect of factor  $a$ .
- The effect of factor  $a$  includes the main effect of  $a$  and the interaction effects that contain  $a$ .
- Currently, contrast only provides large-sample inference.

```
. contrast a
```

```
Contrasts of marginal linear predictions
```

```
Margins      : asbalanced
```

|   |   | df | chi2 | P>chi2 |
|---|---|----|------|--------|
| y | a | 1  | 1.79 | 0.1810 |

- **It is not the test for 2.a from the coefficient table!**

## contrast, small

We need to manually compute the small-sample inference.

- Write your own contrast

$$H_0 : 2.a + \frac{1}{4} \times 2.a\#2.b + \frac{1}{4} \times 2.a\#3.b + \frac{1}{4} \times 2.a\#4.b = 0$$

- Use `test, small`

```
. test ([y]2.a + 0.25*[y]2.a#2.b+0.25*[y]2.a#3.b+0.25*[y]2.a#4.b = 0), small
( 1) [y]2.a + .25*[y]2.a#2.b + .25*[y]2.a#3.b + .25*[y]2.a#4.b = 0
      F( 1, 5.95) =      1.78
      Prob > F =      0.2307
```

- `contrast, small` forthcoming

Thank you!

## References

- [1] W. S. Alnosaier. “Kenward-Roger Approximate F Test for Fixed Effects in Mixed linear models”. PhD thesis. Oregon State University, 2007.
- [2] A. H. Fai and P. L. Cornelius. “Approximate F-tests of multiple degree of freedom hypotheses in generalized least squares analyses of unbalanced split-plot experiments”. In: *Journal of Statistical Computation and Simulation* 54 (1996), pp. 363–378.
- [3] F. G. Giesbrecht and J. C. Burns. “Two-stage analysis based on a mixed model: large-sample asymptotic theory and small-sample simulation results”. In: *Biometrics* 41 (1985), pp. 477–486.

## References (cont.)

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