

## **META-ANALYSIS WORKSHOP**

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# Introduction to Meta Analysis

- Growing in popularity in animal science at apparently 15% per year (Sauvant et al. 2020; *Animal*).
- Likely to keep being important, especially if supplemental electronic submissions of raw data/summary statistics increases in the future.
- “The statistical analysis of a large *collection* of analysis *results* from individual studies for the purpose of integrating the findings” - Glass (1976)
- There are many important issues (publication bias, GIGO, etc.) that will go beyond the scope of a 2 hour workshop.

## Strategy used in today's workshop

- Simulated Data (including some from St. Pierre, 2001)
- Why?
  - Truth is “known” -> so meta-analysis methods could be assessed relative to not only the truth but also to analyses based on raw data (versus using summary statistics from individual studies).
  - Raw data typically not available in meta-analysis (but that will change!)
  - Avoids problems with workshop participants trying to read in data.
- For the vast majority of cases, meta-analysis of original raw data should closely agree with meta-analysis of summary statistics!

## Case #1: A good starting point

**J. Dairy Sci. 84:741–755**

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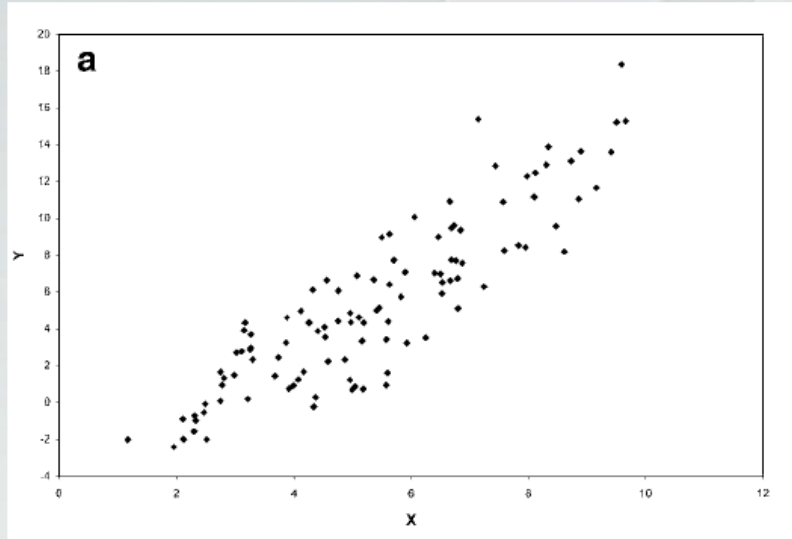
### ***Invited Review: Integrating Quantitative Findings from Multiple Studies Using Mixed Model Methodology***<sup>1</sup>

**N. R. St-Pierre**

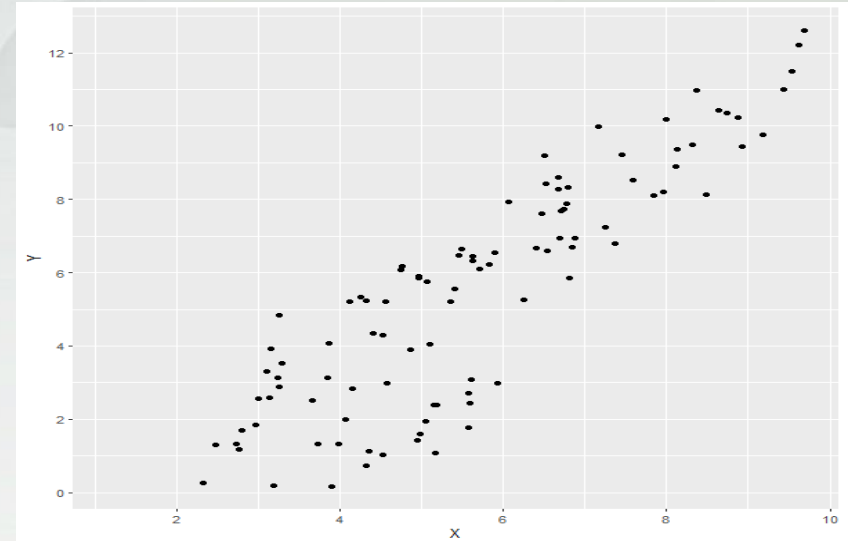
Department of Animal Sciences  
The Ohio State University  
Columbus, OH 43210

# Y vs X

Figure 2a in St-Pierre (2001)



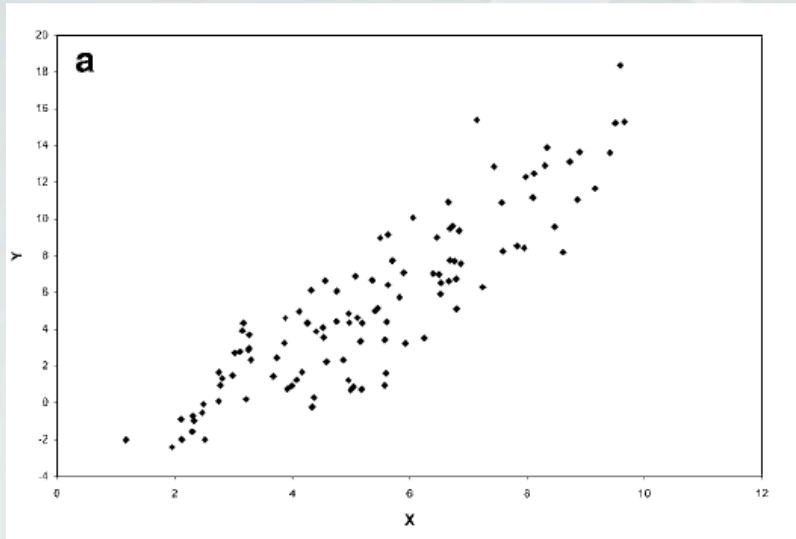
Graph created from data provided at Appendix St-Pierre (2001) (see lab)



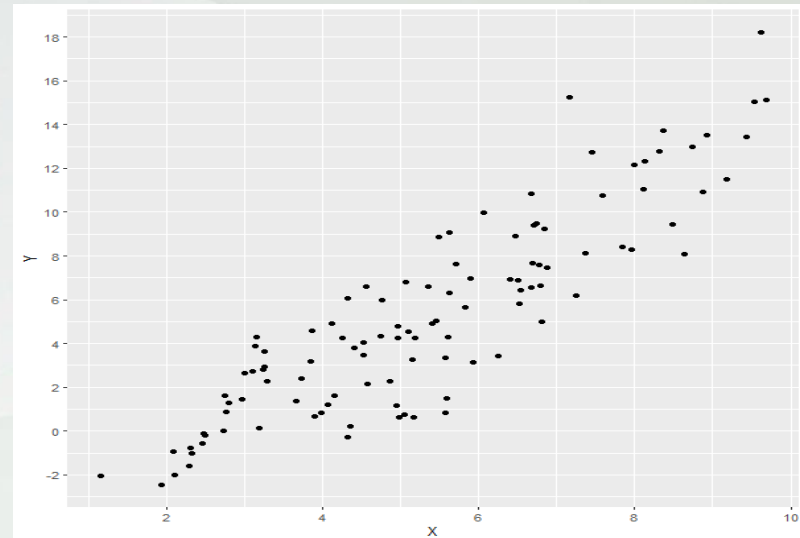
- Wrong data was seemingly provided

# Corrected data provided by Dr. White (forwarded by Dr. St-Pierre)

Figure 2a in St-Pierre (2001)



Corrected data (see lab)



## Data generation

- St-Pierre (2001) simulated data with *study-specific heterogeneity*:

$$y_{ij} = \underbrace{\beta_0 + s_i}_{\text{Study-specific intercept}} + \underbrace{(\beta_1 + b_{1i})}_{\text{Study-specific slope}} x_{ij} + e_{ij}; \quad i=1,2,\dots, n_{\text{study}} = 20, \quad j = 1,2,\dots, n_i$$

- St-Pierre choose  $\beta_0 = 0$  and  $\beta_1 = 1$ , Furthermore,

$$\begin{bmatrix} s_i \\ b_{1i} \end{bmatrix} \sim N \left( \begin{bmatrix} 0 \\ 0 \end{bmatrix}, \begin{bmatrix} 4 & 0.5\sqrt{4}\sqrt{0.04} \\ 0.5\sqrt{4}\sqrt{0.04} & 0.04 \end{bmatrix} \right); \quad e_{ij} \sim N(0, 0.25)$$

- Translation:

- Study specific intercepts have an overall average expected value of 0 with a variance of 4 (sd =2) across studies
- Study specific intercepts have an overall average expected value of 1 with a variance of 0.04 (sd =0.2) across studies
- Residual variability about each study-specific line has sd = 0.5.

Correlation  
= 0.5  
across  
studies


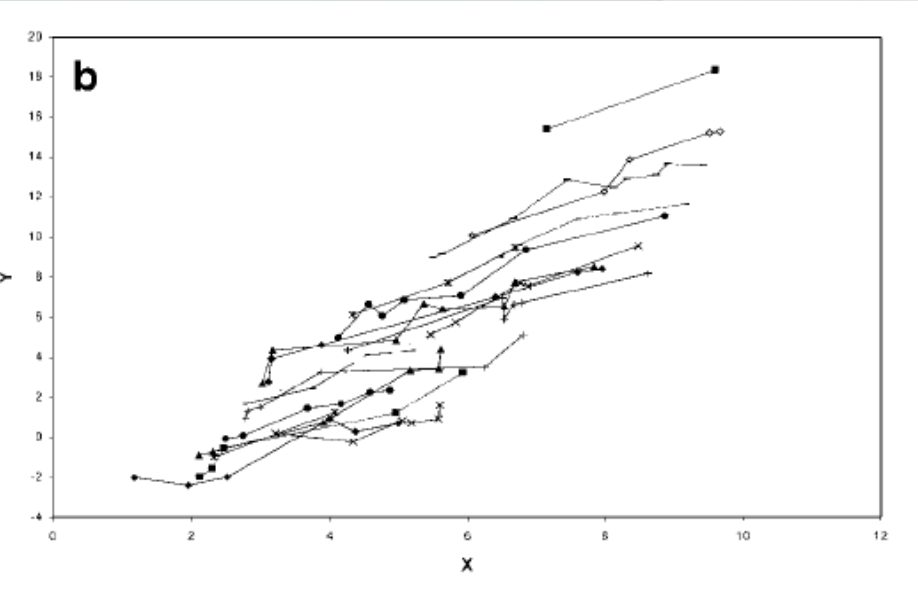
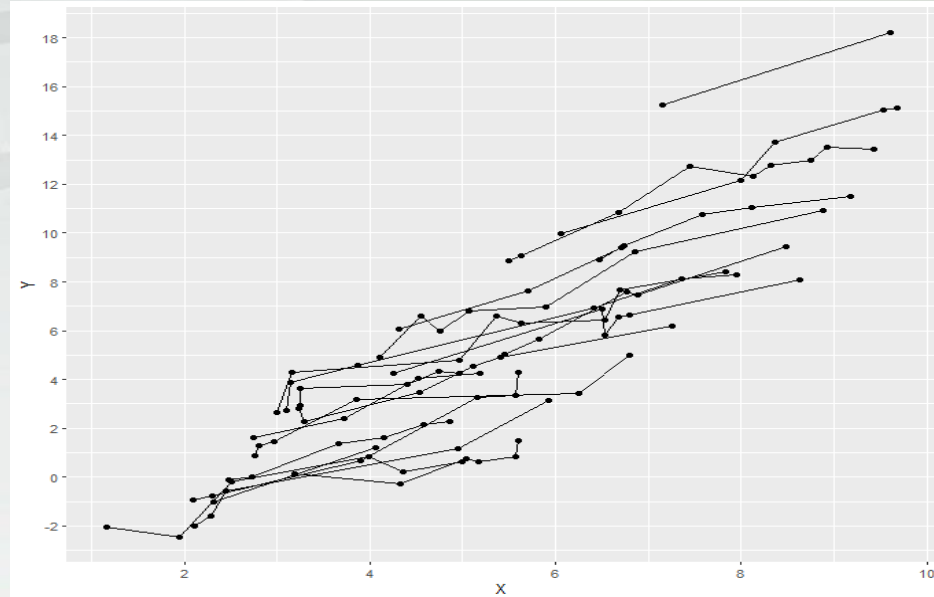


Figure 2b



Generated in R lab



Each line above corresponds to a different study

Goal: to *meta*-estimate the overall intercept ( $\beta_0$ ) and slope ( $\beta_1$ ) !



# Meta-analysis

EFFECT SIZE ( $z_i$ )

- Suppose we only had the study-specific slopes and estimates alongside with the standard errors (St-Pierre did not pursue this)
  - Each meta-analysis “data point” would be a duplet of (1) estimate and (2) std.error

##	Study	term	estimate	std.error	statistic	p.value	nrec
## 1	A	Intercept	-3.07734838	0.76656078	-4.01448711	1.593713e-02	6
## 2	A	X	0.81671421	0.22252478	3.67021698	2.138706e-02	6
## 3	B	Intercept	-4.15298434	0.63281610	-6.56270335	7.195518e-03	5
## 4	B	X	1.17586084	0.16301208	7.21333571	5.492902e-03	5
## 5	C	Intercept	-4.07597045	0.61009504	-6.68087785	2.609649e-03	6
## 6	C	X	1.39429265	0.13995723	9.96227671	5.702866e-04	6
## 7	D	Intercept	-1.80848842	1.09619111	-1.64979300	1.743302e-01	6
## 8	D	X	0.50088152	0.22415810	2.23450111	8.916425e-02	6
## 9	E	Intercept	-3.97906524	NaN	NaN	NaN	2
## 10	E	X	1.27253453	NaN	NaN	NaN	2

- Let's focus entirely on the slope estimates

Can't include Study E...only 2 datapoints!! No se!

# Sampling variances and weights

- Instead of std.error, these are more commonly used in meta-analysis software
- Sampling variance =  $\text{std.err}^2$  ( $s_i^2$ )  $s_i^2$ : Not to be confused with variance of data or residuals!
- Weight =  $(1/\text{std.err}^2)$  ( $w_i$ )  $w_i$ : “precision”
- So a duplet data point might be either one of the following:
  - estimate, sampling variance ( $z_i, s_i^2$ ) popular in meta-analysis software (metafor)
  - estimate, weight ( $z_i, w_i$ ) useful in mixed model analysis

## Common effects (CE) analysis

- Ignores study heterogeneity!



Assumes that variability between studies is simply due to sampling error!

- Working model:

- $Z_i = \zeta + \varepsilon_i$

Residual (within-study) variation

$$\varepsilon_i \sim N(0, s_i^2 = \frac{1}{w_i})$$

Unknown true effect size

- Weighted least squares estimate  $\hat{\zeta} = \frac{\sum_{i=1}^{n_{study}} w_i Z_i}{\sum_{i=1}^{n_{study}} w_i}$

with standard error  $se(\hat{\zeta}) = \sqrt{\left(\sum_{i=1}^{n_{study}} w_i\right)^{-1}}$

## Common effects (CE) analysis

- Three different sets of R codes provided to compute
  - 1. WLS estimate on previous slide.
  - 2. Using linear (mixed) models software
  - 3. Using `metafor` (popular R meta-analysis software package)
    - Option `method = EE`
    - **THIS SHOULD NOT BE YOUR FIRST OPTION!**

# Using linear models software to do CE analysis

(see Madden, LV, H-P Piepho and P.A. Paul. 2016. Statistical models and methods for network meta-analysis. *Phytopathology* 106:792-806)



- Common effect model  $z_i = \zeta + \varepsilon_i$   $\varepsilon_i \sim N(0, s_i^2 = \frac{1}{w_i})$

“Trick:” Same as fitting  $z_i = \zeta + \frac{e_i}{w_i}$   $e_i \sim N(0, \mathbf{1})$  **Hold constant to 1 in software**

Then specify  $w_i$  as a known weight function in the software (R or SAS)

- SAS is especially friendly for fixing variance components to constant values.
- `glmmTMB` seems to be the only R package that easily does this...but doesn't have as many modeling options as SAS.

# Mixed effects **univariate** meta-analysis

Meta-analysis statisticians bicker whether study is fixed or random

- Accommodates study heterogeneity!

Residual (within-study) variation

- Working model:

- $$z_i = \zeta + u_i + \varepsilon_i$$

Unknown true effect size

$$\varepsilon_i \sim N(0, s_i^2 = \frac{1}{w_i})$$

*Between-study heterogeneity:*

$$u_i \sim N(0, \tau^2)$$

In other words:

- $$z_i \sim N(0, \tau^2 + s_i^2)$$

**ONE SHOULD ALMOST ALWAYS EXPECT STUDY HETEROGENEITY!!**

# Mixed effects **multivariate** meta-analysis

- Jointly model study heterogeneity on two (or more) parameters.
  - e.g. **intercept** and **slope**...TOGETHER

$$\begin{bmatrix} z_{i1} \\ z_{i2} \end{bmatrix} = \begin{bmatrix} \zeta_1 + u_{i1} + \varepsilon_{1i} \\ \zeta_2 + u_{i2} + \varepsilon_{2i} \end{bmatrix}$$

Study specific squared  
standard errors

$$\begin{bmatrix} u_{i1} \\ u_{i2} \end{bmatrix} \sim N \left( \begin{bmatrix} 0 \\ 0 \end{bmatrix}, \mathbf{G} = \begin{bmatrix} \tau_1^2 & \tau_{12} \\ \tau_{12} & \tau_2^2 \end{bmatrix} \right) \quad \begin{bmatrix} \varepsilon_{1i} \\ \varepsilon_{2i} \end{bmatrix} \sim N \left( \begin{bmatrix} 0 \\ 0 \end{bmatrix}, \begin{bmatrix} s_{i1}^2 & 0 \\ 0 & s_{i2}^2 \end{bmatrix} \right)$$

- Meta-analysis software (e.g. `metafor` in R) having multivariate estimation capabilities will facilitate different specifications for  $\mathbf{G}$ .
  - Above  $\mathbf{G}$  is said to be “unstructured” (**UN**).

# Mixed effects (ME) analysis

- Workshop will generally present different sets of R codes provided to compute
  - 1. Using linear (mixed) models software
  - 2. Using `metafor` (popular meta-analysis software package)
    - Option method = REML
- Will demonstrate influence/outlier diagnostics with St-Pierre example.
  - Follows closely typical linear model applications.
- How do I know if ME is better than CE? -> Likelihood ratio test/AIC/BIC



## Recap on estimates of $\zeta$ ( $\beta_1$ in St-Pierre)

- Using mixed model (random coefficients) analysis of raw data (deleting two studies with 2 datapoints each)

```
##              Estimate Std. Error t value
## (Intercept) -0.78266    0.50278   -1.557
## X            1.08502    0.05775   18.787
```



Random coefficient  
("random regression")  
model

- Using CE analysis (metafor)

```
## estimate      se      zval      pval      ci.lb      ci.ub
## 1.0864 0.0317 34.3165 <.0001 1.0244 1.1485 ***
```

- Using mixed model analysis (metafor univariate)

```
## estimate      se      zval      pval      ci.lb      ci.ub
## 1.0810 0.0586 18.4410 <.0001 0.9661 1.1959 ***
```



- Using mixed model analysis (metafor multivariate)

```
##              estimate      se      zval      pval      ci.lb      ci.ub
## termIntercept -0.7954 0.4894 -1.6252 0.1041 -1.7546 0.1638
## termX          1.0820 0.0582 18.5847 <.0001 0.9679 1.1961 ***
```



# Validating meta-analytic models

- A good meta-analysis should lead to nearly the same estimates and standard errors as one would get using the correct model on the raw data.
  - Being able to simulate various experimental designs might be pedagogically helpful in that regard (we do that today!)
- Various R packages (`metafor`, `netmeta`) also provide example datasets that are useful to work through as well.
- Linear mixed models allow diagnostic checks as well.
  - **Should be based on studentized residuals.** Regular estimated residuals are not comparable between different studies.

# The completely randomized design

- We'll go through a similar exercise there!

$$y_{ijk} = \mu + \text{Study}_i + \text{Trt}_j + \text{Study} * \text{Trt}_{ij} + e_{ijk};$$

$$i=1,2,\dots, n_{\text{study}}, \quad j=1,2,\dots, n_{\text{Trt}}, \quad k=1,2,\dots, n_{\text{cow}_{ij}}$$

- $\text{Study}_i \sim N(0, \sigma_{\text{Study}}^2);$        $\text{Study} * \text{Trt}_{ij} \sim N(0, \sigma_{\text{Study} * \text{Trt}}^2)$

Study heterogeneity

Treatment effect heterogeneity

- $e_{ijk} \sim N(0, \sigma_e^2)$  between and within cow variability
  - Depending upon trait, one might actually anticipate extensive heterogeneity in VC across studies. Bayesian analyses on raw data then would be ideal

## Fit simple CRD for each study

- Two different sets of analyses to save from each study.
- Contrast-based:
  - Trt A vs Trt B mean difference  $(\hat{\mu}_1 - \hat{\mu}_2) \pm \text{standard errors}$  (**SED** =  $SE(\hat{\mu}_1 - \hat{\mu}_2)$  )
  - **Most popular in the meta-analysis methodology literature.**
- Mean-based (“Arm-based”)
  - Trt A mean  $\hat{\mu}_1 \pm \text{standard errors}$  (**SEM** =  $SE(\hat{\mu}_1)$  )
  - Trt B mean  $\hat{\mu}_2 \pm \text{standard errors}$  (**SEM** =  $SE(\hat{\mu}_2)$  )

Commonly pursued in  
animal/dairy science

## Contrast-based analyses

- Recommendation: **accommodate study-specific heterogeneity!**
- Same as shown previously for univariate analysis on slope (St-Pierre's example)
  - $z_i = \zeta + u_i + \varepsilon_i$

Residual (within-study) variation

$$\varepsilon_i \sim N(0, s_i^2 = SED^2 = \frac{1}{w_i})$$

In other words:

$$z_i \sim N(0, \tau^2 + s_i^2)$$

*Between-study heterogeneity:*  
 $u_i \sim N(0, \tau^2)$

# A comprehensive arm-based analysis

Popular R software (`netmeta`, `metafor`) converts arm-based to contrast based information before analyses

- Modeling extension needed relative to contrast-based analysis.

$$z_{ij} = \zeta_j + u_i + u\zeta_{ij} + \varepsilon_{ij}$$

*Between -study heterogeneity:*

$$u_i \sim N(0, \tau^2) \text{ (or fixed?)}$$

*Between -study*

*inconsistency:*  $u\zeta_{ij} \sim N(0, \omega^2)$

Unfortunately, many scientists don't consider this but most statisticians agree this is required

Residual (within-study) variation

$$\varepsilon_{ij} \sim N(0, s_{ij}^2 = SEM_{ij}^2 = \frac{1}{w_{ij}})$$

Recall the “trick”

Specify  $e_{ij} \sim N(0, 1)$  and weight by  $w_{ij}$

## An equivalent model to that on previous slide

- Multivariate specification...typically used in software packages

$$\begin{bmatrix} z_{i1} \\ z_{i2} \end{bmatrix} = \begin{bmatrix} \zeta_1 + u_{i1} + \varepsilon_{i1} \\ \zeta_2 + u_{i2} + \varepsilon_{i2} \end{bmatrix}; \quad \begin{bmatrix} \zeta_1 \\ \zeta_2 \end{bmatrix} = \begin{bmatrix} \mu_1 \\ \mu_2 \end{bmatrix}$$

$$\begin{bmatrix} u_{i1} \\ u_{i2} \end{bmatrix} \sim N \left( \begin{bmatrix} 0 \\ 0 \end{bmatrix}, \mathbf{G} = \begin{bmatrix} \tau^2 + \omega^2 & \tau^2 \\ \tau^2 & \tau^2 + \omega^2 \end{bmatrix} \right) \quad \begin{bmatrix} \varepsilon_{i1} \\ \varepsilon_{i2} \end{bmatrix} \sim N \left( \begin{bmatrix} 0 \\ 0 \end{bmatrix}, \begin{bmatrix} s_{i1}^2 & 0 \\ 0 & s_{i2}^2 \end{bmatrix} \right)$$

**CS** (compound symmetry) “reasonable” but several others available using either mixed model analyses (SAS or R) or R meta-analysis packages (`metafor`).

A multivariate parameterization allows us to explore alternative specifications to CS (see Madden et al., 2016; Phytopathology)

# Meta-analytic contrast versus arms-based analysis vs analysis of raw data

- Should all give you (nearly) the same answers!!

- Using Raw Data:

```
## contrast estimate      SE df t.ratio p.value
## A - B                -1.92 0.475 24  -4.048  0.0005
```

- Contrast-based meta-analytic

```
## Estimate Std. Error z value Pr(>|z|)
## (Intercept) -1.9266      0.4752  -4.054 5.03e-05 ***
```

- Arms-based meta-analytic

```
## contrast estimate      SE df t.ratio p.value
## A - B                -1.93 0.475 48  -4.054  0.0002
```

25 simulated CRD studies

metafor leads to same test statistic but uses z-test (infinite df). This is typical of meta-analysis software. See code. SAS is more flexible



## Latin square designs across studies

$$y_{ijkl} = \mu + \text{Study}_i + \text{Trt}_j + \text{Study} * \text{Trt}_{ij} + \text{Cow}(\text{Study})_{ik} + \text{Period}(\text{Study})_{il} + e_{ijkl};$$

$$i = 1, 2, \dots, n_{\text{study}}; \quad j = 1, 2, \dots, n_{\text{Trt}}; \quad k = 1, 2, \dots, n_{\text{cow}_{ij}}; \quad l = 1, 2, \dots, n_{\text{period}_{il}}$$

$$\text{Study}_i \sim N(0, \sigma_{\text{Study}}^2); \quad \text{Study} * \text{Trt}_{ij} \sim N(0, \sigma_{\text{Study} * \text{Trt}}^2)$$

$$\text{Cow}(\text{Study})_{ik} \sim N(0, \sigma_{\text{Cow}(\text{Study})}^2); \quad \text{Period}(\text{Study})_{il} \sim N(0, \sigma_{\text{Period}(\text{Study})}^2)$$

$$e_{ijk} \sim N(0, \sigma_e^2) \quad \textbf{within cow variability}$$

# Contrast vs Arm based analysis

- Contrast-based analysis
  - With 3 or more treatments, more than one contrast then!
- Suppose focus was on A vs B contrast!
  - Two potential contrast-based strategies.
    1. Only consider univariate A vs B contrast analysis.
    2. Multivariate analysis considering ALL contrasts

## Contrast-based analysis.

- Univariate: same as before:  $z_i = \zeta + u_i + \varepsilon_i$   $\varepsilon_i \sim N(0, s_i^2 = \text{SED}^2 = \frac{1}{w_i})$   
*Between-study heterogeneity:*  
 $u_i \sim N(0, \tau^2)$

- Multivariate: Include other contrasts.
  - Suppose a three-treatment replicated Latin square

CS

$$\begin{bmatrix} z_{1i} \\ z_{2i} \\ z_{3i} \end{bmatrix} = \begin{bmatrix} \zeta_1 + u_{1i} + \varepsilon_{1i} \\ \zeta_2 + u_{2i} + \varepsilon_{2i} \\ \zeta_3 + u_{3i} + \varepsilon_{3i} \end{bmatrix} \quad \begin{bmatrix} \zeta_1 \\ \zeta_2 \\ \zeta_3 \end{bmatrix} = \begin{bmatrix} \mu_1 - \mu_2 \\ \mu_1 - \mu_3 \\ \mu_2 - \mu_3 \end{bmatrix} \quad \begin{bmatrix} u_{1i} \\ u_{2i} \\ u_{3i} \end{bmatrix} \sim N \left( \begin{bmatrix} 0 \\ 0 \\ 0 \end{bmatrix}, \mathbf{G} = \begin{bmatrix} \tau^2 & \tau_c & \tau_c \\ \tau_c & \tau^2 & \tau_c \\ \tau_c & \tau_c & \tau^2 \end{bmatrix} \right)$$

CS (compound symmetry) “reasonable” but several others available using either mixed model analyses (SAS or R) or R meta-analysis packages (`metafor`)

## Arm-based analysis.

Multivariate: Suppose a three treatment replicated Latin square

$$\begin{bmatrix} Z_{1i} \\ Z_{2i} \\ Z_{3i} \end{bmatrix} = \begin{bmatrix} \zeta_1 + u_{1i} + \varepsilon_{1i} \\ \zeta_2 + u_{2i} + \varepsilon_{2i} \\ \zeta_3 + u_{3i} + \varepsilon_{3i} \end{bmatrix} \quad \begin{bmatrix} \zeta_1 \\ \zeta_2 \\ \zeta_3 \end{bmatrix} = \begin{bmatrix} \mu_1 \\ \mu_2 \\ \mu_3 \end{bmatrix} \quad \begin{bmatrix} u_{1i} \\ u_{2i} \\ u_{3i} \end{bmatrix} \sim N \left( \begin{bmatrix} 0 \\ 0 \\ 0 \end{bmatrix}, \mathbf{G} = \begin{bmatrix} \tau^2 & \tau_c & \tau_c \\ \tau_c & \tau^2 & \tau_c \\ \tau_c & \tau_c & \tau^2 \end{bmatrix} \right)$$

Residual (within-study) variation

$$\varepsilon_{ij} \sim N(0, s_{ij}^2 = \frac{SED_{ij}^2}{2} = \frac{1}{w_{ij}})$$

*Between-study heterogeneity:* CS but many other options are available

Don't use SEM if cow treated as random because between-cow variation is "cancelled out" in treatment comparisons (see Piepho et al., 2012)

The arm-based analysis is “more correct” than the contrast based analyses given model on Slide 25 ((Piepho et al., 2012, Biometrics)).

- If  $\begin{bmatrix} u_{1i} \\ u_{2i} \\ u_{3i} \end{bmatrix} \sim N \left( \begin{bmatrix} 0 \\ 0 \\ 0 \end{bmatrix}, \mathbf{G} = \begin{bmatrix} \tau^2 & \tau_c & \tau_c \\ \tau_c & \tau^2 & \tau_c \\ \tau_c & \tau_c & \tau^2 \end{bmatrix} \right)$  for an arm-based analysis with  $\begin{bmatrix} \zeta_1 \\ \zeta_2 \\ \zeta_3 \end{bmatrix} = \begin{bmatrix} \mu_1 \\ \mu_2 \\ \mu_3 \end{bmatrix}$

- Then for a contrast-based analysis:

$$\begin{bmatrix} \zeta_1 \\ \zeta_2 \\ \zeta_3 \end{bmatrix} = \begin{bmatrix} \mu_1 - \mu_2 \\ \mu_1 - \mu_3 \\ \mu_2 - \mu_3 \end{bmatrix} = \begin{bmatrix} 1 & -1 & 0 \\ 1 & 0 & 1 \\ 0 & 1 & -1 \end{bmatrix} \begin{bmatrix} \mu_1 \\ \mu_2 \\ \mu_3 \end{bmatrix}$$

such that  $\begin{bmatrix} u_{1i} \\ u_{2i} \\ u_{3i} \end{bmatrix} \sim N \left( \begin{bmatrix} 0 \\ 0 \\ 0 \end{bmatrix}, \mathbf{G} = \begin{bmatrix} 1 & -1 & 0 \\ 1 & 0 & 1 \\ 0 & 1 & -1 \end{bmatrix} \begin{bmatrix} \tau^2 & \tau_c & \tau_c \\ \tau_c & \tau^2 & \tau_c \\ \tau_c & \tau_c & \tau^2 \end{bmatrix} \begin{bmatrix} 1 & -1 & 0 \\ 1 & 0 & 1 \\ 0 & 1 & -1 \end{bmatrix} \right)$

## Moderator variables

- Effects of parity, lactation stage, 2<sup>nd</sup> treatment factor, etc.
  - Could add them as additional model factors, including interaction with primary treatment factor
- But more care is needed with Latin squares compared to CRD.
  - e.g. Cows are blocks for treatments but experimental units for parity

# Network meta-analysis

- Suppose focus is on Treatment A vs B.
  - Some researchers will only focus on studies have both Treatments A and B.
  - Direct comparisons
- But suppose some studies include A vs C, some include B vs C.
  - Indirect comparisons between A and B: i.e.  $(A-C) - (B-C) = A-B$ .
- A network meta-analysis accommodates direct and indirect comparisons.
  - Particularly easier to do with arm-based rather contrast-based.
  - See code.
  - Systematic inconsistency: when direct  $\neq$  indirect comparisons

# Can I combine CRD and Latin square (and others) studies?

- Most certainly!
- Network-based arm analysis best suited to capture direct and indirect comparisons.
- Caution.
  - Sampling variances for CRD treatment means =  $s^2 = 1/w = \text{SEM}^2/2$
  - For all other designs, use  $s^2 = 1/w = \text{SED}^2/2$ 
    - Actually, just use  $s^2 = 1/w = \text{SED}^2/2$  FOR ALL DESIGNS!
- Infer upon potential systematic inconsistencies!
  - Effect of design (CRD or Latin Square) on treatment effects






EXECUTIVE OFFICE OF THE PRESIDENT  
OFFICE OF SCIENCE AND TECHNOLOGY POLICY  
WASHINGTON, D.C. 20502

August 25, 2022

MEMORANDUM FOR THE HEADS OF EXECUTIVE DEPARTMENTS AND AGENCIES

FROM: Dr. Alondra Nelson   
Deputy Assistant to the President and Deputy Director for Science and Society  
Performing the Duties of Director  
Office of Science and Technology Policy (OSTP)

SUBJECT: Ensuring Free, Immediate, and Equitable Access to Federally Funded Research

This memorandum provides policy guidance to federal agencies with research and development expenditures on updating their public access policies. In accordance with this memorandum, OSTP recommends that federal agencies, to the extent consistent with applicable law:

1. Update their public access policies as soon as possible, and no later than December 31<sup>st</sup>, 2025, to make publications and their supporting data resulting from federally funded research publicly accessible without an embargo on their free and public release;
2. Establish transparent procedures that ensure scientific and research integrity is maintained in public access policies; and,
3. Coordinate with OSTP to ensure equitable delivery of federally funded research results and data.

# My vision for the future

- Mature raw data repositories
  - Research reproducibility
  - Allow for Bayesian extensions.
    - Model distributions on variance components over studies. Better borrowing of information across studies on variance components.
    - Multivariate analyses involving multiple correlated traits over time.
  - Code also submitted!!