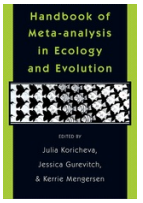

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13

Recovering Missing or Partial Data from Studies: A Survey of Conversions and Imputations for Meta-analysis

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META-ANALYSIS USES SUMMARY STATISTICS like effect sizes to combine information from multiple studies. Yet a common problem encountered when collecting information for calculating effect sizes is the absence of data from published studies. The incomplete reporting of means, correlations, variances, and sample sizes can bias meta-analysis in many ways: reviews will have smaller sample sizes because studies with missing data are often excluded (Orwin and Cordray 1985, Follmann et al. 1992); effect size metrics like Hedges' *d* are disfavored because they require too many within-study statistics; approaches to pooling effect sizes will use less restrictive statistical models such as unweighted analyses (Kelley et al. 2004, Furukawa et al. 2006); and meta-analysis may yield spurious results because excluding studies with missing information could further exacerbate publication bias.

In this chapter, I discuss possible solutions for dealing with partial information and missing data from published studies (Box 13.1). These solutions can improve the amount of the information extracted from individual studies, and increase the representation of data for meta-analysis. I rely heavily on advances and observations from the medical literature; this is necessary given that discussion relating to missing information has received limited attention in ecological and evolutionary meta-analysis (Lajeunesse and Forbes 2003). I begin with a description of the mechanisms that generate missing information within studies, followed by a discussion of how gaps of information can influence meta-analysis and the way studies are quantitatively reviewed. I then suggest some practical solutions to recovering missing statistics from published studies. These include statistical acrobatics to convert available information (e.g., *t*-test) into those that are more useful to compute effect sizes, as well as a few heuristic approaches that impute (fill gaps) missing information when pooling effect sizes (e.g., Follmann et al. 1992, Yuan and Little 2009). Finally, I discuss multiple-imputation methods that account for the uncertainty associated with filling gaps of information when performing meta-analysis.

DEFICIENCIES IN THE LITERATURE

The selective or variable reporting of statistics used to estimate effect sizes, such as means, variances, and sample sizes, can significantly affect meta-analysis and its reliability to synthesize research. A study may report a *t*-test that evaluates the difference between a control and treatment mean, but may not report information on the standard deviations or sample sizes of

BOX 13.1.
Classification of published studies based on what statistical information they lack, and suggested approaches to filling these gaps.

Usefulness for meta-analysis	Study statistics	What is available		Addressing what's missing
high	Completely reported	Has all the data for inclusion	→	Nothing missing!
	Selectively reported	All the data are available but not in forms that are easily integrated into meta-analysis (e.g., data in figures, sample sizes need to be determined from table, *t*-tests and means are not reported, etc.)	→	Extract data from figure or tables (see Chapter 5), convert available statistics (e.g., *t*-test into effect size)
	Partially reported	Has some data (e.g., sample sizes) but is missing information that cannot be estimated directly from what is available (e.g., variance estimates)	→	Recalculation or conversion of available statistics (back calculation from *P*-values), or within-study imputation methods.
	Qualitatively reported	No useful data except for *P*-values or discussion regarding the significance or non-significance of analysis	→	Recalculation of statistics, or use within-study imputation methods or multiple-imputation methods
low	Unreported	No statistics or data are available, although may have specified a protocol for the analysis in the Methods section	→	Exclude from meta-analysis or use an alternative approach to meta-analysis (e.g., vote-count methods)

these means. This is a challenge for meta-analysis because in order for this study to contribute any quantitative information to a review, an effect size must be computed to summarize its findings. Thus, extracting this missing information is important to maintain the scope of the review. I discuss below why there is missing information in published studies before outlining methods useful for recovering or imputing missing information.

Mechanisms that cause data to be missing

There are several mechanisms that can generate gaps of information in published studies. One is the perceived lack of importance. Chan, Hróbjartsson, et al. (2004) found that the lack of clinical importance was the primary reason why medical researchers omitted information from publications. Choosing to omit details of study design (e.g., sample sizes) or analyses ancillary to the main topic under study are examples of this type of reasoning. This also applies to excluding summary statistics such as variances and standard deviations—for example, where the statistical test itself (e.g., *t*-test) is thought to be more noteworthy for describing study outcomes. This issue is further exacerbated by the editorial policies of many journals aiming for brevity and imposing restrictions on the amount of information reported in the main research article (i.e., penalizing studies that overextend pagination with additional publication costs). For example, authors may exclude information when attempting to meet the requirements of editorial policies prior to submitting their research for publication—omitted information might include fully reported and annotated ANOVA tables. These restricted editorial policies often leave authors without any real incentive to fully report results (unless enforced later by referees as a condition of acceptance for publication).

When information is excluded this way, it is assumed to be missing at random, without being related to the outcome of the study. This is because inclusion/exclusion of this information may not affect the interpretation of the study outcome. A more serious nonrandom mechanism that can contribute to missing information is the lack of statistical significance. Chan, Hróbjartsson, et al. (2004) and Chan, Krleza-Jeric, et al. (2004) found that medical studies were half as likely to fully report statistics of nonsignificant outcomes as compared to the significant ones. In ecology, Cassey et al. (2004) also found that studies missing information tended to be nonsignificant or of lower quality. This type of nonrandom reporting is known as dissemination bias. Here, summary information of the data, results, and statistics are partially reported or excluded entirely (e.g., summarized with only a nonsignificant *P*-value), statistical assumptions are not fully addressed, or exact statistical procedures are unspecified (Hahn et al. 2000, Pigott 2001). Given that statistical significance is an important criterion for publication (or even whether the study is submitted for publication; Chapter 14), the motivations for why null research outcomes get less coverage in publications become apparent. For example, it is known that selective reporting of research findings—emphasizing strong positive or negative effects while understating nonsignificant findings—can significantly improve the chances of publishing (Chan, Hróbjartsson, et al. 2004). Yet, when the hypothesis is not falsified, it is unclear whether this outcome is due to errors in biological or statistical assumptions. For example, here it may be difficult to distinguish between a nonexisting biological effect and an existing effect that remains undetected because of low statistical power (Chapter 14). For meta-analysis, when there is dissemination bias for emphasizing significant results, and null outcomes are underreported in the primary research, then this has potential to generate biased review outcomes. This is because studies lacking information (which are more often null, see Cassey et al. 2004) will likely be excluded from the review, further exacerbating statistical problems associated with publication bias (see Chapter 14).

How does variable reporting of statistics affect meta-analysis?

In the previous section, I described mechanisms that contribute to incomplete reporting of statistics within studies. Here I examine how this lack of information can diminish the power of meta-analysis to detect nonzero research outcomes. One approach to handling studies with incomplete information is to exclude them entirely from the meta-analysis. Taken to this extreme, the variable reporting of statistics will decrease the sample size of meta-analysis. Small review sample size will reduce the power to detect significant research outcomes and the ability

to properly evaluate study heterogeneity (Chapter 22). In a Monte Carlo study that simulated studies with incomplete information (e.g., missing means, variances, or sample sizes), Lajeunesse and Forbes (2003) found that a stringent exclusion criterion has the potential to increase the likelihood of making a review level type II error (false negative). This is because meta-analysis, much like a primary study, is sensitive to sampling error when there are too few data for analysis. For example, small review sample sizes (much like small samples within studies) tend to underestimate or overestimate effect sizes, and yield broad confidence intervals (see Figure 22.2 in Chapter 22; Hedges and Olkin 1985).

Rosenthal (1991) refers to this relationship between the meta-analysis sample size and the ability to detect an effect as second-order sampling error; compared to the first-order sampling error of primary studies (Chapter 22). Still, second-order sampling error assumes that studies (irrespective of whether they are included or excluded from analysis) are a *random* sample of a population with common research outcomes. Clearly, publication bias is known to affect the random sampling of studies used in meta-analysis. For example, this occurs when nonsignificant or marginally significant research is less likely to be published and has minor representation in meta-analyses (e.g., file drawer problem, Chapter 14). What is less clear is whether the incomplete reporting of statistics and subsequent exclusion of such studies from meta-analysis can exacerbate this bias. This depends on whether the missing information within studies is omitted completely at random —that is, unrelated to any observed variable, including the missing statistic itself. In this case, the approach of excluding studies with incomplete information would not cause bias, or at least would not exacerbate publication bias, but would simply erode statistical power as predicted by second-order sampling error (Chapter 22).

However, as described earlier (Cassey et al. 2004; Chan, Hróbjartsson, et al. 2004; Chan, Krleza-Jeric, et al. 2004), there is empirical evidence to suggest that studies with partial information are not missing this information at random. It is known that studies with missing information are likely to be nonsignificant or of lower quality, although previous observations implied that they were not (Englund et al. 1999). In terms of meta-analysis, the selective reporting of statistics due to the study's outcome will certainly exacerbate publication bias; low-quality or nonsignificant study outcomes will be vaguely described and only contain partial information of the research. This has the potential to bias conclusions drawn from research syntheses because mostly significant findings with fully reported results are included in the meta-analysis.

A GUIDE TO HANDLING MISSING INFORMATION

I outline below various approaches to handling missing information from published studies. These methods are grouped under three approaches: (a) contacting researchers for missing data, (b) using algebraic recalculations and within-study imputations for estimating effect sizes and variances, and (c) using between-study imputation methods for filling gaps of information when pooling effect sizes. It is important to note that there will always be more uncertainty in the estimation of effect sizes and variances when approximations or imputation techniques are applied, as compared to the case of having a data set with fully reported information (Pigott 1994). However, relative to the alternative of excluding studies with missing information, the need to improve statistical power and issues relating to publication/dissemination bias far outweighs the increased uncertainty associated with imputed analyses.

Contacting researchers for missing data

Before using statistical approximations or imputing data, contacting authors of the publication for the original data is a good start to recovering missing information. Chapters 4 and 5 review

some of the aspects regarding this problem; these include approaches to increase reply success, and potential problems for authors retrieving these data (e.g., data are stored on outdated floppy disks). For example, Chan, Hróbjartsson, et al. (2004) found that multiple sequential questionnaires were required to get a reply from 90% of the primary researchers about missing information (though 80% of the researchers that replied to the first questionnaire denied the existence of missing information). Having access to the raw data is ideal for meta-analysis because precise estimates of effects and variances can be calculated, and sources of bias not described in the original publication can be investigated.

Algebraic recalculations, conversions, and approximations

Partial information can often be recovered by recalculating the available summary statistics or by using approximations when information is limited. For example, if a study reports only *P*-values, these can be calculated directly into *t*-tests or *F*-statistics, which then can be converted into effect sizes. Boxes 13.2 through 13.5 provide a roundup of useful equations to recalculate and convert what is available into various effect size metrics. For further information on this material or for additional examples of more complicated situations with incomplete information, see Fern and Monroe (1996), Glass et al. (1981), Gilpin (1993), Chinn (2000), Lipsey and Wilson (2001), Hozo et al. (2005), Pearson (1932), Wiebe et al. (2006), Rosenthal and Rosnow (1991), Terrell (1982), and Walter and Yao (2007).

These conversions and approximations, however, assume that the original data do not violate assumptions of normality (Lipsey and Wilson 2001). These equations are also limited by the numerical precision of the reported summary statistics, and the efficiency of these conversions and approximations become increasingly unreliable when too few digits are reported. Conversions from *P*-values are particularly sensitive to this problem (Philbrook et al. 2007). Unfortunately, equivalent statistical conversions and approximations for the log response ratio have yet been developed (Gurevitch and Hedges 1999, Hedges et al. 1999, Lajeunesse 2011b). Further, it is always a good practice to test whether studies summarized with conversions or approximations introduce bias to results (especially before pooling results to test ecological hypotheses). This can be evaluated with a sensitivity analysis that contrasts the magnitude and direction of effect sizes from studies with complete and incomplete (but converted) information.

Within-study imputation

When recalculations are impossible, imputation methods can be used to fill gaps of information in order to calculate effect sizes and their variances. To "impute" data means that the missing piece of information is filled with a substitute. For example, without information on the standard deviations (*SD*) of a study, effect size metrics like Hedges' *d* cannot be calculated directly (see definition in Box 13.2; Chapter 6). Imputation methods provide a way to filling this missing *SD* by either using the available data from other studies, or data from previously published meta-analyses. These imputation approaches can be useful given that the standard deviations of the control and treatment means are often not reported in primary studies.

One approach to estimating missing standard deviations is to use the available means ($\overline{X}$) and *SD* (e.g., from a control or treatment groups) from all the studies with complete information in order to calculate the coefficient of variation (e.g., the *SD* to mean ratio; Bracken 1992). For example, the missing *SD* of a given study (denoted with *j*) can be estimated with

$$\tilde{SD}_j = \overline{X}_j \left(\frac{\sum_i^K SD_i}{\sum_i^K \overline{X}_i} \right), \tag{13.1}$$

Box 13.2. Hedges' *d*

key terms

d	effect size
$\bar{X}$	sample mean
T and C	treatment and control groups
SD	standard deviation
n	sample size
J	bias correction factor
s	pooled SD

definition

$$d = \frac{(\bar{X}_T - \bar{X}_C)}{s} J \qquad J = 1 - \frac{3}{4(n_T + n_C) - 9}$$

$$s = \sqrt{\frac{(n_T - 1)SD_T^2 + (n_C - 1)SD_C^2}{n_T + n_C - 2}}$$

approximations

independent *t*-test

$$d = t\sqrt{\frac{n_T + n_C}{n_T n_C}} \qquad d = \frac{2t}{\sqrt{n_{total}}} \qquad d = t_R\sqrt{\frac{2(1 - r_R)}{n_{total}}}$$

n_{total} assumes that $n_T = n_C$, t_R = *t*-test from repeated measures, r_R = corr. between measures

correlation (r)

$$d = \frac{r}{\sqrt{1 - r^2}}\sqrt{\frac{n(n-1)}{n_T n_C}} \qquad d* = \frac{2r}{\sqrt{1 - r^2}}$$

$n = n_T + n_C$, * indicates Cohen's d

F-ratio from one-way ANOVA

$$|d| = \sqrt{\frac{F(n_T + n_C)}{n_T n_C}} \qquad |d| = 2\sqrt{\frac{F}{n_{total}}}$$

n_{total} assumes that $n_T = n_C$

Z-score

$$d = \sqrt{\frac{Z\sqrt{n}}{1 - \sqrt{Z^2 n^{-1}}}}$$

$n = n_T + n_C$

Chi-square (2 x 2 χ^2)

$$d = \sqrt{\frac{\chi^2(n_T + n_C)}{n_T n_C}}$$

imputations and conversions

s (pooled SD)

t-test

$$s = \frac{\bar{X}_T - \bar{X}_C}{t\sqrt{\frac{n_T + n_C}{n_T n_C}}}$$

Mann-Whitney P-value

$$s = \frac{\bar{X}_T - \bar{X}_C}{t(P, df^*)\sqrt{\frac{1}{n_T} + \frac{1}{n_C}}}$$

two-way (factorial) ANOVA

$$s = \sqrt{\frac{SS_B + SS_{A\times B} + SS_e}{df_B + df_{A\times B} + df_e}}$$

one-way ANOVA

$$s = \sqrt{MS_e}$$

one-way ANOVA with g groups

$$s = \sqrt{F^{-1}\frac{\sum n_j \bar{X}_j^2 - \frac{(\sum n_j \bar{X}_j)^2}{\sum n_j}}{g - 1}}$$

ANCOVA

$$s = \sqrt{\left(\frac{MS_e}{1 - r^2}\right)\left(\frac{df_e - 1}{df_e - 2}\right)}$$

$t(P,df)$ = *t*-distribution (Φ), MS = mean squares, e = error, df = degrees of freedom, $df^* = n - 2$, SS = sums of squares, A and B are the model factors, $n = n_T + n_C$

MS_{error}

$$MS_e = \frac{MS_A}{F_A}$$

A = effect of interest

t-test

$$t = \Phi(P, df) \qquad t = \sqrt{F}$$

Φ = *t*-distribution in MS EXCEL as "=TINV(P,df)"
P = P-value, $df = n - 1$,
$n = n_T + n_C$

SD

$$SD = \sqrt{\text{var}} \qquad SD = \frac{IQR_U - IQR_L}{1.35}$$

~~$SD = \frac{SE}{\sqrt{n}}$~~ $\qquad SD = \frac{\text{MAX} - \text{MIN}}{\text{Pearson (1932)}}$

U = upper and L = lower inter-quartile ranges, MAX and MIN ranges, find appropriate values in Pearson (1932) for a given $n = n_T + n_C$

$\bar{X}_T - \bar{X}_C$

ANCOVA

$$\bar{X}_T - \bar{X}_C = \bar{X}_T^{\text{LSM}} - \bar{X}_C^{\text{LSM}} + \beta(\bar{C}_T - \bar{C}_C)$$

LSM = least squares (adjusted) means, C = covariate, β = regression slope with C

Correction: $SD = SE \times \sqrt{n}$

Box 13.3. Correlation coefficient (*r*)

key terms

r	Pearson product-moment correlation
x and y	variables under analysis
n	total sample size

definition

$$r = \frac{n\sum x_i y_i - \sum x_i \sum y_i}{\sqrt{[n\sum x_i^2 - (\sum x_i)^2][n\sum y_i^2 - (\sum y_i)^2]}}$$

conversions and approximations

linear regression

$$r = \beta\left(\frac{SD_x}{SD_y}\right) \quad \text{if } y = \alpha + \beta x$$

SD = standard deviation, α = intercept, β = slope

biserial r (r_b)

$$r \approx r_b$$

point-biserial r (r_{pb})

$$r_b = \frac{r_{pb}\sqrt{n_T n_C}}{u(n_T + n_C)}$$

u = ordinate of unit normal distribution (see Terrell 1982)

independent t-test

$$r_{pb} = \sqrt{\frac{t^2}{t^2 + n_T + n_C - 2}} \qquad r_{pb} = \sqrt{\frac{t^2}{t^2 + df}} \qquad |r_{pb}| = \frac{P}{\sqrt{P^2 + 4}}$$

df = degrees of freedom, $P = P$-value

Hedges' d

$$r = \sqrt{\frac{d^2 n_T n_C}{d^2 n_T n_C + n(n-1)}}$$

$n = n_T + n_C$

F-ratio of one-way ANOVA

$$|r_{pb}| = \sqrt{\frac{F}{F + n_T + n_C - 2}}$$

F-ratio of ANOVA > 2 groups

$$|r_{pb}| = \sqrt{\frac{SS_{\text{between}}}{SS_{\text{between}} + SS_{\text{within}}}}$$

SS = sums of squares

Chi-square

$$|r| = \sqrt{\frac{\chi^2}{n}}$$

$n = n_T + n_C$

Z-score

$$r = \frac{Z}{\sqrt{n}}$$

$n = n_T + n_C$

odds-ratio

$$r = \frac{n_T^A n_C^B - n_C^A n_T^B}{\sqrt{(n_T^A + n_C^A)(n_C^B + n_T^B)(n_T^A + n_T^B)(n_C^A + n_C^B)}}$$

see Box 13.4

coefficient of determination (R^2)

$$|r| = \sqrt{R^2} \qquad r = \frac{\beta\sqrt{R^2}}{|\beta|}$$

β= regression slope

Spearman's rho rank corr. (ρ)

$$r = 2\sin\left(\frac{\pi\rho}{6}\right), \text{ if } n < 90; \quad r = \rho, \text{ if } n \geq 90$$

Mann-Whitney U

$$|r_{pb}| = \frac{1 - 2U}{n_T n_C}$$

Kendall's tau rank corr. (τ)

$$r = \sin\left(\frac{\pi\tau}{2}\right)$$

where $\overline{X}_j$ is the observed mean of the study with missing information, and K is the number of jth studies with complete information. Hereafter, variables accented with ~ indicate the estimate to be imputed when calculating an effect size (see definitions in Boxes 13.2 through 13.5). This approach assumes that the *SD* to mean ratio is at the same scale for all studies (Wiebe et al. 2006), and this assumption should be explored for ecological and evolutionary meta-analyses given that experimental scales can differ tremendously between different taxonomic groups or experimental designs.

Box 13.4. Odds-ratio

key terms

OR	odds-ratio (2 X 2 contingency table)
n	cell frequencies
T and C	treatment and control cell groups
A and B	cell groups A and B

	A	B
T	n_T^A	n_T^B
C	n_C^A	n_C^B

definition

$$OR = \frac{n_T^A n_C^B}{n_C^A n_T^B}$$

approximation

group proportions (P)

$$OR = \frac{P_T^A P_C^B}{P_C^A P_T^B}$$

Box 13.5. *Z*-score

key terms

Z	Z-score
T and C	control and treatment groups
$\overline{X}$	mean
SD	standard deviation

definition

$$Z = \frac{\overline{X}_T - \overline{X}_C}{SD_C}$$

conversions and approximations

Hedges' d

$$Z = \frac{d}{\sqrt{n(d^2+4)}}$$

$n = n_T + n_C$

Correlation coefficient (r)

$$Z = \frac{1}{2}\exp\left(\frac{1+r}{1-r}\right)$$

t-test

$$Z = \frac{t\sqrt{n}}{t+\sqrt{n-1}}$$

$n = n_T + n_C$

Mann-Whitney U

$$Z = \frac{U - 0.5(n_T n_C)}{\sqrt{\frac{n_T n_C (n+1)}{12}}}$$

$n = n_T + n_C$

Kendall's tau rank corr. (τ)

$$Z = \frac{\tau}{\sqrt{\frac{2(2n+5)}{9n(n-1)}}}$$

$n = n_T + n_C$

Another approach to imputing missing data uses regression techniques to predict the missing value given the relationship observed among the statistics of studies with complete information (Buck 1960, Pigott 1994). For example, if a study reports sample sizes but is missing information to calculate a pooled standard deviation s (see definition of Hedges' d in Box 13.2), then a prediction of s can be estimated from linear regression between the observed sample size (n), and s from the studies with complete information. This assumes that n is a good predictor of s. Using the regression equation estimated from studies with complete information, the s of a study with missing information is estimated with:

$$\tilde{s}_j = \alpha + \beta(n_j), \tag{13.2}$$

where α is the intercept and β the slope of the linear regression model of n versus s, and n_j is the observed sample size of the study with missing information. Of course, a nonlinear model or any number of covariates can be included in the model in order to improve the efficiency of the regression to predict missing values.

A comparable approach to the regression method is described by Ma et al. (2008), where missing pooled standard deviations are estimated using information from the other studies in the meta-analysis with complete information. Here, the s of the study with incomplete information is estimated as follows:

$$\tilde{s}_j = \frac{\sum_i^K s_i \sqrt{n_i}}{K\sqrt{n_j}}, \tag{13.3}$$

where K is the number of studies with complete information on s and n. This approach uses sampling theory to predict the expected s (see further details in Ma et al. 2008). Alternatively, Follmann et al. (1992) and Furukawa et al. (2006) describe a more impartial estimate of s (independent of the data used in the meta-analysis) that is derived from a previously published meta-analysis based on similar data. This approach can also be used when information on s is not available for any study. Here, the variances (σ^2) and sample sizes of effect size from each study are used to estimate s as follows:

$$\tilde{s}_j = \sqrt{\frac{\sum_i^K [(n_i - 1)\sigma_i^2]}{\sum_i^K (n_i - 1)}}. \tag{13.4}$$

These approaches to generating imputations for $\tilde{s}_j$ when estimating effect sizes are based on several assumptions. For example, they assume some degree of homogeneity among the observed *SD* and $\overline{X}$ values across studies. Furthermore, unlike effect sizes, imputations are not scaleless estimates; rather, they retain their original units. If there is large variation among estimates, which will be the case when meta-analyses pool research from different species or different measurements of the same ecological of evolutionary construct (e.g., fitness estimated as clutch size or offspring survival), then this may bias imputations. These approaches also assume that information is missing at random and not due to (nonrandom) reporting biases. Unfortunately, it is nearly impossible to test the above assumption in data sets. It is also important to consider that these regression based techniques assume that the missing observations are estimated perfectly by the model. Below, I describe multiple-imputation methods that attempt to account for the error associated with filling gaps of information when observed data are used as the basis for imputation.

Multiple-imputation

Multiple-imputation methods use a random sampling approach to fill gaps of information (Rubin and Schenker 1991). Here, gaps of missing data are filled by sampling the population of observed (available) data, or by sampling a distribution modeled from these available data. These sampling regimes are then repeated and averaged to give an overall "imputed" synthesis. This repetition of sampling is where the "multiple" of multiple-imputation is derived from, because data are filled multiple times to generate complete data sets. These multiple-imputation methods retain the benefits of single-imputation methods where a traditional meta-analysis is performed on imputed data sets. However, they have the advantage that the variability associated with imputing data is explicitly modeled when randomly sampling data; this avoids

treating the imputed values as true observations as in single-imputation approaches. For example, the regression approach described with Equation 13.2 does not include the error associated with intercept (α) and slope (β) estimates. Multiple-imputation methods can account for this source of error.

The most intricate aspect of multiple-imputation methods is the way the data are sampled to fill the gaps of missing information. These sampling procedures can apply maximum likelihood or Bayesian models for imputing data (for further details, see Schafer 1997, Little and Rubin 2002), and require specialized software to hypothesize the distributions of missing data and to perform analyses. For illustrative purposes, I describe the simplest sampling model, known as "hot deck" imputation; this involves sampling data to fill gaps of missing information from the observed data derived from studies with complete information. As in the imputation example described earlier, I will explore the situation where a data set is missing several *SD* for calculating the pooled *s*, in order to estimate an effect size. Here a collection of random samples of *s* are first drawn (with replacement) from the total collection of (available) *observed s*. For example, if there are 4 of 30 studies missing *s*, then four *s* will be sampled from the 26 studies with information. These random samples will form a collection of *possible* samples for the missing data. Then a second random sampling (again with replacement) from this collection of *possible s* will generate the data used to fill the gaps of missing information. The imputed data are sampled from the collection of *possible* rather than *observed* values of *s,* because this will create between-imputation variability among the imputed data sets. These random samples of *s* are then imputed to fill the gaps of missing information in order to form a complete data set, and the whole process is repeated to generate *m* number of complete (but randomly filled) data sets.

After *m* complete data sets are generated, a pooled effect size $\bar{\delta}$ and variance $\sigma^2(\bar{\delta}_l)$ is calculated for each data set using traditional meta-analysis (Chapters 8 and 9). The results of each meta-analysis are then averaged into an overall effect size ($\dot{\delta}$) with a variance of $\sigma^2(\dot{\delta})$. Each *l*th result of *m* meta-analyses are pooled using Rubin's average:

$$\dot{\delta} = \frac{\sum_{l=1}^{m} \bar{\delta}_l}{m}, \tag{13.5}$$

which has a variance of

$$\sigma^2(\dot{\delta}) = \frac{\sum_{l=1}^{m} \sigma^2(\bar{\delta}_l)}{m} + \left(1 + \frac{1}{m}\right)\frac{\sum_{l=1}^{m} (\bar{\delta}_l - \dot{\delta})^2}{m - 1}. \tag{13.6}$$

These results are then treated as the final meta-analysis. Similarly, the total homogeneity test (Chapters 8 and 9) is also averaged across *m* number of data sets as:

$$\dot{Q} = \frac{\sum_{l=1}^{m} Q_l}{m}. \tag{13.7}$$

There is also a general guideline for how many repetitions (*m*) are necessary to get a good estimate of $\dot{\delta}$ and variance $\sigma^2(\dot{\delta})$ that accounts for the between-imputation variability. Surprisingly, these recommended repetitions are few, and Rubin and Schenker (1991) suggest that if 30% of the data are missing, then an *m* of three is sufficient; whereas when 50% of the data are missing, then at least an *m* of five would be necessary. This guideline assumes that the review sample size is large (e.g., $K > 20$) and that there are more studies with complete information than studies missing information. However, given that this technique applies a random sampling approach, many more repetitions ($m > 100$) should be performed, thereby avoiding the sensitivity of resampling techniques to outliers when few replications are performed.

Nonparametric analyses and bootstrapping

An explicit definition of meta-analysis is (a) quantifying research outcomes using effect sizes, and (b) weighting of these effect sizes based on their relative sensitivity to sampling error. Imputation methods are useful to fill gaps of information when estimates of standard deviations are missing (see above). However, when most studies lack information about *SD*, then an effect size metric that does not require *SD* can be paired with a nonparametric bootstrapping approach that uses a simplified weighting scheme. For example, the log response ratio (ln*R*; Gurevitch and Hedges 1999; Chapter 6) is a less restrictive alternative to Hedges' *d* because it only uses the means to calculate an effect:

$$\ln R = \ln\left(\frac{\overline{X}_T}{\overline{X}_C}\right). \tag{13.8}$$

If the standard deviations are available then calculating an effect with Hedges' *d* is preferred (Lajeunesse and Forbes 2003). When standard deviations are missing, but sample sizes are available, then the inverse of a simplified estimate of the variance can be used to weight studies during the meta-analysis (Hedges and Olkin 1985):

$$\sigma^2(\ln R) = \frac{n_T n_C}{n_T + n_C}. \tag{13.9}$$

Bootstrapping methods are then used to estimate the 95% CI around the pooled mean. See Adams et al. (1997) for further details on this approach. However, it should be cautioned that this is a very crude surrogate for traditional meta-analysis (e.g., using the nonsimplified variances of effect sizes for Equation 13.9), and should never be performed as a shortcut to avoid having to extract *SD* from each study. This approach should only be used as a last resort when *SD*s (or standard errors) are impossible to extract from the majority of studies.

EFFECTS OF IMPUTATIONS ON THE OUTCOME OF REVIEWS

Imputation methods are used to fill gaps of information in meta-analysis by using the data already available from studies that have fully reported statistics. These methods can range from simple to very sophisticated models, but because there is a lack of a standardized protocol for implementing the methods, there is the concern that using some models rather than others will introduce bias or generate misleading results (Riley et al. 2004). However, Rubin and Schenker (1991) argue that for most cases of missing information, time and resources should not be focused toward implementing the most sophisticated models, and these advanced methods are mostly useful when a large number of studies lack information. To put this in perspective, Rubin and Schenker (1991) describe the following hypothetical example about the potential for bias (I have modified this slightly for our theme of meta-analysis). If the imputation method does not introduce bias for 75% of the cases of missing information, and there is a deficiency of information in 20% of the studies, then there is a 25% likelihood that imputations will introduce bias in 20% of the information. In this case, the meta-analysis will then only have a 5% bias due to imputation, leaving the remaining 95% of studies unbiased. If there is continued scepticism of the results obtained using imputation methods, then it has been suggested that studies with imputed information could be further downweighted during meta-analysis (Rief and Hofmann 2009). Alternatively, the appropriateness of imputing data into the overall analysis can be evaluated with a sensitivity analysis where imputed studies are included/excluded to assess overall bias (see Riley et al. 2004, Barzi and Woodward 2004).

Despite the potential for bias, reviews applying imputation methods will have improved variance estimates (e.g., smaller 95% CI) over reviews excluding studies with missing information (Philbrook et al. 2007). These improved variance estimates are due to inclusion of more studies when pooling results compared to a review that simply excludes studies with incomplete information (Chapter 22). Further, imputation methods can also potentially improve the representation of null studies or studies from underrepresented moderator groups. Multiple-imputation methods have an additional benefit of providing more conservative results than approaches based on direct within-study imputations (Riley et al. 2004). This is important given that within-study imputations explicitly treat imputed data as real data, and that not accounting for the uncertainty associated with imputed data can result in an underestimation of the pooled variance (Pigott 2001).

CONCLUSIONS AND FUTURE DIRECTIONS

Many of the challenges associated with a lack of information in the literature can be avoided entirely with thorough reporting of means, correlations, standard deviations, and sample sizes of experiments. To address these gaps of information and to establish a uniform reporting standard for journal publications, the medical sciences launched the CONSORT initiative (CONsolidated Standards Of Reporting Trials; see Moher et al. 2001). This initiative provides guidelines for reporting statistics and data in publications, consisting of a 22-item checklist and a flow diagram to help improve the clarity and transparency of the study. Further, the NIH (National Institutes of Health) has an online database (see www.clinicaltrials.gov) where protocols and results of funded studies must be registered (even when the study is not published). This resource is important to help address publication bias while also allowing for the quick recovery of missing information within publications.

Given that many ecological and evolutionary journals have pagination limits and are increasingly pushing for brevity, a standardized guideline would also serve these fields tremendously. This guideline would not only facilitate data extraction for meta-analysis, but would also increase the reliability and repeatability of primary data analysis. Electronic appendixes have improved the availability of data useful for meta-analysis and have made it easier to publish results and findings tangential to the main article. However, the accessibility of this information is still mostly dependent on the reporting practices of the author and on post-submission editorial/reviewer decisions. With a standardized guideline, authors would submit manuscripts that are fully reported and annotated prior to review. This information can then be moved to electronic appendices when necessary. The prospective registration of data sets and supplementary material of published studies is also an emerging alternative (e.g., see DRYAD at datadryad.org). In fact, many journals are adopting policies that encourage authors to submit raw data to these databases. However, to date, the registration of data in freely accessible databases has had limited success; it may require further work for authors to organize data and the usefulness of these data is limited to how well they are annotated (e.g., description of organization and data manipulations).

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