Causal inference with observational data in the presence of unmeasured confounding drivers

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**Code Repository:** <https://github.com/jebyrnes/ovb_yeah_you_know_me>

**App for one simulated dataset:** <https://shiny.umb.edu/shiny/users/jarrett.byrnes/shiny_ovb/>

**App for replicate simulations:** <https://shiny.umb.edu/shiny/users/jarrett.byrnes/ovb_sims/>

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**Abstract**

As ecology tackles progressively larger problems, we have begun to move beyond the scale at which we can conduct experiments to derive causal inferences. Experiments have long been seen as the gold standard for quantifying causal effects in ecological systems. Large-scale observational data, in contrast, has largely been used to either explore ideas derived from experiments or a source of interesting patterns to inspire randomized controlled experiments This avoidance of using observational data for causal conclusions arises from the valid fear of results of unmeasured confounding variables in observational analyses. Unmeasured confounders that influence both the causal variable of interest and effect can bias conclusions - a problem known as Omitted Variable Bias. This phenomenon is what leads to the old saying, “Correlation is not causation.” Many other scientific disciplines, however, cannot do experiments for reasons of ethics or feasibility; they have developed robust approaches for causal inference from observational data. Here we show how Ecologists can harness these tools to derive causal inference from observational data. We begin with the cornerstone of causal inference: using causal diagrams to identify potential known and unknown sources of confounding. We then use a motivating example of assessing the effects of warming on intertidal snails to discuss how ecologists currently handle observational survey data and inference - often incorrectly. We present alternative sampling designs and the statistical designs that make use of them, discuss how they work using the language of causal path diagrams, demonstrate how easily they can be applied to common ecological datasets, and finally how well they are able to overcome problems of unmeasured confounding variables. We present these tools in the hopes that others will pick them up and begin to apply them to their own science as an important complement to experiments for generating meaningful insights into ecological systems.

**Introduction**

As Ecology advances to tackle problems at scales from the continental to global, we are putting our theories to empirical test like never before – working at larger scales in space and time and with unprecedented streams of data. To address fundamental questions in Ecology with these data, we desire to answer questions about causal relationships - either to test basic theory at scale or inform conservation and resource management. Classically in Ecology, understanding causal relationships between variables in nature has been the domain of experiments. Experiments, however, have limitations for generalizing to larger scales and contexts beyond study conditions. As Ecology seeks to address theory and application at scale, we must rapidly move beyond a scale where ideal randomized experiments are possible (reviewed in Kimmel *et al.* 2021), and instead must be able to seize the opportunity of new large-scale sources of observational data.

Our ability to test hypotheses about causal relationships in observational data is limited by two fundamental challenges. First, nature is complex! When we use observational data to attempt to answer causal questions, we face numerous **confounding variables** – variables correlated with the cause and the outcome of interest – that can lead to incorrect estimates of causal effects (Fig. 1). Leaving out confounding variables from an analysisleads to **bias** in our estimate of the relationship between a predictor and its response; the estimate will not be equal to its true value. Even when we know confounders to account for, collecting all data needed to account for each and every one is likely impossible. Second, as humans, we are limited by our ability to imagine how the different elements of complex ecological systems are related. Thinking through the entirety of the natural history of a system to build an analysis of observational data that will enable credible causal inferences is really hard. As a result, causal inference from observational data is often dismissed as impossible due to the potential for spurious correlations, leading to the common saying “correlation is not causation,” and the presentation of the correlation between number of pirates and global average temperature as a cautionary tale of the dangers of observational data. At the core, though, inferring causation from correlations centers on handling the problem of unmeasured confounding variables that influence both a causal variable and the response of interest (Fig. 1).

A diagram of a driver causing a variable bias

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**Figure 1.** A response variable of interest (Y) is driven by both a measured variable (X) and an unmeasured variable (U) as well as other uncorrelated sources of residual variability (e). In one scenario (A), X and U are uncorrelated, and thus the lack of inclusion of U in a statistical model increases the standard error of the estimate of the effect of X on Y, but does not alter the causal identification of the statistical model. However, if U also drives X (B) , or if U and X are driven by a common driver Z (C) the omission of U from a statistical model causes bias in the estimate of the effect of X on Y. The direction of the bias in the estimator depends on the effect of U on Y, with the result that the causal effects are of X on Y are either over- or under-estimated, masking or mimicking a causal effect.

Excluding known but unmeasured, or unknown and unmeasured, confounding variables from an analysis creates what is known as **omitted variable bias** (Rinella *et al.* 2020; Wooldridge 2015). Omitted variable bias (OVB) could be positive or negative. Omitted confounding variables could occur because of missing measurements or due to failures of imagination – simply because we do not yet know confounding variables that are important. For example, one might measure plant communities to study competition, but not measure all the soil abiotic properties that drive all species due to financial or time constraints. Similarly, working with long-term survey data or in human impacted systems, missing data on confounding variables is common, such as when using historical measures of fish abundance to study the impacts of changes in biogenic habitat availability, without measurements of fishing pressure during the same time-period. We have no way of knowing the direction or magnitude of the bias, because knowing all possible confounding variables and their relationships in a system is hard, if not impossible. Measuring, controlling for, or even knowing all potential confounding variables is nearly impossible in complex ecological systems (*reviewed in* Dee *et al.* 2023). In short, in observational data collection and analysis, we are always going to miss something, threatening the validity of our causal inferences.

*Do these challenges mean that we should not try to use observational data for causal inference?* We argue no. Rather than throwing up our hands, discounting and abandoning the use of observational data for causal inference, we suggest that ecologists consider adopting techniques from other disciplines that cannot do experiments – often for logistical or ethical reasons. For instance, it is not ethical to make a person smoke cigarettes daily to test the causal effect of smoking on dementia (Hernan & Robins 2023); one can only manipulate curricula so far in an effort to understand educational outcomes. Thus, disciplines such as psychology, economics, education, epidemiology, sociology, computer science, and more have been building tools to handle OVB in the causal analysis from observational data for decades (Angrist & Pischke 2008; Heckman 2000; Hernan & Robins 2023; Holland 1986; Imbens & Rubin 2015; Morgan & Winship 2015; Pearl 2009; Robins 1989; Rubin 1974, 2005). Some of these tools were even at the center of the 2022 Nobel prize in Economics.

As ecologists, we have a decades-long tradition of considering experiments as a gold standard for causal inference (Benedetti-Cecchi & Cinelli 1997; Carpenter *et al.* 1985; Gotelli & Ellison 2012; Kimmel *et al.* 2021; Lubchenco 1980; Paine 1966; Power 1990; Reichman 1979; Silvertown *et al.* 2006; Underwood *et al.* 1997). However, experiments also rely on assumptions (Kimmel *et al.* 2021), which can be hard to meet in the field, induce artefacts, or rely on conditions that make them hard to generalize to natural ecosystems. Further, this reliance on the primacy of experiments has meant that the tools of other disciplines have been largely absent from the ecologist’s toolbox (but see Butsic *et al.* 2017; Grace 2021; Kendall 2015; Larsen *et al.* 2019; Rinella *et al.* 2020; Shipley 2016 for example). Recently, though, there is a growing interest and use of causal inference in ecology for observational data, including by drawing on a diverse suite of methods from the field of casual inference (Arif & MacNeil 2022, 2023; Dee *et al.* 2023; Dudney *et al.* 2021; Grace & Irvine 2020; Larsen 2013; Larsen *et al.* 2019; MacDonald & Mordecai 2019; Simler-Williamson & Germino 2022). If we are, as a discipline, to move to more widespread use of observational data for causal inference, then we need to carefully consider the problems of such approaches and the techniques we can use to mitigate them.

Here, we aim to provide a guide to readily available ways to cope with Omitted Variable Bias (OVB) for Ecologists. We begin by briefly describing the status quo for how ecologists most often deal with omitted variable bias and associated limitations. After, we review tools for identifying potential sources of omitted variable bias, building on foundation of using directed acyclic graphs that has become increasingly common in ecology (Arif & MacNeil 2023). We then outline sampling and statistical model designs for dealing with omitted variable bias. Most of these statistical model designs are underutilized, if not novel, for ecology. To illustrate problems with OVB and different ways to identify and address it, we present a motivating example that aims to quantify the causal effect of temperature on marine snail abundances. With this example, we demonstrate the conclusions that would be drawn from the typical approaches an ecologist might take with this data (e.g., random effects in a mixed model, *see* Bolker et al. 2009) – and why they fall short of dealing with OVB (i.e., have statistical bias) – compared to several other statistical model designs that can more adequately control for omitted variable. We then present results from simulation analyses showing that these designs – which have seen limited adoption in ecology – are more robust to OVB (unbiased). We provide guidance for choosing among these designs for different data contexts and questions. Our goal is to enable researchers to advance the field of Ecology at scale using observational data.

**How are ecologists coping with Omitted Variables Bias?**

Omitted variable bias is commonly dealt with in one of four ways in Ecology. The first is using randomized controlled experiments. In an ideal, randomized controlled experiment, the effect of confounding variables is eliminated (but see Kimmel *et al.* 2021 on why this can be difficult), because of the random assignment of treatments to units, so that the treatment and control groups have the same level of any confounders on average. However, randomized controlled experiments, particularly at scale, are not always feasible. Second, in observational studies, ecologists primarily attempt to deal with confounding variables by measuring the confounder and controlling for it in a model. As described above, measuring all confounders, however, is often impossible, particularly for retrospective analyses of existing data. Further, all potential confounders in the system might not be known. Third, ecologists sometimes make causal claims rooted in their knowledge of the natural history of a system. These claims can be problematic due to a lack of transparency and potential for incorrect statements of effect size; even the knowledge of the most accomplished naturalist can have gaps in their understanding of a system. Finally, ecologists often qualify their results verbally to avoid making causal claims – even when their research focus is causal understanding, rather than description (but see Laubach *et al.* 2021 on causal aims and claims). This practice muddies the waters and can create confusion over whether an author claiming an association or implying causation while allowing themselves plausible deniability. We feel that given our current need to understand causal relationships from large-scale observational data sets, these solutions are not adequate, and can even lead to misleading inferences. Ecologists have an opportunity and, nay, obligation, to leverage (or at least consider) the solutions to Omitted Variable Bias in causal data analysis that other disciplines have been building for decades. This paper provides an entry point into several approaches and complements recent reviews of what are commonly referred to **quasi-experimental methods** (e.g., Antonakis *et al.* 2010; Arif & MacNeil 2022; Bell *et al.* 2018; Bellemare *et al.* 2020; Butsic *et al.* 2017; the appendices of Dee *et al.* 2023; Ferraro & Miranda 2017; Grace & Irvine 2020; Kendall 2015) by expanding on panel designs for accounting for OVB.

**​​Using DAGs to clarify our causal understanding and assumptions to ferret out Omitted Variables Bias**

Causal diagrams (a.k.a. Structural Causal Models from Grace & Irvine 2020; see Arif & MacNeil 2023 for in depth introductions for Ecologists) are one of the first tools for identifying and addressing omitted variable bias (Arif & MacNeil 2023; Pearl 1995; Pearl *et al.* 2016). Causal diagrams, or Directed Acyclic Graphs (DAGs), visualize our understanding of causal relationships and confounding variables within a system. In doing so, DAGs transparently clarify the assumptions on which one relies for making causal claims about relationships inferred from observed data, including by ruling out potential confounding variables. Critically, a causal diagram needs to include both measured and *unmeasured* confounding variables – and we argue it should be a requirement before conducting an analysis from which one wants to make any causal conclusions. Finally, causal diagrams can also show what variables you should *not* include in an analyses, such as those that cause collider bias – i.e., evaluating a relationship between two variables, but conditioning on something they both cause, such as looking for a relationship between disturbance intensity and herbivory intensity and conditioning on plant abundance, when the latter is caused by the two former (for an excellent discussion of this topic beyond the scope of this manuscript, see McElreath 2020 Chapter 6; Laubach *et al.* 2021; or see Griffith *et al.* 2020 for a Covid-19 example).

If possible, we recommend making a diagram *before* data collection to inform which covariates might be confounding and should be measured if possible. However, due to feasibility constraints or if analyzing pre-existing data, measuring all potential confounders might not be possible. Further, the data could have been collected for another purpose or question, so a set of confounders were deemed unimportant.

**Box 1: A Brief Overview of the Elements of Directed Acyclic Graphs for Causal Analysis**

We briefly review the uses and the elements of causal diagrams, such as the one included in Figure 1, called Directed Acyclic Graphs (DAGs) (Arif & MacNeil 2023; Grace & Irvine 2020; Laubach *et al.* 2021; Pearl 1995). For the variables and implied causal relationships (as paths), we adopt a symbology to differentiate between observed and unobserved variables to reveal where confounding variables might lurk. First, observed variables, things that can be or have been measured, are represented as terms within boxes, as for *X* and *Y* in Figure 1. Second, our DAG in Figure 1 shows *unobserved* (unmeasured) variables contained in ellipses, such as the variable *U.* The error term is shown as *e*. In the case of e - the error term - this is a collection of different variables and influences outside of the scope of analysis. We need not know what they are precisely, but we can trace a causal path between them and other variables in our causal diagram. Finally, variables are connected by paths - i.e., arrows. The direction of these arrows represents a direct causal connection going in the direction the arrow is pointed. This is fundamentally different than the “=” sign in an equation, as there is applied directionality. If the value of a causal variable of interest changes (i.e., via manipulation), there will be a concomitant change in the response variable(s) it affects. If a response variable changes, say via direct manipulation, there will be no associated change in the causal variable of interest.

A common critique is that DAGs do not include feedbacks, to which we respond by asking the reader to think of their definition of causality. Here we adopt the Neyman-Rubin counterfactual causality framework (Holland 1986; Rubin 1974, 2005) where we recognize that cause temporarily precedes effect. Therefore, feedbacks can be handled by thinking about a system with a temporal lag (e.g., Larson *et al.* 2008). If an instantaneous feedback is truly present (albeit rare), or if a time-series of both the driver and response variable is not available, one will likely require other tools such as instrumental variables - something beyond the scope of this manuscript (but see Kendall 2015 for an excellent introduction).

In this article, we emphasize how thinking in terms of graphical causal models helps to determine both where omitted variable bias (OVB) might cause problems in analyses as well as in identifying solutions. As applied researchers, we have found that, rather than creating confusion with complexity, graphical causal models paired with robust statistical approaches for causal inferences have often clarified our own thinking about ecological systems.

After building a DAG, as described in Box 1, one can determine potential sources of omitted variable bias from variables influencing both the cause of interest and outcome that have not been observed in the system (e.g., confounding unobservable variables, *U* in Fig. 1B). Not controlling for this confounding variable opens a “back-door” for causal information to flow between your causal variable of interest and its response variable via an unassessed pathway (Pearl 2009). In the case of Figure 1B, *U* would be folded into a statistical model’s error term. The model’s error term and causal variable of interest would be correlated, leading to a violation of a core assumption of Gauss-Markov, known as an endogeneity problem (Abdallah *et al.* 2015; Antonakis *et al.* 2010).

What is an endogeneity problem? Consider an example of evaluating the relationship between nitrogen availability and plant biomass across a series of fields. If nitrogen availability depends on field soil characteristics, and field soil characteristics also drive plant biomass, then 1) the effects of soil characteristics would be included in the error term so that 2) nitrogen is no longer an **exogenous** (external to the system of interactions) variable. Rather, it is **endogenous** – affected by elements in the error term, which is exogenous.We are no longer estimating the effect of nitrogen controlling for soils. This endogeneity of nitrogen means that the estimate of the nitrogen effect will be wrong – different from the true effect in magnitude or even sign. Note, as discussed below, making field a random effect does not resolve this problem. With random effects, we estimate the variance parameter of fields, not their means; when we estimate the nitrogen effect, the effect of soils differing by fields is not accounted for. Any time a predictor is correlated with random parts of the model – either the error term or random effects – a statistical model will have an endogeneity problem. By drawing a DAG, we can see where those endogeneity problems could be likely to occur.

Once one discovers an endogeneity problem, they can resolve it by including a variable in their analysis that blocks all paths between *X* and *Y* via *U*.This means that the ensuing analysis will satisfy the **back-door criterion** (Pearl 1995, Fig. 2A) – i.e., the endogeneity problem will be solved by controlling for the flow of information from the confounder to the response variable by “shutting the back door” to the error term. Depending on the causal structure of a system and data, there could be many confounding variables to measure and control for. Controlling for these measured confounders as covariates in a statistical model will “shut the back door” and enable causal identification (see Fig 2. and caption for several examples). Without including such confounding variables in a statistical model, this omitted variable will cause Omitted Variable Bias.

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**Figure 2.** Examples of satisfying the back-door criterion with control variables. By including shaded observed variables, either U or W, in a statistical analysis of the effects of X on Y, omitted variable bias is controlled for the results have a causal interpretation. The relationship between the control variable and Y might (A and B) or might (C and D) not have a causal interpretation, depending on the structure of the system. Note, in (D), Q would have also served as an adequate control instead of W. R would have been a bad control.

Understanding how and when to control for these confounding variables is difficult without a causal diagram. With a diagram in hand, it can either be visually obvious or one can utilize a variety of software for analyzing DAGs (e.g., Textor *et al.* 2016) to find “open back-doors” that need to be controlled for in order to eliminate omitted variable bias. Software can also help us identify variables we do not need to control for – e.g., colliders mentioned above or variables that are independent of our response conditioned on the predictors we are interested in (i.e., **conditional independence relationships**). One can evaluate multiple options and find the most efficient (in terms of sampling effort) variable or variables to measure to control for omitted variable bias. Perhaps, most importantly, one can justify their choice of control variables with a DAG, making their assumptions about how a system works before an analysis transparent to readers of their work in the literature.

A causal diagram is, therefore, the first step on the way for identifying potential omitted variable bias. On their own, however, they do not in and of themselves provide a means for statistically controlling for OVB, particularly if we have not measured the confounding variable. Nor does a causal diagram help us in the face of *unknown* confounding variables that we have failed to imagine as part of our system. To address both issues, we must consider the sampling design of our observational studies and how we build statistical models with the data to produce causally identified estimates. To illustrate these, let’s consider an example where we can build a DAG and then consider proper study design and statistical modeling approaches.

**A Problem of Omitted Snails**

To illustrate these empirical challenges and suite of potential solutions, we consider a marine benthic ecosystem, modeled after the Gulf of Maine, USA, where a researcher aims to study the causal effect of temperature on snail abundance. They hypothesize that temperature influences snail metabolic and mortality rates and wish to estimate its effect on snail population abundance. Snail population abundance also driven by recruitment. Regional oceanography (i.e., the flow of major currents and parcels of water that differ in a myriad of properties) drives both water temperature and recruitment. Let us assume that the researcher measured snail abundance and temperature at several sites, but not recruitment or any measurement of oceanography. Thus, recruitment and oceanography are unmeasured or so-called “unobserved” confounding variables that pose threats for bias. An analysis of just the temperature-snail relationship would likely provide biased answers – even answers that were of the wrong sign. Even if the researcher had measured recruitment, though, what if there are other lurking confounding variables? Even if oceanography or recruitment were accounted for, omitted variable bias remains a real possibility – and the estimation of the effect of temperature on snails will be incorrect. Fortunately, our researcher drew out a causal diagram of the system (Fig. 3) and recognized that temperature at the scale of their measurements was also influenced by local variation (e.g., small-scale oceanographic features, weather, or other sources of local or microclimatic variability). With this causal diagram in hand, they realized they could control for both observed and unobserved confounding variables with appropriate sampling and statistical model designs.

## **A black background with a white circle Description automatically generated with low confidence**

**Figure 3.** A system describing the controls of snail abundance in the intertidal. Oceanography drives both temperature and recruitment, both of which drive snail abundance. Temperature, however, is also driven by local influences as well. This could be variability in plot-level temperature within a site – i.e., sources of variation in microclimate - or site-level temperature variability over space or time uncorrelated with local oceanography, recruitment, or other site- or plot-level confounders.

## **Sampling Designs that enable statistical methods to cope with omitted variable bias**

Multiple sampling designs for data collection enable the use of statistical model designs that can address omitted variable bias from confounding variables that vary across space, time, or both. A key feature in these sampling designs is the **nesting** of multiple observations within a cluster or group (e.g. site), such that the causal variable of interest varies across replicates while the confounder varies at the cluster level (Fig 4). Clustered data is often also referred to as a hierarchical or nested sampling design. We use these terms interchangeably. Using our snail and temperature example, we outline different nested sampling designs and discuss how they generate different source of variation in space and time that enable the use of statistical model designs that deal with confounders.

Nested sampling designs can take several forms and generate difference types of variation to study. First, a sampling design could include plots that are sampled within sites that vary across an environmental gradient at a single point in time (Fig. 4A) – a **cross-sectional design**. When sites span large environmental gradients in a causal variable of interest, they also vary in their confounder(s) across the same spatial gradient. In our example (Fig. 3), a spatial gradient in temperature across sites reflects the spatial gradient in oceanography that affects both temperature and recruitment, thus confounding this causal relationship of interest between temperature and snails across sites. However, with data collected from a cross-sectional sampling design, we can use *within*-site variation in temperature to isolate its effect on snails rather than the variation *between* sites, which contains sources of confounding variation.

Second, one could sample the same plots (or sites) repeatedly through time (Fig. 4B) in a **longitudinal** or **panel data design**. This approach leverages variation within-sites through time. As such, longitudinal designs enable many approaches to remove the effects of confounding variables that vary across sites in a similar manner to cross-sectional designs. Thus, we do not need to rely on within-site variation at a single point in time as the signal of our causal variable of interest. Developing an understanding of these two designs and how they can be used to remove variation from confounders is key to confronting OVB and restoring causal identification to models with observational data. They – and further extensions in Box 2 and 3 – pair perfectly with a variety of statistical models to cope with OVB.

A diagram of a design

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**Figure 4.** Visualexamples of clustered/nested/hierarchical study designs with n = 3 per site. In these studies, sites are distributed along a coastline with a corresponding thermal gradient. However, they leverage spatial or temporal clusters to take advantage of temperature variation within sites in a cross-sectional study design (A) or temperature variation across time for a longitudinal (panel) design (B). Open squares are sites. Closed squares are plots within sites. Size of square is proportional to temperature.

## **Statistical Model Designs to Coping with Omitted Variables**

With data and a DAG in hand, there are multiple, well-established statistical model designs for analyzing clustered data to handle omitted confounders for causal analysis. We emphasize the term *‘designs*’ over *‘methods,’* because one could implement these model designs using different estimation approaches (e.g., linear regression, Generalized Linear Models, as a part of Structural Equation Models, or with Bayesian techniques). These statistical model designs have different costs and benefits, and they differ in their assumptions required for interpreting an estimate as a causal effect. Further, most of the following designs allows us to flexibly control for confounding variables that are both known and unknown (see Angrist & Pischke 2008; Dudney *et al.* 2021; Ferraro & Miranda 2017) – something many Ecologists worry about. Thus, we believe these designs are a key advance worth considering for ecologists.

We illustrate the different designs using a common set of terms for causal variables of interest *(x*; e.g. local temperature), responses (*y*; e.g. snail counts), and confounding variables (*w*; e.g. recruitment) in a regression, applied to our example of the snail system in Figure 3. Our example includes data from different sites (*i*) sampled either at multiple time points (*j*) in panel data design or in multiple plots (*j*) in the case of a cross-sectional data design as above. For the sake of simplicity, we assume a linear model form with normally distributed error (), although the framework will work for generalized linear models as well. The system functions such that

(1)

Here, *yij*is the abundance of snails at site *i* in year or plot *j*, is the abundance of snails if the temperature was 0, is the effect of temperature *xij* at site *i* in year or plot *j* on snails, is the effect of recruitment *wi* at site *i* on snail abundance, Our goal is to estimate (the effect of temperature on snail abundance). Due to shared oceanographic influences, *xij* and *wi* are correlated. If we had measured *wi*, then we could include it in our model, and by conditioning on observables with as the effect of *w* on *y*, produce a causally correct estimate of . If the confounder, *w*, was not measured in the design above, and instead a researcher tried to fit the following equation,

(2)

our causal inference about would be incorrect. This is because would now be included in the error term, inducing a correlation between our error and causal variable of interest. This **endogeneity problem** violates the assumptions of the Gauss-Markov theorem and its extensions (Wooldridge 2015) and is what leads to the problem of omitted variable bias (see simulations below to see this bias in action).

## *What Ecologists Typically Do: Random or Mixed Effects Models*

Mixed effects models have been popular in ecology for the past two decades (for a useful review, see Bolker et al. 2009, Schielzeth and Nakagawa 2012, Harrison et al. 2018). Originally used to partition variation in heritability between different relatives (Fisher 1919), **random effects –** the effects of clusters in data assumed to come from a random distribution (but see Gelman & Hill 2006 on the linguistic difficulties of defining random effects) – quickly became a mainstay in the partitioning of variation in randomized experiments with subsamples taken within clusters (Cochran 1937; Eisenhart 1947). They have become a standard part of the toolbox for analyzing ecological experiments (Schielzeth & Nakagawa 2012), and are frequently used when analyzing observational data in ecology.

Random effects account for clustering in our data via the error structure of the model (Bolker *et al.* 2009; Gelman & Hill 2006), rather than estimating cluster means as part of the data generating process of a model (i.e., fixed effects cluster means using the terminology of the mixed models literature). Random effects have the added second benefit of efficiency, costing fewer degrees of freedom to estimate as we assume cluster means follow from a distribution (i.e., estimating a grand mean and variance), rather than directly estimating a separate coefficient for each cluster mean with no relationship to any other cluster mean. With this efficiency can come an improvement in the estimates of *precision* for coefficient estimates for our causal variable of interest (Gelman & Hill 2006) relative to fixed effects cluster means. This improvement in precision contrasts to how cluster robust standard errors – a technique also designed to handle clustering in data - alters the precision of coefficient estimates. Cluster robust standard errors make no assumptions about the distribution of cluster and their means, and they make fewer assumptions about the homogeneity of residuals between clusters (see Box 4 and Oshchepkov & Shirokanova 2022 for an excellent comparison between mixed models and cluster robust standard errors - including when and where to use each, data requirements, and more). Further, as random effects are assumed to be drawn from a common distribution, they have benefits for analyses of unbalanced samples as well as regularizing of cluster means (i.e., shrinkage, drawing them towards the grand mean, see Efron & Morris 1975).

For these reasons, Ecologists conducting a study akin to our snail-temperature example would likely gravitate towards a mixed model to account for site-to-site variability in snail abundances, using a mixed effects model design akin to:

(3)

What is new here relative to eqn. 2 is that is the site-specific deviation at site *i* from our intercept due to random variation which follows a normal distribution. As we will see, because this is a random effect, if site is correlated with temperature, we cannot resolve the problem of OVB with this model.

*What assumptions is a random effects design making when it comes to omitted variables bias?*

Why does the above model not control for omitted confounders via its site effect? Why do mixed effects designs produce incorrect results in the face of omitted confounders (i.e., a statistically biased estimate of the causal effect)? To understand this problem, it is key to remember, that when we model random effects, we are not modeling group means *per se*. Rather, we are modeling correlation in our error structure due to clustering in our data (Bolker *et al.* 2009; Schielzeth & Nakagawa 2012; Wooldridge 2010). The coefficient estimates of the causal variable of interest are unaffected by including or not including a random effect (we recommend you try this with any demo data set you have lying around). This difference – modeling error instead of modeling means *per se* – results in many of the above benefits, but also introduces one new assumption not often considered – a variation on the assumption of endogeneity we call the**Random Effects Assumption**. This assumption states that the random effects do not correlate with any replicate- or lower-level covariates in the regression (Antonakis *et al.* 2021; Wooldridge 2010). This is an extension of the general endogeneity assumption for statistical models discussed above but applied at the level of random effects. In the above model, while site is incorporated into here, the statistical model design is not causally identified due to the violation of the Random Effects Assumptionand will produce biased estimates of .

In a mixed model, the random effects of “site” are part of the error term and assumed to be uncorrelated with temperature to produce an unbiased estimate (Schielzeth & Nakagawa 2012; Wooldridge 2010). However, our causal variable of interest varies at the site level in a way that is confounded with other drivers occurring at the site level, i.e. and are correlated due to having a common driver at the site-level. This correlation and generates a violation of the Random Effects Assumption.

A picture containing circle, moon, astronomy

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**Figure 5.** The system assumed underlying a mixed model (A) versus the system as it is (B). Note that a mixed model does not account for the correlation between site and temperature, nor does it separate out the non-site drivers of temperature. Instead, the effect of temperature on snails is confounded by any correlated site-level drivers that correlate with temperature at the site level.

We can see more clearly how a mixed model would violate the random effects assumption using a path diagram in Figure 5a. In essence, site effects here are site-level residuals drawn from a normal distribution. They represent all other abiotic and biotic forces happening at the site level, but they also assume all are uncorrelated with temperature at the site level. However, given the information in Figure 3, we know that this is not accurate and the key assumption for an unbiased estimator is violated. If we were to take a step back and think about our goals of analysis and our causal understanding, again representing unmeasured quantities in ellipses, what we have is more like Figure 5b. Here, while a random site effect would be wonderful in terms of all the benefits discussed above, we would need to remove the effects of site-level confounders to use it – which is not done with the mixed model design above, as shown in Figure 5a. This example illustrates the difficulty in satisfying the Random Effects Assumption*.* More generally*,* we posit that satisfying this assumption is often quite difficult in Ecology – particular in observational data that spans environmental gradients – yet how badly this assumption is violated the is not well explored or acknowledged widely enough. We need a solution that does not produce biased results due to violating assumptions.

*Enter the Econometric Fixed Effects Design*

The Econometric Fixed Effects Design represents a familiar starting point for many ecologists who are used to using categorical variables in ANOVA and ANCOVA (e.g., Gotelli & Ellison 2012). Before getting into some admittedly confusing language, we note that, for Ecologists, what this design is just using a categorical variable for cluster. The approach is that simple. To get further into the weeds, here we use Fixed Effect in two senses of the phrase to describe this model. The first is the use of the term “fixed effect” is drawn from the econometrics literature, where it refers to attributes of a system (e.g., site, plot, or year) that vary by cluster (i.e., a within cluster intercept) that are encoded in models as dummy variables. In Ecology, this as a categorical predictor representing site, block, or other descriptor of how our data is clustered. In our snail example, would be a site-level time-invariant categorical variable acting as a stand-in for recruitment. We also use “fixed effect” in the language of the mixed model literature – i.e., that the cluster means are estimated as part of the data generating process of the model, not as part of the random error component. We acknowledge that there are many uses and definitions of “fixed effect”, leading to a wealth of confusion with different uses of the term across fields (see Gelman & Hill 2006). We hope to not add to the confusion here but note that both uses of Fixed Effects here are valid for this statistical model design.

Recognizing that confounding variables vary at the cluster-level, and thus by removing the effects of clusters we remove the effects of our confounding variables, we have two options to control for confounding and OVB. First, we can use a bit of algebra known as the **within transformation** or **fixed effects estimator** (Bell *et al.* 2018; Wooldridge 2010)and has some similarities to within-subjects centering in Ecology (van de Pol & Wright 2009). We illustrate this by manipulating the following equation:

(4)

where is our casual variable of interest, and the error term is composed of idiosyncratic (random error), , and , which represent differences across sites *i* including unmeasured confounding variables. To remove the effect of site-level confounding drivers, we transform the data by subtracting this average value from both sides across all years. On the right-hand side we can expand this to subtract . This leads to a transformed model which can generate a causally identified estimate of .

(5)

Using simple algebra, we have removed the confounding influence of time invariant, confounding variables for each site, whether they were observed or not. To achieve the same effect as this group means transformation (see Fig. 6A for how this would look in a causal diagram), we could instead use a model design with a categorical or so-called dummy variables for each cluster (i.e., a 0/1 encoding for each cluster, known as an econometric fixed effect). We can represent this as a site effect in a causal diagram (Fig. 6B). This kind of model design – familiar as an ANCOVA-style model design to many Ecologists – will control for omitted variable bias and produce identical results to the preceding model for (Angrist & Pischke 2008; Wooldridge 2010). For clarity, we can write this model either incorporating the dummy 0/1 variables (*x2i*) and site effects () or with just the site effect alone – i.e., means model notation (Gelman & Hill 2006). Note that unlike random effects in a mixed model design, is not constrained to be drawn from any predefined distribution. We present this without using treatment contrasts (i.e., with as a reference level and as deviation from reference) for clarity.

(6)

Returning to our snail example, with site as an econometric fixed effect as in equation 6, we can control for different sites having different levels of recruitment or other omitted variables correlated with temperature – whether those confounding variables were measured or not. Thus, this design allows us to relax the strong assumption that all confounding variables are observed and measured to interpret as causal (e.g., see Figure 6b which shows we are estimating the effect of temperature controlling for recruitment or any other site covariates). We note that cluster robust standard errors are likely important for both approaches for inference (Abadie *et al.* 2017; see Box 4 and Cameron & Miller 2015). For ecological examples using this design – either dummy coded or the fixed effects transformation – see Dudney et al (2021), Ratcliffe et al.(2023), and Dee et al. (2023) .

The fixed effect design has some drawbacks, despite its simplicity and its strength in controlling for both observed and unobserved confounding variables. First, while fixed effect estimators make much weaker assumptions about confounding variables, these estimators are inefficient compared to random effects. For each fixed effect (each site in our example), we estimate a separate coefficient and thus are estimating more parameters. We therefore need a larger sample size to achieve the same level of precision of our estimate using fixed effects versus random effects, presenting a bias-variance trade-off. However, in the case of omitted variable bias, this framework is still preferable over a mixed model for causal questions, given that it does not have the same endogeneity problem. Second, we lose information about between-site variation, including gradients between sites that may be of interest. These gradients, while confounded with other variables, could be the focus of some research questions which cannot be easily addressed using fixed effect model designs.

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Description automatically generated with low confidence

**Figure 6.** Directed Acyclic Graph representations of different statistical models handling omitted variables in the text.

## *Group Means for Efficiency, Inference, Fun, and Profit*

To study between-site variation and mitigate the loss of efficiency from the fixed effect design, we can step into the world of **correlated random effects designs**. The foundation of correlated random effects model designs is leveraging group means of our causal variable of interestto control for the effects of confounding variables. For every cluster – e.g., each site, year, or region, researchers calculate a group mean of the causal variable of interest to include as a predictor. These group means control for the effects of confounders at the cluster level acting as a proxy for confounders. Using group means of our causal variable also enables us to estimate a coefficient for between cluster gradients in our causal variable of interest as well, although these relationships describe a combination of causal and confounded effects. As our group mean contains the variation due to cluster-level confounded variables, we can now use a random effect for cluster, i.e. make this a hierarchical mixed model. This random effect now encompasses random variation due to cluster without variation due to confounders. By using a random effect for cluster while spending one degree of freedom to estimate a coefficient for our group mean predictor, we gain significantly in efficiency over the fixed effects model.

In Econometrics, this model design is known as a **Mundlak Device** (Mundlak 1978) and has many extensions (e.g., Wooldridge 2021). For clarity, we term it a **Group Mean Covariate** design. For the group mean covariate model design, we use the following equation:

(7)

where accounts for the effect of cluster-level confounders and is a random effect of that cluster (i.e., site). We can see what this looks like as a DAG in Figure 6c. From this diagram, we see that the site mean temperature is controlled for in estimating the temperature effect. The mean temperature of a site is estimated while controlling for each measured temperature.

The site mean temperature coefficient, called a **contextual effect** (Antonakis *et al.* 2021) in the Group Mean Covariate design, shows how changing the mean temperature of a site – and all properties that correlate with site mean temperature – would affect snail abundance were the temperature within a plot to stay the same. For example, *if our plot was 10 degrees C, what would snail abundance be if said plot was in a site with an average temperature of 5 degrees C versus 20 degrees C*? If the contextual effect is 0, then we can conclude that a simple mixed model would have sufficed and that omitted variable bias was not a problem in this particular analysis (Antonakis *et al.* 2021).

The above statistical model design will run into problems, however, if the correlation between our causal variable of interest and its cluster-level mean is too high. To solve this, we need a model design that transforms our causal variable to interest to remove this correlation. We accomplish this with a **Group Mean Centering** design where we subtract the cluster-level mean from the causal variable of interest. We then use this cluster-level anomaly as our predictor variable alongside a cluster level mean as follows:

(8).

Equation 8 decomposes our causal variable of interest into between- and within-cluster terms, an approach already in use in ecology (van de Pol & Wright 2009). The site mean temperature coefficient, , is the between-site effect of a driver of interest and confounders, and the anomaly from the site mean coefficient, , is the within-site temperature effect. Figure 6d shows the DAG for this design and the similarities and key differences with the previous designs. In particular, the interpretation of is different than in the Group Mean Covariate design. for our snail example is now a **between estimator** of the combined effect of moving across gradients in temperature and correlated drivers between the sites. If = , omitted variables are not meaningfully influencing snail abundances; both our between and within site differences are due solely to temperature or multiple confounders have cancelled one another out.

The Group Mean Covariate, Group Mean Centered, and Fixed Effects designs all differ in structure but they will yield the same point estimates of under most conditions, as they all rely on within-site variation in temperature (see simulations below and Wooldridge 2010). Thus, one might ask: *which statistical model design should I use*? This decision depends on the structure and size of one’s data (e.g., how many coefficients do you have the power to estimate given your sample size) and the question of interest (e.g., are you interested in between-site differences?). For example, do you have many sites and are only interested in the causal effect of temperature? Fixed effects design. Do you want to know how plot-level snail abundance would change if the average site temperature changes, but plot temperature stays the same? Group Mean Covariate design. Do you want to understand the effects of temperature while examining the net effect of many forces shaping between-site gradients? Group Mean Centered design. Each design can further be extended to cases where the magnitude of the causal variable of interest’s effect is moderated by the level of confounding variables (i.e., an interaction or “heterogeneous” causal effect, see Box 2).

## *What a Difference Differencing Makes*

Our examples thus far have focused on confounding variables that are unobserved and vary across space (i.e., between sites). We have not discussed omitted confounding variables that differ across time. In the case of omitted confounders varying solely across time and not space (e.g., sites vary randomly in recruitment across space, but year-to-year regional variation in recruitment is correlated with year-to-year regional variation in temperature), we can extend the frameworks presented above, using years as we did sites as clusters. If time-varying confounders are uniform across sites (i.e., are additive with spatial confounders), then we can use an econometric fixed effect of time and an econometric fixed effect of space (a two-way fixed effect or TWFE model design, Wooldridge 2021) or a site-average of predictors and a time-average of predictors (a Two-Way Mundlak model design; Wooldridge 2021). If, however, temporal confounders differ by site, we need a more general solution. If omitted confounders vary spatiotemporally, we can extend our previous framework further using the same principles (see Box 3 and Dee *et al.* 2023). If, however, temporal confounders merely vary in strength from one site to the next, the **first and second difference** statistical model designs provide easy solutions. These statistical model designs deal with both spatial confounders and site-varying temporal confounders.

To illustrate these approaches, consider extending our example so that, in addition to site-level oceanographic recruitment effects, the abundance of snails is influenced by coastal development over time at each site (Fig. 7A). However, rates of development are not the same across all sites. As such, separating the effect of local coastal development from the effect of local temperature variability on snail abundance is difficult. We can see this in a small modification to the dynamics of our system from eq. 1:

(9).

In this scenario, there are both site-specific confounders, represented by and temporal confounders. For our temporal confounder, is a site-specific trend in snails over time (*j*). If there is also a trend in temperature over time (e.g., climate change), our estimation of in any model that did not include our temporal-confounder would suffer from Omitted Variable Bias. One solution to this scenario is to fit a model with an econometric fixed effect of site to account for spatial confounders and a site by time effect to account for the site-level trends. This would lead to twice the number of parameters as the number of sites, however, and might not be a feasible model to fit.

A picture containing black, circle, darkness, astronomical object

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**Figure 7.** Directed Acyclic Graph model representations of different models handling spatial and temporal omitted variables.

Fortunately, there is a simple solution similar to the fixed effects transformation: **temporal differencing**. For each time point in our data, if we subtract the previous time point, we produce a model evaluating the relationship between change in our response variable versus change in our causal variable of interest. Like the fixed effects transformation, the confounding effects of site-level omitted variables that do not have a temporal trend are eliminated. After the transformation, remains as a term to be estimated with an econometric fixed effect, and it will recover an estimate of the trend for each site. This approach has the added benefit of sweeping up other unknown site-level trends into our estimate of . Our first difference model design, represented as a path diagram in Figure 7B, translates to the following with means model notation:

(10)

Here estimates the effect of temperature as before with estimating the site-level trend of other drivers. Note that confounders at the site level, above, are removed algebraically in this design. If there is no temporal trend in temperature, and as such there is no correlation with other site-level trends, we *could* use random effects for the site term. We caution, however, that this adds back the random effects assumption which is unlikely to be met. Note that if the time between sampling events is unequal across sites, we can divide change by time between samples to model change per unit time. Finally, if we are uninterested in site-specific trends, we can calculate the second difference which eliminates the need to estimate . Note that in this second differences statistical model design model is estimating the relationship between acceleration in change in temperature and acceleration in change in snails.

Using either temporal differencing design has several advantages. We again remove the effect of omitted confounders at the site level. We also control for or remove the effects of temporal confounders at the cluster level that have similar trends to our causal variable of interest. Thus, our estimate of a temperature effect is again causally identified. As we are handling two potential forms of omitted variable bias, our analysis is robust to omitted variable bias from two sources of unknown confounders. The main drawback of these approaches is the reduced sample sizes; we lose observations from one or two time periods. This reduction in sample size reduces power and can lead to less precise standard errors, especially in the case of the second difference design. However, this reduction in sample size could be counterbalanced by robustness to violates of assumptions regarding both spatial *and* temporal confounders as well as gains in efficiency from estimating fewer parameters as compared to a fixed effect approach using dummy variables for site-level confounders coupled with also controlling for separate site-level confounded trends. If site-level trends are nonlinear, however, an econometric fixed effect approach or a correlated random effects model to accommodate spatial confounders coupled with nonlinear site-level trends might be more appropriate. This approach can use either polynomials or even Generalized Additive Models to handle temporal confounders (for a polynomial example to deal with space and time see Dee *et al.* 2016). Regardless, temporal differencing can be incredibly useful in cases of both spatial and temporal omitted confounders: a situation all too common in many real ecological systems.

## **Box 2: A Difficult Slope: Omitted Variables that Cause Variation in the Magnitude of the Causal Effect**

Frequently, an omitted confounder does not merely contaminate our estimate of a causal effect but can also lead to model misspecification in the form of missed heterogeneity in the causal effect. This occurs when the causal effect of our variable of interest depends on the level of the confounder itself (i.e., it modifies the causal effect – an interaction effect). In our example, consider that thermal effects in our snail system might depend on levels of recruitment because dense aggregations of intertidal organisms are often better at retaining water and thus resisting desiccation or other forms of thermal stress (e.g., Silliman *et al.* 2011). This is problematic if we have not measured recruitment. In a naive mixed model, we might incorporate this heterogeneity as a random slope. As before, however, the random effects assumption is violated, so a random effects estimator will be biased. To deal with the problem of omitted variable bias in this case, we present two solutions. First, we can use a fixed effects design and include an interaction term between the site dummy variable and our causal variable of interest, allowing us to estimate site-specific temperature effects. Given that we now have site-level slopes, the number of parameters can blow up, leading to this approach being highly inefficient and not advisable for small sample sizes. Instead, we could use correlated random effects approaches with an interaction between the group mean and our causal variable of interest. For example, for a group mean covariate (i.e. Mundlak device) design, we would use the following equation:

This design allows us to examine how site-level confounders – known and unknown – can lead to variation in the effect of our causal variable of interest. It can also show that they have no effect if the estimand for is not different from 0. We could use a similar model for the group mean centered design if deemed appropriate. If we suspect that the magnitude of the temperature effect varied with other non-confounded covariates, we would instead use a random slope. In general, models with interactions representing moderators can provide powerful insights into both the effect of the causal driver of interest as well as how those effects vary.

## **Comparison of Approaches**

To demonstrate the utility the preceding solutions, and the consequences of not using them, we fit a variety of models to simulated data based on a longitudinal study of snail populations at multiple sites based on Figure 3. For a single simulation run, we created a system as follows:

* Oceanography is a variable with a mean of 0 and standard deviation of 1.
* Site mean recruitment is -2 multiplied by the oceanography variable and then rescaled to have a mean of 10 individuals per plot (e.g., so it does not go negative). It is the same in a site across all years.
* Site mean temperature is calculated as twice the oceanography variable and then rescaled to have a mean of 15C.
* Site temperature in year t is determined by site mean temperature and additional variation, with a mean of 0 and standard deviation of 1.

Snail abundance at site *i* in year *t* is then determined in a given year by the following equation (adapted from eqn. 1) corresponding to Fig. 3: Snailsit = Recruitmentit + Temperatureit + Other Driversit with the effect of other drivers varying with a mean of 0 and standard deviation of 1. We then simulate sampling 10 sites over 10 years. We analyzed each single run using all the statistical model designs described above, compared to naive models with no site effect. We also included group mean covariate and group mean centered models without a random effect to demonstrate what a random effect in these models is doing.

We provide results from 100 simulated data sets created as above. Interested users can see the code in Appendix A or can download and run it themselves using the markdown code provided at https://github.com/jebyrnes/ovb\_yeah\_you\_know\_me. To walk through the analysis of a single data set, see Appendix B and Supplementary Data 1. For a more interactive exploration, see the web applications written using R Shiny provided as Appendix C (for one simulated run alone) and Appendix D (with 100 or more replicate simulations exploring the distributions of coefficients).

A graph of different types of temperature

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**Figure 8.** Distribution of point estimates of temperature effects from different models across all 100 simulations. The true effect size (1) is highlighted with a dotted line. Briefly, the Naïve model corresponds to equation 1, Random Effects model to equation 3, the Fixed Effects models to equations 5 and 6, respectively, the Group Mean Covariate models to equation 7and the Group Mean Centered models to equation 8, and the First Differences model to equation 10.

Broadly, our simulations show that the point estimates from the random effects (RE) model - what ecologists typically do - is consistently biased in these simulations and well-below the estimates from both the other designs and the true effect size (Fig. 8, Table 1). Further, not only is the estimated coefficient of the RE model always biased compared to other estimators in our simulations, it is more often within 2SE of 0 than all other models. In most simulations, the 95% confidence intervals of the RE model do not contain the true value of the temperature effect (Table 1).

**Table 1.** Summary results of simulations. Mean and SD of point estimates of temperature effects from different models in the first two columns. Fraction of simulated runs where the mean +/- 2 SE of the temperature effect either overlapped 0 (i.e., high likelihood of committing a type II error) or did not contain the true effect of temperature in the final columns. Models are as in Fig. 8.

| **Model Type** | **Mean Estimate** | **SD Estimate** | **Fraction Sims where 95% CI Contains 0** | **Fraction Sims where 95% CI does Not Contain 1** |
| --- | --- | --- | --- | --- |
| Naive | 0.231 | 0.165 | 0.56 | 0.99 |
| RE | 0.640 | 0.232 | 0.08 | 0.54 |
| FE Using Mean Differencing | 0.985 | 0.215 | 0.00 | 0.05 |
| FE with Dummy Variables | 0.985 | 0.215 | 0.00 | 0.05 |
| Group Mean Covariate | 0.985 | 0.215 | 0.00 | 0.05 |
| Group Mean Centered | 0.985 | 0.215 | 0.00 | 0.05 |
| Group Mean Covariate, no RE | 0.985 | 0.215 | 0.01 | 0.04 |
| Group Mean Centered, no RE | 0.985 | 0.215 | 0.01 | 0.04 |
| First Differences | 0.971 | 0.259 | 0.01 | 0.12 |

Additional explorations show that, in line with the benefits of random effects in mixed models, a site-level random effect is crucial for Group Mean Centered or Group Mean Covariate models when either the study design is unbalanced or there is site-level variation that is uncorrelated with temperature (Appendix A). If our simulation has no site-level variation other than temperature and our confounder, a random effect does not improve either models’ ability to estimate the effect of our causal variable of interest. This assumption is unrealistic for most real data sets, however. As such, we highlight the need for a site level random effect with either of these two designs. In general, we urge researchers to incorporate random effects or robust standard errors as needed to accommodate clustering in the error, per the study design, recognizing the tradeoffs of using both and appropriate context (see Oshchepkov & Shirokanova 2022 for an excellent review).

## **Box 3: Reality Bites: Coping with spatiotemporal omitted confounders**

Spatiotemporal confounding variables – those that are site (or plot) specific and vary through time – pose challenges, and the solutions require more thoughtful study and statistical model design. To illustrate, we consider a scenario where recruitment, a confounding variable related to both snail abundance and temperature, is not static through time but instead varies by site and year (as in a realistic case). For example, sites that experience strong cold-water pulses in a year also experience unusually snail high recruitment in those same years due to oceanographic drivers. The sampling designs for coping with spatiotemporal omitted variables are based on the same principles as cross-sectional and longitudinal sampling, only now we combine the two.

With longitudinal data that includes multiple plots sampled within a site through time, we can flexibly control for this sort of spatiotemporal confounding at the site level by extending the two-way fixed effect designs discussed above. We can add a site-by-time fixed effect, , to our model, in addition to a fixed effect of plot, , where k is a fixed plot within site resampled over time (see below for a discussion of fixed versus re-randomized plots). This produces the following means model:

From this equation, we can see that captures time invariant plot-level confounding effects while captures the effects of spatiotemporal omitted variables at the site by time level. Note, there could be additional spatial or temporal only confounders. This model design sweeps their effects onto the spatiotemporal term.

In small datasets, the above model design can consume degrees of freedom rapidly. For this reason, we can instead use the more efficient correlated random effects model design (e.g., a variation on the Two-way Mundlak model design *sensu* Wooldridge 2021) using site-year means () and plot means () for the entire survey to control for spatiotemporal and plot confounding respectively:

Here the and terms are random effects for plot and unique site-time combinations respectively.

When sampling to handle spatiotemporal confounders, should plots within sites over time be permanent or randomly placed each year? The above models assume permanent plots, so we can eliminate confounding variables at the plot-level that is time invariant over the study period. For this reason, permanent plots help us cope with within-site OVB issues and have higher power to detect change over time (Urquhart & Kincaid 1999). Logistically, however, permanent plots within sites might not be possible. As such, the above models can be modified to drop plot effects; however, they would then assume that there are no confounding differences across plots and could have lower power to detect effects of drivers. We emphasize that the choice of fixed or random plot placement with these designs is a balancing act, however, as fixed plots can lead to a lower sample size due to logistical considerations in many environments, and direct readers to other explorations of this topic (see Gomes 2022 for an excellent elaboration). Finally, without a nested data structure – e.g., plots within sites resampled over years – we cannot include a site by year effect as in the above models. We can attempt to use site-level polynomials or Generalized Additive Models (Wood 2017) to mimic site-by-time effects (for a polynomial example, see Dee *et al.* 2016a), but, this requires knowledge of how the confounder varies at sites over time and extensive testing for robustness to these assumptions. In the many cases this is not possible or inadvisable given the likelihood of creating incorrect causal inference. In those cases, without multiple plots per site over time, “nothing to be done” (Beckett 1954).

In general, we urge caution when dealing with spatiotemporal omitted variables, and careful use of causal diagrams to ensure that we are controlling for a confounder at the relevant spatiotemporal scale. This topic is one that that deserves far more exploration in Ecology. More from other disciplines on this tricky class of problem and approaches can be found from literature outside of the scope of this paper (Athey & Imbens 2017; e.g., Ferraro & Hanauer 2014; Oster 2019).

**Discussion**

We hope that our introduction to statistical and sampling designs to address the problem of omitted variable bias and causal inference from observational data has shown that, through thinking carefully about biological systems, we can draw on a solid set of existing methods to solve this problem. Causal inference from observational data is possible. At the core of these techniques is building an *a priori* causal model of how a system works, and then using that model to guide your choice of sampling designs and statistical methods that you will use to answer your causal questions. Further, these techniques for addressing omitted variable bias are well within the standard statistical abilities of most modern ecologists (see Appendix B for implementation). The results of using the correct models, as seen in at least our toy example, can be profound for our ability to understand biological systems. It is time to begin using these tools to address some of the most pressing questions in the study of nature.

We hope that Ecologists can see the above concepts as part of a generalizable approach to handling confounding variables using clustered data. While we have talked of sites and years, the same concepts apply to studies with cohort effects, individual effects, or other lower levels of clustering as well as to larger-scale studies with not just sites and years but regions and decades. The general suite of approaches remains the same, and potential confounding variables at these different scales can be identified in initial causal diagrams. Cross-sectional and longitudinal sampling designs are generalizable beyond just the simple case presented in our simulation example; for instance, one could adapt the above designs if temperature and recruitment varied temporally at a regional rather than site scale (e.g., sampling plots within a single site or sampling many – both over many years to leverage spatial variation in temperature) or for spatiotemporal designs (see Box 3). Combining these sampling designs with others, such as the classic stratified random sampling design (Foster *et al.* 2018; Grafström & Lundström 2013; Kermorvant *et al.* 2019; Robertson *et al.* 2013; Stevens & Olsen 2004), will allow for the analyses that can improve causal identification and provide more precision in estimation of causal effects over multiple environmental gradients. How to design a study to fully account for confounders, however, will hinge on a causal diagram of the system.

**Box 4: Clustered Robust Standard Errors: An Underutilized Tool in Ecology**

While the focus of this paper is on bias in the estimation of coefficients, many of the issues discussed overlap with issues of non-independence and other violations of assumptions that could generate incorrect standard errors and tests of statistical inference. In light of that, we recommend the use of clustered robust standard errors for some of the models above. Clustered robust standard errors are not commonly used in Ecology (but see examples in Dee *et al.* 2016; Dudney *et al.* 2021) despite being a way to continue to use Ordinary Least Squares and then flexibly apply a post-hoc adjustment to accommodate clustered data, heteroskedasticity, correlation between time points, and other arbitrary correlation structures within the data (Abadie *et al.* 2017; Cameron & Miller 2015). While random effects, autocorrelation structures in statistical models, and more, can address some of the same issues, robust standard errors often provide a simpler solution allowing researchers to not have to make more assumptions about the structure of their data that they are not interested in. There are tradeoffs, however, and as multiple techniques cover similar ground, we recommend looking at comparisons of approaches (e.g., Oshchepkov & Shirokanova 2022). A full discussion or review of robust standard errors is beyond the scope of this paper, but we refer applied researchers to the documentation for the *sandwich* package in R and to comprehensive reviews (e.g., Abadie *et al.* 2017; Cameron & Miller 2015).

The important thing is to be transparent in how we deal with the problem of confounding variables. What are the assumptions you are making to interpret an effect as causal or not? If you are using mixed models, do you meet the random effects assumption? Have you evaluated your residuals to determine if you need to implement robust standard errors? Why did you include some covariates and not others? Do you have a DAG or even a conceptual model of your system that might help a reader understand your thought process? Putting these types of decisions into your work in even a brief sentence – if not a figure or full breakdown in a manuscript supplement (e.g., see Dee *et al.* 2023) – will go far in terms of making your analyses more transparent. It will make your work easier to be built upon to advance science. Even with this transparency, we also must be humble. We must accept that our models and knowledge are imperfect. Someday, someone will come along with a different model or approach that will produce different conclusions and yield new insights. And that is as it should be.

For the approaches we present here are surely not a panacea. They require assumption for causal inferences, as does any approach, including experiments (Kimmel *et al.* 2021). Some assumptions are shared with experiments: i.e., SUTVA – or the stable unit treatment value assumption which has two parts: 1) no interference or “spillovers” across units and 2) no multiple versions of or “hidden variations” in the causal variable of interest (reviewed in Kimmel *et al.* 2021). Most of the models here include assumptions of our causal variable of interest having linear additive effects (Imai & Kim 2021) and that its effects are homogeneous across units and time periods. We have included some discussion of relaxing these assumptions via interactions (i.e., Box 2); however, there is a growing literature on estimating causal effects under more varied forms of heterogeneity (Callaway & Sant’Anna 2021; de Chaisemartin & D’Haultfœuille 2020; Goodman-Bacon 2021; Sun & Abraham 2021). Relaxing this assumption takes more thought and consideration of one’s question of interest and the system dynamics from DAGs.

Further, all of the approaches presented here make the parallel trends assumption. The assumption of parallel trends is most easily understood considering a binary causal driver of interest (i.e., if the driver is present or absent). It implies that, without driver being present, the *difference* in outcomes between different clusters (e.g. sites) after conditioning on any covariates present would be constant through time. This assumption is more likely met with fewer time periods (e.g., two time periods spanning before and after an impact). The assumption can be tested in the pre-treatment period but is untestable after the treatment (for details see Roth 2022). This assumption extends to continuous causal variables. There, we assume the response of interest across clusters would have followed parallel trajectories in the absence of a change in the causal variable and adjusting for other observed covariates. The parallel trends assumption has come under a great deal of scrutiny recently (see review in Roth *et al.* 2023), particularly when changes in the causal variable of interest happen at different points in time across units (called “staggered treatments”, see Baker *et al.* 2022; Marcus & Sant’Anna 2021) and in the face of heterogeneous effects of causal variables (for details see some of the following – Borusyak *et al.* 2023; de Chaisemartin & D’Haultfœuille 2020; Goodman-Bacon 2021; Sun & Abraham 2021). This is a rapidly evolving literature, with many proposed solutions (reviewed in Roth et al. 2023), including for heterogeneous causal effects, non-linear cases, and continuous causal variables as we have in our example (Callaway *et al.* 2021). Many of these solutions are already being implemented in standard software (for a list see Roth *et al.* 2023). Thus, we suggest using the approaches reviewed here in concert with sensitivity tests (Altonji *et al.* 2005; Oster 2019; Rosenbaum 2002) by implementing multiple model designs that make different assumptions in order to probe robustness of results (see Dee *et al.* 2023 for an ecological example).

Finally, we emphasize that this paper provides an entry point into a broader interdisciplinary literature on causal inference in observational data, longitudinal data analysis, and panel regression methods. Indeed, other methods, such as instrumental variables, regression discontinuity designs, and more can be used to eliminate omitted variable bias when their assumptions are met (see reviews and examples in Angrist *et al.* 1996; Arif & MacNeil 2022; Butsic *et al.* 2017; Dee *et al.* 2023; Grace 2021; Kendall 2015). Thoughtful uses of the front-door criterion – the use of mediators between a cause and effect that are unaffected by confounders to resolve a causal relationship – might also prove useful for ecology (Bellemare *et al.* 2020; Pearl *et al.* 2016), although, as of yet, there are no good in the Ecological literature. We urge ecologists, long grounded in experiments, to open themselves to writings in Econometrics, Epidemiology, Computer Science, Public Health, and other disciplines that cannot always do field experiments. Embracing this transdisciplinary approach will enable us to enhance our knowledge of the tremendous advances in causal inference and enable us to explore questions currently beyond our reach. As an incomplete set of starting points for further reading, we recommend Cunningham’s Causal Inference: The Mixtape (2021), McElreath’s chapters on causal diagrams in Statistical Rethinking (2020), Angrist and Pishke’s Mostly Harmless Econometrics (2008), Morgan and Winship’s Counterfactuals and Causal Inference (2015), Sloman’s Causal Models (2005), and Pearl’s Causal Inference in Statistics: A Primer (2016). We also suggest Ecologists interrogate the assumptions and interpretations of their experiments (Kimmel *et al.* 2021). Given how an experiment was designed and run, are its results causally valid with respect to the purported mechanism? It is high time to critically interrogate how to get the robust causal inferences needed to grapple with our rapidly changing world.

## **Conclusion**

“Correlation does not equal causation” rings in many of our heads from our Biostatistics 101 courses. One main reason behind this message is the specter of Omitted Variable Bias from unmeasured confounding variables. This fear has impeded the use of observational data for causal inference in Ecology for much of its history. We hope this review can lift some of that fear and, armed with the tools introduced here and knowledge of a literature beyond this piece, we can move forward as a discipline. With a massively growing volume of observational data, problems at continental to global scales demanding rapid answers, and now, new arrows in our Ecological data analysis quiver, we look forward to seeing the studies and insights from the next generation of Ecologists.

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