Batch Effects are Causal Effects: Applications in Human Connectomics

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Abstract. Batch effects, undesirable sources of variance across multiple experiments, present a substantial hurdle for scientific and clinical discoveries. Specifically, the presence of batch effects can create both spurious discoveries and hide veridical signals, contributing to the ongoing reproducibility crisis. Typical approaches to dealing with batch effects conceptualize 'batches' as an associational effect, rather than a causal effect, despite the fact that the sources of variance that comprise the batch – potentially including experimental design and population demographics – causally impact downstream inferences. We therefore cast batch effects as a causal problem rather than an associational problem. This reformulation enables us to make explicit the assumptions and limitations of existing approaches for dealing with batch effects. We therefore develop causal batch effect strategies – *Causal* DCORR for discovery of batch effects and *Causal ComBat* for mitigating batch effects – which build upon existing statistical associational methods by incorporating modern causal inference techniques. We apply these strategies to a large mega-study of human connectomes assembled by the Consortium for Reliability and Reproducibility, consisting of 24 batches including over 1700 individuals to illustrate that existing approaches create more spurious discoveries (false positives) and miss more veridical signals (true positives) than our proposed approaches. Our work therefore introduces a conceptual framing, as well as open source code, for combining multiple distinct datasets to increase confidence in claims of scientific and clinical discoveries.

1 Introduction

The 21st century has seen the advent of high-throughput techniques for acquiring data on an unprecedented scale. Collection of these datasets often occurs through consortia using a range of technologies across different sites, requiring data to be brought together by aggregation services and hosted by data banks for storage and sharing. These "mega-studies" comprising numerous individual studies serve the useful purpose of facilitating inference on individuals with unprecedented diversity; researchers can subvert traditional sample size and generalizability issues through the use of data from a more diverse sample of the population than could otherwise be collected.

Unfortunately, aggregating data across diverse datasets introduces a source of undesirable variability known as a batch effect. Several strategies have been proposed to define a batch effect. Lazar et al. [22] summarize many of these approaches succinctly: "the batch effect represents the systematic technical differences when samples are processed and measured in different batches and which are unrelated to any biological variation." Unfortunately, this unified description provides limited information about how batch effects manifest, nor how they can be formally characterized and investigated. We have been unable to find a satisfactory technical definition of batch effects in the literature.

Broadly, many approaches model the batch collection or measurement process as a nuisance variable which is to be removed [19, 23, 24, 33, 34, 49, 53], which implies batch effect is a particular component of an associational or conditional model. These approaches typically make strong, potentially unjustified, and often inappropriate parametric assumptions about the data. Two of the most prominent examples of these techniques which can be generalized to many of these other cases are the ComBat and Conditional ComBat batch effect correction procedures [19]. These approaches have demonstrated empirical utility in certain genomics and neuroimaging contexts [34, 54]; however, it remains unclear when these approaches will be successful and when they will fail. Specifically, they could either remove biofidelic variability or fail to remove nuisance variability.

In this work, we develop a unified and systematic approach to the definition, detection, estimation, and mitigation of batch effects. Our main conceptual advance is appreciating that one can view batch effects as causal effects rather than associational effects. Given this understanding, we introduce a formal definition of causal batch effects. This formal definition reveals the limitations of (typically

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inappropriate) assumptions implicit in existing approaches [37, 38, 42]. Methodologically, we introduce two new approaches. First, we developed *Causal* DCORR [44]—building on modern, non-parametric statistical methods—to estimate and detect the presence of batch effects. Second, we developed *Causal* ComBat—an augmentation of the ComBat procedure—which uses causal methods to remove batch effects while limiting the removal of variation due to known demographic variables. Our main empirical contribution is to apply these methods to a large neuroimaging mega-study assembled by the Consortium for Reliability and Reproducibility (CoRR) [55], consisting of more than 1700 connectome measurements across 24 disparate studies. Our investigations reveal that previous strategies fail to differentiate between veridical biological signal and sources of variability due to other experimental design factors. Further, previous strategies for removing batch effects remove more apparently veridical biological signal than *Causal* ComBat.

We believe that this investigation raises significant questions for the validity of downstream inference with or without applying previously proposed batch effect correction procedures to mega-studies. We hope this work contributes to the ongoing effort to improve the validity and reliability of inferences in past and future mega-studies.

2 Methods

For further details on methodological considerations, see Section 5.

2.1 Formally defining batch effects from a causal perspective

Throughout this paper, we use P_X to denote a generic distribution function and f_X to denote a generic probability density or mass function for a random variable X, which we abbreviate P and f for simplicity. We use $P_{X|y}$ to denote the conditional distribution function of the random variable X conditioned on $Y = y$. The corresponding conditional density/mass function is $f(Y = y|X = x)$, which we abbreviate $f(y|x)$. We let Y denote the $y \in \mathcal{Y}$-valued random variable denoting the outcome, T denote the $t \in \{1, \ldots, K\} = [K]$ categorical-valued random variable denoting the batch identity assignment (the *exposure*), x the $x \in \mathcal{X}$-valued random variable denoting measured covariates, and Z the $z \in \mathcal{Z}$-valued random variable denoting unmeasured covariates. We let $\mathbb{P}[T = t|X = x, Z = z]$ denote the probability mass function of the random variable T taking the value t, conditional on the measured and unmeasured covariates X and Z taking values of x and z, respectively. Throughout, we assume that (Y, T, X, Z) are sampled identically and independently from some true but unknown distribution (which implies *exchangeability*). Together, all possible confounding and indirect associations between Y and T can be accounted for by the tuple (X, Z), meaning that X alone may not be sufficient to account entirely for confounding (X and Z *close backdoor paths*). $f(y|t, x, z)$ denotes the true outcome model; note the true outcome model is conditional on both measured *and* unmeasured covariates. In our investigation, the outcome Y is an fMRI connectome, the batch T is the study in which the connectome was acquired, and X are covariates regarding the individual which are known (age, sex, and continent of measurement).

We are interested in estimating the effect of different exposures on the outcome of interest, which can be quantified using the backdoor formula under the assumption that X and Z close all backdoor paths [25, 32, 33, 36]:

$$f_{x,z}(y|t) = \int_{\mathcal{X}\times\mathcal{Z}} f(y|t, x, z) f(x, z) \, \mathrm{d}(x, z), \qquad \forall\, t \in \{1, \ldots, K\}. \tag{1}$$

So our causal estimands will be functions of the set of $\{f_{x,z}(y|t)\}_{t\in\{1,\ldots,K\}}$. Note that the above equation integrates over the *unconditional* distribution of X and Z, $f(x, z)$. This quantity can therefore be thought of as the distribution of the true outcome averaged over *all* measured and unmeasured covariates. This contrasts from the notationally similar, but practically distinct, quantity $f(y|t)$, e.g.:

$$f(y|t) = \int_{\mathcal{X}\times\mathcal{Z}} f(y|t, x, z) f(x, z|t) \, \mathrm{d}(x, z).$$

The key difference is that unlike Equation (1), $f(y|t)$ averages the true outcome distribution, $f(y|t, x, z)$, over the *conditional* distribution of the measured and unmeasured covariates, $f(x, z|t)$. This has the

implication that if $f(x, z|t)$ is not the same as $f(x, z|t')$, $f(y|t)$ represents an average over a different covariate distribution than $f(y|t')$.

Batch Effect Given the above, we formally define the **batch effect** as a causal effect using the backdoor formula (1).

Definition 1 (Batch Effect). *Suppose the setup described above. A batch effect between batches t and t' exists if and only if:*

$$f_{x,z}(y|t) \neq f_{x,z}(y|t').$$

Colloquially, if we seek to detect a batch effect, we seek to be able to characterize when the relationship described above is true. The key limitation of this definition of a batch effect is that, as elucidated in Equation (1), the estimands of interest $f_{x,z}(y|t)$ require an integration over the *unconditional* distribution of both the known *and* unknown covariates, $f(x, z)$, which we will not have in practice due to the fact that the covariates Z are unknown. Therefore, if one were to construct a hypothesis test on the basis of Definition 1, we would be unable to characterize principled estimators of the quantities $f_{x,z}(y|t)$ directly. To this end, we define a sequence of related effects below, and we elucidate the specific sets of progressively less restrictive assumptions about (Y, T, X, Z) under which the existence of the effect of interest implies the existence of a batch effect. The causal claims are only valid insofar as the assumptions upon which they rest adequately characterize the data.

Associational Effect We only observe the pairs (y_i, t_i) for $i \in [n]$. Therefore we will only be able estimate functions of (Y, T).

Definition 2 (Associational Site Effect). *An associational site effect exists between batches t and t' if:*

$$f(y|t) \neq f(y|t').$$

Practically, techniques which aim to address these associational site effects are known as associational site effect correction techniques.

Definition 3 (Associational Site Effect Correction). *Associational site effect correction is the process of estimating and applying a function $\hat{g}$ which is learned from the data (y_i, t_i), where:*

$$v_i = \hat{g}(y_i, t_i).$$

The associational site effect is removed between batches t and t' if $f(v|t) = f(v|t')$. In practice, associational techniques involve approaches for associational site effect detection and correction which *ignore* measured covariates, such as `DCORR` for batch effect detection and `ComBat` for batch effect removal.

When would an associational site effect be equivalent to a causal batch effect? A sufficient assumption for the equivalence of those two effects is that the measured and unmeasured covariates (X, Z) are non-confounding (which is satisfied, for example, whenever (Y, T) is independent of (X, Z)). This assumption, however, is not often a reasonable one to make. Consider, for instance, if in one batch t, we tend to measure older individuals, whereas in another batch t', we tend to measure younger individuals. If age is related to the measurement we obtained, then the differences between $f(y|t)$ and $f(y|t')$ could be due to age or batch identity, and we have no way of differentiating whether the effect is a *bona fide* batch effect versus an associational effect.

Conditional Effect We observe triples (y_i, t_i, x_i) for $i \in [n]$; thus, we will only be able estimate functions of (Y, T, X).

Definition 4 (Conditional Site Effect). *A conditional site effect exists between batches t and t' if:*

$$f(y|t,x) \neq f(y|t',x).$$

Techniques which aim to address these conditional site effects are known as conditional site effect correction techniques.

Definition 5 (Conditional Site Effect Correction). *Conditional site effect correction is the process of estimating and applying a function $\hat{g}$ which is learned from the data (y_i, x_i, t_i), where:*

$$v_i = \hat{g}(y_i, x_i, t_i).$$

The conditional site effect is removed between batches t and t' if $f(v|t,x) = f(v|t',x)$. Conditional techniques involve approaches for batch effect detection and correction that account for measured covariates, such as Conditional `DCORR` for batch effect detection and Conditional `ComBat` for batch effect removal.

When would a conditional site effect be equivalent to a causal batch effect? To answer this question, we first define the propensity score $e(t|x,z)$ [37, 38]; that is, the probability of selection into a particular exposure given one's covariates: $e(t|x,z) = \mathbb{P}[T = t_i | X = x_i, Z = z_i]$. With this definition in hand, a sufficient assumption for the equivalence of those two effects is that both of the following conditions must hold:

1. Conditional on the measured and unmeasured covariates, (X, Z), the exposure is independent of the outcome: $T \perp\!\!\!\perp Y | X, Z$.
2. The covariate distributions overlap; that is, for some $c > 0$, and all $(x,z) \in \mathcal{X} \times \mathcal{Z}$, $c \leq e(t|x,z) \leq 1 - c$, for all $t \in [K]$.

Together, these two conditions are referred to as strong ignorability [37]. If the unmeasured covariates Z are non-confounding, they can be ignored in the above. Note that if the covariate distributions fail to overlap for a pair of exposures, it is impossible to differentiate whether the differences between the outcomes are due to the different covariate distributions or different batches.

In practice, we never know whether the true unmeasured propensities overlap; we can only estimate them from the data. If our estimated propensities do not overlap given finite data, we again cannot reasonably differentiate between differences in the two groups being due to *bona fide* batch effects or empirical differences in the covariate distributions. This motivates a third approach.

Adjusted Effect We again observe triples (y_i, t_i, x_i) for $i \in [n]$. Prior to assessing the equality of any distributions, however, we weight the observations such that the observed covariate distributions are rendered approximately equal; that is, $\widetilde{f}(x|t) \approx \widetilde{f}(x|t')$ for a given $t \neq t'$. These sample adjustments yield adjusted conditional distributions $\left(\widetilde{f}(y|t,x), \widetilde{f}(y|t',x)\right)$ for all pairs $t \neq t'$.

Definition 6 (Adjusted Site Effect). *An adjusted site effect exists between batches t and t' if:*

$$\tilde{f}(y|t,x) \neq \tilde{f}(y|t',x).$$

When would an adjusted site effect be equivalent to a causal batch effect? The overlap assumption stated above is satisfied by construction. Thus, the exposures must be independent of the outcome conditional on any confounding covariates, X and/or Z. Again, if everything is independent of Z, this detail need not be considered.

Techniques which aim to address adjusted site effects are known as adjusted site effect correction techniques.

Definition 7 (Adjusted Site Effect Correction). *Reweight the observations such that $\tilde{f}(x|t) \approx \tilde{f}(x|t')$ via weights w_i for each observation i.*

Adjusted site effect correction is the process of estimating and applying a function $\hat{g}$ which is learned from the reweighted data (y_i, x_i, w_i, t_i), where:

$$v_i = \hat{g}(y_i, x_i, w_i, t_i).$$

The adjusted site effect is removed between batches t and t' if $\tilde{f}(v|t, x) = \tilde{f}(v|t', x)$. In practice, *adjusted* procedures amount to augmenting conditional procedures by first reweighting the measurements across batches on the basis of known confounders. This can be done, for instance, via propensity trimming and matching [42] subjects on the basis of observed covariates. To this end, we develop Causal DCORR to estimate adjusted effects and Causal ComBat to remove adjusted effects, both of which are discussed below.

The adjusted site effect also has limitations. For example, imagine that one batch has more individuals that have had a stroke, but stroke history is unmeasured. Stroke history would be critical to observe if it impacts the outcome. Thus, such effects are only causal under reasonably strong assumptions, specifically that there is no unmeasured confounding.

Crossover Site Effect Here we observe outcomes, exposures, and measured covariates again, but we obtain multiple measurements for each participant, or more specifically, one measurement for each exposure. Thus, we observe for each participant, $\{(y_i^{(t)}, t, x_i^{(t)})\}$ for all $t \in [K]$.

Definition 8 (Crossover Effect). *A crossover effect exists between batches t and t' if:*

$$f\left(y^{(t)}|t, x^{(t)}\right) \neq f\left(y^{(t')}|t', x^{(t')}\right).$$

When would a crossover effect be equivalent to a causal batch effect? Given that we are certain that any *traits* of the participants (i.e., variables that are constant for a given participant, such as genome) are the same across the two groups since the group members are identical. However, *states* may differ as they may be functions of location or time. Therefore, for a crossover effect to be equivalent to a causal batch effect there must be no unmeasured confounding states. For example, if being measured impacts subsequent states, then a crossover effect may not be indicative of a causal batch effect without further assumptions and/or experimental design considerations (such as randomizing exposure order across participants). Detection and correction for crossover effects amount to applying techniques for site effect detection or correction to datasets where each subject is measured in *every* batch.

2.2 Detecting batch effects using Causal Dcorr

At present, literature approaches for detecting the presence of batch effects are limited. Many of the more direct types of detectable effects, such as associational and conditional effects, fail to adaequately account for confounding biases present in the data. We instead propose the use of Causal DCORR, in which a conditional two-sample test is performed on pairs of observational studies which are balanced against measured demographic covariates.

Causal DCORR is performed as follows. Given measurements and covariates from n individuals across 2 batches, each with n_l individuals:

1. Identify the smallest dataset k' as the exposure dataset and the other dataset k as the control dataset.
2. Propensity trim and then match the largest integer less than $n_k/n_{k'}$ control individuals using nearest-neighbor matching to individuals in the exposure dataset. Methods 5 discusses the adjustment procedure in more detail.
3. Discard individuals from the exposure dataset who do not have matches in the control dataset, yielding the exposure cohort.
4. Discard individuals from the control dataset who are not matched to individuals in the exposure cohort.

5. Perform Conditional DCORR [43, 44] on the measurements of the matched exposure and matched control individuals, conditioned on the measured covariates X. The null hypothesis is that the two batches have the same distribution, against the alternative hypothesis that the two batches do not have the same distribution, conditional on the measured covariates X.

Figure 4C illustrates visually the causal procedures employed for demographic balancing. In the event that the conditioning set closes backdoor paths [32, 33], the adjusted effect detected by Causal DCORR is a causal batch effect, and does not require extrapolation assumptions like Conditional DCORR [15, 37, 38, 42]. If the conditioning set does not close backdoor paths, the effect detected is a conditional effect and may yield the detection of demographic effects.

2.3 Mitigating batch effects using Causal ComBat Unfortunately, many existing techniques for the removal of batch effects fail to adequately account for confounding biases that may be present in the data. We instead propose the use of Causal ComBat, in which Conditional ComBat is performed on a subset of observational studies in which all pairs of studies are balanced against measured demographic covariates. Causal ComBat is performed as follows. Given measurements and covariates from n individuals across K batches, each of which has n_k individuals:

1. Identify the smallest dataset k' as the exposure dataset and all $k \neq k'$ datasets as control datasets.
2. Propensity trim and then match the greatest integer less than $n_k/n_{k'}$ control individuals using nearest-neighbor matching to individuals in the exposure dataset. Methods 5 discusses the adjustment procedure in more detail.
3. Discard individuals from the exposure dataset who do not have matches in all K control datasets, yielding the matched exposure cohort.
4. Discard individuals from the control datasets who are not matched to the matched exposure cohort, yielding the matched control cohorts.
5. Perform Conditional ComBat [19] on the measurements of the matched exposure and matched control individuals across the K batches, conditioned on the measured covariates X.

In the event that the conditioning set closes backdoor paths [32, 33], Causal ComBat yields the removal of an internally valid causal effect and does not require extrapolation assumptions, unlike Conditional ComBat [15, 37, 38, 42]. If the conditioning set does not close backdoor paths, the effect removed is a conditional effect and may potentially yield the removal of demographic effects, as we saw in Figure 2. Appendix C depicts the impact on the empirical covariate distribution of the adjustment procedure.

2.4 Batch effects in biological datasets The four effects discussed above have immediate practical implications on measuring batch effects in modern biological datasets. To this end, we demonstrate the applicability of these effect types in the context of a neuroimaging mega-study, in which measurements are collected from individuals across various batches (the *exposures*). The logical process, however, extends beyond this context to many other biological data modalities, such as genomics. Figure 1A shows a directed acyclic graph, or DAG, which underlies a typical mega-study. The exposure is the batch in which participants' data are collected, and the outcomes are the measurements themselves. We seek to estimate the *causal estimand*, which is the causal effect of the exposure to a particular batch on the outcome (the *measurement*). Numerous covariates, both known and unknown, impart potentially confounding biases, in which the variables can influence both the exposure and the outcome. For instance, one batch collected in a children's hospital may tend to over-sample younger individuals relative to other batches, and younger children may have distinct patterns of brain connectivity compared to older children. Unmeasured covariates are often prominent confounders in biological datasets, making proper causal analyses troublesome. *Participant history* involves variables related to specific life experiences, both environmental and societal, that the individual has been exposed to. *Participant traits* are characteristics of a person that remain relatively constant over time. *Participant states* refer to characteristics of a person that change over an individual's lifetime. *Exposure determinants* are factors

which impact batch membership for a particular individual, but do not impact the measurement itself. *Outcome determinants* are factors which do not impact the batch assignment, but impact the outcome.

Figure 1B illustrates the implicit DAGs that are sufficient such that if they characterized the data, then each of the four effect types discussed above become valid causal batch effect estimands. If no covariates exist (observed or unobserved), then an associational effect is a causal effect (Figure 1B.I). Crossover effects can account for many types of measured and unmeasured covariates which are confounding (Figure 1B.III). Because of the crossover property, the batches will be balanced across certain measured and unmeasured covariates, specifically patient history and traits. Hence, many of the confounding variables from Figure 1A are deconfounded. However, unmeasured changes in participant state between different exposure groups (such as measuring individuals only during the daytime in one batch and only during the night time in another batch) remain potential confounders if not carefully balanced across exposure groups through either randomization or direct experimental intervention.

3 Results

3.1 Causal approaches outperform traditional approaches for batch effect detection and correction on simulated data Conditional DCORR and Causal DCORR are used to test for conditional and adjusted effects respectively in Figure 2. Across all simulations, simulated measurements are collected from a gaussian additive model, where the measurement tends to be lower when the covariate is higher, and the measurement tends to be higher when the covariate is lower. Simulated measurements are collected from one of the two batches with equal probability (0.5). In the bottom two simulations, the covariate distribution is equal for the two indicated batches, and both techniques are able to nearly always correctly identify whether or not a batch effect is present. In the top two simulations, however, the covariate distribution in batch 0 tends to favor smaller covariate values, whereas for batch 1 the covariate distribution is higher. This makes isolating the batch effect from the covariate-specific effect difficult without heavy assumptions regarding the measurement distribution, which are often not feasible or well enough established for high dimensional measurements. Conditional procedures struggle with this setting, and nearly always report the incorrect answer (detecting a batch effect when none is present, or vice-versa). On the other hand, causal strategies tend to be far more conservative in these types of difficult settings, and tend to report that any further analysis of the dataset will be inconclusive. These simulations highlight the empirical value of causal techniques, as the ability to conclude that the data do not support conclusions you are trying to make is far more principled than proceeding and doing the *wrong* thing.

Next, we investigate whether causal reasoning is useful in practice for adjusting batch effects. Across all simulations, simulated measurements are collected from an additive gaussian model with either a linear (Figure 3.I to 3.III) or non-linear (Figure 3.IV to 3.VI) covariate-specific effect as well as a batch-specific offset in 3(A). We performed these simulations for cases where the covariate distributions overlap (Figure 3.I and Figure 3.IV), have a moderate degree of overlap (Figure 3.II and Figure 3V), and have limited overlap (Figure 3.III and Figure 3.VI). In the case of limited covariate overlap, the covariate can be thought of as *confounding* the relationship between the batch and the measurement. The *true* signal (solid lines) represent the expected measurement for a particular covariate level. The shaded gray region represents the difference between the true signal in Batch 0 and Batch 1, which comprises the *batch effect*. Across all simulation settings, we ran Conditional `ComBat` (Figure 3.B) or Causal `ComBat` (Figure 3.C), assuming a linear covariate effect, where the fit model is shown in dotted or dashed lines. When the assumptions between the covariate and the measurements are correct, covariate overlap is irrelevant, as the covariate-specific signal can be extrapolated successfully across the entire range of the covariate. When the assumptions between the covariate and the measurements are incorrect, the batch effect can still be removed, as shown in Figure 3.III, when further causal adjustment conditions are satisfied (such as the covariate distributions overlapping). This can be conceptualized as the inaccurate assumptions of the model, in effect, being uniformly *misrepresented* by the model in

each of the two batches, which *still* enables a consistent estimate of the batch effect to be estimated and removed.

When the conditions for a causal adjustment are not satisfied, but `ComBat` is applied anyway, adjustment for batch effects introduces new batch-specific artifacts to the data, as shown in Figure 3.B.V and B.VI. Due to the faulty assumptions of the model, the Conditional `ComBat` corrected signal for Batch 0 is in fact *more different* from the true signal of Batch 1, despite the fact that the true underlying signal is identical across the two batches. When the batch removal strategy fails to mitigate, or *worsens* a batch effect, we term the resulting signal disparity to be a *residual batch artifact*. As shown in the simulation, these artifacts can be arbitrarily large depending on the nature of the incorrect assumption. In this example, the batch effect artifact introduced by conditional `ComBat` exceeds the magnitude of the batch effect in the raw data for V and VI. Simply looking at the points in Figure 3.A.VI, many trained researchers would likely conclude that a line seems reasonable for each batch's measurements with respect to the covariate, as the nonlinear inflection point of the sigmoid falls right where the covariate densities for each batch drop off. Any sort of principled analysis would have to, at best, take a complete guess as to what happens in the region of low covariate coverage for the disparate batches, which in this case, would be entirely wrong and, for practical purposes, could in fact do more harm than good. This presents an enormous point of caution when applying batch effect removal techniques to high-dimensional datasets with confounding, as it is infeasible to explore whether extrapolatory modelling assumptions are within reason on a dimension-by-dimension basis.

On the other hand, as shown in Figure 3.C, Causal `ComBat` first pre-aligns the covariate distributions, and even with model misspecifications, is able to successfully remove a batch effect for the subset of the distribution with sufficient covariate overlap. Significantly, causal strategies *explicitly prohibit* learning about data which falls outside of the region of demographic overlap. When overlap conditions are not met for a portion of the sample space, causal strategies do not do anything, as in C.III and C.VI. Taken together with Figure 2, techniques are therefore more conservative for batch effect detection and mitigation. We believe this to be favorable for batch effect detection and mitigation as, in practice, it is *impossible* to tell whether the assumptions of the model by `ComBat` are sufficient or not.

3.2 The CoRR Studies have disparate demographic characteristics

Figure 4A explores the demographic characteristics for the individuals in the CoRR mega-study. Many of the studies have a narrow age range, and several studies only include females. Because sex [16, 40, 50], age [14, 39, 47], and continent [26] are variables that have been associated with brain connectivity, they serve as conditional covariates used in our investigation.

Figure 4B investigates the level of demographic overlap in the CoRR mega-study, using the distribution-free overlapping index [31], as discussed in Appendix C. Many of the datasets do not overlap at all, and inference on the presence or absence of batch effects would be entirely model-based, as-per Figure 3VI. Further, while some of the datasets overlap, the level of balance varies widely. In the case where demographic imbalances are substantial, the detection or removal of batch effects would be extremely subject to model-based assumptions, as-per Figure 3V. From a causal perspective, this is troublesome, as the covariate records for the CoRR mega-study only include three covariates: age, sex, and continent of measurement. The addition of successive covariates can only reduce the estimated overlap between the pairs of datasets, so having poor overlap on such a coarse set of covariates indicates that the actual demographic overlap may be even lower. This would be problematic if, for instance, unmeasured covariates (such as participant mental health) are confounders.

3.3 Detecting Batch Effects in the CoRR mega-study

Figure 5A explores the four effects defined above in fMRI connectomes from the CoRR mega-study. The majority of associational and conditional effects (>90$\%$) are significant (partial distance correlation two-sample test, BH correction, $\alpha = 0.05$). However, these approaches are overly simplistic for concluding that a causal batch effect is indeed present because they fail to account for non-overlap of the covariate distributions between the subjects.

Effects that account for demographic distributions are examined in Figure 5B. Many pairs of studies could not have an adjusted effect estimated due to poor demographic alignment as shown in Figure 4B, which resulted in no suitable matches existing between the studies, indicated by a red X (279 of 406 pairs of studies). Colloquially, when covariate overlap is moderate or limited as in Figure 3, we cannot tell if effects are misrepresented (or, comparisons are unreasonable entirely) due to demographic imbalance. In this way, causal strategies prepended to batch effect detection and mitigation strategies are *more conservative*, in that they prevent the experimenter from potentially deriving spurious or erroneous conclusions due to confounding biases. Notably, adjusted conditional effects are estimable between all pairs of the American Clique (a group of separate studies consisting of similar demographics collected in North America). After adjustment for the sample characteristics of the demographics associated with individual studies, a majority of adjusted effects (>90$\%$) remain significant (partial distance correlation two-sample test, BH correction, $\alpha = 0.05$). The NKI Rockland Sample takes this a step further, allowing a crossover effect to be determined in a few pairs of batches (purple squares). This study was, in fact, collected on an identical set of participants, in the same location, with the same research technicians, with data varying only in the repetition time for the magnet used in the scanner. Indeed, for two of three comparisons, crossover effects remain prominent. This provides evidence that the parameters under which a study are conducted is a causal predictor of measured connectomes, assuming no participant state confounders are present.

3.4 Causal `ComBat` Produces Disparate Inference from Competing Correction Approaches

At this point, we have demonstrated, through simulation and real examples, if a covariate is a *confounder*, failure to properly account for demographic balancing can, potentially, yield improper detection and mitigation of batch effects and may, in turn, fundamentally alter true signals in the dataset. We saw that, for many of the CoRR [55] datasets, demographic balance was extremely poorly aligned, which allows only a fraction of the original possible comparisons between datasets to be analyzed in a theoretically, and empirically, reasonable manner. The final question we have is: does it matter? Even if we disrupt true signal in the dataset, can we still detect it irrespective of whether the signal is maintained in its unadulterated form?

To this end, we investigate the strength of the sex effect, conditional on age, in the connectomes before and after batch effect correction (Figure 6A). `ComBat` and Conditional `ComBat` are performed on the entire CoRR study (top row), and subsequently all techniques are restricted to the subset of connectomes upon which Causal `ComBat` was executed (the *American Clique*, bottom row). We also compared these techniques to NeuroComBat (Conditional and Causal NeuroH) [11, 34], an implementation of `ComBat` for neuroimaging data. The edges which show a significant, conditional sex effect (partial distance correlation, $\alpha = .05$) are colored from smallest test statistic to largest test statistic (rank = 1, dark purple). Causal approaches produce vastly different statistical inference compared to other correction techniques on the American Clique. Causal approaches were unable to be executed on the set of all studies, because many of the studies in the CoRR dataset do not overlap in terms of their covariate distributions (the red square indicates the analysis is not possible). Next, we seek to answer whether statistical inference for the entire CoRR study (top row) is similar to inference that would be obtained on the American Clique (Figure 6B) using only Causal `ComBat`. We compare the DICE overlap of the top n edges (by effect size) from each of the three non-causal approaches applied to all the data with the top n edges of Causal `ComBat` on the American Clique. A high DICE overlap indicates that the subsets of edges are similar. None of the techniques show high overlap with the edges that are indicated to have a large effect after correction with Causal `ComBat`. Finally, using the raw connectomes, `ComBat`, Conditional NeuroH, and Conditional `ComBat` tend to produce similar inferences, as all have high DICE overlaps near one. In contrast, they all have low overlap with Causal `ComBat` (Figure 6C), with DICE overlap with Causal `ComBat` nearly zero. On the other hand, Causal NeuroH has a high overlap with Causal `ComBat`.

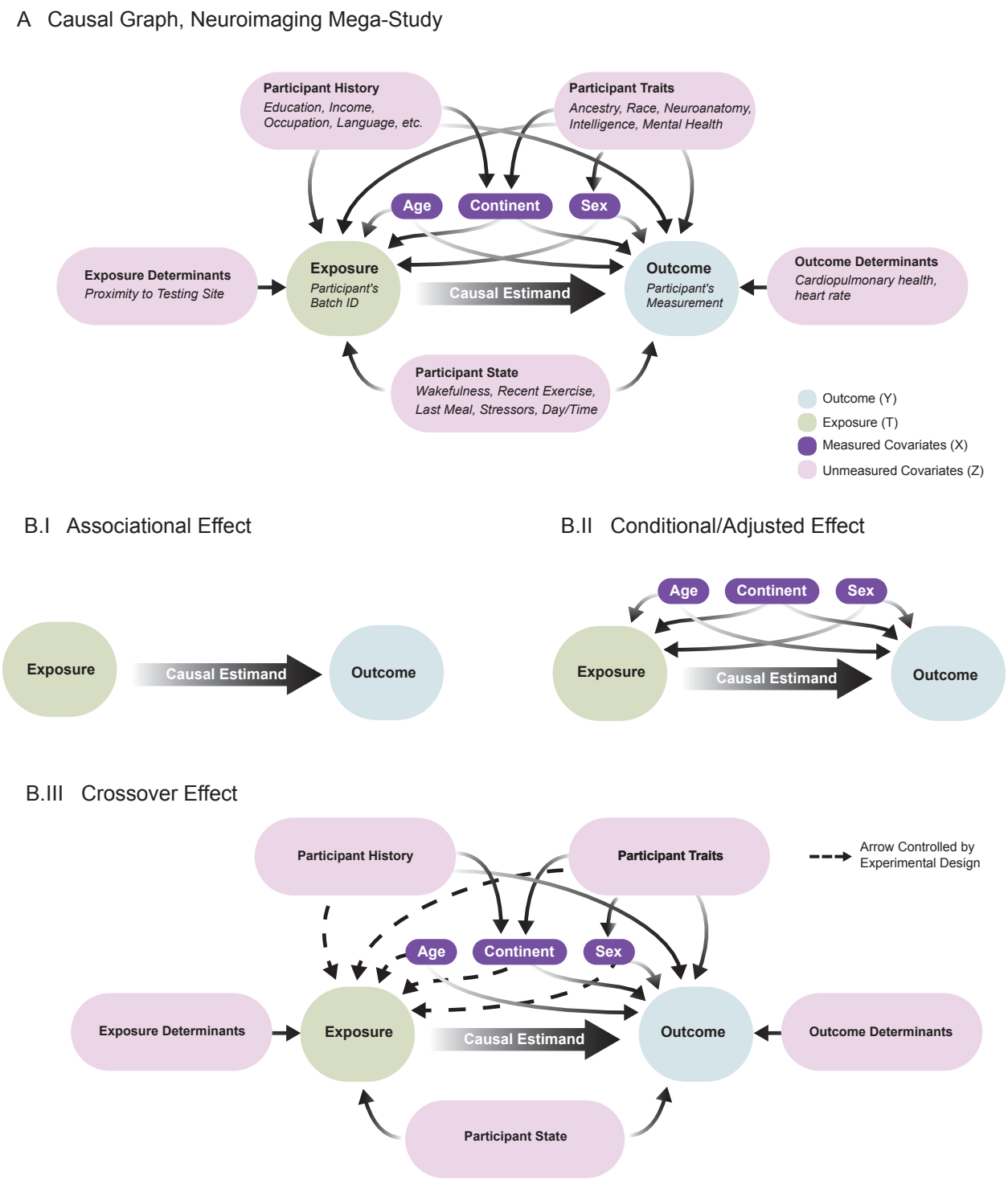

Figure 1: **Causal Graph of Study Covariates**. **(A)** A causal directed acyclic graph (DAG) illustrating potential relationships which can reasonably be assumed to underlie a mega-study. Descriptions reflect possible attributes that might fall into the specific exposures, outcomes, and covariates for a neuroimaging study, for illustration purposes. **(B)** DAGs which illustrate the assumptions which underlie assorted effects in† order for those effects to be causal. Associational effects **(B.I)** are causal when all external covariates are independent the exposure and outcome. Conditional effects and adjusted effects **(B.II)** are causal when the strong ignorability condition holds, and in particular when the measured covariates close backdoor paths. Crossover Effects **(B.III)** are causal when participant states are non-confounding between the exposure and the outcome. The experimental design of a crossover study ensures that other forms of measured and unmeasured covariates are non-confounding.

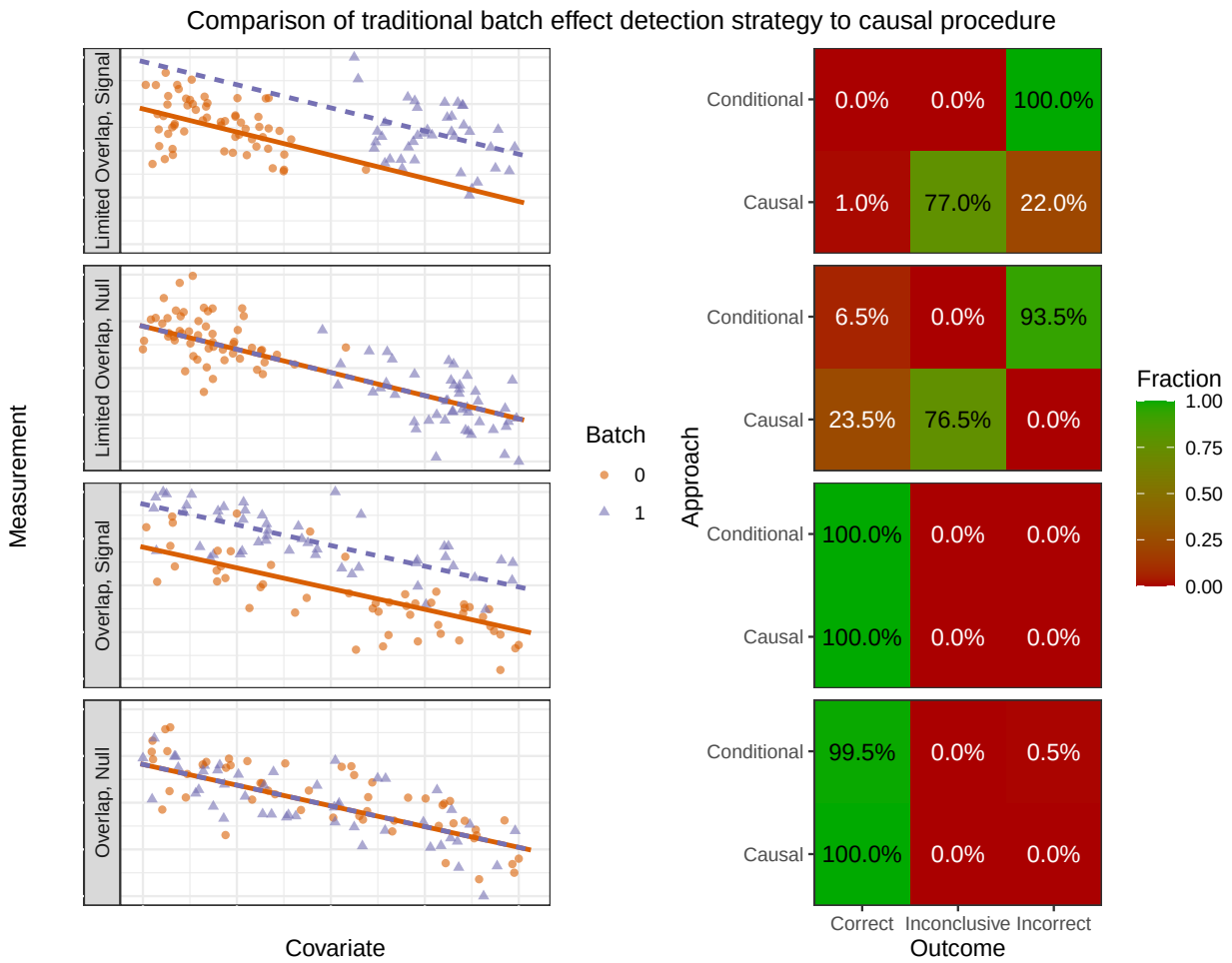

Figure 2: **Empirical simulations demonstrate the utility of causal approaches for batch effect detection**. $n = 400$ simulated univariate measurements are collected from a gaussian additive model (points) with equal probability of being from batch 0 or batch 1 (color). The expected measurement for a given batch at an indicated covariated value is indicated by the lines. The lines overlap when no batch effect is present (null simulations, rows two and four) and do not overlap when a batch effect is present (signal simulations, rows one and three). Tests are performed to determine whether a batch effect is present (or not) using conditional and causal strategies for each of $R = 200$ repeated simulations for each setting. For the top two rows, the covariate overlap between the two batches is limited (batch 0 tends to have lower covariate values, and batch 1 tends to have high covariate values). Consequently, isolating the covariate effect on the measurement from the batch effect on the measurement is difficult. Causal DCORR tends to be sensitive to this type of disparity and reasonably reports that the covariates are inconclusive to support inference for this particular question. On the other hand, Conditional DCORR tends to almost always yield the wrong answer (a batch effect is reported when none is present, and vice versa). Both Conditional and Causal DCORR tend to correctly identify batch effects when covariate overlap is high (bottom two rows). The details of these simulations are found in Appendix B.1.

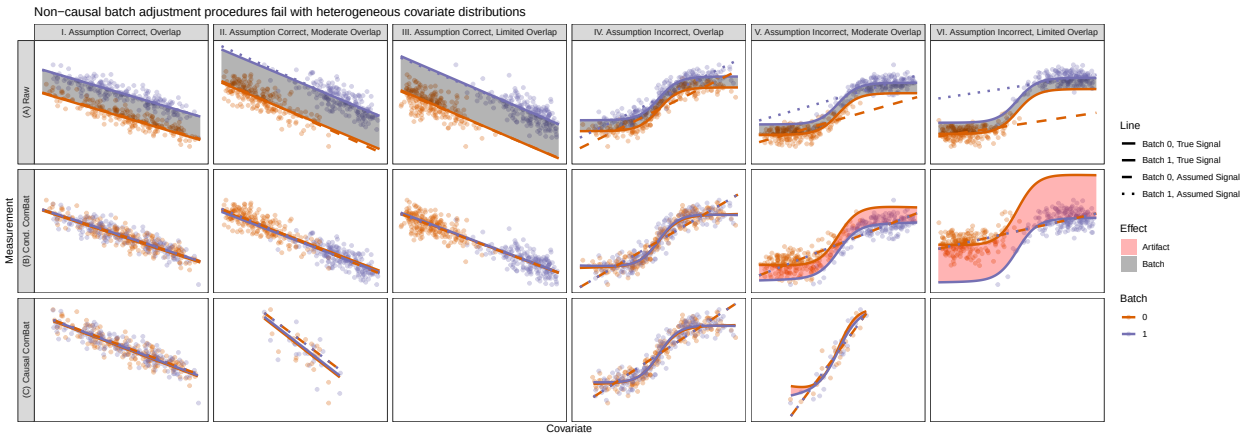

Figure 3: **Empirical simulations exhibit the shortcomings of Conditional** `ComBat`. $n = 400$ simulated univariate measurements are collected from a gaussian additive model (points) with equal probability of being from batch 0 or batch 1 (color). The batch effect (the difference between the two batches) is indicated by the translucent gray box. The expected measurement for a given batch at an indicated covariate value is indicated by the solid lines (the "true signal"). The signal assumed by the model employed is indicated by the dotted line (the "assumed signal"). Columns I to III show examples where the assumptions of `ComBat` are correct, and the fit model closely resembles the true signal in each batch across the covariate range (row A). Consequently, when the batch effect is removed (row B), the signal is consistent between the two batches. On the other hand, columns IV to VI show examples where the assumptions of `ComBat` are not correct. The fit model, a line for each batch, does not resemble the true signal, which is sigmoidal. When the conditions for covariate overlap are met as in IV, the batch effect can still be successfully removed. When the conditions for covariate overlap are not met as in VI, such as by Conditional `ComBat`, attempts to adjust for batch effects introduce a batch-specific artifact that dwarfs the initial batch effect by a factor of approximately 3 (red box). On the other hand, causal approaches facilitate robustness to covariate misspecifications, as in row (C). When demographic overlap is high, the batch effect is mitigated, and when demographic overlap is only moderate, Causal `ComBat` limits inference to the region of covariate overlap between the two batches, yielding a consistent estimate of the batch effect, whereas Conditional `ComBat` introduces a batch artifact of similar magnitude to the original batch effect (B.V). When there is limited demographic overlap (C.III and C.VI), Causal `ComBat` conservatively reports that there is insufficient data for inference. For further technical details of these simulations, see Appendix B.2.

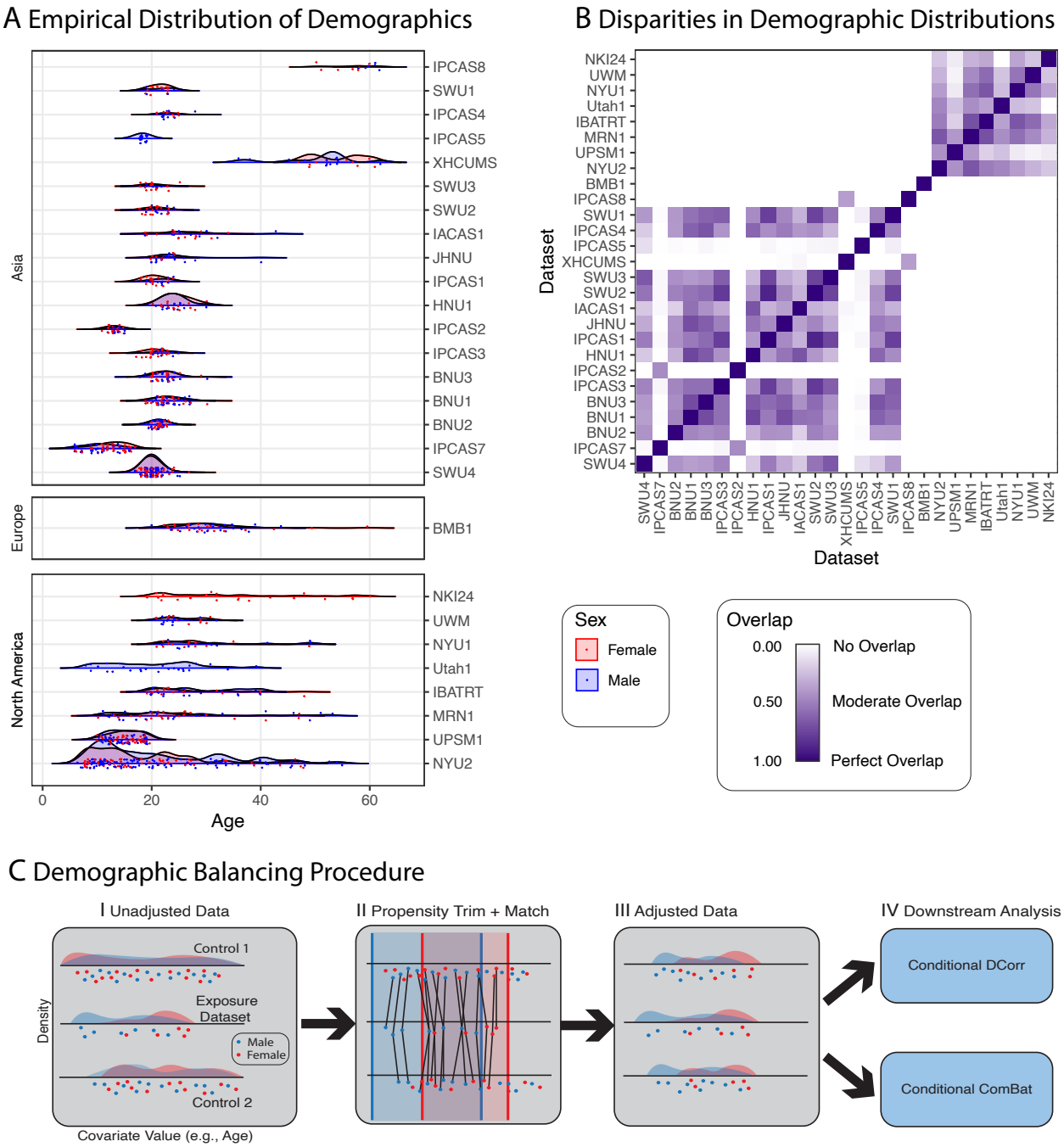

Figure 4: **Demographic data for each of the $N = 24$ studies from the CoRR Mega-Study**. **(A)** Each point represents the age of a participant corresponding to a single measurement, rows are studies, boxes are continents, and color indicates sex. **(B)** Even with only 3 covariates made available (sex, age, continent of measurement) the CoRR studies generally show extremely poor covariate overlap [31]. This makes inference regarding batch effects difficult. **(C)** The demographic balancing procedure, to demographically align poorly balanced datasets using Causal DCORR or Causal ComBat. (C.I) The unadjusted datasets are imbalanced in covariate distributions. The smallest dataset, the *reference*, has a narrower age distribution than the controls. (C.II) Propensity trimming (shaded boxes) and matching (lines) are conducted to identify reasonable matches between the reference and the control datasets. (C.III) The adjusted datasets have far improved demographic overlap after propensity trimming, matching, and removing reference subjects who do not have suitable matches in the control datasets. (C.IV) Downstream batch effect detection via DCORR or correction using ComBat are performed on the data using conditional strategies on the adjusted data.

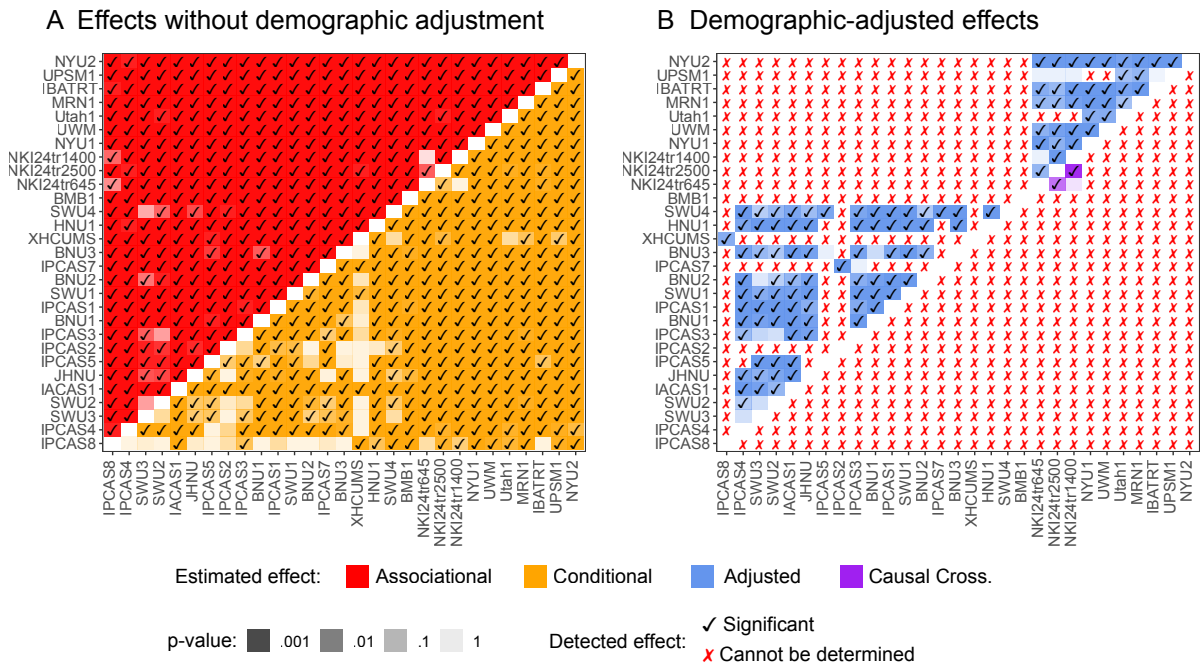

Figure 5: **Comparison of Estimated Effects for CoRR Mega-Study**. Heatmaps indicating the p-value of effect estimates per pair of studies. Studies are organized by continent, followed by the number of samples in the study. Comparisons which are significant at $\alpha = .05$ are indicated by a black check. Since effects are symmetric (an effect between batch t and t' is equivalent to an effect between batch t' and t), we collapse symmetric heatmaps into a single triangle for each effect type. **(A)** Effects which can be estimated but do not make adjustments for demographics. Associational and conditional effects can always be estimated between pairs of studies. (B) Effects which account for demographics through covariate adjustment. Squares in which a causal effect was not estimable are indicated by a red X. Effects which properly account for demographics require covariate overlap, which is indicated in Figure 4B.

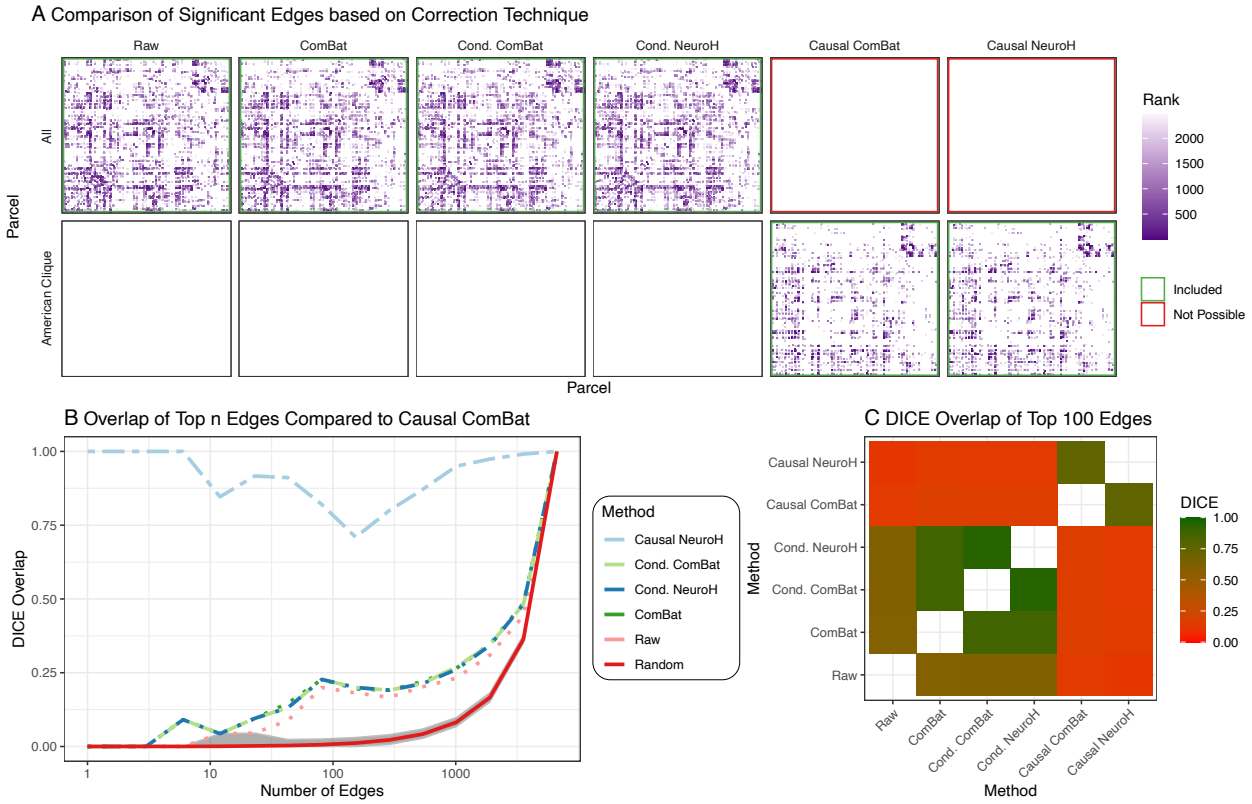

Figure 6: **Significant Edges Before and After Batch Effect Removal**. **(A)** The presence of a sex effect (conditional on individual age) is investigated for each edge in the connectome. The top 100 significant edges are shown in rank-order from largest (rank = 1) to smallest sex effect ($\alpha = .05$, Benjamini Hochberg [2] correction). Analysis is either performed over *all* individuals (top row) or only upon the individuals for which sufficient demographic overlap could be obtained, the *American clique* (bottom row). Causal `ComBat` and Causal NeuroH can only be executed on the American Clique (red square denotes Causal approaches are not possible with *all* studies). **(B)** The DICE overlap of the top n edges of each batch effect removal technique on all the data (green squares, top row) as compared to those from Causal `ComBat` (green square, bottom row). The red line (random) indicates the overlap to be obtained for a particular choice of n to be expected as a result of random chance, and the gray ribbon indicates the 99% confidence interval of the estimate (1000 repetitions). The DICE overlap increases as a function of n, regardless of whether any signal is actually present. **(C)** The DICE overlap of the top 100 edges for all pairs of correction techniques indicated with a green square from **(A)**. Overlap of the top signal edges is high between no correction (raw), `ComBat`, Conditional `ComBat`, and Conditional NeuroH, but all techniques have low overlap with Causal `ComBat`and Causal NeuroH, indicating that Causal approaches yield measurements with signal that the associational approaches fail to identify.

4 Discussion Our primary conceptual contribution is establishing that batch effects can be formalized as causal effects. Given this realization, we propose a framework for quantifying and removing batch effects in high-dimensional datasets featuring non-Euclidean measurements. We propose a non-parametric test for quantifying batch effects, Causal DCORR, and develop a strategy for the removal of batch effects, Causal ComBat, to limit confounding biases. Finally, our neuroimaging use-case shows the utility of the methods developed herein for estimating and removing batch-related effects from large biological datasets. Specifically, our methods identify different causal effects as compared to prior approaches, each of which identifies features similar to a completely unadjusted approach, which is well established in the causal literature to permit numerous false positives and false negatives [7, 10]. Together, our work rigorously defines and studies measurement bias decoupled from demographic confounders in complex, non-Euclidean data.

Together, the conclusions of our work bring into focus the pervasive question of how to properly interpret neuroimaging—or more generally, multi-site scientific—studies.This concern is at the root of any statistical inference task: a conflict between the internal and external validity. Internal validity refers to how well the conclusions generalize from the *sample* population to the *study* population; that is, from the observed samples to other samples that are distributed the same as the observed samples. External validity refers to the degree to which the conclusions generalize to the *target* population; that is, the population to which we wish to apply the conclusions of our inferences. The target population is typically much broader than the study population, to include, for example, all members of the species, or possibly even multiple species.

Through simulation, we demonstrated that minor misspecifications of the statistical model employed for batch effect removal can be disastrous in the presence of confounding biases. Specifically, a minor change of the relationship between the confounder (the covariate) and the measurement from a straight line to a (still monotonic) nonlinearity, the sigmoid, not only inhibited Conditional ComBat from removing a batch effect, but also introduced an artifact that dwarfed the magnitude of the original batch effect itself. As discussed in the Appendix B.2, the resulting estimate of the batch effect must, by construction, be considered neither statistically unbiased nor consistent, thus failing two preconditions for internal validity [51]. Colloquially, the statistical model is *always* wrong, and therefore we *cannot possibly* know whether models employed for batch effect correction will be reasonable to apply to out-of-sample data (e.g., areas of the covariate distribution for which there is no covariate overlap). That is, we cannot tell whether the data we have will fall into Figure 3.III and the assumptions of the batch effect correction technique will be reasonable, or 3.VI where the assumptions of the batch effect correction technique will be entirely unreasonable. On the other hand, causal strategies can help us to apply far more conservative logic, indicating to us when batch effects are unreasonable to estimate. Alternatively, they can aid us to first balance the covariate distributions so that we can avoid the pitfalls of Figure 3.B.V or B.VI.

Given the major shortcomings theoretically and empirically of traditional approaches for detecting and mitigating batch effects, we therefore chose to prioritize the development of strategies which sub-sample individuals into demographically-aligned subsets using causal techniques. In so doing, we prioritized internal over external validity, as internal validity is a prerequisite for external validity. Colloquially, one cannot generalize results of an experiment to a target population if the results are, at best, dubiously applicable to the study population. The trade-off of subsampling individuals is that sample size, sample diversity, and external validity are exchanged for internal validity. We saw this tradeoff materialize dramatically in the CoRR dataset, where over half of all possible dataset pairs could not be assessed for batch effects due to a lack of demographic alignment.

The final hurdle of our analysis, therefore, is to address the question: does the internal validity of batch effect removal techniques actually impact downstream statistical inference? A failure to remove batch effects in an internally valid manner, we believe, presents a substantial hurdle for producing internally valid statistical inference downstream, since downstream statistical inference is a product of the

corrected measurements. Specifically, one can endeavor to mitigate batch effects in one of two complementary ways. First, one can filter individuals by ensuring demographic balancing, and then run the entire analysis only on those individuals (as causal approaches, like Causal `ComBat` or Causal NeuroH, do4). Second, one can run an algorithm for batch effect correction (and potentially benefit from a richer number of samples), and then filter to ensure demographic balancing only when measuring downstream demographic-specific effect sizes (as we did by looking for a sex effect only considering individuals from the Raw, `ComBat`, Conditional `ComBat`, and Conditional NeuroH corrected connectomes in the American Clique). If internally valid, causal batch effect correction techniques may substantially restrict the sample size. Perhaps, even if the batch effect correction technique is not internally valid, measurements corrected using it may still have utility for downstream analysis. We anticipated that the most significant features for the inference task would be, at least, ordered similarly between the two analyses. However, our finding that the analyses produce radically different downstream inferences, even when we restrict the non-causal techniques to the same datasets, suggests that there is a link between downstream conclusions and the internal validity of batch effect correction techniques. Stated another way, when we perform batch adjustment using as few assumptions as possible about the study population through causal techniques, we get extremely disparate downstream scientific conclusions from state-of-the-art conditional techniques. This suggests to us that further work is needed to better understand how the removal of batch effects can be achieved while mitigating the deleterious effects on either internal or external validity through careful consideration of the study populations of analyses.

Biomedical data science, including neuroimaging and connectomics, are plagued by a lack of generalizability and replicability [3, 45]. While many investigations posit that this may be a consequence of small sample sizes or overly simplistic datasets [28, 45] lacking sufficient subject-specific measurements, we argued here that a lack of understanding regarding batch effects, and more fundamentally *causality*, further exacerbates these issues. This work suggests that harmonized analyses should be conducted with both harmonized measurement parameters and demographic distributions. This represents a departure from the manner in which many mega-studies, including so-called harmonized effects, are currently generated [55], in which potentially demographically-disparate populations are analyzed and only loosely harmonized on the basis of the measurement protocols. We saw that post-hoc batch effect detection and removal (and consequently, downstream statistical inference) presents both theoretical and conceptual inconsistencies with regard to internal validity when not first passed through the lens of causality. This problem is highlighted by looking at the poor demographic overlap for popular neuroimaging studies such as CoRR in Figure 4, and in the ABIDE and SRPBS studies detailed in Appendix C. Future work will focus on applying the methods developed here to harmonize mega-studies such as the Adolescent Brain Cognitive Development (ABCD) [20], which includes $N > 12,000$ demographically similar individuals from across the United States, and measurements were produced with a consistent, harmonized measurement protocol. Further, future studies may seek to build upon the NKI-RS and the recent work by Noble et al. [29] by collecting measurements from the same expansive and diverse group of people across multiple neuroimaging sites or scanning protocols. Our work provides a theoretical foundation for evaluating existing neuroimaging studies, such as Noble et al. [29], Yamashita et al. [52], which advocate for the aggregation of studies featuring individuals measured at a wide array of sites (so called *travelling subject* datasets), so that the nature of batch effects can be explored with minimal assumptions needed due to the crossover property. In such datasets, scientists can appreciate internally valid demographic-specific effects on the measurement, and learn more reasonable modeling assumptions, so that perhaps extrapolatory pre- or post-hoc batch effect removal techniques (such as in Figure 3.III) can be employed to mitigate the batch effects in other non-demographic-aligned datasets. Failure to attain a comprehensive understanding of batch effects and the extent to which they pervade statistical inferences, we believe, calls into question the validity of existing results in scientific meta-analyses.

Code Availability The code used for analysis within this manuscript is available at github.com/ebridge2/batch_effects, and a docker container with all software versions is available at hub.docker.com/r/neurodata/batch_effects.

Data Availability The raw data analyzed in this manuscript can be obtained at CoRR Mega-Study. The pre-processed data analyzed in this manuscript is available at neurodata.io/mri.

Acknowledgements The authors are grateful for the support from the National Science Foundation (NSF) administered through NSF Career Award NSF 17-537, the National Institute of Health (NIH) through National Institute of Mental Health (NIMH) Research Project 1R01MH120482-01, and the NIH through Research Project RO1AG066184-01. We also wanted to thank Betsy Ogburn for numerous insightful conversations regarding the presentation and framing of this work.

5 Methods

5.1 Covariate Adjustment The exposed group t is selected to be the smaller of the two groups, and the unexposed group t' is selected to be the larger of the two groups, where n_t is the number of individuals in the exposed group and $n_{t'}$ is the number of individuals in the unexposed group. The "covariate overlap" procedure attempts to ensure positivity of the propensity distribution for the unexposed group (i.e., $e(t'|x) > 0$). Intuitively, we exclude individuals from the unexposed group who do not appear "similar" to individuals in the exposed group. In this work, covariate overlap is established through logistic regression by excluding individuals in the control group with a propensity for exposure lower than 0.01. Similarly, the "covariate balancing" procedure attempts to re-weight observations in the per-batch covariate distributions such that the covariate distributions are approximately equal (i.e., $f(x|t) \approx f(x|t')$). In this work, we perform $k:1$ nearest-neighbor matching using the `MatchIt` package [15]. The number of matches $k = \lfloor \frac{n_{t'}}{n_t} \rfloor$ is chosen to be the largest number of unexposed matches possible. Individuals are balanced on the basis of individual sex, individual age, and individual continent of study. As there are likely many other categories with which brain connectivity may be confounded, we do not believe this covariate set is sufficient to identify a Causal Batch Effect 1, as we would need to be confident that these covariates exhibited the covariate sufficiency property. We perform exact matching on the basis of individual sex and individual continent of measurement, and use a 0.1-standard deviation caliper on the propensity score to obtain at most k matched participants for each treated individual [35].

5.2 Hypothesis Testing Recall that statements of the form $f(y) = g(y)$ against $f(y) \neq g(y)$ are equivalent to $P_f = P_g$ against $P_f \neq P_g$, as probability densities uniquely define distribution functions. Therefore, hypotheses for the effects described in Section 2.1 are natural two-sample and conditional two-sample testing procedures. A natural test statistic for the two-sample testing procedure is the Distance Correlation [44], which is a non-parametric test for testing whether two variables are correlated. A simple augmentation of the distance correlation procedure [41, 48] shows that `dcorr` can be used for the two-sample test, or a test of whether two samples are drawn from different distributions. `dcorr` is exactly equivalent in this context to the Maximum Mean Discrepency (MMD), which embeds points in a reproducing kernel Hilbert Space (RKHS) and looks for functions over the unit ball in the RKHS that maximize the difference of the means of the embedded points. When we instead consider the conditional two-sample test (i.e., a test of $f(y|x) = g(y|x)$ against $f(y|x) \neq g(y|x)$), we instead use the partial distance correlation [43], a kernel-based approach in which the points are embedded in a new, non-linear Hilbert Space, which augments the traditional linear Hilbert Space used in distance correlation to allow the definition of the squared distance covariance. Below, we let $\mathbf{Y} = (y_i) \in \mathcal{Y}^n$ denote realizations across both samples and $\vec{t} = (t_i) \in \{t, t'\}^n$ indicate from which sample each realization is drawn. $\mathbf{X} = (x_i) \in \mathcal{X}^n$ denotes covariates which are known about the objects of interest.

Associational Effect We have the following null and alternative hypotheses:

$$H_0 : f(y|t) = f(y|t') \text{ against } H_A : f(y|t) \neq f(y|t')$$

A test of the preceding hypotheses is performed using the distance correlation, and the natural test statistic is $\texttt{dcorr}(\mathbf{Y}, \vec{t})$.

Conditional Effect We have the following null and alternative hypotheses:

$$H_0 : f(y|t, x) = f(y|t', x) \text{ against } H_A : f(y|t, x) \neq f(y|t', x)$$

A test of the preceding hypotheses is performed using the partial distance correlation, and the natural test statistic is $\texttt{pdcorr}(\mathbf{Y}, \vec{t}|\mathbf{X})$.

Adjusted Conditional Effect We have the following null and alternative hypotheses:

$$H_0 : \tilde{f}(y|t, x) = \tilde{f}(y|t', x) \text{ against } H_A : \tilde{f}(y|t, x) \neq \tilde{f}(y|t', x)$$

Unlike the preceding tests, we instead consider the data $(\tilde{\mathbf{Y}}, \vec{\tilde{t}}, \tilde{\mathbf{X}})$, which are the measurements, sample indicators, and covariates of the n realizations after covariate adjustment. A test of the preceding hypotheses is performed using the partial distance correlation, and the natural test statistic is $\texttt{pdcorr}(\tilde{\mathbf{Y}}, \vec{\tilde{t}}|\tilde{\mathbf{X}})$.

Causal Crossover Effect We have the following null and alternative hypotheses:

$$H_0 : f\left(y^{(t)}\middle|t, x^{(t)}\right) = f\left(y^{(t')}\middle|t', x^{(t')}\right) \text{ against } H_A : H_0 : f\left(y^{(t)}\middle|t, x^{(t)}\right) \neq f\left(y^{(t')}\middle|t', x^{(t')}\right)$$

If the known covariates are identical between batches t and t', we test the preceding hypotheses using the distance correlation, and the natural test statistic is $\texttt{dcorr}(\mathbf{Y}, \vec{t})$. If the known covariates are not identical between batches t and t', we test the preceding hypotheses using the partial distance correlation, and the natural test statistic is $\texttt{pdcorr}(\mathbf{Y}, \vec{t}|\mathbf{X})$.

More Than Two Batches The above approaches generalize sufficiently to K batches using K-sample testing approaches. With f_k for $k \in [K]$ denoting the densities associated with K sites or batches, this motivates hypotheses of the form:

$$H_0 : f_k = f_l \text{ for all } k, l \text{ against } H_A : f_k \neq f_l \text{ for some } k \neq l,$$

which can be tested using the distance correlation or the partial distance correlation as above, with the caveat that $\vec{t}$ becomes the matrix $\mathbf{T} = (t_{i,k}) \in \{0, 1\}^{n \times K}$. Each entry $t_{ik} = 1$ if sample i is in batch k, and 0 otherwise. For the purposes of this manuscript, we focus on the two-batch case.

p-values and Multiple Hypothesis Correction p-values in this manuscript are estimated using permutation testing, which is an approach to obtain the distribution of the test statistic under the null with minimal assumptions and approximations [8]. All p-values are estimated using $N = 10{,}000$ permutations. Across all figures associated with this work, we are concerned with obtaining a proper estimate of the rate at which we detect effects (*discoveries*). Therefore, we control the false discovery rate (FDR) with the Benjamini-Hochberg Correction [2].

5.3 Site Effect Correction To correct for site effects, we compare both z-scoring per-feature within each batch [22] and traditional `ComBat` to Causal `ComBat`.

5.4 Control Numerical Experiments Control experiments are performed to ensure that after batch effect correction, the resulting data maintains interpretability and utility for scientific inquiry. Even if the data is devoid of batch effects, it must still be useful for downstream inference. For our connectome data, we identify two key control scenarios, the preservation of demographic effects and the preservation topological effects, which are desirable to preserve after batch effect correction.

Testing Topological Properties

Demographic Effect Demographic effects are investigated across both the subset of connectomes upon which Causal `ComBat` is executed (the American Clique) and the full dataset. We observe the tuple $(y_i(k,l), s_i, a_i, t_i)$ for $i \in [n]$, and $k, l \in [V]$, where $V = 116$ denotes the number of parcels in the Automated Anatomical Labelling (AAL) parcellation [27]. We suppose that $Y(k,l)$ is the $[0,1]$-valued random variable denoting the weight of edge (k,l), S is the binary-valued random variable denoting the biological sex, A is the positive real-valued random variable denoting age, and T is the $[K]$-valued random variable denoting the batch. We let $\vec{y}(k,l) = (y_i(k,l)) \in [0,1]^n$ denote the realized edge weights, $\vec{s} = (s_i) \in \{0,1\}^n$ denote the realized biological sexes, $\vec{a} = (a_i) \in \mathbb{R}^n$ denote the realized biological ages, and $\vec{t} = (t_i) \in [K]^n$ denote the realized batches. We say that a **demographic sex effect** exists when:

$$f(y|a,s) \neq f(y|a,s')$$

To test for a demographic sex effect, we have the following null and alternative hypotheses:

$$H_0 : f(y|a,s) = f(y|a,s') \text{ against } f(y|a,s) \neq f(y|a,s')$$

We are able to test the preceding hypothesis using the partial distance correlation, and the test statistic is $\texttt{pdcorr}(\vec{y}(k,l), \vec{s}|\vec{a})$.

5.5 Datasets The CoRR Mega-Study [55] is an aggregate dataset consisting of 24 studies collected with a similar goal: assessing the reliability and reproducibility of neuroimaging data. The mega-study consists of 1313 individuals, most of whom are measured numerous times, for a total of $N = 3597$ connectomes. All connectomes are estimated using the `m2g` (MRI to Graphs) pipeline [21], which provides a wrapper for the `CPAC` Pipeline [4]. fMRI scans for each individual are first processed to remove motion artifacts using `mcflirt` [17]. The fMRI scans are then registered to the corresponding individual's anatomical scan using FSL's boundary-based registration (BBR) via `epireg` [13]. A non-linear transformation from the individual's anatomical scan to the MNI152 [9] template is estimtaed using `FNIRT` [18]. Nuisance artifacts are removed by fitting the voxelwise timeseries to a regression model incorporating regressors for the Friston 24-parameter model [12], the top five principal components of the voxelwise timeseries in cerebrospinal fluid `aCompCor` [1], and a quadratic drift term. The adjusted voxelwise timeseries is downsampled to the regions of interest (ROIs) of the Automated Anatomical Labelling (AAL) parcellation [27] by taking the spatial mean signal for each timepoint across voxels within the region of interest. Functional connectivity is estimated using the pairwise correlation between all pairs of ROI timeseries within the AAL parcellation. Parcels are sorted throughout the manuscript according to hemispheric order, in which the parcels are aligned with left hemisphere parcels followed by right hemisphere parcels. Within hemisphere, parcels are sorted by AAL parcel number. For each study, we have baseline covariates for the continent, sex, and the age of participants.

The American Clique The "American Clique" describes a subset of the CoRR Mega-Study in which the sample populations share similarities in sample demographic characteristics. These studies share a demographic focusing on males and females (in roughly equal proportions) of individuals across a wide age range, and include the "NYU2", "IBATRT", "MRN1", "UWM", and "NYU1" studies. The 833 connectomes comprising the studies of the American clique are reduced to the $N = 321$ connectomes with maximal demographic overlap identified through covariate adjustment 5.1.

The NKI Rockland Sample [30] is a single study from the CoRR Mega-Study consisting of 24 individuals, each of whom is measured two times across three functional MRI acquisition protocols, which vary in the repetition time for each slice of the sequence (TR). The data was collected with the intention of investigating the impact of the different MRI protocols in a crossover-randomized approach. Due to the crossover property, evidence in favor of an effect provides strong evidence of a causal batch effect. Images with a TR of 645 millisecond (ms), 1400 ms, and 2500 ms are measured, with the prompt for each subject remaining identical.

References

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Appendix A. Correction for Batch-Related Effects.

Algorithm 1 Causal ComBat. The Causal `ComBat` approach for batch effect correction. Conditional `ComBat` is performed on demographically matched batches to eliminate confounding biases in observational studies. The smallest batch is arbitrarily chosen as the treated batch, and then successive batches are matched against the treated batch. Treated individuals (as well as their matched controls) with no suitable matches in one (or more) batches are eliminated from the analysis. `CovariateMatch()` is a function which takes the treatment and control covariates and matches control individuals to treatment individuals. $\mathcal{I}^k_{mat}$ is a list of the treated individuals with at least one match, and $\mathcal{M}^k_{mat}$ is a list of the treated individual that each control individual was (potentially) matched to. `BalanceCovariates()` uses these lists to identify the treatment individuals who have matches across all control batches and then excludes control individuals who are not matched to treatment individuals with matches across all batches.

Input: The tuples $(\mathbf{Y}^{(k)}, \mathbf{X}^{(k)})$ for $k = 1, \ldots, K$, where $\mathbf{Y}^{(k)} \in \mathbb{R}^{n_k \times p}$ denotes the measurements from batch id k, and $\mathbf{X}^{(k)} \in \mathbb{R}^{n_k \times d}$ denotes the covariates from batch id k, where $N = \sum_k n_k$ is the total number of measurements.

Output: The $N' \times p$ batch effect corrected data, where $N' \leq N$.

function CAUSALCOMBAT($\mathbf{Y}, \mathbf{X}, \vec{t}$)
  $\tilde{\mathbf{Y}}, \tilde{\mathbf{X}}, \tilde{n} = \texttt{BalanceCovariates}(\mathbf{Y}, \mathbf{X})$
  Let $\vec{t} = (1_{\tilde{n}_1}, 2_{\tilde{n}_2}, \ldots, K_{\tilde{n}_K})$ ▷ vector indicating the batch id of each individual
  $\tilde{\mathbf{Y}}_n = \texttt{ComBat}(\tilde{\mathbf{Y}}, \tilde{\mathbf{X}}, \vec{t})$ ▷ Remove the effect due to the batch $\vec{t}$, conditional on the covariates $\mathbf{X}$
  return $\tilde{\mathbf{Y}}_n$ ▷ Return the batch
end function
function BALANCECOVARIATES($\mathbf{Y}, \mathbf{X}$)
  $k' = \text{argmin}_k \, n_k$ ▷ Select treatment study to be the smallest study
  for $k \neq k'$ **do**
    $\mathcal{M}^k_{mat}, \mathcal{I}^k_{mat} = \texttt{CovariateMatch}(\mathbf{X}^{(k')}, \mathbf{X}^{(k)})$ ▷ Covariate match the two studies
  end for
  $\mathcal{I}_{mat} = \bigcap_{k \neq k'} \mathcal{I}^k_{mat}$ ▷ Identify treatment individuals with a control match across all control groups
  $\mathbf{Y}^{(k')} = \mathbf{Y}^{(k')}[\mathcal{I}_{mat}, :]$ ▷ Remove other treatment individuals
  $\mathbf{X}^{(k')} = \mathbf{X}^{(k')}[\mathcal{I}_{mat}, :]$
  $n_{k'} = |\mathcal{I}_{mat}|$ ▷ Number of treated individuals remaining
  for $k \neq k$ **do**
    $\mathcal{J}^k_{mat} = \texttt{which}(\mathcal{M}^k_{mat} \, \%in\% \, \mathcal{I}_{mat})$
      ▷ Control individuals matched to treatment individuals with matches across all groups
    $\mathbf{Y}^{(k)} = \mathbf{Y}^{(k)}[\mathcal{J}^k_{mat}, :]$ ▷ Remove other control individuals
    $\mathbf{X}^{(k)} = \mathbf{X}^{(k)}[\mathcal{J}^k_{mat}, :]$
    $n_k = \left|\mathcal{J}^k_{mat}\right|$ ▷ Number of control individuals remaining
  end for
  $\mathbf{Y} = [\mathbf{Y}^{(1)}; \ldots; \mathbf{Y}^{(K)}]$ ▷ raw measurements across batches
  $\mathbf{X} = [\mathbf{X}^{(1)}; \ldots; \mathbf{X}^{(K)}]$ ▷ covariates across batches
  return $\mathbf{Y}, \mathbf{X}, n$
end function

In Figure 7, we examine the prevalence of effects between different studies. It is important to note that whereas Causal `ComBat` can only be run on the American Clique, both `ComBat` and Z-scoring can be run on all studies. Recall that associational effects investigate whether *any* batch effects are present between pairs of studies (either measurement- or demographics-related). Both `ComBat` and Z-scoring eliminating nearly *all* variability between pairs of studies suggests that `ComBat` and Z-scoring

Figure 7: Empirical distribution of p-values for each estimated effect type by batch correction strategy.

are eliminating variability that is directly related to natural biological variability, which is not a favorable outcome. For both strategies, associational effects are not significant for 100% of comparisons. This is because the studies differ on the basis of demographic covariates possessing signal, and therefore observing no associational batch effects after correction implies we have removed demographic signal. On the other hand, limiting oneself to only pairs of studies in which adjusted effects are estimable with Causal `ComBat` may offer a solution to this undesirable property of Z-scoring and naive `ComBat`.

Appendix B. Simulations.

B.1 Batch Effect Detection Simulations $R = 200$ iterations of each simulation are produced and the following question is asked: do the measurements, conditional on the covariates, differ between batch 0 and batch 1? For each iteration, for each simulation, we sample $n = 100$ points from Batch 0 or Batch 1 with probability 0.5; e.g., $T_i \overset{iid}{\sim} \text{Bern}(0.5)$. The simulation settings are:

Limited Overlap, Signal The covariate distribution is:

$$X_i | T_i = t = \overset{d}{\sim} \begin{cases} \text{Beta}(2, 8) & t = 0 \\ \text{Beta}(8, 2) & t = 1 \end{cases}$$

With $Z_i \overset{iid}{\sim} \mathcal{N}(0, 1)$, the measurement is:

$$Y_i = -2(X_i - .5) + \frac{1}{2} Z_i + T_i.$$

Limited Overlap, Null The covariate distribution is:

$$X_i|T_i = t \overset{d}{\sim} \begin{cases} \text{Beta}(2,8) & t = 0 \\ \text{Beta}(8,2) & t = 1 \end{cases}$$

With $Z_i \overset{iid}{\sim} \mathcal{N}(0,1)$, the measurement is:

$$Y_i = -2(X_i - .5) + \frac{1}{2}Z_i.$$

Overlap, Signal The covariate distribution is $X_i \overset{iid}{\sim} \text{Unif}(0,1)$. With $Z_i \overset{iid}{\sim} \mathcal{N}(0,1)$, the measurement is:

$$Y_i = -2(X_i - .5) + \frac{1}{2}Z_i + T_i.$$

Overlap, Null The covariate distribution is $X_i \overset{iid}{\sim} \text{Unif}(0,1)$. With $Z_i \overset{iid}{\sim} \mathcal{N}(0,1)$, the measurement is:

$$Y_i = -2(X_i - .5) + \frac{1}{2}Z_i.$$

B.2 Batch Effect Removal Simulations $n = 400$ points are sampled from Batch 0 or Batch 1 with probability 0.5; e.g. $T_i \overset{iid}{\sim} \text{Bern}(0.5)$. We have the following 4 simulations, in which the covariates and measurements are normalized to fall on the same scale for visualization purposes:

Assumption Correct, Overlap The covariate distribution is $X_i \overset{iid}{\sim} \text{Unif}(0,1)$. With $Z_i \overset{iid}{\sim} \mathcal{N}(0,1)$, the measurement is:

$$Y_i = -2(X_i - 0.5) + Z_i + T_i.$$

Assumption Correct, Moderate Overlap The covariate distribution is:

$$X_i|T_i = t \overset{d}{\sim} \begin{cases} \text{Beta}(2,6) & t = 0 \\ \text{Beta}(6,2) & t = 1 \end{cases},$$

The measurement is:

$$Y_i = -2(X_i - 0.5) + Z_i + T_i.$$

Assumption Correct, Limited Overlap The covariate distribution is:

$$X_i|T_i = t \overset{d}{\sim} \begin{cases} \text{Beta}(2,8) & t = 0 \\ \text{Beta}(8,2) & t = 1 \end{cases},$$

The measurement is:

$$Y_i = -2(X_i - 0.5) + Z_i + T_i.$$

Assumption Incorrect, Overlap The covariate distribution is $X_i \overset{iid}{\sim} \text{Unif}(-1,1)$. With $Z_i \overset{iid}{\sim} \mathcal{N}(0,1)$, the measurement is:

$$Y_i = 4\text{sigmoid}(8X_i) + Z_i + T_i,$$

where sigmoid(x) is the non-linear sigmoid function; e.g.:

$$\text{sigmoid}(x) = \frac{1}{1 + \exp(-x)}.$$

We chose the sigmoid function because, under the limited overlap covariate regimes employed, where X_i is conditionally (on the batch) beta distributed, the non-linear sigmoid appears, visually, to be locally linear. Therefore, if one were to attempt to argue that exploratory analysis could be employed to post-hoc tune the statistical model employed by `ComBat`, the point of inflection of the sigmoid would not be prominent in either of the batches.

Assumption Incorrect, Moderate Overlap The covariate distribution is:

$$X_i \big| T_i = t \overset{d}{\sim} \begin{cases} \text{Beta}(2,6) & t = 0 \\ \text{Beta}(6,2) & t = 1 \end{cases}.$$

With $Z_i \overset{iid}{\sim} \mathcal{N}(0,1)$, the measurement is:

$$Y_i = 4\text{sigmoid}(8X_i) + Z_i + T_i.$$

Assumption Incorrect, Limited Overlap The covariate distribution is:

$$X_i \big| T_i = t \overset{d}{\sim} \begin{cases} \text{Beta}(2,8) & t = 0 \\ \text{Beta}(8,2) & t = 1 \end{cases}.$$

With $Z_i \overset{iid}{\sim} \mathcal{N}(0,1)$, the measurement is:

$$Y_i = 4\text{sigmoid}(8X_i) + Z_i + T_i.$$

Notation Across all simulations, we term the *raw true signal* at a particular covariate level x to be the quantity:

$$\mathbb{E}_{f_{x,z}(y|t)}[Y_i]$$

where x is the particular covariate level, z are (potential) unknown covariates (which are not present for the purposes of this simulation), and t is the batch.

$n = 100$ triplets (t_i, x_i, y_i) are sampled for each of the four simulations, and are passed to the `ComBat` algorithm to hypothetically detect and remove the batch effect. For a given covariate value x_i and a particular batch t_i, the *raw assumed signal* is the term:

$$\hat{y}_i = \hat{\beta}_x \hat{x}_i + \hat{\beta}_1 \mathbb{1}_{\{t_i=1\}} + \hat{\beta}_t \mathbb{1}_{\{t_i=0\}} + \bar{\mu}$$

where $\hat{\beta}_x$ is the regression coefficient for the covariate x, β_1 is an intercept offset term for batch 1, β_0 is an intercept offset term for batch 0, and $\bar{\mu}$ is the grand mean of the data.

To adjust points for the batch effect, `ComBat` simply removes the estimated batch intercepts; e.g.:

$$y_i^{(a)} = y_i - \left(\hat{\beta}_1 \mathbb{1}_{\{t_i=1\}} + \hat{\beta}_0 \mathbb{1}_{\{t_i=0\}}\right)$$

For a particular batch t, the true signal after adjustment is the term:

$$\mathbb{E}_{f_{x,z}(y|t)}[Y_i] - \left(\hat{\beta}_1 \mathbb{1}_{\{t_i=1\}} + \hat{\beta}_t \mathbb{1}_{\{t_i=0\}}\right)$$

And the assumed signal after adjustment is the term:

$$\hat{y}_i - \left(\hat{\beta}_1 \mathbb{1}_{\{t_i=1\}} + \hat{\beta}_0 \mathbb{1}_{\{t_i=0\}}\right) = \hat{\beta}_x \hat{x}_i + \bar{\mu}$$

It is obvious that after adjustment, the assumed signals for batches 0 and 1 will be equal, as $\hat{\beta}_x \hat{x}_i + \bar{\mu}$ does not depend on t_i.

Addressing the batch effect One way to characterize the batch effect would be analogous to the average treatment effect [37] at a particular covariate level (x, z); e.g.:

$$\text{ATE} = \text{ATE}(x, z) = \mathbb{E}_{f_{x,z}(y|1)}[Y_i] - \mathbb{E}_{f_{x,z}(y|0)}[Y_i]$$

For all simulations, it is clear that the ATE is 1 and does not depend on the covariates.

By definition, a difference in the expectations implies that $f_{x,z}(y|1) \neq f_{x,z}(y|0)$, and a batch effect is present by Definition 1.

It is well understood in the statistical literature that for models of the form $Y_i = g(X_i) + \beta T_i + Z_i$ where $Z_i \overset{iid}{\sim} \mathcal{N}(\mu, \Sigma)$, that as long as either the strong ignorability condition [37] or f is known, the adjustment factor $\hat{\beta}_1 - \hat{\beta}_0$ will be a consistent and unbiased estimate of the ATE [37, 46]. For a non-technical explanation in words, we can obtain reasonable estimates of the ATE in one of two ways (and consequently, account for the batch effect):

1. Extrapolation: if we know $g(x)$, then we can "guess" what $\mathbb{E}_{f_{x,z}(y|t)}[Y_i]$ looks like for values of x that do not exist in our batch, by appropriate estimation of g via the elements of our dataset that we *do* have. In this case, where the model is linear, extrapolation can be performed by linear regression. Once we have identified $g(x)$, we can extrapolate what $g(x)$ looks like for values of x which fall outside the range of our dataset, as in Simulation II.

2. Use asymptotics: if we do not know $g(x)$ but we can reasonably assume that the strong ignorability condition holds, we can leverage asymptotic statistics to conclude that we can still adequately estimate the ATE. Proofs of this result can be found in [37, 38]. In this particular case, $X_i \perp\!\!\!\perp T_i$, which implies the strong ignorability condition [37]. For more trivial reading specific to the case where $X_i \perp\!\!\!\perp T_i$, see [46]. This result is exhibited in Simulation III.

By a similar argument, the estimated batch offset terms, $\hat{\beta}_1$ for batch 1 and $\hat{\beta}_0$ for batch 0, can also be consistently estimated in either of these contexts. In these cases, removal of the estimated offset associated with the particular batch of a measurement is a reasonable approach to removal of the estimated batch effect.

Simulation IV, in which the assumption about $g(x)$ is *incorrect* and X_i is distributed conditionally on T_i (and consequently, the strong ignorability condition will not hold), will not necessarily yield a reasonable estimate of the ATE. In this case, due to the sigmoidal construction and the manner in which Batches 0 and 1 were balanced, we obtain a biased estimate of the ATE, which yields the batch artifact shown in red.

On a technical note, with $a_{x,y}(y|t)$ the distribution of the measurement Y_i after batch adjustment, we say a *residual artifact* is present if a batch effect *still* exists; e.g., if for two batches t and t':

$$a_{x,y}(y|t) \neq a_{x,y}(y|t').$$

Appendix C. Overlap of Empirical Covariates.

The empirical overlap of the covariate distributions is difficult to compute in the case of data without making heavy parametric assumptions. For this reason, we turn to the distribution-free overlapping index [31]. The distribution free overlapping index, $\hat{v}_{kl}$, is computed by first approximating the density of the distribution of the measured covariates for each dataset D, $X = (A, S, C)$, where A is a random variable whose realizations $a \in \mathcal{A}$ are ages, S is a random variable whose realizations $s \in \mathcal{S}$ are sexes (M or F), and C is a random variable whose realizations $c \in \mathcal{C}$ denote continent, using the base R function `stats::density`. The random variable D has realizations $d \in \mathcal{D}$ whose realizations denote dataset. The density $f(a|S = s, C = c, D = d)$ is the conditional density of age, conditional on the individual's sex being s, continent of measurement being c, and dataset being d. The mass $\mathbb{P}(S = s|C = c, D = d)$ is the conditional mass of sex, conditional on the individual's continent of measurement being c, and dataset being d. Finally, the mass $\mathbb{P}(C = c|D = d)$ represents the conditional

mass of an individual's continent of measurement being c, conditional on the dataset being d (0 or 1 for all d, since all individuals from dataset d are either measured on continent c or not). An estimate of the overlap between the two densities, $\hat{v}_{kl}$ between datasets k and l, is computed using the formula:

$$\hat{v}_{kl} = \sum_{c \in \mathcal{C}} \min\Big(\hat{\mathbb{P}}(C = c|D = k), \hat{\mathbb{P}}(C = c|D = l)\Big) \sum_{s \in \{\text{M,F}\}} \min\Big(\hat{\mathbb{P}}(S = s|C = c, D = k), \hat{\mathbb{P}}(S = s|C = c, D = l)\Big) \Bigg[\int_{\mathcal{A}} \min\Big(\hat{f}(a|S = s, C = c, D = k), \hat{f}(a|S = s, C = c, D = l)\Big) \, \mathrm{d}a \Bigg]$$

which is obtained via numerical quadrature.

Intuitively, this can be conceptualized as representing the mass of the "area under the curve" which is shared by the two densities for datasets k and l.

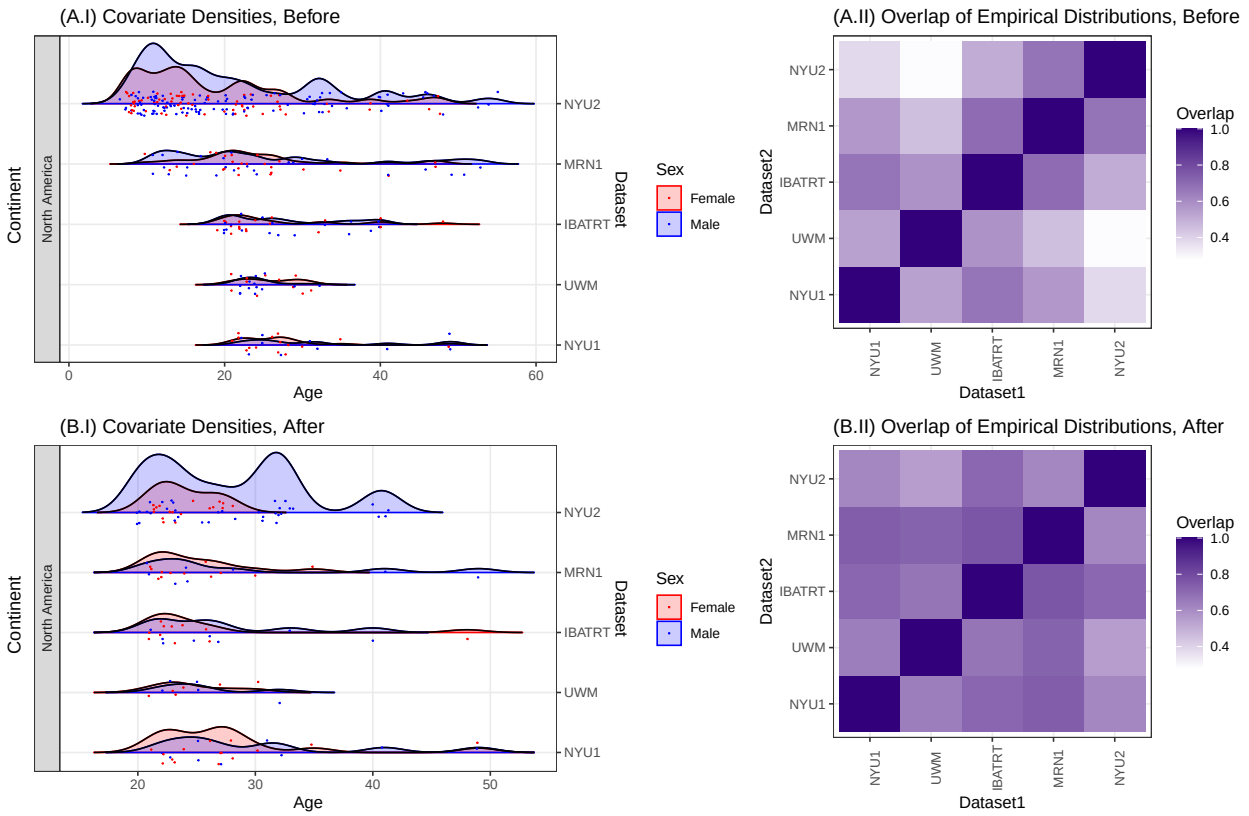

Figure 8: **The overlap of the empirical covariate distributions for the American Clique, before and after adjustment**. **(A)** The empirical distributions of the covariates before adjustment. **(B)** The empirical overlap of the covariate distributions after the adjustment procedure is applied, as discussed in Appendix A.

Batch-Related Effects are reduced with Causal `ComBat` Here we investigate batch-related effects before and after correction. Figure 10 shows average connectomes from the MRN1 and IBATRT studies. With no correction, while the average connectomes appear similar between the two studies, a difference between the average connectomes is present (bottom row). Three different batch effect mitigation strategies (Z-scoring across features within a single batch, `ComBat`, and Causal `ComBat`) all appear to eliminate the differences between the average connectomes. Z-scoring has disrupted fundamental topological properties of the human connectome, as explored in detail in Appendix D. For this reason, we do not consider Z-scoring going forward, and focus instead on variations of the `ComBat` procedure.

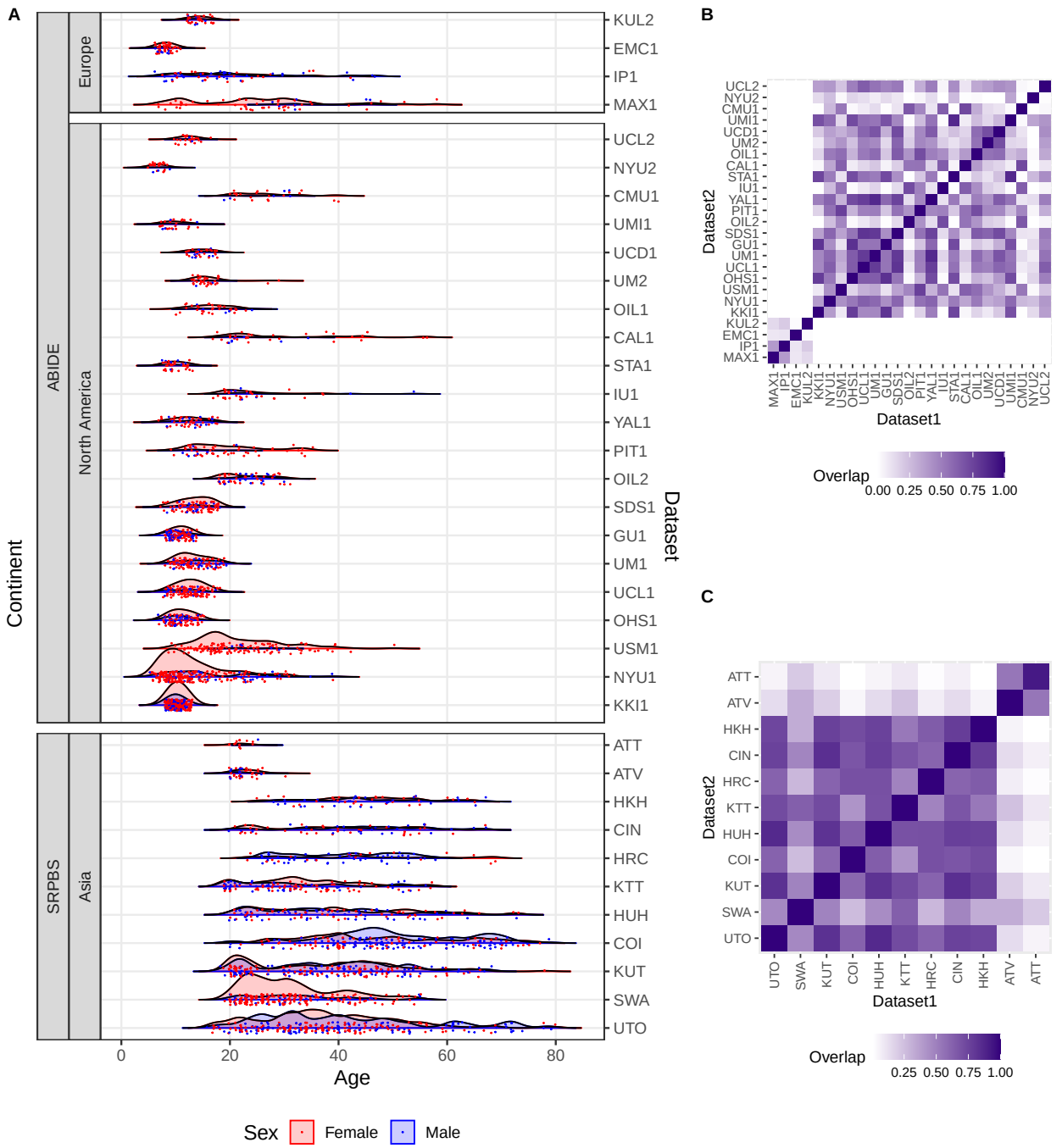

Figure 9: **The overlap of the empirical covariate distributions for two mega-studies. (A)** The empirical distribution of covariates. **(B)** The overlap of covariate distributions given by the distribution-free overlapping index for ABIDE mega-study [5, 6]. **(C)** The overlap of covariate distributions given by the distribution-free overlapping index for the SRPBS mega-study. [52]. Like for the CoRR mega-study, while several pairs of sites have overlapping demographic distributions, many of the sites have extremely poor overlap in both mega-studies. In these cases, attempts to normalize for batch effects using model-based approaches like Conditional `ComBat` would be subject to the pitfalls of Figure 3V or VI if modelling assumptions are not reasonable.

Appendix D. `ComBat` Preserves Topological Properties of fMRI Connectomes. The presence of two prominent topological *signal effects* in human connectomes, homophily and homotopy, are investigated in Figure 11. The left column of Figure 11A looks at the edges comprising these two

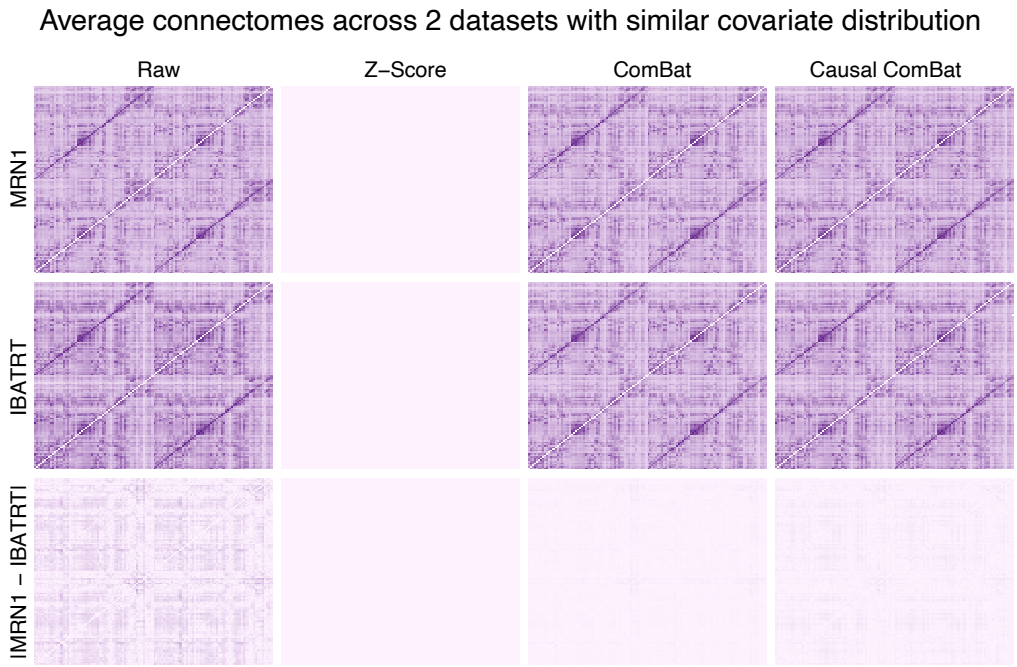

Figure 10: **Distribution of Detected Effects Before and After Correction**. A comparison of the average connectomes from two studies from the same continent, with similar sex and age distributions conditional on sex. While the *Raw* average connectomes appear similar, the absolute difference between the two is appreciable. All of the three adjustment strategies reduce the absolute difference between the average connectomes for the two batches.

disparate community structures. When edges are sorted by hemisphere, the homophilic effect is characterized by a modular two-block structure, with higher connectivity in the lower left and upper right blocks (dark red) than in the two off-diagonal blocks (pink). The homotopic effect is characterized by edges in the off-diagonal band (dark blue) showing higher connectivity than other edges within the connectome (light blue). The right column of Figure 11A looks at a single individual's connectome from the NYU2 study before and after correction. The homotopic property appears to be preserved in only the `ComBat` connectomes, whereas Z-scored connectomes do not appear to preserve this property. In Figure 11B, these two properties are examined statistically for the individuals from the American Clique (Mann-Whitney U Statistic, see Methods 5.4 for details). Points falling along the diagonal line $y = x$ tend to have a similar signal effect before and after batch correction. Whereas `ComBat` strategies tend to preserve the homophilic and homotopic effects, Z-scoring tends to decrease these two topological properties of functional connectomes. This is noted by the fact that the majority of the points for Z-scoring across both effects tend to fall below the $y = x$ line, indicating that the effect size after Z-scoring is lower than the effect size in the raw connectomes.

Figure 12 explores the distribution of edge weights within these two community structures before and after correction. The conclusions are similar in that Causal `ComBat` and `ComBat` preserve the property that the homotopic edges have far higher connectivity than non-homotopic edges.

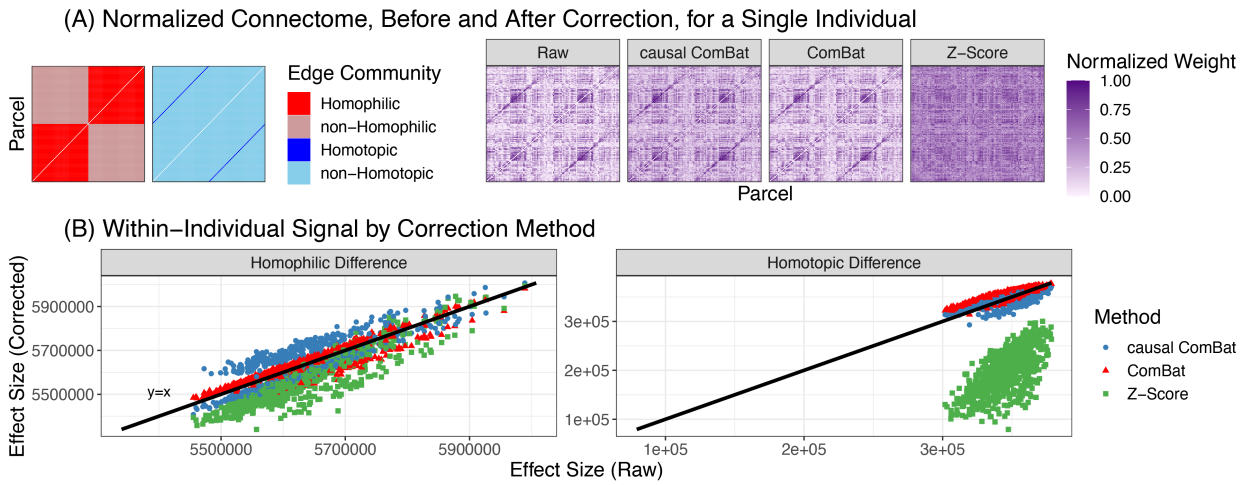

Figure 11: **Preservation of Topological Properties of Connectomes after Batch Correction**. The presence of topological effects is explored in the context of the homophilic and homotopic differences in connectivity in the American Clique. **(A)** (*Left*) A map indicating which edges are associated with homophilic/non-homophilic or homotopic/non-homotopic edge communities. (*Right*) The edge-weight normalized connectome associated with a single individual from the NYU2 study using each removal strategy. **(B)** A scatter plot, showing the effect size (Mann-Whitney U Statistic) before (x axis) and after (y axis) the indicated Batch Effect Correction Method.

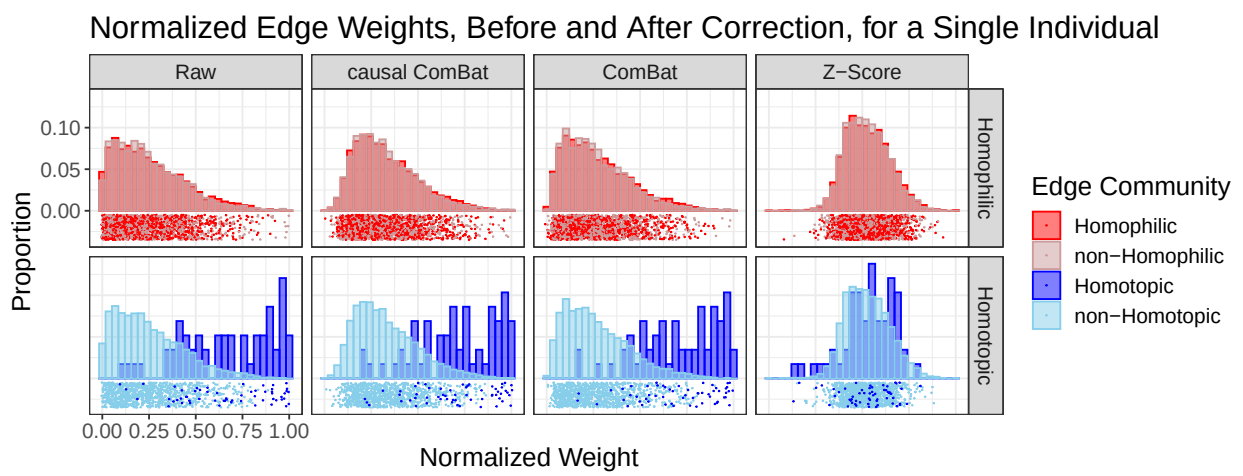

Figure 12: Histogram and rug plot indicating the empirical distribution of the normalized edge weights associated with each of the four edge communities for a single individual's connectome.