Learning to Bound Counterfactual Inference in Structural Causal Models from Observational and Randomised Data

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Abstract

We address the problem of integrating data from multiple observational and interventional studies to eventually compute counterfactuals in structural causal models. We derive a likelihood characterisation for the overall data that leads us to extend a previous EM-based algorithm from the case of a single study to that of multiple ones. The new algorithm learns to approximate the (unidentifiability) region of model parameters from such mixed data sources. On this basis, it delivers interval approximations to counterfactual results, which collapse to points in the identifiable case. The algorithm is very general, it works on semi-Markovian models with discrete variables and can compute any counterfactual. Moreover, it automatically determines if a problem is feasible (the parameter region being nonempty), which is a necessary step not to yield incorrect results. Systematic numerical experiments show the effectiveness and accuracy of the algorithm, while hinting at the benefits of integrating heterogeneous data to get informative bounds in case of unidentifiability.

Keywords: Structural Causal Models; Unidentifiable Counterfactuals; Data Integration.

1. Introduction

Table 1 contains the results of an artificial case study by Mueller and Pearl (2022). It simulates testing a drug that should help patients affected by a deadly disease. The table reports two independent studies carried out on different groups of patients: a randomised control trial (first eight rows) and an observational study (last eight rows). The example is used to advocate taking advantage of multiple studies with structural causal models (SCMs).

It is a matter of fact that allowing models to integrate heterogeneous data brings us closer to real-world problems. Moreover, it offers us the chance to strengthen conclusions compared to the case of single studies. In fact, it is well known that causal, and especially counterfactual, inference may well be unidentifiabile: this means that inference results are going to be interval-valued even in the limit of infinite sample sizes—the narrower the bounds, the more informative the conclusions. But how can we narrow them if increasing the sample size will not do? Using multiples studies. Mueller and Pearl (2022) analytically show in their example that for a typical counterfactual such as the probability of necessity and sufficiency (PNS), we have PNS ∈ [0.28, 0.49] if only the randomised trial is considered, whereas PNS ∈ [0.34, 0.43] is obtained when observational data are taken into account too.

The problem of performing causal inference in SCMs by integrating experimental and interventional studies has however been mostly focused on identifiable queries in the literature (e.g., Bareinboim and Pearl, 2016; Ilse et al., 2021) or on addressing special cases, as
Somewhat in contrast with the trend in the literature, this paper entirely focuses on developing general methods to compute counterfactuals in SCMs under unidentifiability and from any collection of observational and interventional studies. We pursue this objective starting from a representation result in Zaffalon et al. (2020), which permits deriving constraints on the probabilities of an SCM’s exogenous variables from observational data. We extend such a result by showing that the availability of data on different groups of individuals, subject to different studies, induces simultaneous constraints on the exogenous probabilities: it tells us that the feasibility region for those probabilities corresponds to the intersection of the regions obtained in the separate studies. This is the crux why the integration of multiple studies has much potential to strengthening counterfactual bounds.

To practically perform the intersection associated with the simultaneous constraints, we extend to multiple studies the causal expectation-maximisation scheme (the so-called EMCC) originally proposed for a single study by Zaffalon et al. (2021). We prove that the EMCC maintains its convergence and consistency properties in the generalised setup. This allows us to eventually learn the probabilities of exogenous variables from multiple studies by seamlessly iterating the EMCC over the respective datasets and models—nearly as if we had a single big dataset comprising the data from all studies together.

Such an application of the EMCC yields a set of (fully specified) SCMs. Each of them is queried for counterfactual inference and the overall results are aggregated so as to get the approximating bounds we are after. The credible intervals derived by Zaffalon et al. (2022) are eventually used on top of those bounds, in an empirical validation, to obtain guarantees on the quality of the approximation. The results confirm such a quality and, in line with expectations, exhibit some 13–18% shrink of the bounds even with just two studies.

The paper is organised as follows. In Section 2 we review the necessary background material. The problem of addressing partial identifiability with single and multiple studies is discussed in Section 3. The characterisation of the likelihood is in Section 4, while our algorithm is presented in Section 5. An analysis of the motivating example discussed in this Introduction and a numerical validation on a synthetic benchmark are presented in Section 6. Conclusions and outlooks are in Section 7.

2. Background on Bayesian Networks and Structural Causal Models

A generic variable $X$ is assumed to take values from a finite set $\Omega_X$. Denote by $P(X)$ a probability mass function (PMF) over $X$. Given variables $X$ and $Y$, a conditional probability table (CPT) $P(X|Y)$ is a collection of PMFs indexed by the values of $Y$, i.e., $\{P(X|y)\}_{y \in \Omega_Y}$. If all PMFs in a CPT are degenerate, i.e., $\{0, 1\}$-valued, we say that the CPT is degenerate.

A structural equation (SE) $f_X$ associated with variable $X$ and based on the input variable(s) $Y$ is a surjective function $f_X : \Omega_Y \rightarrow \Omega_X$ that determines the value of $X$ from that of $Y$. Such an SE induces the degenerate CPT $P(X|Y)$ via $P(x|y) := [f_X(y) = x]$ for each $x \in \Omega_X$ and $y \in \Omega_Y$, where $[\cdot]$ denotes the Iverson brackets that take value one if the statement inside the brackets is true and zero otherwise.
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| Study       | Treatment | Gender | Survival | Counts |
|-------------|-----------|--------|----------|--------|
| interventional | do(drug)  | female | survived | 489    |
|             | do(drug)  | female | dead     | 511    |
|             | do(drug)  | male   | survived | 490    |
|             | do(drug)  | male   | dead     | 510    |
|             | do(no drug)| female | survived | 210    |
|             | do(no drug)| female | dead     | 790    |
|             | do(no drug)| male   | survived | 210    |
|             | do(no drug)| male   | dead     | 790    |
| observational| drug      | female | survived | 378    |
|             | drug      | female | dead     | 1022   |
|             | drug      | male   | survived | 980    |
|             | drug      | male   | dead     | 420    |
|             | no drug   | female | survived | 420    |
|             | no drug   | female | dead     | 180    |
|             | no drug   | male   | survived | 420    |
|             | no drug   | male   | dead     | 180    |

Table 1: Data from interventional and observational studies on the potential effects of a drug on patients affected by a deadly disease.

Consider a joint variable $V := (V_1, \ldots, V_n)$ and a directed acyclic graph $G$ whose nodes are in a one-to-one correspondence with the variables in $V$ (we use a node in $G$ and its corresponding variable interchangeably). Given $G$, a Bayesian network (BN) is a collection of CPTs $\{P(V_i|\text{Pa}(V_i))\}_{i=1}^n$, where $\text{Pa}(V_i)$ denotes the parents of $V_i$, i.e., the direct predecessors of $V_i$ according to $G$. A BN induces a joint PMF $P(V)$ that factorises as $P(v) = \prod_{i=1}^n P(v_i|\text{pa}(V_i))$, for each $v \in \Omega_V$, where $(v_i, \text{pa}(V_i)) \sim v$, i.e., $v_i$ and $\text{pa}(V_i)$ are the values of $V_i$ and $\text{Pa}(V_i)$ consistent with $v$ for each $i = 1, \ldots, n$.

Now consider two joint variables $V$ and $U$, which we respectively refer to as endogenous and exogenous. A collection of SEs $\{f_V\}_{V \in V}$ such that, for each $V \in V$ the input variables of $f_V$ are in $(V, U)$, is called a partially specified structural causal model (PSCM). A PSCM $M$ induces the specification of a directed graph $G$ with nodes in a one-to-one correspondence with the variables in $(V, U)$ and such that there is an arc between two variables if and only if the first variable is an input variable for the SE of the second. The exogenous variables are therefore root nodes of $G$. We focus on semi-Markovian PSCMs, i.e., those PSCMs that lead to acyclic graphs (see, e.g., Figure 1).

In a PSCM $M$ we obtain a joint state of $V$ from a (joint) state of $U$ by applying the SEs of $M$ consistently with a topological order for $G$. A fully specified structural causal model (FSCM) is just a PSCM $M$ paired with a collection of marginal PMFs, one for each exogenous variable, i.e., $\{P(U)\}_{U \in U}$. As SEs induce (degenerate) CPTs, an FSCM defines a BN based on $G$ whose joint PMF factorises as:

$$P(v, u) = \prod_{V \in V} P(v|\text{pa}(V)) \prod_{U \in U} P(u),$$

(1)
with, for each \( v \in \Omega_V \) and \( u \in \Omega_U \), \((v, \text{pa}(V), u) \sim (v, u)\) and where \( \text{Pa}(V) \) are the parents of \( V \) according to \( G \) (i.e., the inputs of \( SE_f_v \)).

Given the graph \( G \) of a PSCM (or FSCM) \( M \), obtain \( G' \) by removing from \( G \) any arc connecting pairs of endogenous variables. Let \( \{G_c\}_{c \in C} \) denote the connected components of \( G' \). The \( c \)-components of \( M \) are the elements of the partition \( \{V_c\}_{c \in C} \) of \( V \), where \( V_c \) denotes the endogenous nodes in \( G_c \), for each \( c \in C \) (Tian, 2002). This procedure also induces a partition of \( U \), similarly denoted as \( \{U_c\}_{c \in C} \). Moreover, for each \( c \in C \), let \( W_c \) denote the union of the endogenous parents of the nodes in \( V_c \) and \( V_c \) itself. Finally, for each \( V \in V_c \), obtain \( W_V \) by removing from \( W_c \) the nodes topologically following \( V \) and \( V \) itself (note that in the notation we dropped the index \( c \) as this can be implicitly retrieved from \( V \)). Tian (2002) shows that the joint PMF \( P(V) \) obtained by marginalising the exogenous variables from the joint PMF in Equation (1) is a BN, to be called here empirical, that factorises as follows:

\[
P(v) = \prod_{v \in V} P(v|w_v),
\]

(2)

for each \( v \in \Omega_V \), with \((v, w_v) \sim v\) for each \( V \in V \).

In FSCMs, the CPTs in the right-hand side of Equation (2) can be computed through standard BN inference algorithms by simply regarding the FSCM as a BN. With PSCMs, assuming the availability of a dataset \( D \) of endogenous observations, we might also define an empirical BN with the same factorisation and whose CPTs are directly assessed from \( D \).

Observational queries in FSCMs can be addressed in the empirical BN, and the same can be done for PSCMs assuming the availability of the dataset \( D \) of endogenous observations. To perform causal inference, interventions denoted as \( \text{do}(\cdot) \) should be considered instead. In an FSCM or PSCM \( M \), given \( V \in V \) and \( v \in \Omega_V \), \( \text{do}(V = v) \) simulates a physical action on \( M \) forcing \( V \) to take the value \( v \). The original SE \( f_V \) should be consequently replaced by a constant map \( V = v \). Notation \( M\) is used for such a modified model, whose graph is obtained by removing from \( G \) the arcs entering \( V \), and for which evidence \( V = v \) is considered. In an FSCM \( M \), given \( V, W \in V \) and \( v \in \Omega_V \), \( P(w|\text{do}(v)) \) denotes the conditional probability of \( W = w \) in the post-intervention model, i.e., \( P'(w|v) \), where \( P' \) is the joint PMF induced by \( M\).

We call counterfactual those queries embedding a contradiction between intervened and observed states. That is, we observe a variable in a certain state, say \( V = v \), and wonder what would have been the effects (e.g., on another variable \( W \)) of having set the same variable to state \( v' \neq v \). In mathematical parlance, we write it by \( P(W_{v'}|v) \).

Computing counterfactual queries in an FSCM may be achieved via an auxiliary structure called a twin network (Balke and Pearl, 1994). This is simply an FSCM where the original endogenous nodes (and their SEs) have been duplicated, while remaining affected by the same exogenous variables. More general and compact structures might also be considered (Shpitser and Pearl, 2007). Computing a counterfactual in the twin network of an FSCM is analogous to what is done with observational queries provided that interventions and observations are associated with distinct copies of the same variable. BN inference eventually allows one to compute the counterfactual query in such an augmented model.
3. Coping with Partial Identifiability

In this section we formalise the notion of partially identifiable query and the notion of \(M\)-compatibility between a PSCM \(M\) and data (or, more precisely, the empirical PMF induced by these data). We first review the concepts for the case of a single dataset as discussed by Zaffalon et al. (2021), then we extend these ideas to the multiple dataset framework.

3.1. Single Dataset Case

FSCMs permit computing causal queries by BN inference algorithms. Yet exogenous variables are typically latent; their marginal PMFs being unavailable leaves us with PSCMs.

Say that we have a PSCM \(M\) over variables \((U, V)\) together with a dataset \(D\) of endogenous observations. This permits quantifying the empirical BN from which any observational query can be computed. The do-calculus (Pearl, 2009) instead permits reducing identifiable interventional queries on PSCMs to observational ones, which are possibly then computed in the empirical BN. The remaining queries are called unidentifiable.

To start approaching unidentifiable queries in the PSCM \(M\), from \(D\) we first compute the empirical BN inducing the endogenous joint PMF \(\hat{P}(V)\). Then we look for an FSCM consistent with the empirical PMF: that is, a quantification of the marginal PMFs for \(U\), which we represent here via the corresponding vector of parameters \(\theta_U\), which satisfies

\[
\sum_{u \in \Omega_U} \left[ \prod_{U \in U} \theta_u \cdot \prod_{V \in V} P_M(v | \text{pa}(V)) \right] = \hat{P}(v),
\]

for each \(v \in \Omega_V\), with \((v, \text{pa}(V)) \sim v\) and \(\theta_u \sim \theta_u\). If such a \(\theta_U\) exists, we say that the empirical BN is \(M\)-compatible with the original PSCM (Zaffalon et al., 2021). As noticed by Zaffalon et al. (2020), in general there are multiple FSCMs satisfying Equation (3). To compute an unidentifiable causal query in PSCMs, we should therefore find all vectors \(\theta_U\) solving Equation (3) and compute the query for each of them. The result of the unidentifiable query is understood as the interval spanned by the outcomes obtained on all the \((M-)\)compatible FSCMs.
To practically pursue that, it is useful to consider the log-likelihood of $D$ for an FSCM based on $M$, i.e.,

$$LL(\theta_U) := \sum_{v \in D} \log \sum_{u \in \Omega_U} \left[ \prod_{U \in U} \theta_u \cdot \prod_{V \in V} P(v|\text{pa}(V)) \right], \quad (4)$$

with $(u, v, \text{pa}(V)) \sim (u, v)$ and $\theta_u \sim \theta_u$. Interestingly, this function is unimodal.

The idea to be discussed in the rest of the paper is to exploit the following connection between the log-likelihood and the ($M$-)compatible FSCMs:

**Proposition 1 (Zaffalon et al., 2021)** $\theta_U$ satisfies Equation (3) if and only if the log-likelihood in Equation (4) achieves its global maximum at $\theta_U$.

Finally let us note that although all the results in this section refer to a PSCM $M$ paired with an observational dataset, nothing really changes with an interventional dataset, provided that the SEs of the intervened variables are modified as in Section 2. Putting it another way, an interventional dataset for $M$ can be regarded as an observational dataset for the PSCM $M'$ obtained by modifying the SEs of $M$ on the basis of the interventions.

### 3.2. Coping with Multiple, Observational and Interventional, Datasets

Let us define our setup to cope with multiple studies. First of all, we assume that a PSCM $M$ over variables $(U, V)$ characterises our domain of interest. Assume that $d$ independent, observational or interventional, studies are performed in such a domain. For each $k = 1, \ldots, d$, the following objects are defined:

- $D^{(k)}$ is the dataset with the results of the $k$-th study and its size is $N^{(k)} := |D^{(k)}|$
- $M^{(k)}$ is a PSCM over the variables $(U^{(k)}, V^{(k)})$ that is a clone of $M$;
- $V^I_k \subseteq V^{(k)}$ are the intervened variables in $M^{(k)}$ ($V^I_k = \emptyset$ for observational studies);
- $\text{do}(V^I_k = \hat{v}^I_k)$ is the corresponding intervention;
- the SEs of $M^{(k)}$ are the same of $M$ apart from those of the intervened variables $V^I_k$, which are subject to the modification induced by the intervention $\text{do}(V^I_k = \hat{v}^I_k)$;
- $\tilde{P}^{(k)}$ is the joint endogenous PMF associated with the empirical BN one can obtain from the PSCM $M^{(k)}$ and the dataset $D^{(k)}$ (as discussed in Section 2);
- To keep notation short, let $\mathbb{D} := \{D^{(k)}\}^d_{k=1}, \mathbb{M} := \{M^{(k)}\}^d_{k=1}$ and $\tilde{\mathbb{P}} := \{\tilde{P}^{(k)}\}^d_{k=1}$.

The idea here is that each study is subject to the same underlying PSCM but at the same time, each study has its own private data as well as variables. What connects the $d$ separate studies are the unknown chances: we assume that they stay the same across all the studies. Stated differently, we assume that the population of individuals is always the same; and that samples of such a population are independently assigned to the $d$ studies. Estimating $\theta_U$ can then be achieved by aggregating the information collected in the studies.

Before doing that, let us extend the definition of $M$-compatibility, provided in the previous section for a single study, to the current multiple-study setup.
Definition 2 (M-compatibility) We say that data $\mathbb{D}$ and models $\mathbb{M}$ are M-compatible if and only if there is at least an instance $\theta_U$ that can generate all the empirical mass functions $\hat{P}$ through the models in $\mathbb{M}$.

For each $k = 1, \ldots, d$, denote by $\Theta_U^{(k)}$ the set of all and only parameter values $\theta_U$ that generate $\hat{P}^{(k)}$ through $M^{(k)}$. We can think of $\Theta_U^{(k)}$ as defining the set of all and only FSCMs that are compatible with $M^{(k)}$ and the empirical mass function $\hat{P}^{(k)}$ as in Equation (3). In the special case where $\Theta_U^{(k)} = \emptyset$, $\mathbb{D}^{(k)}$ and $M^{(k)}$ are M-incompatible, because $M^{(k)}$ cannot possibly yield mass function $\hat{P}^{(k)}$ irrespective of the parameters $\theta_U$ we may choose for its exogenous variables. This has a simple extension to the general case of M-incompatibility:

**Theorem 3** $\mathbb{D}$ and $\mathbb{M}$ are M-incompatible if and only if $\cap_{k=1}^d \Theta_U^{(k)} = \emptyset$.

**Proof** Let us first prove the direct implication. There are two cases where M-incompatibility can occur. In the first, there is at least a model $M^{(k)}$ that cannot generate the related empirical distribution $\hat{P}^{(k)}$, no matter the choice of $\theta_U$. Whence $\Theta_U^{(k)} = \emptyset$ and as a consequence $\cap_{k=1}^d \Theta_U^{(k)} = \emptyset$. In the second case, we should have $\Theta_U^{(k)} \neq \emptyset$ for all models $M^{(k)}$ and yet there is no single value $\theta_U$ that works for all the models at once, that is, $\cap_{k=1}^d \Theta_U^{(k)} = \emptyset$. The converse implication is analogous.

**Remark 4** Another way to look at Theorem 3 is that $\cap_{k=1}^d \Theta_U^{(k)}$ represents the set of all and only the full specifications of the underlying PSCM $M$ that are M-compatible with all the available data $\mathbb{D}$. Therefore any inference we may want to do on $M$, provided it is compatible with $\mathbb{D}$, can be bounded via those obtained in the FSCMs indexed by $\theta_U \in \cap_{k=1}^d \Theta_U^{(k)}$.

4. Characterising the Log-Likelihood

Let us recall that the $d$ studies are independent but they share the underlying PSCM structure $M$, and moreover they are subject to the same actual chances $\theta_U$. As a consequence, we can write the log-likelihood of the data $\mathbb{D}$ as the sum of the log-likelihoods in the separate studies, i.e.,

$$LL(\theta_U) := \log P(\mathbb{D} | \theta_U, \mathbb{M}) = \sum_{k=1}^d \log P(\mathbb{D}^{(k)} | \theta_U, M^{(k)}) =: \sum_{k=1}^d LL^{(k)}(\theta_U). \quad (5)$$

Let $LL$ denote the global maximum of $LL$ and, similarly, let $LL^{(k)}$ be the global maximum of $LL^{(k)}$. The following result provides a multi-study generalisation of Proposition 1.

**Proposition 5** Condition $\cap_{k=1}^d \Theta_U^{(k)} \neq \emptyset$ holds if and only if $LL = \sum_{k=1}^d LL^{(k)}$.

**Proof** Let us first consider the direct implication. We know that there is $\theta_U$ that renders all the models M-compatible with their data. By Proposition 1, each model $M^k$ achieves its global optimum $LL^{(k)}$ in $\theta_U$, whence $LL(\theta_U) = \sum_{k=1}^d LL^{(k)}$. Since this sum cannot be increased, we deduce that $LL(\theta_U) = LL$. Now on the converse implication. The global optimum $LL$ is the sum of the global optima $LL^{(k)}$. Assume ex-absurdo that $\cap_{k=1}^d \Theta_U^{(k)} = \emptyset$. 
Then no $\theta_U$ optimises all the $LL^{(k)}$ functions simultaneously. Therefore for no $\theta_U$ we have $LL(\theta_U) = \sum_{k=1}^d LL^{(k)}(\theta_U) = \sum_{k=1}^d \prod_{L}^{(k)}$, whence $\prod_{L}^{(k)} < \sum_{k=1}^d \prod_{L}^{(k)}$, a contradiction.

In practice we can decide whether or not an FSCM specification is compatible by simply evaluating the corresponding log-likelihood even in the multi-study case:

Corollary 6 Condition $\cap_{k=1}^d \Theta_{U}^{(k)} = \emptyset$ holds if and only if $\prod_{L}^{(k)} < \sum_{k=1}^d \prod_{L}^{(k)}$.

Finally let us remark that the unimodality of single-study log-likelihoods is inherited by the generalisation in Equation (5). Proofs are analogous to that of Proposition 5.

5. An EMCC for Data Integration

The discussion in the previous section has put set $\cap_{k=1}^d \Theta_{U}^{(k)}$ at the centre of our attention. Unfortunately, obtaining this set is not an easy task in practice as a consequence of an NP-hardness result (Zaffalon et al., 2021, Theorem 2); therefore we need to approximate it.

5.1. Defining the Overall Model

To obtain such an approximation, let us recall that in our assumptions the $d$ PSCMs in $M$ are independent given $\theta_U$, and in particular they do not share variables. Whence we can regard them as an overall graphical model made by a central node for the chances $\theta_U$ from which each model $M^{(k)}$ descends independently of the others. Call the overall model $M^{(0)}$.

The variables in this model are given by the union of those of the separate models, i.e., \{(U^{(k)}, V^{(k)})\}_{k=1}^d (see Figure 2 for a case of two studies). Correspondingly, the dataset for $M^{(0)}$, let us call it $D^{(0)}$, will take the form of a block matrix. Blocks in the diagonal of the matrix will be datasets $D^{(k)}$, $k = 1, \ldots, d$, one after the other. The remaining parts of the matrix will entirely be made of missing values (see Table 2). Those values are missing since the instances in $D^{(0)}$ contain information on exactly one of the models in $M$ at a time.

![Figure 2: The structure $M^{(0)}$ for the model in Figure 1 with the mixed data in Table 1.](image)

Consider the log-likelihood of dataset $D^{(0)}$ for the overall model $M^{(0)}$, i.e.,

$$LL^{(0)}(\theta_U) := \log P(D^{(0)}|\theta_U, M^{(0)})$$

(6)

As the different models in $M$ are independent and the missing values in $D^{(0)}$ are missing at random (the values are missing with probability one), and hence can be dropped from the
Table 2: Dataset $D^{(0)}$ induced by the interventional and observational data in Table 1.

| $V_1^{(1)}$ | $V_2^{(1)}$ | $V_1^{(2)}$ | $V_2^{(2)}$ | Counts |
|-------------|-------------|-------------|-------------|--------|
| drug        | female      | survived    | *           | 378    |
| drug        | female      | dead        | *           | 1022   |
| no drug     | female      | survived    | *           | 420    |
| no drug     | female      | dead        | *           | 180    |
| drug        | male        | survived    | *           | 980    |
| drug        | male        | dead        | *           | 420    |
| no drug     | male        | survived    | *           | 420    |
| no drug     | male        | dead        | *           | 180    |
| *           | *           | drug        | female      | 489    |
| *           | *           | drug        | male        | 511    |
| *           | *           | drug        | male        | 490    |
| *           | *           | no drug     | female      | 510    |
| *           | *           | no drug     | female      | 790    |
| *           | *           | no drug     | male        | 210    |
| *           | *           | no drug     | male        | 790    |

probability formulas, Equation (6) rewrites as:

$$LL^{(0)}(\theta_U) = \sum_{k=1}^{d} \log P(D^{(k)}|\theta_U, M^{(k)}) = \sum_{k=1}^{d} LL^{(k)}(\theta_U) = LL(\theta_U) ,$$  \hspace{1cm}(7)$$

where the last derivation follows from Equation (5). From this we trivially get that for the maximum $\overline{LL}^{(0)}$ of $LL^{(0)}$:

$$\overline{LL}^{(0)} = \sum_{k=1}^{d} LL^{(k)} = \overline{LL} ,$$ \hspace{1cm}(8)$$

where the last step follow from Proposition 5. As a consequence, running the EM algorithm on $D^{(0)}$ with respect to model $M^{(0)}$ and reaching a global optimum point will enable us, though Proposition 5, to sample one element in $\cap_{k=1}^{d} \Theta_U^{(k)}$. Repeating this step with multiple random starting points for the EM will provide the wanted approximation $\overline{\Theta}_U \subseteq \cap_{k=1}^{d} \Theta_U^{(k)}$.

5.2. Simplifying the EM Scheme

Let us simplify the actual application of the EM w.r.t its bare application to $D^{(0)}$ by Equations (7) and (8). Denote by $v_l^{(k)}$ the $l$-th record, with $l = 1, \ldots, N^{(k)}$, of the $k$-th dataset $D^{(k)}$. We start considering the first record of $D^{(0)}$. By construction this record contains information about $V^{(1)}$ as taken from $D^{(1)}$ only, all the other variables from studies with indexes from $k = 2$ to $k = d$ being missing. Whence all these other studies can be ‘marginalised out’ from the record, taking into account that the missingness is at random and that the models in $M$ are independent; thus we are left with computing $P(U^{(1)} = u|v_1^{(1)}, M^{(1)})$ for all $U^{(1)} \in U^{(1)}$, and all values $u \in \Omega_U$. The same will hold up to and including the record $N^{(1)}$ of $D^{(0)}$, which corresponds to the last record of $D^{(1)}$. The next record in $D^{(0)}$ will instead refer to the first record of $D^{(2)}$, namely $v_1^{(2)}$, and we shall compute $P(U^{(2)} = u|v_1^{(2)}, M^{(2)})$ for all $U^{(2)} \in U^{(2)}$ and $u \in \Omega_U$. Again, this will be repeated up to
and including the record $N^{(1)} + N^{(2)}$, and the process will be continued in the same way up to the last record of $D^{(0)}$.

At that point we will have computed expected counts for all the exogenous variables in the $d$ studies. This corresponds to the E-step of an EM scheme. As all these variables are determined by the very same chances $\theta_U$, we can simply add up the expected counts from all the studies and divide them by the overall size $N^{(0)} := \sum_{k=1}^{d} N^{(k)}$ to get a new maximum-likelihood estimate of $\theta_U$. This is the M-step. The two steps are iterated until convergence. Such an overall procedure is iterated $r$ times with different initialisations, thus returning an equal number of estimates for the chances. The pseudo-code is in Algorithm 1 and $P_t$ denotes the joint PMF induced by the FSCM with the chances $\theta_U$.

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**Algorithm 1 (EMCC)**

Input: $r$, $M = \{M^{(k)}\}_{k=1}^{d}$, $D = \{D^{(k)}\}_{k=1}^{d}$

Output: $\bar{\Theta}_U := \{\theta^{(1)}_U, \ldots, \theta^{(r)}_U\} \subseteq \cap_{k=1}^{d} \Theta^{(k)}_U$.

1: for $i \leftarrow 1, \ldots, r$ do
2: $t \leftarrow 0$
3: $\theta^{(t)}_U \leftarrow \text{random.initialisation}()$
4: repeat
5: $t \leftarrow t + 1$
6: for $j \leftarrow 1, \ldots, |U|$ do
7: for $u \in \Omega_{U_i}$ do
8: for $k \leftarrow 1, \ldots, d$ do
9: for $l \leftarrow 1, \ldots, N^{(k)}$ do
10: $n(U_j = u) \leftarrow n(U_j = u) + P_{t-1}(U_j^{(k)} = u | V^{(k)} = v^{(k)}, M^{(k)})$
11: end for
12: end for
13: $\theta^{(t)}_{U_j = u} \leftarrow n(U_j = u) \cdot \left[ \sum_{k=1}^{d} N^{(k)} \right]^{-1}$
14: end for
15: end for
16: $\theta^{(t)}_U \leftarrow \{\theta^{(t)}_{U_j = u}\}_{u \in \Omega_{U_i}}$
17: until $LL(\theta^{(t)}_U) = LL(\theta^{(t-1)}_U)$
18: $\theta^{(i)}_U \leftarrow \theta^{(t)}_U$
19: end for

In summary, computing the expected counts from $D^{(0)}$ can equivalently be done by computing the expected counts sequentially from $D^{(1)}$ to $D^{(d)}$ according to the respective models $M^{(1)}, \ldots, M^{(d)}$, and eventually adding them up. This procedure can be further simplified by noting that we need not use $D^{(0)}$ for this; we can more conveniently create a smaller dataset $\mathcal{D}$, over the variables $(U, V)$ only, by appending each dataset $D^{(1)}, \ldots, D^{(d)}$ one after the other. Then we would directly run the EM on $\mathcal{D}$ just by paying attention to select the correct model $M^{(k)}$ to compute the expected counts, depending on the record under consideration. This has essentially the same complexity of running the original EMCC on dataset $D$. And thanks to the implicit representation via $D^{(0)}$ and $M^{(0)}$, we are guaranteed that the EM on $\mathcal{D}$ will still converge to a stationary point as usual, and that the global maximum will be characterised by value $LL$. 

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6. Empirical Validation
We implemented Algorithm 1 on top of CREDICI, a public library for causal inference.\footnote{http://github.com/idsia/credici.} The causal queries are eventually computed for each one of the $r$ FSCMs returned in output, and their bounds regarded as an inner approximation of the actual ones.

6.1. Back to the Demonstrative Example
For a first validation of our algorithm we consider the integration of the studies in Table 1. We adopt a PSCM over the graph in Figure 1. Its SEs are based on a so-called conservative specification (Zaffalon et al., 2020), which is also called canonical by Zhang et al. (2022). This means having the exogenous parent of an endogenous variable enumerating all the deterministic relations between that variable and its endogenous parents. In our model this implies $|\Omega_U| = 64$. On such a PSCM structure we run Algorithm 1 according to the superstructure in Figure 2 and with the three original datasets as in Table 1.

Once obtained the approximation $\tilde{\Theta}_U$, we use it in the twin network for the graph in Figure 1. In this way, we get the PNS for the causal relation between Treatment and Survival: i.e., $0.00 \leq \text{PNS} \leq 0.43$ if only the observational data are considered and a shrink to $0.34 \leq \text{PNS} \leq 0.43$ if also the interventional datasets are considered. For the ‘conditional PNS’ given the two possible states of Gender, we have instead $0.00 \leq \text{PNS} \leq 0.28$ for females and $0.00 \leq \text{PNS} \leq 0.58$ for males if only observational data are considered. Both intervals shrink to sharp values, respectively $\text{PNS} = 0.28$ for females and $\text{PNS} = 0.49$ for males, if also interventional data are integrated. The results for the PNS computed here with $r = 30$, and rounded to two digits after the decimal point, coincide with those reported by Mueller and Pearl (2022). Yet, the advantage of our procedure is that it can be applied to any causal model. Note that before running our EMCC we checked the $M$-compatibility as in Definition 2. Thanks to Theorem 3 and Proposition 5, this corresponds to computing the log-likelihood for the values returned by a single EM run and compare them with the maxima obtained on the individual models.

6.2. Synthetic Benchmark
For a deeper validation of the EMCC we consider a benchmark of random models and data. First, we use the Erdős-Rényi scheme to uniformly sample directed acyclic graphs. Parentless nodes are regarded as exogenous variables and the other ones as Boolean endogenous variables. SEs and exogenous cardinalities are obtained by sampling (without replacement) the deterministic relations between each endogenous variable and its endogenous parents, letting the states of the exogenous parents index the relations with $|\Omega_U| \leq 64$ for each $U \in U$. On such a PSCM, we sample the ‘ground-truth’ chances $\hat{\theta}_U$, thus obtaining an FSCM. We consequently sample an observational dataset $D^{(1)}$ from the FSCM. Assuming the endogenous variables $V := (V_1, \ldots, V_n)$ sorted in a topological order, we perform an intervention on $V_1$, considering, in order, both its possible values so as to simulate a randomised controlled trial. Let $D^{(2)}$ be the dataset sampled from such a post-interventional model. In our experiments we take $N^{(1)} := 1000$ and $N^{(2)} := 2N^{(1)}$ so as to simulate the effect of unbalanced data. Note that we occasionally increase those starting sizes (in a
proportional way) in case $M$-compatibility fails; we never sample more than 5500 records though. We run Algorithm 1 with $r = 100$, at most, on the original PSCM with: $(O)$ the observational dataset only, $(I)$ the interventional dataset only, and $(O + I)$ the two of them together. As a query we consider, for all the three cases, the PNS obtained by taking $V_1$ as cause and $V_n$ as effect. As we only cope with $M$-compatible data, the bounds for $\text{PNS}_{O+I}$ should be included in those of both $\text{PNS}_I$ and $\text{PNS}_O$. To evaluate the average shrink induced by one study on the other we compute the ratio between the length $L_{O+I}$ of the interval of $\text{PNS}_{O+I}$ and the ones for single studies. We only consider queries that remain unidentifiable even if all the data are available, whence $L_{O+I} > 0$.

This is done on a benchmark of 130 models with sizes ranging from 5 to 15 nodes. In Figure 3 (left) we can see that the shrink is noticeable in both cases, the average values being 13% if the observational data are added to the interventional ones and 18% in the opposite setup. The asymmetry appears to be explained by the presence of unbalanced data, as randomised data weigh more than observational ones in the integration; this is also a double-check about the fact that the EMCC correctly takes into account the relative sizes of multiple data. Interestingly, the observational data lead to a shrink of 13% even though they are half in size of the randomised ones. This is remarkable given that observational data are often regarded as little valuable in comparison to randomised ones. Joining them with SCMs turns them into valuable data too.

Since our EMCC provides an inner approximation of the true bounds, we use in addition the credibility intervals derived in Zaffalon et al. (2022) to estimate the probability $P_{0.1}$ that increasing the length of our interval by 10% at each extreme would allow us to cover the true interval. Figure 3 (right) shows the average values of these probabilities for two increasing values of $r$. EMCC achieves good credibility even with relatively few runs.

![Figure 3: Shrink induced by the integration (left) and credibility vs. EM runs (right).](image)

**7. Conclusions and Outlook**

We have presented an EMCC algorithm that learns the parameters of a partially specified structural causal model from a mix of observational and interventional data.

Our algorithm is approximate: it delivers a set of fully specified SCMs contained in all those that are compatible with the partially specified one. These are queried for counterfactuals, and their aggregated results are used to give inner bounds on unidentifiable queries. Empirical results support the quality of the approximation and confirm the increased informativeness of bounds obtained by merging multiple studies.

As for future work, we would like to compare our EMCC with the MCMC approach recently put forward by Zhang et al. (2022). At the moment it is not clear to us, from the reported experiment, the extent to which their approximate scheme handles heterogeneous
data, and with which accuracy, nor whether their method permits checking \(M\)-compatibility among studies.\(^2\) This is important because \(M\)-incompatibility renders inference not tenable.

More generally speaking, the problem that this work addresses can be regarded as a special case of the fusion framework put forward by Bareinboim and Pearl (2016). In particular, here we do not consider the possibility that different studies can be subject to partially different distributions for the exogenous variables, nor do we consider the problem of selection bias. These are important extensions that we shall consider in future work.

Acknowledgments

This research was partially funded by MCIN/AEI/10.13039/501100011033 with FEDER funds for the project PID2019-106758GB-C32, and also by Junta de Andalucía grant P20-00091. Finally we would like to thank the “María Zambrano” grant (RR_C_2021_01) from the Spanish Ministry of Universities and funded with NextGenerationEU funds.

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\(^2\) The related code does not appear to be publicly available yet.