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# Detecting Dependencies in Sparse, Multivariate Databases Using Probabilistic Programming and Non-parametric Bayes

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## Abstract

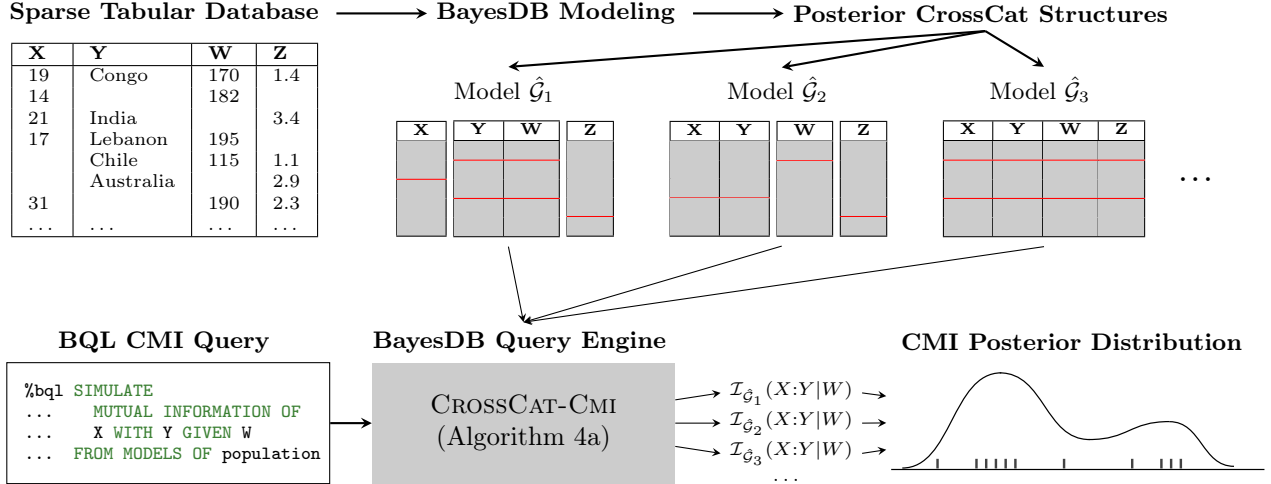
Datasets with hundreds of variables and many missing values are commonplace. In this setting, it is both statistically and computationally challenging to detect true predictive relationships between variables and also to suppress false positives. This paper proposes an approach that combines probabilistic programming, information theory, and non-parametric Bayes. It shows how to use Bayesian non-parametric modeling to (i) build an ensemble of joint probability models for all the variables; (ii) efficiently detect marginal independencies; and (iii) estimate the conditional mutual information between arbitrary subsets of variables, subject to a broad class of constraints. Users can access these capabilities using BayesDB, a probabilistic programming platform for probabilistic data analysis, by writing queries in a simple, SQL-like language. This paper demonstrates empirically that the method can (i) detect context-specific (in)dependencies on challenging synthetic problems and (ii) yield improved sensitivity and specificity over baselines from statistics and machine learning, on a real-world database of over 300 sparsely observed indicators of macroeconomic development and public health.

## 1 Introduction

Sparse databases with hundreds of variables are commonplace. In these settings, it can be both statistically and computationally challenging to detect pre-

dictive relationships between variables [4]. First, the data may be incomplete and require cleaning and imputation before pairwise statistics can be calculated. Second, parametric modeling assumptions that underlie standard hypothesis testing techniques may not be appropriate due to nonlinear, multivariate, and/or heteroskedastic relationships. Third, as the number of variables grows, it becomes harder to detect true relationships while suppressing false positives. Many approaches have been proposed (see [17, Table 1] for a summary), but they each exhibit limitations in practice. For example, some only apply to fully-observed real-valued data, and most do not produce probabilistically coherent measures of uncertainty. This paper proposes an approach to dependence detection that combines probabilistic programming, information theory, and non-parametric Bayes. The end-to-end approach is summarized in Figure 1. Queries about the conditional mutual information (CMI) between variables of interest are expressed using the Bayesian Query Language [18], an SQL-like probabilistic programming language. Approximate inference with CrossCat [19] produces an ensemble of joint probability models, which are analyzed for structural (in)dependencies. For model structures in which dependence cannot be ruled out, the CMI is estimated via Monte Carlo integration.

In principle, this approach has significant advantages. First, the method is scalable to high-dimensional data: it can be used for exploratory analysis without requiring expensive CMI estimation for all pairs of variables. Second, it applies to heterogeneously typed, incomplete datasets with minimal pre-processing [19]. Third, the non-parametric Bayesian joint density estimator used to form CMI estimates can model a broad class of data patterns, without overfitting to highly irregular data. This paper shows that the proposed approach is effective on a real-world database with hundreds of variables and a missing data rate of  $\sim 35\%$ , detecting common-sense predictive relationships that are missed by baseline methods while suppressing spurious relationships that baselines purport to detect.



**Figure 1:** Workflow for computing posterior distributions of the CMI for variables in a data table using BayesDB. Modeling and inference in BayesDB produces an ensemble of posterior CrossCat samples. Each model learns a factorization of the joint distribution of all variables in the database, and a Dirichlet process mixture within each block of dependent variables. For instance, model  $\hat{\mathcal{G}}_1$  specifies that  $X$  is independent of  $(Y, W)$  which in turn is independent of  $Z$ , while in  $\hat{\mathcal{G}}_3$ , all variables are (structurally) dependent. End-user queries for the CMI are expressed in the Bayesian Query Language. The BQL interpreter uses CrossCat structures to optimize the query where possible, by (i) bypassing Monte Carlo estimation completely when the queried variables are structurally independent, and/or (ii) dropping redundant constraints which are structurally independent of the queried variables. Values of CMI returned by each model constitute samples from the posterior CMI distribution.

## 2 Drawing Bayesian inferences about conditional mutual information

Let  $\mathbf{x} = (x_1, x_2, \dots, x_D)$  denote a  $D$ -dimensional random vector, whose sub-vectors we denote  $\mathbf{x}_A = \{x_i : i \in A\}$  with joint probability density  $p_{\mathcal{G}}(\mathbf{x}_A)$ . The symbol  $\mathcal{G}$  refers to an arbitrary specification for the “generative” process of  $\mathbf{x}$ , and parameterizes all its joint and conditional densities. The *mutual information* (MI) of the variables  $\mathbf{x}_A$  and  $\mathbf{x}_B$  (under generative process  $\mathcal{G}$ ) is defined in the usual way [5]:

$$\mathcal{I}_{\mathcal{G}}(\mathbf{x}_A:\mathbf{x}_B) = \mathbb{E}_{(\mathbf{x}_A, \mathbf{x}_B)} \left[ \log \left( \frac{p_{\mathcal{G}}(\mathbf{x}_A, \mathbf{x}_B)}{p_{\mathcal{G}}(\mathbf{x}_A)p_{\mathcal{G}}(\mathbf{x}_B)} \right) \right]. \quad (1)$$

The mutual information can be interpreted as the KL-divergence from the product of marginals  $p_{\mathcal{G}}(\mathbf{x}_A)p_{\mathcal{G}}(\mathbf{x}_B)$  to the joint distribution  $p_{\mathcal{G}}(\mathbf{x}_A, \mathbf{x}_B)$ , and is a well-established measure for both the existence and strength of dependence between  $\mathbf{x}_A$  and  $\mathbf{x}_B$  (Section 2.2). Given an observation of the variables  $\{\mathbf{x}_C = \hat{\mathbf{x}}_C\}$ , the *conditional mutual information* (CMI) of  $\mathbf{x}_A$  and  $\mathbf{x}_B$  given  $\{\mathbf{x}_C = \hat{\mathbf{x}}_C\}$  is defined analogously:

$$\mathcal{I}_{\mathcal{G}}(\mathbf{x}_A:\mathbf{x}_B|\mathbf{x}_C = \hat{\mathbf{x}}_C) = \mathbb{E}_{(\mathbf{x}_A, \mathbf{x}_B)|\hat{\mathbf{x}}_C} \left[ \log \left( \frac{p_{\mathcal{G}}(\mathbf{x}_A, \mathbf{x}_B|\hat{\mathbf{x}}_C)}{p_{\mathcal{G}}(\mathbf{x}_A|\hat{\mathbf{x}}_C)p_{\mathcal{G}}(\mathbf{x}_B|\hat{\mathbf{x}}_C)} \right) \right]. \quad (2)$$

Estimating the mutual information between the variables of  $\mathbf{x}$  given a dataset of observations  $\mathcal{D}$  remains

an open problem in the literature. Various parametric and non-parametric methods for estimating MI exist [21, 22, 15]; see [24] for a comprehensive review. Traditional approaches typically construct a point estimate  $\hat{\mathcal{I}}(\mathbf{x}_A:\mathbf{x}_B)$  (and possible confidence intervals) assuming a “true value” of  $\mathcal{I}(\mathbf{x}_A:\mathbf{x}_B)$ . In this paper, we instead take a non-parametric Bayesian approach, where the mutual information itself is a derived random variable; a similar interpretation was recently developed in independent work [16]. The randomness of mutual information arises from treating the data generating process and parameters  $\mathcal{G}$  as a random variable, whose prior distribution we denote  $\pi$ . Composing  $\mathcal{G}$  with the function  $h : \mathcal{G} \mapsto \mathcal{I}_{\mathcal{G}}(\mathbf{x}_A:\mathbf{x}_B)$  induces the derived random variable  $h(\mathcal{G}) \equiv \mathcal{I}_{\mathcal{G}}(\mathbf{x}_A:\mathbf{x}_B)$ . The distribution of the MI can thus be expressed as an expectation under distribution  $\pi$ :

$$\begin{aligned} \mathbb{P}[\mathcal{I}_{\mathcal{G}}(\mathbf{x}_A:\mathbf{x}_B) \in S] &= \int \mathbb{I}[\mathcal{I}_{\hat{\mathcal{G}}}(\mathbf{x}_A:\mathbf{x}_B) \in S] \pi(d\hat{\mathcal{G}}) \\ &= \mathbb{E}_{\hat{\mathcal{G}} \sim \pi} [\mathbb{I}[\mathcal{I}_{\hat{\mathcal{G}}}(\mathbf{x}_A:\mathbf{x}_B) \in S]]. \end{aligned} \quad (3)$$

Given a dataset  $\mathcal{D}$ , we define the posterior distribution of the mutual information,  $\mathbb{P}[\mathcal{I}_{\mathcal{G}}(\mathbf{x}_A:\mathbf{x}_B) \in S|\mathcal{D}]$  as the expectation in Eq (3) under the posterior  $\pi(\cdot|\mathcal{D})$ . We define the distribution over conditional mutual information  $\mathbb{P}[\mathcal{I}_{\mathcal{G}}(\mathbf{x}_A:\mathbf{x}_B|\hat{\mathbf{x}}_C) \in S]$  analogously to Eq (3), substituting the CMI (2) inside the expectation.

## 2.1 Estimating CMI with generative population models

Monte Carlo estimates of CMI can be formed for models expressed as *generative population models* [18, 28], a probabilistic programming formalism for characterizing the data generating process of an infinite array of realizations of random vector  $\mathbf{x} = (x_1, x_2, \dots, x_D)$ . Listing 1 summarizes elements of the GPM interface.

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**Listing 1** GPM interface for simulating from and assessing the density of conditional and marginal distributions of a random vector  $\mathbf{x}$ .

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`SIMULATE`( $\mathcal{G}$ , query:  $\mathcal{Q} = \{q_j\}$ , condition:  $\hat{\mathbf{x}}_{\mathcal{E}} = \{\hat{x}_{e_j}\}$ )  
 Return a sample  $\mathbf{s} \sim p_{\mathcal{G}}(\mathbf{x}_{\mathcal{Q}} | \hat{\mathbf{x}}_{\mathcal{E}}, \mathcal{D})$ .

`LOGPDF`( $\mathcal{G}$ , query:  $\hat{\mathbf{x}}_{\mathcal{Q}} = \{\hat{x}_{q_j}\}$ , condition:  $\hat{\mathbf{x}}_{\mathcal{E}} = \{\hat{x}_{e_j}\}$ )  
 Return the joint log density  $p_{\mathcal{G}}(\hat{\mathbf{x}}_{\mathcal{Q}} | \hat{\mathbf{x}}_{\mathcal{E}}, \mathcal{D})$

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These two interface procedures can be combined to derive a simple Monte Carlo estimator for the CMI (2), shown in Algorithm 2a.

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### Algorithm 2a GPM-CMI

**Require:** GPM  $\mathcal{G}$ ; query  $\mathcal{A}, \mathcal{B}$ ; condition  $\hat{\mathbf{x}}_{\mathcal{C}}$ ; accuracy  $T$   
**Ensure:** Monte Carlo estimate of  $\mathcal{I}_{\mathcal{G}}(\mathbf{x}_{\mathcal{A}} : \mathbf{x}_{\mathcal{B}} | \mathbf{x}_{\mathcal{C}} = \hat{\mathbf{x}}_{\mathcal{C}})$

- 1: **for**  $t = 1, \dots, T$  **do**
  - 2:    $(\hat{\mathbf{x}}_{\mathcal{A}}, \hat{\mathbf{x}}_{\mathcal{B}}) \leftarrow \text{SIMULATE}(\mathcal{G}, \mathcal{A} \cup \mathcal{B}, \hat{\mathbf{x}}_{\mathcal{C}})$
  - 3:    $m_{\mathcal{A} \cup \mathcal{B}}^t \leftarrow \text{LOGPDF}(\mathcal{G}, \hat{\mathbf{x}}_{\mathcal{A} \cup \mathcal{B}}, \hat{\mathbf{x}}_{\mathcal{C}})$
  - 4:    $m_{\mathcal{A}}^t \leftarrow \text{LOGPDF}(\hat{\mathbf{x}}_{\mathcal{A}}, \hat{\mathbf{x}}_{\mathcal{C}})$
  - 5:    $m_{\mathcal{B}}^t \leftarrow \text{LOGPDF}(\hat{\mathbf{x}}_{\mathcal{B}}, \hat{\mathbf{x}}_{\mathcal{C}})$
  - 6: **return**  $\frac{1}{T} \sum_{t=1}^T (m_{\mathcal{A} \cup \mathcal{B}}^t - (m_{\mathcal{A}}^t + m_{\mathcal{B}}^t))$
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While GPM-CMI is an unbiased and consistent estimator applicable to any probabilistic model implemented as a GPM, its quality in detecting dependencies is tied to the ability of  $\mathcal{G}$  to capture patterns from the dataset  $\mathcal{D}$ ; this paper uses baseline non-parametric GPMs built using CrossCat (Section 3).

## 2.2 Extracting conditional independence relationships from CMI estimates

An estimator for the CMI can be used to discover several forms of independence relations of interest.

**Marginal Independence** It is straightforward to see that  $(\mathbf{x}_{\mathcal{A}} \perp\!\!\!\perp_{\mathcal{G}} \mathbf{x}_{\mathcal{B}})$  if and only if  $\mathcal{I}_{\mathcal{G}}(\mathbf{x}_{\mathcal{A}} : \mathbf{x}_{\mathcal{B}}) = 0$ .

**Context-Specific Independence** If the event  $\{\mathbf{x}_{\mathcal{C}} = \hat{\mathbf{x}}_{\mathcal{C}}\}$  decouples  $\mathbf{x}_{\mathcal{A}}$  and  $\mathbf{x}_{\mathcal{B}}$ , then they are said to be independent “in the context” of  $\hat{\mathbf{x}}_{\mathcal{C}}$ , denoted  $(\mathbf{x}_{\mathcal{A}} \perp\!\!\!\perp_{\mathcal{G}} \mathbf{x}_{\mathcal{B}} | \{\mathbf{x}_{\mathcal{C}} = \hat{\mathbf{x}}_{\mathcal{C}}\})$  [3]. This condition is equivalent to the CMI from (2) equaling zero. Thus by estimating CMI, we are able to detect finer-grained independencies than can be detected by analyzing the graph structure of a learned Bayesian network [30].

**Conditional Independence** If context-specific independence holds for all possible observation sets

$\{\mathbf{x}_{\mathcal{C}} = \hat{\mathbf{x}}_{\mathcal{C}}\}$ , then  $\mathbf{x}_{\mathcal{A}}$  and  $\mathbf{x}_{\mathcal{B}}$  are *conditionally independent* given  $\mathbf{x}_{\mathcal{C}}$ , denoted  $(\mathbf{x}_{\mathcal{A}} \perp\!\!\!\perp_{\mathcal{G}} \mathbf{x}_{\mathcal{B}} | \mathbf{x}_{\mathcal{C}})$ . By the non-negativity of CMI, conditional independence implies the CMI of  $\mathbf{x}_{\mathcal{A}}$  and  $\mathbf{x}_{\mathcal{B}}$ , marginalizing out  $\mathbf{x}_{\mathcal{C}}$ , is zero:

$$\mathcal{I}_{\mathcal{G}}(\mathbf{x}_{\mathcal{A}} : \mathbf{x}_{\mathcal{B}} | \mathbf{x}_{\mathcal{C}}) = \mathbb{E}_{\hat{\mathbf{x}}_{\mathcal{C}}} [\mathcal{I}_{\mathcal{G}}(\mathbf{x}_{\mathcal{A}} : \mathbf{x}_{\mathcal{B}} | \mathbf{x}_{\mathcal{C}} = \hat{\mathbf{x}}_{\mathcal{C}})] = 0. \quad (4)$$

Figure 2 illustrates different CMI queries which are used to discover these three types of dependencies in various data generators; Figure 3 shows CMI queries expressed in the Bayesian Query Language.

## 3 Building generative population models for CMI estimation with non-parametric Bayes

Our approach to estimating the CMI requires a prior  $\pi$  and model class  $\mathcal{G}$  which is flexible enough to emulate an arbitrary joint distribution over  $\mathbf{x}$ , and tractable enough to implement Algorithm 2a for its arbitrary sub-vectors. We begin with a Dirichlet process mixture model (DPMM) [12]. Letting  $L_d$  denote the likelihood for variable  $d$ ,  $V_d$  a prior over the parameters of  $L_d$ , and  $\boldsymbol{\lambda}_d$  the hyperparameters of  $V_d$ , the generative process for  $N$  observations  $\mathcal{D} = \{\mathbf{x}_{[i,1:D]} : 1 \leq i \leq N\}$  is:

### DPMM-PRIOR

$\alpha \sim \text{GAMMA}(1, 1)$

$\mathbf{z} = (z_1, \dots, z_N) \sim \text{CRP}(\cdot | \alpha)$

$\phi_{[d,k]} \sim V_d(\cdot | \boldsymbol{\lambda}_d) \quad d \in [D], k \in \text{UNIQUE}(\mathbf{z})$

$x_{[i,d]} \sim L_d(\cdot | \phi_{[d,z_i]}) \quad i \in [N], d \in [D]$

We refer to [7, 14] for algorithms for posterior inference, and assume we have a posterior sample  $\hat{\mathcal{G}} = (\alpha, \mathbf{z}_{[1:N]}, \{\phi_d\})$  of all parameters in the DPMM. To compute the CMI of an arbitrary query pattern  $\mathcal{I}_{\hat{\mathcal{G}}}(\mathbf{x}_{\mathcal{A}} : \mathbf{x}_{\mathcal{B}} | \mathbf{x}_{\mathcal{C}} = \hat{\mathbf{x}}_{\mathcal{C}})$  using Algorithm 2a, we need implementations of `SIMULATE` and `LOGPDF` for  $\hat{\mathcal{G}}$ . These two procedures are summarized in Algorithms 3a, 3b.

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### Algorithm 3a DPMM-SIMULATE

**Require:** DPMM  $\mathcal{G}$ ; target  $\mathcal{A}$ ; condition  $\hat{\mathbf{x}}_{\mathcal{C}}$

**Ensure:** joint sample  $\hat{\mathbf{x}}_{\mathcal{A}} \sim p_{\mathcal{G}}(\cdot | \hat{\mathbf{x}}_{\mathcal{C}})$

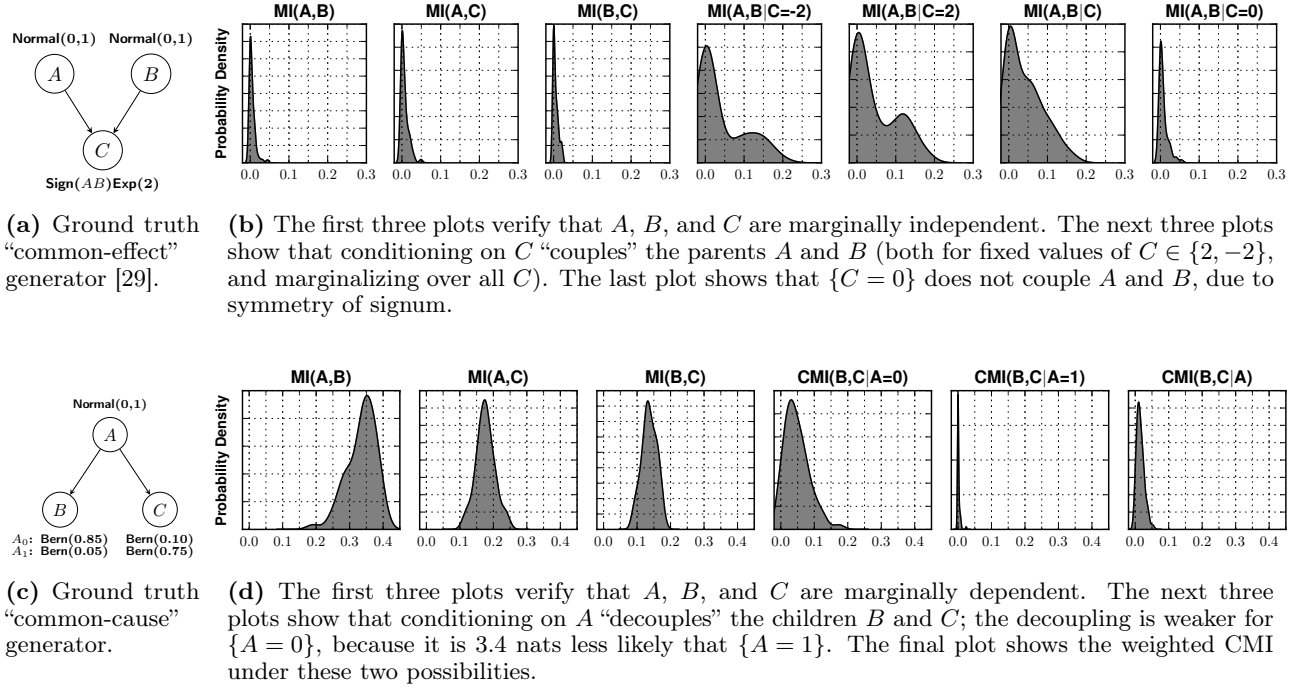
- 1:  $(l_i)_{i=1}^{K+1} \leftarrow \text{DPMM-CLUSTER-POSTERIOR}(\mathcal{G}, \hat{\mathbf{x}}_{\mathcal{C}})$
  - 2:  $z_{N+1} \sim \text{CATEGORICAL}(l_1, \dots, l_{K+1})$
  - 3: **for**  $a \in \mathcal{A}$  **do**
  - 4:    $\hat{x}_a \sim L_a(\cdot | \phi_{[a, z_{N+1}]})$
  - 5: **return**  $\hat{\mathbf{x}}_{\mathcal{A}}$
- 

### Algorithm 3b DPMM-LOGPDF

**Require:** DPMM  $\mathcal{G}$ ; target  $\hat{\mathbf{x}}_{\mathcal{A}}$ ; condition  $\hat{\mathbf{x}}_{\mathcal{C}}$

**Ensure:** log density  $p_{\mathcal{G}}(\hat{\mathbf{x}}_{\mathcal{A}} | \hat{\mathbf{x}}_{\mathcal{C}})$

- 1:  $(l_i)_{i=1}^{K+1} \leftarrow \text{DPMM-CLUSTER-POSTERIOR}(\mathcal{G}, \hat{\mathbf{x}}_{\mathcal{C}})$
- 2: **for**  $k = 1, \dots, K + 1$  **do**
- 3:    $t_k \leftarrow \prod_{a \in \mathcal{A}} L_a(\hat{x}_a | \phi_{[a, k]})$
- 4: **return**  $\log \left( \sum_{k=1}^{K+1} (t_k l_k) \right)$



**Figure 2:** Posterior distributions of CMI under the DPMM posterior, given 100 data points from canonical Bayes net structures. Distributions peaked at 0 indicate high probability of (conditional) independence. In both cases, the posterior CMI distributions correctly detect the marginal, conditional, and context-specific independences in the “ground truth” Bayes nets, despite the fact that both “common-cause” and “common-effect” structures are not in the (structural) hypothesis space of the DPMM prior.

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### Algorithm 3c DPMM-CLUSTER-POSTERIOR

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**Require:** DPMM  $\mathcal{G}$ ; condition  $\hat{\mathbf{x}}_C$ ;  
**Ensure:**  $\{p_{\mathcal{G}}(z_{N+1} = k) : 1 \leq k \leq \max(\mathbf{z}_{1:N}) + 1\}$   
 1:  $K \leftarrow \max(\mathbf{z}_{1:N})$   
 2: **for**  $k = 1, \dots, K + 1$  **do**  
 3:      $n_k \leftarrow \begin{cases} |\{\mathbf{x}_i \in \mathcal{D} : z_i = k\}| & \text{if } k \leq K \\ \alpha & \text{if } k = K + 1 \end{cases}$   
 4:      $l_k \leftarrow \left( \prod_{c \in C} L_c(\hat{\mathbf{x}}_c | \phi_{[c,k]}) \right) n_k$   
 5: **return**  $(l_1, \dots, l_{K+1}) / \sum_{k=1}^{K+1} (l_k)$

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The subroutine DPMM-CLUSTER-POSTERIOR is used for sampling (in DPMM-SIMULATE) and marginalizing over (in DPMM-LOGPDF) the non-parametric mixture components. Moreover, if  $L_d$  and  $V_d$  form a conjugate likelihood-prior pair, then invocations of  $L_d(\hat{\mathbf{x}}_d | \phi_{[d,k]})$  in Algorithms 3a:4 and 3b:3 can be Rao-Blackwellized by conditioning on the sufficient statistics of data in cluster  $k$ , thus marginalizing out  $\phi_{[d,k]}$  [26]. This optimization is important in practice, since analytical marginalization can be obtained in closed-form for several likelihoods in the exponential family [9]. Finally, to approximate the posterior distribution over CMI in (2), it suffices to aggregate DPMM-CMI from a set of posterior samples  $\{\hat{\mathcal{G}}_1, \dots, \hat{\mathcal{G}}_H\} \sim^{\text{iid}} \pi(\cdot | \mathcal{D})$ . Figure 2

shows posterior CMI distributions from the DPMM successfully recovering the marginal and conditional independencies in two canonical Bayesian networks.

### 3.1 Inducing sparse dependencies using the CrossCat prior

The multivariate DPMM makes the restrictive assumption that all variables  $\mathbf{x} = (x_1, \dots, x_D)$  are (structurally) marginally dependent, where their joint distribution fully factorizes conditioned on the mixture assignment  $z$ . In high-dimensional datasets, imposing full structural dependence among all variables is too conservative. Moreover, while the Monte Carlo error of Algorithm 2a does not scale with the dimensionality  $D$ , its runtime scales linearly for the DPMM, and so estimating the CMI is likely to be prohibitively expensive. We relax these constraints by using CrossCat [19], a structure learning prior which induces sparsity over the dependencies between the variables of  $\mathbf{x}$ . In particular, CrossCat posits a factorization of  $\mathbf{x}$  according to a *variable partition*  $\gamma = \{\mathcal{V}_1, \dots, \mathcal{V}_{|\gamma|}\}$ , where  $\mathcal{V}_i \subseteq [D]$ . For  $i \neq j$ , all variables in block  $\mathcal{V}_i$  are mutually (marginally and conditionally) independent of all variables in  $\mathcal{V}_j$ . The factorization of  $\mathbf{x}$  given the

English Summary of CMI Query	CMI Query in Bayesian Query Language	Inference Algorithm Invoked by Query Interpreter
Simulate from the posterior distribution of the mutual information of $(x_1, x_2)$ with $x_3$ , given $x_4 = 14$ .	<b>SIMULATE</b> MUTUAL INFORMATION OF (x1, x2) WITH (x3) GIVEN (x4 = 14) FROM MODELS OF population	1: <b>for</b> $\mathcal{G}_k \in \mathcal{M}$ <b>do</b> 2: $\mathcal{I}_{\mathcal{G}_k} \leftarrow \text{GPM-CMI}(\mathcal{G}_k, \{x_1, x_2\}, \{x_3\}, \{(x_4, 14)\})$ 3: <b>return</b> $(\mathcal{I}_{\mathcal{G}_1}, \dots, \mathcal{I}_{\mathcal{G}_{ \mathcal{M} }})$
Estimate the probability that the mutual information of $(x_1, x_2)$ with $x_3$ , given $x_4 = 14$ and marginalizing over $x_5$ , is less than 0.1 nats.	<b>ESTIMATE PROBABILITY OF</b> MUTUAL INFORMATION OF (x1, x2) WITH (x3) GIVEN (x4 = 14, x5) < 0.1 <b>BY</b> population	1: <b>for</b> $\mathcal{G}_k \in \mathcal{M}$ <b>do</b> 2: <b>for</b> $t = 1, \dots, T$ <b>do</b> 3: $\hat{x}_5^t \leftarrow \text{SIMULATE}(\mathcal{G}_k, x_5, \{(x_4, 14)\})$ 4: $\mathcal{I}_{\mathcal{G}_k}^t \leftarrow \text{GPM-CMI}(\mathcal{G}_k, \{x_1, x_2\}, \{x_3\}, \{(x_4, 14), (x_5, \hat{x}_5^t)\})$ 5: $\mathcal{I}_{\mathcal{G}_k} \leftarrow \frac{1}{T} \sum_t (\mathcal{I}_{\mathcal{G}_k}^t)$ 6: <b>return</b> $\frac{1}{ \mathcal{M} } \sum_j (\mathbb{I}[\mathcal{I}_{\mathcal{G}_k} < 0.1])$
Synthesize a hypothetical dataset with 100 records, including only those variables which are probably independent of $x_2$ .	<b>SIMULATE</b> ( SELECT * FROM VARIABLES OF population WHERE PROBABILITY OF MUTUAL INFORMATION WITH x2 < 0.1 > 0.9) <b>FROM</b> population <b>LIMIT</b> 100;	1: $S \leftarrow \emptyset$ 2: <b>for</b> $x_i \in (x_1, \dots, x_D)$ <b>do</b> 3: <b>for</b> $\mathcal{G}_k \in \mathcal{M}$ <b>do</b> 4: $\mathcal{I}_{\mathcal{G}_k} \leftarrow \text{GPM-CMI}(\mathcal{G}_k, x_i, x_2, \emptyset)$ 5: $p_i \leftarrow \frac{1}{ \mathcal{M} } \sum_k \mathbb{I}[\mathcal{I}_{\mathcal{G}_k} < 0.1]$ 6: <b>if</b> $p_i > 0.9$ <b>then</b> 7: $S \leftarrow S \cup \{x_i\}$ 8: <b>for</b> $t = 1, \dots, 100$ <b>do</b> 9: $s_t \leftarrow \text{SIMULATE}(\mathcal{M}, S, \emptyset)$ 10: <b>return</b> $(s_1, \dots, s_{100})$

**Figure 3:** End-user CMI queries in the Bayesian Query Language for three data analysis tasks; (top) evaluating the strength of predictive relationships; (middle) specifying the amount of evidence required for a “predictively” significant relationship; (bottom) synthesizing a hypothetical population, censoring probably sensitive variables.

variable partition  $\gamma$  is therefore given by:

$$p_{\mathcal{G}}(\mathbf{x}|\mathcal{D}) = \prod_{\mathcal{V} \in \gamma} p_{\mathcal{G}_{\mathcal{V}}}(\mathbf{x}_{\mathcal{V}}|\mathcal{D}_{\mathcal{V}}). \quad (5)$$

Within block  $\mathcal{V}$ , the variables  $\mathbf{x}_{\mathcal{V}} = \{x_d : d \in \mathcal{V}\}$  are distributed according to a multivariate DPMM; subscripts with  $\mathcal{V}$  (such as  $\mathcal{G}_{\mathcal{V}}$ ) now index a set of block-specific DPMM parameters. The joint predictive density  $p_{\mathcal{G}_{\mathcal{V}}}$  is given by Algorithm 3b:

$$p_{\mathcal{G}_{\mathcal{V}}}(\mathbf{x}_{\mathcal{V}}|\mathcal{D}) = \sum_{k=1}^{K_{\mathcal{V}}+1} \left( \frac{\prod_{d \in \mathcal{V}} p_{\mathcal{G}_{\mathcal{V}}}(x_d|\phi_{[d,k]})}{\sum_{k'} n_{[\mathcal{V},k']}} \right). \quad (6)$$

The CrossCat generative process for  $N$  observations  $\mathcal{D} = \{\mathbf{x}_{[i,1:D]} : 1 \leq i \leq N\}$  is summarized below.

**CROSSCAT-PRIOR**

$$\alpha' \sim \text{GAMMA}(1, 1)$$

$$\mathbf{v} = (v_1, \dots, v_D) \sim \text{CRP}(\cdot|\alpha')$$

$$\mathcal{V}_k \leftarrow \{i \in [D] : v_i = k\} \quad k \in \text{UNIQUE}(\mathbf{v})$$

$$\{x_{[i,\mathcal{V}_k]}\}_{i=1}^N \sim \text{DPMM-PRIOR} \quad k \in \text{UNIQUE}(\mathbf{v})$$

We refer to [19, 23] for algorithms for posterior inference in CrossCat, and assume we have a set of approximate samples  $\{\hat{\mathcal{G}}_i : 1 \leq i \leq H\}$  of all latent CrossCat parameters from the posterior  $\pi(\cdot|\mathcal{D})$ .

### 3.2 Optimizing a CMI query

The following lemma shows how CrossCat induces sparsity for a multivariate CMI query.

**Lemma 1.** *Let  $\mathcal{G}$  be a posterior sample from CrossCat, whose full joint distribution is given by (5) and (6). Then, for all  $\mathcal{A}, \mathcal{B}, \mathcal{C} \subseteq [D]$ ,*

$$\mathcal{I}_{\mathcal{G}}(\mathbf{x}_{\mathcal{A}} : \mathbf{x}_{\mathcal{B}} | \hat{\mathbf{x}}_{\mathcal{C}}) = \sum_{\mathcal{V} \in \gamma} \mathcal{I}_{\mathcal{G}_{\mathcal{V}}}(\mathbf{x}_{\mathcal{A} \cap \mathcal{V}} : \mathbf{x}_{\mathcal{B} \cap \mathcal{V}} | \hat{\mathbf{x}}_{\mathcal{C} \cap \mathcal{V}}),$$

where  $\mathcal{I}_{\mathcal{G}_{\mathcal{V}}}(\mathbf{x}_{\mathcal{A} \cap \mathcal{V}} : \emptyset | \hat{\mathbf{x}}_{\mathcal{C} \cap \mathcal{V}}) \equiv 0$ .

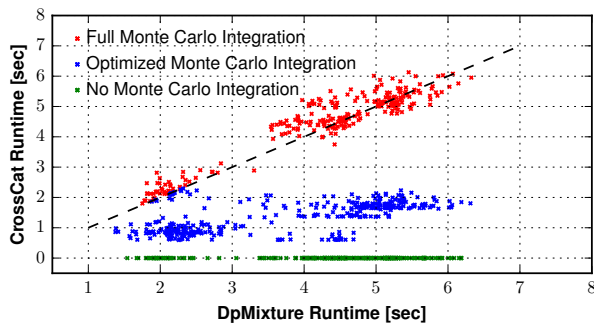
*Proof.* Refer to Appendix A.

An immediate consequence of Lemma 1 is that structure discovery in CrossCat allows us to optimize Monte Carlo estimation of  $\mathcal{I}_{\mathcal{G}}(\mathbf{x}_{\mathcal{A}} : \mathbf{x}_{\mathcal{B}} | \mathbf{x}_{\mathcal{C}} = \hat{\mathbf{x}}_{\mathcal{C}})$  by ignoring all target and condition variables which are not in the same block  $\mathcal{V}$ , as shown in Algorithm 4a and Figure 4.

**Algorithm 4a** CROSSCAT-CMI

**Require:** CrossCat  $\mathcal{G}$ ; query  $\mathcal{A}, \mathcal{B}$ ; condition  $\hat{\mathbf{x}}_{\mathcal{C}}$ ; acc.  $T$   
**Ensure:** Monte Carlo estimate of  $\mathcal{I}_{\mathcal{G}}(\mathbf{x}_{\mathcal{A}} : \mathbf{x}_{\mathcal{B}} | \mathbf{x}_{\mathcal{C}} = \hat{\mathbf{x}}_{\mathcal{C}})$

- 1: **for**  $\mathcal{V} \in \gamma$  **do**
- 2: **if**  $\mathcal{A} \cap \mathcal{V}$  AND  $\mathcal{B} \cap \mathcal{V}$  **then**
- 3:  $i_{\mathcal{V}} \leftarrow \text{GPM-CMI}(\mathcal{G}_{\mathcal{V}}, \mathcal{A} \cap \mathcal{V}, \mathcal{B} \cap \mathcal{V}, \hat{\mathbf{x}}_{\mathcal{C} \cap \mathcal{V}}, T)$
- 4: **else**
- 5:  $i_{\mathcal{V}} \leftarrow 0$
- 6: **return**  $\sum_{\mathcal{V} \in \gamma} i_{\mathcal{V}}$



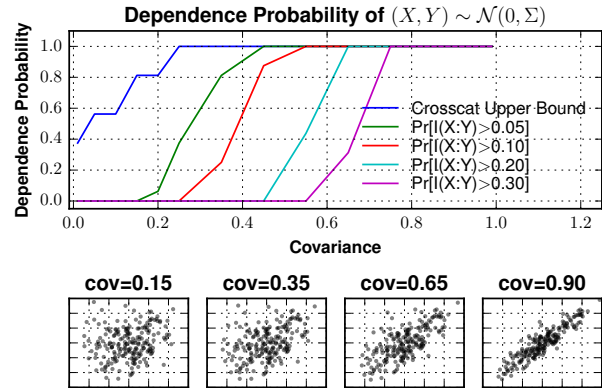
**Figure 4:** Comparing the runtime of CROSSCAT-CMI (Alg 4a) and GPM-CMI (Alg 2a) (using the DPMM), on 1000 randomly generated CMI queries from an 8-dimensional dataset. The dashed curve shows the 45-degree line. The green dots at 0 correspond to CrossCat detecting structural independence between query variables, bypassing Monte Carlo estimation completely. The blue dots (below diagonal) correspond to CrossCat optimizing the Monte Carlo estimator by ignoring constraint variables which are structurally independent of the target variables. The red dots (along diagonal) correspond to CrossCat learning no structural independences, requiring full Monte Carlo estimation and resulting in comparable runtime to DPMM. These three cases correspond to the three posterior CrossCat structures illustrated in Figure 1, when the targets variables are  $X$  and  $Y$  conditioned on  $W$ .

### 3.3 Upper bounding the pairwise dependence probability

In exploratory data analysis, we are often interested in detecting pairwise predictive relationships between variables  $(x_i, x_j)$ . Using the formalism from Eq (3), we can compute the probability that their MI is non-zero:  $\mathbb{P}[\mathcal{I}_{\mathcal{G}}(x_i : x_j) > 0]$ . This quantity can be upper-bounded by the posterior probability that  $x_i$  and  $x_j$  have the same assignments  $v_i$  and  $v_j$  in the CrossCat variable partition  $\gamma$ :

$$\begin{aligned} & \mathbb{P}[\mathcal{I}_{\mathcal{G}}(x_i : x_j) > 0] \\ &= \mathbb{P}[\mathcal{I}_{\mathcal{G}}(x_i : x_j) > 0 \mid \{\mathcal{G} : v_i = v_j\}] \mathbb{P}[\{\mathcal{G} : v_i = v_j\}] \\ & \quad + \mathbb{P}[\mathcal{I}_{\mathcal{G}}(x_i : x_j) > 0 \mid \{\mathcal{G} : v_i \neq v_j\}] \mathbb{P}[\{\mathcal{G} : v_i \neq v_j\}] \\ &= \mathbb{P}[\mathcal{I}_{\mathcal{G}}(x_i : x_j) > 0 \mid \{\mathcal{G} : v_i = v_j\}] \mathbb{P}[\{\mathcal{G} : v_i = v_j\}] \\ &< \mathbb{P}[\{\mathcal{G} : v_i = v_j\}] \approx \frac{1}{H} \sum_{h=1}^H \mathbb{I}[\hat{\mathcal{G}}_h : \hat{v}_{[h,i]} = \hat{v}_{[h,j]}], \quad (7) \end{aligned}$$

where Lemma 1 has been used to set the addend in line 3 to zero. Also note that the summand in (7) can be computed in  $O(1)$  for CrossCat sample  $\hat{\mathcal{G}}_h$ . When dependencies among the  $D$  variables are sparse such that many pairs  $(x_i, x_j)$  have MI upper bounded by 0, the number of invocations of Algorithm 4a required to compute pairwise MI values is  $\ll O(D^2)$ . A comparison of upper bounding MI versus exact MI estimation with Monte Carlo is shown in Figure 5.



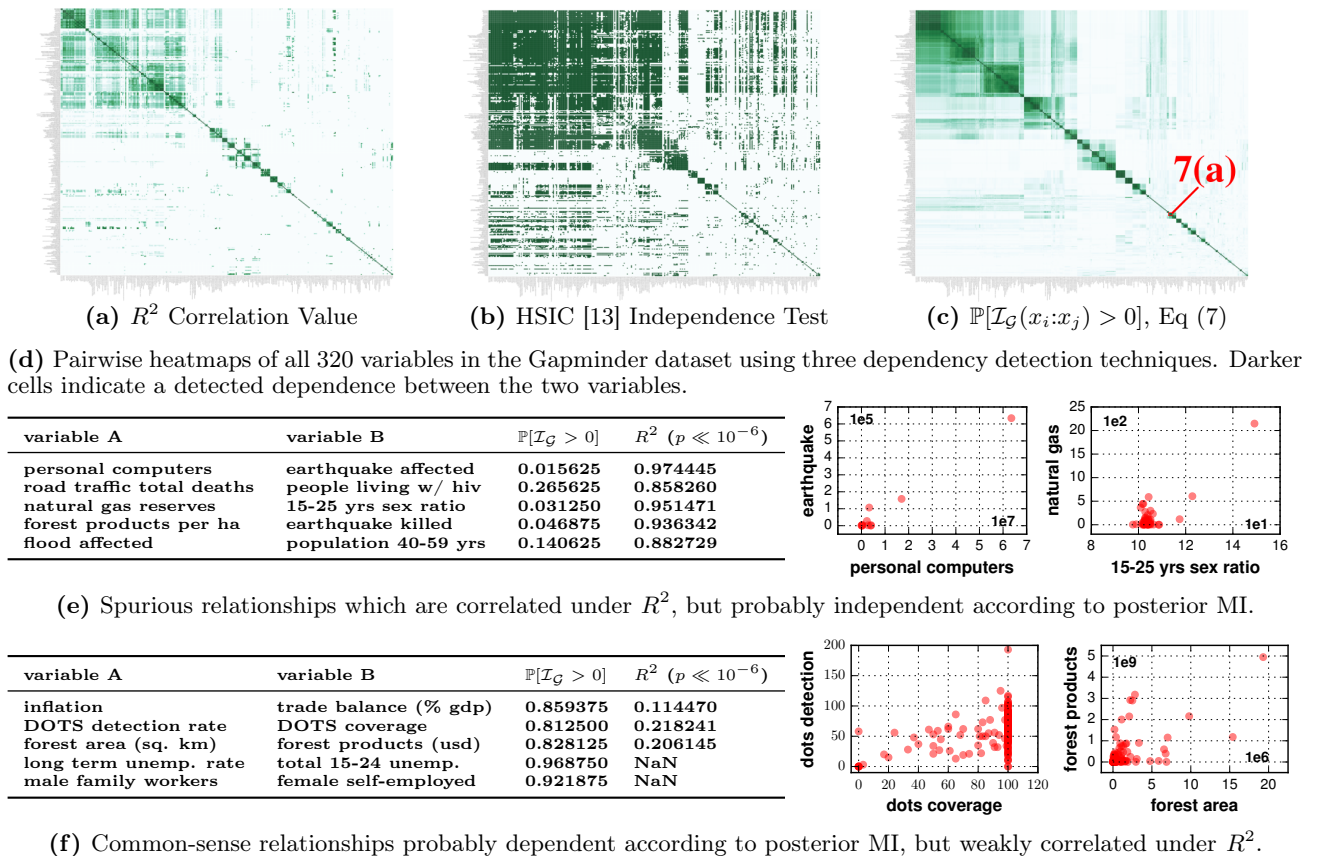
**Figure 5:** Posterior probability that dimensions of a bivariate Gaussian are dependent, vs the covariance (top). The CrossCat upper bound (7) is useful for detecting the existence of a predictive relationship; the posterior distribution of MI can determine whether the strength of the relationship is “predictively significant” based on various tolerance levels (0.05, 0.10, 0.20, and 0.30 nats).

## 4 Applications to macroeconomic indicators of global poverty, education, and health

This section illustrates the efficacy of the proposed approach on a sparse database from an ongoing collaboration with the Bill & Melinda Gates Foundation.<sup>1</sup> The Gapminder data set is an extensive longitudinal dataset of  $\sim 320$  global developmental indicators for 200 countries spanning over 5 centuries [27]. These include variables from a broad set of categories such as education, health, trade, poverty, population growth, and mortality rates. We experiment with a cross-sectional slice of the data from 2002. Figure 6a shows the pairwise  $R^2$  correlation values between all variables; each row and column in the heatmap is an indicator in the dataset, and the color of a cell is the raw value of  $R^2$  (between 0 and 1). Figure 6b shows pairwise binary hypothesis tests of independence using HSIC [13], which detects a dense set of dependencies including many spurious relationships (Appendix B). For both methods, statistically insignificant relationships ( $\alpha = 0.05$  with Bonferroni correction for multiple testing) are shown as 0. Figure 6c shows an upper bound on the pairwise probability that the MI of two variables exceeds zero (also a value between 0 and 1). These entries are estimated using Eq (7) (bypassing Monte Carlo estimation) using  $H=100$  samples of CrossCat. Note that the metric  $\mathbb{P}[\mathcal{I}_{\mathcal{G}}(x_i : x_j) > 0]$  in Figure 6c only indicates the *existence* of a predictive relationship between  $x_i$  and  $x_j$ ; it does not quantify either the strength or directionality of the relationship.

<sup>1</sup>A further application, to a real-world dataset of mathematics exam scores, is shown in Appendix C.





**Figure 6:** Comparing dependences between variables in the Gapminder dataset, as detected by  $R^2$ , HSIC (with Bonferroni correction for multiple testing), and posterior distribution over mutual information in CrossCat.

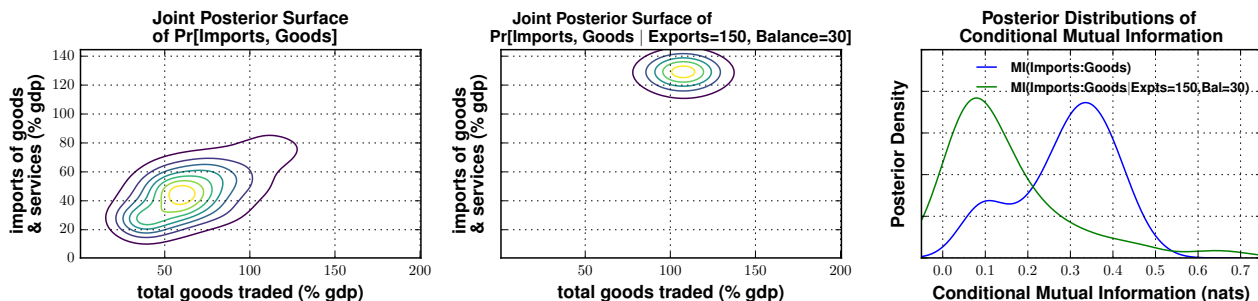
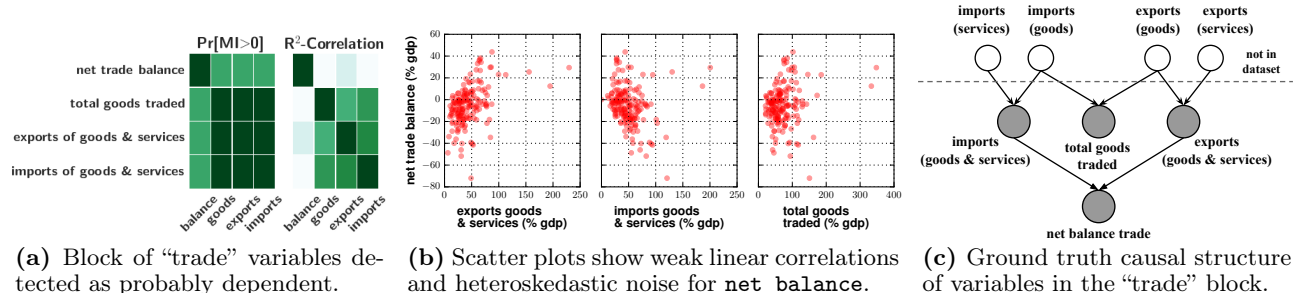
It is instructive to compare the dependencies detected by  $R^2$  and CROSSCAT-CMI. Table 6e shows pairs of variables that are spuriously reported as dependent according to correlation; scatter plots reveal they are either (i) are sparsely observed or (ii) exhibit high correlation due to large outliers. Table 6f shows common-sense relationships between pairs of variables that CROSSCAT-CMI detects but  $R^2$  does not; scatter plots reveal they are either (i) non-linearly related, (ii) roughly linear with heteroskedastic noise, or (iii) pairwise independent but dependent given a third variable. Recall that CrossCat is a product of DPMMs; practically meaningful conditions for weak and strong consistency of Dirichlet location-scale mixtures have been established by [11, 33]. This supports the intuition that CrossCat can detect a broad class of predictive relationships that simpler parametric models miss.

Figure 7 focuses on a group of four “trade”-related variables in the Gapminder dataset detected as probably dependent: “net trade balance”, “total goods traded”, “exports of goods and services”, and “imports of goods and services”.  $R^2$  fails to detect a statistically significant dependence between “net trade balance” and

the other variables, due to weak linear correlations and heteroskedastic noise as shown in the scatter plots (Figure 7b). From economics, these four variables are causally related by the graphical model in Figure 7c, where the value of a node is a noisy addition or subtraction of the values of its parents. Figure 7d illustrates that CrossCat recovers predictive relationships between these variables: conditioning on “exports”=150 and “balance”=30 (a low probability event according to the left subplot) centers the posterior predictive distribution of “imports” around 120, and decouples it from “total goods”. The posterior CMI curves of “imports” and “total goods”, with and without the conditions on “exports” and “balance”, formalize this decoupling (right subplot of Figure 7d).

## 5 Related Work

There is broad acknowledgment that new techniques for dependency detection beyond linear correlation are required. Existing approaches for conditional independence testing include the use of kernel methods [1, 10, 35, 29], copula functions [2, 25, 17], and char-



**Figure 7:** CMI discovers existence and confirms strength of predictive relationships between “trade” variables.

acteristic functions [32], many of which capture non-linear and multivariate predictive relationships. Unlike these methods, however, our approach represents dependence in terms of conditional mutual information and is not embedded in a frequentist decision-theoretic framework. Our quantity of interest is a full posterior distribution over CMI, as opposed to a  $p$ -value to identify when the null hypothesis  $\text{CMI}=0$  cannot be rejected. Dependence detection is much less studied in the Bayesian literature; [8] use a Polya tree prior to compute a Bayes Factor for the relative evidence of dependence versus independence. Their method is used only to quantify evidence for the existence, but not assess the strength, of a predictive relationship. The most similar approach to this work was proposed independently in recent work by [16], who compute a distribution over CMI by estimating the joint density using an encompassing non-parametric Bayesian prior. However, the differences are significant. First, the Monte Carlo estimator in [16] is based on resampling empirical data. However, real-world databases may be too sparse for resampling data to yield good estimates, especially for queries given unlikely constraints. Instead, we use a Monte Carlo estimator by simulating the predictive distribution. Second, the prior in [16] is a standard Dirichlet process mixture model, whereas this paper proposes a sparsity-inducing Cross-Cat prior, which permits optimized computations for upper bounds of posterior probabilities as well as simplifying CMI queries with multivariate conditions.

## 6 Discussion

This paper has shown it is possible to detect predictive relationships by integrating probabilistic programming, information theory, and non-parametric Bayes. Users specify a broad class of conditional mutual information queries using a simple SQL-like language, which are answered using a scalable pipeline based on approximate Bayesian inference. The underlying approach applies to arbitrary generative population models, including parametric models and other classes of probabilistic programs [28]; this work has focused on exploiting the sparsity of CrossCat model structures to improve scalability for exploratory analysis. With this foundation, one may extend the technique to domains such as causal structure learning. The CMI estimator can be used as a conditional-independence test in a structure discovery algorithm such as PC [31]. It is also possible to use learned CMI probabilities as part of a prior over directed acyclic graphs in the Bayesian setting. This paper has focused on detection and preliminary assessment of predictive relationships; confirmatory analysis and descriptive summarization are left for future work, and will require an assessment of the robustness of joint density estimation when random sampling assumptions are violated. Moreover, new algorithmic insights will be needed to scale the technique to efficiently detect pairwise dependencies in very high-dimensional databases with tens of thousands of variables.



## Acknowledgements

This research was supported by DARPA (PPAML program, contract number FA8750-14-2-0004), IARPA (under research contract 2015-15061000003), the Office of Naval Research (under research contract N000141310333), the Army Research Office (under agreement number W911NF-13-1-0212), and gifts from Analog Devices and Google.

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