
Surrogate Bayesian Networks for Approximating Evolutionary Games

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Abstract

Spatial evolutionary games are used to model large systems of interacting agents. In earlier work, a method was developed using Bayesian Networks to approximate the population dynamics in these games. One advantage of that approach is that one can smoothly adjust the size of the network to get more accurate approximations. However, scaling the method up can be intractable if the number of strategies in the evolutionary game increases. In this paper, we propose a new method for computing more accurate approximations by using surrogate Bayesian Networks. Instead of doing inference on larger networks directly, we do it on a much smaller surrogate network extended with parameters that exploit the symmetry inherent to the domain. We learn the parameters on the surrogate network using KL-divergence as the loss function. We illustrate the value of this method empirically through a comparison on several evolutionary games.

1 Introduction

Spatial evolutionary game models have been widely used to model both biological and cultural evolution, e.g., (Durrett and Levin, 1994; Fu et al., 2010; Young, 2001; Sandholm, 2009; De et al., 2017) and a variety of multi-agent systems topics (Axtell, 2002; Tuyls and Parsons, 2007; Ponsen et al., 2009; Phelps et al., 2010; Morales et al., 2018). Most work on evaluating these games involves computationally expensive simulations, an approach that often does not scale well for spatial structures (Shakarian et al., 2012). Other lim-

itations on validation (Herd et al., 2013) and variability (Manzo and Matthews, 2014) make it difficult to apply simulations towards the analysis of many evolutionary games. To address these limitations, moment closure methods such as pair approximation (Hauert and Szabó, 2005; Fu et al., 2010; Kuehn, 2016; Overton et al., 2019; Kuga et al., 2021) have been developed to approximate the dynamics of these games.

Symmetric Dynamic Bayesian Network Approximation

In (Hsiao et al., 2021), a novel generalization of pair approximation using Bayesian networks was introduced to approximate the dynamics of spatial evolutionary games. That method, which we will call Symmetric Dynamic Bayesian Network Approximation (SD-BNA), takes advantage of the inherent symmetry in spatial Markov processes. Like pair approximation, the population dynamics of a spatial evolutionary game are analyzed by computing the transition probabilities of a local neighborhood of agents around an arbitrary focal agent. This computation is represented as a probabilistic inference problem on individual Bayesian networks that represent a single time-step of the local neighborhood. This allows for much more tractable approximation than a direct computation on the full population.

One of the advantages of the SD-BNA approach is that it is possible to adjust the size of the Bayesian network representing the local neighborhood to get more accurate approximations of the population dynamics. However, scaling up the method for more accurate results can still be intractable, as the induced width of the network depends directly on the size of the local neighborhood represented and the number of strategies in the evolutionary game. To address this issue, we propose a new method for computing approximate inference on larger Bayesian networks in SD-BNAs using what we will call *surrogate* Bayesian networks.

Contributions We propose a novel method for performing approximate inference on evolutionary game Bayesian networks.

- We introduce the concept of a surrogate Bayesian network, a subset of an evolutionary game Bayesian network with added parameters that exploit the symmetry inherent in these models.
- We formulate the process of learning the parameters for surrogate Bayesian networks as a KL-divergence minimization problem between the surrogate network and the original larger network.
- We introduce a novel sample-search algorithm for generating high value samples for the KL-divergence minimization problem.
- We provide an empirical comparison of our method with other approximate inference algorithms such as Abstraction Sampling on a variety of evolutionary games.

2 Related Work

Our work is similar to variational inference approaches. One can make the analogy that the smaller surrogate Bayesian network serves as the parameterized distribution in a variational inference approach and our goal is to minimize the KL-divergence between this parameterized distribution and the one we are approximating (the larger network). However, compared to previous work on variational Bayesian network approximation such as the edge-deletion approach in (Choi and Darwiche, 2006), a major difference is that our surrogate networks are always a strict subset of the network we want to approximate. This lets us formulate our optimization problem in a different way, since data points sampled from a larger network are full configurations of the smaller surrogate network. Our surrogate networks also contain parameter sharing by exploiting the symmetry present in SD-BNAs.

3 Background

3.1 Evolutionary Game Theory

Evolutionary Game Theory (EGT) provides a framework for modeling the time evolution of a population of agents that interact through strategic games whose outcome determines each individual’s evolutionary fitness. These models disregard any game-theoretic assumptions of rationality and instead assume individuals reproduce or change strategies based on a predetermined population update rule. More concretely, consider a population of agents $\{X_1, \dots, X_N\}$ that play an iterated stage game over a finite time horizon $t \in [0, \dots, T]$. An evolutionary game is (S, U, F) :

- $S = \{s_1, \dots, s_M\}$: a set of M strategies where s_i is the i -th strategy in the set of possible strategies

S and $\mathbf{s}(t = 0) = (s_1^0, \dots, s_n^0)$ denotes the initial strategy profile which is a strategy assignment to each agent in the population.

- $U : S^N \rightarrow \mathbb{R}^N$: the payoff (or utility) function that maps the strategy profile to corresponding payoff values for each agent.
- $\Pr(\mathbf{s}^{t+1} = \mathbf{s}' | \mathbf{s}^t = \mathbf{s}) = F(\mathbf{s}', \mathbf{s}, U(\mathbf{s}))$: an update rule giving the transition probabilities given the current strategy assignment and payoff values.

Spatial Evolutionary Game Spatial evolutionary games are an extension of evolutionary games to model interactions among agents in a structured population. For example, agents may interact more frequently with agents in a neighborhood around them or the utility received from their interactions may be weighted accordingly to some network structure. These models are useful in examining how network structure influences the evolution of agent behavior. More concretely, a spatial evolutionary game is (S, U, F, G) where

- S , U , and F are analogous components to those in well-mixed evolutionary games, but they can now also depend on a spatial structure G .
- $G \in \{0, 1\}^{N \times N}$ is a spatial or network structure that specifies the strength of interactions between agents. An example payoff function is:

$$U_i(\mathbf{s}) = \sum_{j=1}^N G_{ij} \text{Pay}[s_i, s_j] \quad (1)$$

Population Dynamics In non-spatial evolutionary games, it is common to refer to agents as *indistinguishable*, i.e., we don’t care exactly which agent is playing which strategy. Instead we are typically interested in population-level aggregated quantities such as the population profile $\mathbf{p} = \{p_{s_1}, \dots, p_{s_M}\}$, where p_{s_i} is the proportion of the population that is currently playing strategy s_i . One of the ways to visualize a population’s time evolution is to plot these quantities as a function of time as in Fig. 4. In spatial games, the specific distributions of strategies (whether it is uniform or clustered) through the population can make a significant difference. To address this, we define higher-order aggregate quantities such as $p_{s_i s_j}$ which denotes the proportion of pairs of adjacent agents playing strategy s_i and s_j respectively. These second order quantities give an insight to the clustering behavior of different strategies in the population. For analysis on spatial games, it is then common to assume that pairs of agents are *indistinguishable*. While not completely accurate, it is necessary to make such assumptions to make sure the analysis of the population remains tractable.

3.2 Bayesian Networks

A Bayesian Network is a graphical model (X, D, F) , consisting of a discrete variable set $X = \{X_1, X_2, \dots, X_N\}$, a set of corresponding domains: $D = \{D_{X_1}, D_{X_2}, \dots, D_{X_N}\}$, and a set of parent functions $F = \{F_1, F_2, \dots, F_N\}$. Each X_i is associated with a parent function $F_i = P(X_i | pa_i)$ where pa_i is the set of parent variables of X_i .

Given a graphical model with variables $\{X_1, \dots, X_N\}$, a common task is to compute the marginals, $P(X_i = s), \forall s$ in its domain for some variables X_i . A special case is computing a normalization constant known as the partition function:

$$Z = \sum_x \prod_i F_i(x) \quad (2)$$

where the \sum_x refers to a summation over all possible configurations of the variables in the model. We can also define the partition function conditioned on certain variable assignments:

$$Z(X_1 = s) = \sum_{x|X_1=s} \prod_i F_i(x) \quad (3)$$

where the summation is over all configurations where $X_i = s$. In inference benchmarks, conditioned variables are termed *evidence*. To compute the marginal probability of a variable we can simply compute $Z(X_i = s)/Z$. One of the benefits of working with Bayesian networks is that we know that the partition function $Z = 1$ and so we can just compute $P(X_i = s) = Z(X_i = s)$.

Exact inference (e.g. computing the partition function) on a Bayesian Network is typically done using bucket elimination (aka variable elimination) or joint-tree algorithm Darwiche (2009); Dechter (2013) where messages of the form λ_{B_i} :

$$\lambda_{B_i} = \sum_{X_i} \prod_{F_j \in B_i} F_j \quad (4)$$

are computed from functions F_j placed in individual buckets B_i which are processed to eliminate X_i along a given variable ordering.

However, those algorithms can run into complexity issues where computing a message can take too much time/space. In these cases, many approximate inference techniques exist. One scheme is (Weighted) Mini-Bucket Elimination (WMBE) Dechter and Rish (2003); Liu and Ihler (2011), an extension of bucket elimination, where the message in bucket elimination is replaced with a weighted geometric mean across smaller internal mini-bucket MB_i partitions in each

bucket:

$$\lambda_{B_i} = \left(\sum_{X_i} \prod_{F_j \in MB_i} F_j^{\frac{1}{p_j}} \right)^{p_j} \quad (5)$$

The partition function can also be computed in a stochastic manner using sampling algorithms (Darwiche, 2009; Koller and Friedman, 2009). In this work, we will compare with more recent sampling algorithms such as Abstraction Sampling (Broka et al., 2018; Kask et al., 2020) which have been shown to be competitive on inference benchmarks. Other algorithms for evaluating Bayesian Networks optimization tasks can also be relevant (Marinescu and Dechter, 2009).

3.3 Symmetric Dynamic Bayesian Network Approximations

A Symmetric Dynamic Bayesian Network Approximation (SD-BNA) (Hsiao et al., 2021) is an iterative method for approximating the forward dynamics of a spatially structured multi-agent population. Given a population profile $\mathbf{p}(t)$ at time t , each iteration of a SD-BNA takes the population profile to the next timestep $\mathbf{p}(t+1)$. It can be shown that a special case of this approximation is computationally equivalent to a pair approximation model, a common approximation technique in the evolutionary game literature (Hsiao et al., 2021). A primary advantage of a SD-BNA is that it allows for the exploration of higher order approximations beyond pair approximation which can yield better accuracy with respect to the underlying stochastic model (Hsiao et al., 2021).

SD-BNA for spatial Markov processes Consider a multivariate Markov process defined over N indistinguishable agents situated on a network G that take a strategy in the set S . We assume that the transition probability of an agent X_i depends locally on its neighborhood $Nb(X_i)$ for each iteration:

$$\begin{aligned} P(X_i(t+1) = s | \mathbf{X}(1), \dots, \mathbf{X}(t-1)) \\ = P(X_i(t+1) = s | X_i(t), X_j(t), \forall j \in Nb(X_i)). \end{aligned} \quad (6)$$

Following the conventions in (Hsiao et al., 2021), we can construct a Dynamic Bayesian Network (DBN) (Murphy, 2002) that completely captures the above Markov process. Each node in the DBN corresponds to an agent in the spatial evolutionary game. Because the DBN is highly symmetric, we get an additional benefit from the indistinguishability property: the marginal distributions $P(X = s) = P(Y = s)$ are identical for any two arbitrary agents X and Y . This property also applies to any pairs of adjacent agents: $P(Nb(X)|X) = P(Nb(Y)|Y)$ where $Nb(X)$ is a neighboring adjacent agent of X and $Nb(Y)$ is a neighboring

adjacent agent of Y . From this point on, to make notation easy, we will refer to a single unindexed agent X (we can denote this as the focal agent, and the location of this agent is marked as a dark circle in Figures 3 and 5). We define the following population level aggregate terms:

$$\begin{aligned} p_{s_i} &= P(X = s_i) \\ p_{s_i s_j} &= P(X = s_i, Nb(X) = s_j) \end{aligned} \quad (7)$$

At $t = 0$, we are given $p_{s_i}(0)$ and $p_{s_i s_j}(0)$ which is an initial distribution of the population. By *Symmetric Dynamic Bayesian network approximation* we refer to the following iterative method for approximating the time evolution of p_{s_i} and $p_{s_i s_j}$:

- Choose a representative subset of agents to be the *input neighborhood* $I \subset [1, \dots, M]$ and a subset $O \subset I$ to be the *output neighborhood*. It is necessary for every node in O to have a fully defined transition probability conditioned on the nodes in I as in Eq. 6. For example, in the simplified diagram of Fig. 1, $I(T - 1)$ consists of the three nodes at $T - 1$ within the highlighted area and $O(T)$ consists of the the single node at time T within the highlighted area.
- Define the distribution of $I(t)$ using some function of $P(X_t)$ and $P(X_t, Nb(X)_t)$.
- Using the Markov process defined in Eq. 6, construct a Bayesian network B that transform the strategies of each agent in $I(t)$ to the agents at $O(t + 1)$.
- Use a probabilistic inference algorithm (Darwiche, 2009; Dechter, 2013) such as Bucket Elimination (Dechter, 1999) to query $p_{s_i}(t + 1)$, $p_{s_i s_j}(t + 1)$ for time $t + 1$. These distributions are defined over the agents in the output $O(t + 1)$.

To summarize, a separate 2 timestep Bayesian network is constructed for each iteration that takes the strategies of each agent from t to $t + 1$. Using a probabilistic inference algorithm, we query the probabilities $P(X_{t+1})$ and $P(X_{t+1}, Nb(X)_{t+1})$ and we repeat the process at the next timestep by defining the distribution of the next input set $I(t + 1)$ using the quantities we queried. More information is described in an earlier paper (Hsiao et al., 2021).

Symmetric Dynamic Bayesian Network Approximation as a truncation The SD-BNA can be considered to be a truncation approximation of the exact Dynamic Bayesian Network (DBN) for Eq. 6. We truncate the DBN temporally and spatially (blue and red respectively in Fig. 1). We approximate the

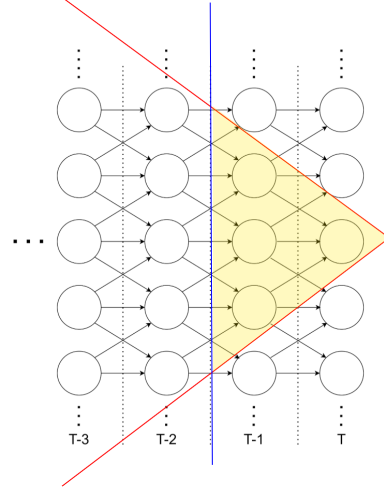


Figure 1: SD-BNA as a DBN truncation

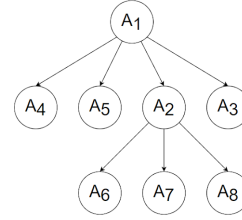


Figure 2: Tree approximation for input neighborhood definition

distribution of $I(t + 1)$ using quantities queried from $O(t + 1)$ in the previous network. This can be thought of as a type of moment closure approximation (Kuehn, 2016). In previous work (Hsiao et al., 2021), the distributions are closed at the pair level and a tree approximation is used to model the distribution of input nodes at $t + 1$. For example, if the input consists of 8 nodes $I = (A_1, \dots, A_8)$ with A_1 being the focal node in the left network of Fig. 3, we can specify a tree approximation as in Fig. 2 where:

$$\begin{aligned} P(A_1 = s_i) &= p_{s_i} \\ P(A_2 = s_i, A_1 = s_j) &= p_{s_i s_j} \end{aligned} \quad (8)$$

and so forth for each node in the tree.

4 Problem Statement

In Hsiao et al. (2021), it was shown that increasing the number of nodes in the input and output sets produce SD-BNAs that give more accurate approximations of the underlying dynamics. However, it is computationally expensive to evaluate large SD-BNAs. The induced width of the resulting Bayesian Network is proportional to the number of nodes in the input and output sets and the number of strategies in the evolu-

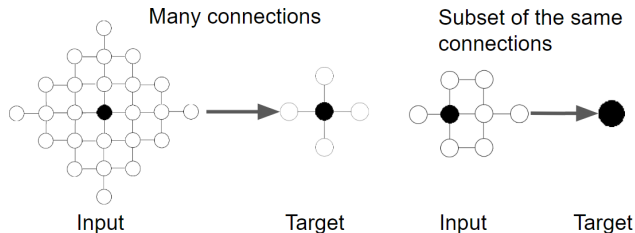


Figure 3: The input and output sets for a 25 node SD-BNA (left) and 8 node SD-BNA (right). Focal node is blackened.

tionary game is the base of the exponent (analogous to the domain size of each variable in the network).

One might consider a straightforward approach of applying approximate inference techniques to the larger SD-BNA models. An example of a state-of-the-art approximate inference technique is Abstraction Sampling (AS) (Broka et al., 2018; Kask et al., 2020). We can apply AS instead of Bucket Elimination as our inference routine to compute $p_{s_i s_j}(t+1)$.

However, as can be seen in the right most graph in Fig. 4 on the Deadlock evolutionary game, simply replacing exact inference with Abstraction Sampling runs into several limitations. Specifically:

- Accuracy: It can take many samples for AS on a 25 node network to produce better results compared to exact inference on an 8 node network.
- Time: Running exact inference on 8 node network is much faster than AS on a 25 node network.
- Noise: Without sufficient sample convergence in AS, it is difficult to determine certain quantities such as the location of inflection points, which can impact qualitative results.

To address these issues, we propose a method that combines the estimate from the smaller network with estimates from the larger network.

5 Surrogate Maximum Likelihood Models

Consider an 8 node SD-BNA and a 25 node SD-BNA for approximating a spatial evolutionary game located on a grid structure (each agent has four neighbors). For the purpose of this paper, we will only focus on 8 and 25 node SD-BNAs (the number of nodes referring to the size of the input set including the focal node as in Fig. 3), but in principle this work can also be extended to other pairs of SD-BNAs with the smaller network serving as the surrogate of the larger network.

A key observation we can make is that the smaller 8 node network is a subset of the larger 25 node network. Our idea is to extend the 8 node SD-BNA with additional parameterized nodes/connections so it can approximate the 25 node network. We first give an initial explanation of the basic idea of our approach (termed the basic MLE algorithm) in Section 5.1. In Section 6, we develop an improved algorithm termed KL-search for inference by devising a sample/search method for generating informative samples for the basic MLE algorithm.

5.1 Parameterizing the new edges

In the current setting of the 8 node network we approximate the query $p_{s_i s_j}$ as $\approx P(X_{t+1}, Nb(X)_t)$, when we really want $P(X_{t+1}, Nb(X)_{t+1})$. In order to increase accuracy we propose to add a new set of 4 dummy nodes $Nb(X)_{t+1}$ that capture the output neighborhood. We add new connections (edges) from the input neighborhood to the output neighborhood as seen in Fig. 5. For these new connections, we define these new connections as a simple conditional probability table (CPT) conditioned on two nodes in the input neighborhood. In essence, we add new CPTs of the form $\theta_{x,y,z} = p_{x|yz}$. Since we inherit the assumption that all neighboring nodes are indistinguishable from 25 node network, all CPTs are identical and we can share parameters across them.

Given a 25 node SD-BNA model and an 8 node extended model, the **basic MLE algorithm** for learning the extended 8-node network is as follows:

1. Forward sample the 25 node SD-BNA model for a full configuration of every variable in the 25 node network. Denote each full configuration as an individual data point \mathbf{x}^j .
2. The 8-node network is fully observed for each data since its variables are subsumed in the large network we can derive the likelihood expression:

$$\begin{aligned}
 \mathcal{L}(\theta) &= \prod_{j=1}^L P_{\theta}(\mathbf{x}^j) \\
 &= \prod_{j=1}^L P_{\theta}(Nb(X^{(j)})_{t+1} | X_t^{(j)}, Nb(X^{(j)})_t) \cdot C \\
 &= \prod_{j=1}^L \theta(Nb(X^{(j)})_{t+1}, X_t^{(j)}, Nb(X^{(j)})_t) \cdot C
 \end{aligned} \tag{9}$$

where $X_t^{(j)}$ denotes the assignment to X for the j -th data point and at time t . C is some constant that doesn't depend on θ and can be ignored when

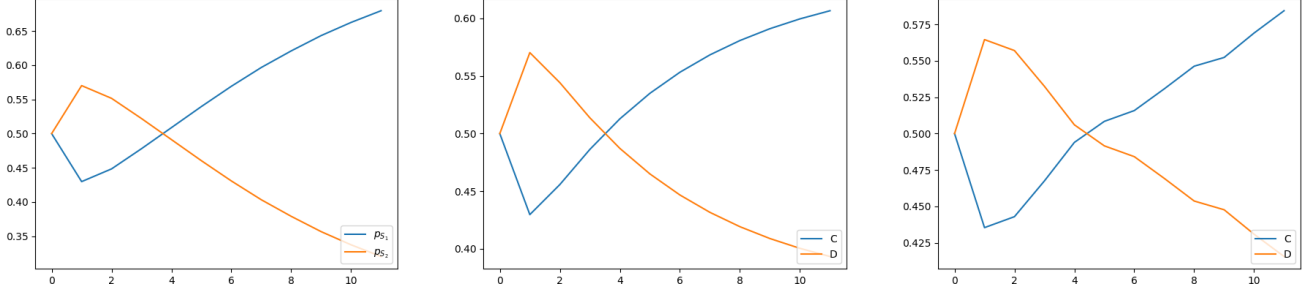


Figure 4: Simulation ground truth (left), compared with exact 8 node SD-BNA result (center), and approximate Abstraction Sampling result on 25 node SD-BNA (right) on the Deadlock evolutionary game.

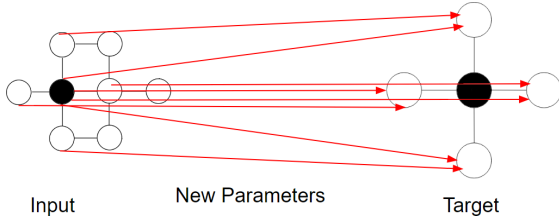


Figure 5: New parameters (edges) to add to 8 node network for MLE estimation.

maximizing the corresponding sum of log likelihoods.

3. Maximize the log likelihood $\log \mathcal{L}(\theta)$ subject to symmetry constraints:

$$p_{s_i}(t+1) = \sum_{s_j, s_k \in S} \theta_{s_i, s_j, s_k} \cdot p_{s_j s_k}(t), \quad \forall s_i \in S \quad (10)$$

We can pre-compute $p_{s_i}(t+1)$ on a non-parameter extended 8 node network and use this to constrain our log likelihood maximization derived from Eq. 9:

$$\begin{aligned} \theta^* = & \\ \arg \max_{\theta} & \sum_{j=1}^L \log \theta(Nb(X^{(j)})_{t+1}, X_t^{(j)}, Nb(X^{(j)})_t) \\ \text{subject to} & \\ p_{s_i}(t+1) = & \sum_{s_j, s_k \in S} \theta_{s_i, s_j, s_k} \cdot p_{s_j s_k}(t), \quad \forall s_i \in S \end{aligned} \quad (11)$$

This can be solved with existing constrained maximization solvers such as sequential least squares Kraft (1988) or trust-region algorithms which can be found in the SciPy python package (Virtanen et al., 2020).

Once θ^* is learned, we can evaluate the forward dynamics (compute $p_{s_i, s_j}(t+1)$) on the optimal extended network B_{θ^*} .

6 KL-based Search Tree Exploration

In the previous section we used Monte Carlo forward sampling to generate the samples. **Key idea: instead of drawing random samples, we will combine sampling with search aiming for diverse samples that are likely to reduce the KL-divergence between our surrogate model (the 8 node model) and the model we are approximating (the 25 node model).**

From this point onward, we'll refer to the the 25 node model as model A and the 8 node model as model B for simplicity. Furthermore, we will assume bi-valued variables and use P_A , and P_B to denote distributions on model A and model B , respectively, and use P_{B_θ} for the distribution of the extended model B parameterized by θ .

Informative sample generation In order to guarantee that all the samples are different and aim towards meaningful samples we generate a fixed number L of partial configurations from the large network A using best-first search along some variable ordering guided by a heuristic function. For example, the first two nodes that are generated are associated with the root variable X_1 and represent the partial configurations $(X_1 = 0)$ and $(X_1 = 1)$. In the best-first search, we want a heuristic that will explore branches of high difference between the models. To do this, we define a KL heuristic for the partial configuration $(X_1 = 0)$ as:

$$h_{kl}(X_1=0) = [\log(P_A(X_1=0)) - \log(P_B(X_1=0))] \cdot P_B(X_1=0) \quad (12)$$

Once we have L leaf nodes (representing a partial configuration) we extend each to a full configuration by forward sampling the rest of the variables using the 25 node network yielding a data point \mathbf{x}^k conditioned on the node's partial configuration.

Since it is difficult to directly compute $P_A(X_1 = 0)$ and $P_B(X_1 = 0)$ in the KL heuristic, we approximate

these terms using a weighted mini-bucket elimination (WMBE) heuristic (Liu and Ihler, 2011) with an i-bound of 10 (this is just an estimate of our Bayesian network’s partition function conditioned on a node’s partial configuration).

Once we have L full samples, we solve for θ^* that minimizes the following loss function:

$$\theta^* = \arg \max_{\theta} \sum_{j=1}^L \log P_{B_{\theta}}(\mathbf{x}^j) \cdot P_A(\mathbf{x}^j)$$

subject to

$$p_{s_i}(t+1) = \sum_{s_j, s_k \in S} \theta_{s_i, s_j, s_k} \cdot p_{s_j s_k}(t), \quad \forall s_i \in S \quad (13)$$

with an additional term $P_A(\mathbf{x}^k)$ where each θ expression is also multiplied with the probability of the sample $P(\mathbf{x}^k)$. We can justify this as the loss function because at the limit of large L , this loss function is equivalent to minimizing KL divergence. This is formally stated in the following Theorem. The full **KL-Search** algorithm is shown in Algorithm 1.

Theorem 6.0.1 (Asymptotic Convergence of KL-Search Minimization). *Let θ_L be the result of KL-Search Minimization [Algorithm 1] given L samples. Then given a family of extended networks B_{θ} parameterized by θ :*

$$\lim_{L \rightarrow \infty} \theta_L = \arg \min_{\theta} D_{KL}(P_A || P_{B_{\theta}}) \quad (14)$$

Proof [See Supplemental]

6.1 Scaling up to more strategies

To scale up the method to handle evolutionary games with more strategies, the major computational bottleneck is in computing $P_A(X_1 = 0)$ in Eq. 12 using our WMBE approximation. While we can feasibly evaluate this quantity in 25 node networks having 3 or less strategies, WMBE heuristics for approximating $P_A(X_1 = 0)$ become difficult to evaluate directly in 25 node networks with 4 or more strategies. Therefore, instead of computing $P_A(X_1 = 0) \approx WMB(X_1 = 0)$, we propose an easier to compute heuristic such as:

$$P_A(X_1 = 0) \approx \hat{Z}_A(X_1 = 0) \quad (15)$$

where \hat{Z}_A is a stochastic estimate of the partition function conditioned on $(X_1 = 0)$:

$$\hat{Z}_A(X_1 = 0) = \frac{1}{N} \sum_{i=1}^N \hat{Z}_A(x^{(i)}), \quad x^{(i)} \sim P_A(x | X_1 = 0) \quad (16)$$

We propose a quick estimate for the partition function to be evaluated from a single sampled configuration ($N = 1$). We’ll call this new method **Fast KL-search**.

Algorithm 1: KL-Search Minimization

Input: Two Bayesian networks: a large network A , a smaller network B , and a parameterized extended network B_{θ} such that all nodes in B are in A ($B \subset A$), a variable ordering o over A , initial distribution $p_{yz}(t)$, and pre-computed output distribution $p_x(t+1)$

Parameters: Number of samples L

Output: θ , estimated parameters that minimize difference between A and B_{θ}

$T \leftarrow$ the OR-search tree on A using ordering o ;

$OPEN \leftarrow \{\langle root(T), 0 \rangle\}$;

// frontier nodes are ordered by the 2nd value for $i = 1 \rightarrow L$ do

$v \leftarrow OPEN.dequeue()$; // remove the node of highest priority

for $u \in children(v)$ do

$h_{kl}(u) \leftarrow [\log(P_A(u)) - \log(P_B(u))] \cdot P_B(u)$;

Append $\langle u, h_{kl}(u) \rangle$ to $OPEN$;

end

end

Let X be an empty list;

for $v \in OPEN$ do // leaf nodes

Forward sample x , a full configuration of A conditioned on the partial configuration represented by v ;

Append x to X ;

end

Solve $\theta^* = \arg \max_{\theta} \sum_{j=1}^L \log P_{B_{\theta}}(\mathbf{x}^j) \cdot P_A(\mathbf{x}^j)$, subject to

$p_{s_i}(t+1) = \sum_{s_j, s_k \in S} \theta_{s_i, s_j, s_k} \cdot p_{s_j s_k}(t), \quad \forall s_i \in S$;

Return θ^* ;

6.2 Learning and Inference

KL-Search (Algorithm 1) and Fast KL-search (Algorithm 1 with a simplified heuristic) both work over one timestep of the evolutionary game. The θ^* obtained as the return value from these algorithms minimizes the kl divergence between models for a single timestep. The optimal θ value can change each time iteration and is dependent on the current values of $p_{s_i}(t)$ and $p_{s_i s_j}(t)$. Thus the full algorithm for our approach has two parts: learning (KL-Search) followed by inference (SD-BNA). Our goal in the empirical results section is to determine what methods reduce the single iteration error the most, so we will use the measure $D_{KL}(P_{sim}(X_1 | Nb(X)_1) || P_{method}(X_1 | Nb(X)_1))$ evaluated at $t = 1$ where P_{sim} is the probability estimated using the average of many simulations and P_{method} is the probability estimated using a given method. Finding the most effective intervals to interleave learning with inference will be future work.

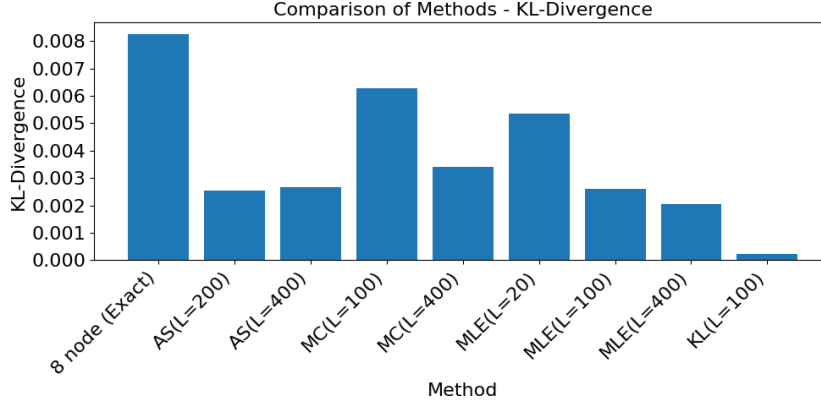


Figure 6: Sample efficiency comparison (measured using average KL divergence) on the Deadlock evolutionary game. Results are averaged across 10 separate runs for each method

7 Empirical Results

The central task of our empirical evaluation is estimating $P(X_{t+1}|Nb(X)_{t+1})$ to compute $p_{s_i s_j}$ at each time step in a SD-BNA. Therefore, we focus on evaluating the accuracy of different approaches for estimating these quantities. For this, we will use the divergence measure $D_{KL}(P_{sim}(X_1|Nb(X)_1)||P_{method}(X_1|Nb(X)_1))$ (as mentioned in Section 6.2) to evaluate the effectiveness of different approximate inference algorithms.

For our comparisons in Fig. 6, 7, and 8, we test our algorithms on a variety of SD-BNAs constructed from different evolutionary games with KL-divergence results. In each of these experiments, the goal is to minimize the KL-divergence with respect to the ground truth estimate from the simulation.

For an initial comparison in Fig. 6, we use the Deadlock game (see Table 2) from Fig. 4. The methods used in the initial comparison include:

- 8 node (exact): the estimate obtained from exact inference on the 8 node network.
- AS: Abstraction Sampling on a 25 node SD-BNA with (200, 400) samples.
- MC: Forward sampling on a 25 node SD-BNA with (100, 400) samples.
- MLE: The surrogate network approach from Section 5 with (20, 100, 400 data points) without doing KL-search to generate the data points.
- KL: The estimate obtained using θ^* from Algorithm 1.

In the initial tests on the DLK game, the KL-search approach outperforms all of the other methods in terms of KL-divergence.

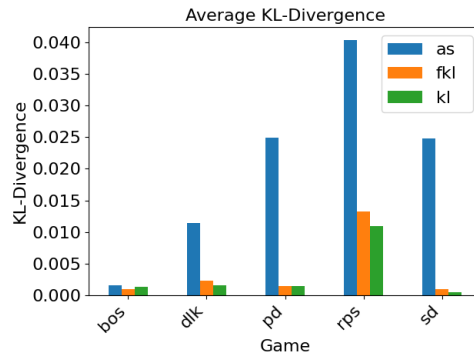


Figure 7: Average KL divergence between simulation and [abstraction sampling (as), KL-search using WMBE (kl), and KL-search using a single configuration sample (fkl)].

7.1 Comparison of Methods

We compare KL-search (Algorithm 1), Fast KL-search (Algorithm 1 with Eq. 15), and Abstraction Sampling using the same average KL divergence metric as in Fig. 6. For these set of tests, we average the results of 30 separate runs for each game and allow each method to generate 100 samples for each run.

The main results are displayed in Fig. 7, which compares the three methods across 5 different evolutionary games (Table 2). Both the Fast KL-search (denoted fkl in the figure) and the regular KL-search with WMBE heuristic perform much better than Abstraction Sampling in all games.

Larger Games The only method that can run on games with more than 3 strategies is Fast KL-Search. As mentioned earlier, with 4 or more strategies, the WMBE heuristic is hard to compute because of its inherent table representation of the CPTs which become

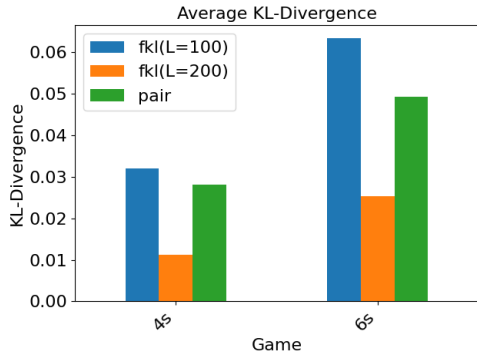


Figure 8: Average KL divergence between simulation and [pair approximation (pair), and KL-search using a single configuration sample (Fast KL-search) at 100 and 200 samples (fkl(L=100), fkl(L=200))] on games with a high number of strategies.

too large. in Fig. 8, we show a comparison with the method known as pair approximation Fu et al. (2010). We observed that in these larger games, more than 100 samples are needed for Fast KL-Search to outperform pair approximation.

Time Comparison A comparison of time per probe/sample for the experiments from Fig. 7 and 8 is shown in Table 1. For example, for $|S| = 2$ on KL-Search, we average the time taken for the experiment on the 2 strategy (bos, dlk, pd, and sd) games and divide by $4 \cdot 30 \cdot 100$ samples.

Fast KL-Search actually takes more time than normal KL-Search, as the time for the latter is frontloaded in computing the initial WMBE tree. For individual samples, the WMBE heuristic takes less time than evaluating an entire sample as in Fast KL-Search. As expected, both methods take much less time than Abstraction Sampling.

One sample in AS is a full probe that expands $O(d \cdot h)$ nodes in a search tree where d is the number of abstract states and h is the tree’s depth. This takes $O(d \cdot h \cdot L)$ time where L is the number of samples. For KL-Search and Fast KL-Search, only L nodes in the search tree need to be expanded to get L samples, so the final time is just $O(L)$. The following table summarizes this:

AS	KL-Search	Fast KL-Search
$O(d \cdot h \cdot L) \cdot O(1)$	$O(L) \cdot O(1)$	$O(h) \cdot O(L)$

8 Conclusion

We have introduced a novel approach for performing approximate inference on evolutionary game Bayesian networks. Our method, based on optimizing param-

Table 1: Time per sample (s) with amortized initial (WMBE for AS/KL) and post-processing (KL minimization for KL/FKL) time (each time is computed by averaging over at least 3000 samples from the experiments for Fig. 7 and 8).

$ S $	AS	KL-Search	Fast KL-Search
2	0.1175	0.01419	0.01624
3	0.2203	0.03063	0.03725
4	-	-	0.1630
6	-	-	0.7299

Table 2: Evolutionary Game Payoff Matrices

Game Name	Payoff Matrix
Prisoner’s Dilemma (pd)	$\begin{pmatrix} 2 & -1 \\ 3 & 0 \end{pmatrix}$
Snowdrift (sd)	$\begin{pmatrix} 2 & 1 \\ 3 & 0 \end{pmatrix}$
Battle of the Sexes (bos), symmetric version, (Cooper et al., 1989)	$\begin{pmatrix} 0 & 1 \\ 2 & 0 \end{pmatrix}$
Deadlock (dlk)	$\begin{pmatrix} 5 & -4 \\ 3 & -5 \end{pmatrix}$
Rock Paper Scissors (rps)	$\begin{pmatrix} 0 & -1 & 1 \\ 1 & 0 & -1 \\ -1 & 1 & 0 \end{pmatrix}$

eterized surrogate Bayesian Networks, leverages the symmetry present in SD-BNAs to combine the efficient computation of smaller SD-BNAs with the more accurate results of larger SD-BNAs. We introduce a novel sample-search approach to generate high value samples for this optimization problem, and empirically demonstrate its effectiveness when compared to existing approximate inference techniques such as Abstraction Sampling.

For future work, it may be interesting to extend this technique to domains beyond spatial evolutionary games. It should be possible to apply SD-BNAs to any general spatial Markov process with a high degree of symmetry. Other spatial Markov processes such as voter models and SIS models could be a valid area of application. It may also be interesting to see if this technique could be applied to general Bayesian network inference on networks with a high degree of structure.

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