Distributed and Online Maintenance of Graphical Models in Apache Flink

Abstract

With the growing need for large scale data analysis, distributed machine learning has grown importance in recent years. The raw data is described by large number of interrelated variables and an important task is to describe the joint probability distribution over these variables, allowing simultaneously interferences and predications to be made. Directly modeling of joint probability distribution of all these variables may be infeasible, since the complexity of such model grown exponential with the number of variables. We focus on Bayesian Networks, the father of graphical models and present a different communication-efficient approach using the well-known method of Functional Geometric Monitoring, for continuously learning and maintenance of Bayesian Networks in a distributed streaming environment. Finally, the experimental results confirmed the functionality of proposed method.

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Chapter 1:

Introduction

1.1 Objective

The present thesis proposes a system capable of construction and maintenance of the well-known graphic model, namely Bayesian Networks, on data referring to large volume of data, that is evolving, distributed and multidimensional, while using the minimal communication cost. The purpose of the system is the maintenance and the continuously parameter learning using communication-efficient algorithms on distributed continuously model based on the Maximum Likelihood Estimation (MLE) algorithm.

The first approach based on using approximate distributed counters with the combinations of the algorithms BASELINE, UNIFORM and NON_UNIFORM. These algorithms propose the way which we can define the approximation factor ε on each counter, which aims to provide appropriate error guarantees of the joint probability distribution of MLE. The system supports two types of fundamental approximate distributed counters, the first refers to the RANDOMIZED counters and the second one refers to the DETERMINISTIC counters. This approach leads to exponential reduction on communication cost compared to conservative approach of EXACTMLE that is the algorithm which uses EXACT counters.

Moreover, the system supports the maintenance of a special-case of Bayesian Networks, the Naïve-Bayes Classifiers (NBC). The implementation of the system takes part on Apache Flink and Apache Kafka.

The present thesis except of the first approach, proposes an alternative approach of the maintenance and the continuously parameter learning of Bayesian Networks. In particular, this approach using the well-known method of Functional Geometric Monitoring in combination with the algorithm BASELINE and UNIFORM which define with appropriate way the available error budget. The idea behind the using of Functional Geometric Monitoring method is now each counter we do not need to treat individually but the approximate distributed counters we can treat as frequency vectors that the state which is used corresponds to vectors, specifically to frequency vectors. This approach leads to the reduction of communication cost up to one order of magnitude to the previous approach and up to two orders of magnitude to EXACTMLE. Finally, the experimental evaluation confirms that the proposed approach can handle with quite satisfied way large data volumes providing the appropriate scaling.

The present thesis integrates the widely known method of Laplace Smoothing for handling the zero parameters and proposes the method of Dummy Father (DF) in combination with the NON_UNIFORM algorithm. Experimental evaluation confirms that leads to a 50% reduction of communication cost.

1.2 Thesis Outline

The thesis is organized as follows: **Chapter 2** provides the necessary theoretical background, covering crucial concepts related to Bayesian Networks and Naïve Bayes Classifiers. Each concept is illustrated with a relevant example. Additionally, a detailed analysis is conducted for the Forward Sampling Algorithm and the method of Laplace Smoothing. Furthermore, the chapter delves into the Maximum Likelihood Estimate algorithms used for parameter learning, and introduces the Distributed Continuous Model, the model employed in this thesis. The analysis within Chapter 2 offers a comprehensive exploration of these topics, providing valuable insights into their implementation and implications.

In **Chapter 3**, it contains the definition of the problem and the general approach that is used for both approaches. In **Chapter 4**, it contains the analysis of the problem, particularly the analysis of the first approach considering the approximate distributed counters, which in this case, we treat as individual entities. Finally, it contains the analysis of the second approach, which employs Functional Geometric Monitoring (FGM). In **Chapter 5**, it contains the design and implementation of the proposed system. In **Chapter 6**, it contains the experimental evaluation for each approach from different perspectives. Finally, in **Chapter 7**, it contains the conclusions, future work, and extensions of the system.

Chapter 2:

Theoretical Background

2.1 Notation

Throughout this thesis, the notations used are primarily based on [1].

Random variables are denotated using capital Latin letters X, Y, Z while their corresponding values are represented using the lowercase Latin letters x, y, z, respectively. Moreover, the notation $Val(X)$ denotes the set of values of random variable X. When referring to categorical (discrete) random variables, we use the notation $x^1, \dots, x^k$ to enumerate the values of random variable X, according to the fact that the continuous random variable X contains k different values. Additionally, $\boldsymbol{X}, \boldsymbol{Y}, \boldsymbol{Z}$ represent sets of random variables while $\boldsymbol{x}, \boldsymbol{y}, \boldsymbol{z}$ contains the values of the set from random variables, accordingly we can define $Val(\boldsymbol{X})$ so in this case we refer to the set of values from the set of random variables $\boldsymbol{X}$**.**

Moreover, the function $|\cdot|$ denotes the cardinality of the corresponding function-relation expect when defined differently. For instance, $|Val(X)|$ corresponds to the number of values of the random variable X or equivalently the number of values contained in the set of values of random variable X. In most cases, we use the $P(x)$ for $P(X = x)$, given the fact that the x refers to the values of the random variable X. Finally, we consider $P((X = x) \cap (Y = y))$ to be equivalent to $P(X = x, Y = y)$ or $P(x, y)$ or $\mathrm{P}(X, Y)$.

Suppose we have a set of random variables $\boldsymbol{X} = \{X_1, \dots, X_n\}$. The joint probability distribution over the set $\boldsymbol{X}$ is denoted as $P(X_1, \dots, X_n)$ *or* $P(\boldsymbol{X})$ while the distribution $P(X_i)$ refers to the marginal distribution of the random variable X_i. When referring to conditional probability distribution *(CPDs)*, we use the notation $P(X \mid Y)$ where X, Y represent any random variable. Finally, we use the ξ to denote a full-assignment of random variables from any set of random variables $\boldsymbol{X}$.

The two most fundamental rules are used and are worth-mentioning is the Chain Rule [1] and Bayes Rule [2]. Both rules based on widely known method of conditional probability. We provide the definition of conditional probability below.

Suppose α, β refers to any two events. The conditional probability of β given α is defined as:

$$Conditional\ Probability: \ P(\beta \mid \alpha) = \frac{P(a \cap \beta)}{P(\alpha)}$$

The conditional probability is defined only when the denominator is greater than zero i.e., $P(\alpha) > 0$.

The first rule, the Chain Rule, states that if $\alpha_1, \dots, \alpha_\kappa$ is a sequence of events, then:

$$Chain\ Rule: P(a_1 \cap \dots \cap a_k) = P(a_1) \cdot P(a_2|a_1) \cdots P(a_k \mid a1 \cap \dots \cap a_{k-1})$$

If the sequence of events consists of independent events, meaning $P(a_i \cap a_j) = P(a_i) \cdot P(a_j)$ for each $i, j \in \{1, \dots, \kappa\}$, then:

$$P(a_1 \cap \dots \cap a_k) = P(a_1) \cdot P(a_2) \cdots P(\alpha_\kappa)$$

The second rule, *Bayes' Rule*, is an immediate consequence of the definition of conditional probability, if α, β represents any two events, then:

$$Bayes'\ Rule: P(\alpha \mid \beta) = \frac{P(\beta \mid \alpha) \cdot P(\alpha)}{P(\beta)}$$

Graphs

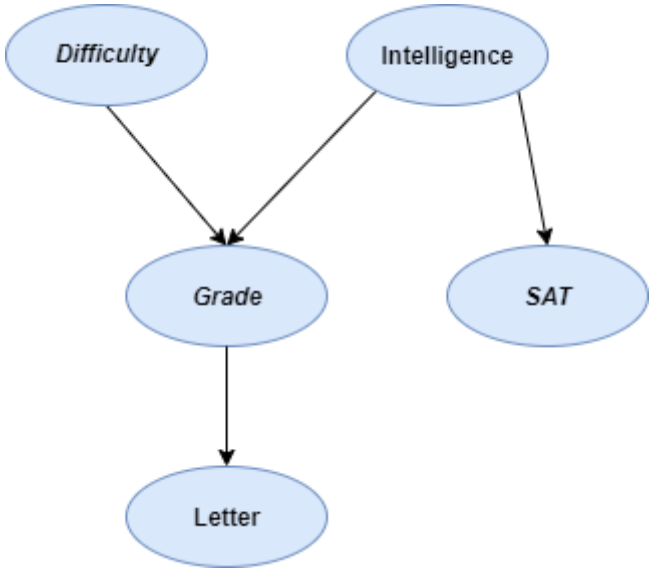

Figure 1: Directed Acyclic Graph (DAG) of the Student Bayesian network

This section contains the most fundamental notations used throughout this thesis regarding graphs. More details represented in [1, Ch. 2].

The most primary *data structure* used is this thesis is the well-known structure of *graph*. A graph consists of a set of nodes $\mathcal{V}$ and a set of edges $\mathcal{E}$. Hereafter, we will use the notation $\mathcal{G}(\mathcal{V}, \mathcal{E})$ or $\mathcal{G}(\mathcal{X}, \mathcal{E})$ to denote a graph $\mathcal{G}$, where the $\mathcal{V} = \{V_1, \dots, V_n\}$ represents the set of nodes and the $\mathcal{E} = \{E_1, \dots, E_n\}$ denotes the set of edges, respectively.

In particular, we focus on *Directed Acyclic Graph (DAG)*. In this case each pair of nodes $V_i, V_j \in \mathcal{V}$ is exclusively connected by a directed edge $V_i \to V_j$. The set of edges $\mathcal{E}$ contains all the possible pairs of connected nodes. Additionally, the *acyclic* property of the graph ensures that there is no *directed path* $V_1, \dots, V_k$ where $V_1 = V_k$ which would represent a *loop*.

Given a *directed acyclic graph* $\mathcal{G}(\mathcal{X}, \mathcal{E})$, for any edge $X_i \to X_j \in \mathcal{E}$ where $X_i, X_j \in \mathcal{X}$ then the node X_j is the *child* node of X_i . We will use the notation $Child(X_j)$ to express the set of nodes that are parents of X_j. Similarly, we will use the notation $Par(X_i)$ to denote the set of nodes that are parents of X_i. Additionally, the notation $NonDescedants(X_i)$ will be used to represent the set of nodes that are not *descendants* of X_i.

Figure 2 represents an instance of a *DAG* where the set of nodes $\mathcal{V}$ is as follows:

$$\mathcal{V} = \{Difficulty, Intelligence, Grade, SAT, Letter\}$$

While the set of edges is as follows:

$$\mathcal{E} = \{\ Difficulty \rightarrow Grade\ , Intelligence \rightarrow Grade\ ,\ \ Intelligence \rightarrow SAT\ , Grade \rightarrow Letter\ \}$$

Using the previous statements, we can make the following declarations for the node $Grade$:

$$\mathrm{P}ar(Grade) = \{Difficulty, Intelligence\}$$

$$\mathrm{C}hild(Grade) = \{Letter\}$$

$$NonDescedants(Grade) = \{SAT\}$$

2.2 Bayesian Networks

2.2.1 Introduction to Bayesian Networks

Bayesian Networks [3] represents an intersection between *graph theory* and *probability theory*, aiming to facilitate the modeling of probabilistic and causal inferences in *real-world* applications [4].

Bayesian Networks can be applied in various fields. For instance, they can be used as decision-support systems, specifically in sensor validation systems [5]. The basic idea is to determine whether a sensor is faulty by analyzing a set of sensor readings (represented through the Bayesian Network) that contribute to the overall system operation.

Another application of Bayesian Networks is in medical diagnosis systems [4, Ch.2]. In this case, the objective is to diagnose a disease based on patient findings. The basic idea can be expressed as follows:

$$diagnosis = max_i P(D_i|E)$$

Generally, $P(D_i|E)$ represents the probability of disease D_i given a set of evidence E, which includes observed patient symptoms and laboratory examination results. Examples of such networks include MUNIN [6], used for diagnosing neuromuscular disorders, and HEPAR2 [7], used for diagnosing liver disorders.

Bayesian Networks have various applications, including cybersecurity [8]. In this context, Bayesian Networks are utilized as real-time security analysis systems that determine whether the input is malicious or benign.

One specific type of Bayesian Networks that falls under the category of Classifiers is Naïve Bayes Classifiers (See Chapter 2.3). Naïve Bayes Classifiers find applications in diverse fields. Some well-known examples include Document Classifiers [4, Ch.11] and Information Retrieval systems [4, Ch.12].

The graphical models we are referring to initially belong to the category of probabilistic graphical models, specifically Bayesian Networks. As previously mentioned, Bayesian Networks are graphical models with a fundamental characteristic represented by a graph (See Chapter 2.1). The use of a graph provides a compact representation of the joint probability distribution, typically defined in a high-dimensional probability space.

The representation of a graph has two perspectives. The first perspective pertains to representing the set of independencies among the nodes. The second aspect involves utilizing these independencies to decompose the initial distribution into smaller factors, typically defined in lower-dimensional probability spaces. This approach allows us to avoid working with the high-dimensional probability space of the joint probability distribution.

Probability queries

Except for learning parameters (See Chapter 2.5), which define the joint probability distribution of a Bayesian Network, another objective is to estimate queries related to the distributions of random variables. This specific category of queries is referred to as probability queries. Probability queries consist of two parts:

- The first part pertains to the evidence, which comprises a subset $\boldsymbol{E}$ of random variables accompanied by an instance $\boldsymbol{e}$ of values from those random variables. We also use queries where the evidence is the empty set, i.e., $\boldsymbol{E} = \emptyset$.
- The second part relates to the *query variables*. Generally, this set consists of a subset $\boldsymbol{Y}$ of random variables. In most cases, the query variables pertain to the entire set of random variables in the network, rather than a subset. This implies querying the joint probability distribution of the network.

$$Probabilty\ queries: P(\boldsymbol{Y} \mid \boldsymbol{E} = \boldsymbol{e})$$

The main objective is to estimate the *probability queries* over the *joint probability distribution*, assuming that $\boldsymbol{E} = \emptyset$. We refer to these queries as follows:

$$P(\boldsymbol{Y}) = P(Y_1, \dots, Y_n)$$

Assuming a set of random variables $\boldsymbol{X} = \{X_1, \dots, X_n\}$**,** where each variable represents a binary value (e.g., the outcome of a coin toss), the objective is to estimate the *joint probability distribution* $P(X_1, \dots, X_n)$ defined by the random variables in set $\boldsymbol{X}$. In the simplest case, this would require $2^n - 1$ parameters, with one parameter for each possible assignment of values $x_1, \dots, x_n$ from the random variables. However, managing the joint probability distribution becomes infeasible from various perspectives. This includes the challenge of allocating sufficient heap space to store all the different parameter values of the joint distribution, as well as the substantial volume of datasets required to estimate the parameters, which exponentially increases with the number of random variables.

Now, let's assume that the set $\boldsymbol{X}$ consists of *marginally independent* random variables. This means that the distributions for any pair of random variables X_i, X_j are independent ($X_i \perp X_j$). By applying the Chain Rule (See Chapter 2.1), we can express the joint probability distribution as follows:

$$P(X_1, \dots, X_n) = P(X_1) \cdot \dots \cdot P(X_n)$$

Using the *independence* property among the random variables, now we can define the *joint probability distribution* exclusively using the *marginal distribution* $P(X_i)$ of the random variables $\boldsymbol{X}$. Exploiting the previous statement, if θ_{X_i} denotes the parameter which defines the *marginal probability distribution* $P(X_i)$ of the binary-*valued* variable.

By utilizing the independence property among the random variables, we can define the *joint probability distribution* exclusively using the *marginal distribution* $P(X_i)$ of the random variables $\boldsymbol{X}$. Expanding on the previous statement, if θ_{X_i} denotes the parameter that defines the *marginal probability distribution* $P(X_i)$ of a binary-valued variable X_i

$$Marginal\ probability\ distribution: P(X_i = x_i) = \theta_{x_i} = \begin{cases} \theta_i\,, & where\ x_i = x_i^1 \\ 1 - \theta_i\,, & where\ x_i = x_i^0 \end{cases}$$

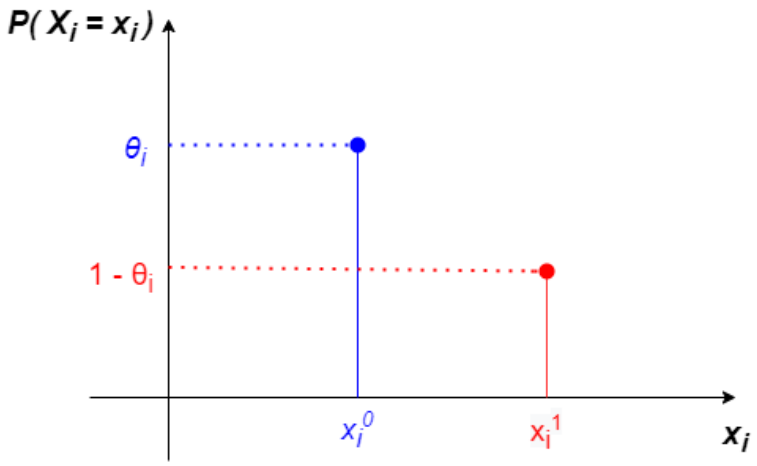

Figure 2: Probability mass function(pmf) from a binary-valued random variable X_i

Now the only requirement to define the *joint probability distribution* is to determine the parameters $\theta_{X_1}, \dots, \theta_{X_n}$ for distributions of random variables $X_1, .., X_n$. In conclusion, the joint probability distribution defines as follows:

$$P(x_1, \dots, x_n) = \prod_{i=1}^{n} \theta_{X_i}$$

In this way we successfully reduce the initial space of *joint probability distribution* from a subspace of $\mathbb{R}^{2^n}$ to an *n-dimensional manifold* of $\mathbb{R}^{2^n}$. Additionally, we achieve to obtain linear dependence on the number of random variables.

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The previous example represents an ideal scenario that is difficult to achieve in *real-world* applications due to the presence of dependencies among different random variables. In most cases, it is more reasonable to consider *conditional independences* among different random variables as an alternative approach. By incorporating *conditional independences* and *Directed Acyclic Graph (DAG)*, we can effectively model and represent Bayesian Networks.

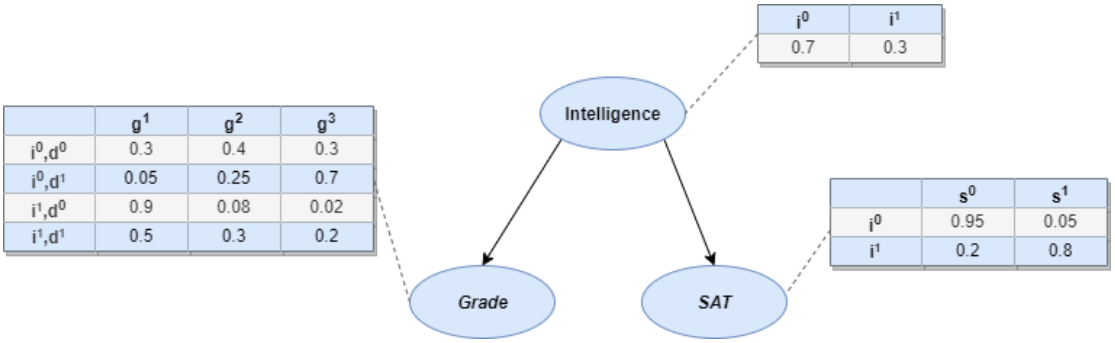


Figure 3: Part of the graph from Student Bayesian Network

Let's assume the *Bayesian Network* from *Figure 3*. The network consists of the nodes *Intelligence(I), Grade(G), SAT(S)*. The random variable I contains two values $Val(I) = \{i^1, i^0\}$, where i^1 refers to *high intelligence students* and i^0 refers *low intelligence students*. Similarly, the random variable S contains two values $Val(S) = \{s^1, s^0\}$, where s^1 denotes a *high score* and s^0 denotes a *low score*. Finally, the random variable G has three values $Val(G) = \{g^1, g^2, g^3\}$, where g^1, g^2, g^3 correspond to grades A, B, C , respectively. In this case, the direct approach to *joint probability distribution* of the three variables requires 12$(2 \cdot 2 \cdot 3)$ parameters, with each parameter representing the probability of the combination of values from three variables.

The property of versatile independence among random variables can't be applied due to *dependencies* among them (for instance, the grade of student affects the student's *intelligence* up to a certain point). We assume the *conditional independency*: $(S \perp G \mid I)$ meaning that the random variable *Grade(G)* is independent from the random variable *SAT(S)* given the random variable *Intelligence(I).*

Using the previous *conditional independence*, we can express the *joint probability distribution* using the following equation:

$$P(I, G, S) = P(S, G \mid I) \cdot P(I) = P(S \mid I) \cdot P(G \mid I) \cdot P(I)$$

Even in the simplest case, with the usage of one *conditional independence*, we can separate the *joint probability distribution* into smaller independent factors, which contributes to a more compact representation of initial distribution. Now, the number of parameters required to define the *joint distribution* is 7 parameters (the difference between them is not significant, but it increases as the number variables and *conditional independencies* also increases, the example is illustrative), one parameter for the distribution $P(I)$, two parameters for the distribution $P(S)$ and four parameters for the distribution $P(G)$.

The separation of *joint probability distribution* into smaller factors highlights the property of *modularity.* This means that the insertion or deletion of a random variable affects only a specific part of joint distribution rather than the entire as in direct approach of distribution. In the direct approach, we would need to renumerate all the possible combinations of values from the new set of random variables. Moreover, the factors of joint *probability distribution* compromise the main characteristic so the *Maximum Likelihood Estimation* (*MLE – See. Chapter 2.5*) can be applied in a distributed environment (*See Chapter 2.7*).

In conclusion, the representation of *Bayesian Network* through a *directed acyclic graph (DAG)* offers two advantages:

- A compact representation of set of *conditional independences* among the random variables that define the *joint probability distribution*.
- A mechanism that provides a compact representation of *joint probability distribution(factors)*. Through the process of *factorization,* we can avoid the initial *high-dimensional* space and instead work with a product of factors corresponding to *lower-dimensional* spaces.

2.2.2 Bayesian Network Semantics

This section presents the most essential definitions regarding the *Bayesian Networks*.

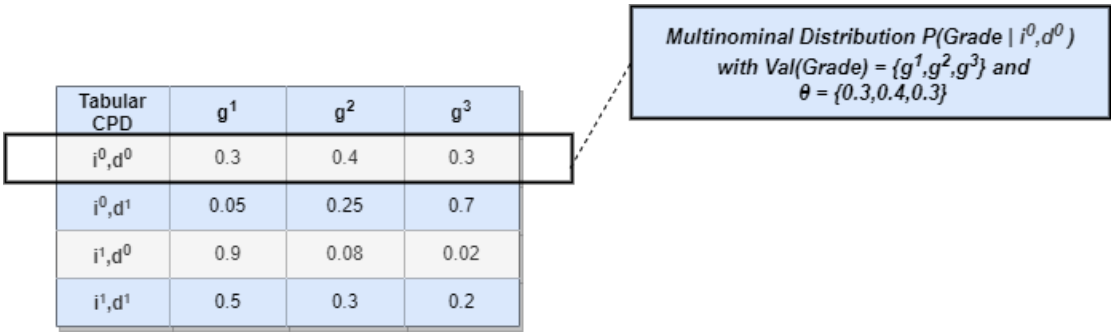
A *Bayesian Network structure, denoted as* $\mathcal{G}(\mathcal{X}, \mathcal{E})$ is a *directed acyclic graph* (*DAG – See Chapter 2.1*), where the nodes correspond to the set of random variables $\mathcal{X} = \{\mathrm{X}_1, \dots, X_n\}$ and the set of *directed edges* $\mathcal{E}$ corresponds to the *conditional independences* among nodes. Each *directed edge* indicates a *direct dependence* among the involved random variables. We denote $Par(X_i)$ as the set of parents nodes of X_i and $NonDescedants(X_i)$ as the set of nodes that are not *descendants'* nodes of X_i. The graph $\mathcal{G}$ can express the set of *conditional independences*, referred as *local independences* and denotated as $I_\ell(\mathcal{G})$, with the following equation:

$$P(X_1, \dots, X_n) = \prod_{i=1}^{n} P(\, X_i \mid Par(X_i)\,)$$

The latter equation is known as *chain rule of Bayesian Networks*. Each factor of product $P(\, X_i \mid Par(X_i)\,)$ corresponds to well-known *local conditional probability distributions (CPDs)*.

The random variables used in this thesis belong to the category of *categorical-discrete* random variables. As a result, the *conditional probability distributions (CPDs)* of these variables fall into the well-known category of *Tabular CPDs*. Each *CPD* $P(\, X_i \mid Par(X_i)\,)$ can be represented as table where each entry corresponds to the probability associated with a combination of values between X_i and $Par(X_i)$(*See Figure 4*).

Each row of *Tabular CPD* $P(\, X_i \mid Par(X_i) = \boldsymbol{x_i}\,)$ represents a *multinomial distribution* with $k = Val(X_i)$ *states* where $\boldsymbol{x_i} \in Val(Par(X_i))$ and the corresponding probabilities(*parameters*) $p_i \in [0,1]\ for\ each\ i \in Val(X_i)\ and\ \sum_{i=1}^{Val(X_i)} p_i = 1$. For each row of *Tabular CPD* we require a *k-dimensional parameter vector* to define the corresponding *multinomial distribution*. We denote the set of required parameters for all distributions(rows) of the CPD $P(\, X_i \mid Par(X_i)\,)$ of variable X_i as θ_{X_i}. Additionally, we use $\theta = \{\theta_{X_1}, \dots, \theta_{X_n}\}$ to represent all the parameters required for all *CPDs* in the *Bayesian* network $\mathcal{G}(\mathcal{X}, \mathcal{E})$, which is necessary to estimate the *joint probability distribution* of the network.



Tabular CPD	g^1	g^2	g^3
i^0,d^0	0.3	0.4	0.3
i^0,d^1	0.05	0.25	0.7
i^1,d^0	0.9	0.08	0.02
i^1,d^1	0.5	0.3	0.2

Figure 4: Tabular CPD of Grade node

We consider a *Bayesian Network* $\mathcal{G}(\mathcal{X},\mathcal{E})$, where $\mathcal{X}$ consists of n *binary* random variables. It can be proven that direct approach to *joint probability distribution* requires $2^n - 1$ parameters. However, by factorizing the *joint probability distribution* based on the graph $\mathcal{G}$ and assuming that k is the maximum number of parents nodes for any variable, we can demonstrate that the number of parameters required for the *joint probability distribution* is less than $n \cdot 2^k$. This approach allows us to avoid *exponential independence* on the number of nodes n, which can be infeasible for large values of n. Instead, the *exponential independence* remains only on the number of nodes k, which is advantageous since a random variable usually depends on a small number of random variables in the network. In most cases we observe that $n \ll k$. The latter property highlights one the main benefits of *Bayesian Network* because we achieve exponentially smaller number of parameters for joint probability distribution.

Discretization

When a Bayesian Network involves *continuous* random variables, the initial step is to convert these variables into discrete. This conversion can be accomplished through a process known as *discretization*. This serves as a *pre-processing step* that utilizes the available information for each random variable, before proceeding to learn the parameters of *joint probability distribution*. Various method can be employed for discretization, and detailed descriptions of these methods can be found in [9]. In this context, we specifically focus and support a specific method, namely *equal width binning*, which is akin to constructing an *equal width histogram.*

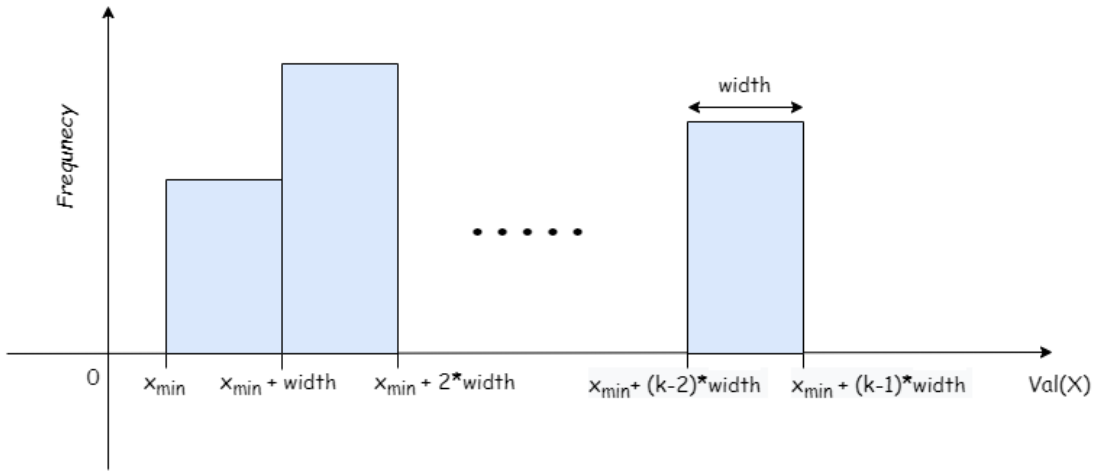


Figure 5: Equal width binning

The objective of the *equal width binning* is to divide the range of values of a continuous random variable into k equally-sized buckets, where k is a *user-defined* parameter. It is important to note that this method may not be suitable for *skewed* distributions, although there are more advanced techniques available to address this issue. However, such advanced methods are beyond the scope of this thesis.

Given a continuous random variable X with $Val(X) \in [x_{min}, x_{max}]$ and assuming k represents the number of *buckets*, the width of each *bucket* can be calculated as follows:

$$width = \frac{x_{max} - x_{min}}{k}$$

While creating the *bucket boundaries*, they are defined in the following manner:

$$x_{min} + i \cdot width \, , where \; i = 1, \dots, k-1$$

The method falls under the *unsupervised setting* as it does not take into account any available *class labels*. Additionally, it belongs to the category of *global methods*, where the *partitions(buckets)* are created based on the entire *continuous space* defined by the random variable, independent of other variables. It is also considered as a *static* method, as it requires a *user-defined* parameter that determines the maximum number of *buckets-partitions* to be created.

It is important to note that the *discretization* method is not combined with others aspects, such as *Bayesian Structure Learning*. In this thesis, *discretization* is used exclusively as a *pre-processing step.*

2.2.3 *Student Bayesian Network*

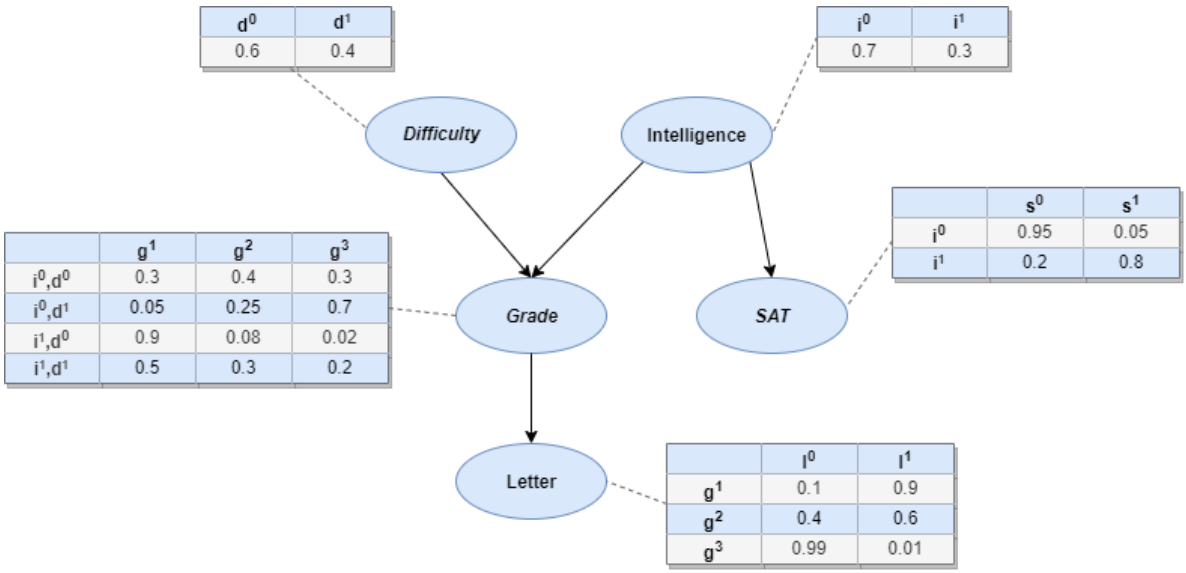


Figure 6: Student Bayesian Network accompanied with CPDs

Given the previous information, we can now examine a comprehensive example of a *Bayesian Network*. We will refer to it as the *Student Bayesian Network* (*Figure 6*). The *Student Network* $\mathcal{G}(\mathcal{X}, \mathcal{E})$ consists of five nodes: the Intelligence (I), the Difficulty(D), the Grade(G), the *SAT grade*(S) and the quality of recommendation letter(L):

$$\mathcal{X} = \{Difficulty(D), Intelligence(I), Grade(G), SAT(S), Letter(L)\}$$

All the random variables in the network are *binary-valued*, except for the $Grade(G)$, which is a *ternary-valued* variable. The set of *local conditional independences* $I_l(\mathcal{G})$ based on $\mathcal{G}(\mathcal{X}, \mathcal{E})$, can be defined as follows:

$$For\ Intelligence, Difficulty\ nodes: (I \perp G)$$

$$For\ Letter\ node: (L \perp I, D, S \mid G)$$

$$For\ Grade\ node: (G \perp S \mid I, D)$$

$$For\ SAT\ node: (S \perp D, G, L \mid I)$$

Given the $\mathcal{G}(\mathcal{X}, \mathcal{E})$ and $I_l(\mathcal{G})$, we can express the *joint probability distribution* of $\mathcal{G}$ with the following way (*chain rule of Bayesian Networks*):

$$P(I, D, S, G, L) = P(I) \cdot P(D) \cdot P(G \mid I, G) \cdot P(S \mid I) \cdot P(L|G)$$

In this case, the number of parameters required to define the *joint probability distribution* is 15. We need one parameter for each *binomial distribution* of $Intelligence, Difficulty$ nodes, 2 parameters for each of the four *multinomial distributions* of $Grade$ node, one parameter for each of the two *binomial distributions of* SAT node and one parameter for each of the three *binomial distributions of* $Letter$ node. On the other hand, the direct approach to *joint probability distribution* requires 47 parameters$(2^4 \cdot 3)$.

Example of probability queries in the Student Bayesian Network

The objective is to estimate *probability queries* on *joint probability distribution*. Based on *Student Example*, an example of probability query can be formulated in the following manner:

$$P(i^1, d^0, g^2, s^1, l^0) = P(\, i^1) \cdot P(d^0) \cdot \; P(g^2) \cdot \; P(s^1) \cdot \; P(l^0) = 0.004$$

The query expresses the probability of intelligent student; the probability of a low difficulty subject; the probability that an intelligent student takes B on a low difficulty subject; the probability that an intelligent student has high *SAT score* and the probability that a student has B grade and takes a weak recommendation letter.

2.3 Naïve Bayes Classifiers

2.3.1 Introduction to Naïve Bayes Classifiers

Initially, we focus on a special case of *Bayesian Networks*, namely the well-known *Naïve Bayes Classifiers* [10]. The *Naïve Bayes Classifier* is an intersection between the *graph and probabilistic theory*. In this case, the *classification* is based on the widely known rule of *Bayes'* theorem, which is described analytically below.

Naïve Bayes Classifiers can be applied to a variety of *real-word* applications. They are commonly used as *Documents Classifiers* and particularly effective in *email spam filtering*. They are also utilized in *Medical Diagnosis Systems* and *Credit-Card Fraud Detection Systems* In addition, they have proven to be valuable in the field of *Sentiment Analysis*. Furthermore, can be integrated into *recommender* systems [11], where they work in conjunction with the *collaborative filtering* methods to create scalable hybrid *recommender system* that achieve improved *accuracy* compared to the other existing systems. In this case, the *Naïve Bayes Classifier* functions similarly to *Documents Classifiers*, but the set of *class labels* represents a set of *recommendations*.

Considering the process of classification, the objective is to construct a function that assigns class *labels* to instances taking into account the available set of *attributes*. *Both the attribute and the class label set are known in advance, making it a supervised setting.*

2.3.2 Naïve Bayes Classifiers Semantics

The *Naïve Bayes Classifier* operates by learning the *CPDs* of each *feature* X_i given the *class variable* C, denoted as $P(X_i|C)$, assuming that each *feature* X_i is independent from others given the *class variable* C*(naïve Bayes assumption)*. *Classification* is performed using *Bayes' Rule*, where the *class label* c^i with the highest *posterior probability* given the *input feature vector* $\boldsymbol{x}$, $P\big(C = c^i \,\big|\, \boldsymbol{x}\big)$ is selected.

We provide the most fundamental definitions around *Naïve Bayes Classifiers*.

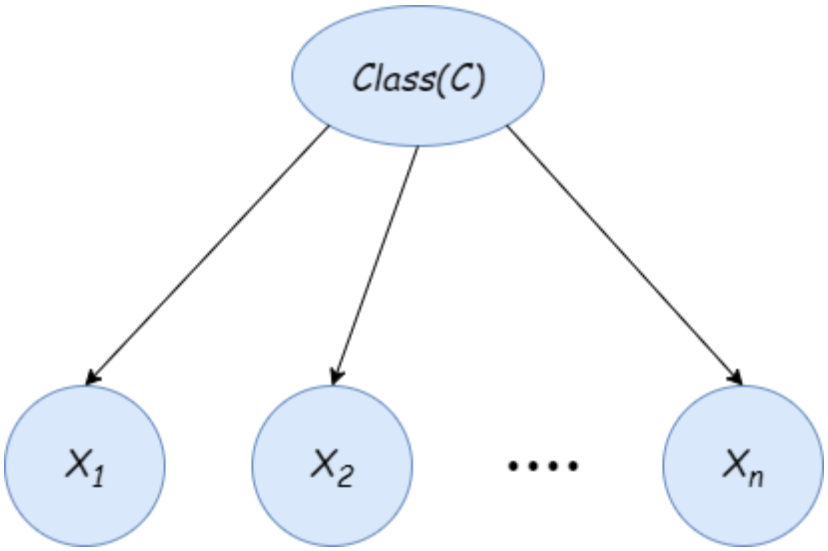


Figure 7: Naïve Bayes Classifier

A *Naïve Bayes Classifiers structure* $\mathcal{G}(\mathcal{X}, \mathcal{E})$ is a *directed acyclic graph* (*Figure 7*), where the nodes correspond to the set of random variables $\mathcal{X} = \{X_1, \dots, X_n, C\}$ and the set of *directed edges* $\mathcal{E}$ represents the *conditional independences* among nodes. In this case, the set of variables $\mathcal{X}$ can be divided into two disjoint subsets. The first subset refers to the set of features, denoted as $\{X_1, \dots, X_n\} \subseteq \mathcal{X}$ assuming that the number of features is n. The second subset pertains to the *class variable* $C \subseteq \mathcal{X}$, with the set of *class labels* consisting of $Val(C) = \{c^1, \dots, c^k\}$, where k represents the number of class labels.

In the context of *Naïve Bayes Classifiers*, the so-called *naive Bayes assumption* it holds, which states that the *features* are *conditionally independent* given the *class label.* Furthermore, for each *feature* node X_i with $i \in \{1, .., n\}$, holds that $Par(X_i) = C$. As a result, the set of *conditional independences* $I_\ell(\mathcal{G})$ can be expressed as follows:

$$For\ each\ variable\ X_i : (X_i \perp \boldsymbol{X_{-i}} \mid C)$$

$$where\ the\ set\ \boldsymbol{X_{-i}} = \{X_1, .., X_n\} - \{X_i\}.$$

Given the *structure* of *Naïve Bayes Classifiers* $\mathcal{G}(\mathcal{X}, \mathcal{E})$ and the corresponding set of *local independencies* $I_\ell(\mathcal{G})$, we can express the *joint probability distribution* $P(\mathcal{X})$ as follows:

$$P(C, X_1, \dots., X_n) = P(C) \cdot \prod_{i=1}^{n} P(X_i \mid C)$$

Each factor $P(X_i \mid C)$ corresponds to the *local conditional probability distributions (CPDs)* of *feature* X_i. Similar to *Bayesian Networks*, we can express the *joint probability distribution* as product of these factors(*factorization*). In this case, the *joint probability distribution* consists of the prior distribution $P(C)$ and the set of *CPDs* $P(X_i|C)$ where each of them represents a *multinomial* distribution. This approach allows us to significantly reduce the number of parameters required for the *joint probability distribution*.

The random variables used in this context belong to the category of *categorical-discrete* random variables. Therefore, the *conditional probability distributions (CPDs)* of these variables belong to the well-known category of *Tabular CPDs*. For *continuous* variable, we employ method of *discretization (See Chapter 2.2)*. In conclusion, the *Multinomial Naïve Bayes Classifier* used throughout this thesis.

Each *CPD* $P(X_i \mid C)$ can be represented as a *table* where each entry corresponds to the probability of a combination values of X_i and the *class variable* C. Additionally, each *CPD* characterized by a set of parameters, denoted as θ_{X_i}.

Given a *Naïve Bayes Classifier* consists of n *binary- valued features* and a *binary-valued class variable*, we can prove that the number of independent parameters in the *factorized joint probability distribution* is $2n + 1$. This means that the number of parameters is linearly dependent on the number of features n, in contrast to the direct approach of *joint probability distribution* where the dependence on number of *features* is exponential ($2^n - 1$ parameters). Despite the strong assumptions of *independence* among *features*, the simplicity and the linear dependence on set of *features* result in a small number of required parameters. This property makes *Naïve Bayes Classifier* applicable in many cases involving *high-dimensional feature vectors.*

Despite its simplicity and the strong assumptions of independence, which may not hold in *realistic* scenarios, the *Naïve Bayes Classifier* performs quite well even when compared to more sophisticated *classifier* like *C4.5*, as described in detail in [12]. The success of *Naïve Bayes Classifiers* as noted in [13], can be attributed to the fact that the *classification error* is not necessarily related to the quality of *fit* of the *joint probability distribution* (appropriateness of *conditional independencies*). In other words, the *estimation error* of *joint probability* does not necessarily result in *classification errors*. The *classification* of *class labels* is not highly *sensitive* to the *errors* in estimating *instance probabilities*.

Regarding the process of *Classification*, we consider a *Naïve Bayes Classifiers structure* $\mathcal{G}(\mathcal{X}, \mathcal{E})$ with the set of *features* corresponding to $\{\mathrm{X}_1, \dots, X_n\} \subseteq \mathcal{X}$ and a c*lass variable* $C \subseteq \mathcal{X}$ where the values of the variable are represented as $Val(C) = \{c^1, \dots, c^k\}$. The objective, for any *n-dimensional vector* $\boldsymbol{x} = [x^1, \dots, x^n]$ is to determine the *class label* with the highest *posteriori probability* given an n-*dimensional vector*. To achieve this, we select the *class label* that maximizes the following expression:

$$class\ label = \arg max_{c^i \in Val(C)} P(C = c^i | \boldsymbol{x})$$

Our goal is to maximize the probability $P(C|\boldsymbol{x})$. By applying *Bayes' rule*, the probability is defined as follows:

$$P\big(C = c^i \big| \boldsymbol{x}\big) = \frac{P(\boldsymbol{x}|C = c^i) \cdot P\big(C = c^i\big)}{P(\boldsymbol{x})}\ for\ each\ c^i \in Val(C)$$

2.3.3 Spam classification problem

Considering the previous statements, we will now present a complete example of a *Naïve Bayes Classifier*. Our focus is on determining whether an *email* is spam or nor, based on its context. This example falls within the broader field of *Document Classification*. We assume that the *class variable* C is a *binary valued* variable, with values represented as $Val(C) = \{spam, non\_spam\}$.

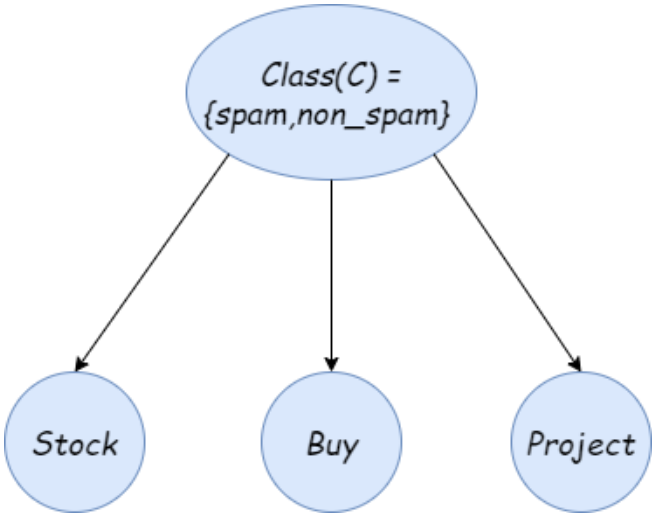


Figure 8: Naïve Bayes Classifier for spam filtering

The context of each email consists of a *bag-of-words*, where each *word* represents a *feature*. In this example, we assume three *features* corresponding to the words "Stock», «Buy" and "Project". Each feature is accompanied by its *CPD* $P(W_i|C)$, where $W_i \in \{Stock, Buy, Project\}$. The network structure is illustrated in *Figure 8*. The set of features generally encompasses a large set of *keywords* used to define the *class label*.

Applying the *naïve Bayes assumption,* the *joint probability distribution* is defined as follows:

$$P(C, Stock, Buy, Project) = P(C) \cdot P(\, Stock \mid C\,) \cdot P(\, Buy \mid C\,) \cdot P(\, Project \mid C\,)$$

Our goal is to *classify* an email into one of the two *class labels*. Assuming that the email contains the words *stock, buy* but does not contain the word project, the *input feature vector* can be represented as follows: $\boldsymbol{x} = [stock, buy, \neg project]$. To determine the *class label*, we need to calculate the *posteriori probabilities* given $\boldsymbol{x}$**,** which can be defined as follows:

$$For\ the\ class\ label\ spam:$$

$$\mathrm{P}(spam \mid \boldsymbol{x}) = P(\boldsymbol{x}|spam) \cdot P(spam)$$
$$= P(stock|spam) \cdot P(buy|spam) \cdot P(\neg project|spam) \cdot P(spam)$$

$$For\ the\ class\ label\ non\_spam:$$

$$\mathrm{P}(non\_spam \mid \boldsymbol{x}) = P(\boldsymbol{x} \mid non\_spam\ ) \cdot P(non\_spam)$$
$$= P(stock \mid non\_spam) \cdot P(buy \mid non\_spam) \cdot P(\neg project \mid non\_spam) \cdot P(non\_spam)$$

The *class label* is determined by comparing the probabilities $\mathrm{P}(spam \mid \boldsymbol{x})$ and $\mathrm{P}(non\_spam \mid \boldsymbol{x}\ )$**,** and selecting the one with the highest value.

2.4 Forward Sampling

In this section, we present the *Forward Sampling* algorithm [14] which is used to generate all the *training instances*. The *training instances* are used for the experimental evaluation of the proposed approaches.

For the generation of *training instances*, each instance consists of a *full particle* of all the variables in the *Bayesian* network $\mathcal{G}(\mathcal{X}, \mathcal{E})$, confirming that the setting is *supervised*.

We focus on estimating *probabilities queries* $P(\boldsymbol{Y} = \boldsymbol{y})$ based on the *joint probability distribution* $P(\mathcal{X})$ of the network $\mathcal{G}$, where $\boldsymbol{Y} \subseteq \mathcal{X}\ and\ \boldsymbol{y} \in Val(\mathcal{Y})$. However, we do not consider *conditional probability queries* of the form $\boldsymbol{P}(\boldsymbol{Y} = \boldsymbol{y} \mid \boldsymbol{E} = \boldsymbol{e})$**,** where $\boldsymbol{Y}, \boldsymbol{E} \subseteq \mathcal{X}$, $\boldsymbol{y} \in Val(\boldsymbol{Y})$ and $\boldsymbol{e} \in Val(\boldsymbol{E})$.

We have chosen the *Forward Sampling* algorithm to generate full *particles* for the purpose of estimating queries on the *joint probability distribution*. Unlike other algorithms like *Rejection Sampling* and *Likelihood Weighting* [15], which are typically used for generating *full particles* to estimate *conditional probability queries*.

In certain cases, when dealing with highly skewed distributions where only a small number of variables have negligible probability distribution, alternative algorithms like *Deterministic Search* may be necessary. However, since these cases are beyond the scope of this thesis, we have opted to utilize the *Forward Sampling* algorithm.

The algorithm based on the concept of generating data for each variable according to its probability distribution. The first step in implementing the algorithm is to establish a *topological order* of the *DAG (Directed Acyclic Graph)* representing the Bayesian network $\mathcal{G}$. This ordering ensures that each node X_i is preceded before any node X_j in the sequence, meaning there no directed paths from X_i to X_j. This step is crucial as it guarantees that data for each node's parent nodes is generated before the node itself.

Based on the ordering of nodes, the algorithm proceeds by sampling for each node according to its corresponding *CPD* $P(X_i \mid Par(X_i))$. The process is repeated for each node in the ordering. Once the process is completed for all nodes, a *particle* is generated. Below we describe the algorithm.

Algorithm 1: *Forward Sampling in BNs*

Input:

Bayesian Network Structure $\mathcal{G}(\mathcal{X}, \mathcal{E})$ *with* $\mathcal{X} = \{X_1, \ldots, X_n\}$
T *number of full particles*

Output: T full particles

1. *Let* $X_1, \ldots, X_n$ *be a topological ordering of Bayesian Network*
2. **For** 1 **to T**
3. *Initialize an empty instantiation* $\boldsymbol{t}$
4. **Foreach** *node* **from** *topological ordering* $X_1, \ldots, X_n$
5. *Get the values of parents of* X_i *from* $\boldsymbol{t}$
6. *Sample* x_i *from* $P(X_i | Par(X_i))$
7. *Add value* x_i *to* $\boldsymbol{t}$
8. **End**
9. **return** $\boldsymbol{t} = (x_1, \ldots, x_n)$
10. **End**

The process of generating a *particle* is descibed analytically below. We will use the *Student* (*See Chapter 2.2.3*) as an example. Assuming that the generated sequence of the topological order is as follows: $Difficulty(D), Inteligence(I), Grade(G), SAT(S), Letter(L)$, the algorithm operates as follows:

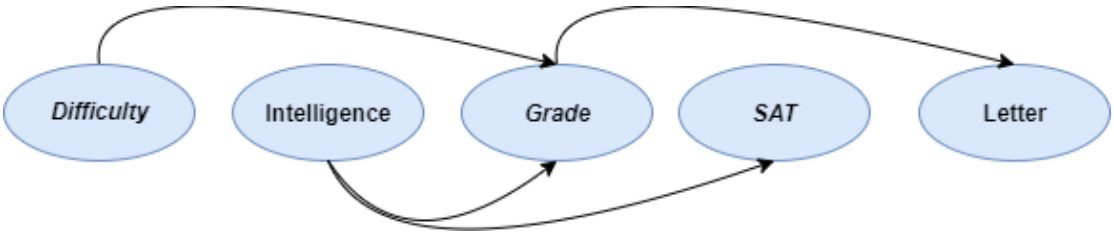


Figure 9: Topological ordering of Student Bayesian Network

1. Initially, we sample from the distribution $P(D)$ for the $Difficulty$ node, assuming $Difficulty = d^0$
2. Next, we sample from the distribution $P(I)$ for the $Inteligence$ node, assuming $Inteligence = i^0$.
3. Then, we sample from the distribution $P(G | I = i^0, D = d^0)$ for the $Grade$ node, assuming $Grade = g^2$.
4. Subsequently, we sample from the distribution $P(S | I = i^0)$ for the SAT node, assuming $SAT = s^0$.
5. Finally, we sample from the distribution $P(L | G = g^2)$ for the $Letter$ node, assuming $Letter = l^0$.
6. As a result, the particle corresponds to $D = d^0, I = i^0, G = g^2, S = s^0, L = l^0$.

Analysis of Forward Sampling algorithm

Given a dataset $D = \{\xi[1], \ldots, \xi[M]\}$ of full particles, which is generated by sampling, applying the *convergence bounds* [1, Ch. 17], we can estimate the expected value of any function using the following method:

$$E_D(f) = \frac{1}{M}\sum_{m=1}^{M} f(\xi[m]) \ \ where\ M : the\ size\ of\ particle\ set$$

Our goal is to estimate *queries* of the form $P(\boldsymbol{Y} = \boldsymbol{y})$**,** where the only requirement is to know the number of particles that contain the $\boldsymbol{y}$**.** The probability can be defined as follows:

$$P_D(\boldsymbol{y}) = \frac{1}{M}\sum_{m=1}^{M} \boldsymbol{I}\{y[m] = \boldsymbol{y}\}$$

Where the function $\boldsymbol{I}$ refers to an indicator function, defined as:

$$\begin{cases} 1\,, if\ y[m]\ contains\ the\ \boldsymbol{y} \\ 0\,, otherwise \end{cases}$$

Considering the complexity of the algorithm of *Forward Sampling*, assuming M corresponds to the total number of generated *full particles*, $n = |\mathcal{X}|$ denotes to the number of nodes of the network, $p = \max_i |Par(X_i)|$ denotes the maximum number of parents nodes for any variable, and $d = \max_i |Val(X_i)|$ denotes the maximum number of values for any variable, then the complexity of the algorithm is $O(M \cdot n \cdot p \cdot\ logd)$. This considers that the sampling for any variable is $O(logd)$ and the indexing time required to retrieve the values of parents nodes for any distribution using the appropriate data structure is $O(p)$.

Sampling distribution

Regarding to the scope of this thesis, our focus is on *categorical* random variables. We assume a *multinomial* distribution $P(X)$ with values $Val(X) = \{x^i, \ldots, x^k\}$, which is defined by the parameters $\theta_1, \ldots, \theta_k$, respectively. The sampling process (*Figure 10*) can be summarized in the following three steps:

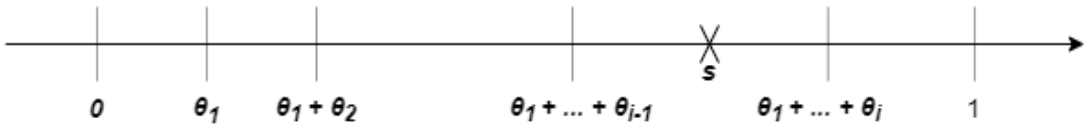


Figure 10: Sampling of a multinomial distribution

1. Initially, we generate a uniformly sampled value $\boldsymbol{s}$ from the interval $[0,1]$.
2. Then, we divide the interval into k sub-intervals: $[0, \theta_1), [\theta_1, \theta_1 + \theta_2), \ldots$ where the *i sub-interval* is defined as $[\sum_{j=1}^{i-1} \theta_j\ , \sum_{j=1}^{i} \theta_j)$
3. If the sampled value $\boldsymbol{s}$ falls within the $\boldsymbol{i-th}$ sub-interval, the generated values is x^i(the interval boundaries can be determined using the method of binary search in $O(logk)$ time).

Estimation Quality Analysis

The quality of the estimation obtained from the sampling method, which measures the proximity to the *joint ground truth distribution* of *Bayesian Network* $\mathcal{G}$, is largely determined by the number of generated *particles*. In cases where we aim to quantify the *error guarantees* of the estimation, we can achieve using the following theorem.

We assume that $P(Y = y)$ represents the *ground truth joint distribution*, derived from the *true values* of parameters, $P_D(Y = y)$ denotes the distribution obtained from the set of generated *particles*, which is equivalent to the distribution obtained through the *MLE* algorithm. M represents the number of *particles*.

Theorem 1[1, Corollary 12.2]: Assuming $M \geq \frac{3\ln\left(\frac{2}{\delta}\right)}{P(y)\varepsilon^2}$, we can provide an (*ε, δ)-approximation* of the *joint ground truth* distribution as follows:

$$(1-\varepsilon) \leq \frac{P_D(y)}{P(y)} \leq (1+\varepsilon)\ with\ probability\ 1-\delta$$

To guarantee an *ε relative error* with an *error probability* up to δ from the *joint ground truth* distribution, the size of the sample depends logarithmically on $\frac{1}{\delta}$, quadratically on $\frac{1}{\varepsilon}$ and linearly on $1/P(y)$. However, a problem with this approach arises when the distribution $P(y)$ is unknown, making difficult to determine the appropriate sample size for achieving a "good" estimation quality. While there are other *error guarantees* [1, Ch. 17] for the estimation, our main concern is the *relative error guarantees*.

An extension of the previous theorem involves assuming the prior learning of the parameters of *local CPDs* of *Bayesian Network* $\mathcal{G}$, which is defined as follows:

Theorem 2[1, Corollary 17.3]: Under the assumptions $P(\ X_i \mid Par(X_i)\ ) \geq \lambda\ \forall i, X_i, Par(X_i)$ and $M \geq \frac{(1+\varepsilon)^2}{2\lambda^{2(d+1)}\varepsilon^2}\log\frac{nJ^{d+1}}{\delta}$, the following equation holds:

$$e^{-n\varepsilon} \leq \frac{P_D(y)}{P(y)} \leq e^{n\varepsilon}\ with\ probability\ 1-\delta$$

where $J = max_{i=1}^{n}\ J_i\ με\ J_i = |Val(X_i)|, d = max_{i=1}^{n}|Par(X_i)|$ και $n = |\mathcal{X}|$.

In this scenario, the required number of *particles* to ensure a "good" estimation depends not only on *ε, δ* but also on J, d, n which take into account the structure of *Bayesian Network* $\mathcal{G}$.

To ensure the correctness and quality of the estimation, it is necessary to bound, if feasible the values of joint *truth probability* of *queries* (e.g., quantifying $P(Y) \geq 0.1$ for all the queries). This allows for determining an appropriate size of the query set in order to control the distribution.

2.5 Learning parameters

Our goal is to learn the *parameters* of *joint probability distribution* of the *Bayesian Network Structure* $\mathcal{G}(\mathcal{X}, \mathcal{E})$. Given a known network structure known, we attempt to learn the parameters from the dataset D. To accomplish this, we utilize the *Maximum Likelihood Estimation* (*MLE*) algorithm, which will be discussed and analyzed below. The dataset consists of instantiations of *full assignments* confirming the *supervised* setting.

The objective is to construct a model M, which falls under the category of *parametric models* and is characterized by a parameter set θ. Our primary concern is that the obtained *joint probability distribution* closely matches the distribution of the dataset. Therefore, the selection of parameters is defined in such way that the available *training instances* achieve the highest probability, making them the *most probable*.

2.5.1 Maximum Likelihood Estimation (MLE)

Assuming a Bayesian Network Structure $\mathcal{G}(\mathcal{X}, \mathcal{E})$ with the set of variables corresponds to $\mathcal{X} = \{X_1, \dots, X_n\}$.

Given a dataset $D = \{\, \xi[1], \dots, \xi[M] \,\}$(*training dataset*) consisting of *independent* and *identically distributed*(*i.i.d.*) samples from the *joint probability distribution* $P(\mathcal{X})$ of $\mathcal{G}$(*See. Chapter 2.4*). Each $\xi[i]\ for\ i \in \{1, \dots, M\}$ represents an *instantiation* of *full assignments* of $\mathcal{X}$. Our objective is to determine the set of parameters θ that define the required parameters for each *CPD* of each variable.

The first step in defining the *likelihood function* of parameters θ given the dataset D, is as follows:

$$likelihood : L(\theta : D) = P(D|\theta)$$

Similarly, we can define the *log-likelihood* function which commonly used (usually we calculate $\log \mathrm{P}(\xi|\theta)$ to avoid *overflow* problems), as follows:

$$log - likelihood : l(\theta : D) = logP(D|\theta)$$

It is worth mentioning that the *negated form* of the *log-likelihood* is referred as the loss *function*, which measures the *loss* given the learning parameters for any *instance* ξ.

$$loss\ function :\ loss(\xi|\theta) = -logP(\xi|\theta)$$

Regarding the fact that the dataset $D = \{\, \xi[1], \dots, \xi[M] \,\}$ consists of *i.i.d instances*, we can redefine the *likelihood function*, as follows:

$$L(\theta : D) = P(D|\theta) = \prod_{i=1}^{M} P(\, \xi[i] :\ \theta)$$

To maximize the *likelihood function*, we want to select the parameters θ that maximize the *likelihood* function. Assuming $\hat{\theta}$ represents the set that maximize the *likelihood function*, the following equation holds:

$$\text{Maximum Likelihood Estimation} : L\big(\hat{\theta} : D\big) = max_{\theta \epsilon \Theta} L(\theta : D)$$
$$where\ \Theta\ denotes\ the\ hypothesis\ space$$

Exploiting the *Bayesian network structure*, we can define the *likelihood function*, as follows:

$$L(\theta : D) = P(D|\theta) = \prod_{i=1}^{M} P_G(\xi[i] : \theta)$$

$$= \prod_{i=1}^{M} \prod_{j=1}^{n} P(x_i[m] \mid Par(X_i)[m] : \theta)$$

$$= \prod_{i} \left[\prod_{m} P(x_i[m] \mid Par(X_i)[m] : \theta) \right]$$

Each factor in brackets denotes the *condition likelihood function* of the random variable X_i given $Par(X_i)$. Assuming θ_{X_i} denotes the set of parameters that defines the *CPD* $P(X_i|Par(X_i))$, the following equation holds:

$$L(\theta : D) = \prod_{i} L_i(\theta_{X_i} : D)$$

Each factor denotes the *local likelihood* of the random variable X_i and is defined as follows:

$$L_i(\theta_{X_i} : D) = \prod_{m} P(x_i[m] \mid Par(X_i)[m] : \theta_{X_i})$$

The latter property is known as the *global decomposability* of the *likelihood function*. Assuming that each θ_{X_i} is independent of θ_{X_j} for each $\neq j$ with $i, j \in \{1, \dots, n\}$, we can maximize each *local likelihood function* independently from the others and combine them to obtain the *MLE*. This property, along with the property of *local decomposability* constitutes the ideal scenario to apply in a *distributed* environment.

Given a dataset $D = \{ \xi[1], \dots, \xi[M] \}$ and the corresponding Bayesian *Network Structure* $\mathcal{G}(\mathcal{X}, \mathcal{E})$, assuming θ_{X_i} is independent of θ_{X_j} for each $i \neq j$ with $i, j \in \{1, \dots, n\}$ and $\hat{\theta}_{X_i}$ maximizes the *local likelihood function* $L_i(\theta_{X_i} : D)$ of random variable X_i then the set $\hat{\theta} = \{\hat{\theta}_{X_1}, \dots, \hat{\theta}_{X_n}\}$ maximizes the το *likelihood function* $L(\theta : D)$.

Beyond the property of *global decomposability* of the *likelihood* function, the property of *local decomposability* also holds. Given the *tabular CPD* $P(X_i \mid Par(X_i))$ of random variable X_i with $Par(X_i) = \boldsymbol{U}$, which is our primary concern, we can redefine the *local likelihood function* with the following manner:

$$L_i(\theta_{X_i} : D) = \prod_{m} P(x_i[m] \mid Par(X_i)[m] : \theta_{X_i})$$

$$= \prod_{m} \theta_{x_i[m] \mid Par(X_i)[m]}$$

$$= \prod_{\boldsymbol{u} \in Val(\boldsymbol{U})} \left[\prod_{x \in Val(X_i)} \theta_{x_i|\boldsymbol{u}}^{M[\boldsymbol{u}, x_i]} \right]$$

Where $M[\boldsymbol{u}, x_i]$ represents the counter of the combination of values $X_i = x_i$ and $Par(X_i) = \boldsymbol{u}$ in D.

Considering the latter equation, we achieve to concentrate all the references of the parameter $\theta_{x_i|\boldsymbol{u}}$ for each $x_i \in Val(X_i)$ together. We attempt to maximize the parameters $\theta_{x_i|\boldsymbol{u}}$ taking into account the restriction $\sum \theta_{x_i|\boldsymbol{u}} = 1$ for each $\boldsymbol{u} \in Val(\boldsymbol{U})$. The latter property demonstrates the property of *local decomposability*, now we can maximize the parameters $\theta_{x_i|\boldsymbol{u}}$ for each $\boldsymbol{u} \in Val(\boldsymbol{U})$ independently from the others.

Maximum Likelihood Estimate

We can prove that the *maximum likelihood estimate* $\hat{\theta}_{X_i}$ of θ_{X_i} of *tabular CPD* $P(X_i \mid Par(X_i))$, which predisposes that the *likelihood function* is derivable, defined as follows:

$$Maximum\ likelihood\ estimate: \ \hat{\theta}_{X_i} = \frac{C_i(x_i, x_i^{par})}{C_i(x_i^{par})}$$
$$for\ each\ x_i \in Val(X_i), x_i^{par} \in Par(X_i)$$

Where $C_i(x_i, x_i^{par})$ denotes the number of instances $(X_i = x_i, Par(X_i) = x_i^{par})$ in D and $C_i(x_i^{par})$ denotes the number of *instances* $(Par(X_i) = x_i^{par})$ in D. To obtain the maximum likelihood estimate the only requirement is to maintenance the counters $C_i(x_i, x_i^{par})$ and $C_i(x_i^{par})$ for each random variable X_i of the network and for each $x_i \in Val(X_i)$ and $x_i^{par} \in Val(Par(X_i))$. *Algorithm 2* summarize the *MLE* algorithm.

Algorithm 2: *Maximum likelihood Estimation (MLE)*

Input:
Bayesian Network Structure $\mathcal{G}(\mathcal{X}, \mathcal{E})$
$\boldsymbol{D} = \{ \xi[1], \dots, \xi[M] \}$ *of full assignments*
Output:
$\hat{\theta} = \{\widehat{\theta_{X_1}}, \dots, \widehat{\theta_{X_n}}\}$

1. // Count
2. **Foreach** $\xi[1]$ **from** $\boldsymbol{D}$
3. **Foreach** X_i **from** $\mathcal{X}$
4. Increment count(x_i, x_i^{par})
5. Increment count(x_i^{par})
6. **End**
7. **End**
8.
9. // Estimation
10. **Foreach** X_i **from** $\mathcal{X}$
11. **Return** $\widehat{\theta_{X_i}} = F_i(x_i, x_i^{par})$ / $F_i(x_i^{par})$
12. **End**

Given a *Bayesian Network Structure* $\mathcal{G}(\mathcal{X}, \mathcal{E})$, the *MLE* of the *joint probability distribution* can be defined as follows:

$$P(\mathcal{X}) = \prod_{i=1}^{n} \theta_{X_i} = \prod_{i=1}^{n} \frac{C_i(x_i, x_i^{par})}{C_i(x_i^{par})}$$

MLE consistency

The algorithm *MLE* also holds the property of *consistency* [1, Theorem 16.1]. Given a sequence of *i.i.d* samples $D_M = \{\xi[1], .., \xi[M]\}$ from the distribution $P(\mathcal{X})$, then the property of *consistency* demonstrates as follows:

$$\lim_{M \to \infty} P_{D_M}(A) = P(A)$$

For large dataset the *empirical distribution* approaches the obtained distribution of the *MLE* algorithm that is close enough to the initial distribution $P(\mathcal{X})$ with high probability, specifically the probability convergences to 1 as $M \to \infty$.

Data fragmentation and overfitting

One of the restrictions of the *learning parameters* of a *Bayesian Network* given *training instances*, constitutes the fact that an increase to the number of parents nodes for any node leads to exponential increase to *parents assignments* of the node and simultaneously leads to exponential decrease to the number of data for each *parent assignment*. This phenomenon denoted as data *fragmentation*, where the dataset divided to a large number of small subsets. In case, the size of dataset is limited then someone subset is also limited and therefore this scenario can be led to *overfitting* (large number of zeros in distribution).

2.6 Laplace Smoothing

An issue during the process of the *MLE* algorithm in both *Bayesian Network* and *Naïve Bayes Classifier*, arises when the size of *training instances* is very limited (of course, this can also occur when the size of dataset is large but combined usually with *highly skewed distributions*), is that the dataset may not be representative of the *joint probability distribution*, as it may lack data for certain variables in the network, particularly those with small parameter values θ_{X_i}.

When we encounter situations where there is no data available for specific values of network nodes, estimating queries on the joint probability distribution becomes challenging. Treating these missing parameters as zero does not accurately reflect the truth, as it does not necessarily mean that these values do not exist. The problem becomes apparent when we have no data for a *non-zero parameter* θ.

Attempting to answer *user-posed queries* involving values or combination of values that have small probabilities and small θ values (usually occurring when the queries refer to *highly unlikely queries*, *queries* quite small *joint probability distribution* that is unlikely to happen) leads to a zero estimation. Consequently, this results in a non-pragmatic scenario where the estimation of *joint probability distribution* does not reflect the truth due to the absence of data for certain parameters.

To address this problem, one effective approach is the widely known method of *Laplace smoothing*. *Laplace smoothing* can be applied in both *zero* and *non-zero* parameters although our primary focus is on the *zero* parameters. The method works as follows: for each *zero parameter*, we add $\lambda\,(pseudocount)$ occurrences of the parameter value regardless of whether the value has been observed in the dataset. Since the parameter θ_{X_i} represents a probability, it is necessary to normalize it by the number of values of variable X_i and multiplying it by the value of parameter λ. Assuming θ_{X_i} corresponds to the *CPD* $P(X = x_i \mid Par(X_i))$ of random variable X_i, the following equation holds when *Laplace Smoothing* is applied:

$$Maximum\ likelihood\ estimate\ with\ Laplace\ Smoothing$$

$$P(X = x_i \mid Par(X_i)) = \frac{count\big(X = x_i\ and\ Par(X_i)\big) + \lambda}{count\big(Par(X_i)\big) + \lambda \cdot Val(X_i)}\ \ where\ \lambda > 0$$

We can demonstrate the application of the *Laplace Smoothing* using the following examples. Assuming a *biased coin* with two faces $\{Head(H), Tail(T)\}$ and one toss which resulted to $Head$. Estimating the parameters given the result of the previous toss and the *MLE* algorithm, then:

$$Maximum\ Likelihood\ estimate$$

$$p(H) = \frac{1}{1} = 1\,, \qquad p(T) = \frac{0}{1} = 0$$

Regarding both of estimations, none of them are consistent. This example demonstrates the problem of *overfit* of the *MLE* algorithm which confirms the fact when the size of dataset is small and the number of parameters quite large then the *MLE* leads to *overfit* (most of parameters consider as zero which is not reflect the reality).

The following equation holds when *Laplace Smoothing* is applied and assuming $\lambda = 1$:

$$Maximum\ Likelihood\ estimate\ with\ Laplace\ Smoothing$$

$$p(H) = \frac{1 + 1}{1 + 2} = \frac{2}{3}\,, \qquad p(T) = \frac{0 + 1}{1 + 2} = \frac{1}{3}$$

The application of *Laplace Smoothing* leads to a more pragmatic scenario and simultaneously results in preventing the problem of *overfitting,* even when the dataset is quite small.

By varying the value of parameter λ, we can define the added *smoothing-regularization* on parameter. The larger the value of λ, more the distribution approaches the uniform distribution. Regarding *zero parameters*, both the numerator and denominator of the previous equation are zero regardless of the value of λ. In this case the distribution accurately approaches the uniform distribution.

Although, in most cases the numerator is zero. Considering the experimental evaluation, the value of λ where the quality of the obtained estimation is quite "good" is achieved when $\lambda = 1$.

Another advantage of this method is the effect of the parameter based on the size of dataset. As the dataset size increases, the influence of λ diminishes, which is desirable since a larger dataset is more reliable. When considering a zero parameter, as soon as data about it is detected, it is converted into a *non-zero* parameter. This marks the point at which the usage of *Laplace Smoothing* method is discontinued. In the context of this thesis, the *Laplace Smoothing* method is exclusively applied to zero parameters in both *Bayesian Networks* and *Naïve Bayes Classifier*. Otherwise, the parameter estimation relies solely on the dataset.

2.7 Distributed Continuous Model

This section describes the mode used throughout this thesis, namely the *Continuous Distributed Monitoring Model* [16]. The model represents an intersection between the *communication model*, where $k \geq 2$ *sites* exist and our objective is the *one-shot computation* of a specific function and the *data stream model* where $k = 1$(only one site) and our objective is the *continuous monitoring* of a specific function.

This model simulates most of the *learning tasks* over *big data streaming* systems, which involve enormous volumes of datasets (on the order of *Petabytes*). These datasets are streaming and distributed and our aim is to ensure *real-time* responses.

The *Continuous Distributed Monitoring Model* consists of a set of *observers*, each of which tracks only one part of the observations. The objective is to estimate a function over the union of the observation for each time.

For instance, the function can be the counting of the observation set (*count-tracking problem* – which is our primary concern), where the function represents a *linear* and *monotonic increasing function*. Of course, there are more complex function, such as the *second frequency moment* F_2 which can be applied to various situations, such as *estimating join sizes*.

Our goal is to minimize the *communication cost* among observes(*communication-efficient*). To achieve this, it is usually necessary to provide an approximate estimation of the corresponding function (*approximate answers*).

We assume that the observation set for each observer represents a *high-speed, high-volume* and *high-throughput data streams* so approaches such as *periodic polling* or *centralization* of *streams* may be infeasible.

Specifically, we assume k *sites* (or *workers*) and the set of *sites* denoted as $S = \{S_1, .., S_k\}$. Each site S_i receives a stream of observations with varied rate probably. Also, we assume that the $A_i(t)$ corresponds to a *multiset of elements (bag of elements*) which have received from the site S_i up to the time t and $A(t) = \uplus_i A_i(t)$ with $i \in \{1, \dots, k\}$ which corresponds to the union of stream of all sites, with $\uplus$ denotes *multiset addition*.

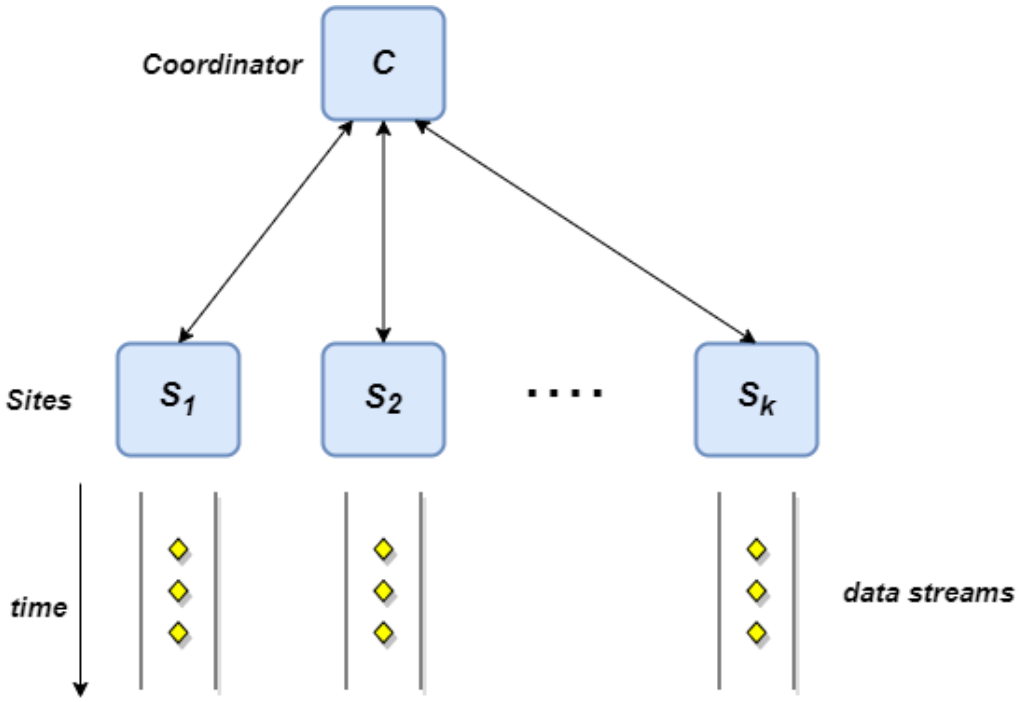


Figure 11: Distributed Continuous Model

Beyond the individual sites, there exists a designated site known as the *Coordinator*. The *Coordinator* communicate directly with each site S_i and therefore, there is a *two-way communication channel* between the *Coordinator* and each one of the k *sites* (*Figure 11*). Although, there is no direct communication channel among the sites themselves, this does not pose a limitation. By utilizing the Coordinator as an intermediate node, sites can communicate through the *Coordinator*. The *downstream communication cost* refers to the number of messages sent from the *sites* to the *Coordinator*, while *upstream communication cost* refers the number of messages sent from the Coordinator to the sites.

Our goal is to monitor the function over the union of the data streams. We except the Coordinator to continuously maintain the value $f\big(A(t)\big)$ for any given time t. For instance, in the case of *count-tracking problem*, the function can be defined as follows: $f\big(A(t)\big) = |A(t)|$.

Our primary focus is on the *value monitoring*, where for any time t we aim to provide an estimation $\hat{f}(A(t))$ of the function $f(A(t))$ while also ensuring *error guarantees*. We seek an *ε,δ-approximation* of the function $f(A(t))$ for any given time, which can be defined as follows:

$$(1-\varepsilon)\cdot f\big(A(t)\big) \leq \hat{f}\big(A(t)\big) \leq (1+\varepsilon)\cdot f\big(A(t)\big)\ with\ probability\ 1-\delta\ ,\forall\ t$$

The analysis of the *MLE* algorithm reveals a crucial component: the maintenance of the necessary counters for each *CPD* of the network, considering the *Continuous Distributed Model*. We refer to these counters as *distributed counters* (*See Chapter 4.1.1*). Additionally, the maintenance of *distributed counters* is accompanied by minimal communication cost (*communication efficient*). This problem is widely known as *count-tracking* problem and has been discussed analytically on [17] and [20]. The *count-tracking* problem can be viewed as the maintenance of F_1 *frequency moment*.

Chapter 3:

Problem statement

3.1 Problem definition

The general idea of the problem is to design a system which is capable of maintaining necessary *distributed counters* with minimal communication cost(*communication-efficient*), while providing *error guarantees* for the maintained model. These systems consist of *massive, dynamic, high-throughput* and *distributed data sources*, where centralizing datasets may be *inefficient* and *infeasible* due to the *enormous communication cost*.

Our aim is to design a system capable of effectively maintaining a graphical model over distributed and streaming datasets, with a specific emphasis on providing an accurate approximation of the Maximum Likelihood Estimate (MLE) at any given time.

The only requirement to obtain the *maximum likelihood estimate* is to have the *counters* for the parameters defined for each *CPD* in the network. We aim to maintain a collection of *distributed counters* necessary for estimating the MLE. However, in a distributed environment, utilizing EXACT *counters* (*See Chapter 4.1.1*), where each site sends an *update* message to the Coordinator whenever receives an event, communication cost becomes the bottleneck of the entire system.

To address this problem, a *tradeoff* between *efficiency* and estimation *quality* is needed. Instead of using *Exact MLE*, which incurs substantial *communication cost*, it is preferable to utilize an *accurate approximate* of *MLE* with lower *communication cost*. By leveraging the property of independence among the parameters and appropriately allocating the available error budget to different and independent parameters (known as *slack allocation problem*), that firstly provides the error of *joint probability distribution* remains within acceptable bounds and secondly the *communication cost* is as little as possible, then we can provide an *accurate approximate* of *MLE* with minimal communication cost.

Using both the first approach which involves a collection of *approximate distributed counters* treating each counter individually, and the proposed approach utilizing the method of *Functional Geometric Protocol (FGM)*, we can achieve our objective. This involves the utilization of the *BASELINE, UNIFORM, NON_UNIFORM* [18] algorithms, which define the appropriate way to divide the available *error budget* and are discussed and analyzed below.

Given a *Bayesian Network structure* $\mathcal{G}(\mathcal{X}, \mathcal{E})$, the probability $\hat{P}(\mathcal{X})$ represents the *EXACTMLE* of the *joint probability distribution* of the network $\mathcal{G}$. Furthermore, given an *approximation factor* ε, where $\varepsilon \in [0,1]$, an *ε-approximation* of *MLE* is the *joint probability distribution* $\tilde{P}(\mathcal{X})$ for each $\boldsymbol{x} \in Val(\mathcal{X})$, if and only if the following equation holds:

$$\varepsilon - approximation\ of\ MLE$$

$$e^{-\varepsilon} \leq \frac{\tilde{P}(\boldsymbol{x})}{\hat{P}(\boldsymbol{x})} \leq e^{\varepsilon}$$

Similarly, given an additional parameter *δ,* where $\delta \in [0,1]$, then $\tilde{P}(\mathcal{X})$ refers to an *(ε,δ)-approximation*, if and only if the following equation holds:

$$(\varepsilon, \delta) - approximation\ of\ MLE$$

$$e^{-\varepsilon} \leq \frac{\tilde{P}(\boldsymbol{x})}{\hat{P}(\boldsymbol{x})} \leq e^{\varepsilon}\ with\ probability\ 1-\delta$$

Our objective is to maintain an *(ε,δ)-approximation* of *MLE*, at any given time. Given a *Bayesian Network structure* $\mathcal{G}(\mathcal{X}, \mathcal{E})$, the *EXACTMLE* of *joint probability distribution* $\tilde{P}(\mathcal{X})$ (*See Chapter 2.5*) can be defined as follows:

$$\tilde{P}(\mathcal{X}) = \prod_{i=1}^{n} \theta_{X_i} = \prod_{i=1}^{n} \frac{C_i\left(x_i, x_i^{par}\right)}{C_i\left(x_i^{par}\right)}$$

Where the $C_i\left(x_i, x_i^{par}\right)$ represents the number of *events* $(X_i = x_i, Par(X_i) = x_i^{par})$, and $C_i(x_i^{par})$ represents the number of *events* $(Par(X_i) = x_i^{par})$.

Assuming $A_i\left(x_i, x_i^{par}\right)$, $A_i\left(x_i^{par}\right)$ represents the *approximate version of the distributed counters* $C_i\left(x_i, x_i^{par}\right)$, $C_i(x_i^{par})$*,* respectively, for any *input vector* $\boldsymbol{x} = [x_1, \dots, x_n]$, and given an *approximation factor ε*, we want the following statement to hold true at any time:

$$e^{-\varepsilon} \leq \frac{\tilde{P}(\boldsymbol{x})}{\hat{P}(\boldsymbol{x})} = \prod_{i=1}^{n} \left(\frac{A_i\left(x_i, x_i^{par}\right)}{C_i\left(x_i, x_i^{par}\right)} \cdot \frac{C_i\left(x_i^{par}\right)}{A_i\left(x_i^{par}\right)} \right) \leq e^{\varepsilon}$$

Definition of Classification problem

Beyond the scope of the *Bayesian Networks*, we focus on a special case of them, namely *Naïve Bayes Classifier*. Given the collection of the *approximate distributed counters*, we need to redefine the *Classification* problem. Assuming a *Naïve Bayes Classifier* $\mathcal{G}(\mathcal{X}, \mathcal{E})$ and an *approximation factor ε*, for any *input vector* $\boldsymbol{x}$ (or known as *evidence*), the *class label* c^i resolve the *Bayesian classification* problem with *ε error*, if:

$$\hat{P}\left(C = c^i \middle| \boldsymbol{x}\right) \geq (1-\varepsilon) \cdot max_{c^i \in Val(C)} \hat{P}\left(C = c^i \middle| \boldsymbol{x}\right)$$

We choose the *class label* c^i that the *conditional probability* is close to the highest probability. Given an *(ε,δ)-approximation* of the *MLE* of *joint probability distribution* of a *Naïve Bayes Classifier*, the *class label* c^i resolves the *Bayesian Classification* problem with *ε error* [18, Lemma 13].

Consequently, at any time we want an *(ε,δ)-approximation* of *the MLE* of the *joint probability distribution* of *Bayesian Network* over the *distributed continuous model*, while using the minimal communication cost (*communication efficient*).

3.2 The general approach

This section describes the general approach used both the first approach (*See Chapter 4.1*) and second approach (*See Chapter 4.2*). The general approach can be summarized in the following four algorithms.

The first algorithm is the *INITIALIZATION* (Algorithm 1) algorithm. This algorithm is used by the sites, including the Coordinator. It is executed first and is responsible for *initializing* all the *approximated distributed counters* required from each *CPD* of the *Bayesian Network*, which are necessary for estimating the *MLE* of the *joint probability distribution* of the network. The first parameter refers to the *Bayesian Network* to be used, the second parameter refers to the type of the *approximate distributed counter*(*type_counter*) that will be used regarding the first approach while refers to the type of the *frequency vector* that will be used considering the second approach. The last parameter, *schema_error*, specifies the algorithm to be used and defines the appropriate value of the *approximation factor ε* for each of the available *counters*, choosing from the *BASELINE, UNIFORM* and *NON_UNIFORM* algorithms.

Algorithm 1: *INITIALIZATION*

Input:

type_counter: corresponds to one of the four available algorithms (RANDOMIZED, DETERMINISTIC, EXACT, CONITNUOUS)
schema_error: corresponds to one of the three available algorithms (BASELINE, UNIFORM, NON_UNIFORM)
Bayesian Network Structure $\mathcal{G}(\mathcal{X}, \mathcal{E})$ *, where* $\mathcal{X} = \{X_1, .., X_n\}$ *are the nodes of Bayesian Network*

1. **Foreach** X_i **from** $\mathcal{X}$
2. *// Generate all the distributed counters from node* X_i *based on type of counter*
3. *GENERATE_DIST_COUNTERS* (*type_counter*, X_i)
4.
5. *// Initialize the distributed counters based on error schema*
6. **Foreach** $A_i\left(x_i, x_i^{par}\right)$ **from** $X_i \cap Par(X_i)$
7. *INITIALIZE_DIST_COUNTER* ($A_i\left(x_i, x_i^{par}\right)$, *schema_error*)
8. **Foreach** $A_i\left(x_i^{par}\right)$ **from** $Par(X_i)$
9. *INITIALIZE_DIST_COUNTER* ($A_i\left(x_i^{par}\right)$, *schema_error*)
10. **End**

The second algorithm is responsible for managing the events and is called the *UPDATE* algorithm *(Algorithm 2)*. It is exclusively used by the sites to handle the received *data stream* of *training instances*. Its objective is to manage the corresponding *input vector* while providing the necessary increments to the *distributed counters*.

Algorithm 2: UPDATE

Input: $\boldsymbol{x} = < x_1, \dots, x_n >$ *is a full particle of nodes from Bayesian Network*

1. **Foreach** x_i **from** $\boldsymbol{x}$
2.
3. **If**(X_i *has parents*) **then**
4. *// Get the counters correspond to the parents' nodes of* X_i
5. *GET_COUNTER* (x_i^{par})
6. *INCREMENT_DIST_COUNTER* (x_i^{par})
7. **End**
8.
9. *// Get the counters correspond to the* X_i *node*
10. *GET_COUNTER* (x_i)
11.
12. *// Increment the distributed counters for the* X_i *node*
13. *INCREMENT_DIST_COUNTER* (x_i)

The algorithm responsible for handling the messages between the *sites* and the *Coordinator* and vice versa is called the *HANDLE_MESSAGE algorithm (Algorithm 3)*. It is used by both sides, the *sites* while receiving messages from the *Coordinator* and the *Coordinator* while receiving messages from the *sites* (*two-way communication channel*). Depending on the type of messages (*type_message*), it performs the corresponding action. The action usually involves either sending a message (such as *broadcasting* a value from the Coordinator to sites) or *updating* the value of a variable. Both the type of message and the subsequent sequence of actions are defined by the corresponding approach.

Algorithm 3: *HANDLE_MESSAGE*

Input:
type_message: corresponds to one of the available types of messages
message: corresponds to a message

1. *// Handle the message based on the type of it*
2. *HANDLE_MESSAGE* (*type_message*)
3. *UPDATE_COUNTERS ()*

Finally, the algorithm responsible for estimating *probability queries* is the *ESTIMATE algorithm (Algorithm 4)*, which is used exclusively by the Coordinator. When receiving *queries*, the Coordinator only needs to estimate the value of the *joint probability distribution* of the query.

Algorithm 4: *ESTIMATE*

Input: $\boldsymbol{x} = < x_1, \dots, x_n >$ *is a full particle of nodes from Bayesian Network*
Output: *Return the estimated probability from event*

1. **Foreach** x_i **from** $\boldsymbol{x}$
2. *// Get the counters for the parameter* θ_{X_i}
3. *GET_COUNTER*$\left(x_i, x_i^{par}\right)$
4. *GET_COUNTER*$\left(x_i^{par}\right)$
5.
6. *// Estimate the parameter for the specific* X_i
7. *ESTIMATE_PAR* **(**θ_{X_i}**)**
8. *UPDATE_EST_PROBABILITY* (θ_{X_i})
9. **End**
10. **Return** *EST_PROBABILITY*

Chapter 4:

Problem analysis

4.1 A first approach

The first approach to the problem is the maintenance of a collection of *approximate distributed counters*, treating each counter *individually*. We need to define the appropriate value of the *approximation factor ε* among the given *approximate counter*s, aiming to achieve an ε-*approximation* of the *MLE* of *joint probability distribution*, while using the minimum communication cost.

This can be achieved using the three algorithms *BASELINE, UNIFORM, NON_UNIFORM* [18], which define the way to divide the *approximation factor ε* among the *approximate distributed counters*. The implemented type of *approximate distributed counter* are the *RANDOMIZED counter* and the *DETERMINISTIC counter*, which are discussed and analyzed below.

EXACT counters

The first solution to provide a *continuous maintenance* of the *MLE*, which also requires the *continuous maintenance* of corresponding *counters*, is the *EXACT counters* (*Algorithm 1,2*). This way, the Coordinator maintains the *EXACTMLE* of the *joint probability distribution* at any time, but the communication cost quickly becomes the *bottleneck* of the entire system.

Algorithm 1: *Exact Counter* (*EXACT*) - *Worker*

Input: $\boldsymbol{x} = < x_1, \dots, x_n >$ *is a full particle of nodes from Bayesian Network*

```
1.  If (received = `INPUT`)
2.      Foreach x_i from x
3.          If( X_i has parents) then
4.              // Get the counters correspond to the parents' nodes of X_i
5.              GET_COUNTER (x_i^par)
6.              INCREMENT_ COUNTER (x_i^par)
7.              SEND_MESSAGE (x_i^par, `INCREMENT`)
8.          End
9.
10.         GET_COUNTER (x_i)
11.         INCREMENT_COUNTER (x_i)
12.         SEND_MESSAGE (x_i , `INCREMENT`)
13.     End
14. End
```

The idea behind the *EXACT counter* is that for each increment on the counter, the site also sends a message to the Coordinator (*Algorithm 1*) to update the value of the counter *(Algorithm 2*). However, this approach leads to a loss of the benefit of the distributed environment, as the communication cost quickly becomes substantial.

Given a Bayesian Network Structure $\mathcal{G}(\mathcal{X}, \mathcal{E})$, which consists of n nodes, using *EXACT counters,* we can prove that total communication cost required to continuously maintain the MLE of the του $\mathcal{G}$ is equal to $O(m \cdot n)$, where m is the number of *observations*. This corresponds to sending m messages of size n. It is evident that the *communication cost* increases linearly with the number of the *observations* in *data stream*. Therefore, it is necessary to find a way to avoid this linear dependence on the number of the *observations*.

Algorithm 2: Exact Counter (*EXACT*) - *Coordinator*

Input:

type_message: corresponds to one of the available types of messages
message: corresponds to a message

1. **If** (*type_message = `INCREMENT`*)
2. *GET_COUNTER_MSG (message)*
3. *UPDATE_COUNTER*

4.1.1 Approximated Distributed counters

In order to mitigate the linear dependency on the number of *training instances*, it is necessary to maintain an *(ε,δ)-approximation* of the *MLE* of the Bayesian Network $\mathcal{G}(\mathcal{X}, \mathcal{E})$. To accomplish this, appropriate *approximate distributed counters* are employed, which accompanied with the minimal *communication cost.* The implemented types of counters are the *RANDOMIZED* and the *DETERMINISTIC* counters, which are discussed in detail. The *Table 2* provides the space and communication complexity of each counter, while the *Table 1* presents the notations used for both on *RANDOMIZED* and *DETERMINISTIC counters*.

Count-Tracking problem

Each *site* S_i, where $i \in \{1, \dots, k\}$, maintains a *local counter* n_i, initially set to zero. As data is received, each *site* S_i increments its *local counter* $n_i(t)$, where $n_i(t)$ denotes the value of the n_i at the time t. Additionally, assuming each *update* for each site follows the format $\langle i, c \rangle$, each site S_i updates the *local counter* $n_i(t)$ by c (*Cash register model*), where $c > 0$ and specifically $c = 1$, allowing only *insertions*. As a result, each *local counter* n_i represents a *linear, monotonic increasing* functions and accordingly the total counter.

Our objective is for the Coordinator to maintain an *(ε,δ)-approximation* of the *total counter* $n(t) = \sum_{i=1}^{k} n_i(t)$ at any given time, where $0 \leq \varepsilon, \delta \leq 1$.This can be defined as follows:

$$(1 - \varepsilon) \cdot n(t) \leq \hat{n}(t) \leq (1 + \varepsilon) \cdot n(t) \; with \; probability \; 1 - \delta$$

While also ensuring the minimal *communication cost*, it has been mentioned in [19], the minimum required *communication cost* to maintain such a counter is equal to $O(k/\varepsilon \cdot logN)$, where N denotes the final value of the total counter n and k denotes the number of *sites.*

Notations	*Description*
$\boldsymbol{n_i}$	*Local counter of* S_i
$\boldsymbol{n}$	*Total counter*
$\boldsymbol{\bar{n}_i}$	*Last sent value of* S_i *to Coordinator*
$\boldsymbol{p}$	*Probability* $p \in [0,1)$ *. Initially,* $p = 1$
$\boldsymbol{\hat{n}_i}$	*The estimator of* n_i
$\boldsymbol{\hat{n}}$	*The estimation over the sites (sum of* $\hat{n}_i$*)*
$\boldsymbol{\bar{n}}$	*The last broadcast value from the Coordinator*
$\boldsymbol{\lfloor x \rfloor_2}$	*The next power of 2 less than* x
$\boldsymbol{n_i'}$	*The last update of the* n_i *on Coordinator*
$\boldsymbol{n'}$	*The sum of* n_i'
$\boldsymbol{N}$	*The final value of the counter*
$\boldsymbol{\varepsilon}$	*Approximation factor*
$\boldsymbol{\delta}$	*Delta, refers to randomized counters*
$\boldsymbol{k}$	*The number of sites*

Table 1: Notation summary

4.1.1.1 Randomized Counters

The *RANDOMIZED counter* is the first implemented and discussed in detail below. It has been proven to have the *lower communication cost* in the *count-tracking* problem, as stated in [19]. The communication cost is $O(\sqrt{k}/\varepsilon \cdot logN)$, and as the name suggests, it utilizes a *randomized* algorithm. By employing *randomization*, the communication cost is reduced by $\sqrt{k}$ compared to any *deterministic* method.

By utilizing the *randomization* method, we can continuously maintain an *unbiased estimator* for n_i, such that $E[\hat{n}_i] = n_i$, while the *variance* of *estimator* is $Var[\hat{n}_i] = (\varepsilon n)^2/k$.

Given the *variance* of each *estimator* is $(\varepsilon n)^2/k$, we can prove the total variance is $(\varepsilon n)^2$. By applying the property of the *independence of* $n_i's$, the following holds:

$$Var[\hat{n}] = Var\left[\sum_{i=1}^{k} \hat{n}_i\right] = \sum_{i=1}^{k} Var[\hat{n}_i] = k \cdot Var[\hat{n}_i] = (\varepsilon n)^2$$

The proceeding statement is sufficient to produce an *estimator* $\hat{n}$ with an error εn and a probability $1 - \delta$, by utilizing the *Chebyshev's inequality*.

Therefore, given the *variance* of each *unbiased estimator* $\hat{n}_i$ is $(\varepsilon n)^2/k$, it is sufficient to support an *error* equal to $\varepsilon n/\sqrt{k}$, compared to $\varepsilon n/k$ which is required for any *deterministic* method. As a result, we achieve an improvement of $\sqrt{k}$. This is demonstrated by utilizing Chebyshev's *inequality*, where the following statement must hold:

$$\frac{Var[\hat{n}_i]}{(error)^2} \leq 1 \Rightarrow error \geq \varepsilon n/\sqrt{k}$$

Each *site* S_i sends the last value of the local counter n_i to the Coordinator with a probability p when receives an event that increments the *local counter* n_i. Regarding the estimation of the *local counter* n_i on Coordinator, the following applies:

$$\hat{n}_i = \begin{cases} \bar{n}_i - 1 - 1/p\,, if\ \ \bar{n}_i\ exists \\ 0\,, \qquad\qquad otherwise \end{cases}$$

Where $\bar{n}_i$ represents the *last update* on Coordinator for the *local counter* n_i, while the total estimation of the total count n is the sum of the corresponding $\hat{n}_i$ i.e., $\hat{n} = \sum_{i=1}^{k} \hat{n}_i$.

We can prove that the $\hat{n}_i$ is an *unbiased estimator* with *variance* $Var[\hat{n}_i] \leq 1/p^2$, considering the fact that the *total estimation* $\hat{n}$ is an *unbiased estimator* with *variance* $Var[\hat{n}] \leq k/p^2$. Setting the probability appropriately $p = \Theta(\sqrt{k}/\varepsilon n)$, is sufficient, then the variance of the total estimator is $Var[\hat{n}] = (\varepsilon n)^2$, which is sufficient to maintain an *estimator* $\hat{n}$ with *error* εn with probability $1 - \delta$ at any time. The proof discussed in detail on [19].

Considering that the n is not accessible from all sites at any time and $p = \Theta(\sqrt{k}/\varepsilon n)$, it is sufficient each *site* S_i has a *constant-factor approximation* of the n in each *round*. To do so, not only each *site* S_i sends an *increment* message to the Coordination with probability p(*INCREMENT*), but also each site S_i sends an additional message whenever the *local counter* n_i doubles (*DOUBLES*). When the Coordinator receives the *DOUBLES* message, it then updates the variable $n' = \sum_{i=1}^{k} n_i'$, where n_i' denotes the *last update* of *local counter* n_i on Coordinator. When n' doubles (more precisely, when changes by factor between 2 and 4), the Coordinator broadcasts the n' at all sites and then a new round begins. This way ensures that each site always has a *constant-factor approximation* of n in each *round*, which is used from sites to define the probability p. We assume $\bar{n}$ represents the last broadcast value of n'.

While $\bar{n} \leq \sqrt{k}/\varepsilon$ then we set $p = 1$. As a result, the first $O(\sqrt{k}/\varepsilon)$ elements will be sent to the Coordinator due to the probability $p = 1$. When $\bar{n} > \sqrt{k}/\varepsilon$, we set $p = 1/\lfloor \varepsilon\bar{n}/\sqrt{k} \rfloor_2$. While the $\bar{n}$ increased in each round, accordingly the probability decreased (more precisely, the probability sub-halved in each round).

At the beginning of each round the probability decreased, so we need to adapt the values of $\bar{n}_i$ on the Coordinator to ensure that the whole system runs with the new probability p. This can be achieved with the following manner: each *site* S_i decides with probability $p = 1/2$, if the $\bar{n}_i$ remains the same. If decide to change it, then each *site* S_i flips a *coin* with probability $1/p$ (with the new p) repeatedly. For each failed *coin flip* decreases, the $\bar{n}_i$ by 1 until a *successful coin flip* or $\bar{n}_i = 0$. At the end, each *site* S_i sends a message to the Coordinator with the new value of $\bar{n}_i$. The last step is necessary because of ensuring to prevent the *bias* will be generated on the estimation *estimator* $\hat{n}_i$ with the change of p. The whole process summarized in *Algorithms 3,4*.

Algorithm 3: *Randomized Counter (RC) - Worker*

Input: *epsilon, delta*
type_message: *corresponds to one of the available types of messages*

1. **If** (n_i *increment by one*)
2. *SEND_MESSAGE* (n_i,p,`*INCREMENT*`)
3. *UPDATE* ($\bar{n}_i$)
4. **If** (n_i *doubles*)
5. *SEND_MESSAGE* (n_i', p=1, `*DOUBLES*`)
6. *UPDATE* ($\bar{n}_i$)
7. **If** (*type_message = `UPDATE`*)
8. *// New round begins*
9. *UPDATE* ($\bar{n}$)
10. **If** ($\bar{n} < \sqrt{k}/\varepsilon$) *Set* p=1
11. **Else**
12. *Set* $p = 1/\lfloor \varepsilon\bar{n}/\sqrt{k} \rfloor_2$
13. **If** (p *halved*)
14. *// Adjust the* n_i
15. *SEND_MESSAGE* (n_i,$p = \frac{1}{2}$,`*INCREMENT*`)
16. **If** (*loose flip*)
17. *While (Flip until succeed)*
18. *SEND_MESSAGE* **(**n_i*-num_of_failures*,$p = 1$,`*INCREMENT*`**)**
19. *UPDATE* ($\bar{n}_i$)

Regarding the communication cost of the *RANDOMIZED counter*, the cost can be analyzed as follows. In each round, the communication cost consists of the communication cost of the broadcast of the value $\bar{n}$ from the Coordinator (*upstream communication cost*), resulting in a cost of $O(k)$. Additionally, the *communication cost* required to send the *sites* on the Coordinator*(downstream communication cost*) , which equals to $O(np)$. Combining these costs, the communication cost per round is $O(k + np) = O(k + \sqrt{k}/\varepsilon) = O(\sqrt{k}/\varepsilon)$. Considering that there are $logN$ rounds, the total communication cost is $O(\sqrt{k}/\varepsilon \cdot logN)$.

Algorithm 4: *Randomized Counter (RC) - Coordinator*

Input: *type_message corresponds to one of the available types of messages*

1. **If** (*type_message = `INCREMENT`*)
2. *UPDATE* ($\bar{n}_i$)
3. *CALCULATE* ($\hat{n}_i$)
4. **If** (*type_message = `DOUBLES`*)
5. *UPDATE* (n_i')
6. *UPDATE* (n')
7. **If (**n'*doubles***)** *// Change by factor between 2 and 4*
8. *// New round begins*
9. *Set* $\bar{n} = n'$
10. *BROADCAST*($\bar{n}$,`*UPDATE*`)

4.1.1.2 Deterministic Counters

The second counter implemented and discussed in detail below, is the *DETERMINISTIC counter*. Similar approaches have been used in [17] and [20]. As the name suggests, we focus on *deterministic* methods while ensuring an *ε-approximation* of the *counter*. At any time t the following statement holds:

$$(1-\varepsilon)\cdot n(t) \leq \hat{n}(t) \leq (1+\varepsilon)\cdot n(t)$$

The algorithm operates as follows. Given a *ε-approximation* of the *counter*, the *maximum error* that can be supported on Coordinator at any time is εn. Considering the independent of the k sites, we can easily prove that the *maximum error* at each site, while ensuring an *ε-approximation*, equals $\varepsilon n/k$.

The whole process summarized in *Algorithms 4,5*. Since each site cannot know the exact value of n at any time, although it is sufficient for each site to maintain a constant *factor approximation* of the n through $\bar{\boldsymbol{n}}$ at each *round*, where $\bar{\boldsymbol{n}}$ denotes the last broadcast value of the Coordinator. Initially, we set $\bar{\boldsymbol{n}} = 0$. Now, each *site* S_i sends a message on the Coordinator whenever the $n_i > \varepsilon\bar{n}/k$(*INCREMENT*). When the Coordinator receives k such messages, indicating that the maximum error has been reached, it broadcasts a message to all sites in order to receive the *local counters* from each site *(DRIFT)*. Upon receiving a *DRIFT* message, the Coordinator updates the value of $\bar{\boldsymbol{n}}$**.** When k messages have been received (one from each site), the Coordinator broadcasts an *UPDATE* message to all *sites* with the new value of the $\bar{\boldsymbol{n}}$**.** marking the beginning of a new round. Finally, it can be observed that the first $O(k/\varepsilon)$ elements will be sent to the Coordinator, as $\varepsilon\bar{n}/k \leq 1$.

Algorithm 4: *Deterministic Counter (DC) - Worker*

Input: *epsilon*
type_message corresponds to one of the available types of messages

```
1.  If (type_message = `INPUT`)
2.      Increment n_i // local drift
3.  If (n_i > εn̄/k )
4.      SEND_MESSAGE (n_i,p = 1,`INCREMENT`)
5.      Reset the local counter n_i // local drift
6.
7.  If (type_message = `DRIFT`)
8.      SEND_MESSAGE (n_i,p = 1,`DRIFT`)
9.      Reset the local counter n_i // local drift
10.
11. If (type_message = `UPDATE`)
12.     // New round begins
13.     UPDATE (n̄)
```

The communication cost of the *DETERMINISTIC counter* can be analyzed as follows. In each round, the communication cost consists of the communication cost of the broadcast of both the value $\bar{n}$ and a *DRIFT* message from the Coordinator (*upstream communication cost*), resulting in a cost of $O(k)$. Additionally, the communication cost required from the sites to the Coordinator *(downstream communication cost)* resulting in a cost of $O(k + k/\varepsilon)$. Combining these costs, the communication cost per round is $O(k + k/\varepsilon) = O(k/\varepsilon)$. The

Coordinator broadcasts the updated value of $\bar{n}$ each time it increases by a factor of $1 + \sum_{i=1}^{k} \varepsilon/k = 1 + \varepsilon$. This implies that the number of rounds is bounded by $O(\log_{1+\varepsilon} N)$. Therefore, the total communication cost is $O(k/\varepsilon \cdot logN)$.

***Algorithm 5**: Deterministic Counter (DC) – Coordinator*

Input: *type_message corresponds to one of the available types of messages*

```
1.  If (type_message = `INCREMENT`)
2.      UPDATE (n̄_i)
3.      CALCULATE (n̂_i)
4.      If (num_messages_inc = k)
5.          BROADCAST(`DRIFT`)
6.
7.  If (type_message = `DRIFT`)
8.      UPDATE (n̄)
9.      If (num_messages_drift = k)
10.       // New round begins
11.       BROADCAST(n̄,`UPDATE`)
```

Count-Tracking probelm	*Space (per site)*	*Communication cost*
EXACT	$O(1)$	$O(N)$
RANDOMIZED	$O(logN)$	$O(\sqrt{k}/\varepsilon \cdot logN)$
DETERMINISTIC	$O(logN)$	$O(k/\varepsilon \cdot logN)$

Table 2: Space and communication complexity for each counter

4.1.1.3 Comparison between RANDOMIZED and DETERMINISTIC

The only difference between the counters is the dependence on the number of sites k, specifically the *RANDOMIZED counter* has an improvement by factor of $\sqrt{k}$. The latter confirmed through experimental evaluation, where the change of the communication cost of the *RANDOMIZED counter* was smaller compared to the *DETERMINISTIC counter* when varying the number of sites k.

The reasons for implementing the *DETERMINISTIC counter* are twofold. Firstly, it relates to the completeness of the problem. We want to address the problem by considering how each *approximate counter* can be adapted. Secondly, we observe that when the number of sites is small, the *DETERMINISTIC counter* exhibits a *lower communication cost*.

In the *DETERMINISTIC counter*, the quantity $\varepsilon \cdot \bar{n}_{DC}/k$ defines when a message is sent, whereas for the *RANDOMIZED counter*, it is the probability $p = 1/\lfloor \varepsilon \cdot \bar{n}_{RC}/\sqrt{k} \rfloor_2$. The values of $\bar{n}_{DC}$ and $\bar{n}_{RC}$ determine the number of messages will be sent, considering the values of the ε, k constant.

In most cases, we observe that $\bar{n}_{RC} < \bar{n}_{DC}$, indicating that the number of messages required for the *DETERMINISTIC counter* to reach the value $\bar{n}_{DC}$ is bigger. Assuming the *DETERMINISTIC counter* sends a message with probability p', which is determined by the quantity $\varepsilon \cdot \bar{n}_{DC}/k$. Despite $\bar{n}_{RC} < \bar{n}_{DC}$ resulting in a larger number of messages to achieve the probability p', henceforth the $p' > p$. Although the *DETERMINISTIC counter* sends more messages to reach the value of $\bar{n}_{DC}$, it gains an advantage due to $p' > p$.

When the difference between $\bar{n}_{RC}$ and $\bar{n}_{DC}$ remains small, which is primarily defined by the number of *sites* k, the advantage gained from the DETERMINISTIC counter is larger. With smaller number of sites, the difference between them becomes less significant, and the advantage of the *DETERMINISTC counter* is amplified. However, when the difference between $\bar{n}_{RC}$ and $\bar{n}_{DC}$ is substantial, the advantage of the *DETERMINISTC counter* diminishes. This is because the number of messages required to reach the value of $\bar{n}_{DC}$ is significantly larger than the number of messages to reach the value $\bar{n}_{RC}$, reducing the impact of the probability p'. This occurs when $\bar{n}_{DC} \gg \bar{n}_{RC}$.

Based on the experimental evaluation, it is more preferable to use *DETERMINISTC counter* when the number of sites is small, while the *RANDOMIZED counter* is more suitable when the number of sites is large.

As shown in *Figure 12*, we measure the values of $\bar{n}_{RC}$ and $\bar{n}_{DC}(y - axis)$ while varying the number of *sites* k, assuming $\varepsilon = 4 \times 10^{-4}, \delta = 0.25$ and $k \in [2,30]$. As the number of sites increases, the difference of values $\bar{n}_{RC}$ and $\bar{n}_{DC}$ also becomes significantly larger.

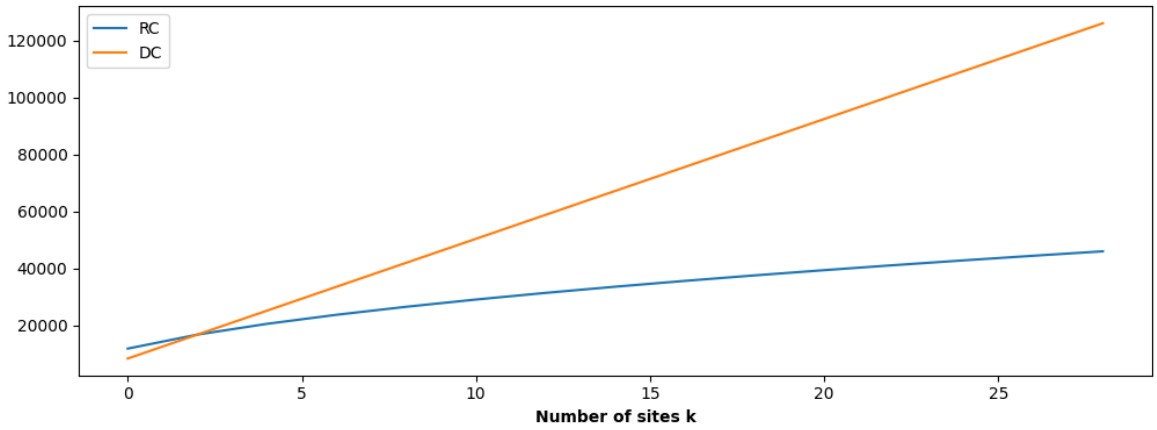


Figure 12: $\bar{n}_{RC}$ and $\bar{n}_{DC}$ varying the number of sites k

4.1.2 Analysis of BASELINE, UNIFORM and NON_UNIFORM

Apart from the general approach and the previously discussed *approximated distributed counters*, the remaining analysis focuses on how to allocate the available error budget among the approximate *distributed counters* $A_i(x_i, x_i^{par})$, $A_i(x_i^{par})$, while ensuring an *(ε,δ)-approximation* of *the MLE* at any time.

This section introduces and examines the *BASELINE, UNIFORM, NON_UNIFORM* algorithms, which provide the way to divide the available error budget.

The analysis includes the *RANDOMIZED counter*. The *Table 3* presents the results each one of algorithm. In the case of the *DETERMINISTIC counter,* the difference lies in the parameters δ and k. Specifically, the *DETERMINISTIC counter* exhibits a linear dependency on the number of sites k, while it does not depend on δ.

Given a Bayesian Network Structure $\mathcal{G}(\mathcal{X}, \mathcal{E})$, where the number of nodes denoted as $\mathcal{X} = \{X_1, \dots, X_n\}$, which constitutes a *Bayesian Network* with n nodes. Additionally, J_i represents the domain cardinality of the X_i node, denoted as $J_i = |Val(X_i)|$ for each $i \in \{1, \dots, n\}$, while the K_i represents the domain *cardinality* of *parents* nodes of X_i , denoted as $K_i = |Val(Par(X_i))|$ for each $i \in \{1, \dots, n\}$. Finally, the k denotes the number of *sites*.

Additionally, we assume $J = max_{i=1}^{n} J_i$ denotes the node with the largest set of values in the network, $d = max_{i=1}^{n} |Par(X_i)|$ denotes the maximum number of parents node for any variable in the network and the parameters ε, δ within the range of $0 \leq \varepsilon, \delta \leq 1$.

BASELINE

The *BASELINE* algorithm is the first algorithm introduced. The *approximation factor* for each *approximate distributed counter* $A_i(x_i, x_i^{par})$, $A_i(x_i^{par})$, is assigned to $\frac{\varepsilon}{3n}$. The *BASELINE* algorithm ensures an *(ε,δ)-approximation* of *MLE* of the *joint probability distribution* of the network $\mathcal{G}$ at any time. The proof discussed in detail in [18, Section IV-C]. The error budget is divided uniformly among the counters.

The total communication cost given *m training instances*, is:

$$O\left(\frac{n^2 \cdot J^{d+1}\sqrt{k}}{\varepsilon} \cdot \log\frac{1}{\delta} \cdot \log \mathrm{m}\right)$$

In this case, by replacing the value of the approximation factor ε, the *communication cost* of each *approximate distributed counter* is $O(\frac{n \cdot \sqrt{k}}{\varepsilon} \cdot \log\frac{1}{\delta} \cdot \log \mathrm{m})$ messages. Additionally, for each $i \in \{1, \dots, n\}$, there are at most J^{d+1} *counters* $A_i(x_i, x_i^{par})$ and J^d *counters* $A_i(x_i^{par})$, for each $x_i \in Val(X_i)$ and $x_i^{par} \in Val(Par(X_i))$. Combing them, the total communication cost is $O(\frac{n^2 \cdot J^{d+1}\sqrt{k}}{\varepsilon} \cdot \log\frac{1}{\delta} \cdot \log \mathrm{m})$ messages. By using the *BASELINE* algorithm, we manage to avoid the linear dependency on the number of *training instances m*, as the dependency is logarithmic.

UNIFORM

A different approach to the problem leads to the *UNIFORM* algorithm. The *approximation factor* for each *approximate distributed counter* $A_i(x_i, x_i^{par})$, $A_i(x_i^{par})$, is $\frac{\varepsilon}{16\sqrt{n}}$. By employing the *UNIFORM* algorithm, we again ensure an *(ε,δ)-approximation* of the *MLE* of *joint probability distribution* of the network $\mathcal{G}$. The proof described in detail in [18, Section IV-C]. The error budget is uniformly divided among the counters.

The total communication cost given *m training instances*, is:

$$O\left(\frac{n^{3/2} \cdot J^{d+1}\sqrt{k}}{\varepsilon} \cdot \log\frac{1}{\delta} \cdot \log \mathrm{m}\right)$$

The *communication cost* for each *approximate distributed counter* is $O(\frac{\sqrt{nk}}{\varepsilon} \cdot \log\frac{1}{\delta} \cdot \log \mathrm{m})$ messages, given the *approximation factor* is $\frac{\varepsilon}{16\sqrt{n}}$. For each $i \in \{1, \dots, n\}$, there are at most J^{d+1} *counters* $A_i(x_i, x_i^{par})$ and J^d *counters* $A_i(x_i^{par})$, for each $x_i \in Val(X_i)$ and $x_i^{par} \in Val(Par(X_i))$. Combing them, the total communication cost is $O(\frac{n^{3/2} \cdot J^{d+1}\sqrt{k}}{\varepsilon} \cdot \log\frac{1}{\delta} \cdot \log \mathrm{m})$ messages. The dependency on the number of *training instances* is logarithmic and we achieve an improvement of $\sqrt{n}$ on the communication cost compared to the *BASELINE* algorithm.

NON_UNIFORM

The two previously algorithms uniformly divide the available among the *counters*. None of them consider elements related to the structure of a node, such as the *domain cardinality* and the number of parents nodes. Now, the difference is the *NON_UNIFORM* includes such elements. The available *error budget* is no longer uniformly divided among the counters, but the *approximation factor* for each *approximate distributed counter* $A_i(x_i, x_i^{par})$, $A_i(x_i^{par})$ is related to both $J_i = |Val(X_i)|$ and $K_i = |\, Val(Par(X_i))\,|$.

In this case, there is partition between the counters. For each *approximate distributed counter* $A_i(x_i, x_i^{par})$, the *approximation factor* is defined with the following manner:

$$v_i = \frac{(J_i K_i)^{\frac{1}{3}} \cdot \varepsilon}{16a}, where\ \alpha = \left(\sum_{i=1}^{n} (J_i K_i)^{\frac{2}{3}}\right)^{1/2}$$

While for each *approximate distributed counter* $A_i(x_i^{par})$, the *approximation factor* is defined with the following manner:

$$\mu_i = \frac{(K_i)^{\frac{1}{3}} \cdot \varepsilon}{16\beta}, where\ \beta = \left(\sum_{i=1}^{n} (K_i)^{\frac{2}{3}}\right)^{\frac{1}{2}}$$

By applying the values of v_i, μ_i, we ensure an *(ε,δ)-approximation* of the *MLE* of the *joint probability distribution* of the network $\mathcal{G}$. The proof is discussed in detail in [18, Section IV-C].

In this case, the *approximation factor* of each *approximate distributed counter* $A_i(x_i, x_i^{par})$ depends on both J_i and K_i. This means that the error is proportional to both the set of values of X_i and the domain cardinality of parents nodes of X_i. On the other hand, the *approximation*

factor of each *approximate distributed counter* $A_i(x_i^{par})$ solely depends on K_i, meaning that the error is only proportional to the domain cardinality of parents nodes of X_i.

The total communication cost given *m training instances* is:

$$O(\Gamma \cdot \frac{\sqrt{k}}{\varepsilon} \cdot \log \frac{1}{\delta} \cdot \log \mathrm{m}) \text{, όπου } \Gamma = \left(\sum_{i=1}^{n} (J_i K_i)^{\frac{2}{3}}\right)^{3/2} + \left(\sum_{i=1}^{n} (K_i)^{\frac{2}{3}}\right)^{3/2}$$

The *communication cost* of each *approximate distributed counter* $A_i(x_i, x_i^{par})$ is $O(\frac{\sqrt{k}}{v_i} \cdot \log\frac{1}{\delta} \cdot \log \mathrm{m})$ messages. For each node X_i, the counters $A_i(x_i, x_i^{par})$ are defined by both J_i and K_i , so there are at most $J_i \cdot K_i$ *counters*. Combining them, the total communication cost for all counters $A_i(x_i, x_i^{par})$ for each node X_i is:

$$M_1 = \sum_{i=1}^{n} \frac{J_i \cdot K_i \cdot \sqrt{k}}{v_i} \cdot \log\frac{1}{\delta} \cdot \log \mathrm{m}$$

Replacing the v_i , we can redefine the M_1 with the following manner:

$$M_1 = \left(\sum_{i=1}^{n} (J_i \cdot K_i)^{2/3}\right)^{3/2} \cdot \frac{\sqrt{k}}{\varepsilon} \cdot \log \frac{1}{\delta} \cdot \log \mathrm{m}$$

Accordingly, for each node X_i there are at most K_i *counters* $A_i(x_i^{par})$, for which the commination cost is $O(\frac{\sqrt{k}}{\mu_i} \cdot \log\frac{1}{\delta} \cdot \log \mathrm{m})$ messages. Combing them, the total communication cost for all the nodes is (replacing also the μ_i):

$$M_2 = \left(\sum_{i=1}^{n} K_i^{2/3}\right)^{3/2} \cdot \frac{\sqrt{k}}{\varepsilon} \cdot \log \frac{1}{\delta} \cdot \log \mathrm{m}$$

The total communication cost is $M_1 + M_2 = O(\Gamma \cdot \frac{\sqrt{k}}{\varepsilon} \cdot \log \frac{1}{\delta} \cdot \log \mathrm{m})$ messages. The linear dependency on the number of training instances also remains.

	Approximation Factor	*Communication Cost*
BASELINE $A_i(x_i, x_i^{par}), A_i(x_i^{par})$	$\frac{\varepsilon}{3n}$	$O\left(\frac{n^2 \cdot J^{d+1}\sqrt{k}}{\varepsilon} \cdot \log\frac{1}{\delta} \cdot \log \mathrm{m}\right)$
UNIFORM $A_i(x_i, x_i^{par}), A_i(x_i^{par})$	$\frac{\varepsilon}{16\sqrt{n}}$	$O\left(\frac{n^{3/2} \cdot J^{d+1}\sqrt{k}}{\varepsilon} \cdot \log\frac{1}{\delta} \cdot \log \mathrm{m}\right)$

NON_UNIFORM $A_i(x_i, x_i^{par})$	$v_i = \frac{(J_i K_i)^{\frac{1}{3}} \cdot \varepsilon}{16a}$ $\alpha = \left(\sum_{i=1}^{n} (J_i K_i)^{\frac{2}{3}} \right)^{1/2}$	$O(\Gamma \cdot \frac{\sqrt{k}}{\varepsilon} \cdot \log \frac{1}{\delta} \cdot \log m)$ $\Gamma = \left(\sum_{i=1}^{n} (J_i K_i)^{\frac{2}{3}} \right)^{3/2} + \left(\sum_{i=1}^{n} (K_i)^{\frac{2}{3}} \right)^{3/2}$
$A_i(x_i^{par})$	$\mu_i = \frac{(K_i)^{\frac{1}{3}} \cdot \varepsilon}{16\beta}$ $\beta = \left(\sum_{i=1}^{n} (K_i)^{\frac{2}{3}} \right)^{\frac{1}{2}}$	

Table 3: Approximation factor and Communication Cost for algorithms

4.1.2.1 Dummy Father

During the evaluation of the *NON_UNIFORM* algorithm, where the *approximation factor ε* is proportional to both J_i and K_i, we observed a problematic situation related to the *orphan nodes*, that is $Par(X_i) = \emptyset$. By applying the *NON_UNIFORM* algorithm, the *approximation factor ε* for each node is zero due to the $K_i's$ node is also zero. As a result, we need to maintain the *EXACT counter* for each $x_i \in Val(X_i)$ of such node. Consequently, when the number of orphan *nodes* is significant incurring quite high *communication cost* for maintaining them.

To prevent this problem, we suggest for each *orphan node* X_i, the insertion of a *dummy parent node (Dummy father -- Figure 13*). Specifically, for each such node, we set $K_i = 1$. With the insertion of the node managing to avoid the maintenance of the *EXACT counter* for each *counter* $A_i(x_i, x_i^{par})$ relating to *orphan node* X_i.

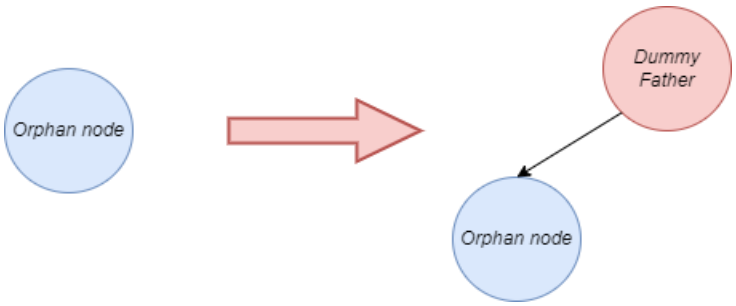


Figure 13: Dummy Father

Moreover, we achieve to increase the value of $= \left(\sum_{i=1}^{n} (J_i K_i)^{\frac{2}{3}} \right)^{1/2}$, which leads to a slightly larger *approximation factor* for the rest of the counters. This also leads to slightly *lower communication cost*. The primary advantage is the avoidance of maintaining the *EXACT counters*, which mainly contributes to the reduction of the communication cost is achieved.

The *NON_UNIFORM* algorithm is combined with *Dummy Father* method in experimental evaluation. We achieve to reduce the *communication cost* by a percentage is ranged in $0 - 50\%$ related to the *NON_UNIFORM* (*See. Chapter 6.3.5*). To mention that the reduction percentage is achieved, mainly depends on the topology of the *Bayesian Network*. The reduction percentage varied among the different *Bayesian Networks* because the reduction depends on whether the network contains orphan nodes or not.

4.1.2.2 Comparison among BASELINE, UNIFORM, NON_UNIFORM algorithms

Generally, comparing the previous algorithms, the following statement holds: *BASELINE < UNIFORM < NON_UNIFORM*.

The difference between *BASELINE* and *UNIFORM* directly reflected from the communication cost. In most cases, the *BASELINE* is better than *UNIFORM* as $\frac{\varepsilon}{16\sqrt{n}} > \frac{\varepsilon}{3n}$, so the *communication cost* for each *approximate distributed counter* of *UNIFORM* algorithm is lower. However, when the number of nodes $n \leq 29$, the *BASELINE* appears better than the *UNIFORM* as $\frac{\varepsilon}{16\sqrt{n}} < \frac{\varepsilon}{3n}$ and so the *communication cost* for each *approximate distributed counter* of *BASELINE* algorithm is lower. Both *BASELINE* and *UNIFORM* have the same dependency on the k, ε, δ and m parameters, although the only difference is on the n parameter, specifically the *UNIFORM* algorithm is better by a factor of $\sqrt{n}$.

Regarding the *UNIFORM* and *NON_UNIFORM* algorithm, the *NON_UNIFORM* is at least as good as the *UNIFORM* algorithm, given the *NON_UNIFORM* algorithm exploits more information of the network. Both *UNIFORM* and *NON_UNIFORM* have the same dependency on k, ε, δ and m parameters, the point which differs is on the parameters J_i, K_i, respectively. When the differences of J_i, K_i among nodes are significant, then the *NON_UNIFORM* prevails. However, when the values of J_i and K_i are quite close, the *UNIFORM* algorithm appears slightly better, which is confirmed on the experimental evaluation because the *Bayesian Networks* are used, do not appear significant differences on parameters J_i, K_i among the available nodes.

4.1.3 Communication cost of Naïve Bayes Classifier

This section presents the *communication cost* for each of the three algorithms for the *Naïve Bayes Classifiers*.

Given a *Naïve Bayes Classifier* $\mathcal{G}(\mathcal{X}, \mathcal{E})$, where the set of nodes is denoted as $\mathcal{X} = \{\mathrm{X}_1, \dots, X_n, C\}$. In this case, K_i for each node X_i represents the domain cardinality of the *class variable* C, where $K_i = J_c$ for each $X_i \in \mathcal{X} - \{C\}$. Additionally, the maximum number of parents nodes that exist in the graph is 1, so $d = 1$.

Based on *Table 3*, the total communication cost of *BASELINE* algorithm is:

$$BASELINE\ with\ \text{Naïve Bayes Classifier: } O\left(\frac{n^2 \cdot J^2\sqrt{k}}{\varepsilon} \cdot \log\frac{1}{\delta} \cdot \log \mathrm{m}\right)$$

For the *UNIFORM* algorithm the total communication cost is:

$$UNIFORM\ with \text{ Naïve Bayes Classifier: } O\left(\frac{n^{3/2}\cdot J^2\sqrt{k}}{\varepsilon}\cdot \log\frac{1}{\delta}\cdot \log \mathrm{m}\right)$$

Regarding the *NON_UNIFORM* algorithm, for each *approximate distributed counter* $A_i\left(x_i, x_i^{par}\right)$, the *approximation factor* is defined as follows:

$$v_i = \frac{(J_i)^{\frac{1}{3}}\cdot\varepsilon}{16a}\ , where\ \alpha = \left(\sum_{i=1}^{n}(J_i)^{\frac{2}{3}}\right)^{1/2}$$

While, for each *approximate distributed counter* $A_i\left(x_i^{par}\right)$, the *approximation factor* is defined as follows:

$$\mu_i = \frac{(K_i)^{\frac{1}{3}}\cdot\varepsilon}{16\beta} = \frac{\varepsilon}{16\sqrt{n}}\ , \text{όπου } \beta = \sqrt{n\cdot(J_c)^{2/3}}$$

The total communication cost is required of the *NON_UNIFORM* algorithm for the *Naïve Bayes Classifier*, given *m training instances,* is:

$$NON\_UNIFORM\ with \text{ Naïve Bayes Classifier}$$

$$O\left(J_c\cdot\left(\sum_{i=1}^{n}(J_i)^{\frac{2}{3}}\right)^{3/2}\cdot\frac{\sqrt{k}}{\varepsilon}\cdot\log\frac{1}{\delta}\cdot\log \mathrm{m}\right)$$

In all cases for all algorithms, we achieve logarithm dependency on the number of *training instances*.

4.2 A second approach

The second approach proposed for solving problem, while ensuring an (*ε,δ)-approximation* of the *MLE* of the *joint probability distribution* of the *Bayesian Network Structure* $\mathcal{G}(\mathcal{X}, \mathcal{E})$ over the *Distributed Continuous Model*. Instead of treating each counter individually, the approach views the counters collectively as *vectors* and specifically as *frequency vectors*. This shift allows for a more general and effective approach to be applied to solving the problem, leading to improved results, as discussed in detail below. To achieve this, we incorporate the method of *Functional Geometric Monitoring* [21] in combination with *BASELINE* and *UNIFORM* algorithms. These algorithms are solely used to define the appropriate value of the *approximation factor ε* among the *counters*.

The *NON_UNIFORM* algorithm is not used in this approach. As mentioned before, the *approximation factor ε* defined by the *NON_UNIFORM* is specialized for each *approximate counter*, while in this case, we utilize *frequency vectors*. The goal is to have algorithms can universally be applied to all the counters, and therefore we have selected the *BASELINE* and *UNIFORM* algorithm for this purpose. By leveraging the concept of frequency vectors and combining it with the BASELINE and UNIFORM algorithms, we can effectively address the challenges posed by MLE tracking-problem.

The *Functional Geometric Monitoring (FGM)* method has been chosen due to its significant benefits in terms of *communication cost* and *scalability* of the system compared to other methods, particularly its predecessor, the *Geometric Monitoring (GM)* [22]. *FGM* represents the successor of the *GM* method, offering improved performance and capabilities

The *FGM* constitutes a universally applicable method that can be employed for various monitoring problems. It is independent of the monitoring problem, as it employs a *problem-specific family of functions*, known as *safe function* which will be discussed in detail later. The method of the *FGM* can be integrated with ease in any stream *processing framework* like *Apache Flink* [23] and *Apache Spark* [24], providing a general and powerful tool for monitoring a wide range of problems.

Furthermore, the *FGM* method can be provably adapted under adverse conditions of the monitoring problem, regarding *tight monitoring bounds* (making it a suitable choice for our purposes). Additionally, the *FGM* method can be easily adapted in the presence of *skew distribution* among *sites*.

4.2.1 Functional Geometric Monitoring (FGM)

Given the number of sites k, where each *site* S_i with $i \in \{1, \dots, k\}$ maintains a *frequency vector* of *counters* $\boldsymbol{S_i}(t)$(*local state vector*), which is updated in an appropriate manner (*See Chapter 3.2*), while receiving data. In addition, the *global state* vector $\boldsymbol{S}(t)$ refers to sum of the corresponding *local states* $\boldsymbol{S_i}(t)$, denoted as $\boldsymbol{S}(t) = \sum_{i=1}^{k} \boldsymbol{S_i}(t)$. Our primary concern is the region of the *continuous query (Q)*, aiming for the Coordinator to continuously maintains an ε-*approximation* of *query value* of the *global state vector* $S(t)$, defined as follows:

$$Q\big(\boldsymbol{S}(t)\big) \in (1 \pm \varepsilon) Q(\boldsymbol{E}(t))$$

With $\boldsymbol{E}(t) = \sum_{i=1}^{k} \boldsymbol{E_i}(t)$, where $\boldsymbol{E_i}$ denotes the *estimated vector* on Coordinator for each *site* S_i. To maintain the previous equation, each *site* S_i needs to periodically send a message to the Coordinator, particularly at each round, informing how the *local state vector* $\boldsymbol{S_i}(t)$ has varied from the received *local data stream*. The Coordinator maintains an *estimator vector* $\boldsymbol{E_i}$ for each *site* S_i. Therefore, each time the site sends such a message to the Coordinator, it sends its *drift vector* $\boldsymbol{X_i}(t) = \boldsymbol{S_i}(t) - \boldsymbol{E_i}$. The Coordinator updates the $\boldsymbol{E_i}$ by adding the $\boldsymbol{X_i}$(*vector addition*). More details are discussed in [21].

The *Functional Geometric Monitoring* (FGM) ensures the *safety* of the entire system, the value of the *monitoring query* falls within the desired bounds, utilizing a *safe function* φ. The *safe function* denotes a *real function* that is defined by the monitoring problem. Particularly, the safe function employed to each *site* S_i, where each site S_i needs to monitoring its $\varphi(\boldsymbol{X_i})$ as its *drift vector* $\boldsymbol{X_i}$ varies. It is sufficient to prove that if the sum $\psi = \sum_{i=1}^{k} \varphi(\boldsymbol{X_i}) > 0$, then the *safety* of the entire system is ensured. The *safe zone composition* and quality criteria of *safe zones* are discussed in detail in [25].

The analysis of the MLE algorithm primarily centers around the *monitoring* of *frequency moments* F_p. The objective is to effectively maintain the *counters* $A_i(x_i, x_i^{par})$, $A_i(x_i^{par})$ within a given *Bayesian Network Structure* $\mathcal{G}(\mathcal{X}, \mathcal{E})$, where the set of nodes is denoted as $\mathcal{X} = \{X_1, \dots, X_n\}$.Therefore, the problem can be framed as the continuous maintenance of the F_1 *frequency moment* of a *vector* $\boldsymbol{x} = [x_1, \dots, x_n]$. The F_1 *moment*, also known as the $l^1\ norm$, is defined as follows:

$$\|\boldsymbol{x}\|_1 = \sum_{i=1}^{n} |x_i|$$

Regarding our case, each x_i of the *frequency vector* $\boldsymbol{x}$ corresponds to the counters $A_i(x_i, x_i^{par})$, $A_i(x_i^{par})$. Therefore, the $\boldsymbol{x}$ contains all the counters of each node X_i in the network $\mathcal{G}$. The *frequency* of each counter $A_i(x_i, x_i^{par})$ and $A_i(x_i^{par})$ is maintained, representing the number of times appears in the data stream.

Furthermore, when monitoring the F_1 *frequency moment*, we employ *safe functions* that are defined as follows:

$$\|\boldsymbol{x} + \boldsymbol{E}\|_1 - T$$

In the context of continuous querying, the threshold for each round will vary and is equivalent to $(1 + \varepsilon)\|\boldsymbol{E}\|_1$. Therefore, the safe function can be defined as follows:

$$\|\boldsymbol{x} + \boldsymbol{E}\|_1 - (1 + \varepsilon)\|\boldsymbol{E}\|_1$$

Our objective is to continuously maintains an *ε-approximation* of the *MLE* of a *Bayesian Network* $\mathcal{G}(\mathcal{X}, \mathcal{E})$. To achieve this, we need to address two prerequisites. The first prerequisite involves dividing the available error budget among the counters in a way that provides an *ε-approximation* of the *MLE*. Since the *counters* are framed as *frequency vectors* and the *safe function* follows the previous format, it is evident that the *approximation factor ε* must be the same for all *counters*. This immediately implies that the *BASELINE* and *UNIFORM* algorithms are the only ones that can be applied. The second prerequisite is to ensure an *ε-approximation* for each counter $A_i(x_i, x_i^{par})$ and $A_i(x_i^{par})$ for each X_i, given that the *error budget* has been appropriately allocated among the counters.

By applying the previous formulation of the safe function, it becomes evident that the maximum error at each round is proportional to $\varepsilon\|\boldsymbol{E}\|_1$. However, it is insufficient for ensuring an *ε-approximation* for each *counter* $A_i(x_i, x_i^{par})$, $A_i(x_i^{par})$. The reason is that the *error* is determined by the sum of the values of all the counters, which it not accurately represent the error for each individual counter. To illustrate this point, we consider a *frequency vector* that contains one small counter and several high counters. The error at each round will be affected for the values of the high counters. As a result, the changes of the small counter may not be detected because its changes will be smaller than the overall error influenced by the high counters. Consequently, the error calculation is based on the sum of all counter values, which does not accurately reflect the error for each specific counter.

We propose a *safe function* in the format $\|\boldsymbol{x} + \boldsymbol{E}\|_1 - T$, but the *threshold* T is defined as follows:

$$T = \|\boldsymbol{E}\|_1 + minViolatedValue$$

$$\text{where } minViolatedValue = \varepsilon \cdot \min_{i} \boldsymbol{E}$$

The $minViolatedValue$ is defined based on the value of the approximation factor ε and the minimum value among counters on E. This approach ensures an *ε-approximation* for each *counter* $A_i(x_i, x_i^{par})$ and $A_i(x_i^{par})$ for each X_i. By calculating the *error* at each round using the minimum value among *counters*, we obtain the least possible *error*. By ensuring that there is no *violation* for the minimum counter, we infer that there are no *violations* for the other counters because they must change by an amount greater than what is defined. Although this approach may result in more *rounds*, treating the counters collectively and each message on the Coordinator contains information for all the available counters, significantly reduces the communication cost.

Despite the *error* defined by the minimum *counter* value, which is significantly small, the *FGM* method offers the advantage of treating the counters collectively. This means that for each *update* message from each site S_i, the Coordinator receives information for all counters. As a result, the communication cost is significantly reduced, as confirmed by the experimental evaluation. We achieve an improvement of *10x* in communication cost over the first approach and an improvement of *100x* in communication cost compared to *EXACTMLE*. Moreover, the *FGM* provides a *scalable* and *high-throughput* solution for the problem, as demonstrated in the experimental evaluation.

Rebalancing

Our objective is the round lasts longer, which is desirable as it allows for better summarization of the *local streams* on *local state vectors*. Our goal is to minimize the upstream communication cost associated with the estimated vector $\boldsymbol{E}$ at the beginning of each round, whenever possible. While the condition $\psi = \sum_{i=1}^{k} \varphi(\boldsymbol{X_i}) > 0$ does not necessarily imply a significant movement of the *global state* $\boldsymbol{S}(t)$ relative to $\boldsymbol{E}$, the *safe function* may be quite useful. Instead of broadcasting a new *safe function* to the *sites* (incurring *upstream communication cost*), the Coordinator broadcasts a *scaling factor* λ. This *scaling factor* is then used by the *sites* to appropriately adjust their *drift vectors*. By doing so, we reduce the communication cost associated with broadcasting an estimated vector. In experimental evaluation, the FGM method is used in conjunction with the *rebalancing* method.

Chapter 5:

Design and Implementation of the system

5.1 Apache Flink

The *Apache Flink* [23] is an *open-source* framework used for *distributed stream data processing*. The core of the Flink constitutes the streaming engine, which provides the ability to perform stateful operators over *unbounded data streams*, while guaranteeing *in-memory* speed for computations. The Flink is designed to integrate easily on various *cluster environments* such as Hadoop, Yarn *and Kubernetes*.

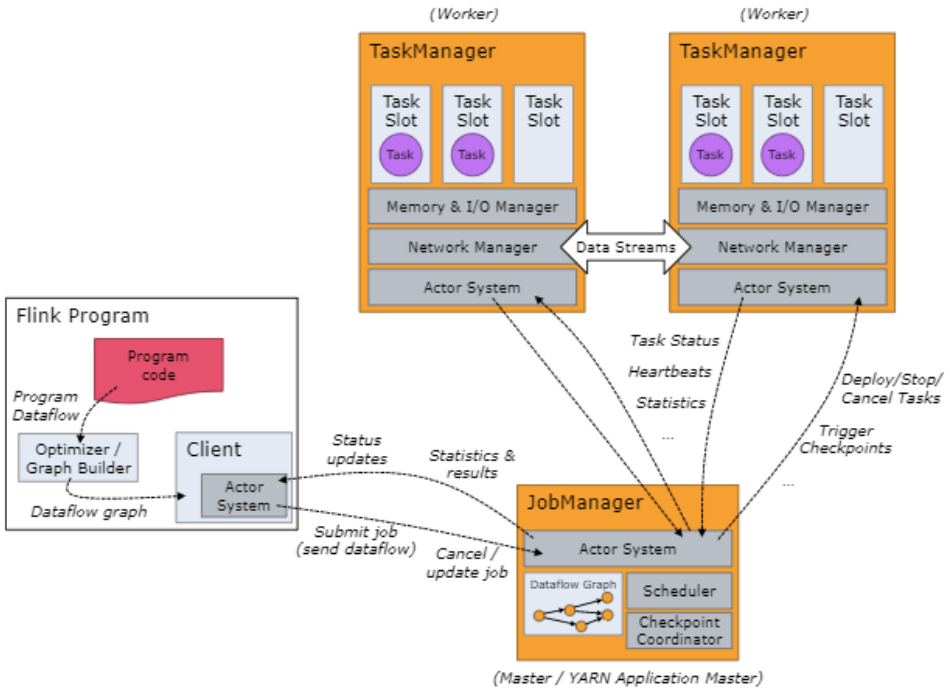


Figure 14: Apache Flink

The Apache Flink consists of two *processes*: the *Job Manager* and the *TaskMangers* (*Figure 14*). The *Job Manger* is responsible for coordinating the entire execution process of the application, while each TaskManager is responsible for the execution *tasks(operators)* of the *dataflow*, as well as buffering and the *exchange* of *data streams*.

Furthermore, the Flink provides a wide range of *APIs* that can be used for developing our application. One of the most significant *API* is the one that contains the *stateful operators*. These operators allow us to save *states* while processing the dataset. Each *state* can be framed as a *snapshot* of the operator at a given time, which keeps track information related to the operator. In our approach, both each site and Coordinator represent a *stateful operator*.

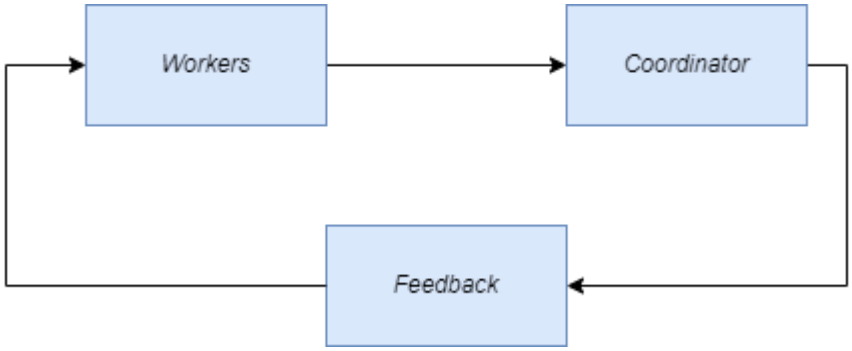


Figure 15: Feedback loop

Between the sites and the Coordinator there was a *feedback loop*. It can be represented as the *redirecting* of the one operator output to the previous one *(Figure 15*). The feedback loop can be met in cases related to the *continuously maintenance* of someone model, which is equivalent to our problem. The *Apache Flink* provides the *Iterative Stream* operator for implementing the *feedback loop*. Given that the version of the Flink used for executing all the experiments was on early stage (See *Chapter 6*), we decided to use a *Kafka topic* as feedback loop.

5.2 Apache Kafka

The *Apache Kafka* [26] is an open-source platform that provides the capability of *distributed event streaming*. The *Kafka* has emerged as the successor to the *traditional messaging* systems, offering essential characteristics such as *high-throughput, high-reliability, scalability* and *durability*, which are crucial for processing *distributed streaming data sources*. In *Apache Kafka* the datasets are stored in *topics*, which are further divided into *partitions* to ensure *scalability* and *reliability* of the system. Typically, there are more than one *Kafka broker* which constitutes a *Kafka cluster*. The *Kafka* offers two primary *services*: *Kafka consumer* and *Kafka producer*. The *Kafka consumer* used to read data from a topic while the *Kafka producer* is responsible for publishing data to a topic.

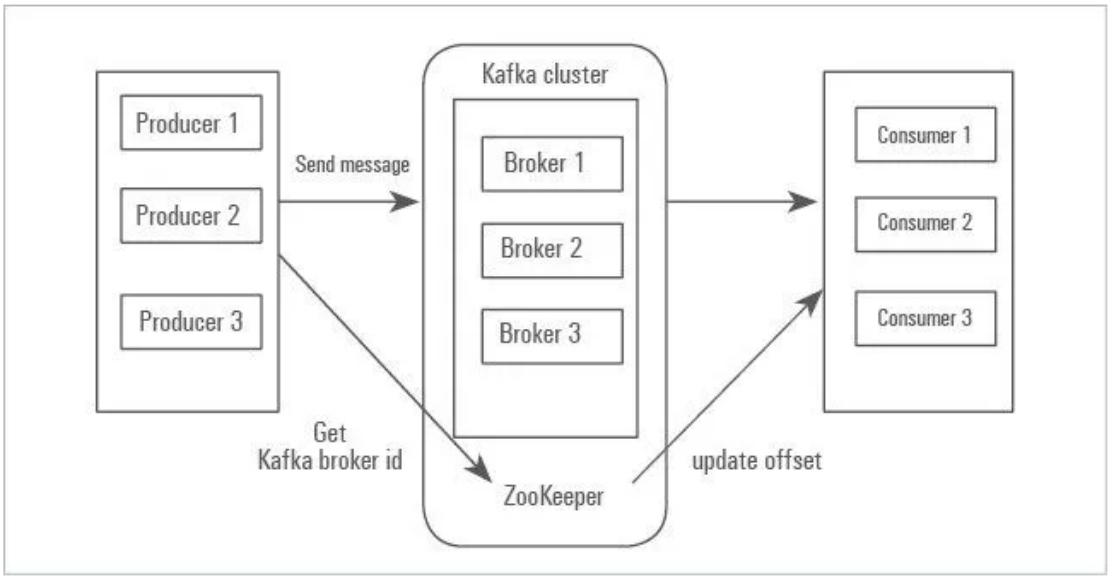


Figure 16: Apache Kafka

In our system, we utilize *Kafka* used for reading *data streams* that are directed to the sites and for implementing the *feedback loop*. For the *feedback loop*, a *Kafka topic* is used as a *buffer* between the producer and the *consumer*. In this context, the *producer* represents the *Coordinator* which produces all the necessary control messages while the *consumer* represents the *sites*, which needs to consume and process the messages sent by Coordinator.

5.3 System Architecture

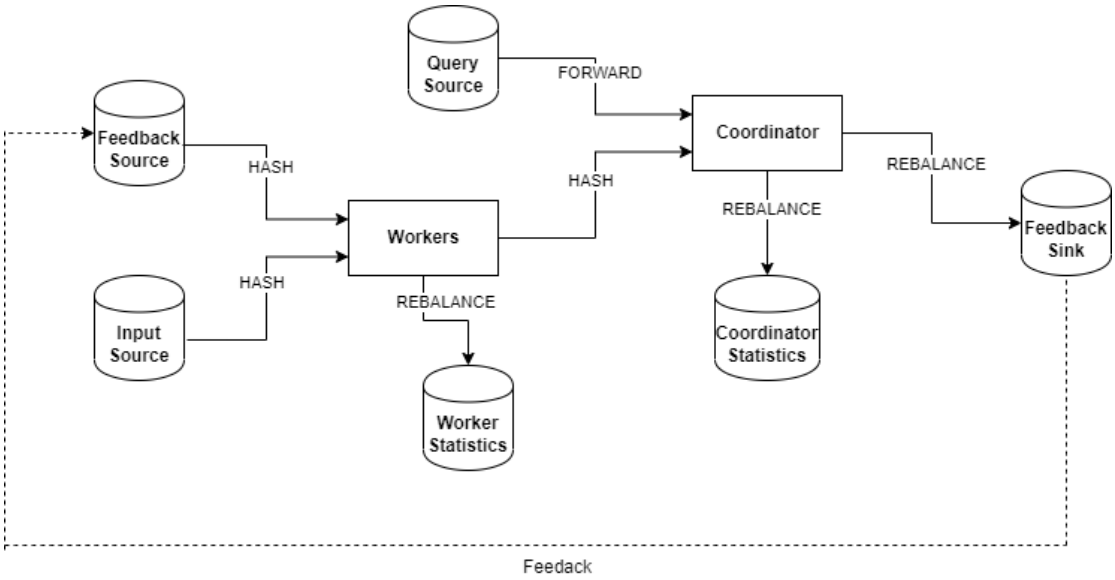


Figure 17: System Architecture

Both *Apache Flink* and *Apache Kafka* are utilized in the implementation of our system. Figure 17 provides an abstract view of our system architecture.

The *Input Source operator* is responsible for reading the incoming dataset from a *Kafka topic* which serves as the Input Source. It is responsible for defining the dataset in the appropriate format. Each input is represented as a tuple, following a specific format:

$$< value, worker_{id} >$$

The $value$ denotes the *input feature vector* of a *Bayesian Network* (or a *Naïve Bayes Classifier*), while the $worker_{id}$ serves as a *pseudo-key* used for distributing the dataset among *Workers*. It ensures that the dataset is evenly distributed among the workers, following a horizontal partitioning strategy.

Each *Worker* represents a two-input operator, therefore can be framed as a *keyed co-process operator*. The first input refers to the incoming dataset which needs to be processed, while the second input refers to the *Feedback Source*. In this context, the *Feedback Source* contains the control messages that are sent by the Coordinator. Additionally, *Feedback Source* and *Feedback Sink* denote the same *topic* (*feedback topic*), which acts as a *buffer* between the *Coordinator* and the *Workers*. Specifically, the *Coordinator* acts as *Kafka Producer* in *Feedback Sink*, while the *Workers* acts as *Kafka Consumers* in *Feedback Source*. This achieves a *two-way communication channel* between *Coordinator* and *Worker* (*feedback loop*).

Accordingly, the Coordinators is treated as a two-input operator and can be also implemented as a *keyed co-process operator*. The first input corresponds to the messages received from Workers, while the second input comes from the *Query Source*. In this context, the *Query Source* can treat either *testing source* which include *queries* used to evaluate the quality of *joint probability distribution* estimation, or as *query source* which contains *user-posed queries* related to the *joint probability distribution* of a *Bayesian Network*.

The exchanged messages between the Coordinator and Worker are represented as a triplet, following a specific format:

$$< value, worker_{id}, type\_message >$$

The value field represents the content of the message, which could be a value of an *approximate distributed counter* or a *frequency vector* in case of the *FGM* method. The $worker_{id}$ field is used differently depending on the direction of the message flow. For messages from Workers to *Coordinator*, it denotes the $cord_{id}$, while for messages from the *Coordinator* to Workers, it represents the $worker_{id}$ indicating the intended Worker to receive the message. Finally, the $type\_message$ field defines the message type based on the specific action performed.

Each message, in addition to the three fields, in case of the *approximate distributed counters* and are treated as individual entities, the message needs to include another one field related to the counter that messages is referring to. The following mechanism is also used to retrieval of the counters during the update process. Specifically, each counter in *Bayesian Network* is unique characterized from the following fields:

$$< counterName, counterValue, counterParentsName, counterParentsValue >$$

While in *Naïve Bayes Classifier*, each counter is uniquely characterized from the following fields:

$$< index, counterValue, classValue >$$

Where the index field denotes the position of counter value in *input feature vector*.

In case each message contains all the previous fields, the size of message will be significantly large. Instead of each counter characterized by a *unique key* corresponded to a long number. This number is generated by hashing all the fields of each counter, using an appropriate hash function (*Figure 18*).

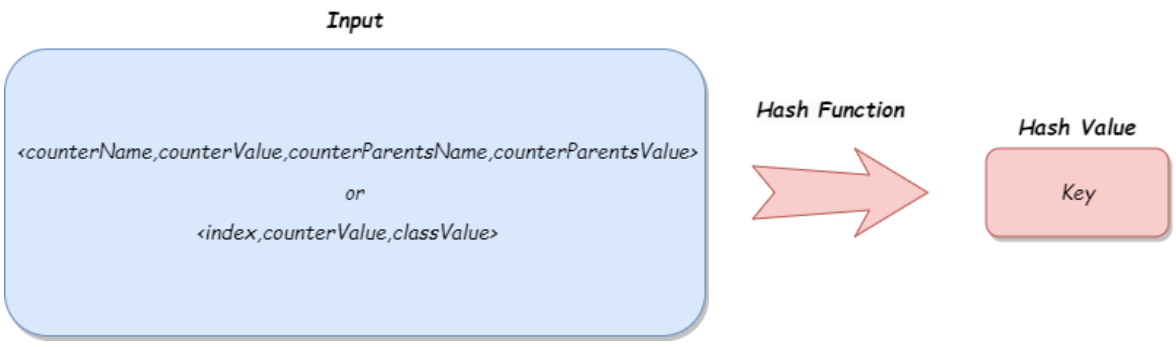


Figure 18: Hashing

Apparently, the hashing process is not performed each time a message is sent, instead it is carried out during the process of the *Initialization*. Each counter is converted into a *unique key* that will be used throughout the entire process. This allows us to reduce the size of each message and create a fast retrieval mechanism for the counters, utilizing an appropriate structure (*Hash Map)*.

Both the *Worker* and *Coordinator* components include a *side-output*, which serves as a *logging* mechanism. This mechanism enables us to log various important metrics related to our system, including *throughput*, *communication cost* at a given time, and more.

For further details on the *project structure* and *setup,* can be found in Appendix. Additionally, the code for the project is available at [27].

Chapter 6:

Experimental evaluation

The experimental evaluation comprises a wide range of experiments covering both the first approach (*See. Chapter 4.1*) and the proposed approach (*See Chapter 4.2*). The first section validates the functionality of the proposed approach, while the second section refers to the system's capability to handle large volume of datasets. The third section provides a comparison between the two approaches. All the experiments are conducted using *Bayesian Networks*, with similar results observed for *Naïve Bayes Classifiers*.

In the first approach, we conducted experiments using two types of counters: *RANDOMIZED* and *DETERMINISTIC* counter, in conjunction with the *BASELINE*, *UNIFORM* and *NON_UNIFORM* algorithms. For the second approach, which utilizes the FGM method, we conducted various experiments using the *BASELINE* and *UNIFORM* algorithms. It should be noted that the Bayesian Network structure is predetermined, and our objective is to learn the parameters.

Testing Setup

All the experiments described in this thesis were conducted on the *SoftNet Cluster* of the *SoftNet lab* [28]. The *SoftNet Cluster* is composed of *12 Quad Core Xeon X3323 2.5GHz,8 GB DDR3 RAM*. The version of *Apache Flink version* is the *1.10.0* and the version of the *Apache Kafka Connector version* is the *1.9.3* .

6.1 Datasets

All the *Bayesian Networks* used in our experiments are *real-world Bayesian Networks* and available in the repository [29]. Additionally, the *Bayesian Networks* had been extensively studied to prior studies. We selected *Bayesian Networks* from different size categories. Specifically, we chose the *ALARM* [30] as a *small size network* (≤ 40 *nodes*), the *HEPAR2* [7] as a *medium size network*(≤ 100 *nodes*) and the *LINK* as a *large size network* (≤ 1000 *nodes*). Finally, all the *Bayesian Networks* in our experiments refers to *Discrete Bayesian Networks*.

Table 4 provides an overview of the *Bayesian Networks* used in the experiments. It includes the number of nodes in each Bayesian Network, which corresponds to the size of the *input feature vector*. The second column indicates the number of edges, representing the number of *conditional dependencies* among the nodes in each *Bayesian Network*. Additionally, table displays the number of parameters required to define the *joint probability distribution* of each *Bayesian Network*, while the last column indicates the number of counters required to maintenance, for estimating the parameters of each *Bayesian Network*.

Dataset	*Number of nodes*	*Number of edges*	*Number of parameters*	*Number of counters*
ALARM	*37*	*46*	*509*	*983*
HEPAR II	*70*	*123*	*1453*	*2816*
LINK	*724*	*1125*	*14211*	*26609*

Table 4: Bayesian Networks

Training Data

Regarding the *training dataset*, we generated datasets for each *network* from the *joint probability distribution* using the *Forward Sampling method* (*See Chapter 2.4*). The size of datasets for each network varied from $5K$ to $50M$. These generated datasets were used exclusively for learning the parameters of each Bayesian *Network*.

Testing Data

The *testing dataset* contains *queries* about specific *events*, with the objective of evaluating the *accuracy* of the system. Particularly, we measure the system's ability to accurately estimate the probability of various events. To accomplish this, we generate *1000 events* based on the *joint probability distribution* of the *Bayesian Network*. The probability of these events is estimated using the learning parameters of the trained network. All events in the testing dataset pertain exclusively to probability queries regarding the joint probability distribution. It is important to note that there are no limitations on values of the probability events. The testing *dataset* encompasses both *highly unlikely* and *highly likely* queries, with the only requirement being that the assigned probabilities must be non-negative, in adherence to the basic probability axiom.

6.2 Performance metrics

Communication cost

The illustrated *communication cost* represents the total number of bytes of messages. Encompassing both the *upstream* and *downstream communication cost*.

Error to Ground Truth (GT)

For each *testing event*, we calculate the probability using the *learning parameters* of the *approximate model*, which corresponds to the *trained network*. We then compare this probability to the *ground truth* probability *event* obtained using the values of *ground truth* parameters of the network. Consequently, the metric measure to the *error* of the *ground truth (GT)* probability, denoted as *Error to GT*.

Error to EXACTMLE

For the *BASELINE*, *UNIFORM* and *NONUNIFORM* algorithms, we measure the *error* in relation to *EXACTMLE* and denote it as *Error to EXACTMLE*.

6.3 Experimental Results

For all the following experiments are reported the mean value of five independent *runs*. Furthermore, the *Bayesian Networks* do not appear significant differences between J_i, K_i among the nodes, resulting the differences among *BASELINE*, *UNIFORM* and *NONUNIFORM* algorithms both of approaches are negligible. We focus on differences between of two approaches. We set $k = 16$, $\varepsilon = 0.1$ and $\delta = 0.1$, unless otherwise specified.

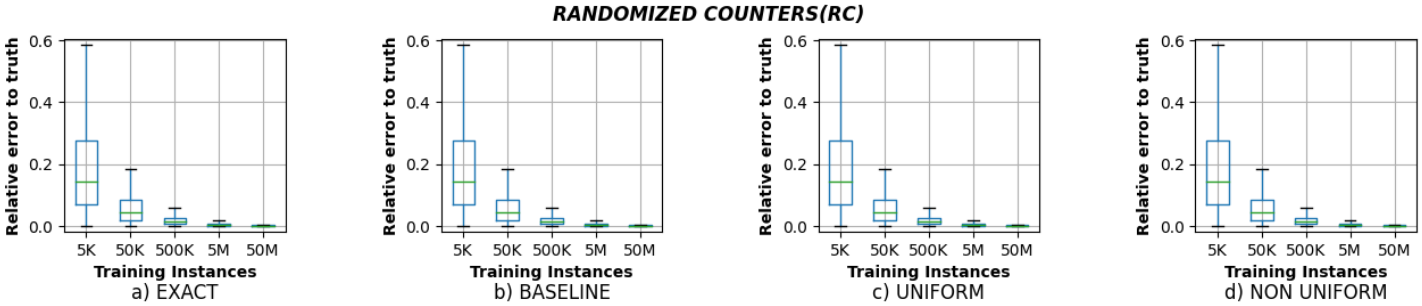
We present the results of four categories of experiments. The first category measures the *communication cost* while varying the number of *training instances*, and the second category examines the *communication cost* while varying the *approximation factor ε*. Last but not least, the third category measures the *communication cost* while varying the number of the *workers*. Lastly, int the fourth category we evaluate the scalability of the system. In all cases, we compare the two approaches themselves and each approach with *EXACT counters*, that is the *EXACTMLE*.

6.3.1 Communication cost related to the number of training instances

The first category focuses on the communication cost while varying the number of *training instances*. The size of datasets ranges from $5K$ to $50M$ and the dataset used is the *HEPAR II*.

In this category, we compare the *Error to GT* between the two approaches. For the first approach, we measure the error for both RANDOMIZED and *DETERMINISTIC* counters, while for the second approach, we use the *FGM* method. The *Error to GT* represents the *absolute error* of the *probability queries*.

As the number of training instances increases for both approaches, the error decreases. This is expected because with more training instances, more information about the parameters is obtained, resulting in more accurate parameter estimation. Furthermore, the *interquartile range* shrinks with the increase in training instances, indicating a reduction in the variance of the *probability queries* errors. Both approaches achieve good accuracy, for instance, after $5M$ *instances* the median error is less than 1% for each approach. The diagrams illustrating the *error to GT* of the *HEPAR II* network in both approaches, can be found in the Appendix.



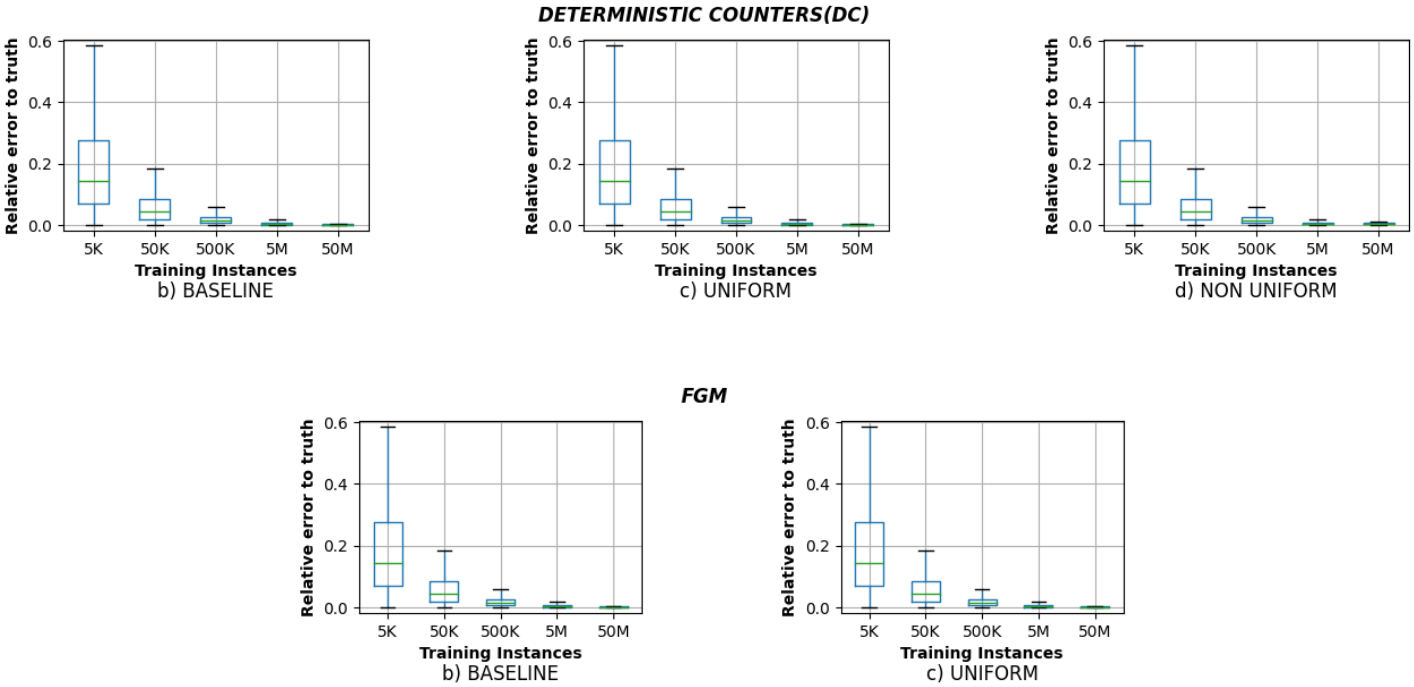


Figure 19: Error to GT related to the training instances for both approaches, for the HEPAR II dataset

We compare the *Error to EXACTMLE* in relation to the number of *training instances* for both approaches. In this case, the *Error to EXACTMLE* represents the *mean absolute error* of the probability *queries*. This error can be attributed to two sources: *statistical error* and *approximation error*. The *statistical error* arises due to the number of training instances and depicts the error relating to *ground truth values* of the parameters. The *approximation error*, on the other hand, captures the error between the learnt model and the model obtained using *EXACT counters*, which is influenced by the *approximation factor ε*.

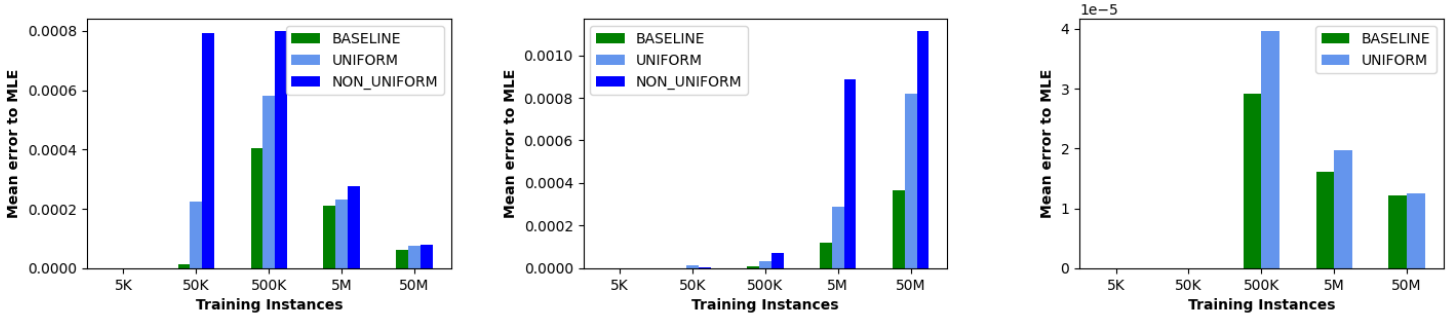


Figure 20: Error to EXACTMLE related to the number of training instances for both approaches for the HEPAR II dataset

Our objective is to control the *approximation error* to the *EXACTMLE*. We observe that for both approaches the error approximately remains bounded as the number of training instances is varied. The latter confirms the functionality of each approach. We guarantee for each approach combined with the *BASELINE, UNIFORM* and *NON_UNIFORM* algorithms that the error is always bounded, where the *error guarantees* are always specified by the *approximation factors ε, δ.* For small number of training instances ($\leq 50K$), the error is negligible due to the *tight bounds* for each counter. The latter holds due to the fact that the values of the counters are quite small in this case. For example, when $\varepsilon = 0.1$ the approximation factor for each counter is roughly in the order of 10^{-4}, therefore the *bounds* are extremely tights for small values of the counters.

The *BASELINE* obtains the smallest *error*, which corresponds to the best *accuracy*, closely followed by the *UNIFORM* and *NON_UNIFORM* algorithms. The latter holds due to the fact that the *BASELINE* algorithm accompanied by more *tight bounds* for each *counter* compared to the others. The purpose of this experiment is to prove the functionality both of approaches and not to infer results among the BASELINE*, UNIFORM* and *NON_UNIFORM* algorithms.

Additionally, we measure the *communication cost* related to the number of *training instances* for both approaches. Note that the y-axis is in logarithmic scale.

Firstly, there are no significant differences among the *BASELINE, UNIFORM* and *NON_UNIFORM* algorithms. As mentioned earlier, there are no significant differences between $J_i \; and \; K_i$ among the nodes of the *HEPAR II* network. Generally speaking, the *UNIFORM* and *NON_UNIFORM* algorithm is quite close while both algorithms appear to be better than the *BASELINE* algorithm as the number of training instances increases.

As the number of training instances increases, the difference to *EXACTMLE* also increases for both approaches. This desirable as it proves that both approaches can handle large volumes of datasets sufficiently while using as little communication cost as possible. In the case of the first approach, both *RANDOMIZED* and *DETERMINISTIC* counters achieve up to an order of magnitude less communication cost of *EXACTMLE*. This practically means that they send 10 times fewer messages than *EXACTMLE*. On the other hand, the second approach achieves up to two orders of magnitude less communication cost of EXACTMLE, which means that it sends 100 times fewer messages than *EXACTMLE*.

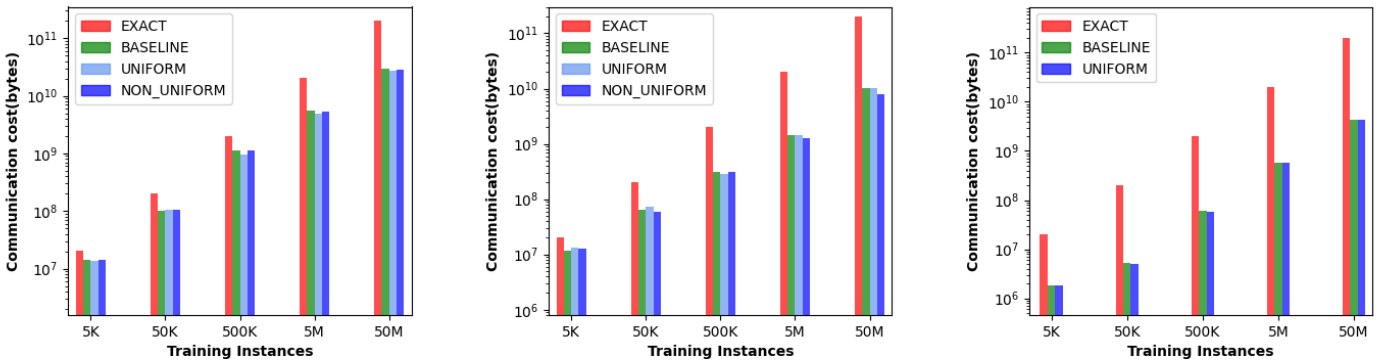


Figure 21: Communication cost related to the number of training instances for both approaches from the HEPAR II dataset

The communication cost tends to increase logarithmically with the number of training instances. This trend is particularly evident when examining the LINK dataset. The results for both the LINK and ALARM datasets can be found in the Appendix.

In Figure 22, for each approach among the *BASELINE, UNIFORM* and *NON_UNIFORM* algorithms are used the algorithm which resulted on the lowest communication cost. We observe that the proposed approach outperforms the first approach, which utilizes *individually approximate distributed counters* (either *RANDOMIZED* or *DETERMINISTIC*), by up to an order of magnitude in terms of communication cost. When comparing the *RANDOMIZED* and *DETERMINISTC* counters, we observe that *DETERMINISTC* achieves an 50% improvement in communication cost (*See. Chapter 4.1.1.3*).

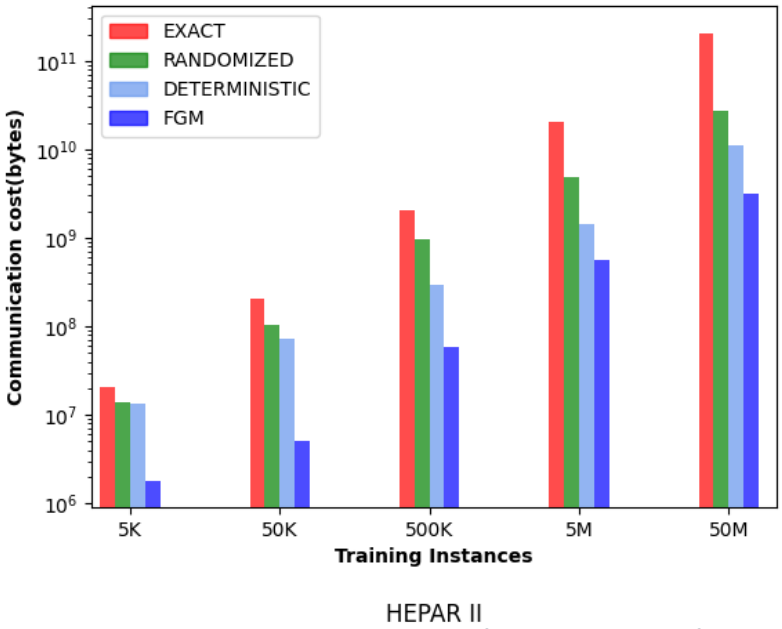
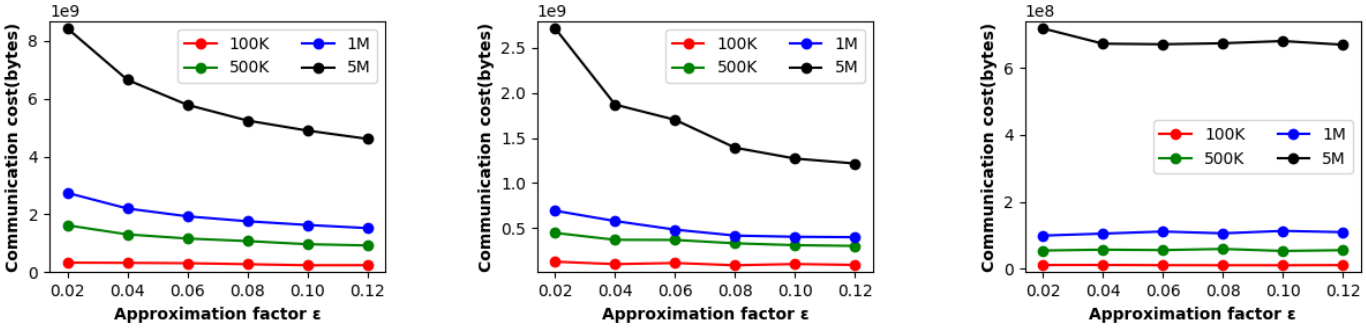


Figure 22: Communication cost related to the number of training instances for both approaches from HEPAR II dataset -Best results

6.3.2 Communication cost related to the approximation factor ε

In this section, we compare the *communication cost* in relation to the *approximation factor ε*. We vary the *approximation factor ε* in the range of $[0.02,0.12]$ with an increment of 0.02 and measures the *communication cost* for both approaches. The size of datasets is $100K, 500K, 1M, 5M$ respectively, using the *HEPAR II dataset*. The results for both approaches combined with the *UNIFORM* algorithm are presented here, while the results of the other algorithms can be found in Appendix.

For both approaches and all algorithms, we observe that the *communication cost* does not closely follow the changes in the approximation factor *ε*. This implies that the *communication cost* is not sensitive to variations in the *approximation factor ε* for both approaches. In the first approach, with both types of counters, we initially observe a reduction in the communication cost by around $15\% - 20\%$ when the approximation factor ε changes from 0.02 to 0.04. However, this reduction gradually diminishes as the *approximation factor ε* increases. On the other hand, the communication cost of the second approach remains stable across different values of the approximation factor *ε*. In other words, the approximation factor ε has little impact on the communication cost of the FGM method. This can be attributed to how we define the safe functions to achieve our objective.



a) RC - UNIFORM b) DC - UNIFORM c) FGM - UNIFORM

Figure 23: Communication cost related to the approximation factor ε, for HEPAR II dataset and UNIFORM algorithm

By comparing the two approaches in terms of the impact of the *approximation factor ε*, we find that the proposed approach achieves better results. Both types of counters in the first approach exhibit a similar dependency on the *approximation factor* ε. Note that the y-axis of the Figure 24 is in logarithmic scale.

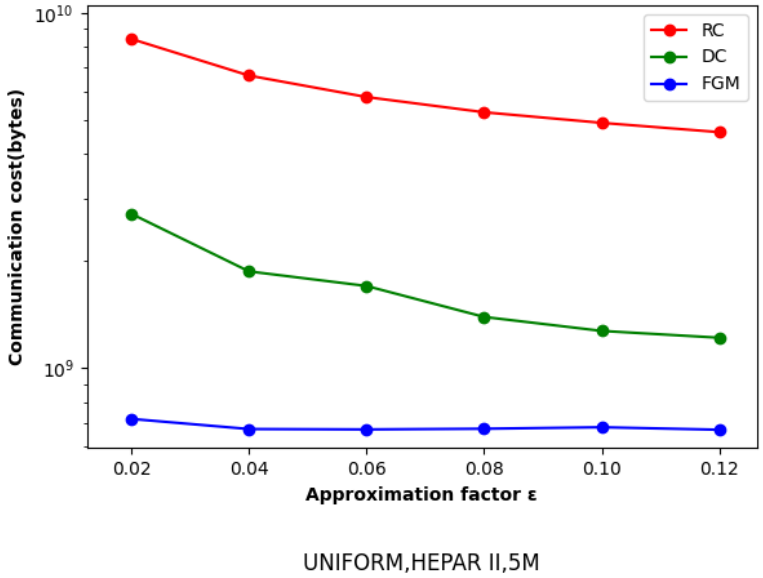


Figure 24: Communication cost related to the approximation factor ε for both approaches, for HEPAR II dataset and UNIFORM algorithm

Furthermore, we provide a diagram depicting the *Error to GT* in relation to *approximation factor ε* for both approaches using the *UNIFORM* algorithm. The results of other algorithms exhibit similar trends. In this case, the error denotes the *mean absolute error* of the *probability queries*.

As the *approximation factor ε* increases, the *error* does not show significant changes (although some differences exists but they are not significant). This is due to the fact that the *approximation factor ε* only controls the *approximation error*, which is considerable smaller than the *statistical error* (up to two orders order of magnitude smaller). As a result, the impact of the approximation error is overshadowed, leading to negligible changes in the overall error. On the other hand, we do observe changes in the error among different datasets. Specifically, the error decreases as the number of training instances increases. This is attributed to the reduction in statistical error as more training instances are utilized. Lastly, the accuracy achieved is quite good given the probabilities of the queries, the accuracy is less than 6% for both approaches.

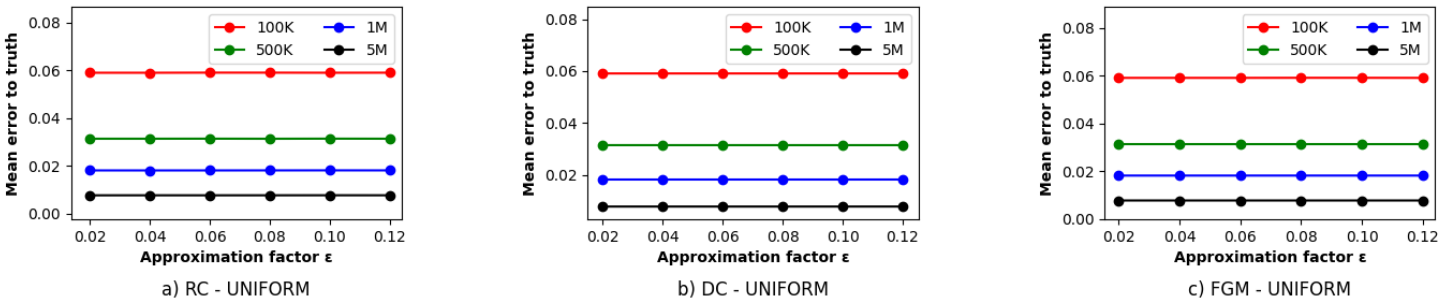


Figure 25: Error to GT related to the approximation factor ε for both approaches, για το dataset from HEPAR II dataset and UNIFORM algorithm

6.3.3 Communication cost related to the number of workers

In this section we compare the *communication cost* in relation to the number of sites. Specifically, the number of sites is varied in range of $[2,64]$. The size of dataset is $500K$ and refers to *HEPAR II* dataset. We present the communication cost for both approaches using the *UNIFORM* algorithm, while the results of the other algorithms can be found in Appendix. Note that the y axis is in logarithmic scale.

Upon analysis, we observe the *communication cost* increases sub-linearly with respect to the number of sites for both approaches. The first approach, utilizing RANDOMIZED counters, demonstrates the most favorable dependency on the communication cost, in line with the theoretical results. On the other hand, both the FGM and *DETERMINISTIC counters* exhibit similar results in the terms of their dependency on the number of sites.

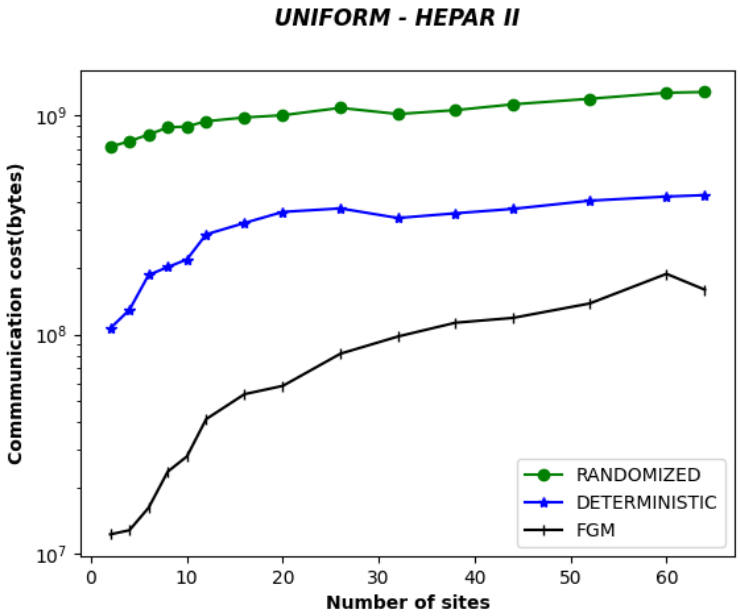


Figure 26: Communication cost related to the number of workers sites for both approaches, from the HEPAR II dataset and UNIFORM algorithm

6.3.4 Scalability

Until now, we measure the *communication cost* for different parameters of our system. In this section, we evaluate the performance of our system for both approaches. using two metrics: the *throughput* and *runtime*. The *throughput*(*events/sec*) denotes the average of training instances that the system can handle per second, while the runtime*(sec)* represents the time between the first and last message received from the Coordinator during the training process.

We conduct two categories of experiments to evaluate the system's performance using these metrics. In the first experiment, we measure the two metrics varying the number of sites. In the second experiment we measure the two metrics varying the number of parallelism. The parallelism can be interpreted as the number of subtasks or the size of resources utilized by the system.

In each experiment, we compare the two approaches themselves and each approach with the EXACTMLE. All the experiments are conducted using the *HEPAR II* dataset with a size of $500K$ instances. We present the results using the metric of *throughput*, the results of *runtime* can be found in Appendix. To mention that the results of *runtime* are similar to the *throughput*, but with a focus on reducing the runtime.

In the first experiment, we measure both *throughput(event/sec)* and runtime*(sec)* in relation to the number of sites. The number of sites is varied in the range of $[2,10]$ with step of 2. Note that the number of sites does not include the Coordinator.

In the first approach using both *RANDOMIZED* and *DETERMINISTIC counter*, we observe that the throughput does not increase proportionally to the number of sites, after the number of sites exceeds 6. This suggests that adding more sites does not significantly improve the system's throughput beyond a certain point. As the number of sites increases, the *communication cost* also increases. Notable, the largest increase in the communication cost is observed when using small number of sites *(Figure 26)*, therefore we choose the number of sites is on the range of $[2,10]$.

The augmentation in the *communication cost*, particularly in the initial state where all the counters appeared to have *violations*, resulting to a significant increase in the volume of messages sent to the Coordinator. As a consequence, *backpressure* generated on the sites. The *backpressure* appears only to the initial stage where the counters are quite small accompanied by tight bounds. It is important to note that this backpressure is temporary and tends to diminish over time. In contrast, we observe that the *throughput* of the EXACTMLE remains relatively stable regardless of the number of sites, indicating that its communication cost is indeed substantial, resulting in lasting backpressure on the sites. As a result, it does not scale well in terms of the number of sites.

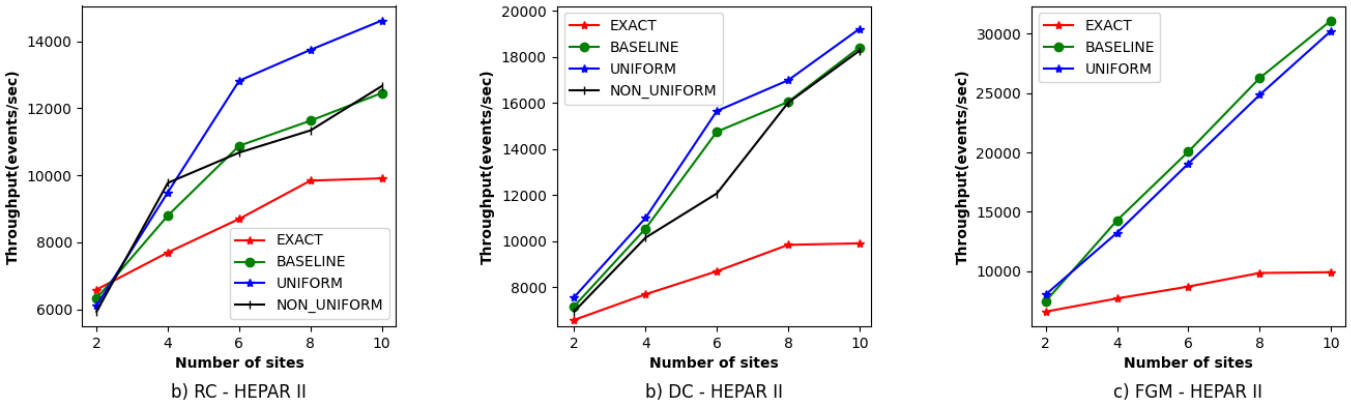
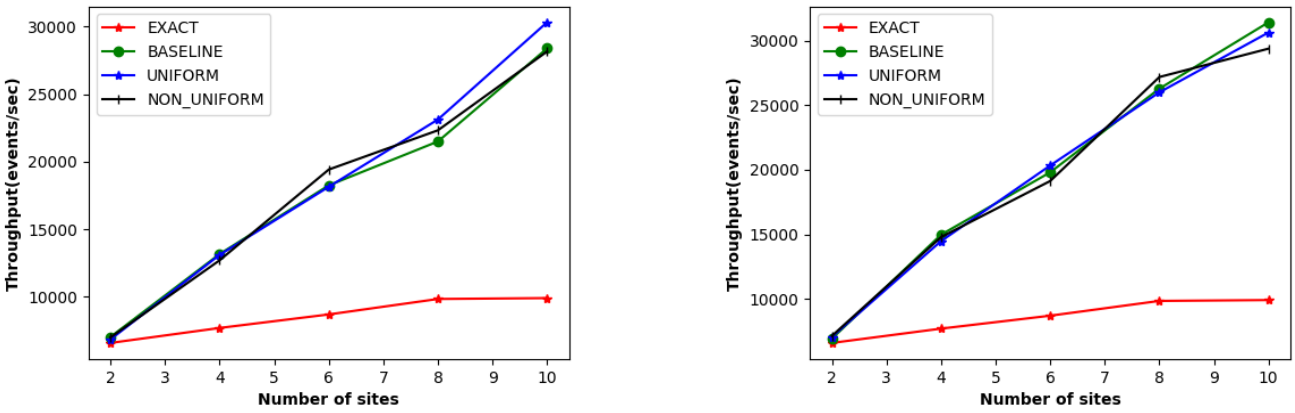


Figure 27: Throughput(events/sec) related to the number of sites for both approaches, for HEPAR II dataset

Considering the second approach, we observe that the *throughput* increases linearly according to the number of sites, indicating that there is no *backpressure* on the sites. As a result, the proposed approach achieves the ideal scaling without experiencing backpressure issues. The differences observed between the two approaches suggest variations in their communication cost. Specifically, the second approach exhibits significantly lower communication costs compared to the first approach. Furthermore, differences in *throughput* and *runtime* among the *BASELINE, UNIFORM* and *NON_UNIFORM* algorithms can be attributed to variations of their *communication costs*, which are directly proportional to their differences.

We measure the *throughput* and the *runtime* of the first approach after the initial state, where all the counters appeared with violations. We observe that the *throughput* increases proportional to number of sites, while the *runtime* decreases proportionally to the number of sites for both type of counters. This confirms that the *backpressure* after the initial state begins to diminish over time, and as a result, the first approach with both type of counters achieves ideal scaling.



a) RC - HEPAR II, after initial state

b) DC - HEPAR II, after initial state

Figure 28: Throughput(events/sec) related to the number of sites for the first approach for HEPAR II dataset HEPAR II, after the initial state

We present a comparison of the two approaches in terms of throughput (Figure 29). The chosen algorithm for each approach among the *BASELINE, UNIFORM* and *NON_UNIFORM* algorithms is the one that achieves the best performance i.e., the algorithm with the highest *throughput* for each approach (while for the *runtime* is used the algorithm with the lowest runtime). For the first approach, the *throughput* is measured without considering an initial state. We observe that the proposed approach achieves higher throughput than first approach, indicating differences in their communication cost are significant. Furthermore, both the second and the first approaches demonstrate higher *throughput* compared to the *EXACTMLE*, indicating the substantial differences in their communication cost.

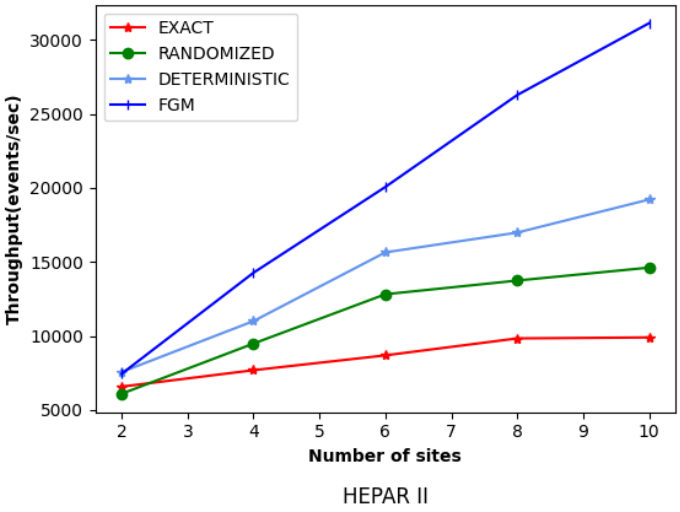


Figure 29: Throughput(events/sec) related to the number of sites for both approaches, for HEPAR II dataset -Best results

In the second experiment, we measure the *throughput(event/sec)* and the *runtime(sec)* in relation to the number of parallelism. Specifically, the parallelism is varied in the range of [2,16] with a step of 2 while the number of *sites* remain fixed at 16.

Similar to the findings in the previous experiment, we observe that in the first approach, as the number of parallelism increases, the variations in both *throughput* and the *runtime* do not increase proportionally to the number of sites.

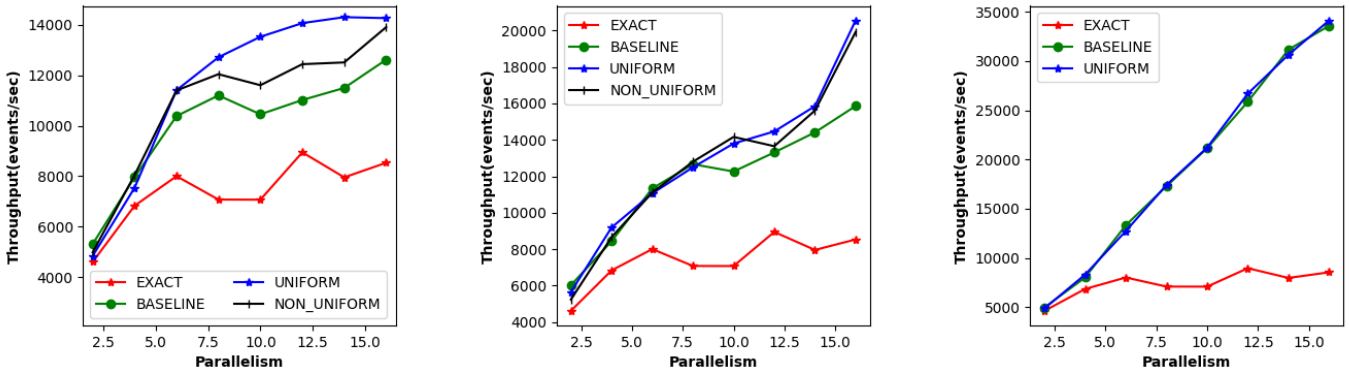
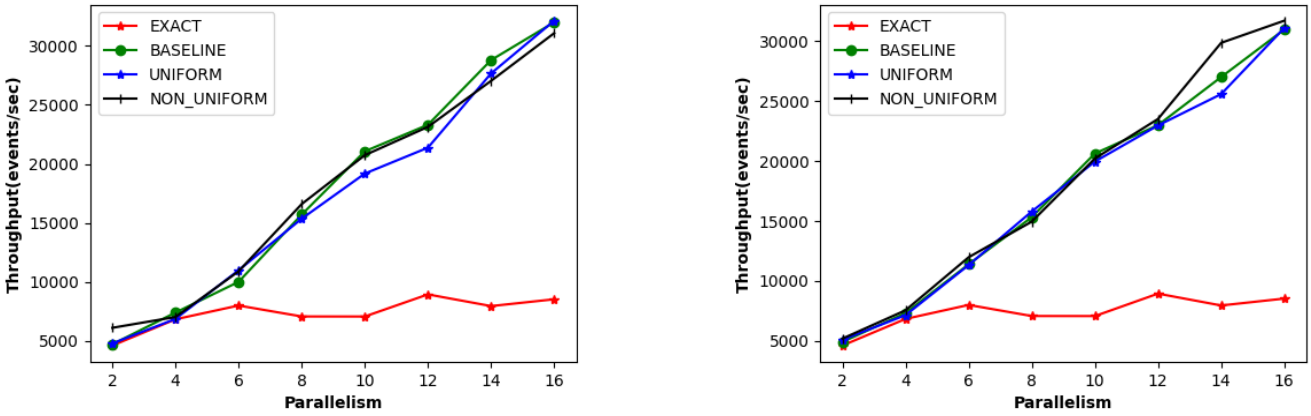


Figure 30: Throughput(events/sec) related to the number of parallelism for both approaches for HEPAR II dataset

This can be attributed to the fact that as the number of parallelism increases, the rate at which messages arrive to the Coordinator surpasses the rate at which the messages can be processed, resulting in *backpressure* on the sites. The *backpressure* is observed only in the first approach, particularly during the initial state where all the counters have tight bounds and violations are more common. This leads to a significant increase in the communication cost. However, as the system progresses beyond the initial state, the *backpressure* gradually diminishes (*Figure 31)*, where we measure the *throughput* after the initial state for both types of the counters in relation to the number of sites.



a) RC - HEPAR II, after initial state

b) DC - HEPAR II, after initial state

Figure 31: Throughput(events/sec) related to the number of parallelism for the first approach for HEPAR II dataset, after the initial state

Considering the second approach, we observe that the increase in the *throughput* is linear in relation to the number of the parallelism, indicating that there are no backpressure issues on the sites. This suggests that the proposed approach achieves ideal scaling in terms of parallelism (i.e., the number of resources can be utilized of the system).

On the other hand, the *throughput* of the *EXACTMLE* remains relatively stable to the increase of the number of parallelism, indicating that the rate at which the messages arrived at the Coordinator is substantial. This is due to the *communication cost* associated with the *EXACTMLE* is substantial. As a result, *backpressure* consistently generated on the sites. Therefore, the *EXACTMLE* does not achieve the desired scaling in relation to the number of *resources*.

We present a comparison of the two approaches in terms of the parallelism (*Figure 32*). Among the *BASELINE, UNIFORM* and *NON_UNIFORM* algorithms, for each approach is used the algorithm that achieves the best performance for each approach is selected (in the *runtime*, the algorithm with the lowest runtime, respectively). The proposed approach outperforms both types of counters in terms of throughput, indicating its ability to effectively utilize the available resources and achieve optimal scaling of the system. The significant difference in throughput between the two approaches highlights the difference in their communication costs. Additionally, the *throughput* of both the first and second approach are better than that of the *EXACTMLE*, which confirms their differences on *communication cost*.

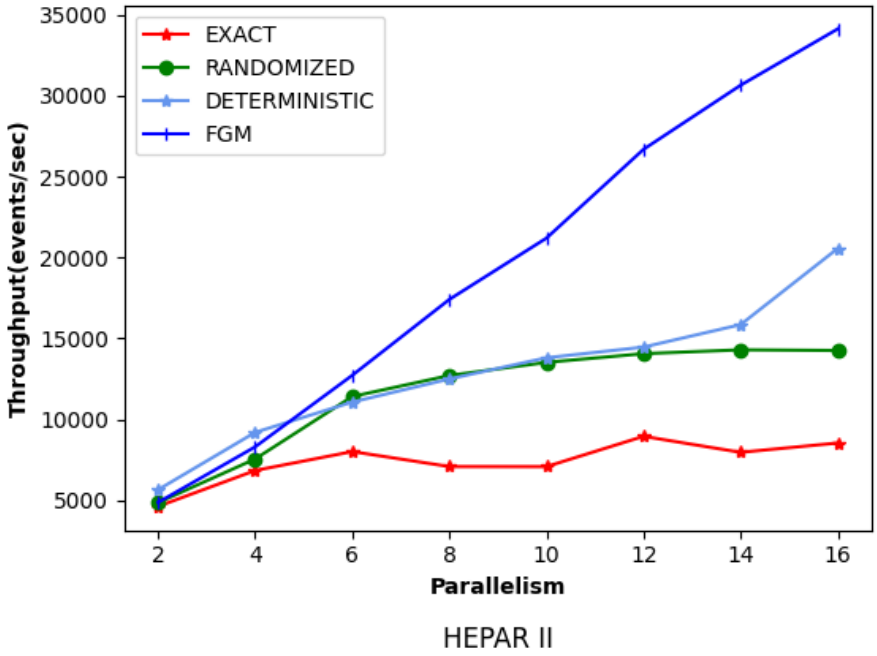


Figure 32: Throughput(events/sec) related to the number of parallelism for both approaches for HEPAR II dataset- Best results

6.3.5 Dummy Father

In this section, we present the results of the *Dummy Father (DF)* in conjunction with the NON_*UNIFORM* algorithm. The results are exclusively focuses on the first approach (*See Chapter 4.2.1*).

We measure the *communication cost* of the *NON_UNIFORM* combined with the *Dummy Father (DF)* method and then compare the results to the *communication cost* of the *NON_UNIFORM* algorithm, using both the *RANDOMIZED* and *DETERMINISTIC counters* of the first approach. The *datasets* are varied in the range of $5K$ to $50M$ and are related to the *HEPAR II* and *ALARM* dataset, respectively. Note that the y-axis is in logarithmic scale.

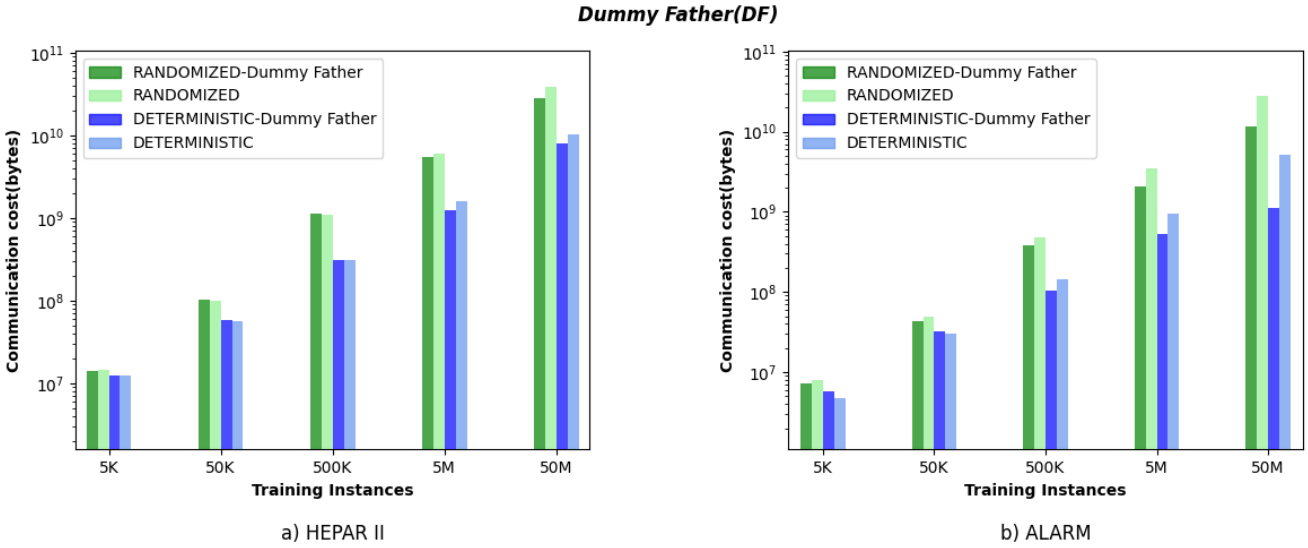


Figure 33: Communication cost in conjunction with the Dummy Father (DF) method for HEPAR II, ALARM datasets

As the number of training instances increases, the difference in communication cost begins to increase as well. This is because each counter is required to send fewer messages. We achieve a 40% reduction in *communication cost* of the *RANDOMIZED counters* and a 50% reduction in *communication cost* for the *DETERMINISTIC counters.* To mention that the reduction in *communication cost* is attributed to the prevention of maintaining *EXACT counters* for *orphan* nodes. Therefore, the differences may vary among different networks. Specifically, in case of the *ALARM* dataset, we are able to prevent the maintenance of *26 EXACT counters*, while in *HEPAR II* we are able to prevent the maintenance of *18 EXACT counters*.

Chapter 7:

Conclusions

7.1 Conclusions

We propose a different approach for learning parameters ensuring the continuously maintenance of a *Bayesian Network* over the *continuous distributed model*, using *FGM* method. We achieve a reduction on communication cost compared to the EXACTMLE, while ensuring error *guarantees* on the estimation of the *probabilities queries* of the *joint probability distribution* of a *Bayesian Network*, with the latter be confirmed from the experimental evaluation. Additionally, we present a comprehensive and extensive analysis from the first approach using both the RANDOMIZED and *DETERMINISTIC* counters combined with the *BASELINE, UNIFORM* and *NON_UNIFORM* algorithms. Finally, we integrate both approaches into a *distributed streaming framework* like *Apache Flink*.

7.2 Future Work

There are several extensions that can be explored for both approaches. One interesting extension is the *structure* learning of a *Bayesian* Network, where the structure of the *Bayesian* Network is assumed to be known in advance, now the learning of the structure is accomplished in an online fashion as new data is received at the sites. Considering the second approach, another interesting extension is the search of "better" safe functions. This could potentially lead to further reduction in communication cost by optimizing the selection of safe functions. Additionally, the adaptation of the *Graphical Model sketches* [32] could be explored to achieve a reduction in communication cost. *Graphical sketches* provide a *space-efficient* representation of the entire *joint probability distribution*, allowing for more efficient communication compared to *frequency vectors*, while ensuring the appropriate *error guarantees*.

Appendix

Experimental results

Communication cost related to the number of training instances

We present the *mean error to GT* for both approaches. To mention that the differences among the *BASELINE, UNIFORM* and *NON_UNIFORM* algorithms are not significant because the *statistical error* outweighs the *approximation error*. As a result, the dominant factor is the *statistical error*, and there are no differences among the algorithms. The *error* decreases as the number of *training instances* increases which can be attributed to the decrease in the *statistical error*. In terms of accuracy, both approaches perform quite well. For example, for the datasets exceeding $50K$ training instances, the error is less than 10% for each approach. The captured error is considered good when considering the *probability queries*.

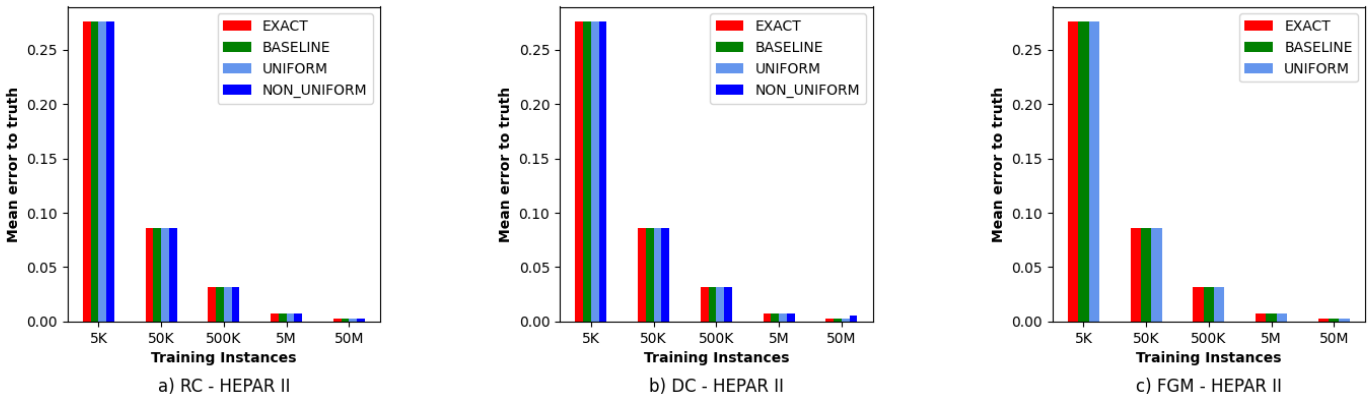
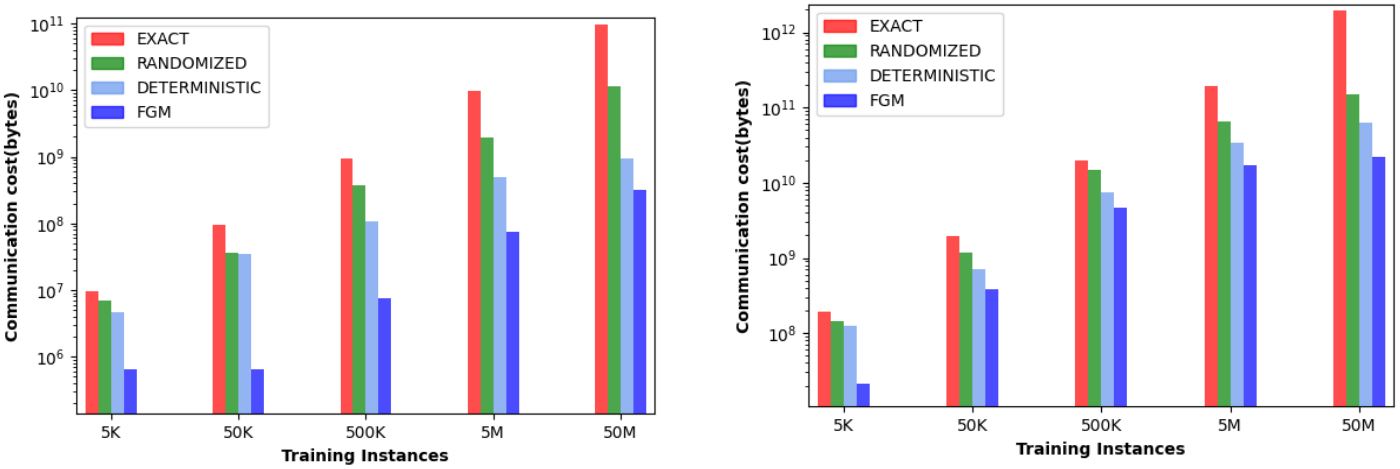


Figure 34: Mean error to GT related to the number of training instances for both approaches for HEPAR II dataset

We analyze the *communication cost* in relation to the number of *training instances* for both approaches using the *LINK* and *ALARM* dataset. For each approach and network, among the *BASELINE, UNIFORM* and *NON_UNIFORM* algorithms are selected the algorithm with the best performance



a) ALARM

b) LINK

Figure 35: Communication cost related to the number of training instances for LINK, ALARM datasets

Communication cost related to the approximation factor ε

We present the *communication cost* in relation to the *approximation factor ε*, using the *BASELINE, UNIFORM* and *NON_UNIFORM* algorithms for each approach.

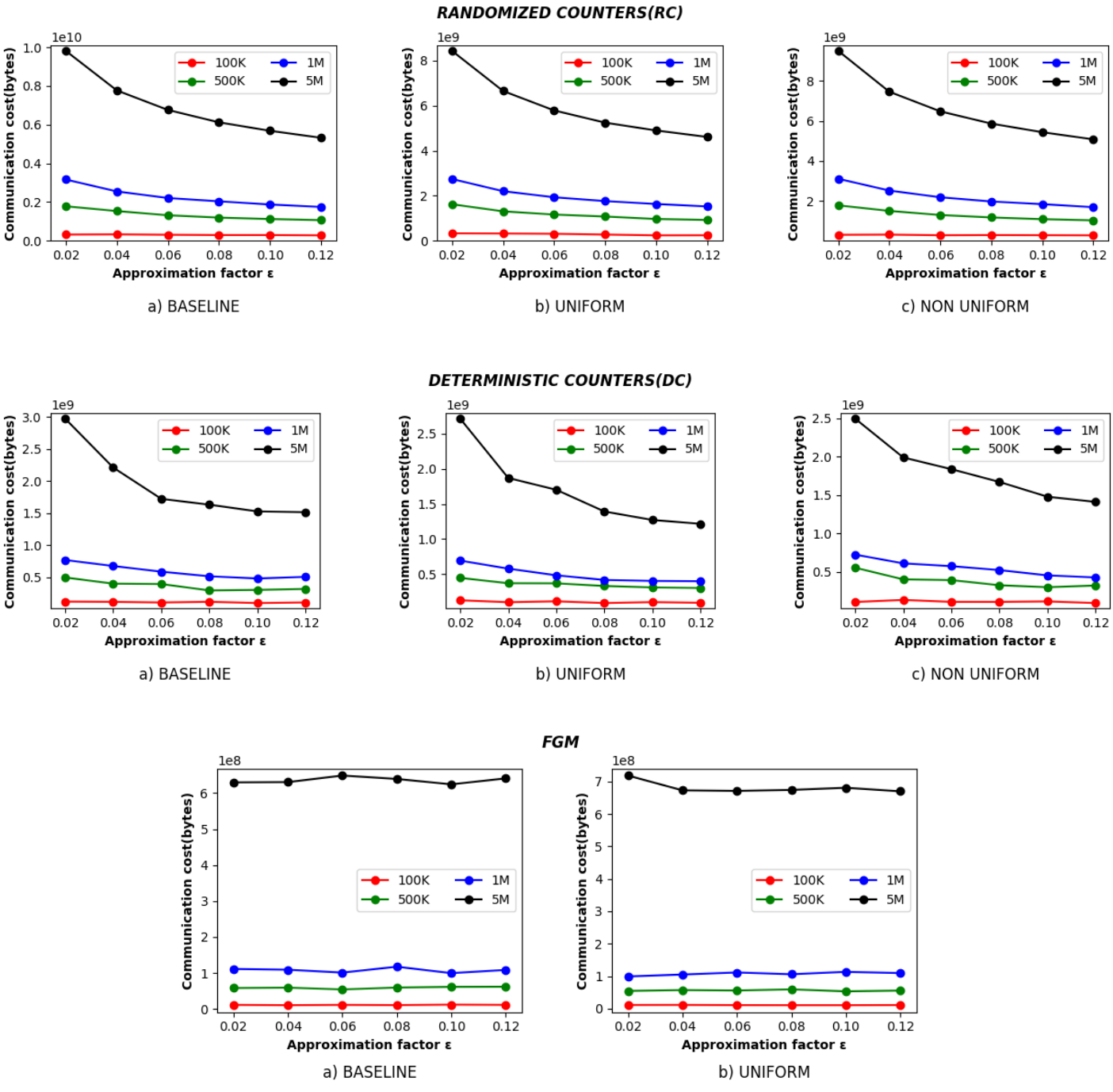


Figure 36: Communication cost related to the approximation factor ε for both approaches for HEPAR II dataset

Communication cost related to the number of workers

We present the *communication cost* in relation to the number of sites, using the *BASELINE, UNIFORM* and *NON_UNIFORM* algorithms for each approach.

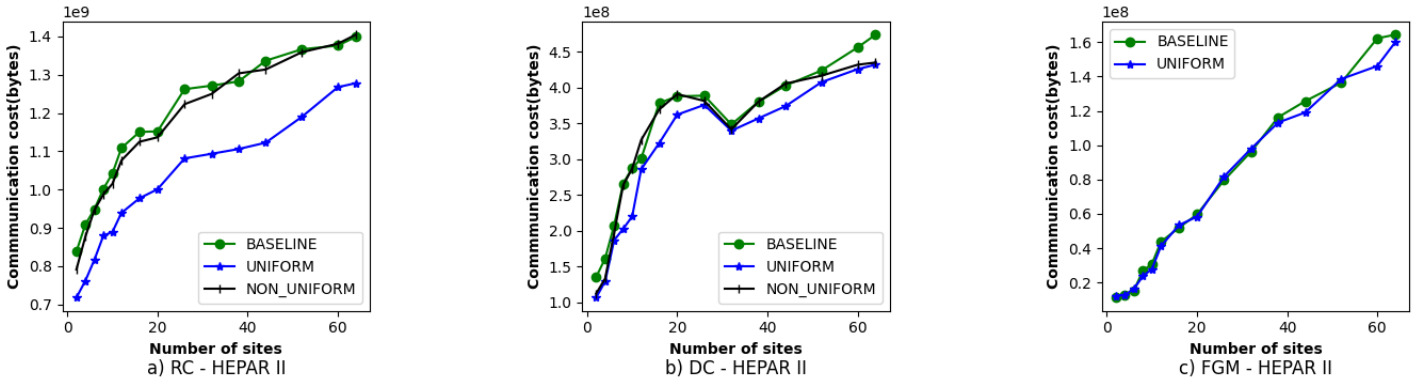


Figure 37: Communication cost related to the number of sites for both approaches for HEPAR II dataset

Scalability

Runtime related to the number of sites

We present the *runtime(sec)* in relation to the number of sites using the *BASELINE, UNIFORM* and *NON_UNIFORM* algorithms for each approach.

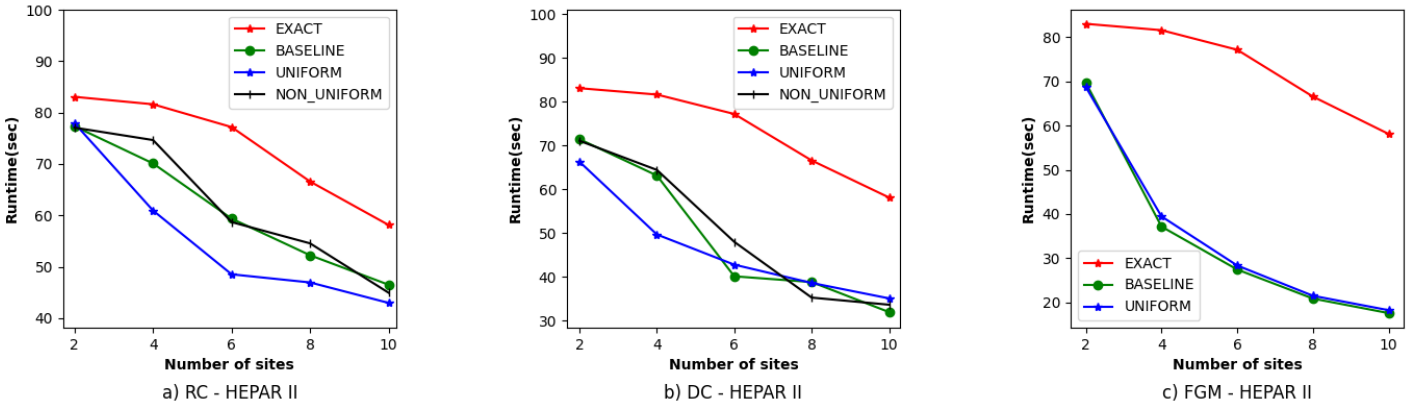
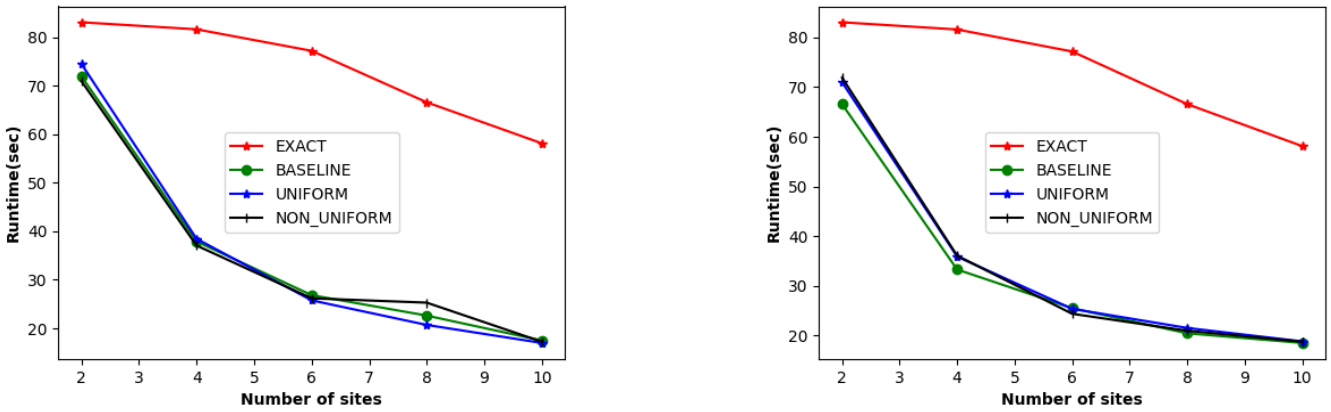


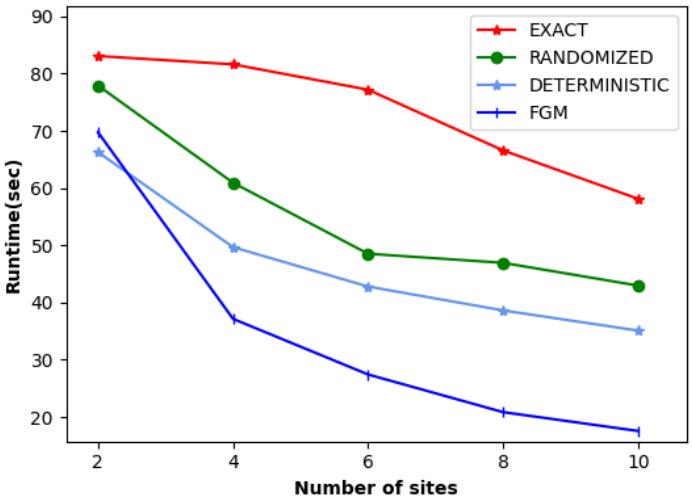
Figure 38: Runtime(sec) related to the number of sites for both approaches for HEPAR II dataset



a) RC - HEPAR II, after initial state

b) DC - HEPAR II, after initial state

Figure 39: Runtime(sec) related to the number of sites for the first approach for HEPAR II dataset, after the initial state

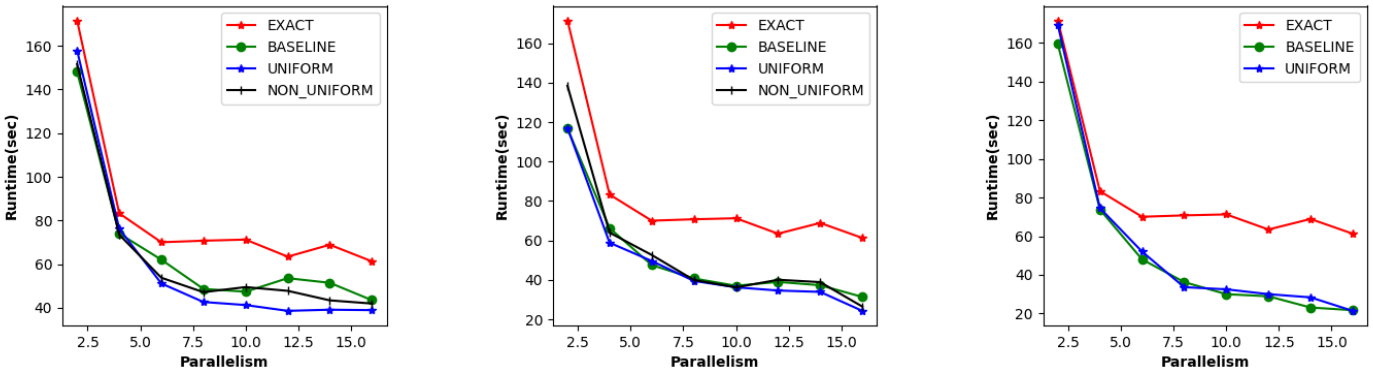


HEPAR II

Figure 40: Runtime(sec) related to the number of sites for both approaches for HEPAR II dataset - Best results

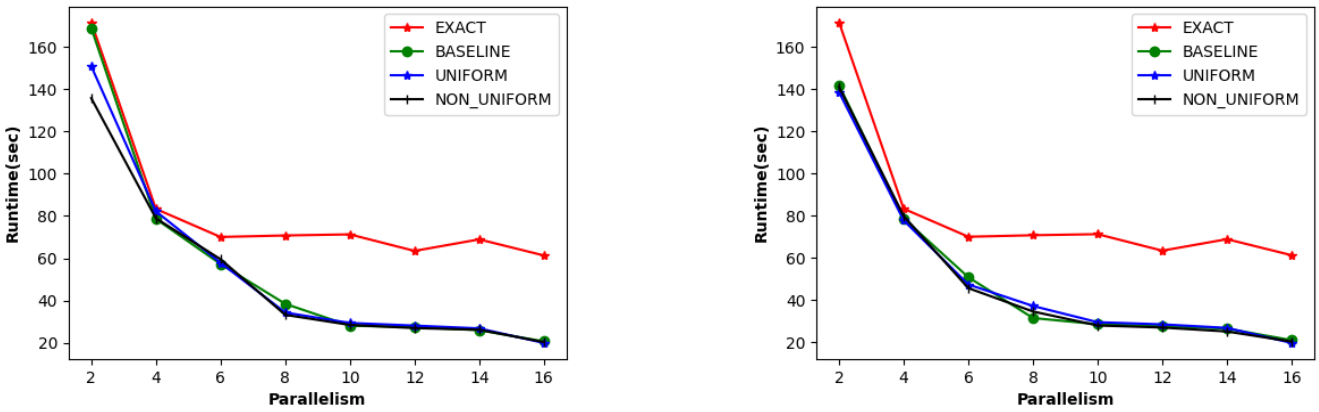
Runtime related to the number of parallelism

We present the *runtime(sec)* in relation to the number of parallelism using the *BASELINE, UNIFORM* and *NON_UNIFORM* algorithms for each approach.



a) RC - HEPAR II b) DC - HEPAR II c) FGM - HEPAR II

Figure 41: Runtime(sec) related to the number of sites for both approaches for HEPAR II dataset



a) RC - HEPAR II, after initial state b) DC - HEPAR II, after initial state

Figure 42: Runtime(sec) related to the number of sites for the first approach for HEPAR II dataset, after the initial state

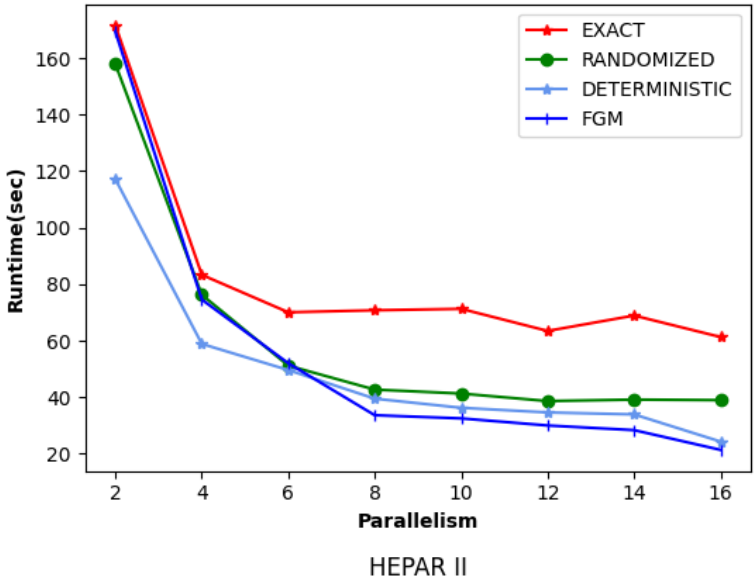


Figure 43: Runtime(sec) related to the number of sites for both approaches for HEPAR II dataset - Best results

Project Structure

In the following figure, the abstract structure of the project is presented. It depicts how the packages are organized, which will be discussed in details below.

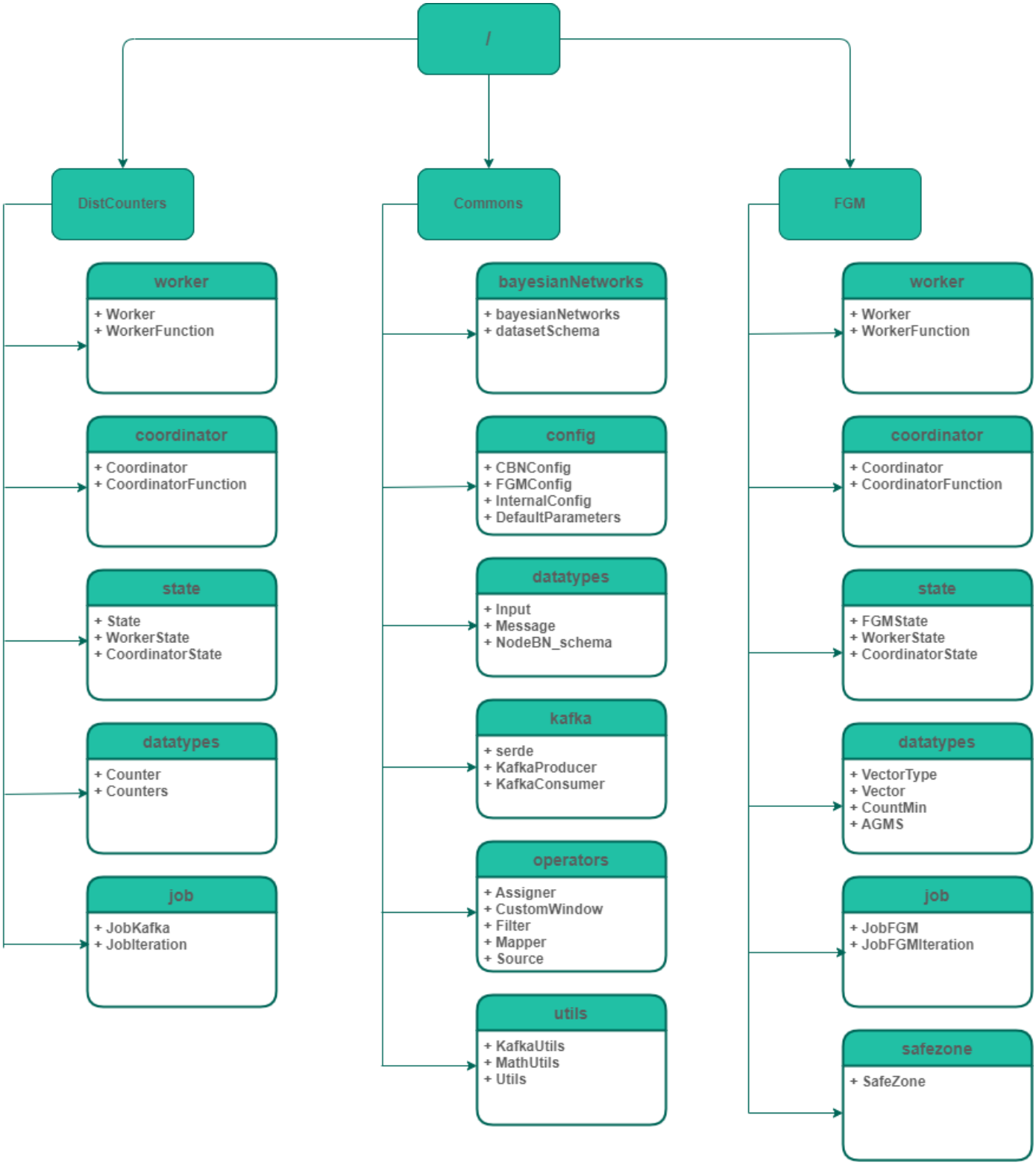


Figure 44: Project Structure

As depicted, the project structure is divided into three essential categories: the *DistCounters* the *FGM* and the *Commons*. DistCounters represents the Approximate Distributed Counters, FGM represents the components specific to the second approach, and Commons represents the shared components used by both approaches. We present a summary of the main components in each category.

DistCounters-FGM

- ***worker****:* The package includes two components: the *Worker* and the *WorkerFunction*. The *Worker* component contains the rudimentary logic for each *Worker*, such as managing the *Input Source* and receiving control messages from the Coordinator(*Feedback Source*). The *WorkerFunction* component provides the necessary functionality specific to each Worker and is defined based on the selected approach.
- ***coordinator****:* The package consists of two components: the *Coordinator* and the *CoordinatorFunction*. The *Coordinator* component handles the basic logic used by the Coordinator, which includes managing messages from the Workers and handling the *probability queries (Query Source)*. The *CoordinatorFunction* component provides all the functionality for the Coordinaotor and is defined based on the selected approach.
- ***state:*** The package consists of three components, but in this case, there is a hierarchical relation among them: the *State*, the *WorkerState* and the *CoordinatorState*. The *State* component contains the shared elements used by both sides (*Worker-Coordinator*). It serves as a base component inherited by both *WorkerState* and *CoordinatorState*. T *State* component includes elements related to the setup of the entire pipeline of the system and will be discussed in detail in the following section. The *WorkerState* component includes elements from the *State* component and the additional state for each Worker. For example, the *approximate distributed counter* regarding the first approach while the *frequency vectors* considering the *FGM* protocol. The *CoordinatorState* follows a similar pattern, inheriting elements from the *State* component and maintaining state specific to the Coordinator based on the selected approach (*approximate distributed counters* or *frequency vectors*).
- ***datatypes:*** The package contains the basic *datatypes* utilized by both the *WorkerState* and the *CoordinatorState*. In the first approach, the fundamental element utilized by the sites is the *Counter*, which represents an *approximated distributed counter*. In the second approach, the key element is the *Vector*, which defines a *frequency vector*. As mentioned earlier, the FGM method constitutes an independent monitoring method. Thus, we also implement another essential element called *sketches*. Particularly, it includes two well-known and basic sketches: the *Fast-AGMS sketch* [33] and the *CountMin sketch* [34]. These sketches can be used to for monitoring in conjunction with the appropriate safe function.
- ***safezone:*** This package is specifically related to the FGM method and focuses on the *safe functions*. It provides the necessary functionality to define and utilize the appropriate safe function based on the monitoring requirements. The package ensures compatibility with the specific datatype provided by the system.
- ***job:*** This package encompasses the entire inferred pipeline by combining all the components. The first pipeline refers to the one that utilizes a Kafka topic as feedback

loop, while the second pipeline refers the one that utilizes the *Iterative Stream operator* provided from Apache Flink. These pipelines orchestrate the flow of data and processing within the system.

Commons

- ***bayesianNetworks:*** This package serves as a repository for all the available *Bayesian Networks* that are integrated into the system, where each network accompanied by the *schema* of the dataset. The *schema* defines the format of the *input feature vector* for a *Bayesian Network*. Therefore, for the insertion of a new *Bayesian Network* or *Naïve Bayes Classifier* to the system, it is necessary to define both the *bayesiaNetwork* itself and its corresponding *datasetSchema*.
- ***config***: This package consists of three individual components***:*** the *InternalConfig*, the *CBNConfig* and *FGMConfig*. The *InternalConfig* contains shared parameters by both approaches (*DistCounter - FGM*) required for the setup of the entire pipeline. The *CBNConfig* includes parameters specific to the *DistCounter*, while the *FGMConfig* includes the parameters related to the *FGM* protocol. These parameters are further discussed in detail in the *Project Setup* section.
- ***datatypes:*** This package comprises the basic shared *datatypes* utilized by both approaches. Specifically, it includes the format of the *Input Source* and the format of messages (*Message*) exchanged between the Coordinator and the Workers and vice versa.

Project Setup

This section represents the description of the parameters need to be defined by the user in order to run an example of our system.

Distributed Counters Configuration

Parameter: typeCounter
Description: This parameter defines the type of counter to be used as basic component during the process. There are four available types of counters: RANDOMIZED, DETERMINISTIC, CONTINUOUS and EXACT counter.

FGM Configuration

Parameter:typeState
Description: This parameter defines the type of state to be used by both sides(workers-coordinator) during the process. There are three available types of state: VECTOR, Fast-AGMS and COUNT_MIN sketches.

Parameter: enableRebalancing
Description: This parameter enables/disables the rebalancing mechanism of the FGM protocol. Moreover, it works in conjunction with the value of lambda. The default value of lambda is 2.

Parameter: width, depth
Description: These parameters are only applicable if the type of state chosen is one of the available types of sketches. They determine the width and the depth of the sketch to be used as the state of the Workers and Coordinator.

Common Configuration

Parameter: typeNetwork
Description: This parameter defines the type of network to be used during the process. There are two available types of networks: BAYESIAN, NAÏVE

Parameter: BNSchema
Description: This parameter defines the specific network to be used during the process. There are built-in network options availabel. Here are some of the available network options: SACHS, ALARM, HEPAR2, LINK, MUNIN, and EARTHQUAKE.

Parameter: datasetSchema
Description: This parameter defines the schema of the dataset to be used during the process. Similar to the network schema, there are built-in dataset schema options available. Here are some of the available schemas options: SACHS, ALARM, HEPAR2, LINK, MUNIN, and EARTHQUAKE.

Parameter: errorSetup
Description: This parameter defines the algorithm used to adjust the error between the available counters. There are three available options: the BASELINE, UNIFORM, and NON_UNIFORM algorithms.

Parameter: workers
Description: This parameter defines the number of workers/sites (not including the Coordinator) to be used during the process.

Parameter: parallelism
Description: This parameter defines the parallelism i.e. the number of subtasks to be used by each pipeline operator during the process.

Parameter: eps
Description: This parameter specifies the epsilon value that defines the accuracy of the estimated joint probability distribution (user-defined error guarantees).

Parameter: delta
Description: This parameter specifies the delta value that defines the likelihood of the estimated joint probability distribution (user-defined error guarantees).

Parameter: inputTopic
Description: This parameter defines the Kafka topic to be used as the input for the Workers.

Parameter: feedbackTopic
Description: This parameter defines the Kafka topic to be used as feedback loop between the Workers and the Coordinator.

Below are two complete examples demonstrating the application of the aforementioned parameters. The first example corresponds to DistCounters method, while the second example corresponds to the FGM method.

In both examples, the dataset is the **HEPAR2** using **sourceHEPAR2** as inputTopic and **fdHEPAR2** as feedbackTopic. Furthermore, the number of workers is equivalent to **8** while the number of parallelism is equal to **4**. Finally, the accuracy set to **0.1** and the likelihood of the estimated joint probability distribution is **90%**(error guarantees).

--inputTopic sourceHEPAR2 --feedbackTopic feedbackHEPAR2 --workers 8 --parallelism 4 --eps 0.1 --delta 0.25 --errorSetup UNIFORM --typeCounter RANDOMIZED --queriesSize 1000 --bn HEPAR2 --datasetSchema HEPAR2

The only change in order for the previous example to be applied to the second approach, is the *typeCounter* to be replaced by the *typeState*, which is accompanied by the appropriate system type provided (for example, *VECTOR*).

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