MiSoSouP: Mining Interesting Subgroups with Sampling and Pseudodimension

Matteo Riondato
Labs
Two Sigma Investments, LP
New York, NY, USA
matteo@twosigma.com

Fabio Vandin
Department of Information Engineering
Università di Padova
Padova, Italy
fabio.vandin@unipd.it

"Miso makes a soup loaded with flavour that saves you the hassle of making stock." – Y. Ottolenghi

ABSTRACT

We present MiSoSouP, a suite of algorithms for extracting high-quality approximations of the most interesting subgroups, according to different interestingness measures, from a random sample of a transactional dataset. We describe a new formulation of these measures that makes it possible to approximate them using sampling. We then discuss how pseudodimension, a key concept from statistical learning theory, relates to the sample size needed to obtain an high-quality approximation of the most interesting subgroups. We prove an upper bound on the pseudodimension of the problem at hand, which results in small sample sizes. Our evaluation on real datasets shows that MiSoSouP outperforms state-of-the-art algorithms offering the same guarantees, and it vastly speeds up the discovery of subgroups w.r.t. analyzing the whole dataset.

CCS CONCEPTS

• Mathematics of computing → Probabilistic algorithms; • Information systems → Data mining; • Theory of computation → Sketching and sampling; Sample complexity and generalization bounds;

KEYWORDS

Pattern Mining, Statistical Learning Theory

ACM Reference Format:

1 INTRODUCTION

A fundamental task within data mining is subgroup discovery [8, 10, 32], which requires to identify interesting subsets (the subgroups) of a dataset, for which the distribution of a specific feature (the target) within the subgroup largely differs from the distribution of that feature in the entire dataset. The notion of interestingness is captured by a formally-defined measure of quality that combines the frequency of the subgroup in the dataset and the difference between the mean of the target within the subgroup and the mean of the target in the entire dataset. Subgroup discovery is a broadly applicable task and is relevant in many domains: in market basket analysis, it uncovers groups of customers with a particular interest in buying a product; in social networks, it identifies members attracted to a given topic; in biomedicine, it discovers groups of patients associated with a clinical phenotype (e.g., response to therapy).

Many exact algorithms for subgroup discovery have been proposed [10, 32] (see also the comprehensive reviews by Herrera et al. [5] and Atzmueller [2]). They naturally require to process the entire dataset, but the sheer amount of data may render such (full) computation infeasible. A general approach to deal with very large datasets is to only analyze a small random sample of the data. Random sampling has been successful in many areas of knowledge discovery, such as frequent itemsets mining [21, 22] and graph analysis [23]. The main challenge in using sampling for subgroup discovery is understanding how close the qualities of the subgroups observed in the sample are to their exact values, which are unknown as they can only be obtained by processing the entire dataset. Solving this challenge requires the derivation of a sample size $S$ such that, with high probability, on a sample of size $S$, all the sample qualities are within $\epsilon$ from the exact ones, where $\epsilon$ is an user-specified parameter (to be fixed with domain knowledge) controlling the maximum allowed error.

The derivation of such sample size for subgroup discovery is more complex than in other scenarios (e.g., than in frequent itemsets mining [21, 22]), since estimating the quality of a subgroup requires to approximate both the frequency of the subgroup in the dataset and the mean of the target within the subgroup. The latter is an especially challenging inferential task since the target mean is a conditional expectation. This increased complexity is reflected in the lack of rigorous sampling algorithms for subgroup discovery, with even popular approaches [25] not providing rigorous quality guarantees on their output, as we discuss in the supplementary materials [24].
1.1 Contributions
The main focus of this work is the extraction of a high-quality approximation of the top-$k$ most interesting subgroups from a random sample of the dataset. Our contributions are the following.

- We precisely define the concept of $\varepsilon$-approximation of the set of top-$k$ subgroups according to various interestingness measures, extending and strengthening an existing definition by Scheffer and Wrobel [25, Def. 2]. The user-defined parameter $\varepsilon$ controls the quality of the approximation.
- We give a new formulation of the 1-quality, one of the key measures of subgroup interestingness, and as a consequence also of other fundamental measures. This novel formulation is crucial to enable the estimation of the interestingness of subgroups from a sample.
- We present MiSoSouP, a suite of algorithms that use random sampling to extract, with probability at least $1 - \delta$, $\varepsilon$-approximations of the set of top-$k$ interesting subgroups from a small random sample of the dataset. MiSoSouP is the first algorithm to obtain such approximations, while previous work [25] does not actually provide rigorous guarantees (see the supplementary materials [24]). The only parameters of MiSoSouP are $\varepsilon, k$, and the confidence parameter $\delta$, which are all easily interpretable, therefore making our algorithms very practical.
- We derive the sample size employed by MiSoSouP using pseudodimension [19], a key concept from statistical learning theory [30]. We show an upper bound to the pseudodimension of the task of subgroup discovery, which is independent from the size of the dataset and only depends on properties of the set of possible subgroups (i.e., the language) and on the number of columns of the dataset. The computation of the upper bound is essentially cost-free. To the best of our knowledge, ours is the first application of pseudodimension to the field of subgroup discovery, and in general to pattern mining.
- We perform an extensive experimental evaluation showing that MiSoSouP identifies rigorous approximations to the most interesting subgroups using a small fraction of the dataset, and it provides a significant speed-up w.r.t. other sampling approaches with the same guarantees.

2 RELATED WORK
Many measures for evaluating the quality (i.e., interestingness) of subgroups have been proposed in the literature, and many subgroup discovery algorithms are available. We discuss some of the measures in Sect. 3, and refer the reader to the surveys by Herrera et al. [5] and Atzmueller [2] for details about the algorithms. In this work we treat these algorithms as black-boxes: we run them on a small random sample of the dataset and we are interested in how well the so-obtained collection of interesting subgroups approximates the one we would obtain by mining the whole dataset.

Scheffer and Wrobel [25] first studied the use of sampling for subgroups: they present GSS, a progressive sampling algorithm to compute an approximation of the most interesting subgroups. Unfortunately, the analysis of GSS has some issues. The first concern is that the quantities of interest (e.g., the number of subgroups at iteration $i$) are random variables, while the analysis assumes that they are fixed values. Another major issue is that the analysis uses a Chernoff bound for the probability of deviation for the unusualness of a subgroup, but such bound cannot be employed since the unusualness is a conditional probability, hence it cannot be obtained as the average of a binary function over all transactions in the sample. Other issues and possible partial solutions are discussed more in depth in the supplementary materials [24]. Even when (partially) corrected, the analysis of GSS relies on the availability of probabilistic confidence intervals on the estimated quality of each subgroup under consideration, and then on a union bound over all possible subgroups, in order to obtain simultaneous guarantees on the confidence intervals of all subgroups. The union bound is, by design, loose in many practical situations, effectively assuming that the considered events are independent. As a results, the stopping condition used by GSS cannot be satisfied at small sample sizes. MiSoSouP instead relies on pseudodimension [19], which allows us to use very small sample sizes.

Some works focused on the issue of the statistical significance of subgroups. Duivesteijn et al. [3] designed a permutation-based approach to estimate the distribution of false discoveries, which is used to assess the ability of various quality measures to distinguish between statistically significant patterns and false discoveries. Van Leeuwen and Ukkonen [29] showed that several real datasets contain large numbers of high-quality subgroups, many more than are expected from randomly drawn subgroups. Terada et al. [27] introduced LAMP, a method to identify a minimum generalization threshold to find subgroups while bounding the family-wise error rate (FWER), where the significance of a subgroup is given by its association with a binary target variable as assessed by Fisher exact test. Minato et al. [15] subsequently improved LAMP by employing a more efficient mining strategy. We do not investigate the issue of statistical significance of subgroups, but one of the quality measures we study (i.e., the 1/2-quality measure, see Sect. 3) is a proxy for the z-score, a well-defined measure of statistical significance.

Our approach is orthogonal to heuristic approaches that sample subgroups to speed-up the discovery of interesting subgroups [17]. In contrast, MiSoSouP samples transactions while providing rigorous guarantees on the relation between the qualities of the subgroups obtained from the sample and their exact qualities (i.e., obtained from the entire dataset). In fact, any exact or heuristic algorithm can be used to mine the sample from MiSoSouP while maintaining the aforementioned guarantees for the resulting subgroups. The use of sampling is also orthogonal to techniques that aim at reducing the redundancy in the output collection of subgroups [28]. Indeed these approaches could be applied to the collection of subgroups obtained by MiSoSouP.

Pseudodimension [19] is a key concept from statistical learning theory [30]. Like many other measures of sample complexity, such as Rademacher averages, it has long been considered only of theoretical interest, but recent applications [4, 7, 20, 22, 23] of these quantities have shown that they can be extremely useful in practice, especially on very large datasets. Pseudodimension is closely related to the concept of Vapnik-Chervonenkis dimension that has been used in the context of frequent itemsets mining by Riondato and Upfal [21]. Despite the relative similarity between subgroup discovery and frequent itemset mining, using pseudodimension
for the former presents significant challenges, such as lack of anti-
monotonicity in the quality measures, that do not allow to use
the same approach by Riondato and Upfal [21]. To the best of our
knowledge, ours is the first application of concepts from statistical
learning theory to the task of subgroup discovery.

3 PRELIMINARIES

In this section we formally introduce the core definitions and theo-
rems that we use throughout the article.

3.1 Subgroup discovery

We now define the fundamental concepts of subgroup mining [9]
and the quality measures used to rank the subgroups.

Let \( \mathcal{D} \) be a \textit{dataset}, i.e., a bag of \((z+1)\)-dimensional
tuples, known as \textit{transactions}, over the attributes \(\{A_1, \ldots, A_z, T\}\).
The attributes \(A_i, 1 \leq i \leq z\) are known as \textit{description}
attributes, while \(T\) is the \textit{target} attribute. Transactions take value in
\(Y_1 \times \cdots \times Y_z \times Y_T\), where each \(Y_i\) is the (categorical or numerical) domain
of attribute \(A_i\), while \(Y_T\) is Boolean (i.e., \(Y_T = \{0, 1\}\)).

A \textit{subgroup} is a conjunction of disjunctions of conditions on the
description attributes. An example of subgroup is: \((A_1 = \text{“blue”} \lor
A_1 = \text{“red”}) \land (A_2 > 4)\). A transaction \(t \in \mathcal{D}\) supports a subgroup
\(A\) if the values of \(t\)’s attributes satisfy \(A\). The \textit{cover} \(\mathcal{C}_D(A)\) of \(A\) on
\(\mathcal{D}\) is the bag of transactions in \(\mathcal{D}\) that support \(A\). The \textit{generality}
g\(_D\)(\(A\)) of a subgroup \(A\) on \(\mathcal{D}\) is the ratio between the size of the
cover of \(A\) on \(\mathcal{D}\) and the size of \(\mathcal{D}\):

\[
g_D(A) = \frac{|\mathcal{C}_D(A)|}{|\mathcal{D}|} .
\]

Given a bag \(\mathcal{B}\) of transactions, let

\[
\mu(\mathcal{B}) = \frac{1}{|\mathcal{B}|} \sum_{t \in \mathcal{B}} t.T
\]

be the \textit{target mean} of \(\mathcal{B}\), where \(t.T\) denotes the value in the target
attribute of the tuple \(t\). If \(\mathcal{B} = \emptyset\), \(\mu(\mathcal{B}) = 0\). The \textit{target mean of a
subgroup} \(A\) on \(\mathcal{D}\) is

\[
\mu_D(A) = \mu(\mathcal{C}_D(A)) .
\]

The \textit{unusualness} \(u_D(A)\) of \(A\) on \(\mathcal{D}\) is the difference between the
target mean of \(A\) and the target mean of \(\mathcal{D}\):

\[
u_D(A) = \mu_D(A) - \mu(\mathcal{D}) .
\]

The generality and the unusualness are used to define quality mea-
sures for the subgroups (see Sect. 3.1.1).

A \textit{description language} \(\mathcal{L}\) is a set of subgroups that are of potential
interest, and is \textit{fixed in advance} by the user before analyzing the
dataset. It could be a superset or a subset of the subgroups that
actually appear in the dataset, and it expresses the constraint that
only subgroups in the description language should be considered
in the mining process. For example, given some integer \(m\), one may
consider the description language of all and only the subgroups
composed of up to \(m\) conjunctions of equality conditions on the
attributes.\(^{1}\)

3.1.1 Quality measures. A \textit{quality measure} for the subgroups in
\(\mathcal{L}\) on a dataset \(\mathcal{D}\) is a function \(\phi_{\mathcal{D}} : \mathcal{L} \to \mathbb{R}\) which assigns
a numerical score to each subgroup \(A \in \mathcal{L}\) based on its generality
and unusualness. In this work we consider the most popular subgroup
quality measures [10], which differ from each other for the relative
weight given to generality and unusualness.

Definition 3.1 ([8, 18, 32]). Let \(p \in \{1/2, 1, 2\}\). The \textit{p-quality of a
subgroup} \(A\) on a dataset \(\mathcal{D}\) is

\[
q^{(p)}_D(A) = (\|\mathcal{D}\| \mu_D(A))^p u_D(A) .
\]

The 1-quality is also known as \textit{Weighted Relative Accuracy}
(WRAcc).\(^{3}\) The 1/2-quality is proportional to the \textit{z-score} \(\text{z}^\text{stat}\) for the
statistic \(\mathcal{C}_D(A)/u_D(A)\), which can be used to test whether a sub-
group shows statistical association with the target variable. Thus,
the 1/2-quality can be used as a proxy for the statistical significance
of the subgroup \(A\) [8, 25, 29]. The domain \(Y_T\) of the target attribute
is Boolean, thus \(q^{(p)}_D(A) \in [-1, 1]\) for any subgroup \(A\). There exist
variants of the \(p\)-qualities that consider the \textit{absolute value} of the
unusualness [25]. MiSoSouP can be easily adapted to work with
such measures.

3.1.2 Subgroup discovery task. Fix \(p \in \{1/2, 1, 2\}\). Let \(\mathcal{L}_D\) be
the subset of \(\mathcal{L}\) containing only the subgroups of \(\mathcal{L}\) that actually
appear in \(\mathcal{D}\) (i.e., those with generality strictly greater than zero).
We do not assume to know \(\mathcal{L}_D\); it is needed for the following
definition. Assume to sort the subgroup in \(\mathcal{L}_D\) in decreasing order
according to their \(p\)-quality in \(\mathcal{D}\), ties broken arbitrarily. Let \(k > 0\)
be an integer and let \(r^{(p)}_D(k)\) be the \(p\)-quality of the \(k\)-th subgroup
in the sorted order.

Definition 3.2. The \textit{subgroup discovery task} consists in extracting
the set \(\text{TOP}_p(k, \mathcal{D})\) of the \(k\)-top subgroups in \(\mathcal{L}_D\) w.r.t. the \(p\)-quality
in \(\mathcal{D}\), i.e., the set of subgroups with \(p\)-quality at least \(r^{(p)}_D(k)\):

\[
\text{TOP}_p(k, \mathcal{D}) = \left\{ A \in \mathcal{L}_D : q^{(p)}_D(A) \geq r^{(p)}_D(k) \right\} .
\]

\(\text{TOP}_p(k, \mathcal{D})\) may contain more than \(k\) elements when many
subgroups have \(p\)-quality equal to \(r^{(p)}_D(k)\).\(^{5}\)

A variant of the task allows the user to specify a constraint on the
minimum generality of returned subgroups. MiSoSouP can handle
this case with minor modifications.

3.1.3 Approximations. We want to obtain an \(\varepsilon\)-approximation
to the \textit{set} \(\text{TOP}_p(k, \mathcal{D})\) from a small \textit{random sample} of the dataset,
where \(\varepsilon \in (0, 1)\) is an user-defined parameter that controls the
maximum acceptable error. Formally this concept is defined as
follows.

Definition 3.3. Let \(\varepsilon \in (0, 1)\). An \(\varepsilon\)-approximation to \(\text{TOP}_p(k, \mathcal{D})\)
is a set \(\mathcal{B}\) of pairs \((A, q_A)\) where \(A\) is a subgroup and \(q_A\) is a value
in \([-1, 1]\), and \(\mathcal{B}\) is such that:

\(^1\)We use \(|\mathcal{B}|\) to denote the size of a bag \(\mathcal{B}\), i.e., the number of elements in \(\mathcal{B}\), counting
repeated elements multiple times.

\(^2\)Scheffer and Wrobel [25] use the term \textit{statistical unusualness}. We choose to drop the
adjective to avoid confusion with \textit{statistical significance}.

\(^3\)Van Leeuwen and Ukkonen [29] denote the 1/2-quality as “WRAcc”, but all other
references we found (e.g., [5, 12]) use this name to denote the 1-quality.

\(^4\)The \textit{z-score} for a test statistic \(X\) is \((X - \mathbb{E}[X]) / \sigma_X\), where \(\mathbb{E}[X]\) is the expectation
and \(\sigma_X\) is the standard deviation of \(X\) (under the null hypothesis). For subgroups,
under the null hypothesis of no association of a subgroup with the target variable,
the \textit{z-score} is \(\left|\mathcal{C}_D(A)/\mu_D(A) - \mathcal{C}_D(A)/u_D(A)\right|\sqrt{\mathcal{C}_D(A)/\mu_D(A)} / \sqrt{\mathbb{E}[\mathcal{D}]/(1 - \mu_D(A))}\).

\(^5\)This definition of the task is therefore slightly different from the one given in [25,
Definition 1], where the size of \(\text{TOP}_p(k, \mathcal{D})\) is limited to exactly \(k\) elements.
We now introduce the main concepts and results on A TOP \cite{26} and by Anthony and Bartlett \cite{1}.

H×\f to our settings. discuss them in an extended version of this work.

(1) for any A ∈ TOP_p(k, D), there is a pair (A, q_A) ∈ B; and
(2) there is no pair (A, q_A) ∈ B such that q_p(A) < r_p(k) − ε;
(3) for each pair (A, q_A) ∈ B, |q_p(A) − q_A| ≤ ε/4.

MiSoSouP computes (with high probability) an ε-approximation from a random sample of the dataset.

An ε-approximation can act as a set of candidates for TOP_p(k, D), as it contains a pair (A, q_A) for each subgroup A in this set. Scheffer and Wrobel \cite{25, Definition 2} present a slightly different definition of approximation. Such an approximation is not a set of candidates for TOP_p(k, D), and in particular its intersection with this set may be empty. On the other hand, if we sort the pairs in an ε-approximation by decreasing order of their second component, ties broken arbitrarily, the set of the subgroups in the first k pairs according to this order is an approximation in the sense defined by Scheffer and Wrobel \cite{25}. The choice of ε, similar to the choice of k in Def. 3.2 must be informed, at least in part, by domain knowledge. The quantity 1 − µ(D) can act, in some sense, as an upper bound to the possible choice of ε, as no subgroup can have 1-quality greater than this quantity. Approximations guaranteeing a multiplicative bound on the error are also possible and we will discuss them in an extended version of this work.

3.2 Pseudodimension

We now introduce the main concepts and results on VC-dimension \cite{31} and pseudodimension \cite{19}, specializing some of them to our settings. \footnote{For an in-depth discussion of these topics see, e.g., the books by Shalev-Shwartz and Ben-David \cite{26} and by Anthony and Bartlett \cite{1}.}

3.2.1 VC-dimension. Let W be a finite domain and let R ⊆ 2^W be a collection of subsets of W, where 2^W is the set of all subsets of W. We call R a range set on W, and call its members ranges. The set A ⊆ W is shattered by R if {R ∩ A : R ∈ R} = 2^A. The VC-dimension VC(W, R) of (W, R) is the size of the largest subset of W that can be shattered by R.

3.2.2 Pseudodimension. Pseudodimension \cite{19} is an extension of VC-dimension \cite{31} to real-valued functions, defined as follows.

Let F be a family of functions from a finite domain H onto [a, b] ∈ R. In this work H will be the dataset D, and F will contain one function f_A for each subgroup A ∈ L (see Sect. 4.1.1). Consider, for each f ∈ F, the subset R_f of H × [a, b] defined as

\[ R_f = \{(x, t) : t ≤ f(x)\}. \]

Let

\[ F^+ = \{R_f, f ∈ F\}, \]

be a range set on H × [a, b]. The pseudodimension PD(F) of F is the VC-dimension of (H × [a, b], F^+) \cite[Sec. 11.2]{1}:  

\[ PD(F) = VC(H × [a, b], F^+) . \]

3.2.3 Uniform convergence. Let S = \{x_1, \ldots, x_l\} be a bag of elements of H, sampled independently and uniformly at random, with replacement. For each f ∈ F, define

\[ m_H(f) = \frac{1}{|H|} \sum_{x ∈ H} f(x) \quad \text{and} \quad m_S(f) = \frac{1}{l} \sum_{i=1}^{l} f(x_i) \]  

We call m_S(f) the empirical average of f on S. It holds \[E][m_S(f)] = m_H(f).\] The following result connects an upper bound to the pseudodimension of F to the number of samples needed to simultaneously approximate all the expectations of all the functions in F using their sample averages.

**Theorem 3.4** (\cite{11}). Let PD(F) ≤ d. Fix ξ, η ∈ (0, 1). When S is a collection of
\[ |S| = \left( \frac{b - a}{\xi^2} \right) \left( d + \log \frac{1}{\eta} \right) \]  
elements sampled independently and uniformly at random with replacement from H, then, with probability at least 1−η over the choice of S, it holds
\[ |m_H(f) − m_S(f)| < \xi \quad \text{for every} \quad f ∈ F . \]

The following two lemmas by Riondato and Upfal \cite[Lemmas 3.7 and 3.8]{23} are useful when proving upper bounds to the pseudodimension of a family of functions.

**Lemma 3.5.** If B ⊆ H × [a, b] is shattered by F^+, it may contain at most one element (d, x) ∈ H × [a, b] for each d ∈ H.

**Lemma 3.6.** If B ⊆ H × [a, b] is shattered by F^+, it cannot contain any element in the form (d, a), for any d ∈ H.

4 ALGORITHMS

In this section we present MiSoSouP, our suite of algorithms to compute ε-approximations of TOP_p(k, D). We present only the case for p = 1, and discuss the variants for the other p-qualities in the supplementary materials \cite{24}.

4.1 MiSoSouP for 1-quality

We start by introducing a family P of functions which we use to give a novel expression for the 1-quality of a subgroup. We then present a sufficient condition for extracting an ε-approximation from a sample, and derive bounds to the sample size sufficient to ensure that the condition holds with high probability. Finally, we describe the algorithm.

4.1.1 A novel formulation of the 1-quality. The family P contains one function ρ_A from D to \{−µ(D), 0, 1 − µ(D)\} for each subgroup A ∈ L, defined, for t ∈ D, as:

\[ ρ_A(t) = \begin{cases} 1 & \text{if } t ∈ C_D(A) \text{ and } t.T = 1 \\ −µ(D) & \text{if } t ∈ C_D(A) \text{ and } t.T = 0 \\ 0 & \text{otherwise} \end{cases} . \]

We assume to know the exact value of µ(D), which is a standard and reasonable assumption (made also by Scheffer and Wrobel \cite{25}), since µ(D) can be computed with a very quick scan of the target attribute on D, or kept up-to-date while collecting the data.

The 1-quality of a subgroup A can be expressed as the average over the transactions in the dataset of the function ρ_A:

\[ m_D(ρ_A) = \frac{1}{|D|} \sum_{t ∈ D} ρ_A(t) \]

\[ = \frac{1}{|D|} \left( (1 − µ(D))µ_D(A)[C_D(A) − µ(D)][C_D(A)(1 − µ_D(A))] \right) \]

\[ = \frac{|C_D(A)|}{|D|} (µ_D(A) − µ(D)) = g_D(A)q_D(A) = q_D^{(1)}(A) . \]
This equivalence is a novel insight of crucial importance to enable the efficient estimation of the 1-quality from a sample of the dataset.

Let now \( S = \{ t_1, \ldots, t_L \} \) be a collection of transactions sampled uniformly and independently at random with replacement from \( \mathcal{D} \).

It holds, following the same steps as in (2), that

\[
m_S(\rho_A) = \frac{1}{L} \sum_{i=1}^{L} \rho_A(t_i) = g_S(A)(\mu_S(A) - \mu(\mathcal{D}))
\]

Note that this quantity is different from \( \bar{q}_S^{(1)}(A) \), as it uses \( \mu(\mathcal{D}) \) rather than \( \mu(S) \). As mentioned earlier, it is reasonable to assume knowledge of \( \mu(\mathcal{D}) \). We define the approximate 1-quality of \( A \) on \( S \) as

\[
\bar{q}_S^{(1)}(A) = m_S(\rho_A)
\]

4.1.2 Sufficient condition for an \( \varepsilon \)-approximation. We now show a condition on the sample \( S \) that is sufficient to allow the computation of an \( \varepsilon \)-approximation of \( \text{TOP}_1(k, \mathcal{D}) \) from \( S \). Assume to sort the subgroups in \( \mathcal{L} \) in decreasing order by their approximate 1-quality on \( S \), ties broken arbitrarily. Let \( r_S^{(1)}(k) \) be the approximate 1-quality on \( S \) of the \( k \)-th subgroup in this order.

**Theorem 4.1.** If \( S \) is such that

\[
|\bar{q}_S^{(1)}(A) - q_D^{(1)}(A)| \leq \frac{\varepsilon}{4} \quad \text{for every } A \in \mathcal{L},
\]

then the set

\[
\mathcal{B} = \left\{ (A, \bar{q}_S^{(1)}(A)) : \bar{q}_S^{(1)}(A) \geq r_S^{(1)}(k) - \frac{\varepsilon}{2} \right\}
\]

is an \( \varepsilon \)-approximation to \( \text{TOP}_1(k, \mathcal{D}) \).

**Proof.** Equation (3) holds in particular for subgroups appearing in the pairs in \( \mathcal{B} \). Thus, \( \mathcal{B} \) satisfies Property 3 from Definition 3.3.

It holds

\[
r_S^{(1)}(k) \geq r_D^{(1)}(k) - \frac{\varepsilon}{4}
\]

because all the subgroups in \( \text{TOP}_1(k, \mathcal{D}) \), which are at least \( k \), have, from (3), approximate 1-quality in \( S \) at least \( r_D^{(1)}(k) - \varepsilon/4 \).

Another consequence of (3) is that

\[
r_S^{(1)}(k) \leq r_D^{(1)}(k) + \frac{\varepsilon}{4}
\]

because only subgroups with exact 1-quality in \( \mathcal{D} \) strictly greater than \( r_D^{(1)}(k) \) can have an approximate 1-quality in \( S \) strictly greater than \( r_D^{(1)}(k) + \varepsilon/4 \), and there are only at most \( k - 1 \) such subgroups.

It then holds from (6) and (3) that

\[
\bar{q}_S^{(1)}(Z) \geq r_S^{(1)}(k) - \frac{\varepsilon}{2} \quad \text{for all } Z \in \text{TOP}_1(k, \mathcal{D})
\]

Thus \( \mathcal{B} \) satisfies Property 1 of Definition 3.3.

Let now \( A \) be any subgroup with \( q_S^{(1)}(A) < r_S^{(1)}(k) - \varepsilon \). It follows from (3) that

\[
\bar{q}_S^{(1)}(A) \leq r_S^{(1)}(k) - 3\varepsilon/4,
\]

and using (5) we get

\[
\bar{q}_S^{(1)}(A) < r_S^{(1)}(k) - \varepsilon/2,
\]

hence \( (A, \bar{q}_S^{(1)}(A)) \notin \mathcal{B} \), as required by Property 2 of Definition 3.3.

4.1.3 Loose bounds to the sufficient sample size. Intuition correctly suggests that if the sample \( S \) is large enough, then with high probability over the choice of \( S \), \( S \) satisfies the condition in (3), allowing the computation of an \( \varepsilon \)-approximation of \( \text{TOP}_1(k, \mathcal{D}) \) from \( S \). To warm up, and as a baseline, we first present a loose bound on how large \( S \) should be for the above to happen.

**Theorem 4.2.** Let \( \delta \in (0, 1) \), \( \varepsilon \in (0, 1) \), and \( k \geq 1 \). Let \( S \) be a collection of

\[
|S| \geq \frac{16}{\varepsilon^2} \left( \ln |\mathcal{L}_D| + \ln \frac{2}{\delta} \right)
\]

transactions sampled uniformly at random with replacement from \( \mathcal{D} \). With probability at least \( 1 - \delta \) (over the choice of \( S \)), the set

\[
\mathcal{B} = \left\{ (A, \bar{q}_S^{(1)}(A)) : \bar{q}_S^{(1)}(A) + \frac{\varepsilon}{2} \geq r_S^{(1)}(k) \right\}
\]

is an \( \varepsilon \)-approximation to \( \text{TOP}_1(k, \mathcal{D}) \).

The proof is in the supplementary material [24]. It uses Hoeffding’s inequality [6] and the union bound [16, Lemma 1.2].

The quantity in (7) is a loose upper bound to the sample size sufficient to probabilistically obtain an \( \varepsilon \)-approximation, due to the use of the union bound. It is also somewhat intuitive that the sample size should not depend on just the size of \( \mathcal{L}_D \), but on a quantity that better describes the relationship between the language and the dataset, as will be the case for the sample size used by MiSoSouP. Another drawback is that the sample size in (7) can only be computed when the size of \( \mathcal{L}_D \) is known, which is almost never the case. A loose upper bound to \( |\mathcal{L}_D| \) can be computed with a full scan of the dataset, which is potentially expensive (see details in Sect. 5). The sample size used by MiSoSouP, presented next, does not suffer from these downsides.

4.1.4 Bounds to the pseudodimension and to the sample size. In this section we present a novel upper bound to the number of samples needed to satisfy the condition in (3), and therefore compute a high-quality approximation of \( \text{TOP}_1(k, \mathcal{D}) \). It relies on the following bound to the pseudodimension [19] (see Sect. 3.2) of the family \( \mathcal{P} \) introduced in Sect. 4.1.1.

**Theorem 4.3.** Let \( d \) be the maximum number of subgroups from \( \mathcal{L} \) that may appear in a transaction of \( \mathcal{D} \). Then, the pseudodimension \( PD(\mathcal{P}) \) of \( \mathcal{P} \) satisfies

\[
PD(\mathcal{P}) \leq \lceil \log_2 d \rceil + 1.
\]

We need some intermediate results before proving this theorem.

Define, for every subgroup \( A \in \mathcal{L} \), the range

\[
R_A = \{(t, x) : t \in \mathcal{D} \text{ and } x \leq r_A(t)\},
\]

and let \( \mathcal{R} = \{R_A : A \in \mathcal{L}\} \) be a range set on \( \mathcal{D} \times [-\mu(\mathcal{D}), 1 - \mu(\mathcal{D})] \).

Lemma 3.6 tells us that only subsets of \( \mathcal{D} \times [-\mu(\mathcal{D}), 1 - \mu(\mathcal{D})] \) may be shattered by \( \mathcal{R} \). The following lemmas further restrict the collection of sets that may be shattered.

For any \( x \in (-\mu(\mathcal{D}), 1 - \mu(\mathcal{D})) \) let

\[
c(x) = \begin{cases} 1 - \mu(\mathcal{D}) & \text{if } 0 < x \leq 1 - \mu(\mathcal{D}) \\ 0 & \text{if } -\mu(\mathcal{D}) < x \leq 0 \end{cases}
\]

**Lemma 4.4.** A set \( B \subseteq \mathcal{D} \times (-\mu(\mathcal{D}), 1 - \mu(\mathcal{D})) \) is shattered by \( \mathcal{R} \) if and only if the set

\[
B' = \{(t, c(x)) : (t, x) \in B\}
\]
is also shattered by $\mathcal{R}$. Note that $|B| = |B'|$. 

Proof. It follows from the definition of $\mathcal{R}_A$, $A \in \mathcal{L}$, that $(t, x)$ belongs to all and only the $\mathcal{R}_A$’s that $(t, c(x))$ belongs to. Hence if $B$ is shattered then the same ranges that shatter it also shatter $B'$, and vice versa.

The equality $|B| = |B'|$ follows from 1) the fact that clearly it is impossible that $|B'| > |B|$; and 2) Lemma 3.5 as it ensures that if $B$ is shattered then it cannot contain more than a single element $(t, y)$ for a fixed $t \in \mathcal{D}$ and some $y \in (\mu(D), 1 - \mu(D))$, hence it is impossible that two or more elements of $B$ are mapped by $c(\cdot)$ to the same element of $B'$.

Lemma 4.5. Let $t \in \mathcal{D}$ be any transaction such that $t.T = 0$. No $B \subseteq \mathcal{D} \times \{0, 1 - \mu(D)\}$ such that $(t, 1 - \mu(D)) \in B$ can be shattered by $\mathcal{R}$.

Proof. There is no subgroup $A \in \mathcal{L}$ such that $(t, 1 - \mu(D)) \in \mathcal{R}_A$, thus, for any $B$ containing $(t, 1 - \mu(D))$, it is impossible to find an $A \in \mathcal{L}$ such that $\mathcal{R}_A \cap B = \{(t, 1 - \mu(D))\}$, hence $B$ cannot be shattered. □

Lemma 4.6. Let $t \in \mathcal{D}$ be any transaction such that $t.T = 1$. No $B \subseteq \mathcal{D} \times \{0, 1 - \mu(D)\}$ such that $(t, 0) \in B$ can be shattered by $\mathcal{R}$.

Proof. The element $(t, 0)$ belongs to $\mathcal{R}_A$ for any $A \in \mathcal{L}$, so for any $B$ containing $(t, 0)$, it is impossible to find an $A \in \mathcal{L}$ such that $\mathcal{R}_A \cap B = \emptyset$, hence $B$ cannot be shattered. □

It follows from Lemmas 3.6, 4.4, 4.5 and 4.6 that, to prove Theorem 4.3, we can focus our attention only on trying to shatter subsets of $\mathcal{D} \times [-\mu(D), 1 - \mu(D)]$ containing elements that are either in the form $(t, 1 - \mu(D))$ with $t.T = 1$, or in the form $(t, 0)$ with $t.T = 0$. The two following lemmas show upper bounds to the sizes of such subsets that can be shattered by $\mathcal{R}$. Theorem 4.3 is then an immediate consequence.

Lemma 4.7. Let $B \subseteq \mathcal{D} \times \{0, 1 - \mu(D)\}$ be a set that is shattered by $\mathcal{R}$ and such that $B$ contains an element $(t, 1 - \mu(D))$, for some $t \in \mathcal{D}$. Then it must be

$$|B| \leq \lfloor \log_2 d \rfloor + 1,$$

for $d$ as in Theorem 4.3.

Proof. The proof is in part inspired by the one for [21, Theorem 4.5]. Consider one of the elements in the form $(t, 1 - \mu(D))$ belonging to $B$. By hypothesis there is at least one such element. Let us denote it as $a = (t, 1 - \mu(D))$.

Denote the $2^{[B]^{-1}}$ non-empty subsets of $B$ containing $a$ as $C_i, 1 \leq i \leq 2^{[B]^{-1}}$, labelling them in an arbitrary order. Since $B$ is shattered, for each of the $C_i$’s there must be a $\mathcal{R}_A$ such that $\mathcal{R}_A \cap B = C_i$. Since $C_i \neq C_j$ for each $i \neq j, 1 \leq i, j \leq 2^{[B]^{-1}}$, it must hold $\mathcal{R}_A \neq \mathcal{R}_A$. The element $a$ belongs to each $\mathcal{R}_A$, $1 \leq i \leq 2^{[B]^{-1}}$. From Lemma 4.5 it follows that, since $B$ is shattered, then it must be $t.T = 1$. Thus the element $a$ belongs to all and only the ranges $\mathcal{R}_Z$ for $Z \in \mathcal{L}$ such that $t \in C_{\mathcal{D}}(Z)$. There are at most $d$ such $Z$’s, hence it must be $2^{[B]^{-1}} \leq d$. □

Lemma 4.8. Let $B \subseteq \mathcal{D} \times \{0, 1 - \mu(D)\}$ be a set that is shattered by $\mathcal{R}$ and such that $B$ contains an element $(t, 0)$, for some $t \in \mathcal{D}$. Then it must be

$$|B| \leq \lfloor \log_2 d \rfloor + 1,$$

for $d$ as in Theorem 4.3.

Proof. Consider one of the elements in the form $(t, 0)$ that belong to $B$. By hypothesis there is at least one such element. Let us denote it as $a = (t, 0)$. The proof is similar to the one for Lemma 4.7, but with one profound difference, i.e., we essentially consider the subsets of $B$ that do not contain $a$.

Denote the $2^{[B]^{-1}}$ subsets of $B$ not containing $a$ as $C_i, 1 \leq i \leq 2^{[B]^{-1}}$, labelling them in an arbitrary order. Note that there must be an $i$ such that $C_i = \emptyset$. Since $B$ is shattered, for each of the $C_i$’s there must be a subgroup $A_i$ such that $\mathcal{R}_{A_i} \cap B = C_i$. Since $C_i \neq C_j$ for each $i \neq j, 1 \leq i, j \leq 2^{[B]^{-1}}$, it must hold $\mathcal{R}_{A_i} \neq \mathcal{R}_{A_j}$. The element $a$ does not belong to any $\mathcal{R}_{A_i}, 1 \leq i \leq 2^{[B]^{-1}}$. From Lemma 4.4 it follows that, since $B$ is shattered, then it must be $t.T = 0$. Thus the element $a$ does not belong only to the ranges $\mathcal{R}_Z$ for $Z \in \mathcal{L}$ such that $t \in C_{\mathcal{D}}(Z)$. There are at most $d$ such $Z$’s, hence it must be $2^{[B]^{-1}} \leq d$. □

It is common to choose $\mathcal{L}$ to be the set of subgroups involving up to $c$ conjunctions of simple equality conditions on the attributes, for some $c \geq 1$. The following corollary is a reformulation of Theorem 4.3 using the maximum number of subgroups from $\mathcal{L}$ that may appear in a transaction of $\mathcal{D}$ for such cases.

Corollary 4.9. Let $c$ be the number of description attributes in $\mathcal{D}$ (i.e., not counting the target attribute). Let $\mathcal{L}$ be the set of subgroups of conjunctions of equality conditions on up to $c$ attributes, for some $1 \leq c \leq C$. Then

$$PD(P) \leq \left\lfloor \log_2 \sum_{i=1}^{c} \binom{c}{i} \right\rfloor + 1. \quad (8)$$

We conjecture that these bounds to the pseudodimension are strict, in the sense that there are datasets attaining the bounds. We will investigate this conjecture in the extended version of this work.

By combining Theorem 4.3 with Theorem 3.4 we obtain the following result.

Theorem 4.10. Let $\delta \in (0, 1), \varepsilon \in (0, 1)$, and $k \geq 1$. Let $d$ as in Theorem 4.3. Let

$$S = \frac{16}{\varepsilon^2} \left( \lfloor \log_2 d \rfloor + 1 + \ln \frac{1}{\delta} \right). \quad (9)$$

The probability that a collection $\mathcal{S}$ of $S$ transactions sampled independently and uniformly at random with replacement from $\mathcal{D}$ satisfies (3) is at least $1 - \delta$.

The improvement of (9) over (7) is evident: $\lfloor \log_2 d \rfloor + 1$ is usually much much smaller, potentially orders of magnitude so, than $\ln |\mathcal{L}|$.

4.1.5 The algorithm. We now have all the ingredients to describe and analyze MIsoSoU+, our algorithm for extracting, with probability at least $1 - \delta$ (over the runs of the algorithm), an $\varepsilon$-approximation to TOP$_1(k, \mathcal{D})$. The input of the algorithm is the tuple $(\mathcal{D}, k, \varepsilon, \delta)$. 

MiSoSouP-1 starts by creating the sample $S$ by drawing $S$ transactions independently and uniformly at random with replacement from $D$, for $S$ as in (9). An exact algorithm for subgroup discovery is used to extract from $S$ the set $B$ defined in (4). Any exact algorithm can be used for the discovery step, but it needs to be slightly modified to use $q_1^S(A)$ as measure for the interestingness of a subgroup $A$, instead of $q_1^D(A)$. This modification is straightforward. The set $B$ is then returned in output. By combining Theorem 4.1 with Theorem 4.10 we obtain the following result on the quality guarantees of MiSoSouP-1.

**Theorem 4.11.** With probability at least $1 - \delta$ (over its runs), MiSoSouP-1 outputs an $\varepsilon$-approximation to $\text{TOP}_1(k, D)$.

## 5 EXPERIMENTAL EVALUATION

We now discuss our experimental evaluation to assess the performances of MiSoSouP. We report here a subset of the results for $p = 1$. Additional and qualitatively similar results for the other measures are available in the supplementary materials [24].

### 5.1 Goals

Our experiments have two goals: 1) evaluate the speed-up of MiSoSouP w.r.t. sampling-based approximation algorithms offering the same quality guarantees; and 2) evaluate the quality of the approximations returned by MiSoSouP, in terms of the accuracy of the estimates of the quality of the returned subgroups, and of the number of returned subgroups.

### 5.2 Baselines

We compare the performances of MiSoSouP against a baseline algorithm $\text{UB}$.\(^7\) Like MiSoSouP, $\text{UB}$ computes, with probability at least $1 - \delta$, an $\varepsilon$-approximation to $\text{TOP}_p(k, D)$ by analyzing a sample of the dataset. The only difference between MiSoSouP and $\text{UB}$ is that $\text{UB}$ uses, as sample size, the r.h.s. of (7) (or similar equations for $p \neq 1$). We use $\text{UB}-1$ to denote the variant of $\text{UB}$ for 1-quality. As is evident from (7), $\text{UB}$ requires, to compute its sample size, the number of subgroups in $L$ that actually appear in $D$ or an upper bound to such number. An upper bound can be computed by considering the size of the (effective) domains of the columns in the dataset, and taking the sum, over all $r$-subsets $C$ of columns, for $r$ from 1 to some $\text{maxlen}$, of the products of the sizes of the column domains in $C$. Computing the sizes of the column domains requires a linear scan of the dataset. Despite the fact that this step can be relatively expensive and its cost grows with the size of the dataset, we do not include the time for such computation in the runtime of UB we report, therefore favoring UB in our comparisons. Note that MiSoSouP relies on (8) to compute the upper bound $d$ to the pseudodimension used in (9) to obtain its sample size, and the cost of evaluating the r.h.s. of (8) is essentially nil, as all values are known by MiSoSouP, since $L$ and thus $c$ are fixed in advance, and the number of columns of $D$ is an immediately available quantity.

We do not compare MiSoSouP with algorithms that mine the whole dataset and output the exact collection $\text{TOP}_p(k, D)$ because MiSoSouP (and also $\text{UB}$) have sample sizes that are independent on the size of the dataset, while an exact algorithm would take time proportional to this quantity. As a result, on modern-sized datasets, an exact algorithm is always much slower than a sampling-based algorithm. We also do not to compare against GSS [25] because the algorithm does not actually offer the claimed guarantees (see the supplementary materials [24]). Additionally, an implementation is not available.

### 5.3 Datasets and languages

We use datasets from the UCI repository [14]. Since these datasets are quite small for today’s standards, we replicate them 20,000 times (i.e., each transaction is copied 20,000 times) and then shuffle the order of the transactions in the replicated copy. This way, we obtain significantly larger datasets while preserving the distribution of the $p$-qualities of the subgroups appearing in the original datasets. This approach does not change the search space of any algorithm and does not give any advantage to MiSoSouP over UB. Table 1 shows the descriptive statistics of the datasets we used. We consider the description language $L$ of subgroups of up to “Max. Length” conjunctions of equality conditions.

### 5.4 Implementation and environment

We implemented MiSoSouP and UB in C++17. The implementation uses a simple exhaustive search algorithm for extracting the subgroups from the sample (any algorithm can be used for this step, we just found it more practical to write our own implementation than to modify an existing implementation of a more efficient algorithm). We run our experiments on a cluster of GNU/Linux machines, except for the timing experiments, which were performed on a machine with an AMD Phenom™ II X4 955 processor and 16GB of RAM, running FreeBSD 12. The code is included in the supplementary materials [24].

### 5.5 Parameters

We report results for $k \in \{10, 50, 100, 200, 500, 1000, 2000\}$, $r \in \{0.05, 0.02, 0.01, 0.0075\}$, and for $\delta = 0.1$. We tested different values for $\delta$, but given that both MiSoSouP and UB have (the same) logarithmic dependence on $\delta$, varying $\delta$ has limited quantitative effect and no qualitative effect. We run MiSoSouP and UB five times for each combination of parameters: the results were extremely stable and we report them for a randomly chosen run among the five.

### 5.6 Results

We first show the results on runtime and sample sizes (Sect. 5.6.1), then discuss the accuracy of the estimates of the 1-qualities obtained by MiSoSouP-1 (Sect. 5.6.2), and finally analyze the number of false positives it reports (Sect. 5.6.3).

<table>
<thead>
<tr>
<th>Dataset</th>
<th>Size</th>
<th>Attributes</th>
<th>Max. Length</th>
</tr>
</thead>
<tbody>
<tr>
<td>Car</td>
<td>$6912 \times 10^4$</td>
<td>6</td>
<td>4</td>
</tr>
<tr>
<td>Mushroom</td>
<td>$32496 \times 10^4$</td>
<td>22</td>
<td>4</td>
</tr>
<tr>
<td>Tic-Tac-Toe</td>
<td>$3832 \times 10^4$</td>
<td>9</td>
<td>5</td>
</tr>
</tbody>
</table>

Table 1: Characteristics of the datasets

---

\(^7\)UB was not presented before in the literature. We introduce it only for comparison with MiSoSouP, which, as we will see, offers several practical advantages.
over the part of the running time that depends on the size of the sample, thus the reduction in MiSoSouP-1’s runtime w.r.t. UB-1’s is not proportional to the reduction in the sample size. The sample-size-dependent costs dominate when \( \varepsilon \) is small (larger sample sizes) and in these cases the speed-up becomes essentially equal to the reduction in the sample size.

5.6.2 Accuracy. We evaluate the accuracy of the output of MiSoSouP-1 by measuring, for each subgroup \( A \) in the output, the absolute error \( \text{err}^{(A)} = \frac{q^{(A)}}{S} - q^{(A)} \). The quality guarantees of MiSoSouP-1 ensure that, with probability at least \( 1 - \delta \), the absolute error is bounded by \( \varepsilon/4 \) for all subgroups. A first important result is that the above was true in all the thousands of runs of MiSoSouP-1 we performed, i.e., not just with probability \( 1 - \delta \). Hence MiSoSouP-1 has, in practice, even higher confidence than it guarantees theoretically. We will further comment later on this aspect. In the six rightmost columns of Table 2 we report the minimum, first quartile, median, third quartile, and maximum absolute error, and the value of \( \varepsilon/4 \) for comparison. We report results for \( k = 1000 \) (the full table for all values of \( k \) is available in the supplementary materials [24], with qualitatively similar results). We can see that not only the maximum absolute error was approximately between two to seven times smaller than the maximum allowed (\( \varepsilon/4 \)), but the majority of the distribution of the error (over the subgroups) is highly concentrated around values that are often orders of magnitude smaller, with the median being at times even more than 100 times smaller than \( \varepsilon/4 \). Additionally we see how, as \( \varepsilon \) decreases, the distribution of the error becomes more concentrated, with the maximum values decreasing faster than the third quartiles and the medians.

A possible explanation for the fact that the estimation of the 1-qualities is much better than what is guaranteed by the theory is that the analysis uses an upper bound to the pseudodimension, which itself is a worst-case measure of complexity. This looseness is

<table>
<thead>
<tr>
<th>Dataset</th>
<th>( \varepsilon )</th>
<th></th>
<th>Reduction w.r.t. UB-1</th>
<th>Runtime (s)</th>
<th>Reduction w.r.t. UB-1</th>
<th>Min.</th>
<th>1st Q.</th>
<th>Median</th>
<th>3rd Q.</th>
<th>Max.</th>
<th>( \varepsilon/4 )</th>
</tr>
</thead>
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<td>0.76</td>
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<td>125</td>
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<tr>
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<td>&lt; 0.01</td>
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<td>8.20</td>
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<td>4.98</td>
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<td>0.17</td>
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<tr>
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<td>&lt; 0.01</td>
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<td>0.64</td>
<td>1.11</td>
<td>5.14</td>
<td>18.75</td>
<td></td>
</tr>
</tbody>
</table>

Table 2: Sample size, runtime, and accuracy (absolute error) evaluation for MiSoSouP-1
somewhat inevitable, but it suggests that there is room for improvement in the analysis. We plan to investigate the use of Rademacher averages [11] to obtain tighter sample-dependent bounds to the deviations of the sample qualities from their exact values.

5.6.3 Output properties. The set of subgroups returned by MiSoSouP-1 is a superset of $\text{TOP}_p(k, \mathcal{D})$. This was always the case in all the runs, so the recall of MiSoSouP-1 is, in practice, 100%. MiSoSouP-1 therefore effectively exceeds the theoretical guarantees it offers. As for the precision, we must remark that a sampling-based algorithm can obviously not guarantee 100% precision, especially if it gives 100% recall like MiSoSouP-1 does.

Nevertheless, MiSoSouP-1 guarantees that False Positives (FP), i.e., subgroups not in $\text{TOP}_p(k, \mathcal{D})$ that may be included in the output, can only be among those subgroups with 1-quality in $\mathcal{D}$ at least $r^{(1)}_\mathcal{D}(k) - \epsilon$, i.e., at most $\epsilon$ less than the 1-quality of the top-$k$th subgroup in $\mathcal{D}$. The number of these “acceptable” FP depends on the distribution of the 1-qualities in the dataset, and cannot be controlled by the algorithm. Thus, the precision may be very low if there are many (potentially $\gg k$) subgroups that would be acceptable FP, and these FP are the price to pay for the speed-up in analyzing the dataset. It is arguable that in these cases the exact choice of $k$ becomes somewhat arbitrary, because there are many subgroups with $p$-qualities very close to each other. In any case, the output of MiSoSouP-1 is a superset of $\text{TOP}_p(k, \mathcal{D})$ and can be refined to obtain this set with a fast linear scan of the dataset.

We report in Table 3, for the Mushroom dataset, the number of FP in the output and to what percentage of the acceptable FP that number corresponds to. The tables for other datasets are available in the supplementary materials [24]. As expected, for a fixed value of $k$, the number of FP included in the output decreases as $\epsilon$ becomes smaller, but notice that the percentage may not decrease because the set of acceptable FP changes with $\epsilon$. The absolute number of FP tends to grow with $k$, because the number of acceptable FP also tends to grow with $k$, which is a consequence of the power-law distribution of the qualities of the subgroups.

In the end, the amount of FP is either a small number (either in absolute terms or relatively to $k$) or a relatively small fraction of the total number of acceptable FP. This fact can be explained by the “excessive” accuracy of MiSoSouP-1 in estimating the 1-quality of the subgroups, as discussed in Sect. 5.6.2. As mentioned, MiSoSouP-1 gives no guarantees that only a small subset of the acceptable FP would be included in the output, so the fact that in most cases less than half of them are actually present is a witness to the good performances of the algorithm.

6 CONCLUSIONS

We introduced MiSoSouP, the first family of algorithms based on random sampling that compute probabilistically-guaranteed high-quality approximations of the collection of the top-$k$ most interesting subgroups in a dataset. Our analysis relies on pseudodimension, a fundamental concept from statistical learning theory. This connection is novel for subgroup discovery.

Our experimental evaluation shows that MiSoSouP requires much smaller sample sizes than state-of-the-art solutions to obtain approximations with the same guarantees, therefore providing the first viable tool to efficiently identify the most interesting subgroups for ever-more-massive datasets.

Our algorithms hinge on defining quality measures as averages of specific functions. This approach can be used in concert with Rademacher averages to design progressive-sampling methods for subgroups discovery, as done for other mining tasks [22]. We will investigate this direction in the near future.

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REFERENCES


| $\epsilon$ | $k$ | $|\text{TOP}_p(k, \mathcal{D})|$ | FP | % of all Acceptable FP |
|-----------|-----|-----------------|-----|-------------------------|
| 0.05      | 10  | 10              | 29  | 19.72                   |
|           | 50  | 50              | 120 | 22.64                   |
|           | 100 | 100             | 232 | 25.86                   |
|           | 200 | 200             | 399 | 32.83                   |
|           | 500 | 546             | 764 | 34.80                   |
|           | 1000| 1013            | 850 | 17.63                   |
|           | 2000| 2004            | 4030| 15.26                   |
| 0.02      | 10  | 10              | 14  | 56.00                   |
|           | 50  | 50              | 48  | 57.83                   |
|           | 100 | 100             | 57  | 40.42                   |
|           | 200 | 200             | 141 | 51.64                   |
|           | 500 | 546             | 361 | 59.66                   |
|           | 1000| 1013            | 284 | 42.83                   |
|           | 2000| 2004            | 949 | 31.96                   |
| 0.01      | 10  | 10              | 2   | 14.28                   |
|           | 50  | 50              | 17  | 36.95                   |
|           | 100 | 100             | 26  | 45.61                   |
|           | 200 | 200             | 46  | 34.07                   |
|           | 500 | 546             | 67  | 18.55                   |
|           | 1000| 1013            | 129 | 41.88                   |
|           | 2000| 2004            | 455 | 48.50                   |
| 0.0075    | 10  | 10              | 2   | 100.00                  |
|           | 50  | 50              | 8   | 34.78                   |
|           | 100 | 100             | 26  | 78.78                   |
|           | 200 | 200             | 35  | 35.00                   |
|           | 500 | 546             | 47  | 16.60                   |
|           | 1000| 1013            | 92  | 46.23                   |
|           | 2000| 2004            | 246 | 36.71                   |

Table 3: Output evaluation for MiSoSouP-1 on Mushroom