A Survey on Techniques for Identifying and Resolving Representation Bias in Data

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The grand goal of data-driven decision-making is to help humans make decisions, not only easily and at scale but also wisely, accurately, and just. However, data-driven algorithms are only as good as the data they work with, while data sets, especially social data, often miss representing minorities. Representation Bias in data can happen due to various reasons ranging from historical discrimination to selection and sampling biases in the data acquisition and preparation methods. One cannot expect AI-based societal solutions to have equitable outcomes without addressing the representation bias. This paper surveys the existing literature on representation bias in the data. It presents a taxonomy to categorize the studied techniques based on multiple design dimensions and provide a side-by-side comparison of their properties. There is still a long way to fully address representation bias issues in data. The authors hope that this survey motivates researchers to approach these challenges in the future by observing existing work within their respective domains.

CCS Concepts: • Information systems → Data management systems;

Additional Key Words and Phrases: Databases, Responsible Data Science, Fairness in Machine Learning, Bias Detection

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1 INTRODUCTION

Data-driven decision-making shapes every corner of human life today, from autonomous vehicles to healthcare, and even in predictive policing and criminal sentencing. A critical question, particularly in applications impacting human beings, is how trustworthy the decision made by the system is. It is easy to see that the accuracy of a data-driven decision depends, first and foremost, on the data used to make it. After all, the system learns the phenomena that data represent. As a first step, we may desire that the data should represent the underlying data distribution from which the production data will be drawn. But that is not enough since it only tells us about the overall model performance. Although a system may generally perform well in terms of accuracy, it could fail for less populated regions in the data that do not have enough representation. These regions may matter greatly because they frequently represent some minority sub-population in society. They could also represent critical cases that may not happen very often but have a determining impact on the correctness of the decision made. In short, if data is not representative of a given subpopulation, the outcome of the decision system for that subpopulation may not be trustworthy.
Representation Bias happens when the development (training data) population under-represents (and subsequently fails to generalize well) for some parts of the target population [69]. Representation bias in data can originate from how (and from where) the data was originally collected or be caused by the biases introduced after collection, whether historically, cognitively, or statistically. Representation bias can happen due to selection bias, i.e., when the sampling method only reaches a portion of the population or the population of interest has changed or is distinct from the population used during model training. For example, a survey to measure illegal drug use of teenagers could be biased if it only includes high school students and ignores home-schooled students or dropouts. Another potential reason is the skewness of the underlying distribution. Suppose the target population for a particular medical data set are adults aged in the range of 18-60. There are minority groups within this population: for example, pregnant people may make up only 5% of the target population. Even with perfect sampling and identical population, the model is prone to be less robust for the group of pregnant people because it has fewer data to learn from [69]. Furthermore, even if we carefully arrange for uniform sampling by age, we may find that sampling is non-uniform for pregnant people: for example, there may be proportionately fewer pregnant people over 40. If some group is a minority in the underlying distribution, then even random sampling will not help the under-representation issue for this group.

Without a systematic approach to data collection, representation bias is almost always guaranteed. For example, in a survey data collection, a crucial step is to identify all the sub-populations in the underlying distribution based on the desired demographic information and ensure that the survey reaches all of them while enough samples are collected from each. However, the problem is that data scientists usually do not have any control over the data collection process, resulting in the utilization of “found data” in most data-driven decision-making systems. Therefore, with no guarantee on the aforementioned steps in the data collection process, the found data is most likely a biased sample.

Representation bias in data is not a new problem, and has been a known issue in data mining and statistics communities. However, with the emergence of responsible data science and trustworthy AI, it has been addressed with greater vigor and from a brand new perspective in recent years. This survey discusses techniques for identifying and resolving representation bias in data sets, introducing a taxonomy to classify these techniques based on multiple dimensions. While most of the work covered is recent, older work is also included where relevant.

In Section 2, we explain the notion of representation bias, explaining the reasons that give rise to it, and present techniques for measuring this phenomenon. In Section 3 we propose a taxonomy to categorize different approaches to representation bias, based on factors such as objectives and capabilities. We discuss each factor, and provide a side-by-side comparison of the reviewed techniques. In Sections 4 and 5, we follow the guidelines from our taxonomy to investigate the details of each work, explain its novelty, and discuss its pros and cons. Finally, in Section 6, we discuss aspects that have been noticed less in the existing lines of work and propose some possible directions for the researchers to investigate.

The scope of the studies reviewed in this survey is bounded to representation bias in tabular data. To the best of our knowledge, the effort to address representation bias for many other data types is limited. In Section 6, we briefly discuss representation bias for other data types such as image data.

2 AN OVERVIEW OF REPRESENTATION BIAS

With the abundance of data collected from a wide range of contexts, we are transitioning from decision-making based on intuition and observations to potentially far more success-prone decision-making based on the data. Data-driven decision-making suggests that every decision should generalize based on the information set verifying its effectiveness and performance. This entails the fact that every decision is only as good as the data used to make it [10]. The quality
of underlying data can be questionable for numerous reasons that affect the precision of the decision. Yet, one of the most important, yet less noticed, aspects of data quality is being representative for all the possible subgroups influenced by that decision. This representativeness originates from how the data has been collected. With a prospective data collection approach such as through a survey or a scientific experiment, data scientists may be able to specify requirements like representation in data. However, more often than not, data, now known as found data, is collected independently in a process that data scientist has limited or no control over. Besides, it is important to note that while data must follow the actual production distribution, this is not sufficient for the development of representative data. The data must include enough examples from less popular regions if these regions are to be handled well by the system.

In today’s data-driven world, Automated Decision Systems (ADS) are widely used in various fields of social life, such as fire prevention by predicting high-risk buildings and recruiting automation by screening out competitive candidates. However, historical data used for decision-making might not be objective; it could inherit historical biases to the algorithm design. For responsible development of ADS, it is essential to analyze the representation to avoid the potential risks of injustice. For example, an attempt of the Boston government [24] using a system to assign students to schools near their residential areas was found problematic as it ignored the fact that top schools are typically less common in the underprivileged districts. For systems that rely on the machine learning algorithms, without a careful inspection of the training data quality, underrepresentation of minority groups may cause discrimination in the prediction results [7, 17, 46]. For example, StyleGAN [38], one famous algorithm for auto-generating eerily realistic human faces, is also producing white faces more frequently than faces of people of color. It appears that the problem is inherited from the training data sets, which defaults to white features. As a result, recent research has started to explore the relationship between machine learning bias and the inadequate sample sizes [17, 58]. In critical areas, such as health care, representation bias is also a crucial problem. First of all, there are group-specific patterns in the health care data. For example, many diseases are correlated with demographic factors like race, gender, etc. Ashkenazi Jewish women are known to have a higher risk of breast cancers [22]; the likelihood of many diseases, including obesity, hypertension, diabetes, and high total cholesterol, also varies across racial/ethnic groups [1]. Therefore, the medical datasets’ diversity, especially the demographical diversity, is vital when making further use of the collected data. Besides, as health data are usually sensitive, patients’ willingness to share the data might vary [19]. As a result, ensuring the representativeness of the collected data is essential to avoid inaccurate or biased results in the downstream usage of the data.

2.1 Reasons for Representation Bias

Representation bias happens for a variety of reasons with no consensus on an exact set of grounds. With that in mind, we seek the origins for representation bias in one or more of the following:

**Historical Bias.** Historical bias is “the already existing bias due to the socio-technical issues in the world” [50]. An example of historical bias can be found in Google’s image search result. Searching for term ‘CEO United States’, the results are dominated by images of male CEOs and showing fewer female CEO images. This is due to the fact that only 8.1% of Fortune 500 CEOs are women, causing the search results to be biased towards male CEOs. This problem has previously been shown for a variety of job titles such as ‘CEO’ in [42] and Google had alleged to have resolved it. These search results are indeed reflecting the reality, however, whether the search algorithms should mirror this reality or not may depend on the application and is another issue to consider.

**Underlying Distribution Skew.** The underlying distribution that data is collected from may lack an equal ratio or sufficient representation for all of its subpopulations. In such cases, the underlying distribution is inherently skewed,
and there are no discriminatory motives behind it. For example, according to the US Census Bureau [2], around 7% of the US population is of Asian descent while 75% of the population is White. Collecting a uniform sample from the US society, the Asian community is considered a minority in the outcome sample and naturally less represented. However, this is a reflection of the underlying distribution that the data has been collected from. This reflection of reality may lead to discrimination against this subpopulation in some applications.

Selection Bias. Selection bias is introduced to the data when one fails to ensure proper randomization in the selection of people, groups, or tuples of data for analysis. Therefore, the collected sample may not be representative of the population to be analyzed. Sampling bias, which is a type of selection bias, happens on account of a non-random sampling of a population, causing some subpopulation to have less likelihood of being included than the rest, resulting in a biased sample in which all subjects are not equally represented. Although sampling bias and selection bias are often used interchangeably, it is important to differentiate between them as sampling bias reduces the external validity of a test which is the generalizability of its results to the entire population, while selection bias mainly addresses internal validity for differences or similarities found in the sample at hand. In this regard, errors happening during the assemblage of the sample lead to sampling bias, while any errors in any in later steps cause selection bias [3]. An example of this kind of bias would be a predicting the potential winner of an election by asking 1000 voters about their candidate. This would be valid only if the sample of 1000 voters is representative of the entire constituency. However, imagine a situation where we limit the poll to 1000 white middle-class college students. In such circumstance, votes of important parts of the constituency such as (ethnic minorities, older adults, blue-collar workers) will most probably be underrepresented in the sample. Therefore, any algorithm built on this sample is less likely to be able to successfully predict the outcome of the election. Self-selection bias is another closely related concept to selection bias, happening due to different reasons, usually more intentional rather than inadvertently. This bias occurs in situations such as in research projects where the intention of the participants whether to participate in the research or not creates abnormal or undesirable conditions. Consider an example where researchers mail in ballots to the households in a particular district, trying to survey the number of people who are able to read. The results of this survey are affected by the fact that only people who can read can return the ballots, introducing self-selection bias to the results [66].

Faulty representation for some subpopulations can be explained in terms of biases existing in the data. Biases have been studied in the statistical community for a long time [57] but social data, increasingly the source of data for policy decision making, presents different challenges [9, 10, 59]. At a high level, bias in social data means certain subpopulations in data are more heavily weighted or represented due to systematic favoritism. It is a deviation from expectation in data and is recognized as a subtle error that sometimes goes unnoticed, causing skewed outcomes, low accuracy levels, and analytical errors. These biases are sometimes introduced to the data due to cognitive biases [31, 32] in human reporting or a flawed data collection or preprocessing. We refer the reader to [29, 59] for more information about the general topic of biases in social data, the origins, and various types. In the next section, we will look into the reasons that give rise to representation bias in data.

2.2 Measuring Representation Bias

In this section, we discuss the measures that have been proposed to evaluate representation bias in data.

2.2.1 Representation Rate. Representation rate is a metric defined in [14] to identify representation bias with respect to the base rates. Base rate, also known as “prior probability”, refers to the class probability unconditioned on any observation. In the existing works [40, 65], equal base rate is defined as having an equal number of objects for different
subgroups in the data set. In other words, the objects in the selected set should have an equal chance of belonging to each subgroup. Consider data set \( D \) with \( n \) tuples and let \( n_i \) be the number of tuples belonging to subgroup \( i \). That is, for all possible subgroups \( i, j \) in \( D \), they are represented if \( n_i = n_j \).

Next, we present the definition of representation rate. For a threshold \( \tau \in (0, 1] \), data set \( D \) following the distribution \( p : \Omega \to [0, 1] \) is said to have representation rate of \( \tau \) with respect to a protected attribute \( t \) if for all \( z_i, z_j \in \Omega_t \), we have \( \frac{P[Z = z_i]}{P[Z = z_j]} \geq \tau \). That is, for all possible subgroups \( i, j \) we have \( \frac{n_i}{n_j} \geq \tau \). The closer \( \tau \) to zero, the more biased \( D \) is. Representation rate sometimes fails to adequately capture representation bias. That is because, in practice, it rarely happens that all subgroups have (almost) the same number of objects.

2.2.2 Data Coverage. The notion of data coverage has been studied across different settings in \([4, 5, 7, 8, 37, 46, 52, 70]\) as a metric to measure representation bias. At a high level, coverage is referred to having enough similar entries for each object in a data set. For better understanding, let us go over a definition for generalized notion of coverage. Consider a data set \( D \) with \( n \) tuples, each consisting of \( d \) attributes \( X = \{x_1, x_2, \cdots, x_d\} \). Attribute values may be non-ordinal categorical (e.g. race) or continuous-valued (e.g. age). Ordinal attribute values are normalized to lie in the range \([0, 1]\), with values drawn from the set of rational or real numbers. For every tuple \( t \in D \), \( t[i] \) shows the value of \( t \) on attribute \( x_i \in X \). In practice, the data scientist may be interested in studying coverage over a subset of attributes, called "attributes of interest". Examples of attributes of interest are gender, race, salary, etc. Subsequently, \( X \) is assumed to be the set of attributes of interest. The data set also contains target attributes \( Y = \{y_1, \cdots, y_F\} \) that may or may not be considered for the coverage problem.

Given a query point \( q \in [0, 1]^d \), where \( q[i] \) shows the value of \( q \) with regard to \( x_i \in X \), \( q \) is not covered by the data set \( D \), if there are not "enough" data points in \( D \) that are representative of \( q \). In order to generalize the notion of coverage, \( G(q) \) is defined as the universe of tuples that would represent \( q \) and let \( G_D(q) = G(q) \cap D \). In other words, \( G_D(q) \) are the set of tuples in \( D \) that represent \( q \). Using this notation, coverage of \( q \) is defined as the size of \( G_D(q) \). That is, \( \text{cov}(q, D) = |G_D(q)| \). Given a coverage threshold value \( k \), \( q \) is covered if \( \text{cov}(q, D) > k \). Similarly, a group \( G \) is not covered if \( G \cap D < k \). The uncovered region in a data set is the collection of tuples that are not covered by it.

It is important to have a high enough coverage for all meaningful sub-populations in data regardless of the data space to make sure they are adequately represented. Coverage thresholds are expected as an input to the problem and are supposed to be determined through statistical analyses as they are application-specific and vary by context. By borrowing the concept from statistics and central limit theorem, the rule of thumb suggests the number of representatives be around 30 or as [67] suggests, for each "minority subpopulation" a minimum of 20 to 50 samples is necessary.

3 TAXONOMY

Figure 1 depicts the classification we propose in this survey to categorize different techniques based on their objectives, capabilities, and assumptions. This section discusses our classification dimensions and their impact on the design of techniques addressing representation bias. For each dimension, we will go through a detailed description of the research work that addresses it and its novelty, in sections 4 and 5.

3.1 Identification of Representation Bias

Depending on the attribute type, existing works for identifying representation bias in data can be classified into techniques for discrete or continuous space. In this section, we will introduce these techniques and will leave the technical details to future sections.
3.1.1 Discrete Attribute Space. One aspect of studying representation bias is by merely focusing on purely discrete data sets or over one or a combination of discrete attributes in an arbitrary one. Let us begin with an example to better observe representation bias in discrete data sets:

**Example 1.** Consider the Adult data set [41] with a list of discrete attributes with categorical non-ordinal values like race, sex, education, work class, marital status, etc. that contribute to predicting whether an individual makes greater than $50K annually or not. If there are not enough entries matching a specific subpopulation (e.g. race=Asian AND gender=Female), it may not be a suitable data set on which to train a system to make a decision for that group.

The existing work has evaluated representation bias in discrete space using the discrete notion of coverage measure and representation rate. Many critical research fields have targeted the problem of identifying representation bias from different perspectives. For example, in machine learning it is important to identify underrepresented subgroups in the data used to build the models as they are at a higher risk of experiencing unfairness in downstream data-driven algorithms [7, 37]. Another closely related problem in machine learning is model validation by finding problematic regions in data that the model will perform poorly [18, 61, 62, 70].

The majority of the existing works focus on studying representation bias for data sets that populate data in just a single table [7, 37]. However, in the real world, data is more commonly stored and integrated into databases with multiple tables. In order to analyze the representation bias, a combinatorial number of attribute-value combinations from different tables needs to be explored. In this process, joining the tables, constructing indexes at run time, and combining the predicate results across tables can be computationally expensive [46]. Later in section 4.1 we will study the techniques for identifying representation bias for both single and multiple related data sets.

3.1.2 Continuous Attribute Space. Data in the real world often consists of a combination of continuous and discrete values. To better understand representation bias in continuous data sets, let’s look into an example:

**Example 2.** Consider an employment application screening example. While the model can discriminate with respect to categorical attributes like sex and race, it may also discriminate based on continuous-valued attributes such as age (e.g., because most tech workers and job applicants are young). If there are not enough entries for different age ranges (e.g. age>40) in a data set, it may not be trained with enough data to make a decision for those ranges.
Regarding the example above, simple solutions like binning age into "young" and "old" can transform the continuous space into discrete. However, they may lead to coarse groupings that are sensitive to the thresholds chosen. It may be inappropriate to treat a 35-yo as young but a 36-yo as old. In [8], the authors extend the notion of coverage to continuous space for identifying representation bias. We will discuss the detailed techniques in Section 4.1.

3.1.3 Related Concepts and Techniques. There’s a rich line of work from several disciplines, namely, database management and data-mining [21, 44, 47, 48] on the problem of discovering interesting patterns, regularities, or finding empty space in the data (particularly largest empty space recognition). It is a parallel and relatively similar problem to identifying representation bias in data sets. However, we should keep in mind that these two problems have different perspectives and target separate issues despite all the similarities. The largest empty-space recognition problem is usually stated as: given a space containing \( n \) points, compute the largest regions that do not contain any of the points in their interior. Some techniques put restrictions on the shape of the empty region being (axis parallel) hyper-rectangles or hyper-spheres, while some are independent of it. In section 4.3, we will review such problems related to the problem of identifying representation bias.

3.2 Resolving Representation Bias

After identifying representation bias in data, the next step is presenting a remedy for it. The first approach to tackling this problem is adding more data while hoping to address the under-representation issues. However, it may not always be possible since adding more data is not free. When adding more data is not feasible, the current research suggests preventive solutions such as informing the user about the representation bias issue or rewriting queries to meet the representation constraints. With that being said, we would like to emphasize the necessity of human-in-the-loop in the resolution process. It is vital to notice that not all the under-represented regions in data are meaningful, and some may even be invalid. Therefore a domain expert must evaluate and semantically validate the identified groups/regions.

In the following, we will introduce state-of-the-art techniques for resolving representation bias. We will go through the details of each work in section 5.

3.2.1 Adding More Data. Enriching the data set with more data is the best way to address the under-representation issues. However, it may not be as simple as that. Adding more data is not free, and some questions need to be answered before taking any action. Considerations such as whether the data should be added only to the under-represented regions, resulting in changes to the underlying distribution, or data should be equally added to the underlying distribution. Furthermore, there are not always opportunities for adding more data through data collection or integration. In these cases, the existing research has acquired techniques like data augmentation to potentially improve whatever data is available and address the lack of representation issues. We will look into the details of the works in this category in section 5.1.

Data Collection. Data collection is usually costly. If the data are obtained from some third party, there may be a direct monetary payment. If the data are directly collected, there may be a data collection cost. In all cases, there is a cost to cleaning, storing, and indexing the data. To minimize these costs, as little additional data as possible should be acquired to meet the representation constraints. In [7], it suggests that the smallest number of additional data points are needed to hit all the large uncovered spaces. In [70], the authors provide solutions to acquire the right amount of data for data slices such that both accuracy and fairness are improved.
Data Augmentation. Data augmentation techniques [11, 14, 15, 30, 35, 64] increase the size of data by adding partially altered duplicates of already existing tuples or generate new synthetic entries from existing data. Some of the existing works adopt these techniques by adding synthetic points with different values for the attribute of interest for representation. Consequently, the new data set has an equal number of elements for different values of the attribute of interest, resulting in potentially resolving the underrepresentation issues.

Data Integration. In data integration, data is consolidated from different sources into a single, unified view. Integration consists of several steps including cleansing, ETL mapping, transformation, entity resolution, and data deduplication. Regarding insufficient representation, data integration [55, 56] concerns with how to query the multiple data sources at hand such that the count for the underrepresented groups in data is satisfied in a cost-efficient manner.

3.2.2 No More Data Available to Add. It is not always possible to add more data to the data sets as there might be complications such as unknown underlying distribution, lack of additional data, etc. Existing work suggests alternative solutions to tackle these scenarios, such as informing the users about the deficiencies in the data set or raising warnings at query time. Furthermore, by adding proper constraints on the queries with respect to the attributes of interest, an effort is made to ensure the proper representation. We will look into the details of the works in this category in section 5.2.

Generating Proper Warning Signal. Generating proper signals for the trustworthiness of the analysis [8] occurs when querying about a particular data point that might potentially be concerning due to belonging to an underrepresented subpopulation. Whether to consider the outcome and how to take action is left to the model user.

Data Labels and Data Sheets. Annotating data sets with representation information [27, 51, 52, 68] informs the data scientist about the potential deficiencies due to representation bias when the model is being constructed. This is a signal to investigate the fitness of data for a particular task before building the models.

Query Rewriting. Consider a data set with some interesting attributes (for example, gender, race, age) that are prone to be underrepresented and a query over the data. Now suppose that some representation constraints are given with respect to the result of a query when executed over the data set (for example, the number of females to be greater than a given threshold), but when the query is executed over the data set, results do not satisfy the required constraints. The idea of query rewriting [4, 5, 65] is to minimally rewrite the transformation queries so that certain representation constraints are guaranteed to be satisfied in the result of the transformation.

In Fig. 2, we present an overview of the algorithms/techniques described in this survey and present a side by side comparison between them based on different properties. Each technique is associated with its reference paper and is examined based on the following properties:

- **Attribute Type** specifies whether the data is in discrete or continuous space.
- **Relation Model** specifies whether data is in a single or multiple tables.
- **Task** specifies whether the algorithm identifies or resolves insufficient representation.
- **Time Complexity** states the worst-case time complexity of the technique or provides information on its running time.
- **Technique** briefly mentions the general idea of the proposed approach.
| Algorithm/Method                              | Attribute Type | Relation Model | Task                                      | Time Efficiency                                      | Technique                                                                 |
|----------------------------------------------|----------------|----------------|-------------------------------------------|------------------------------------------------------|---------------------------------------------------------------------------|
| Pattern-Breaker [7]                          | Discrete       |                | Identification                           | Pruning descendants of a MUP                        |                                                                           |
| Pattern-Combiner [7]                         | Continuous     |                | Identification                           | Pruning ancestors of a MUP                          |                                                                           |
| Deep-Diver [7]                               | Continuous     |                | Identification                           | Pruning both descendants and ancestors of a MUP     |                                                                           |
| Decision Tree Training [18]                  | Continuous, Discrete | Multi | Identification                           | Practical ML algorithm                              | Decision tree optimized on the classification results                     |
| Lattice Searching [18]                       | Continuous     |                | Identification                           | Heuristics for NP-hard problem                      | BFS over the lattice of data slices                                       |
| SliceLine Enumeration Algorithm [62]         | Continuous     |                | Identification                           | Fast and exact enumeration algorithm                | Linear-algebra-based exact slice enumeration algorithm                    |
| COUNTATA [52]                                | Continuous     |                | Identification                           | Pattern-based labels                                |                                                                           |
| Pattern Count-based Labels [51]              | Continuous     |                | Identification                           | Heuristics for NP-hard problem                      | Pattern count based labels                                               |
| P-Walk [46]                                  | Continuous     |                | Identification                           | Heuristics for NP-hard problem                      | Priority-based MUP searching                                              |
| FindBHR [47]                                 | Continuous     |                | Identification                           | O(n^{3d-1}d^{3}(log n)^2)                          | Discovering holes in the data                                             |
| FindMEHR [48]                                | Continuous     |                | Identification                           | Practical ML algorithm                              | Decision tree for discovering holes in the data                           |
| Maximal Empty Rectangles 2D [21]             | Continuous     |                | Identification                           | O(nm)                                                | Discovering holes in 2D data                                              |
| Maximal Empty Rectangles [21]                | Continuous     |                | Identification                           | O(d^2n^2)                                           | Discovering holes in high-dimensional data                                |
| DevExplorer [61]                             | Continuous     |                | Identification                           | O(n^2m)                                              | Discovering holes in data                                                |
| Shapley Slice Ranking Mechanism [23]         | Continuous     |                | Identification                           | O(n^2 m)                                             | Ranking slices based on Shapley value                                    |
| FairVis [12]                                 | Continuous     |                | Identification                           | O(n^2)                                               | Clustering data set to find problematic subgroups                         |
| Uncovered-2D [6]                             | Continuous     |                | Identification                           | O(k^n log n)                                        | k-th Voronoi diagram                                                      |
| Uncovered-MD [8]                             | Continuous     |                | Identification                           | O((Nnd + T) log N)                                   | ε-net approximation                                                       |
| Iterative Algorithm for Slice Tuner [70]     | Continuous     |                | Resolution                               | Dominated by data acquiring time                    | Periodically updating learning curves for dependent slices               |
| One-Shot Algorithm [70]                      | Continuous     |                | Resolution                               | O(KU)                                                | Amortization technique to reduce number of model trainings               |
| Greedy Fairness-aware Data Augmentation [64] | Continuous     |                | Resolution                               | 1 – 1/e approximation                                | Augmenting minority group instances to reach ideal data set              |
| Coverage-based rewriting baseline Algorithm with Pruning [5] | Continuous, Discrete | Multi | Resolution                               | Dominated by search time                            | Query rewrite such that representation constraints are met               |
| Coverage-based rewriting baseline Algorithm with Pruning with Iteration [5] | Continuous, Discrete | Multi | Resolution                               | Dominated by search time                            | Query rewrite such that representation constraints are met               |
| Dynamic Programming Algorithm for Data Distribution Tailoring [55] | Continuous, Discrete | Multi | Resolution                               | Exact Dynamic Programming                           |                                                                           |
| Equi-cost Binary [55]                        | Continuous     |                | Resolution                               | O(max(Q_i))                                         | Special case for binary valued attribute with equal collection cost       |
| Coupon Collector [55]                        | Continuous     |                | Resolution                               | O(mmax(Q_i))                                        | Approximation via instances of coupon collector                          |
| Upper Confidence Bound [55]                  | Continuous     |                | Resolution                               | O(nm \sum 1/p_i)                                    | Modeled as multi-armed bandit                                            |
| Query-2D [8]                                 | Continuous     |                | Resolution                               | O(k + log n)                                        | Trust signal                                                             |
| Query-MD [8]                                 | Continuous     |                | Resolution                               | O(log N)                                             | Trust signal                                                             |
| Datasheets for Data sets [27]                | Continuous     |                | Resolution                               | Not Applicable                                       | Describes Data sets from Representation Perspectives                      |
| MithraLabel [68]                             | Continuous     |                | Resolution                               | Not Applicable                                       | Describes Data sets from Representation Perspectives                      |
| Re-weighting [14]                            | Continuous     |                | Resolution                               | O(d)                                                 | Re-weighting data to meet representation constraints                     |

Fig. 2. Properties of different techniques for identifying and resolving representation bias.
4 IDENTIFYING REPRESENTATION BIAS

In this section, we study the works focused on identifying representation bias in data. Depending on the attribute type, we categorize the techniques into two classes depending on whether they target the problem in discrete or continuous space.

4.1 Discrete Attribute Space

Techniques in this category assume data with categorical-valued attributes and propose solutions for identifying the subpopulations with insufficient representation in discrete data sets. The works in this category are classified into two categories of addressing the problem in a single or multi relation data sets.

4.1.1 Single Relation. We begin with [7] that identifies representation bias in discrete space using the discrete notion of coverage measure. For cases where attributes of interest are non-ordinal categorical, coverage in discrete space is defined as having “enough” entries in data set matching a particular pattern. A pattern is a string that specifies a subgroup (e.g. gender=male, race=white) that matches possible values over a subset of attributes of interest. For example, consider a data set with three binary attributes of interest $A_1, A_2, A_3$. The pattern $P = X01$ specifies all the tuples for which $A_2 = 0$ and $A_3 = 1$ ($A_1$ can have any value). Coverage is usually discussed for groups given by the combinations of attribute-value assignments. A constant value is considered as the threshold for coverage, meaning that a minimum number of entries equal to the threshold value should exist from a subpopulation to be covered.

**Definition 4.1 (coverage in discrete space).** Given a data set $D$ over $d$ attributes with data domains $c = \{c_1, \ldots, c_d\}$, and a Pattern $P$ based on $c$ and $d$, the coverage of $P$ is the number of items in $D$ that match $P$. Formally: $\text{cov}(P, D) = |\{t \in D | M(t, P) = \top\}|$.

An item $t$ matches a pattern $P$ (written as $M(t, P) = \top$), if for all $i$ for which $P[i]$ is deterministic, $t[i]$ is equal to $P[i]$. Formally:

$$M(t, P) = \begin{cases} \top, & \forall i \in [1, d] : P[i] = X \text{ or } P[i] = t[i] \\ \bot, & \text{otherwise} \end{cases} \quad (1)$$

A pattern $P$ is said to be covered in a data set $D$ if its coverage is greater than or equal to the specified threshold: $\text{cov}(P, D) \geq \tau$. Otherwise, the pattern $P$ is uncovered.

In discrete data sets, there are multiple attributes each having multiple possible values that form a combinatorial number of possible patterns. Patterns as mentioned before, are the combination of some or all attributes-values; hence each pattern can have multiple children and parents (for example, considering attributes gender and race and their possible combinations, Female is the parent of Hispanic-Female, Black-Female, Asian-Female, White-Female, etc.). Depending on the size and skew in data sets, the coverage of patterns could be different and they try to identify patterns that don’t have sufficient coverage in an efficient way. If a pattern is uncovered, all of its children are also uncovered and it suggests that uncovered patterns should be identified in a way that they are not dominated by more general ones. In a more formal way, they introduce the notion maximal uncovered patterns (MUPs) as a pattern $P$ that its coverage is less than $\tau$, while for any pattern parent of $P$, their coverage is greater than or equal to $\tau$. The main goal in [7] is to find all the MUPs. No polynomial time algorithm can guarantee the enumeration of the set of MUPs, however, they propose several algorithms inspired by set enumeration and Apriori algorithm for association rule mining to efficiently address this problem.
Naive algorithm is a baseline that does a single pass over the data set with a counter for each pattern and then compares all pairs of the uncovered patterns to check if one is dominated by the other and if so remove the former from the list of uncovered patterns as it is not maximal.

Next they introduce Pattern Graph data structure that exploits the relationship between patterns to do less work than computing all uncovered patterns only to remove the ones that are not maximal. The parent-child relationship between the patterns is represented in a graph that can be used to find better algorithms. Pattern-Breaker starts from the top of the graph where the general patterns are and moves down by breaking each pattern into more specific ones. If a pattern is uncovered, then all of its descendants are also uncovered and they can not be a MUP, even if they have a parent that is covered. Therefore, this subgraph of the pattern graph can be pruned. The issue with Pattern-Breaker is that it explores the covered regions of the pattern graph and for the cases that there are a few uncovered patterns, it has to explore a large portion of the exponential-size graph. The algorithm for Pattern-Breaker is brought in Algorithm 1.

To tackle the issue in Pattern-Breaker, they propose Pattern-Combiner algorithm that performs a bottom-up traversal of the pattern graph. It uses an observation that the coverage of a node at level of the pattern graph can be computed as the sum of the coverage values of its children. The problem with Pattern-Combiner is that it traverses over the uncovered nodes first and therefore, it will not perform well for the cases that most of nodes in the graph are uncovered. The algorithm for Pattern-Combiner is brought in Algorithm 2.

In fact, for the cases that most of the MUPs are placed in the middle of the graph, both Pattern-Breaker and Pattern-Combiner will not be efficient as they should traverse half of the graph. Therefore, they propose Deep-Diver, a search algorithm that quickly finds the MUPs, and use them to limit the search space by pruning the nodes both dominating and dominated by the discovered MUPs. Each MUP is the child of a covered node, instead of doing a Breadth-First-Search over the patterns, Deep-Diver does a Depth-First-Search and takes a path down to find an uncovered node. The algorithm for Deep-Diver is brought in Algorithm 3.

Algorithm 1 Pattern-Breaker [7]

Input: Data set $D$ with $d$ attributes having cardinalities $c$ and threshold $\tau$

Output: Maximal uncovered patterns $M$

1: $Q = \{XX\cdots X\} // start$ from the root
2: $M = \{\}; Q_p = \{\}$
3: for /* each level of the graph */ $l = 0$ to $d$ do
4:   if $Q$ is empty then break
5:   $Q_n = \{\}$
6:   for $P \in Q$ do
7:     flag = false
8:     for $P'$ in parents($P$) do
9:       if $P' \notin Q_p$ or $P' \in M$ then flag = true; break
10:      if flag then continue
11:     $cnt = cov(P, D)$
12:     if $cnt < \tau$ then
13:       add $P$ to $M$
14:     else
15:       add children of $P$ based on Rule 1 to $Q_n$
16:   $Q_p = Q; Q = Q_n$
17: return $M$
Algorithm 2 Pattern-Combiner [7]

\textbf{Input:} Data set \( \mathcal{D} \) with \( d \) attributes having cardinalities \( c \) and threshold \( \tau \)

\textbf{Output:} Maximal uncovered patterns \( \mathcal{M} \)

1. \( \text{count} = \text{new hash()} \)
2. \( \text{for } \forall P \in \{v_1v_2 \cdots v_d \mid v_i \in c[A_i]\} \) \( \text{do} \)
3. \( \text{cnt} = \text{cov}(P, \mathcal{D}) \)
4. \( \text{if } \text{cnt} < \tau \) \( \text{then } \text{count}[P] = \text{cnt} \)
5. \( \text{if } \text{count is empty } \text{then return } \emptyset \)
6. \( \text{for } \ell = 0 \text{ to } d \) \( \text{do} \)
7. \( \text{nextCount} = \text{new hash()} \)
8. \( \text{for } P \in \text{count.keys} \) \( \text{do} \)
9. \( \mathcal{P}' = \text{generates nodes at } \ell - 1 \text{ based on Rule 2 on } P \)
10. \( \text{for } P' \in \mathcal{P}' \) \( \text{do} \)
11. \( i = \text{the index of right-most } X \text{ in } P' \)
12. \( \mathcal{P}'' = \{P''|\forall j \neq i : P''[j] = P'[j] \text{ and } P''[i] \in c[A_i]\} \)
13. \( \text{cnt} = \sum_{P'' \in \mathcal{P}''} (\text{count}[P''] \text{ if } P'' \in \text{count.keys} \text{ else } \tau) \)
14. \( \text{if } \text{cnt} < \tau \) \( \text{then } \text{nextCount}[P'] = \text{cnt} \)
15. \( \text{for } P \in \text{count.keys} \) \( \text{do} \)
16. \( \text{if } \text{parents}(P) \cap \text{nextCount.keys} = \emptyset \) \( \text{then} \)
17. \( \text{add } P \text{ to } \mathcal{M} \)
18. \( \text{if } \text{nextCount is empty } \text{then break} \)
19. \( \text{count} = \text{nextCount} \)
20. \( \text{return } \mathcal{M} \)

In [37], a system is designed on top of the methods and algorithms proposed in [7] to investigate representation bias over the intersection of multiple attributes using the notion of coverage.

Next work by Chung et al. [18] propose SliceFinder as a solution to address a similar problem to identifying representation bias is data. The goal is to find out if a model underperforms on some particular parts of data (referred as a data slice) because the overall model performance can fail to reflect that of smaller data slices. A slice is a conjunction of attribute-value pairs (similar to patterns in the [7]) and is considered problematic if the classification loss function takes very different values between the slice and the rest of the data. Enumeration of all possible slices is not practical and searching for the most underperforming slices can be deceptive since model’s performance over smaller slices can be noisy or they may be too small to have considerable impact on model’s quality. The goal is to identify the largest and most problematic slices that the model does not perform well for. Finding the most problematic slices requires a balance between the significance of the difference in loss and the magnitude of the slice. To do so, the disparity between the loss of a slice and its counterpart is calculated using a loss function like logarithmic loss such that the difference is always non-negative (slice has higher loss than its counterpart). To determine if the difference is significant, they suggest treating each slice as a hypothesis and perform two tests to determine 1) if the loss disparity is statistically significant (not observed by chance) and 2) whether the effect size of the disparity is large enough (how problematic the slice is). Therefore, they find a handful of the largest problematic slices, by taking all problematic slices with effect size larger than a threshold and rank them by size (number of entries).

In order to search for problematic slices, they propose three algorithms including a baseline. The idea for the Clustering baseline is to group similar examples in clusters each as a data slice and if a model performs unsatisfactory for a cluster, user can examine examples in the cluster more carefully. As convenient as it may sound, there are major
Algorithm 3 Deep-Diver [7]

Input: Data set $D$ with $d$ attributes having cardinalities $c$ and threshold $\tau$
Output: Maximal uncovered patterns $M$

1. Let $S$ = an empty stack
2. push $X \cdots X$ to $S$
3. while $S$ is not empty do
   4. $P = \text{pop a node from } S$
   5. $\text{uncoveredFlag} = \text{a flag indicating if } P \text{ is uncovered}$
   6. if $P$ is dominated by $M$ then
      7. continue
   8. else if $P$ dominates $M$ then
      9. $\text{uncoveredFlag} = \text{true}$
   10. else
      11. $cnt = \text{cov}(P, D)$
      12. $\text{uncoveredFlag} = cnt < \tau$
      13. if $\text{uncoveredFlag}$ is true then
         14. Let $S' = \text{an empty stack}$
      15. while $S'$ is not empty do
         16. $P' = \text{pop a node from } S'$
         17. $P' = \text{generates parent nodes of } P' \text{ by replacing one deterministic cell with } X.$
         18. for $P'' \in P'$ do
            19. $cnt' = \text{cov}(P'', D)$
            20. if $cnt' < \tau$ then push $P''$ to $S'$; break
         21. add $P$ to $M$
      22. else
      23. $Q = \text{generate nodes on } P \text{ and } c \text{ based on Rule 1}$
      24. push $Q$ to $S$
   25. return $M$

concerns such as the difficulty of clustering for high dimensional data and user-provided number of clusters that crucially affects the quality of clusters.

Next, they propose Decision Tree Training method in which, they train a decision tree to partition examples into slices defined by the tree. To find the $k$-problematic slices, they perform a Breadth-First-Search on the decision tree in which slices in each level are sorted based on increasing number of literals, decreasing slice size, and decreasing effect size and filtered whether they are statistically significant and have large enough effect-size. The advantage of using decision tree approach is its natural interpretability and the fact that it needs to be expanded a few levels to find the top-$k$ problematic slices. Conversely, decision tree is optimized for classification results and may not find all problematic slices. Besides, in cases of overlapping data slices, decision tree will find at most one of them.

To overcome the aforementioned problems, they propose Lattice Searching algorithm, in which slices form a lattice and problematic slices can overlap. Lattice searching follows the same procedure as decision tree training algorithm to search for the problematic slices as shown in Algorithm 4. Lattice search can be more expensive than decision tree training approach and cannot address the scalability issue searching over exponential size of data slices and therefore, they suggest employing parallelization and sampling techniques.

Next work, SliceLine [62], expands on the idea of [18] for exact slice enumeration to find real top-$k$ problematic data slices. None of the prior methods are able to find the real top-$k$ problematic slices and this uncertainty creates trust
Algorithm 4 Lattice Searching Algorithm [18]

Input: Lattice root $R$, max. number of slices to return $k$, effect size threshold $T$, significance level $\alpha$

Output: Problematic slices $S$

1. $S \leftarrow []$
2. $C \leftarrow PriorityQueue()$
3. $N \leftarrow []$
4. $S \leftarrow 1$
5. $E \leftarrow ExpandSlices([R], L)$
6. $W \leftarrow \alpha$
7. while True do
8.     for $slice \in E$ do
9.         if EffectSize(slice) $\geq T$ then
10.            C.push(slice)
11.        else
12.            N.append(slice)
13.     while $C$ not empty do
14.         slice $\leftarrow C$.pop()
15.         if IsSignificant(slice, $W$) then
16.             S.append(slice)
17.             if $|S| = k$ then
18.                 return $S$
19.                 $W \leftarrow UpdateWealth(W, 0)$
20.         else
21.             N.append(slice)
22.             $W \leftarrow UpdateWealth(W, 0)$
23.     $L \leftarrow L + 1$
24.     $E \leftarrow ExpandSlices(N, L)$
25.     if $E$ is empty then
26.         break
27. return $S$

Pastor et al. [61] propose the notion of divergence to estimate different classification behavior in subgroups compared to the overall data set. Divergence measures the difference in statistics such as False Positive Rate and False Negative Rate between a subgroup and the entire data set. However similar to [18], to recognize the problematic subgroups, they only consider the most frequent patterns with a size larger than a threshold and discard smaller subgroups. Once subgroups with high divergence are recognized, they check whether they are statistically significant and not due to fluctuations caused by finite size of data set. Next using the notion of Shapley value, they investigate which attributes in each problematic subgroup are contributing the most to the local and global divergence. DivExplorer algorithm (brought in Algorithm 6) extracts frequent subsets of attribute values and estimates their divergence.
Algorithm 5 SliceLine Enumeration Algorithm [62]

**Input:** Feature matrix $X_0$, errors $e$, $K = 4$, $\sigma = 32$, $\alpha = 0.5$, $\lceil L \rceil = \infty$

**Output:** Top- $k$ slices $TS$, Top- $k$ scores, errors, sizes $TR$

1. // data preparation (one-hot encoding $X$)
2. $f_{dom} \leftarrow \text{colMaxs}(X_0)$  // $1 \times m$ matrix
3. $f_b \leftarrow \text{cumsum}(f_{dom}) - f_{dom}$
4. $f_e \leftarrow \text{cumsum}(f_{dom})$
5. $X \leftarrow \text{oneHot}(X_0 + f_b)$  // $n \times l$ matrix
6. // initialization (statistics, basic slices, initial top- $k$)
7. $\bar{e} \leftarrow \text{sum}(e) / n$
8. $[S, R, c_I] \leftarrow \text{createAndScoreBasicSlices}(X, e, \bar{e}, \sigma, \alpha)$
9. $[TS, TR] \leftarrow \text{maintainTopK}(S, R, 0, 0, K, \sigma)$
10. // level-wise lattice enumeration
11. $L \leftarrow 1$, $\lceil L \rceil \leftarrow \min(m, \lceil L \rceil)$  // current/max lattice levels
12. $X \leftarrow X[c_I]$  // select features satisfying $s_0 \geq \sigma$ and $s_e > 0$
13. **while** nrow($S$) > 0 and $L < \lceil L \rceil$ **do**
14. $L \leftarrow L + 1$
15. $S \leftarrow \text{getPairCandidates}(S, R, TS, TR, K, L, \bar{e}, \sigma, \alpha, f_b, f_e)$
16. $R \leftarrow \text{matrix}(0, \text{nrow}(S), 4)$, $S_2 \leftarrow [S, cl]$
17. **for** $i$ in nrow($S$) **do**  // parallel for
18. $R_i \leftarrow \text{evalSlices}(X, e, \bar{e}, S_2^T, L, \alpha)$
19. $[TS, TR] \leftarrow \text{maintainTopK}(S, R, TS, TR, K, \sigma)$
20. **return** decodeTopK($TS, f_b, f_e$), $TR$

Algorithm 6 DivExplorer Algorithm [61]

**Input:** $D$, $u$, $v$, $o$, $f$, $s$

**Output:** FP divergence $FP_D$

1. $o(D) = \text{computeOutcomeFunction}(D, o, f)$
2. $T_D, F_D, \perp = \text{OutcomeOneHotEncoding}(o(D))$
3. $FI_{\text{withoutOutcomes}} = []$
4. **for** step$_i$ in Frequent Pattern Mining steps **do**
5. $l_{\text{step}_i} = \text{extractItemsets}(D, \text{step}_i)$
6. **for** $I$ in $l_{\text{step}_i}$ **do**
7. $T_I, F_I, \perp = \text{cardinalityOutcomes}(I, (T_D, F_D, \perp_D))$
8. **if** $(T_I + F_I + \perp_I) / \text{len}(D) \geq s$ **then**
9. $FI_{\text{withoutOutcomes}}.\text{append}(I, (T_I, F_I, \perp_I))$
10. $FP_f = \text{evaluateFunction}(FI_{\text{withoutOutcomes}}, f)$
11. $FP_{\Delta_f} = \text{divergence}(FP_f, f(D))$
12. **return** $FP_{\Delta_f}$

Farchi et al. [23] propose Shapley Slice Ranking Mechanism with focus on Error concentration (SSR-E) as an approach to rank data slices by the order of being problematic. However, they assume the slices are given as an input and they use the notion of Shapley value to rank the slices. They model the slices as players in a cooperative game and capture the importance of error concentration and statistical significance of the slices by defining various characteristic foundations.

Cabrera et al. [12] propose a system called FairVis that employs a different approach to generate subgroups in the combinatorially large space. They perform a clustering on the training data set to find statistically similar subgroups and
then use an entropy technique to find important features that are more dominant in that subgroup. When a feature’s entropy is close to zero, it means that it is concentrated in one value, which makes the feature more dominant in that subgroup. Next, they calculate a fairness score on the clusters and present the subgroups to the user sorted by the score. Once a problematic subgroup has been identified, users can compare them with similar subgroups to discover which value differences impact performance or to form more general subgroups with fewer number of features. The similarity between a pair of subgroups is calculated by summing the Jensen Shannon divergence between all features.

Finally, in [43], Lees et al. suggest to explore each subpopulation’s sample complexity bounds for learning an approximately fair model with a high probability. Sample complexity provides a lower limit on the count of training samples that are necessary from the subpopulations to learn a fair model. They demonstrate that a classifier can be representative for all subgroups if adequate population samples exist and the model dimensionality is aligned with subgroup population distributions. In case the sampling bias of the subpopulations are not met, human interventions in the data collection process by correcting representation bias (for example, collecting more data for underrepresented subpopulations) is recommended.

4.1.2 Multiple Relations. In real-world data analysis, the data to be analyzed is obtained through complex operations, e.g., table joins and predicate combinations, in databases with multiple relations. Due to the sheer data volume, determining adequate coverage can require a prohibitively long execution time. In [46], Lin et al. focus on the threshold-defined coverage identification in the multiple table scenario. Following the definition of the data pattern and the maximal uncovered pattern (MUP) in the single table scenario, coverage with multiple relations can be defined as follows:

**Definition 4.2 (Coverage with Multiple Relations).** Given a database $\mathcal{D}$ with multiple tables $\{T_1, \cdots, T_n\}$, an attribute set $\mathcal{A}$, and a data pattern $\mathcal{P}$, the coverage of a data pattern $\text{cov}(\mathcal{P})$ is defined as the number of records in the join table $\times_{T}$ that satisfies $\mathcal{P}$. With the fixed coverage threshold $\tau$, pattern $\mathcal{P}$ is a covered pattern if $\text{cov}(\mathcal{P}) \geq \tau$. Otherwise, this pattern is said to be uncovered.

The coverage analysis for multiple relations contains two important steps: (1) For a given data pattern, determine the coverage for this data pattern via the efficient conjunctive COUNT query execution. (2) In the lattice space of the pattern graph, design search algorithms to identify the set of MUPs. The authors design a highly parallel index scheme to handle joins and cross-table predicate combinations to efficiently compute the number of records for each given group. As discussed in [7], MUP identification problem is an NP-hard problem. To traverse the combinatorially large search space of the pattern graph, [46] designs a priority-based search algorithm that could minimize the number of computations to assess the count for a given group. As shown in Algorithm 7, the priority-based algorithm keeps searching the nodes with higher pruning efficiency. When a node is dominated by MUPs or dominates a covered pattern, it prunes this branch based on the coverage monotonicity property. The priority of the nodes is computed by a heuristic priority scoring function:

$$\text{priority} = \omega_p \times n_p + \omega_c \times n_c$$

where $n_p$ and $n_c$ are the number of parent nodes and child nodes for each data pattern, $\omega_p$ and $\omega_c$ are the weights for parents and children. With a higher weight for child nodes, the priority algorithm would be close to top-down BFS, while with a higher weight for parent nodes, the algorithms is more likely to traverse deep to the lower layers.

Besides, as the number of patterns does not need the exact counts for the patterns, we only need to determine whether the database contains more records than the given threshold or not. Therefore, this paper also provides a
A sampling-based approximate algorithm for coverage identification, which allows more efficient computation with smaller data sizes.

**Algorithm 7 P-WALK Coverage Analysis Algorithm [46]**

**Input:** Pattern graph $G(A)$, coverage threshold $\tau$

1. **procedure** INITIALIZATION
2. $neighbors \leftarrow$ empty priority queue sorted nodes by the priority scoring function
3. $C$ an empty set to store covered nodes
4. Maximal uncovered patterns $M$
5. **procedure** COVERAGEASSESSMENT
6. push the root node $P = XX...X$ to neighbors
7. while $neighbors$ is not empty do
8. $p = pop a node from neighbors$
9. if $p$ is dominated by $M$ or $p$ dominates $C$ then continue
10. $cov(p) = COUNT_PATTERN_COVERAGE(p)$
11. if $cov(p) \geq \tau$ then
12. push all children of $p$ into neighbors
13. push $p$ into $C$
14. else
15. Initialize stack $S' \leftarrow$ empty stack
16. push all parents of $p$ into $S'$
17. while stack $S'$ is not empty do
18. $p' = pop a node from S'$
19. if $cov(p') < \tau$ then
20. if all parents of $p'$ are covered then
21. push $p'$ into $M$
22. else push all uncovered parents into $S'$
23. else push $p'$ into $C$
24. return maximal uncovered patterns $M$

### 4.2 Continuous Attribute Space

Techniques in this category assume data with continuous-valued attributes and propose solutions for identifying representation bias in such data sets.

Following a similar definition of coverage discussed earlier in section 4.1, they extend the notion of coverage to continuous space for identifying representation bias in [8]. A query point in a continuous data space is covered if there are enough number of data points in its neighborhood. The collection of all the uncovered query points in the space shape the uncovered region. They formally define coverage in continuous space as:

**Definition 4.3 (Coverage in continuous space).** Given a data set $D$ with $d$ attributes $X = \{x_1, x_2, \ldots, x_d\}$, query point $q \in [0,1]^d$, a distance function $\Delta : \mathbb{R}^d \times \mathbb{R}^d \rightarrow \mathbb{R}$, a vicinity value $\rho$, and a threshold value $k$, the coverage of $q$ by $D$ is verified as follows:

$$ cov_{\rho,k}(q, D) = \begin{cases} 
true & \text{if } |\{t \in D \mid \Delta(t, q) \leq \rho\}| \geq k \\
false & \text{otherwise} 
\end{cases} $$

17
For each tuple \( t \in \mathcal{D} \), let \( \sigma_t \) be the hyper-sphere with radius \( \rho \) centered at it. Note that any point within the hyper-sphere \( \sigma_t \) has the distance less than \( \rho \) from \( t \). As a result, any query point in the space that falls within less than \( k \) hyper-spheres contains less than \( k \) tuples in its neighborhood is uncovered. The total uncovered region \( \mathcal{U} \) is the set of points that are not covered by \( \mathcal{D} \). Formally, \( \mathcal{U} = \{ q \in [0, 1]^d \mid cov(q, \mathcal{D}) = false \} \).

Depending on the number of attributes in a data set, they propose two algorithms for identifying uncovered regions in data.

First algorithm known as Uncovered-2D studies coverage over two-dimensional data sets where \( \mathcal{X} = \{ x_1, x_2 \} \). In order to find the number of circles that a query point falls into and consequently discovering the uncovered region, Uncovered-2D makes a connection to \( k \)-th order voronoi diagrams. Consider a data set \( \mathcal{D} \) and its corresponding \( k \)-th order voronoi diagram. For every tuple \( t \in \mathcal{D} \), let \( \sigma_t \) be the \( d \)-dimensional sphere (\( d \)-sphere) with radius \( \rho \) centered at \( t \). Consider a \( k \)-voronoi cell \( \mathcal{V}(S) \) in the \( k \)-th order voronoi diagram \( \mathcal{V}_k(\mathcal{D}) \). Any point \( q \) inside the intersections of the \( d \)-spheres of tuples in \( S \), i.e. \( q \in \bigcap_{t \in S} \sigma_t \), is covered, while all other points in the region are uncovered. Formally:

\[
\forall q \in \mathcal{V}(S) : Cov_{\rho,k}(q, \mathcal{D}) = \begin{cases} 
\text{true} & \text{if } q \in \bigcap_{t \in S} \sigma_t \\
\text{false} & \text{otherwise}
\end{cases}
\]

Algorithm 8 Uncovered-2D [8]

Input: data set \( \mathcal{D} \), \( k \), \( \rho \)

1: function \textsc{Identify}(\mathcal{D}, k, \rho)
2: \( \mathcal{V} \leftarrow \mathcal{V}_k(\mathcal{D}) \); \( \mathcal{U} \leftarrow \{ \} \)
3: for \( \mathcal{V}(S) \in \mathcal{V} \) do
4: \( C \leftarrow \bigcap_{t \in S} \sigma_t \)
5: \( \mathcal{U}.add(\mathcal{V}(S) \setminus C) \)
6: return \( \mathcal{U}, \mathcal{V} \)
7: function \textsc{Report}(\mathcal{U})
8: \text{map} \leftarrow 2D \text{ map of } [0, 1] \times [0, 1]
9: for \( \langle x_1, x_2 \rangle \in \text{map} \) do
10: if \( \langle x_1, x_2 \rangle \in \mathcal{U} \) then \text{color}[x_1, x_2] \leftarrow \text{red}
11: else \text{color}[x_1, x_2] \leftarrow \text{green}

The algorithm starts by constructing the \( k \)-th order voronoi diagram of the data set and then for each voronoi cell \( \mathcal{V}(S) \) in the diagram, it computes the intersection of the circles of the tuples in \( S \) and marks the portion of \( \mathcal{V}(S) \) that falls outside it as uncovered. After identifying the uncovered region, a 2D map of \( \{ x_1, x_2 \} \) value combinations is used to report the region to the user. Uncovered-2D algorithm is brought in Algorithm 8.

The algorithm for the 2D case can be extended to the general case by relaxing the assumption on the number of attributes to discover the exact uncovered region, however, due to the curse of dimensionality, the search size space explodes as the number of dimensions increase and as a result, the algorithm will not be practical. Therefore, they propose a randomized approximation algorithm based on the geometric notion of \( \epsilon \)-net.

The idea is to take random samples from the space (every sample is a potential query point) and check whether each point is covered or not labeling them as +1 if uncovered and −1 otherwise. If we have enough samples in this collection it forms an \( \epsilon \)-net that the uncovered region can be learned using it. The problem with Uncovered-MD is that, theoretically speaking in adversarial cases, the number of samples may be exponentially large to the number of
dimensions, however, in practice the adversarial case is unlikely to happen since the boundary complexity depends on the number of arcs constructing it which can be significantly less than the theoretical upper-bound provided for the number of samples. }

Uncovered-MD algorithm is brought in Algorithm 9.

Algorithm 9

Uncovered-MD [8]

Input: Data set \( \mathcal{D} \), \( k \), \( \rho \), \( \varepsilon \), and \( \phi \)

1: function Identify(\( \mathcal{D} \), \( k \), \( \rho \), \( \varepsilon \), \( \phi \))
2: \( T \leftarrow \) a set of i.i.d samples according to \( \phi \)
3: \( N_S \leftarrow \) an initial value // based on \( n, d \)
4: repeat
5: \( S \leftarrow \) \( N_s \) i.i.d samples from \([0,1]^d\)
6: for \( s \in S \) do
7: \( \text{if } |\{ t \in \mathcal{D} \mid \Delta(t,s) \leq \rho \} | \geq k \text{ then } t[s] \leftarrow +1 \)
8: \( \text{else } t[s] \leftarrow -1 \)
9: \( \mathcal{U}_a \leftarrow \text{classifier}(S,t) \)
10: \( \text{Error}\leftarrow \text{error}(\mathcal{U}_a, T) \)
11: \( N_s \leftarrow 2 \times N_s \)
12: until \( \text{Error} \leq \varepsilon \)
13: return (\( \mathcal{U}_a \), \( S \), \( t \))

function Report(\( S \), \( t \))

14: \( T \leftarrow \text{DecisionTree}(S,t); \text{desc} \leftarrow \{ \}
15: for \( l \in T.\text{leaves} \) do
16: \( \text{if } l.\text{label} = +1 \text{ then} \)
17: \( \text{add } (\text{PathFromRoot}(l), l.\text{entropy}) \text{ to } \text{desc} \)
18: return \text{desc}

4.3 Related Concepts and Techniques

Problems related to lack of representation are also critical in the data mining field. Many of the data mining approaches focus on the discovery of frequent patterns, while the alternative problem, the discovery of empty regions is also an important task in discovering rules or regularities that exist in the data. For example, empty regions could warn us about some unexpected missing value combinations. There are many works [21, 44, 47, 48] focus on the search of interesting holes in the databases. The papers focus on the discovery of regions that has fewer records than the given threshold (could be 0), which are called maximal hyper-rectangles (MHR). This problem has also been discussed in the computational geometry field with the purpose to produce run-time bounds [16, 20, 53, 54, 60].

FindMHR firstly [47] solves the problem of identifying empty regions \( (N = 0) \) in the high-dimensional data space with continuous values. In Algorithm 10, the main idea is to start with one MHR which occupies the entire space \( S \). As each point incrementally adds to \( S \), the algorithm updates the set of MHRs by computing the new upper and lower bound for each new hyper-rectangles.

However, in large data set settings, the main drawback of this algorithm is the necessity for calculating and storing every empty hyper-rectangle in memory. In addition, it requires that every element be processed before anything can be known about the size of large holes. In [44], the authors propose a Monte Carlo algorithm for finding holes in high dimensional data that reduces the complexity of the previous algorithm from exponential to polynomial time with respect to the number of dimensions. In Algorithm 11 and Algorithm 12, first the data is normalized from 0 to 1 in each
Woodstock '18, June 03–05, 2018, Woodstock, NY
Nima Shahbazi, Yin Lin, Abolfazl Asudeh, and H. V. Jagadish

Algorithm 10 FindMHR [47]

1: Insert($T$, $\{(S_l_1, S_u_1), \cdots, (S_l_k, S_u_k)\}$)
2: for each point $X$ in the database do
3: $RL = \text{ContainmentSearch}(T, X)$
4: for each point $H = ((L_i, U_i), \cdots, (L_k, U_k))$ in $RL$ do
5: if $X$ is on a surface of $H$ then
6: insert $X$ into the set of bounding points in that surface
7: else delete $(T, H)$
8: for each dimension $i$ do
9: $L'_i = \{l \in L_i | l(i) < X(i)\}$
10: $U'_i = \{u \in U_i | u(i) < X(i)\}$
11: $L''_i = \{l \in L_i | l(i) > X(i)\}$
12: $U''_i = \{u \in U_i | u(i) > X(i)\}$
13: if $L'_j$ and $U'_j$ not empty for all $j \neq i$ and $\text{BigEnough}(H' = ((L'_1, U'_1), \cdots, (L_i, X(i)), \cdots, (L'_k, U'_k))$ then
14: Insert($T$, $H'$)
15: if $L''_j$ and $U''_j$ not empty for all $j \neq i$ and $\text{BigEnough}(H'' = ((L''_1, U''_1), \cdots, (X, U_i), \cdots, (L''_k, U''_k))$ then
16: Insert($T$, $H''$)
17: Sort and report all the MHRs in $T$ according to their sizes

In [21], they utilize a technique similar to [6], which improves the memory efficiency of [47]. They proposed an algorithm for the 2D space while proposing an extension to handle the multi-dimensional data sets. The extension...
work [48] (described in Algorithm 13), built upon [47], can handle the mixture of continuous and discrete attributes, which makes use of the decision tree model to overcome the shortcomings of the previous work and also provide practical algorithms to reduce the time complexity. It trains a decision tree to divide the space into filled and empty regions and then identifies maximal holes using the filled regions generated in the decision tree.

Algorithm 13 FindMHR [48]

1. procedure FindMHR(data, projections)
2. for all \( k \in \text{projections} \) do
3. \( r \leftarrow \text{rand}(0,1) \)
4. \( L_k, U_k \leftarrow \text{findBoundingPoints}(r, \text{projections}) \)
5. \( ehr \leftarrow \text{createR}(U, L) \)
6. \( mehr \leftarrow \text{expandRectangle}(ehr, \text{projections}) \)
7. return \( mehr \)

In this section, we study the works focusing on resolving representation bias in data. We categorize the techniques into two classes: first, techniques that resolve representation bias by adding more data to the data set when possible and second, a variety of approaches when adding data is not an within reach.

5 RESOLVING REPRESENTATION BIAS

A Survey on Techniques for Identifying and Resolving Representation Bias in Data Woodstock ’18, June 03–05, 2018, Woodstock, NY
5.1 Adding More Data

5.1.1 Data Collection. Collecting data is not free as it is associated with costs at different stages of the data management pipeline. In this regard, we want to make sure that the right amount of data that serves the purpose is collected while the expenses are minimized.

For resolution purposes Asudeh et al. [7] suggest identifying the smallest number of additional data points needed to hit all the large uncovered spaces. Given the combinatorial number of patterns, it is not feasible to cover all of the patterns in practice. To do so, they determine the patterns for the minimum number of items that must be added to the data set to reach a desired maximum covered level or to cover all patterns with at least a specified minimum value count. This problem translates to a hitting set instance which can be viewed as a bipartite graph with the value combinations in the left side and the uncovered patterns in the right. There is an edge between a combination and a pattern if the combination matches the pattern. The objective is to select the minimum number of nodes in the left side that hit all the patterns in the right. The hitting set problem is NP-complete and the greedy approach in Algorithm 14 guarantees a logarithmic approximation ratio for it.

```
Algorithm 14 Greedy [7]
Input: The bit vector \( f_i \), best-known hit-count \( c_{\text{max}} \), inverse indices \( I \), and the current level \( i \), the set of uncovered patterns to hit \( M \)
Output: The set of value combinations to collect
1: function hit-count(\( f_i \), \( c_{\text{max}} \), \( I \), \( i \))
2: for value \( v_j \) in \( c_i \) do
3: \( b[v_j] = f_i \land I_{A_j} \)
4: \( \text{cnt}[v_j] = \text{number of 1's in } b[v_j] \)
5: if \( i = d \) then
6: \( \vartheta_{\text{max}} = \text{argmax } \text{cnt}[j] \)
7: return \( \text{max}(\text{cnt}[\vartheta_{\text{max}}], c_{\text{max}}), \vartheta_{\text{max}} \)
8: sort values \( v_j \) in \( c_i \) based on \( \text{cnt}[j] \), descendingly
9: for \( j = 1 \) to \( c_i \) do
10: if \( \text{cnt}[v_j] < c_{\text{max}} \) then
11: break
12: \( \text{tmp}_{\text{cnt}}, \text{tmp} = \text{hit-count}(b[v_j], c_{\text{max}}, I, i + 1) \)
13: if \( \text{tmp}_{\text{cnt}} > c_{\text{max}} \) then
14: \( \text{retval} = \text{join}(\text{tmp}, v_j) \)
15: \( c_{\text{max}} = \text{tmp}_{\text{cnt}} \)
16: return \( c_{\text{max}} \), retval
17: 
18: function greedy()
19: \( f_i \) = a bit vector of size \( |M| \) with all bits being 1
20: \( I \) = inverted indices of attribute values to \( M \)
21: \( V = \{ \} \)
22: while \( \exists 1 \leq j \leq |M| \) s.t. \( f_i[j] = 1 \) do
23: \( c_{\text{max}}, v = \text{hit-count}(f_i, 0, I, 1) \)
24: add \( v \) to \( V \) and update the \( f_i \) accordingly
25: return \( V \)
```

In another work, Tae et al. [70] focus on acquiring right amount of data for data slices such that both accuracy and fairness are improved. Acquiring same amount of data for all slices may not have the same cost-benefit and it can
bias the data and affect model’s accuracy for other regions. Therefore, they propose a few data acquisition strategies (including 3 baselines) such that the models are accurate and fair for different slices. Baselines include acquiring same amount of data for all slices, acquiring data for all slices such that in the end they all have the same amount of data (Water filling algorithm) and acquiring data in proportion to original data distribution. None of the baselines solve the problem in an optimal way and in many cases increase the loss and unfairness of the models. This leads to the selective data acquisition problem that is defined as given a data set, a set of data slices, a model trained on the data set, a cost function for data acquisition and a data acquisition budget, acquire examples for each slice such that the model’s average loss and average unfairness over all slices are minimized while the overall cost for data collection fits the budget.

The idea is to estimate the learning curves of slices, which reveal the cost benefits of data acquisition. The impact of data acquisition on model’s loss is significant at first but then gradually is stabilized to the point where it is not worth the effort anymore. Given the learning curves, Slice Tuner uses the learning curves to determine how much data to acquire per slice in order to optimize the model accuracy and fairness across the slices while using a limited data acquisition budget. However, in reality, learning curves are not perfectly generated because slices may not have sufficient data for the model loss to be measured. Besides, acquiring data for one slice may affect the loss of the model on some other slices and eventually change their learning curves. So it is important to generate learning curves that are reliable enough to still benefit Slice Tuner given these issues.

Selective data acquisition problem can be considered in two different settings: for the cases that slices are independent from each other, it is only needed to solve the optimization problem once. Since the objective for minimizing loss and unfairness is global, the optimization should be done on all slices. The One-shot algorithm updates the learning curves and solves the optimization problem to determine the amount of data that needs to be acquired for each slice. When slices are dependent Slice Tuner iteratively updates the learning curves as more data is acquired. Besides, the iterative updates make the learning curves more reliable, as they are updated whenever enough influence happens, irrespective of its direction. The Iterative algorithm (Algorithm 15) limits the change of imbalance ratio to determine the amount of data to obtain for each slice.

5.1.2 Data Augmentation. In [64], Sharma et al. propose a novel data augmentation method to address lack of representation of subgroups in a data set. For a data set with a protected attribute having a privileged and unprivileged subpopulation, they create an ideal world data set: for every data sample, a new sample is created that has the same label and features as the original sample except for that it has the opposite protected attribute value. The synthetic tuples are then sorted in order of their closeness to the original training distribution and added to the real data set to create intermediate data sets. As a result, this new data set has an equal number of entries for privileged and unprivileged sub-populations, while the label is not dependent on the the protected attribute anymore, therefore potentially removing representation bias from the model built on the data set. Although, there is concern over polluting the data set with too many synthetic entries, by selectively adding the synthetic points that are closest to the original distribution in every increment. The user can see the effect of an augmentation technique that improves fairness while keeping the overall accuracy nearly constant.

Sometimes, the real-world training data could predominately be composed of majority examples with a small percentage of outliers or interesting minorities. For example, in applications like fraud detection, disease diagnoses, and the detection of oil spills, the majority of the records are negative while there is a small number of positive “interesting” records. Machine learning models trained on such imbalanced data sets are highly likely to have poor performance.
Algorithm 15 Iterative algorithm for Slice Tuner [70]

Input: The slices \( S \), budget \( B \), minimum slice size \( L \), and data acquisition cost function \( C \)

1: \( \text{sizes} \leftarrow \text{SliceSize}(S) \)
2: \( T \leftarrow 1 \)
3: if \( \exists i \text{ sizes}(i) < L \) then
4: \( \text{num\_examples} \leftarrow \max(L \times 1 - \text{sizes}, 0) \)
5: \( \text{sizes} \leftarrow \text{sizes} + \text{num\_examples} \)
6: \( B \leftarrow B - \sum_i (C(i) \times \text{num\_examples}[i]) \)
7: \( IR \leftarrow \text{GetImbalanceRatio}(\text{sizes}) \)
8: while \( B > 0 \) do
9: \( \text{num\_examples} \leftarrow \text{OneShot}(\text{sizes}, B) \)
10: \( IR \leftarrow \text{GetImbalanceRatio}(\text{sizes} + \text{num\_examples}) \)
11: if \( IR > T \) then
12: \( \text{target\_ratio} \leftarrow IR + T \times \text{Sign}(\text{After\_IR} - IR) \)
13: \( \text{change\_ratio} \leftarrow \text{GetChangeRatio}(\text{sizes}, \text{num\_examples}, \text{target\_ratio}) \)
14: \( \text{num\_examples} \leftarrow \text{change\_ratio} \times \text{num\_examples} \)
15: \( IR \leftarrow \text{GetImbalanceRatio}(\text{sizes} + \text{num\_examples}) \)
16: \( B \leftarrow B - \sum_i (C(i) \times \text{num\_examples}[i]) \)
17: \( T \leftarrow \text{IncreaseLimit}(T) \)
18: \( IR \leftarrow \text{After\_IR} \)
19: return
20: function \( \text{GetImbalanceRatio}(\text{sizes}) \)
21: return \( \max(\text{sizes}) \)
22: return \( \min(\text{sizes}) \)

Oversampling is one of the most commonly used methods to enhance the model performance in this case. The naive uniform oversampling algorithms simply duplicates the minorities uniformly at random and are subject to a higher risk of model over-fitting. The Synthetic Minority Oversampling Technique (SMOTE) [15] is a better alternative, which generates synthetic records of minorities based on their \( k \)-Nearest minority neighbors. There is a rich line of works that extend the SMOTE algorithm, for example, the SMOTE-borderline algorithms [30], which classified the minorities into noise, danger, and safe and only use the danger minorities for data augmentation; and the extension of SMOTE for high-dimensional data [11]. In [35], they suggest two techniques for resolving representation bias including an oversampling baseline by duplicating the instances from the minority subgroups to achieve balance. The idea of their main approach is using SMOTE as an augmentation technique. They propose two approaches to create the instances, first, producing instances based on a given attribute and populating the minority subgroup for a given attribute. Second, by generating instances based on a given attribute with respect to class, meaning that instances from the underrepresented subgroup of a given attribute are generated to deal with subgroup’s class imbalance.

Finally, Celis et al. [14] present a data preprocessing method towards mitigating representation bias. The goal of this approach is to learn a distribution that resolves representation bias while remaining closest possible to the original distribution. Learning a distribution in polynomial time to the dimension of the domain (versus domain size that can be exponential) guarantees the scalability of their method. They propose a framework based on the maximum entropy principle claiming that of all the distributions satisfying observed constraints, the distribution should be chosen that is “maximally non-committal” with regard to the current state of knowledge meaning that it makes fewest assumptions.
about the true distribution of the data. Using this principle, probabilistic models of data are learned from samples by obtaining the distribution over the domain that minimizes the KL-divergence with regards to a “prior” distribution such that its expectation follows the empirical average derived from the samples. Their approach for preprocessing data benefits from the maximum entropy framework by combining re-weighting and optimization approaches. Maximum entropy frameworks can be specified by a prior distribution and a marginal vector, providing a simple way to enforce constraints for sufficient representation. Using a re-weighting algorithm, Celis et al. specify the prior distribution by carefully choosing weights for each tuple such that desired fairness measures are satisfied data is debiased from representation bias. The algorithm for the re-weighting approach is brought in Algorithm 16. Next, a marginal vector is chosen as the weighted average vector of samples to meet the representation rate constraints. Having defined the optimization program, they solve the dual form using Ellipsoid algorithm as it can be done in polynomial time in the dimension of data.

Algorithm 16 Re-weighting [14]

Input: Data set \( S := \{(X_\alpha, Y_\alpha, Z_\alpha)\}_{\alpha \in S} \subseteq X \times Y \times \Omega \), frequency list \( \{n_\alpha\}_{\alpha \in S} \), parameter \( \tau \in (0, 1] \)

1. for \( y \in Y \) do
2. \( c(y) \leftarrow \sum_{\alpha \in S} 1(Y_\alpha = y).n_\alpha \)
3. \( c(y, 0) \leftarrow \frac{1}{\tau} \sum_{\alpha \in S} 1(Y_\alpha = y, Z_\alpha = 0).n_\alpha \)
4. \( c(y, 1) \leftarrow \sum_{\alpha \in S} 1(Y_\alpha = y, Z_\alpha = 1).n_\alpha \)
5. \( w \leftarrow 0 \)
6. for \( \alpha \in S \) do
7. \( w(\alpha) \leftarrow \frac{n_\alpha.c(Y_\alpha)/c(Y_\alpha,Z_\alpha)}{W} \)
8. \( W \leftarrow \sum_{\alpha \in S} w(\alpha) \)
9. return \( \{w(\alpha)/W\}_{\alpha \in S} \)

5.1.3 Data Integration. Nargesian et al. [55] suggest Data Distribution Tailoring (DT) as resolving insufficient representation of subgroups in a data set by integrating data from multiple sources in the most cost effective manner such that subgroups in the data set meet the count distribution specified by the user. Depending on our knowledge about data source distributions, DT can be defined from two different perspectives, first, When the user is aware of the data source sizes and total number of tuples belonging to each subgroup, and second, when such knowledge about the data sources does not exist.

For the cases when the group distributions are known, the process of collecting the target data set is a sequence of iterative steps, where at every step, the algorithm chooses a data source, queries it, and if the obtained tuple contributes to one of the groups for which the count requirement is not yet fulfilled, it is kept, otherwise discarded. To do so, they first propose a Dynamic Programming (DP) algorithm. An optimal source at each iteration minimizes the sum of its sampling cost plus the expected cost of collecting the remaining required groups, based on its sampling outcome. The dynamic programming analysis evaluates this cost recursively by considering all future sampling outcomes and selecting the optimal source in each iteration accordingly. The drawback to the DP algorithm is that it quickly becomes intractable for cases that count requirements are not small. However, they provide a special case for when the (sensitive) attribute of interest is binary like gender (male, female) and the cost to query data is similar from all sources. Similar to the previous algorithm, process of collecting the target data is a sequence of iterations where, at every iteration, we should select a data source to query. At each iteration, the algorithm finds corresponding data sources for each group and then depending on which group is in the minority, it queries the proper data source. The algorithm stops when the
Algorithm 17 Equi-cost Binary [55]

Input: Group counts \( q_1 \) and \( q_2 \); data sources \( \mathcal{L} = \{D_1, \ldots, D_n\} \)
Output: \( O \), target data set

1: \( O \leftarrow \{\} \)
2: \( O_i^j \leftarrow 0, \forall 1 \leq i \leq n, 1 \leq j \leq 2 \)
3: while \( (q_1 > 0 \text{ OR } q_2 > 0) \) do
4: \( D_k \leftarrow \arg\max_{D_k \in \mathcal{L}} \left( \frac{N_k^j - O^j_k}{N_k} \right) \), \( D_{k'} \leftarrow \arg\max_{D_{k'} \in \mathcal{L}} \left( \frac{N_{k'}^j - O^j_{k'}}{N_{k'}} \right) \)
5: \( p_1 \leftarrow \frac{N_k^1 - O^1_k}{N_k}, p_2 \leftarrow \frac{N_{k'}^1 - O^1_{k'}}{N_{k'}} \)
6: \( D_1 \leftarrow D_k \text{ if } (q_2 == 0 \text{ OR } p_1 < p_2) \text{ else } D_1 \leftarrow D_{k'} \)
7: \( s \leftarrow \text{Query}(D_1) \)
8: \( j \leftarrow \mathcal{G}(s) // \text{ the group of } s \)
9: if \( (s \notin O \text{ AND } q_j > 0) \) then
10: add \( s \) to \( O \), \( q_j \leftarrow q_j - 1 \); \( O_i^j \leftarrow O_i^j + 1 \)
11: return \( O \)

Algorithm 18 Coupon Collector [55]

Input: Group counts \( q_1, \ldots, q_m \); data sources \( \mathcal{L} = \{D_1, \ldots, D_n\} \)
Output: \( O \), target data set

1: \( O \leftarrow \{\} \)
2: \( O_i^j \leftarrow 0, \forall 1 \leq i \leq n, 1 \leq j \leq m \)
3: while \( \exists q_j > 0, \forall 1 \leq j \leq m \) do
4: \( \text{min} \leftarrow \infty \)
5: for \( j = 1 \) to \( m \) do
6: if \( q_j == 0 \) then continue
7: \( x \leftarrow \arg\max_{D_k \in \mathcal{L}} \left( \frac{(N_k^j - O^j_k)}{N_k} \right) \)
8: if \( (N_k^j - O^j_k)/N_k < \text{min} \) then \( i \leftarrow x \)
9: \( s \leftarrow \text{Query}(D_i) \)
10: \( j \leftarrow \mathcal{G}(s) // \text{ the group of } s \)
11: if \( (s \notin O \text{ AND } q_j > 0) \) then
12: add \( s \) to \( O \), \( q_j \leftarrow q_j - 1 \); \( O_i^j \leftarrow O_i^j + 1 \)
13: return \( O \)

count requirements of both groups are satisfied then returns the target data set. The algorithm is shown in Algorithm 17.

Finally, as an alternative for the DP algorithm, they propose an approximation algorithm for the general case. They model the problem as \( m \) instances of the "coupon collector’s problem", where every \( j \)-th instance aims to collect samples from the \( j \)-th group and then using the union bound, they come up with an upper-bound on the expected cost of this algorithm. The algorithm first identifies the minority groups and then queries its corresponding data source and updates the target data accordingly. The algorithm is shown in Algorithm 18.

For the cases where the group distributions are unknown, they model DT as a “Multi-armed bandit problem”. Every data source is an arm and we want to select arms in order to collect the required tuples for each group. Every arm has an unknown distribution of different groups and a query to an arm has a cost. As the bandit strategy, they adopt “Upper Confidence Bound (UCB)” to balance between exploration and exploitation. At every iteration, for every arm, UCB computes confidence intervals for the expected reward, and selects the arm with the maximum upper-bound of reward to be explored next. Finally, they argue that reward of obtaining a tuple from a group is proportional to how rare this
was verified, otherwise, why not? Does the data set identify any subpopulations such as race, gender, age group, etc.

Algorithm 19 Upper Confidence Bound [55]

Input: Group counts \(q_1, \ldots, q_m\); data sources \(\mathcal{L} = \{D_1, \ldots, D_n\}\); underlying distribution of groups \(p^1, \ldots, p^m\)

Output: \(O\), target data set

1. \(O \leftarrow \{\}; t \leftarrow 0; \text{cost} \leftarrow 0\)
2. \(O_j \leftarrow 1, \forall i \in [1, n]\)
3. \(O_j' \leftarrow 0, \forall i \in [1, n], j \in [1, m]\)
4. for \(i = 1\) to \(n\) do // query each data source once
   5. \(s \leftarrow \text{Query}(D_i); \text{cost} \leftarrow \text{cost} + C_i; t \leftarrow t + 1;\)
   6. if \((s \notin O \text{ AND } q_j > 0)\) then
      7. add \(t\) to \(O\); \(q_j \leftarrow q_j - 1\); \(O_j' \leftarrow 1\)
8. while \(\exists q_j > 0, \forall i \leq j \leq m\) do
9. for \(i = 1\) to \(n\) do
10. \(R[i] \leftarrow \frac{1}{C_i} \sum_{j=1}^{m} q_j' \frac{1}{p_j}; U[i] \leftarrow \sqrt{2 \ln t/O_i}\)
11. \(D_i \leftarrow \arg\max_{k} U[k]; \text{cost} \leftarrow \text{cost} + C_i;\)
12. \(s \leftarrow \text{Query}(D_i);\)
13. \(j \leftarrow \mathcal{G}(s) /\text{ the group of } s\)
14. \(O_j \leftarrow O_j + 1; t \leftarrow t + 1; \text{cost} \leftarrow \text{cost} + C_i;\)
15. if \((s \notin O \text{ AND } q_j > 0)\) then
16. add \(s\) to \(O\); \(O_j' \leftarrow O_j' + 1; q_j \leftarrow q_j - 1\)
17. return \(O\)

group is across different data sources or in other words, what is the expected cost one needs to pay in order to collect a tuple from that group. The algorithm is shown in Algorithm 19

5.2 No More Data Available to Add

5.2.1 Generating Proper Warning Signal. After identifying the uncovered regions in the data set, [8] generates a trust signal for any arbitrary point in the query space. The warning signal states whether the query point is covered or not. For the 2D case, the idea is to find the Voronoi cell that the query point belongs to and check the point’s distance to all the points from data set that fall into that cell. If either of the distances are larger than the vicinity threshold, the query point is uncovered and a warning signal is generated. For the MD case, the classifier trained on the last iteration of the Uncovered-MD algorithm is used to determine the coverage of the query point by the data set.

5.2.2 Data Labels and Data Sheets. In [27], the authors propose a list of questions that data set collectors should have in mind before the procedure and respond after the collection is done. Users can then make informed decisions about the fitness of the data set for their tasks. A number of these questions address the representativeness of the data set such as whether the data set includes all possible instances or is a sample (not necessarily random) of a larger set and if it’s the latter, what is the larger set? Is the sample representative of the larger set and if so how the representativeness was verified, otherwise, why not? Does the data set identify any subpopulations such as race, gender, age group, etc. and, if so, how are these subpopulations identified and what is the distribution of them like in the data set? Does the data set include attributes that can be considered sensitive like racial or ethnic origins, sexual orientations, religious beliefs, political opinions, etc.

Some research proposes using data labels to help the data users to choose the appropriate datasets for their tasks. Information about data coverage is important to the data set profiling. MithraLabel [68] provides a set of visual widgets delivering information about the data set along different tasks on representativeness of minorities, bias, correctness, coverage in terms of MUPs, outliers and much more. In [51, 52], the authors design a “coverage label” of compact
size that can be used to efficiently estimate the counts for each combination of discrete attributes (data pattern). They provide a trade-off between the label size and the estimation error of pattern counts. The label model is built upon an estimation function that allows the users to estimate the count of every pattern. The authors design a label for a given subset $S$ which stores the pattern count for each possible pattern over $S$ and the value count of each value appearing in the data set. The identification of the optimal labels is an NP-hard problem. The authors also present an optimized heuristic for optimal label generation.

5.2.3 Query Rewriting. Accinelli et al. [5] propose an approach for rewriting filter and merge operations in preprocessing pipelines into the closest operation, so that the unprivileged groups are sufficiently represented. This is motivated by the fact that underrepresentation of a subpopulation in an initial or intermediate data set in preprocessing pipelines may lead to underrepresentation of that subpopulation in any future analyses. To do so, they provide an approach that minimally rewrites the transformation operation such that coverage constraints are ensured to be met in the transformed outcome. Many potential re-writings could exist, however, their proposed sample-based approximate approach finds the minimal rewriting of the original query. Queries are transformed into a canonical form as a preprocessing step. Next, the search space of potential re-writings is discretized, in such order that an approximation of the optimal solution can be determined in the next step, by inspecting the succeeding finite set of points. The modified input query meeting coverage constraints can be acquired by examining the grid resulting from the preprocessing step, in an order that ensures the fast identification of the closest rewriting, and by confirming constraint satisfaction using a sample-based approach. The coverage-based rewriting is approximate as a result of the discretization of the search space and of the error in estimating cardinalities and constraint satisfaction on the sample. They propose 3 algorithms including a baseline for coverage-based query rewriting. Coverage-based Rewriting Baseline $\text{CRBase}$ visits the grid by an increasing order of distance from the first cell of the grid. During the visit, we look for the cell corresponding to the query with the minimum cardinality that satisfies coverage-based constraints. $\text{CRBase with Pruning (CRBaseP)}$ adds some pruning rules to reduce the search space and $\text{CRBase with Pruning with Iteration (CRBasePI)}$ further optimizes $\text{CRBaseP}$ by iteratively increasing the number of bins during the search up to a given maximum. As a result, each iteration increases the precision by which they refine the query and compute the cardinalities.

Since the proposed methods in [5] are approximate, they further expand their approach in [4] by introducing some measures for computing the appearing errors. These errors include approximation error resulting from the usage of the grid for the discretization of the query search space, the approximation error correlated with the usage of a sample during the preprocessing and processing phases and finally the error related to the detected optimal rewriting.

6 DISCUSSION

6.1 Expanding The Scope to Other Data Types

We reviewed the techniques on identifying and resolving representation bias mostly in tabular data data sets. The existing research has briefly investigated these issues in other data types such as multimedia [13, 26, 71], text [33, 49], graphs, streams [25], spatio-temporal [28], etc. Still, identification and resolving biases in visual data sets has drawn more attention from different research communities and in this section we present a review of the existing works.

In particular, Hu et al. [34] propose a crowd-sourcing workflow to facilitating sampling bias discovery in visual data sets with the help of human-in-the-loop. This workflow takes a visual data set as input, and outputs a list of potential biases of the data set. There are three steps in this workflow. The first step is Question Generation and the crowd inspects random samples of images from the input data set and describes their similarity using a question-answer pair. The next
Algorithm 20 Coverage-based Rewriting Baseline with Pruning [5]

**Input:** $Q$: a sensitive selection monotone query, $CC$: a set of coverage-based constraints, $I$: a database instance

**Output:** $\min$: index of a coverage-based rewriting of $Q$ with respect to $CC$ and $I$

```plaintext
1: function CRBase($Q$, $CC$, $I$)
2:    $Space \leftarrow$ all the indexes in the CMG
3:    $\min \leftarrow (n - 1, ..., n - 1)$
4:    $\hat{a} \leftarrow (0, ..., 0)$
5:    if not Check($Q_{\min}(I), CC$) then
6:        return ⊥
7:    else
8:        while $Space \neq 0$ do
9:            $\hat{a} \leftarrow$ Next($\hat{a}, Space$)
10:       if Check($Q_{\hat{a}}(I), CC$) then
11:           $Space \leftarrow Space / UR(\hat{a})$
12:          if $|Q_{\hat{a}}(I)| < |\min(I)|$ then
13:              $\min \leftarrow \hat{a}$
14:          else
15:             if $|Q_{\min}(I)| < |\hat{a}(I)|$ then
16:                $Space \leftarrow Space / UR(\hat{a})$
17:        return $\min$
```

Answer Collection in which the crowd reviews separate random samples of images from the input data set and provides answers to questions generated in the earlier step. Finally, in the third step called Bias Judgement, the crowd judges if the statements about the visual data set automatically generated through the accurate questions and answers collected in the former steps reflect the real world.

Torralba et al. [72] perform some experiments on famous image data sets to measure the bias. To correctly measure a data set’s bias, it should be compared the real visual world, which would have to be in form of a data set, which could also be biased and consequently, not a viable option. Therefore, they suggest Cross-data set Generalization by training a model on a data set and testing it on another and assuming that the training data set is truly representative of the real world, the model should perform well otherwise it means that there are biases such as selection and capture present in the data set. Next, knowing that data sets define a visual phenomenon not only by what it is but also by what it is not, they argue about Negative Set Bias and whether negative samples are representative of the rest of the world or even sufficient. To do so, they run an experiment such that for each data set, they train a classifier on its own set of positive and negative instances and then during testing, the positives come from that data set, but the negatives come from all data sets combined. The performance of the models show how good the data set is representing the rest of the world.

Another work by Schaaf et al. [63] focuses on measuring bias in image classification tasks by means of attribution maps. Attribution maps seek to explain image classification models, such as CNNs, by demonstrating the importance of each individual pixel of the input image on the outcome. To do so, they propose a four step process to indicate their usefulness. First, they generate artificial data sets with known bias. For example, they generate a biased fruit data set where apples are all on tree backgrounds, while other fruits have different backgrounds, and an unbiased data set where all fruits have different backgrounds. Next, they train biased CNN models and then generate attribute maps using different attribution techniques such as Grad-CAM, Score-CAM, Integrated Gradients and epsilon-LRP. Finally, they quantitatively evaluate attribution maps’ ability to detect bias using metrics such as Relevance Mass Accuracy (RMA), Relevance Rank Accuracy (RRA) and Area Over The Perturbation Curve (AOPC). Their results partly confirms the ability
of attribution maps to quantify bias. However, in some cases attribution maps provide inconsistent results for different metrics.

Jaipuria et al. [36] propose a bias mitigation approach by using aimed synthetic data augmentation that combines the advantages of gaming engine simulations and sim2real style transfer techniques to bridge the gaps in real data sets for vision tasks. However, instead of blindly collecting more data or mixing data sets that often ends up in worse final performance, they suggest a smarter approach to augment data regarding the task-specific noise factors. The results consistently indicate that through adding synthetic data to the training set, a noticeable improvement occurs in cross-data set generalization in contrast to merely training on original data, for a training set of equal size.

Wang et al. [73] build a tool named REVISE for identifying and mitigating bias in visual data sets. Their scope is limited to three set of metrics: 1) Object-based that focuses on statistics about object frequency, scale, context, or diversity of representation 2) Person-based that examines the representation of people from various demographics in the data set, and allows the user to assess what potential downstream consequences this may have in order to consider how best to intervene. It also builds on the object-based analysis by considering how the representation of objects with people of different demographic groups differs. 3) Geography-based that considers the portrayal of different geographic regions within the data set and is deeply intertwined with the previous two, as geography influences both the types of objects that are represented, as well as the different people that are pictured. REVISE accepts annotated image data sets as input and depending on the annotations it provides insights on the data sets based on each of the three categories of metrics explained above. Metrics such as object count, scale, co-occurrence, scene diversity, etc. for Object-based category, person prominence, appearance differences and contextual representations for Person-based and geography distributions based on people, language, weather and etc. for Geography-based category. REVISE doesn’t claim to find all the visual biases and it’s limited to the available annotations accompanying the data.

Li et al. [45] propose REPAIR, a resampling based bias mitigation approach that is formulated as an optimization problem. REPAIR assigns a weight to the instances that the classifier built on a feature representation can penalize more easily. This is implemented through a deep neural network as feature extractor for the representation of interest and learning an independent linear classifier to classify the extracted features. Next, bias mitigation is defined as maximizing the ratio between the loss of the classifier on the reweighted data set and the uncertainty of the ground-truth labels. Lastly, the problem is reduced to a minimax problem, that can be solved by alternatingly updating the classifier coefficients and the dataset resampling weights, through stochastic gradient descent.

Finally in [39], Khosla et al. propose an algorithm that learns the visual world model and the biases for each data set. The key observation is that all data sets are sampled from a common visual world (a more general data set). A model trained on this data set would have the best generalization ability, however making such data set is not realistic. Therefore, they suggest to define the biases associated with each data set and approximate the weights for the visual world by removing the bias from each data set. The visual world model performs well on average, but not necessarily the best on any specific data set, since it is not biased towards any one data set. On the other hand, the biased model, built by combining the visual world model and the learned bias, performs superior on the data set that it is biased towards but not necessarily extend to the rest of data sets. In this regard, they propose a maxed-margin learning discriminative framework to collectively learn the weight vector correlated to the visual world object model and a set of bias vectors, for each data set such that when combined with the visual world weights lead to an object model specific to the data set.
6.2 Conclusion

In this paper, we surveyed techniques for identification and resolution of representation bias in data. We provided an thorough overview on the problem definition, the causes and how to measure and quantify this phenomena. We then presented a classification based on multiple dimensions such as type of task, attribute type, relation model, etc. and then had a side by side comparison of the techniques. We discussed the details of several algorithms to illustrate the different challenges and the problems they address. We envision the following research directions to be important to pursue:

- **Addressing representation bias in other types of data sets.** As we discussed in section 6, with the extension of the problem scope to new data types such as multimedia, text, graphs, streams, spatio-temporal, etc., new challenges arise and the current solutions may not be directly extendable. Therefore, it is crucial that representation bias is addressed in a data type specific manner.

- **More metrics for measuring representation bias.** Existing works have introduced coverage and representation rate for measuring representation bias. However, each metric has potential shortcomings that provide new research opportunities. Furthermore, when it comes to data quality and trust measures in data, there is no such a thing as “enough” and there is always room for improvement.

Finally, it is critical to note that although representation bias is an important matter, it does not necessarily imply poor and groundless decision making of the system. To clarify more, we investigate this in a task-specific context. In a classification setting, having representation bias in regions far from the boundary is likely to be immaterial since those points may not contribute to refining the boundary. In a regression setting, in regions of the training data where the fluctuation of the value that is to be predicted is not much, representation bias is much less important than in regions that have a higher fluctuation. Therefore, it is safe to say that representation bias is problematic in the regions where the model behind decision system fails to interpolate properly based on the current data sample.

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