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A scalable software solution for anonymizing high-dimensional biomedical data

--Manuscript Draft--

Manuscript Number:	GIGA-D-20-00292R1
Full Title:	A scalable software solution for anonymizing high-dimensional biomedical data
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Abstract:	Background: Data anonymization is an important building block for ensuring privacy and fosters the re-use of data. However, transforming the data in a way it preserves the privacy of subjects while maintaining a high degree of data quality is challenging and particularly difficult when processing complex datasets that contain a high number of attributes. In this paper we present how we extended the open source software ARX to improve its support for high-dimensional, biomedical datasets. Findings: For improving ARX's capability to find optimal transformations when processing high-dimensional data, we implement two novel search algorithms. The first one is a greedy top-down approach and is oriented on a formally implemented bottom-up search. The second is based on a genetic algorithm. We evaluated the algorithms with different datasets, transformation methods and privacy models. The novel algorithms mostly outperformed the previously implemented bottom-up search. Additionally, we extended the graphical user interface to provide a high degree auf usability and performance when working with high-dimensional datasets. Conclusion: With our additions we have significantly enhanced ARX's ability to handle high-dimensional data in terms of processing performance as well as usability and thus can further facilitate data sharing.
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Response to Reviewers:	Dear Dr. Edmunds, we are pleased to submit a revised version of our manuscript GIGA-D-20-00292R1 entitled "A scalable software solution for anonymizing high-dimensional biomedical data" by Thierry Meurers, Raffael Bild, Kieu-Mi Do and Fabian Prasser for consideration for publication in GigaScience. We thank the reviewers and the editor for the helpful and constructive feedback. The most important changes to our manuscript are: 1) We added an additional figure (Figure 4) to Section 2.3 ("Integrating Anonymization

Algorithms for High-Dimensional Data”), which illustrates how the novel algorithms search the solution space.
2) We have added a new subsection (Section 4.2 “Limitations”) to the discussion section in which we describe limitations of our study.
3) We have more clearly emphasized the contributions of our work in sections “Introduction”, “Principal results” and “Comparison with prior work”.
4) We have provided more details on why we chose to implement a genetic algorithm, how we decided on its exact design and how we determined the parameterization used in the experiments.
5) We have revised various parts of the manuscript to address minor comments by the editor and the reviewers and performed some editorial changes to improve the readability of the paper.

A detailed overview of our changes regarding the reviewers’ comments is listed in the point-by-point-response below.

With kind regards,
Thierry Meurers

Editor (Scott Edmunds)

Comment 1: Please register any new software application in the bio.tools and SciCrunch.org databases to receive RRID (Research Resource Identification Initiative ID) and biotoolsID identifiers, and include these in your manuscript. This will facilitate tracking, reproducibility and re-use of your tool. Please also follow the software citation guidelines for software discussed here https://f1000research.com/articles/9-1257/v2

Response: We thank the editor for pointing this out. We registered ARX to bio.tools (https://bio.tools/arx) and SciCrunch.org (SCR_021189) and included the IDs in the “Availability of supporting source code and requirements” Section of the revised manuscript. Furthermore, we changed the citation of ARX to comply to the software citation guidelines mentioned.

Reviewer #1

Comment 1: The manuscript is clear, and well-written overall. The manuscript has sufficient originality, and undertaken problem is of practical nature. Although the results presented in the manuscript seem promising and overall approach is contributing to the body of the literature, I encourage the authors to please consider the attached file suggestions/comments to improvise the presented work more prior to its publication.

Response: We thank the reviewer for this positive feedback! We have addressed the individual comments contained in the attached file as described below.

Comment 2: In figure 1, I would recommend adding a one comprehensive in terms of data input overview, intermediate steps with two proposed methods illustration or formalization,
and final output after passing through all steps.

Response: We thank the reviewer for this very good suggestion. Figure 1 is part of Section 2.1 (“Fundamentals of Data Anonymization”) and it is meant to only provide a general overview of how data can be altered in the context of anonymization. For this reason, we added an additional figure (Figure 4) to Section 2.3 (“Integrating Anonymization Algorithms for High-Dimensional Data”), which illustrates how the novel algorithms search the solution space.

Comment 3: In my opinion, section I should include some more recent and pertinent studies. Authors can possibly include the recent and closely related studies,

- Majeed, A., & Lee, S. (2020). Anonymization Techniques for Privacy Preserving Data Publishing: A Comprehensive Survey. IEEE Access.
- Majeed, A., & Lee, S. (2020). Attribute susceptibility and entropy based data anonymization to improve users community privacy and utility in publishing data. Applied Intelligence, 1-20.
- Majeed, A., Ullah, F., & Lee, S. (2017). Vulnerability-and diversity-aware anonymization of personally identifiable information for improving user privacy and utility of publishing data. Sensors, 17(5), 1059

Response: We thank the reviewer for providing this list of recent studies in the field. We included the first study listed (survey article by Majeed & Lee) to the manuscript's introduction section (Section 1), where it fits well as it is a recent survey on the topic.

Comment 4: The limitations of the presented study are not provided by the authors. It would be better to highlight them in the revised work.

Response: We agree with the reviewer that more information on the limitations of our work were needed. We have added a corresponding section to the discussion section (Section 4.2 "Limitations") in which we address 1) the dependence of our benchmark results on the datasets and privacy models used, as well as 2) the difficulty of properly parameterizing genetic algorithms in general.

Comment 5: Some more and pertinent keywords can be added related to subject matter presented in this paper.

Response: We thank the reviewer for this suggestion. We added three additional keywords (privacy preserving data publishing, biomedical data, data protection) to further describe the paper's subject.

Comment 6: All symbols can be written in math mode for better readability of the manuscript.

Response: We thank you for this suggestion. We replaced all symbols in the manuscript using the math mode.

Comment 7: Some examples and scenarios that emphasize the technical contribution of this paper can be explained in the revised work.

Response: We thank the reviewer for pointing out that this required further clarification. We rewrote parts of Section 4.1 ("Principal results") to provide a better understanding of scenarios where using the new algorithms can be beneficial: "Evaluating the newly implemented algorithms showed that they are particularly useful in scenarios where high-dimensional data needs to be anonymized." Furthermore, we added a synthesis of our results to underline the most important results (see the next comment below).
To highlight the novelty of our work in the context of genetic anonymization algorithms, we rewrote Section 4.3 ("Comparison with Prior Work"): "It has been demonstrated multiple times that genetic algorithms can be used for anonymizing data. However, previously described solutions were mostly tailored towards specific types of data or privacy and transformation models. […] Our work is different from these approaches, because it integrates a genetic algorithm into ARX in such a way that it can be used to anonymize datasets using a variety of privacy models, quality models and data transformation schemes.".
Finally, we have also added a concise numbered list of our contributions to the introduction section (see also our reply to Comment 11 below).

Comment 8: Some detailed synthetises of the results obtained from experiments can be provided for
the better readership of this article before conclusion section.

Response: We thank the reviewer for this suggestion. We rewrote parts of Section 4.1.("Principal Results") to provide a more thorough synthesis the results obtained: "Evaluating the newly implemented algorithms showed that they are particularly useful in scenarios where high-dimensional data needs to be anonymized. Using global generalization, they clearly outperformed the previously implemented bottom-up search (i.e. better performance in 5 of the 6 experiments). A similar result was observed when using local generalization. Averaged over all experiments, the new algorithms achieved a utility of 76.5 % (genetic algorithm) and 75.1 % (top-down algorithm), which is significantly higher than that provided by the bottom-up approach (60.2%). Especially when anonymizing the dataset with the largest solution space (credit card), the new algorithms often performed significantly better, both in terms of scalability and utility. Additionally, the results obtained when processing low-dimensional data showed that heuristic algorithms can be helpful to improve computational efficiency even in scenarios where optimal algorithms could be used. The top-down approach required the least amount of time on average to find an optimal solution (4.0 s), followed by the bottom-up approach (6.3 s), the genetic algorithm (9.9 s) and the optimal search strategy (14.1 s)."

Comment 9: All figures must be placed on the appropriate position in the revised work.

Response: Thanks for pointing this out. We carefully revised the positioning of our figures and moved one figure (Fig. 5) closer to the corresponding text in the manuscript. Furthermore, we have noticed that one of the figures was wrongly numbered and fixed this as well. Following the author guidelines of GigaScience, all figures are submitted in separate files and their position within the main manuscript is indicated using placeholders and captions.

Comment 10: This manuscript categorization can be written concisely in the introduction section of the revised work.

Response: We thank the reviewer for this suggestion. We added the type of our manuscript (Technical Note) to the introduction (Section 1).

Comment 11: Contribution can be presented with bullets concisely in the revised work.

Response: Thank you for this suggestion. We rewrote the end of the introduction (Section 1) to provide a concise overview of our contributions which are: "(1) extending ARX's user interface with additional views that simplify the management of high-dimensional data, (2) implementing two novel heuristic anonymization algorithms and (3) evaluating the novel algorithms regarding their performance for anonymizing low-dimensional and high-dimensional datasets."

Reviewer #2

Comment 1: This is a very interesting and valuable result. However, there are several concerns.

Response: We thank the reviewer for this kind and positive feedback! We have addressed the concerns raised as described below.

Comment 2: There is not enough convincing explanation for the reason for applying genetic algorithm. There are several methods for optimization including simulated annealing. Moreover, as the author mentioned, there was already an attempt to apply genetic algorithm for data anonymization (Wan et al.). To promote the novelty of the presenting study, it needs to provide more robust explanation for selecting genetic algorithm for this project.

Response: We thank the reviewer for pointing out that this needed to be clarified. We integrated the genetic algorithm into ARX as it is a well-known population-based metaheuristic. In contrast to single-solution based approaches (like, for example, greedy heuristics or simulated annealing) multiple candidate solutions are maintained which results in a high degree of diversification and lowers the risk of getting stuck in local optima. We added these details to Section 2.3 (“Integrating Anonymization Algorithms for High-Dimensional Data”) of the revised manuscript.

Other papers using genetic algorithms for data anonymization are tailored towards a specific type of data (e.g. the approach implemented by Wan et al. is exclusively used for anonymizing genetic data, which is a process that is very different from the process focused on in our work) or only allow for specific anonymization procedures (e.g. by partitioning the data to fulfill k-anonymity). Integrating a genetic algorithm into the generic data anonymization core provided by ARX enables using a genetic anonymization algorithm for a wide range of tabular datasets using a wide range of privacy models and data transformation methods. We have added these additional aspects highlighting the novelty of our work to Section 2.3 (“Integrating Anonymization Algorithms for High-Dimensional Data”) when introducing the algorithm and also rewrote parts of Section 4.3 (“Comparison to prior work”) to make this clearer.

Comment 3. Genetic algorithm is little bit complicate to handle. Author showed the detailed parameter setting for the present study. It is necessary to provide a reference as well as scientific reasons for setting parameters. In addition, why do the authors use 'triangle pattern' in genetic algorithm for this research?

Response: We agree with the reviewer that these points require a careful consideration. Both, the parametrization as well as the ‘triangle pattern’ were inspired by the work of Wan et al.. For our first submission, we run preliminary benchmarks in which we individually varied a subset of the parameters, which resulted in setting the productionFraction to 0.2 (instead to 0.8 as suggested by Wan et al.). For the new revision of the manuscript, we conducted a systematic evaluation of all parameters and also checked whether the ‘triangle pattern’ is advantageous for our use case. Evaluating the parametrization was done as follows: (1) we started with the recommendations made by Wan et al., and, (2) performed a systematic analysis of the influence of parameters by individually altering them and running the evaluation benchmarks. The detailed procedure and its results are described in a supplementary file (see Supplementary Table S2) which is also referenced in the revised version of Section 2.5.3 (“Parametrization”). The results confirmed that setting the productionFraction to 0.2 improves the algorithm’s performance in our experiments. Additionally, the preliminary experiments also showed that decreasing the subpopulationSize from 100 to 50 leads to further improvements in our setting. Although the difference caused by the reduction of the subpopulationSize was only small, we repeated our experiments with this configuration and updated the figures in the paper.

Moreover, we performed another set of experiments to compare different variants of the genetic algorithm to motivate the use of the “triangle pattern”. We investigated three variants: approach 1 used a dual-population algorithm with “triangle pattern” (as proposed by Wan et al.), approach 2 used a dual-population algorithm without “triangle pattern” and approach 3 used a single-population algorithm without “triangle pattern”. Running our experiments showed that approach 1 (“triangle pattern” with dual-population) offers the best average performance. This can be explained by the triangle-pattern covering a larger part of the overall solution space in the beginning. We added this explanation to Section 2.3 (“Integrating Anonymization Algorithms for High-Dimensional Data”) when explaining the initialization procedure and included the results of the preliminary benchmark in the supplementary file (see Supplementary Table S1).

Comment 4: Authors introduced several approaches (#1. top-down #2. bottom-up #3. genetic algorithm). Genetic algorithm showed better performance for the complex and high dimensional datasets but lower performance for the low dimensional datasets. If the authors propose some guidance to select the appropriate algorithm for data anonymization, it would be very helpful for general users of ARX solution.

Response: We thank the reviewer for this suggestion. Generally recommending a

	specific algorithm is difficult due to the performance being highly dependent on the dataset anonymized and the configuration utilized. Nevertheless, we revised Section 4.1 ("Principal results") to contain a concise summary of our evaluation results and highlighted ARX's capability of automatically deciding whether it is feasible to calculate an optimal solution or whether a heuristic search is required. Furthermore, we mentioned that ARX provides means to easily try out different algorithms and compare their results to facilitate the selection of a method well suited in a specific context.
Additional Information:	
Question	**Response**
Are you submitting this manuscript to a special series or article collection?	No
Experimental design and statistics Full details of the experimental design and statistical methods used should be given in the Methods section, as detailed in our Minimum Standards Reporting Checklist. Information essential to interpreting the data presented should be made available in the figure legends. Have you included all the information requested in your manuscript?	Yes
Resources A description of all resources used, including antibodies, cell lines, animals and software tools, with enough information to allow them to be uniquely identified, should be included in the Methods section. Authors are strongly encouraged to cite Research Resource Identifiers (RRIDs) for antibodies, model organisms and tools, where possible. Have you included the information requested as detailed in our Minimum Standards Reporting Checklist?	Yes
Availability of data and materials All datasets and code on which the conclusions of the paper rely must be either included in your submission or deposited in publicly available repositories	Yes

(where available and ethically appropriate), referencing such data using a unique identifier in the references and in the “Availability of Data and Materials” section of your manuscript. Have you have met the above requirement as detailed in our Minimum Standards Reporting Checklist?	

A scalable software solution for anonymizing high-dimensional biomedical data

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Abstract

Background: Data anonymization is an important building block for ensuring privacy and fosters the re-use of data. However, transforming the data in a way it preserves the privacy of subjects while maintaining a high degree of data quality is challenging and particularly difficult when processing complex datasets that contain a high number of attributes. In this paper we present how we extended the open source software ARX to improve its support for high-dimensional, biomedical datasets.

Findings: For improving ARX's capability to find optimal transformations when processing high-dimensional data, we implement two novel search algorithms. The first one is a greedy top-down approach and is oriented on a formally implemented bottom-up search. The second is based on a genetic algorithm. We evaluated the algorithms with different datasets, transformation methods and privacy models. The novel algorithms mostly outperformed the previously implemented bottom-up search. Additionally, we extended the graphical user interface to provide a high degree auf usability and performance when working with high-dimensional datasets.

Conclusion: With our additions we have significantly enhanced ARX's ability to handle high-dimensional data in terms of processing performance as well as usability and thus can further facilitate data sharing.

Keywords

data privacy, anonymization, de-identification, heuristics, genetic algorithm, software tool, privacy preserving data publishing, biomedical data, data protection

1 Introduction

Big data technologies and latest data science methods promise to be valuable tools for providing new insights into the development and course of diseases. These insights can be used to derive new preventive, diagnostic and therapeutic measures [1]. Implementing these methods in practice requires access to comprehensive, multi-level datasets of high quality. At a large scale, this can only be achieved by fostering the reuse of data from different contexts and the sharing of data across institutional boundaries. The reuse of data is also in line with the FAIR (Findable, Accessible, Interoperable, Reusable) data principles and supports the reproducibility of research. However, in the context of biomedical research, sharing data is challenging as it is important to account for ethical aspects [2], privacy concerns as well as data protection laws like for example the US Health Insurance Portability and Accountability Act (HIPAA) [3] or the European General Data Protection Regulation (GDPR) [4].

One important building block for ensuring privacy is to provide safe data that minimizes disclosure risks [5]. This can be achieved by employing data anonymization techniques, that transform the data to mitigate privacy risks [6], [7]. Typically, the anonymization process is not limited to the removal of directly identifying attributes such as the name, telephone number or insurance id number. Instead, it must also account for attributes like the postal code, age and gender that could be combined to re-identify individuals or derive sensitive personal information [8]–[10]. However, transforming the data will also have an impact on its usefulness and striking the right balance between privacy and data quality is challenging and particularly difficult when working with high-dimensional datasets that contain a high number of attributes. The complexity of this task is also demonstrated by several re-identification attacks [11], [12]. To mitigate risks and put anonymization in practice, tools that implement formal approaches based on mathematical and statistical models can be utilized. An example of such a tool is the open source software ARX [6], [13]. It is focused on biomedical data and has been mentioned in several official policies and guidelines [14], [15], used in research projects [16]–[18], and enabled several data publishing activities [19]–[21].

Versions of ARX up to 3.8.0 were only able to process datasets with a limited number of attributes that could be considered during anonymization (up to about 15). The reason for this were twofold: (1) the software only had limited support for anonymization algorithms able to process high-dimensional data, (2) the graphical user interface was not designed to work with datasets containing a high number of attributes.

In this Technical Note, we describe our efforts to overcome these limitations by (1) extending ARX's user interface with additional views that simplify the management of high-dimensional data, (2) implementing two novel heuristic anonymization algorithms and (3) evaluating the novel algorithms regarding their performance for anonymizing low-dimensional and high-dimensional datasets.

2 Materials and Methods

In this section, we will first provide some fundamental details about data anonymization. Second, we will present important properties of the ARX Anonymization Tool that had an influence on our design decisions. Third, we will present the extensions implemented into ARX. Finally, we will provide insights into our experimental setup.

2.1 Fundamentals of Data Anonymization

When anonymizing a dataset the first step is to remove all attributes that directly identify the individuals. Thereafter, the dataset is modified or noise is introduced so that the risk of identified or identifiable individuals of being linked to one or multiple records of the dataset or to sensitive information in general is lowered [7]. This step involves the usage of mathematical or statistical privacy models used to quantify the risk of privacy breaches as well as quality models that measure the usefulness of the output data. For (1) measuring privacy risks, (2) measuring data quality and (3) transforming the data a variety of models can be employed and combined.

< Figure 1 >

Figure 1: Exemplary anonymization process.

Figure 1 shows a simplified example of an anonymization process. The transformation involves different procedures such as (1) randomly sampling the records, (2) aggregating values by replacing them with their mean, (3) suppressing values, (4) masking trailing characters of strings, (5) categorizing numerical values and (6) generalizing categorical attributes. These transformations may reduce the fidelity of the data but also reduce the risk of linkage attacks and the attacker's accuracy when linking records. Furthermore, an additional uncertainty could be created by introducing noise. The transformed output data of the example fulfills two frequently used privacy models: k-Anonymity with $k = 3$ [22] and (ε, δ)-Differential Privacy with $\varepsilon \approx 0.92$ and $\delta \approx 0.22$ [23].

The simple example demonstrates the variety of possibilities available for transforming data. Furthermore, it also suggests why it is often not feasible to search the entire solution space of all potential output datasets when processing more complex data. For this kind of tasks, solutions that try to determine a good transformation scheme on a best-effort basis, e.g. based on heuristic strategies [24]–[26] or clustering algorithms [27]–[29], have been developed. An overview of common types of approaches is provided by Fung et al. [7].

2.2 The ARX Anonymization Tool

ARX supports a variety of privacy models, quality models and data transformation schemes and allows for their arbitrary combination [6]. For transforming the data, it relies on domain generalization hierarchies which describe how values can be transformed to make them less unique. For each hierarchy it is possible to define multiple levels of generalization that cover an increasing range of the attribute’s domain.

< Figure 2 >

Figure 2: Generalization hierarchies (a) and structure of the solution space (b) used by ARX.

The basic solution space that is utilized by ARX is given by all possible combinations of generalization levels defined by the hierarchies. An example is provided in Figure 2. Each possible generalization is called a generalization scheme. Mathematically, the solution space is a lattice [30], [31], which grows exponentially in size regarding the number of attributes that need to be protected [25]. As ARX is also able to apply different generalization schemes automatically to different parts of the input dataset the size of the solution space may grow further by a multiplicative factor representing the number of rows [6]. ARX supports different algorithms for finding optimal solutions within solution spaces of tractable size [32] as well as a heuristic algorithm for larger search spaces that tries to determine a good transformation scheme on a best-effort basis [25].

In addition to its anonymization engine, ARX also features a cross-platform graphical user interface. An overview of the different perspectives provided by the platform is shown in Figure 3.

< Figure 3 >

Figure 3: Basic perspectives of the graphical interface of the ARX Data Anonymization Tool.

In the *configuration* perspective it is possible to define risk thresholds for different types of attacks, to prioritize attributes by importance, to model the background knowledge of possible attackers and to define transformation methods and rules. In the *exploration* perspective, relevant anonymization strategies are visualized for the input data and a categorization according to output data quality is supported. A further perspective supports the manual *quality analysis* of the output data. Different methods for measuring the information content of the output data, descriptive statistics and methods for comparing the usefulness of the input and output data for different application scenarios are provided. In a *risk analysis* perspective, it is possible to visually compare input and output data using different risk models. However, in the user interface it is challenging to support high-dimensional datasets. For example, several perspectives and views of the software display lists of all attributes of the dataset loaded, which can become confusing and lead to performance problems on some platforms with an increasing number of attributes.

2.3 Integrating Anonymization Algorithms for High-Dimensional Data

As mentioned before, the anonymization procedures supported by ARX are built around a basic operator that searches through the generalization lattice. In prior work we have already integrated a greedy best-first bottom-up search algorithm into the software [25]. This algorithm starts at the bottom generalization scheme, which applies no generalization to the data. It then “expands” this generalization scheme, by applying all generalization schemes to the input dataset that can be derived by increasing one of the generalization levels. The quality of the resulting output dataset is computed for all these schemes, and the process is repeated by expanding the generalization resulting in the dataset with highest quality. This process is then repeated until a user-specified period of time has passed. During the execution of the algorithm, a list of all generalization schemes that have been evaluated is stored and, in each iteration, the scheme with the highest output data quality that has not yet been expanded is expanded. For further details we refer interesting readers to the original publication [25].

It must be noted that this process is only suitable for processing dataset of medium dimensionality (about 15 attributes) for several reasons. First, the search process may become trapped in local minima, as there is no significant diversification of the solutions considered. Second, the process naturally favors transformation schemes located in the lower part of the search space (i.e. schemes that apply a low degree of generalization). While this makes sense for anonymization processes that only apply generalization, the method reaches its limits with the complex transformation operations supported in newer versions of ARX in which different transformation schemas are used to transform different parts of a dataset. In this case, a better overall solution can sometimes be determined if outliers are transformed more strongly.

For this reason, we have integrated two new algorithms for processing high-dimensional data into the software. Figure 4 illustrates how the algorithms search through the solution space to find a good solution. Although the process shown in the figure is simplified, it illustrates that both approaches follow completely different concepts.

< Figure 4 >

Figure 4: Simplified illustration of (a) the top-down approach and (b) the genetic algorithm searching the solution space. Solutions considered are represented as dots. The best solution found is circled.

The first algorithm closely resembles the bottom-up greedy best-first search but performs this process top-down. We will not describe it in further detail, as this is a straight-forward extension of the process described in the previous paragraphs.

The second algorithm applies a genetic optimization process to the anonymization problem. Genetic algorithms search for solutions in a heuristic manner that is oriented on the process of natural selection [33]. During the search, the solutions are considered chromosomes or individuals that carry the solution's properties encoded as a list of genes. The set of candidate solutions/individuals is called population. Mostly, the initial population is created by randomly generating individuals. Thereafter, the algorithm works iteratively. By crossing (i.e. randomly combining the properties of two individuals) and mutating (i.e. randomly altering the properties of individuals) selected individuals contained in the population each iteration will result in a new, so-called, generation. Whether and how an individual is altered is determined by its fitness which usually is calculated using the cost function of the investigated optimization problem. Once reaching a predefined limit of iterations the fittest individual is considered the optimal solution. However, there is no guarantee that a globally optimal solution can always be found.

We opted for the genetic algorithm as it is one of the most well-known population-based meta-heuristics. In comparison to single-solution based algorithms (e.g. simulated annealing or the greedy heuristics described above) population-based approaches maintain multiple candidate solutions which potentially results in a high degree of diversification and a decreased risk of getting stuck in local optima [34]. Moreover, genetic algorithms have already been successfully applied for anonymizing data in previous work. However, prior approaches were often limited to a specific kind of data or privacy model (see Section 4.3 "Comparison with Prior Work"). The genetic algorithm implemented into ARX is based on the work by Wan et al. [35]. Wan et al. employed the algorithm for anonymization genomic data using a game-theoretic privacy model, which was already successfully adapted and integrated into ARX in prior work [36].

For our work we significantly modified the algorithm to make it compatible with the types of solution spaces used by ARX and to integrate it with the privacy and quality models supported by the software. Instead of a binary string every individual carries a list of numerical values representing a generalization scheme. The list’s length equals the number of attributes that need to be transformed and the i-th value of the list represents the generalization level of the i-th attribute. When generating new individuals or altering single genes we choose a random value in between the lowest and highest generalization level available for the corresponding attribute. The populations are implemented in a matrix like structure with the rows of this matrix representing individuals (generalization scheme) and columns their genes (generalization level of an attribute). ARX’s privacy and quality models have been integrated via the fitness function. ARX always automatically alters the output of any given transformation in such a way that the required privacy guarantees are provided. This is achieved by suppressing records [37]. The suppression of records is captured by a decrease in data quality. Hence, we defined the fitness of a transformation to equal output data quality, which not only measures the transformation’s direct impact on data quality but also implicitly captures how well the required privacy guarantees are achieved.

The algorithm itself works as follows:

- **Initialization:** During the initialization two equally sized subpopulations are created. Following the approach of Wan et al., the first individuals of the first subpopulation are generated in the form of a “triangle pattern” using the lowest and highest generalization levels. An example is provided in Figure 5. The remaining individuals of the first subpopulation as well as the entire second subpopulation is filled by randomly creating individuals. The motivation behind this approach is based on properties of genetic data [38]. To determine whether the initialization procedure is also favorable in our case, we performed experiments in which we compared the initialization strategy proposed by Wan et al. with a completely random initialization in a single- as well as a dual-population setting (see Supplementary Table S1). The experiments showed that using the “triangle pattern” performs well when processing low-dimensional data and significantly outperforms other approaches when processing high-dimensional datasets. This can be explained by the fact that the pattern creates populations that cover a larger part of the solution space in the beginning.

< Figure 5 >

Figure 5: Initialization of the first subpopulation for a solution space with the highest generalization levels of [3,1,5,3,1].

- **Iteration:** After initializing the subpopulations the algorithm’s main loop is started. The algorithm stops after reaching a pre-defined number of iterations or time limit. Within the loop the following steps are executed:

  Step 1: Sorting: The individuals contained in the subpopulations are sorted by their fitness in descending order.

  Step 2: Selection: The fittest individuals of the current population will simply be copied to the next generation without being modified. We refer to this fraction of individuals as *elite fraction*.

  Step 3: Crossover: Next, the so-called *crossover fraction* of the new generation is populated. For this purpose, two parent-individuals from the *production fraction* of the current population are crossed to generate a new child-individual. The probability of being chosen as a parent increases with the fitness. The crossover is performed in a randomized fashion. For every gene it is decided randomly from which of the two parents it is inherited.

  Step 4: Mutation: The rest of the new generation is populated by randomly choosing individuals of the current generation and mutating them by altering their genes. The number of changed genes is randomly chosen between 1 and an upper bound which is calculated by multiplying the *mutation probabilit*y with the number of available genes.

  Step 5: Swapping: Additionally, it is possible that the fittest individuals are swapped between the two subpopulations. How often they are changed depends on the *immigration interval* which refers to the number of iterations between the swaps. The number of exchanged individuals can be controlled by the *immigration fraction*.

2.4 Extending the User-Interface for High-Dimensional Data

ARX is implemented as a cross-platform program using Java and executed on the Java Virtual Machine. The Graphical User Interface (GUI) is implemented using the Standard Widget Toolkit (SWT), which enables implementing native GUIs on three supported platforms: Windows, Linux and MacOS.

For improving the GUI's usability when working with high-dimensional datasets we made use of two SWT-based components provided by the Eclipse Nebula Project [39]. The first is NatTable. Based on the idea of virtual tables it ensures that the GUI remains responsive and provides a high rendering performance when displaying large datasets. The second is Pagination Control. This component is used to display a navigation page when working with tables used to configure a potentially large number of attributes.

Additionally, ARX features a mechanism that automatically detects the type of an attribute to ease the initial import of data as well as the ability to configure multiple attributes at once. These last two features are also available for smaller dataset but are especially helpful when working with high-dimensional datasets.

2.5 Experimental Design

2.5.1 Experiments

With the extensions described in this article, ARX now supports three algorithms for anonymizing high-dimensional data: (1) the initial bottom-up search, (2) the new top-down search and (3) the new genetic search algorithm. We performed a series of experiments, to study how well these algorithms work for different types of data to provide users with insights into which algorithm should be used in which context. In total, we conducted two experiments:

(1) **Low dimensional data:** We compared the algorithms to the optimal algorithm already supported by ARX [32] in the low-dimensional setting. We did this for two reasons. First, heuristic algorithms might also be relevant when anonymizing low-dimensional data if they significantly outperform optimal algorithms in terms of the time needed to find the optimal

solution. Second, experiments with low-dimensional data might provide insights into basic strengths and weaknesses of the approaches. To this end, we compared the overall execution time of ARX's optimal algorithm with the time needed by the heuristic algorithms to find the optimal solution.

(2) **High-dimensional data:** Here, we use the three heuristic algorithms to anonymize high-dimensional datasets. This experiment was performed to determine whether the novel approaches (genetic and top-down) offer an advantage over the bottom-up algorithm. To this end, we executed the algorithms with different time limits and compared the quality of their results.

2.5.2 Privacy, quality and transformation model

To investigate a broad spectrum of anonymization problems, we decided to utilize different privacy and data transformation models.

For measuring and managing privacy risks, we used two models:

(1) **Distinguishability:** To implement restrictions on the distinguishability of data, we utilized the well-known and relatively strict k-anonymity model. A dataset is k-anonymous if every record cannot be distinguished from at least $k-1$ other records in respect to attributes that may be used to de-anonymize the data [40]. As a parameter we used $k=5$ which is a common recommendation [41].

(2) **Population uniqueness:** ARX also supports statistical models that estimate disclosure risks by estimating the fraction of records in a dataset that are expected to be unique in the overall population. Compared to k-anonymity, this is a relatively weak privacy model. For our experiments we enforced a uniqueness of $1\ \%$ within the US population and relied on the model introduced by Pitman to estimate population characteristics [42], [43].

For transforming data, we also used two common models:

(1) **Global generalization**: With this model, the values in a dataset are generalized based on user-defined hierarchies. In this process, it is guaranteed that all values of an attribute are generalization to the same level of the associated hierarchy. To prevent overgeneralization, records can also be removed from the dataset.

(2) **Local generalization:** With this model, data is also transformed by generalization, but values of the same attribute in different records can be transformed differently. Records may also be removed, but this is typically not required due to the flexibility of the transformation model.

In ARX, local transformations are implemented by using an iterative process in which the dataset is automatically partitioned and different transformation schemes are applied to different partitions [6]. In our experiments with local generalization, we used 100 iterations and different time limits for individual iterations.

To quantify data quality, we decided to use the intuitive “Granularity” model [44], which measures the value-level precision of the output data. The measurements are normalized with $0\ \%$ representing a dataset from which all information has been removed and $100\ \%$ corresponding to a completely unmodified dataset [6].

2.5.3 Parameterization

While the top-down and bottom-up search algorithms do not require any additional parameterization, the genetic search algorithm features multiple configuration parameters, which are shown in Table 1. In ARX, these parameters are presented as configuration options to the users.

Table 1: Parameters of the genetic algorithm and the values employed in the experiments.

Parameter	Description	Value
Elite fraction	Fraction of individuals that is directly copied to the next generation.	0.2

Crossover fraction	Fraction of individuals that is replaced by new individuals that are generated by crossing two parents from the production fraction.	0.4
Production fraction	Fraction of individuals used as parents when generating crossover individuals.	0.2
Mutation probability	Used to calculate the upper bound of changed genes when mutating individuals.	0.05
Immigration fraction	The fraction of individuals that is swapped between the subpopulation.	0.2
Immigration Interval	Number of iterations between swaps.	10
Iterations	Number of iterations performed by the GA	50
Subpopulation size	Number of individuals contained in each of the subpopulations.	100

Table 1 also shows the parameters used in our evaluation. Regarding all but one parameter we followed the suggested configuration by Wan et al. [35] for all parameters that are applicable to our setting. We made this decision based on a set of experiments performed in preparation of our evaluation in which we individually altered all parameters and examined their effect on the performance of the algorithm (see Supplementary Table S2). This process showed that setting the production fraction to 0.2 (instead of 0.8 as suggested by Wan et al.) improves execution times when processing low-dimensional datasets and data utility when processing high-dimensional datasets. The fact that almost the same parameters work well in our setting as well as in the experiments by Wan et al., although very different anonymization procedures are being investigated, can be seen as an indicator of the robustness and generality of this parameterization.

2.5.4 Technical Setup

We repeated each experiment five times and report the average for two reasons: first, it is well known that execution times of JVM-based programs vary slightly due to effects from functionalities, such as just-in-time compilation. Second, the genetic algorithm is randomized and hence may perform slightly different in each execution.

The experiments were performed on a desktop computer with an AMD Ryzen 2700X processor (8 cores, 3.7-4.3 GHz) running 64-bit Windows 10 (version 1909) and a 64-bit Oracle JVM (version 1.8.0).

2.5.5 Datasets

For evaluating the performance of the heuristic algorithms, we used six different real-world datasets. An overview of the properties of the datasets is shown in Table 2. Most of them have already been utilized in previous evaluations of data anonymization algorithms.

As low-dimensional datasets we choose (1) an excerpt of the 1994 US census dataset (*Census income*) which can be considered the de-facto standard for evaluating anonymization algorithms, (2) data from a nationally representative U.S. time diary survey and (3) results from the integrated health interview series collecting data on the health of the U.S. population.

As high-dimensional datasets we included (1) data from the responses to the American Community Survey (ACS) which captures demographic, social and economic characteristics of people living in the U.S., (2) a credit card client dataset from Taiwan used to estimate costumers default payments and (3) answers to a psychological test designed to measure someone's Machiavellianism from the open-source psychometrics project. As attributes that needed to be transformed, we selected variables that are typically associated with a high risk of re-identification. These included demographic data, timestamps, spatial information, medical attributes and payment histories.

Table 2: Overview of the datasets used for comparing the algorithms.

Name	#Attributes	#Records	Solution space size	Category
Census income [45]	9	30,162	12,960	Low dimensional
Time use [46]	9	539,254	34,992	Low dimensional
Health interviews [47]	9	1,185,424	25,920	Low dimensional
Census community [48]	30	68,725	203,843,174,400	High dimensional
Credit card [49]	24	30,000	49,478,023,249,920	High dimensional

Psychology test [50]	16	73,489	85,030,560	High dimensional

3 Results

3.1 Experimental results

3.1.1 Low-dimensional data

The results of the first set of experiments are displayed in Figure 6. For each heuristic algorithm, it shows the time in seconds needed to determine the optimal solution (and the overall execution time for the optimal algorithm) using the global transformation model. We did not use the local transformation model in this experiment, as the underlying algorithm is heuristic in nature (independently of the actual search strategy used) and can therefore not be used to compare the time needed to achieve a specific result in terms of output data quality [6].

< Figure 6 >

Figure 6: Time required for finding an optimal solution for different low-dimensional datasets and privacy models in dependence to the used algorithm.

As can be seen, heuristic approaches provided a valuable alternative to the optimal approach even in low-dimensional settings. When aiming for a threshold on distinguishability, the bottom-up and top-down search algorithms almost always outperformed the optimal algorithm. On average, the genetic algorithm was slower than the other heuristic approaches, because it aims at diversifying the solutions considered, which is not a desirable feature in low-dimensional settings. Whether the top-down approach or the bottom-up approach performed better was associated with the degree of generalization required and hence with the fact whether the optimal solution is located more closely to the top or to the bottom of the lattice.

When optimizing for a threshold on population uniqueness the optimal algorithm outperformed the heuristic approaches in two out of three cases. This can be explained by the fact that calculating population uniqueness is much more computationally complex than checking for k-anonymity, as bivariate non-linear equation systems need to be solved. As a consequence, execution times are not dominated by the time needed to transform the dataset but by the time needed to evaluate the privacy model. The optimal approach implements a wide variety of pruning strategies that reduce the number of transformations that need to be checked [37], which cannot be implemented by the heuristic algorithms. The genetic algorithm provided the worst overall performance, as it tries to look at a diverse set of potential solutions.

3.1.2 High-dimensional data

The results of the experiments with high-dimensional data are displayed in Figure 7 and Figure 8. We compared the development of output data quality for the different algorithms over time and present two different types of results. For global transformation we continuously measured the development of output data quality over time. For local transformation we present the output data quality achieved with different time limits as the heuristic nature of the local transformation algorithm implemented in ARX makes it difficult to directly track the progress [6].

< Figure 7 >

Figure 7: Global generalization: Quality improvement over time for different high-dimensional datasets and privacy models in dependence to the used algorithm.

Figure 7 shows the development of output data quality over time when using the global transformation model until the results of all three algorithms stabilized. As can be seen, all algorithms almost always eventually found a solution with comparable quality. However, when enforcing a threshold on population uniqueness on the credit card dataset, the bottom-up algorithm exhibited sub-optimal performance. Moreover, in most cases the genetic and top-down approach found better solutions much quicker than the bottom-up algorithm. When comparing the different algorithms to each other it can be seen that the genetic algorithm was generally good at quickly determining a relatively good solution while the top-down algorithm provided a good balance of optimization speed and quality of its overall output. It can also be seen that output data quality was higher when reducing population uniqueness compared to reducing distinguishability, as the former model is weaker than the latter (see Section 2.5.2).

Figure 8 provides additional insights by presenting the results for the local transformation model.

< Figure 8 >

Figure 8: Local generalization: Achieved quality for different high-dimensional datasets depending on the privacy models and used algorithm.

Again, the time axis covers the time that was needed for the solutions of the different algorithms to stabilize. As can be seen, the results are quite similar to the results obtained using the global transformation model, apart from the fact that the overall output data quality is higher with this transformation method. The genetic algorithm is good at very quickly finding a relatively good transformation and in most cases all algorithms finally found a comparable solution. The credit card dataset is a notable exception. In this case, the bottom-up algorithm provided the best result when reducing population uniqueness and the top-down approach provided the best result when reducing distinguishability. It is notable that the genetic algorithm performed best for short time limits in the former case, as the credit card dataset results in the largest solution space and the evaluation of individual solution candidates is expensive for population uniqueness. Moreover, good solutions were not located close to the top or bottom of the search space. This is exactly the scenario in which one would expect good performance from a genetic search process.

3.2 Extended User-Interface

In the updated version of the ARX GUI, seven views of the software distributed over all four perspectives have been extended using the pagination feature. We note that this extension is graceful, meaning that it is only activated when a high-dimensional dataset is loaded into the software (an according threshold can be specified in the tool's settings). As an example, the pagination feature of a view in ARX's quality analysis perspective is shown in Figure 9.

< Figure 9 >

Figure 9: Screenshots from the “Classification model” tab before (left) and after (right) adding the pagination feature.

Further features that are important for managing high-dimensional data with ARX, such as auto-detection of data types and options to configure multiple attributes at once, are located in different parts of the GUI, such as data import and hierarchy creation wizards as well as the software’s main toolbar.

4 Discussion

4.1 Principal results

In this paper we presented the results of our efforts to improve the ability of the ARX Anonymization Tool to handle high-dimensional data. For this purpose, we extended the graphical user interface and introduced and evaluated two new heuristic anonymization algorithms. One of the algorithms, top-down search, complements the existing greedy bottom-up search algorithm. The other approach is based on a genetic algorithm and aims at diversifying the potential solutions considered using the process of natural selection.

Evaluating the newly implemented algorithms showed that they are particularly useful in scenarios where high-dimensional data needs to be anonymized. Using global generalization, they clearly outperformed the previously implemented bottom-up search (i.e. better performance in 5 of the 6 experiments). A similar result was observed when using local generalization. Averaged over all experiments, the new algorithms achieved a utility of 76.5 % (genetic algorithm) and 75.1 % (top-down algorithm), which is significantly higher than that provided by the bottom-up approach (60.2 %). Especially when anonymizing the dataset with the largest solution space (credit card), the new algorithms often performed significantly better, both in terms of scalability and utility. Additionally, the results obtained when processing low-dimensional data showed that heuristic algorithms can be helpful to improve computational efficiency even in scenarios where optimal algorithms could be used. The top-down approach required the least amount of time on average to find an optimal solution (4.0

s), followed by the bottom-up approach (6.3 s), the genetic algorithm (9.9 s) and the optimal search strategy (14.1 s).

Making a general recommendation for one of the algorithms is difficult based on the results of our experiments. For helping users to decide on an algorithm, ARX automatically determines whether it is feasible to calculate an optimal solution or whether a heuristic algorithm should be used. Also, ARX provides means to easily try out different algorithms and compare their results to enable users to determine which approach works best in which specific context.

4.2 Limitations

Our result show that the performance of the algorithms studied strongly depends on the dataset anonymized and the configuration utilized. While the new heuristic algorithms typically exhibited significantly improved performance in comparison to the methods previously implemented in ARX, this is not guaranteed to always be the case.

The exact operations of the genetic algorithm can be optimized by adjusting its parameterization. In our experiments, we used the parameterization by Wan et al. and additionally tuned the parameters for optimal average performance. Therefore, we chose a single parameterization in all our experiments. Optimizing the parameters for specific use cases could therefore lead to further improvements. For this reason, the GUI and API of ARX allow the user to easily change the parameterization of the genetic algorithm.

4.3 Comparison with Prior Work

It has been demonstrated multiple times that genetic algorithms can be used for anonymizing data. However, previously described solutions were mostly tailored towards specific types of data or privacy and transformation models.

Examples of approaches which focus on a specific type of data include the algorithm by Wan et al. [35], which targets genomic data and which we have adopted to general tabular data in this work, and the approach for anonymizing graphs presented by Casas-Roma et al. [51].

Regarding specific privacy and transformation models, genetic algorithms have also been used in clustering-based anonymization processes. To reduce distinguishability, such algorithms partition the records of a dataset into several groups with each of the groups containing at least k members, hence implementing the k-anonymity model. Solanas et al. [52] demonstrated how the computationally challenging partition step which aims at maximizing homogeneity within the groups can be performed using a genetic algorithm. In their approach, the number of genes equals the number of records in the dataset with the i-th gene representing the group of the i-th record. The groups are encoded as an alphabet with a fixed size as the maximal number of different groups can be derived from k and the number of records in the dataset. Lin et al. [27] described how the scalability of the clustering process can be improved for large datasets by encoding the solution using the entire population instead of a single individual. Finally, focusing on data transformations, Iyengar [44] has demonstrated how a genetic algorithm can be used to determine intervals for generalizing values. In simplified terms each individual is a binary string with a length derived from the number of processed attributes and the number of their distinct values. A value of 1 in the string implies that a value is used as an interval boundary.

Our work is different from these approaches, because it integrates a genetic algorithm into ARX in such a way that it can be used to anonymize datasets using a variety of privacy models, quality models and data transformation schemes.

Heuristics anonymization algorithms comparable to the bottom-up approach evaluated in our paper include DataFly [24] and iGreedy [26]. Both use global generalization and are focused on k-anonymity only. They are based on a bottom-up search and follow the concept of minimal anonymization meaning they terminate as soon as they find a transformation that fulfills the requested privacy properties. In previous work we have already shown that the bottom-up algorithm implemented by ARX outperforms these approaches [25]. Furthermore, other researchers have focused on top-down search strategies. Important examples include the work of He et al. [53] who proposed a greedy top-down algorithm to partition a dataset and apply local generalization as well as the Top-Down Specialization method described by Fung et al. that iteratively specializes attributes until violating the anonymity requirements [54].

5 Conclusion and future work

With the work presented in this article we have significantly enhanced ARX's ability to handle high-dimensional data, both in the GUI and the Application Programming Interface (API). All features described in this article are available as open source software and are included in the latest release of the software [13].

In future work, we plan to add additional features to improve ARX's performance for high-dimensional data. While ARX already supports a wide range of data transformation models, we believe that the addition of further transformation methods would have the largest impact. One important example is sub-tree generalization, which provides a good balance between improved output data quality and interpretability of output datasets [55]. Moreover, we plan to add further methods from the area of statistical disclosure control, such as Post-Randomization (PRAM), that can be used to inject uncertainty into data with little impact on its usefulness [56].

Availability of supporting source code and requirements

Project name: ARX Anonymization Tool

Project home page: https://arx.deidentifier.org/

GitHub repository: https://github.com/arx-deidentifier/arx

Operating system(s): Platform independent

Programming language: Java 8

Other requirements: None

License: Apache License 2.0

RRID: SCR_021189

bio.tools ID: arx

Project name: Benchmark of ARX's Heuristic Algorithms

GitHub repository: https://github.com/arx-deidentifier/genetic-benchmark

Operating system(s): Platform independent

Programming language: Java 8, Python 3

Other requirements: None

License: Apache License 2.0

Availability of supporting data

The datasets used to benchmark the algorithms are publicly available. The corresponding download URLs are referenced in Table 2 in Section 2.5.5. Additionally, the datasets are part of a GitHub repository containing our benchmarking code (https://github.com/arx-deidentifier/genetic-benchmark). The repository also contains the generalization hierarchies used for anonymizing the data and the raw benchmark results as .csv files.

Competing interests

The authors declare that there is no conflict of interest.

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Author Contributions

R.B. initiated and conceptualized the work. F.P., K.D. and T.M. implemented the novel anonymization algorithms and integrated them into ARX. F.P. and T.M. reworked the user-interface of ARX. T.M. programmed the framework used to evaluate the novel algorithms and performed the benchmarks. T.M. and F.P. drafted the manuscript. R.B. and K.D. revised the manuscript and provided important suggestions for further improvements. All authors read and approved the final manuscript.

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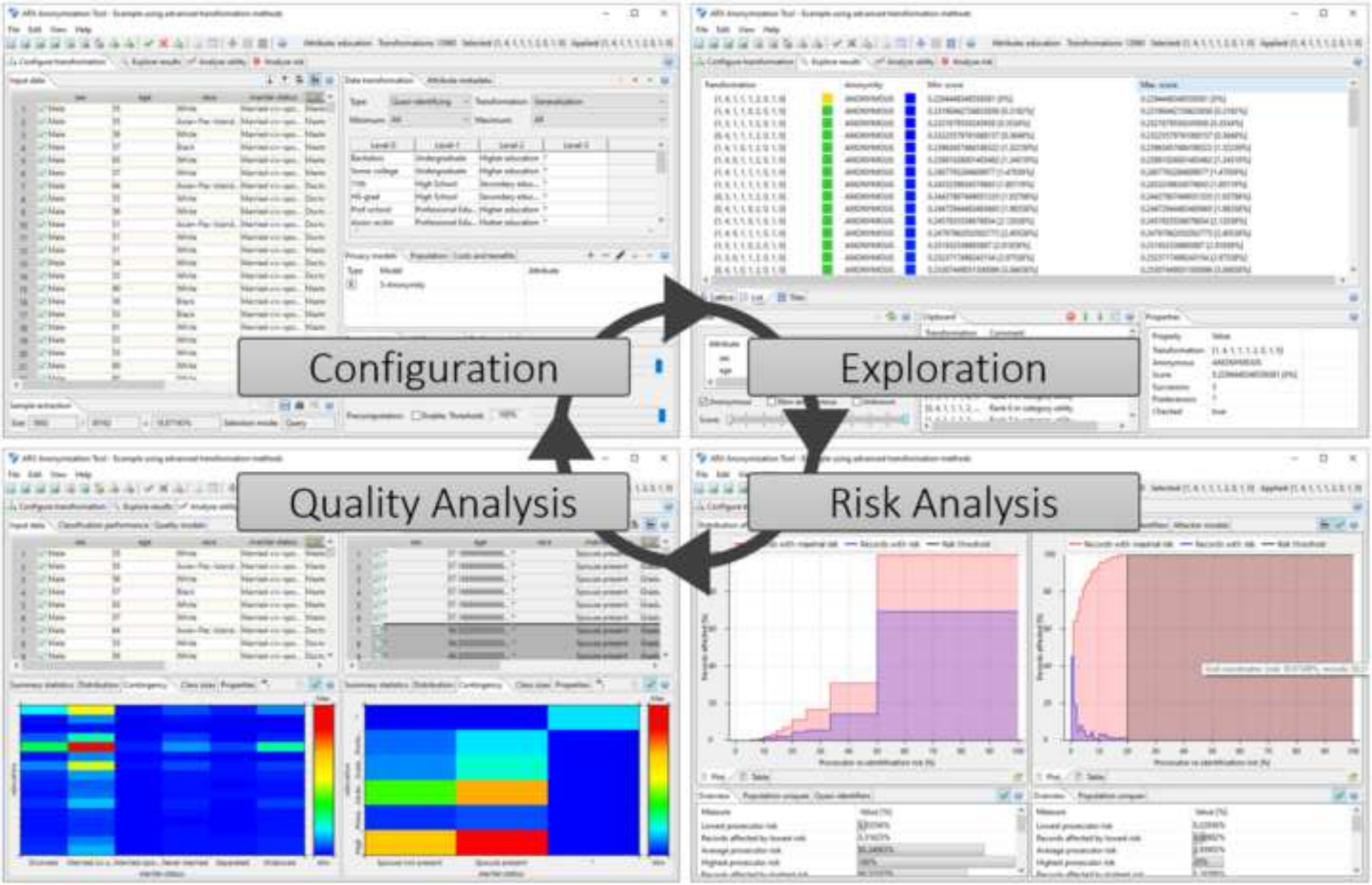
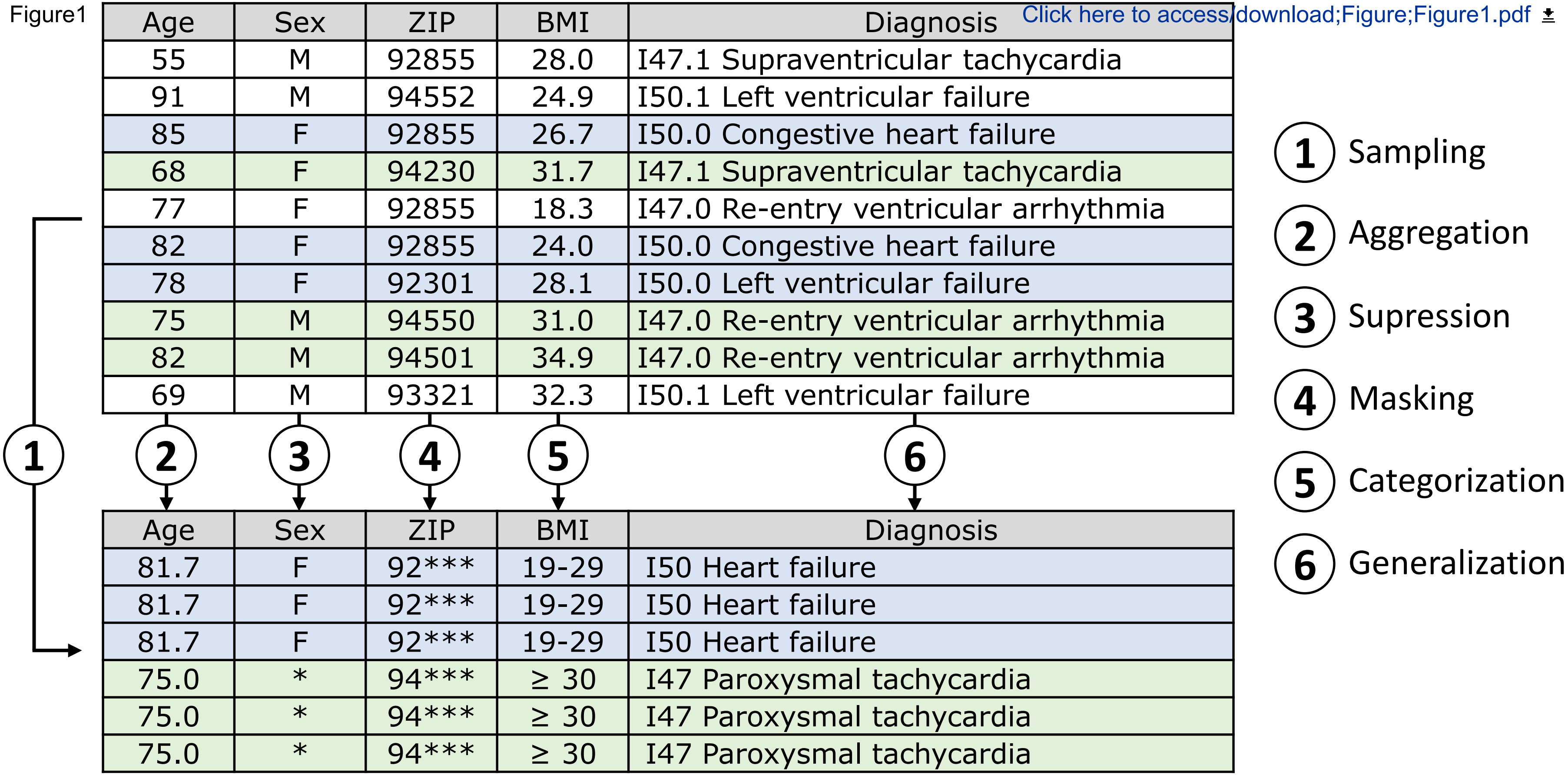

Configuration
Exploration
Quality Analysis
Risk Analysis

Figure1



Age	Sex	ZIP	BMI	Diagnosis
55	M	92855	28.0	I47.1 Supraventricular tachycardia
91	M	94552	24.9	I50.1 Left ventricular failure
85	F	92855	26.7	I50.0 Congestive heart failure
68	F	94230	31.7	I47.1 Supraventricular tachycardia
77	F	92855	18.3	I47.0 Re-entry ventricular arrhythmia
82	F	92855	24.0	I50.0 Congestive heart failure
78	F	92301	28.1	I50.0 Left ventricular failure
75	M	94550	31.0	I47.0 Re-entry ventricular arrhythmia
82	M	94501	34.9	I47.0 Re-entry ventricular arrhythmia
69	M	93321	32.3	I50.1 Left ventricular failure

Age	Sex	ZIP	BMI	Diagnosis
81.7	F	92***	19-29	I50 Heart failure
81.7	F	92***	19-29	I50 Heart failure
81.7	F	92***	19-29	I50 Heart failure
75.0	*	94***	≥ 30	I47 Paroxysmal tachycardia
75.0	*	94***	≥ 30	I47 Paroxysmal tachycardia
75.0	*	94***	≥ 30	I47 Paroxysmal tachycardia

① Sampling
② Aggregation
③ Supression
④ Masking
⑤ Categorization
⑥ Generalization

Figure2

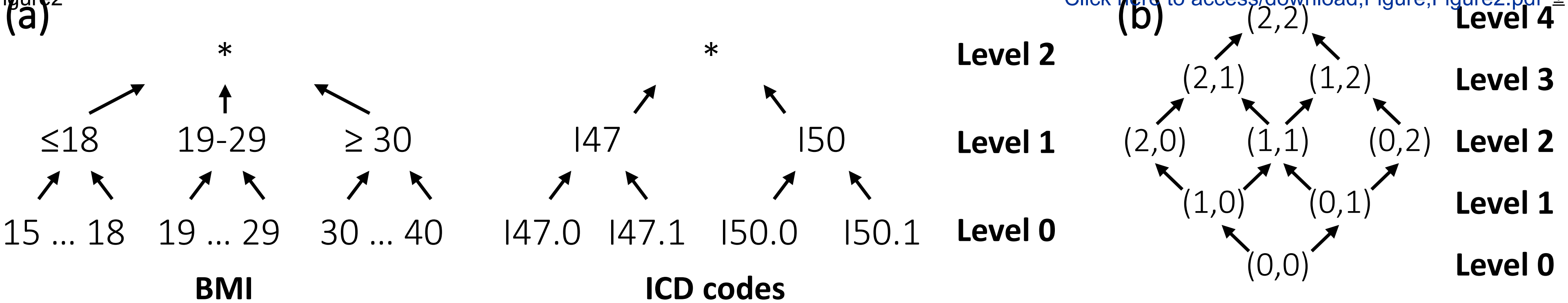

(a)
*
≤18
19-29
≥ 30
15 … 18
19 … 29
30 … 40
BMI
*
I47
I50
I47.0
I47.1
I50.0
I50.1
ICD codes
Level 2
Level 1
Level 0
(b)
(2,2)
(2,1)
(1,2)
(2,0)
(1,1)
(0,2)
(1,0)
(0,1)
(0,0)
Level 4
Level 3
Level 2
Level 1
Level 0

Figure4

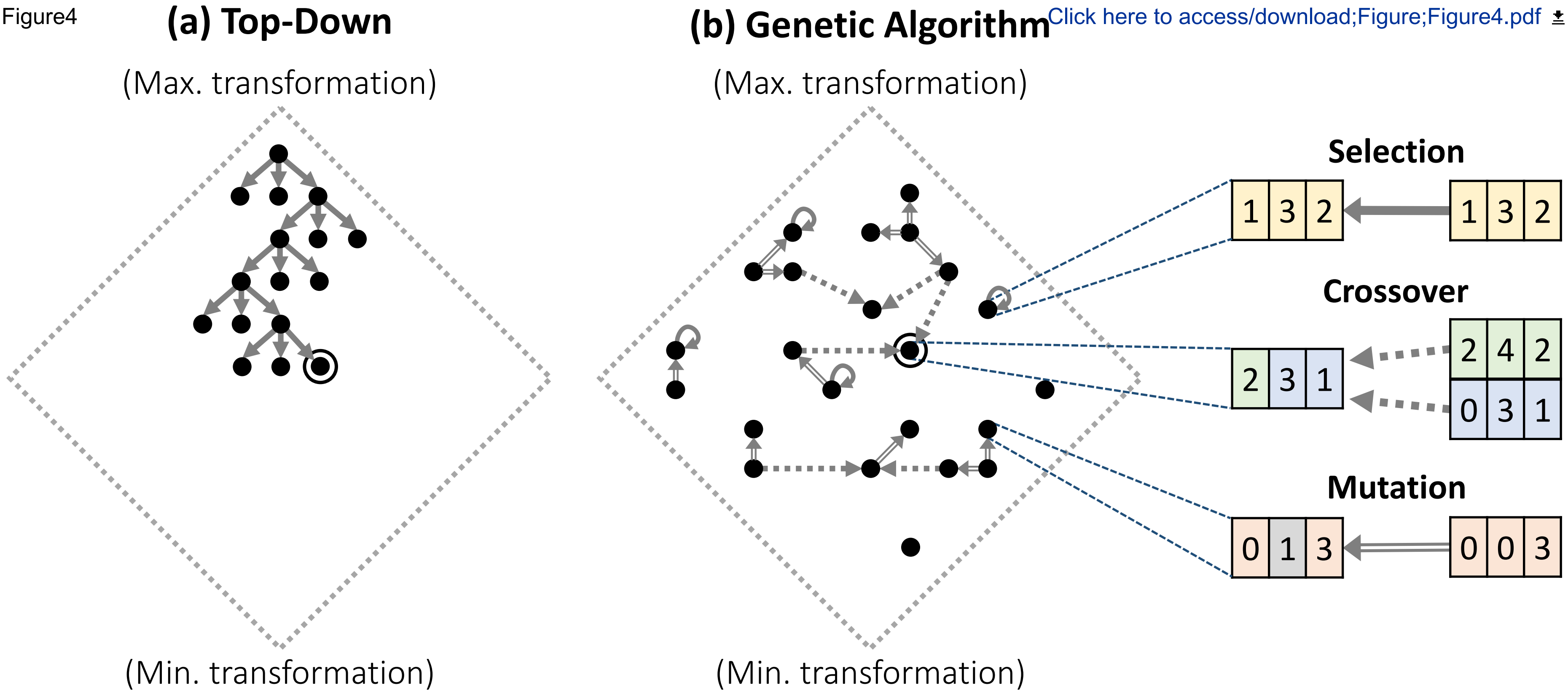
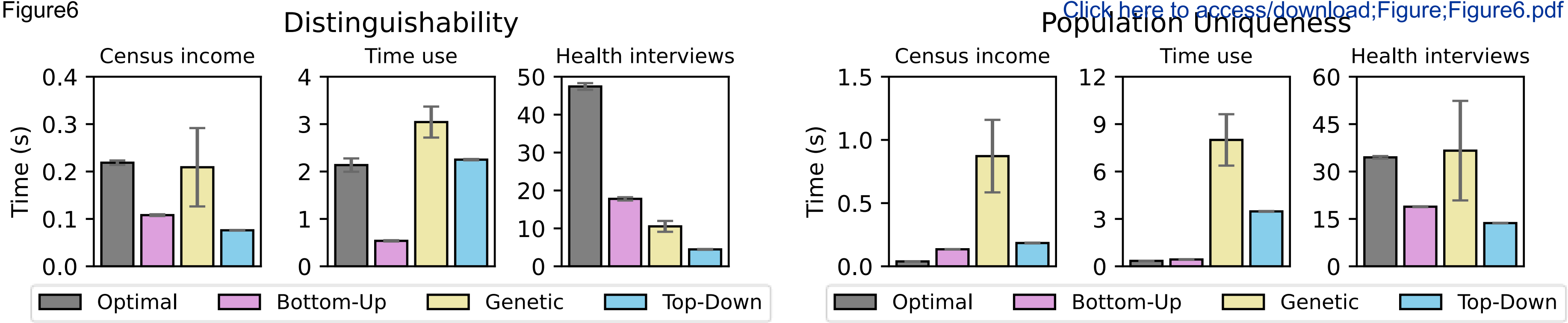

(a) Top-Down
(Max. transformation)
(Min. transformation)
(b) Genetic Algorithm
(Max. transformation)
(Min. transformation)
Selection
1 3 2
1 3 2
Crossover
2 3 1
2 4 2
0 3 1
Mutation
0 1 3
0 0 3

Figure5

#	Individual	
1	[**3**, 0, 0, 0, 0]	Filled using a „triangle“ pattern
2	[**3**, **1**, 0, 0, 0]	
3	[**3**, **1**, **5**, 0, 0]	
4	[**3**, **1**, **5**, **3**, 0]	
5	[**3**, **1**, **5**, **3**, **1**]	
6	[2, 0, 4, 2, 1]	Randomly generated
	⋮	
n	[1, 1, 3, 2, 0]	

Figure6


Distinguishability
Census income
Time use
Health interviews
Time (s)
0.0
0.1
0.2
0.3
0.4
0
1
2
3
4
0
10
20
30
40
50
Population Uniqueness
Census income
Time use
Health interviews
Time (s)
0.0
0.5
1.0
1.5
0
3
6
9
12
0
15
30
45
60
Optimal
Bottom-Up
Genetic
Top-Down

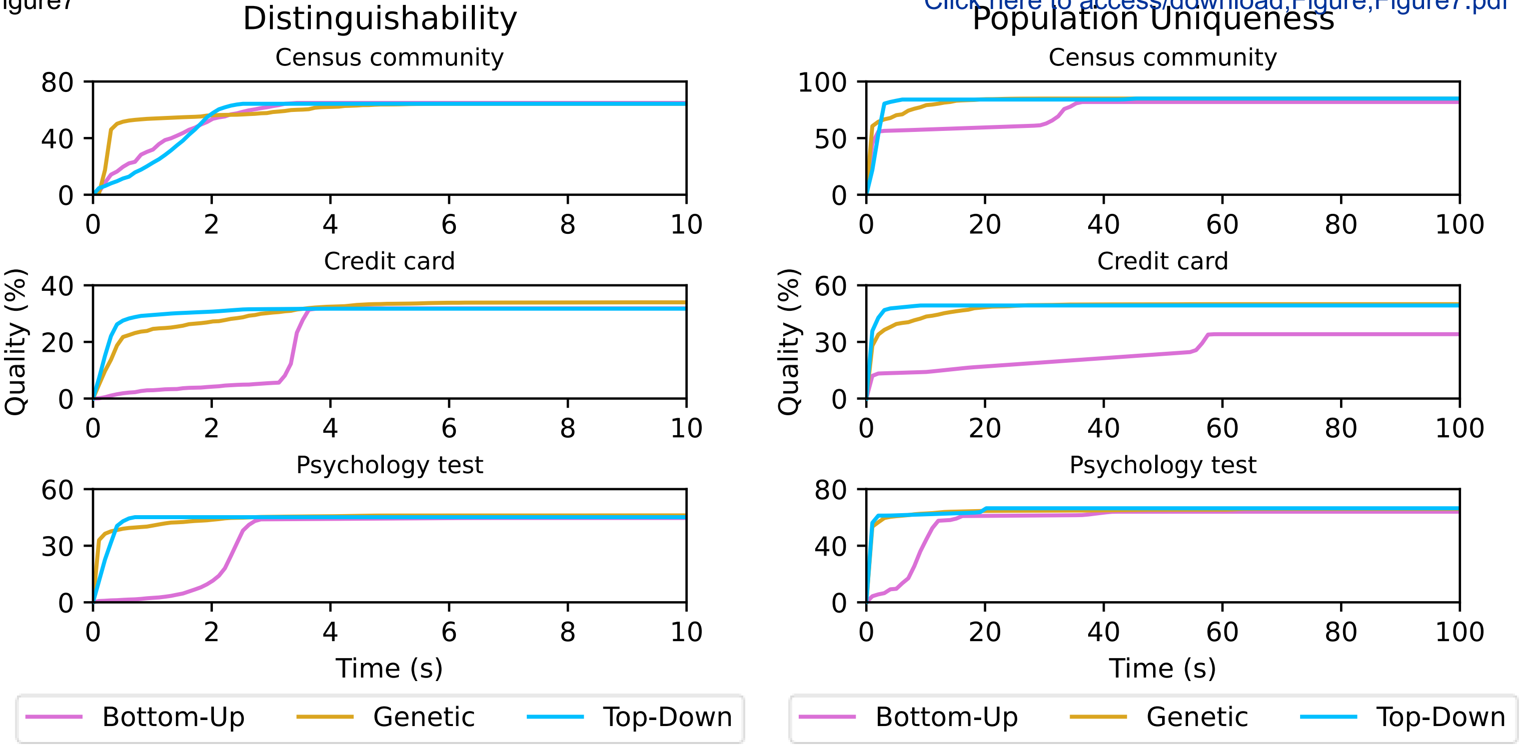

Distinguishability
Population Uniqueness
Census community
Credit card
Psychology test
Quality (%)
Time (s)
0
2
4
6
8
10
20
40
60
80
100
30
50
Bottom-Up
Genetic
Top-Down

Figure8

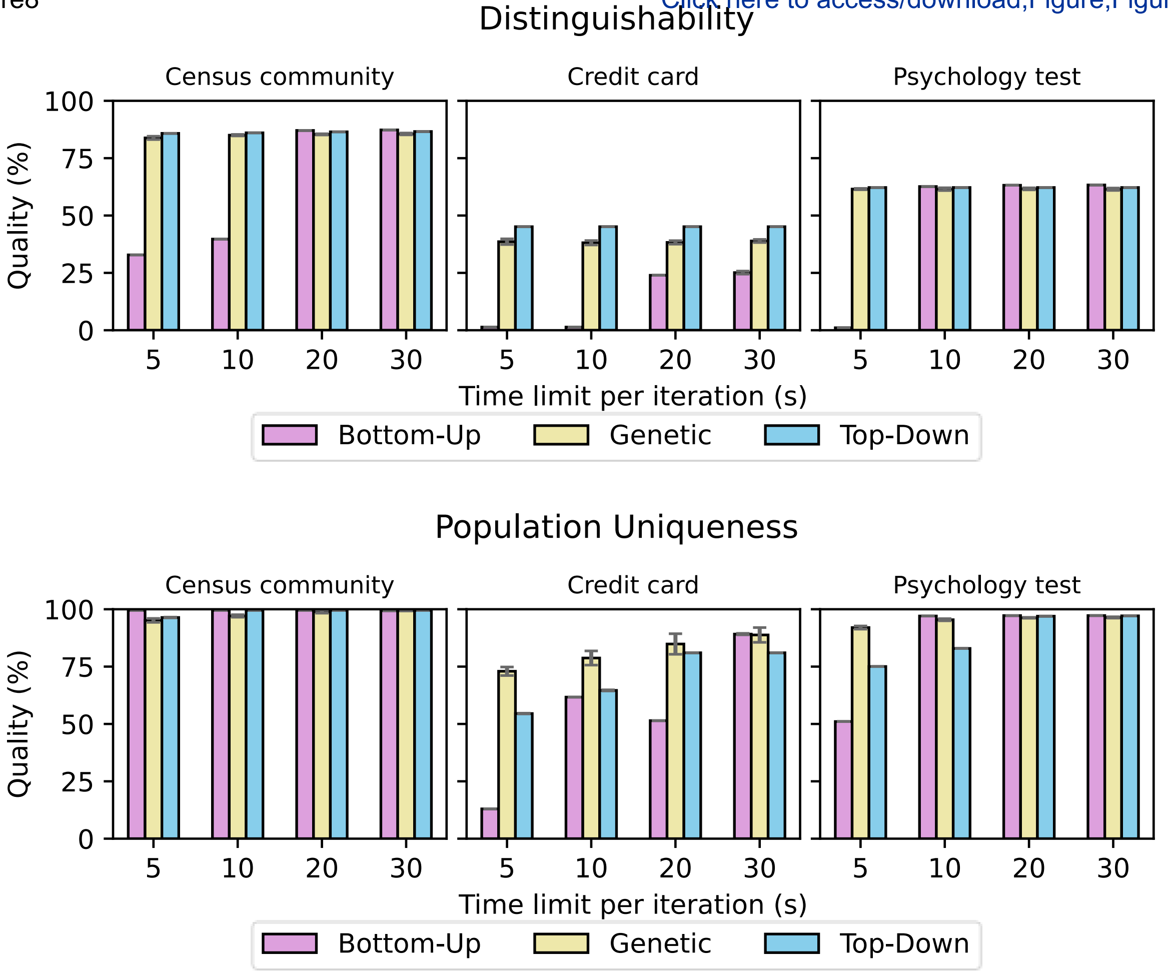
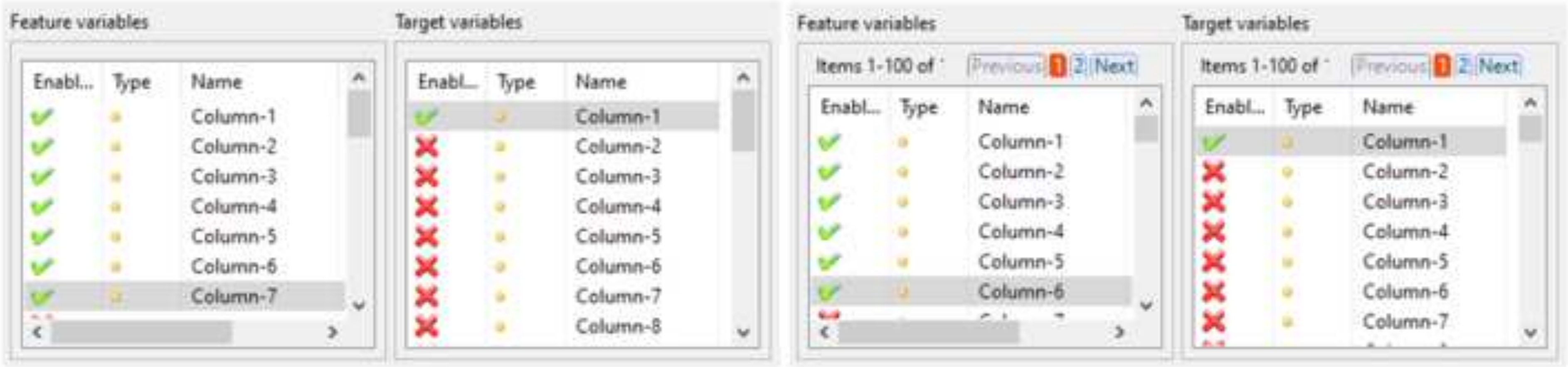

Distinguishability
Census community
Credit card
Psychology test
Quality (%)
0
25
50
75
100
5
10
20
30
Time limit per iteration (s)
Bottom-Up
Genetic
Top-Down
Population Uniqueness
Census community
Credit card
Psychology test
Quality (%)
0
25
50
75
100
5
10
20
30
Time limit per iteration (s)
Bottom-Up
Genetic
Top-Down

Figure9



Feature variables

Enabl...	Type	Name
✓	●	Column-1
✓	●	Column-2
✓	●	Column-3
✓	●	Column-4
✓	●	Column-5
✓	●	Column-6
✓	●	Column-7

Target variables

Enabl...	Type	Name
✓	●	Column-1
✗	●	Column-2
✗	●	Column-3
✗	●	Column-4
✗	●	Column-5
✗	●	Column-6
✗	●	Column-7
✗	●	Column-8

Feature variables

Items 1-100 of

Enabl...	Type	Name
✓	●	Column-1
✓	●	Column-2
✓	●	Column-3
✓	●	Column-4
✓	●	Column-5
✓	●	Column-6

Target variables

Items 1-100 of

Enabl...	Type	Name
✓	●	Column-1
✗	●	Column-2
✗	●	Column-3
✗	●	Column-4
✗	●	Column-5
✗	●	Column-6
✗	●	Column-7