SBA Research



Anonymisation and Fingerprinting of Microdata: A Genetic Algorithm for Finding Optimal Set for Data Distribution

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Stadt Wion





Introduction Motivation

- Tracing the unauthorised usage of anonymised data
- <u>Our objective</u> is to enable a system that allows:
 - 1. sharing *k*-anonymous data with multiple recipients
 - 2. <u>tracing</u> the shared copies in cases of unauthorised redistribution or unauthorised usage
 - identify the recipient of the anonymised data copy
 - identify own signature to prove the ownership of the original data

Introduction Ownership protection via a traceable marker

- **Fingerprinting**: embedding (hiding) a traceable marker into data that:
 - Identifies the owner
 - Identifies the recipient
- Fingerprinting of microdata:
 - Fingerprint generation $F(SK, id) \rightarrow [1,0]^{l}$
 - Fingerprint translates to a pattern of modifications of data values

Original data				Fingerprinted data 1				Fingerprinted data 2				
Name	Sex	Birthdate	Disease	Name	Sex	Birthdate	Disease		Name	Sex	Birthdate	Disease
Bob	М	19.03.1970	Chest pain	Bob	М	21.03.1970	Chest pain		Bob	М	21.03.1970	Chest pa
Dave	М	20.03.1970	Short breath	Dave	М	20.03.1970	Short breath		Dave	М	20.03.1970	Short br
Alice	F	18.04.1970	Obesity	Alice	F	18.04.1970	Short breath		Alice	F	18.04.1970	Chest p
Eve	F	21.04.1970	Short breath	Eve	F	21.04.1970	Short breath		Eve	F	21.04.1970	Short bi

Introduction Fingerprinting & anonymisation

- Requirements:
 - Allow sharing *k*-anonymised data
 - Trace unauthorised re-distribution of data
- Idea: "reuse" the modification from anonymisation for tracing
- Fingerprint: *unique generalisation pattern*

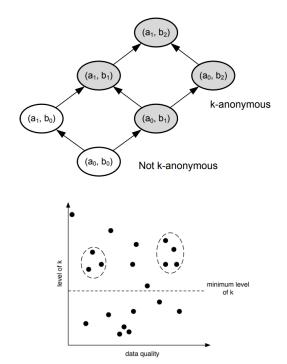
Original data							
Name	Sex	Birthdate	Disease				
Bob	М	19.03.1970	Chest pain				
Dave	М	20.03.1970	Short breath				
Alice	F	18.04.1970	Obesity				
Eve	F	21.04.1970	Short breath				

2-anonymous set 1 [0,2]							
Name	Sex	Birthdate	Disease				
*	М	1970	Chest pain				
*	М	1970	Short breath				
*	F	1970	Obesity				
*	F	1970	Short breath				

2-anonymous set 2 [1,1]							
Name Sex		Birthdate	Disease				
*	*	03.1970	Chest pain				
*	*	03.1970	Short breath				
*	*	04.1970	Obesity				
*	*	04.1970	Short breath				

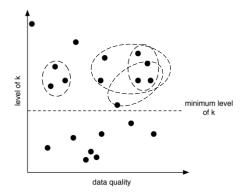
Introduction Fingerprinting & anonymisation: the algorithm

- 1. Obtain all generalisation patterns given the dataset and hierarchies
- 2. Discart those not satisfying *k*-anonymity
- 3. Cluster the fitting generalisation patterns on their max *k* and *some* utility metric
- 4. Treat the cluster as a group of equally good solutions for distribution
- 5. Collusion filter



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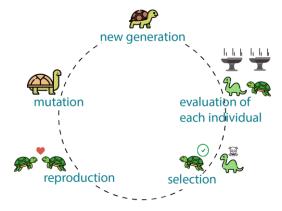
- Select a subset of generalisation patterns (anonymous data sets) where:
 - All elements satisfy minimum privacy criterium
 - The elements have similarly good utility
 - The subset is large *enough* for sharing with recipients

Problem statement

- **Problem statement**: find a subset of n(S) *k*-anonymous datasets $S = \{s_1, s_2, ..., s_{n(S)}\}$ such that:
 - Total utility loss, $loss(S) = \frac{\sum_{i=1}^{n} s_{i}}{n}$ is minimised
 - Variation coefficient of the loss, $cv(S) = cv(loss(s_1), loss(s_2), ..., loss(s_n))$ is minimised
 - Cardinality *n(S)* is maximised
- **Objective function**: $\min f(S) = 1 \frac{n n_{min}}{n_{max} n_{min}} + loss(S) + cv(S)$

Genetic Algorithm

- **Genetic algorithm (GA)**: metaheuristic for solving optimisation problems inpired by natural selection
 - 1. Initialisation
 - 2. Evaluation using *fitness function*
 - 3. Selection
 - 4. Crossover / Reproduction
 - 5. Mutation

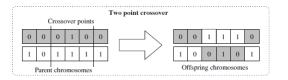


Solution with GA: formulation

• Fitness function: $\min f(S) = 1 - \frac{n - n_{\min}}{n_{\max} - n_{\min}} + loss(S) + cv(S)$

transformation	LM	sup. records	Precision	AES
[0,4,0,0,1,0,0,1,0]	0.2210	9.77%	0.2037	28.3195

- **Genotype** (chromosomes) of a candidate solution $S = \{s_1, s_2, ..., s_n\}$: $[1,0]^{n_{max}}$
- **Crossover**: two-point crossover

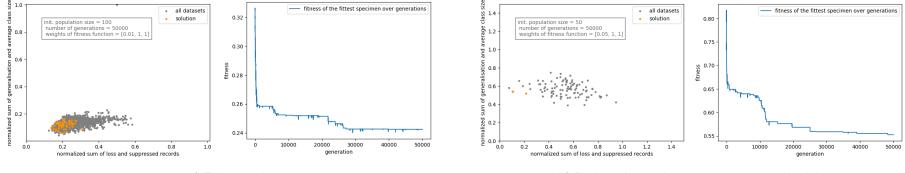


Mutations:

- <u>Replacing gene within the candidate solution</u>: with a probability of 40% we replace genes from the candidate solution with new data points from the dataset. The amount of replaced data points is between zero and a third of the size of the candidate solution (the amount is chosen randomly)
- <u>Adding/removing a gene:</u> with a probability of 60% we add a new gene or delete one. The probability of choosing to add/remove a random data point from the dataset to the candidate solution is 50%.

Results

- Adult Census: search space of 1,197 3-anonymous data sets
- Flash k-anonymisation algorithm within ARX toolbox



a) Full search space

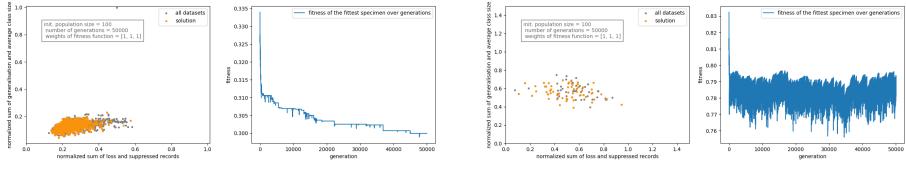
b) Reduced search space: top 100 optimal datasets

Fig1: Reduced weight of subset size n(S) in the fitness function

Kohlmayer, Florian, et al. "Flash: efficient, stable and optimal k-anonymity." 2012 International Conference on Privacy, Security, Risk and Trust and 2012 International Conference on Social Computing. IEEE, 2012.

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Results

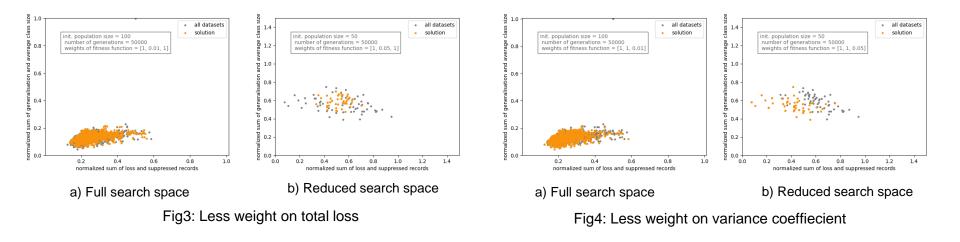


a) Full search space

b) Reduced search space: top 100 optimal datasets

Fig2: Equal weights for subset size, total loss and variance of the subset

Results



Concluding remarks and next steps

- Collusion filter after GA
 - Making sure that the recipients cannot avoid being traced by collaborating
- More privacy concerns for data subjects by sharing multiple anonymised copies?

Comparison to sequential approach: k-anonymisation then fingerprinting

Merci!

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