

Generating Synthetic Data Mimicking the Real Cancer Population

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Intro

What Is Synthetic Data?

Synthetic data are “any production data applicable to a given situation that are not obtained by direct measurement”. The synthesized data might be directly obtained by perturbing the real data or based on some assumptions, distributions and frequency tables which might follow a particular real situation.

Why We Produce It?

- For the confidentiality purpose to protect disclosure risk
- For the Research Purpose
- For uniformity of evaluating some procedures or software

Synthetic Data for the De-duplication & Record Linkage Purpose

The real data set is dirty. Some entities exist multiple times. The formats of fields are not the same, and there might be variety kinds of typos. Therefore if we want to synthesize a real data for the de-duplication or record linkage purpose, we need to consider all of these situations.

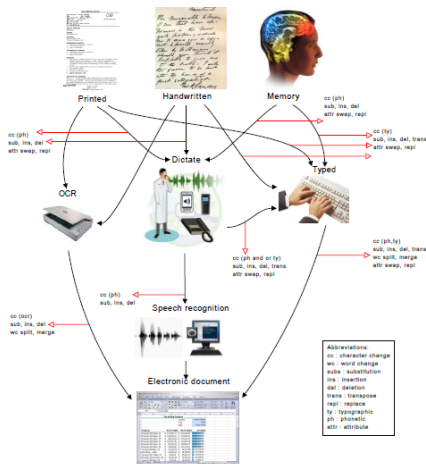
Purpose & Goal of This Research:

Generating A Synthetic Data Mimicking the Real Cancer Population

- We need to consider different possibilities of errors that might happen in the real situation for the fields
- We need to incorporate frequency distributions or tables obtained from registered data or online reliable sources.

Cont'd Purpose & Goal of This Research:

- To have different scenarios we make fields dependent. For example a specific kind of cancer could be dependent to the gender. Or cancer and blood pressure could vary based on the age.
- We consider Zipf, Uniform, or Poisson distributions for randomly selecting units that need to be duplicated.
- Matching variables that we considered are: First name, Last name, SSN, DOB, State, Zipcode, Age, Phone Number, Cancer, Blood pressure, etc.



Software

1. DBGen (C programming) developed around 1990s; producing US mailing address
2. GeCo (Python programming) developed from 2002-2008; for the special purpose of bio-medical studies

Both programs are capable of producing one synthesized data set with **unique IDs**, duplication and errors.

We should give them the frequency tables not the full raw data set.

DBGen

1. We cannot incorporate as many errors as we want
2. We can generate fields such as: First Name, Middle Initial, Last Name, Street Number, P.O. Box, Apartment Number, City, State, Zipcode.
3. We can consider Insertions, deletions, replacements, swapping, and other errors.
4. The program is old and not handy. For changing it, we need to write a lot of codes

Cont'd DBGen

```

sepideh@sepideh-Latitude-E5450: ~/Desktop/Sepideh/NCI/Softwares/dbgen/dbgen
File Edit View Search Terminal Help

Random Database Generator - v2.0
Computer Science - University of Illinois, Springfield
.....Uniform
Database Size
Number of Records      379109
Number of Clusters    > 379109

Other types of errors
Swap First & Last      0.00%
No middle initial     0.00%
Chg. first for initial 0.00%
Chg. last name        0.00%

Social Security Numbers
Generate SSN          100.00%
Error Probability      0.00%

Addresses
Use P.O. Box          0.00%
Change Address        0.00%

Street Number
Typo. Error Prob.     0.00%

Street Names
Typo. Error Prob.     0.00%
Single Error Prob.    0.00%
Insertions            40.00%
Deletions             20.00%
Replacements          20.00%
Swappings             20.00%

.....Page 1 of 2.....More>
Commands: (q)uit (g)enerate (a)ppend (s)ave (r)estore (c)hange s(e)ed (o)ther

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sepideh@sepideh-Latitude-E5450: ~/Desktop/Se
File Edit View Search Terminal Help

Random Database Gen
Computer Science - University
.....
City, State, Zip
Typo. Error Prob.    > 0.00%
Single Error Prob.   0.00%
Change Zip Code      0.00%
Change State         0.00%
Number of States     50

Types of Typos
Same row in keyboard 0.00%
Same column in keyboard 0.00%
Homologous           0.00%
Change First Letter  0.00%
Consonant Change     0.00%
Cons. Order          rstnlchdpghfbywvxqkj

Files
Output File          output.db
Names DB             /home/sepideh/Desktop/S
es.gazamer File      params.gen
<More>.....Page 2 o
Commands: (q)uit (g)enerate (a)ppend (s)ave

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An Empirical Study (DBGen)

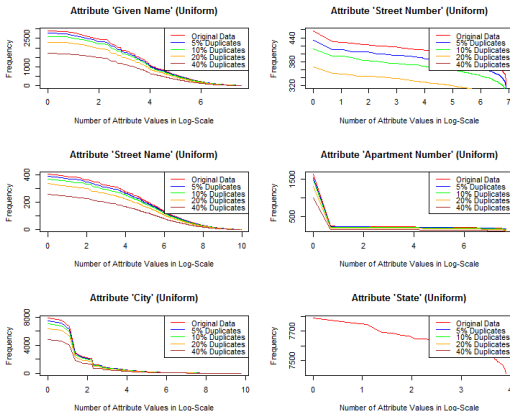
To test whether the DBGen (since it is old) is good for generating data, we implemented an experimental study. We assumed n (number of units) = c (number of clusters)

I generated an error free data set based on the frequency tables coming from Automated Vital Statistics System under the Institute for Social, Behavioral, and Economic Research at the University of California, Santa Barbara, CA 93106. Number of girls = 240311 and boys = 252972.

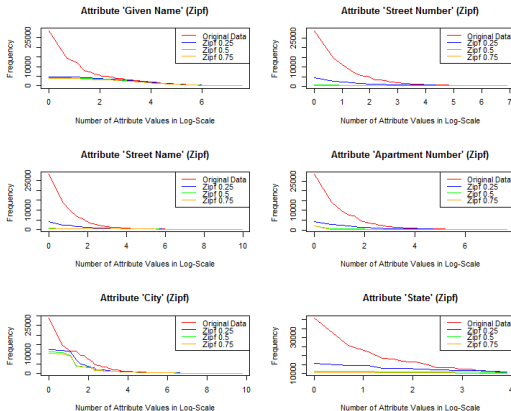
DBGen Evaluation

To evaluate the duplicated data set, we considered %5, %10, %20, and %40 duplication. Then we selected six attributes with their frequency distributions, Average Frequencies, and Standard Deviations.

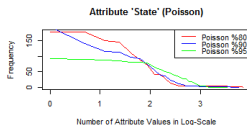
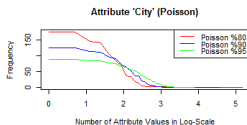
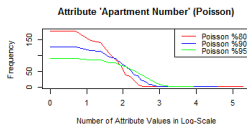
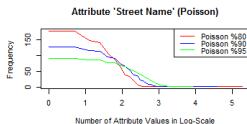
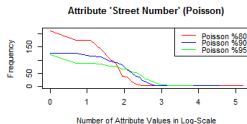
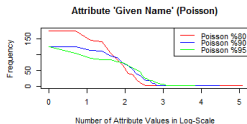
DBGen Evaluation



DBGen Evaluation



DBGen Evaluation



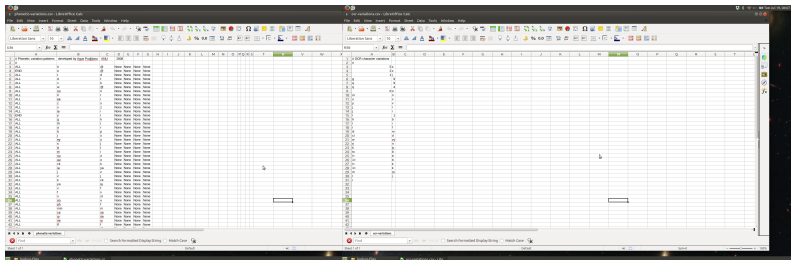
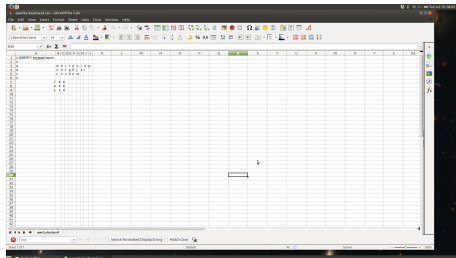
GeCo

1. Capable of incorporating variety kinds of errors, missing values, etc.
2. We can consider dependent attributes.
3. We need to define the number of duplication; otherwise, the program does not work.
4. Writing codes in Python is usually easier rather than C.

GeCo (As Our Final Focus)

We wrote codes and merged them with the original GeCo codes. I produced a big data set with variety of errors. Since the ids are unique just per data set not across the data set (generating the data is based on random process), we split the data set into 2 data set with different sizes after permutation for the purpose of record linkage. Unique IDs make it easy to evaluate the matching process since we have the true situations.

GeCo (Some Possible Errors)



How the Produced Data Sets Look Like?

The image displays two side-by-side screenshots of Microsoft Excel spreadsheets, each showing a large dataset of synthesized cancer-related information. The left spreadsheet is titled 'Libraries Data' and the right is 'Libraries Data - Copy'. Both spreadsheets have a similar structure with columns for various attributes. The data appears to be organized into rows, with some rows highlighted in green. The columns include identifiers, accession numbers, lengths, GC content, and other genomic or library-related metrics. The spreadsheets are shown in a standard Excel interface with toolbars and status bars visible.

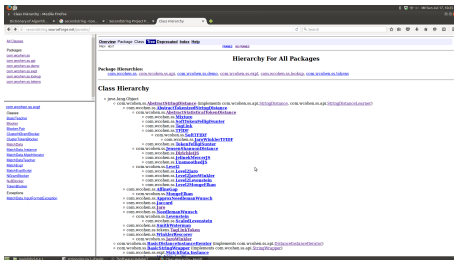
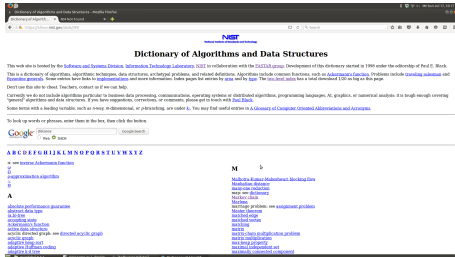
This screenshot shows a single Microsoft Excel spreadsheet titled 'Libraries Data'. It contains a large dataset of synthesized cancer-related information. The columns include identifiers, accession numbers, lengths, GC content, and other genomic or library-related metrics. The data is organized into rows, with some rows highlighted in green. The spreadsheet is shown in a standard Excel interface with toolbars and status bars visible.

Febrl (for de-duplication and record linkage)- Beyond the Contract

Febrl is a program in Python which needs different packages and features on the computer for its implementation. Its installation is time-consuming and different per PC. It has different versions. I considered Febrl 0.4.1 (Dec 2008). It also has a data generator module called dsgen which is not error free and handy. It contains a GUI. But we are considering the main Python codes to add some other criteria.

1. Indexing 2. Standardization 3. De-duplication, 4. Record Linkage, 5. Evaluation

Febri (For Adding Features)



Febri (GUI)

Febri - (None)*

File Tools Help

Execute New Open Save Quit

Standardization Deduplication
Grouping Linkage

Data Explorer Index Compare Log

First data set type: CSV COL TAB SQL Missing values: View Data Edit Data

Filename: censusTexts... Use headerline Stop fields

Record identifier field: (None)

SOURCE IDENTIFIER	SURNAME	GIVENNAME	INITIALS	ZIPCODE	SUBURB
A ID4447124106822810001	ANDERSON			4848	BASSWOOD
A ID4447124106822810003	ANDERSON			4848	BASSWOOD
A ID4447124106822810004	ANDERSON			4848	BASSWOOD
A ID4447124106822810002	ANDERSON			4848	BASSWOOD
A ID4447124106881610001	AQUINO	CLARA	J	656	STARKEY

Second data set type: CSV COL TAB SQL Missing values: View Data Edit Data

Filename: censusTexts... Use headerline Stop fields

Record identifier field: (None)

SOURCE IDENTIFIER	SURNAME	GIVENNAME	INITIALS	ZIPCODE	SUBURB
B ID444611561	AHREWS	MARITZA	A	345	71ST
B ID444611562	AHREWS	MARINHA	B	345	71ST
B ID4447124106879931001	BENETAS	LEHARD	A	560	STARKEY
B ID4447124106879931003	BENETAS	SAMMY	R	560	STARKEY
B ID4447124106879931002	BENETAS	DOLORES	R	560	STARKEY

Generated Febri Python code for data set installation (see Log page for generated code).

Febri - (None)*

File Tools Help

Execute New Open Save Quit

Standardization Deduplication
Grouping Linkage

Data Explorer Index Compare Log

weight vector classification method: Nearest

Nearest comparison value: 0.5 Nearest method: Nearest Selection nearest: 100 Select unique weight vectors

Nearest comparison value: 0.5 Nearest method: Nearest Selection nearest: 100 Select unique weight vectors

Random selection method: (None)

Stop two classification method: SUM Normal type: RDB C 18

Generated Febri Python code for classification (see Log page for generated code).

Some Future Steps

- Considering more other specific scenarios for the cancer population
- Availability of real data set or frequency tables for some cancer population
- Febrl applications (Beyond the contract)
- Time and Energy

Thank You!

Questions: smosafer@umd.edu