

# Data Deidentification Research and Resources from the NIST Collaborative Research Cycle

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**Christine Task, Knexus Research**  
with content from  
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**NIST**

NATIONAL INSTITUTE OF  
STANDARDS AND TECHNOLOGY  
U.S. DEPARTMENT OF COMMERCE

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# National Institute of Standards and Technology

Measurements essential  
to commerce, trade,  
and innovation

Federal role  
established in the  
U.S. Constitution



# Why does NIST research privacy?

NIST seeks to facilitate organizations and individuals deriving benefits from data while simultaneously encouraging effective management of risks to individuals' privacy.

NIST seeks to be the world's leader in creating critical measurement solutions and promoting equitable standards.

NIST is a trusted leader in metrology and provides independent, and transparent technical guidance for the benefit of all.

This talk focuses on a NIST metrology program for data **deidentification techniques**.

Deidentification includes any processing to microdata that produces microdata in the same schema and is *intended* to be resistant to individual reidentification: SDC, synthetic data, differential privacy.

This past year we've launched a massive community benchmarking and meta-analysis project, collecting metrics, algorithms and data samples from stakeholders, researchers and statistical agencies around the world— and making them all freely available and easy to use. We'll give you a tour, and you can check the QR code to access it all yourselves.



[https://pages.nist.gov/privacy\\_collaborative\\_research\\_cycle/](https://pages.nist.gov/privacy_collaborative_research_cycle/)



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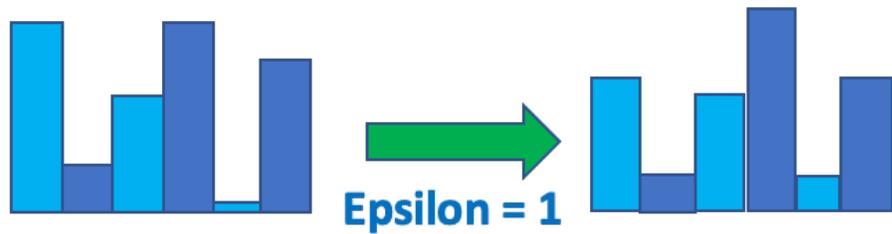
The diagram illustrates the Collaborative Research Cycle as a continuous loop. It features three main components: 'Research' (top left, with a magnifying glass icon), 'Engineering' (top right, with a gear icon), and 'Engagement' (bottom center, with a group of people icon). Curved arrows connect these components in a clockwise direction: from Research to Engineering, from Engineering to Engagement, and from Engagement back to Research.

## Collaborative Research Cycle

Welcome to the homepage of the Collaborative Research Cycle (CRC), hosted by the [NIST Privacy Engineering Program](#)

- Home
- Participate
- Results Blog
- Techniques
- Archive & Tools
- How to Cite

**DP Histogram:** Add randomized noise to counts



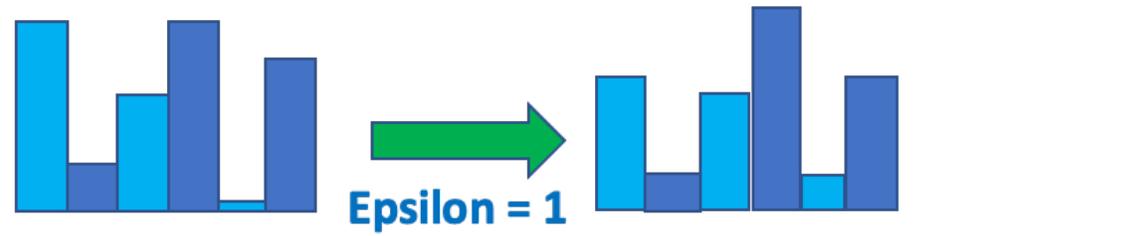
Differential Private Histogram ( $\epsilon = 10$ )

PATECTGAN Differential Private GAN ( $\epsilon = 10$ )

CART-model Synthesis (non-DP synthetic)

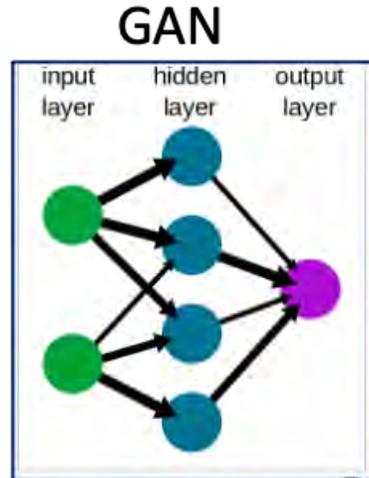
Cell Suppression ( $k = 6$ )

## DP Histogram: Add randomized noise to counts



Differential Private Histogram ( $\epsilon = 10$ )

**DP GAN:** Add randomized noise while training an ML model to reproduce the distribution.



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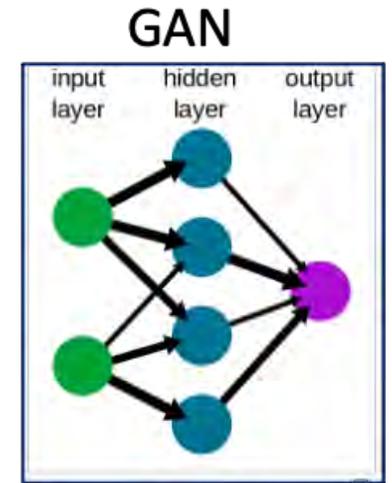
# Algorithms: A Sample of Four Deidentification Approaches

**DP Histogram:** Add randomized noise to counts



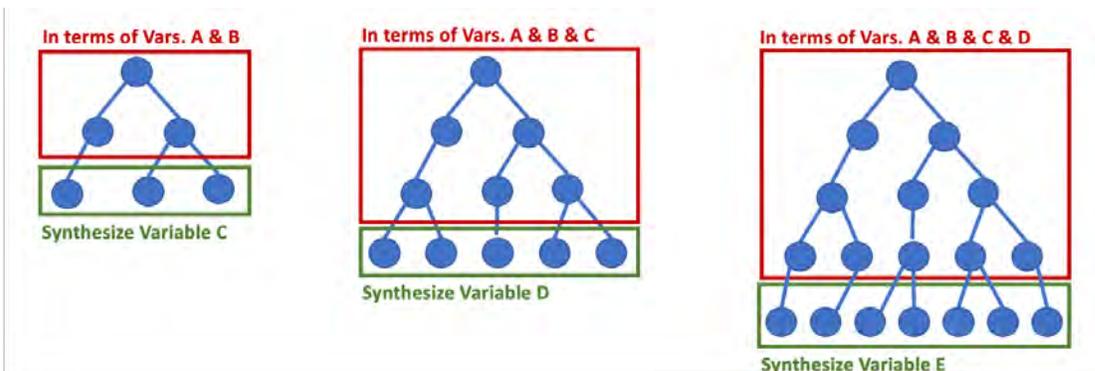
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**CART:** Use a sequence of decision trees to generate new values for every feature, one at a time.

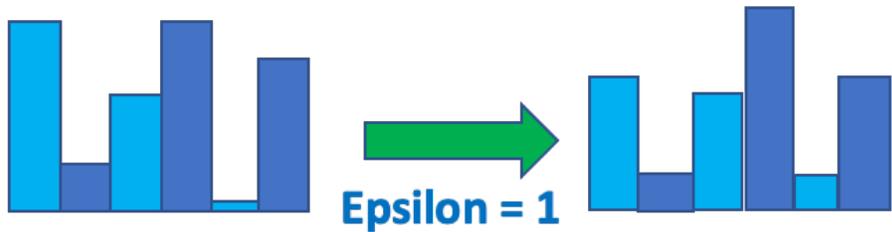


CART-model Synthesis (non-DP synthetic)

Cell Suppression ( $k = 6$ )

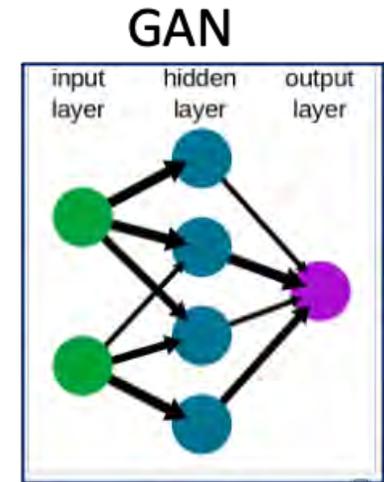
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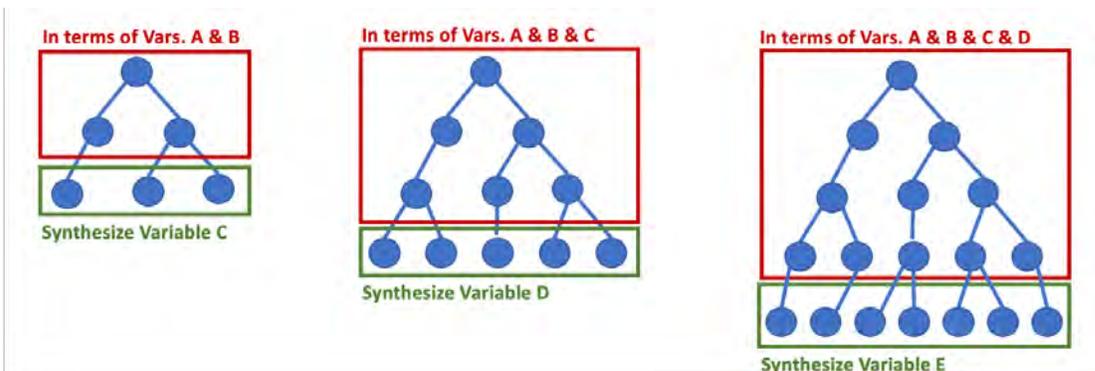
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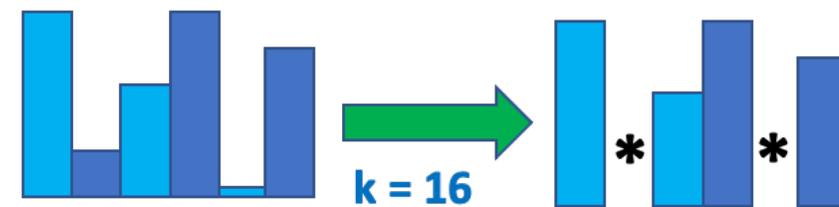
PATECTGAN Differential Private GAN ( $\epsilon = 10$ )

**CART:** Use a sequence of decision trees to generate new values for every feature, one at a time.



CART-model Synthesis (non-DP synthetic)

**Cell Suppression:** Redact small counts



Cell Suppression ( $k = 6$ )

# Data: Diverse Community Excerpts Benchmark Data

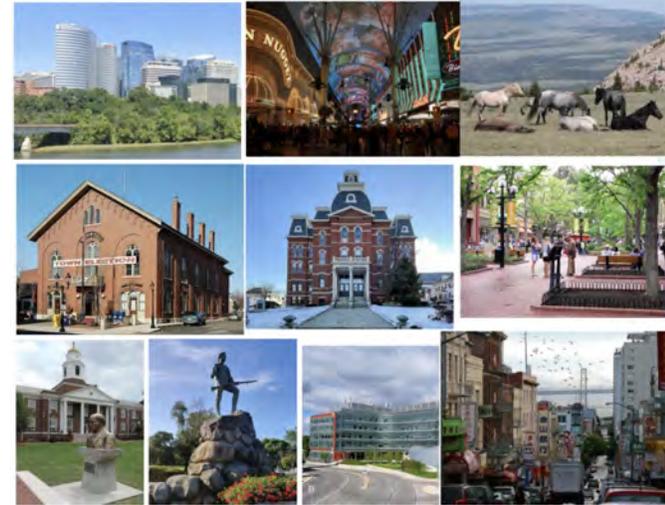
## Excerpts of 2019 American Community Survey Data

Tractable schema size for research: 22 Data Features + Weights

Curated to focus on geographies (PUMA) with challenging distributions

| Feature Name | Feature Description                              |
|--------------|--|
| PUMA         | Public use microdata area code                   |
| AGEP         | Person's age                                     |
| SEX          | Person's gender                                  |
| MSP          | Marital Status                                   |
| HISP         | Hispanic origin                                  |
| RAC1P        | Person's Race                                    |
| NOC          | Number of own children in household (unweighted) |
| NPF          | Number of persons in family (unweighted)         |
| HOUSING_TYPE | Housing unit or group quarters                   |
| OWN_RENT     | Housing unit rented or owned                     |
| DENSITY      | Population density among residents of each PUMA  |

|           |  |
|-----------|--|
| INDP      | Industry codes   |
| INDP_CAT  | Industry categories                                      |
| EDU       | Educational attainment                                   |
| PINCP     | Person's total income in dollars                         |
| PINCP_DEC | Person's total income in 10-percentile bins              |
| POVPIP    | Income-to-poverty ratio (ex: 250 = 2.5 x poverty line)   |
| DVET      | Veteran service connected disability rating (percentage) |
| DREM      | Cognitive difficulty                                     |
| DPHY      | Ambulatory (walking) difficulty                          |
| DEYE      | Vision difficulty  |
| DEAR      | Hearing difficulty                                       |



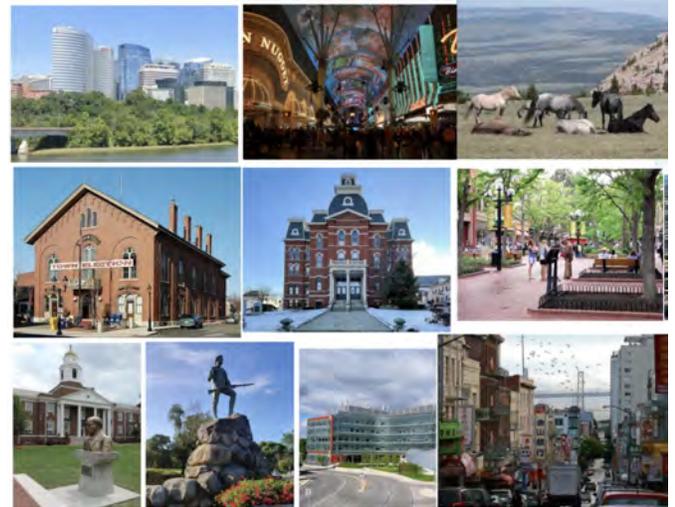
<https://github.com/usnistgov/SDNist/tree/main/nist%20diverse%20communities%20data%20excerpts>

# Data: Diverse Community Excerpts Benchmark Data

Excerpts of 2019 American Community Survey Data  
 Tractable schema size for research: 22 Data Features + Weights  
 Curated to focus on geographies (PUMA) with challenging distributions  
 Recommended Feature Subsets provided for small schema approaches

| Feature Name | Feature Description                              |
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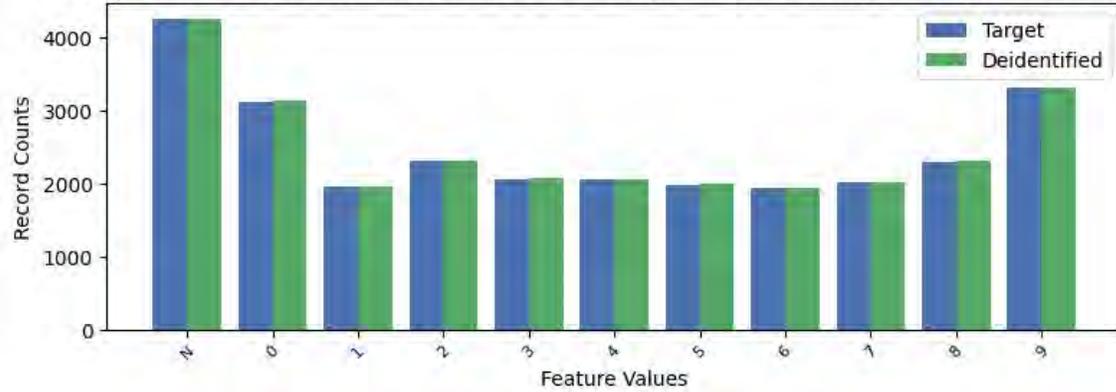


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The next few slides will use the "Demographic-focused" Feature Subset

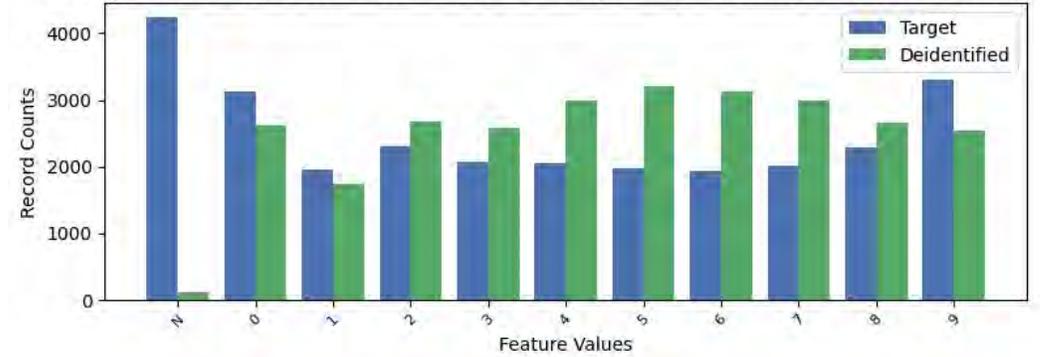
# Metrics: Univariate

PINCP\_DECILE: Person's total income rank (with respect to their state) discretized into 10% bins.



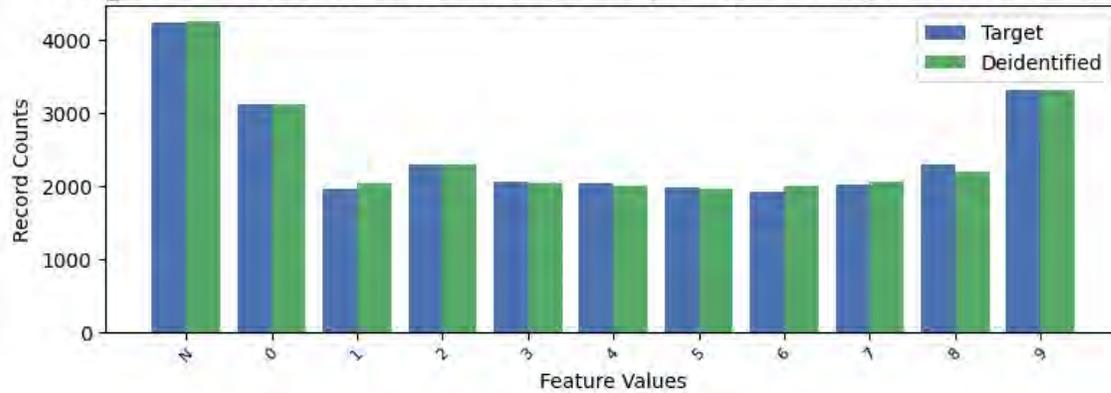
**Differential Private Histogram ( $\epsilon = 10$ )**

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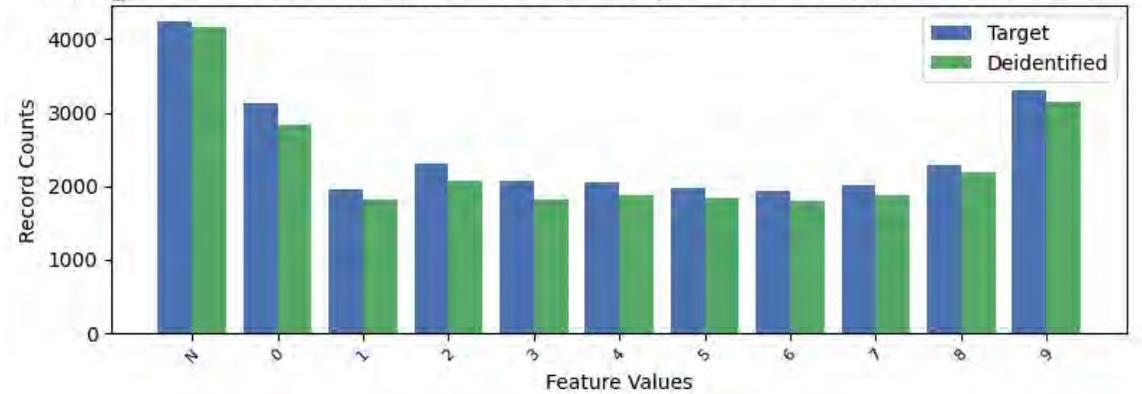
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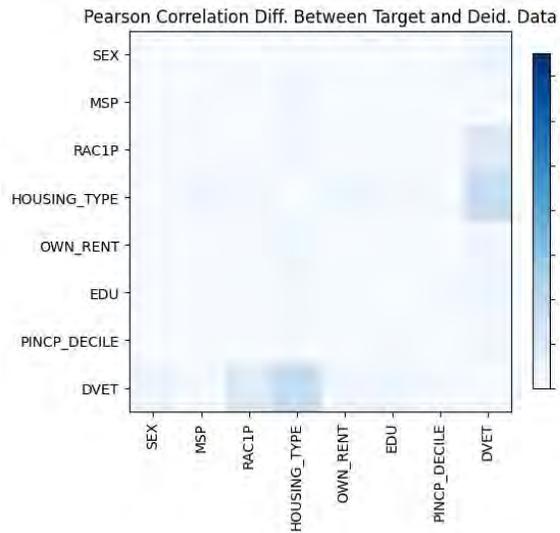
**CART-model Synthesis (non-DP synthetic)**

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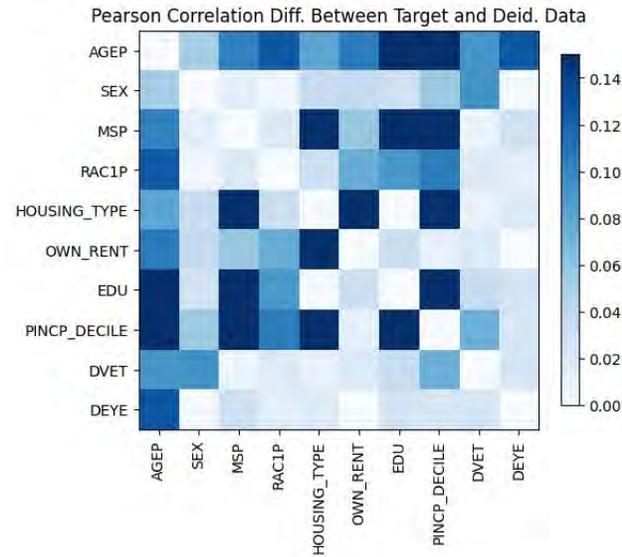


**Cell Suppression ( $k = 6$ )**

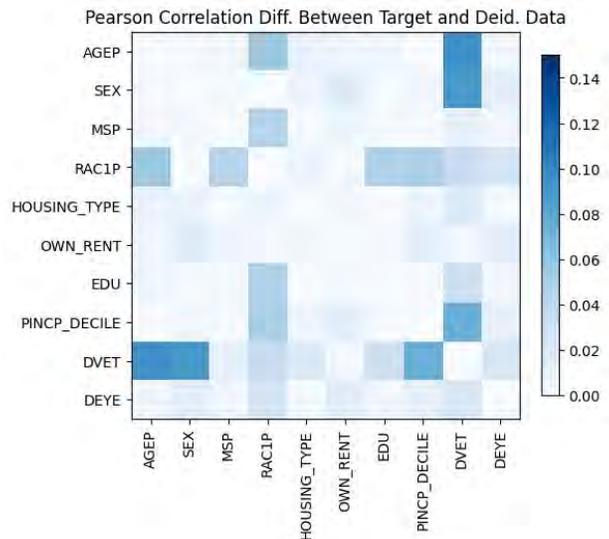
# Metrics: Pairwise Correlations



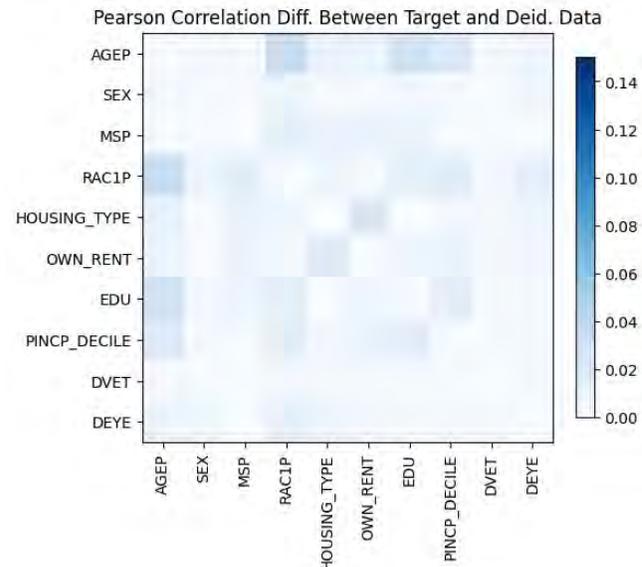
**Differential Private Histogram ( $\epsilon = 10$ )**



**PATECTGAN Differential Private GAN ( $\epsilon = 10$ )**



**CART-model Synthesis (non-DP synthetic)**



**Cell Suppression ( $\kappa = 6$ )**

**Pairwise Correlations:** A key goal of deidentified data is to preserve the feature correlations from the target data, so that analyses performed on the deidentified data provide meaningful insight about the target population. Which correlations are the deidentified data preserving, and which are being altered?

The [Pearson Correlation](#) difference was a popular utility metric during the [HLG-MOS Synthetic Data Test Drive](#). Note that darker highlighting indicates pairs of features whose correlations were not well preserved by the deidentified data.

**998**

Equivalent to a **90%** uniform random subsample of the input target data.

**Differential Private Histogram ( $\epsilon = 10$ )**

**805**

Less than a **1%** uniform random subsample of the input target data.

**PATECTGAN Differential Private GAN ( $\epsilon = 10$ )**

**984**

Equivalent to a **40%** uniform random subsample of the input target data.

**CART-model Synthesis (non-DP synthetic)**

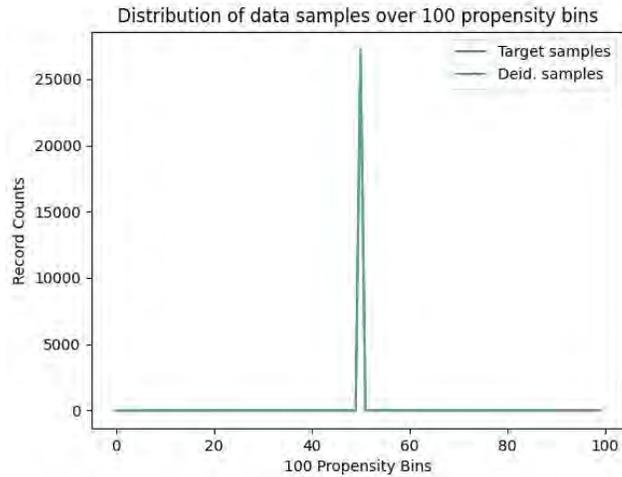
**977**

Equivalent to a **20%** uniform random subsample of the input target data.

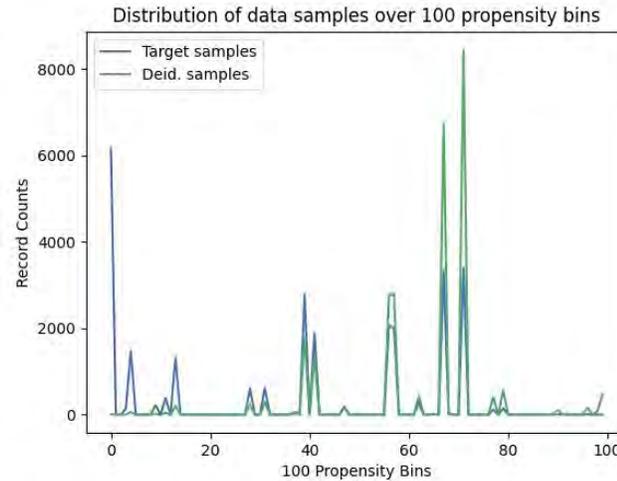
**Cell Suppression (k = 6)**

**K-marginal Similarity:** checks how far the shape of the deidentified data distribution has shifted away from the target data distribution, using many 3-dimensional snapshots of the data, averaging the density differences across all snapshots. It was developed as an efficient scoring mechanism for the NIST Temporal Data Challenges, and can be applied to measure the distance between any two data distributions. A score of 0 means zero overlap, while a score of 1000 means the two distributions match identically. More information can be found [here](#).

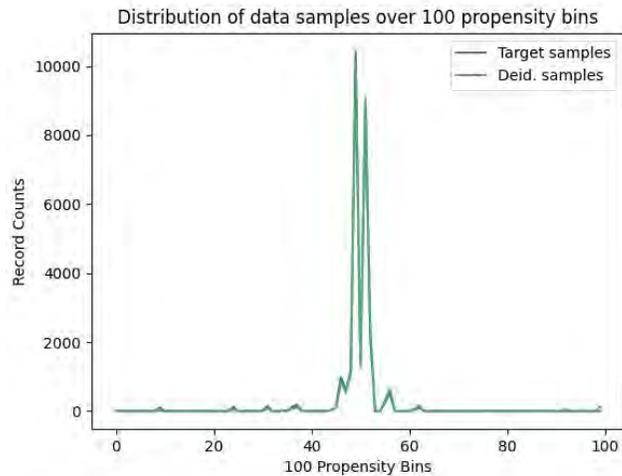
# Metrics: Propensity



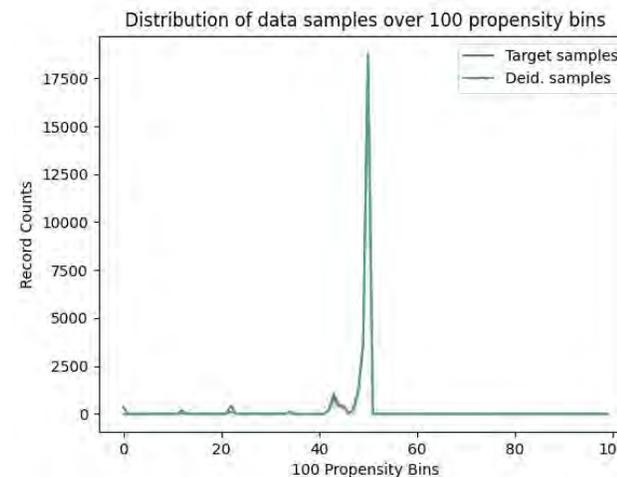
**Differential Private Histogram ( $\epsilon = 10$ )**



**PATECTGAN Differential Private GAN ( $\epsilon = 10$ )**



**CART-model Synthesis (non-DP synthetic)**

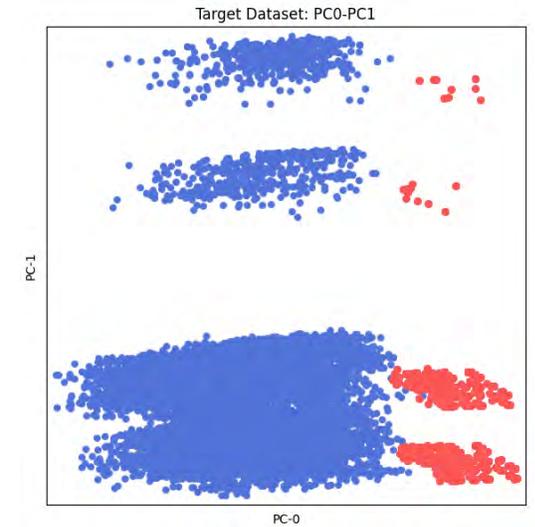
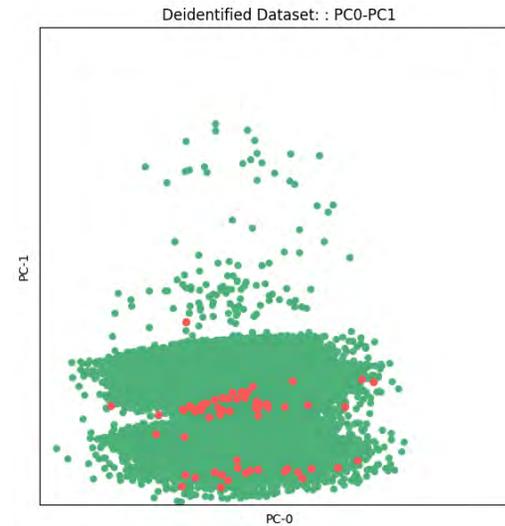
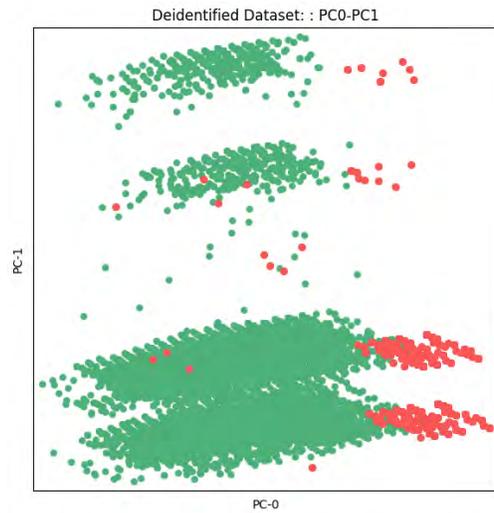


**Cell Suppression ( $k = 6$ )**

## Propensity Metrics:

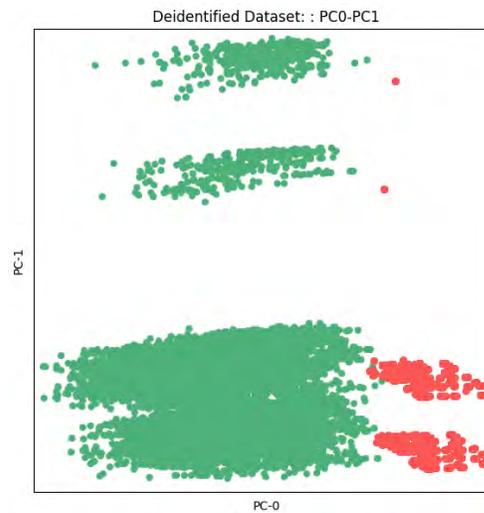
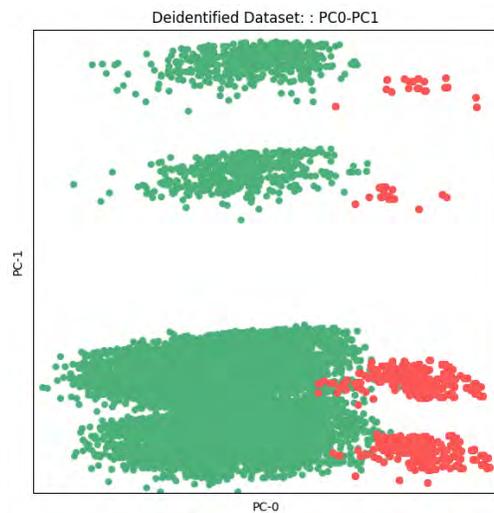
Can a decision tree classifier tell the difference between the target data and the deidentified data? If a classifier is trained to distinguish between the two data sets and it performs poorly on the task, then the deidentified data must not be easy to distinguish from the target data. If the green line matches the blue line, then the deidentified data is high quality. Propensity based metrics have been developed by [Joshua Snoke and Gillian Raab](#) and [Claire Bowen](#)

# Metrics: Pairwise PCA



**Differential Private Histogram ( $\epsilon = 10$ )**

**PATECTGAN Differential Private GAN ( $\epsilon = 10$ )**



**CART-model Synthesis (non-DP synthetic)**

**Cell Suppression ( $k = 6$ )**

**PCA Metric** visually compares a synthetic data set with the original input data. It plots high dimensional data as a 2D scatterplot using the first two principal component axes; each point represents an individual in the data. Good synthetic data should recreate the shape of the original data with new points (new synthetic individuals). The plot above shows the shape of the original sensitive data; the synthetic data generators are trying to reproduce this distribution. To display more detail, we've used **red points** to highlight records that represent **children** (MSP value = 'N')

# Metrics: Consistency Checks

| Inconsistency Group | Number of Records Inconsistent |
|---------------------|--------------------------------|
| Age                 | 17                             |
| Work                | 0                              |
| Housing             | 42                             |

**Differential Private Histogram ( $\epsilon = 10$ )**

| Inconsistency Group | Number of Records Inconsistent |
|---------------------|--------------------------------|
| Age                 | 517                            |
| Work                | 0                              |
| Housing             | 122                            |

**PATECTGAN Differential Private GAN ( $\epsilon = 10$ )**

**Age Inconsistencies:** These inconsistencies deal with the AGE feature; records with age-based inconsistencies might have children who are married, or infants with high school diplomas

**Work Inconsistencies:** These inconsistencies deal with the work and finance features — such as high incomes while being in poverty.

**Housing Inconsistencies:** Records with household inconsistencies might have more children in the house than the total household size, or be residents of group quarters (such as prison inmates) who are listed as owning their residences.

| Inconsistency Group | Number of Records Inconsistent |
|---------------------|--------------------------------|
| Age                 | 59                             |
| Work                | 0                              |
| Housing             | 0                              |

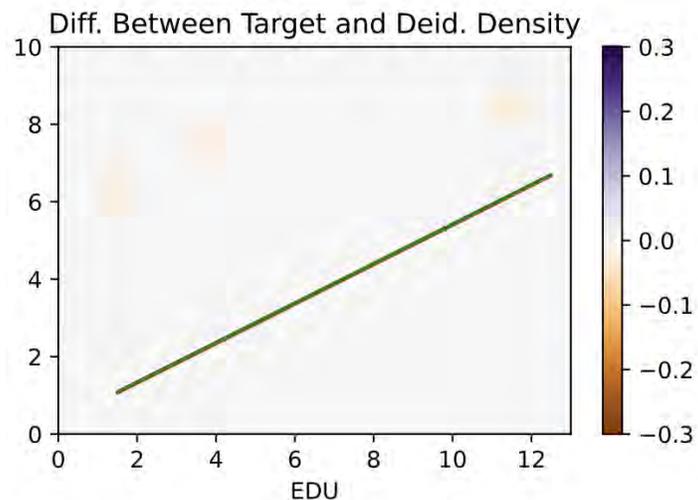
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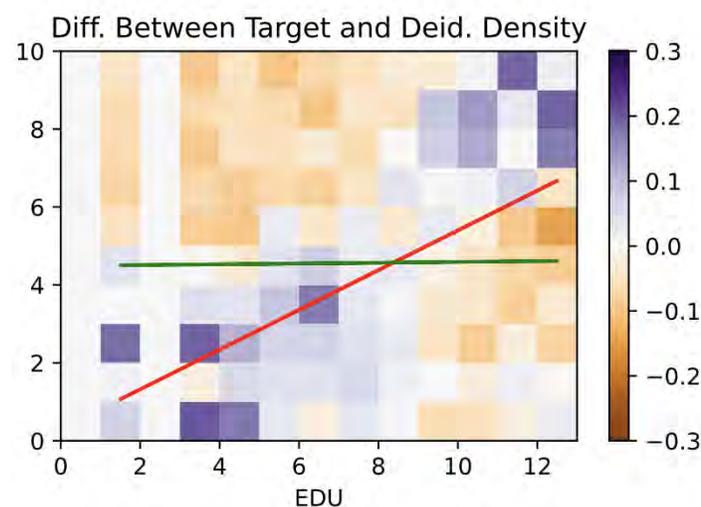
**Cell Suppression ( $k = 6$ )**

# Metrics: Unique Exact Match Rate

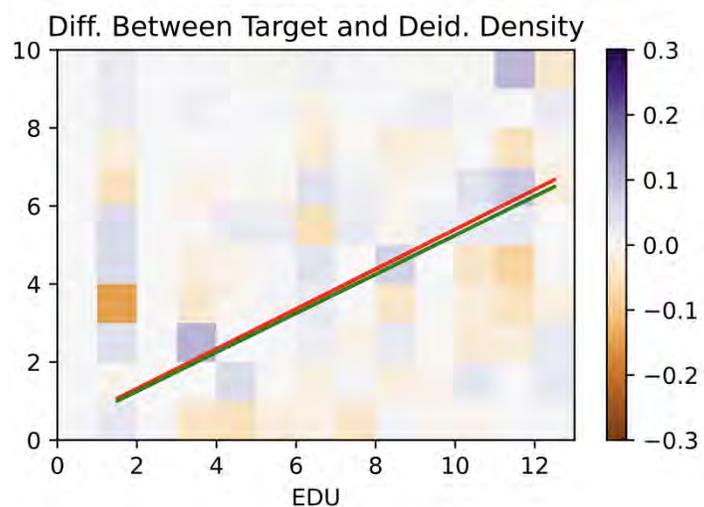
|   |   |  |
|---|---|--|
| <p>Percent of unique Target Data records exactly matched in Deid. Data:<br/><b>100%</b></p> <p><b>Differential Private Histogram (<math>\epsilon = 10</math>)</b></p> | <p>Percent of unique Target Data records exactly matched in Deid. Data:<br/><b>7.1%</b></p> <p><b>PATECTGAN Differential Private GAN (<math>\epsilon = 10</math>)</b></p> | <p><b>Unique Exact Match Rate:</b><br/>This is a count of unique records in the target data that were exactly reproduced in the deidentified data. Because these records were unique outliers in the target data, and they still appear unchanged in the deidentified data, they are potentially vulnerable to reidentification.</p> |
| <p>Percent of unique Target Data records exactly matched in Deid. Data:<br/><b>20.32%</b></p> <p><b>CART-model Synthesis (non-DP synthetic)</b></p>                   | <p>Percent of unique Target Data records exactly matched in Deid. Data:<br/><b>48.5%</b></p> <p><b>Cell Suppression (k = 6)</b></p>                                       |  |



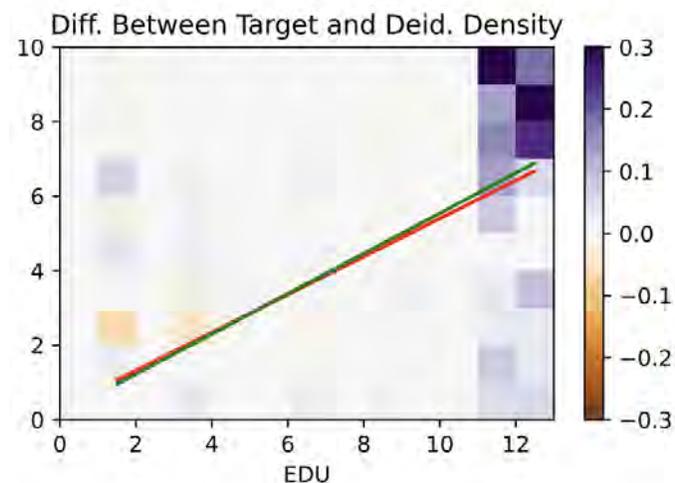
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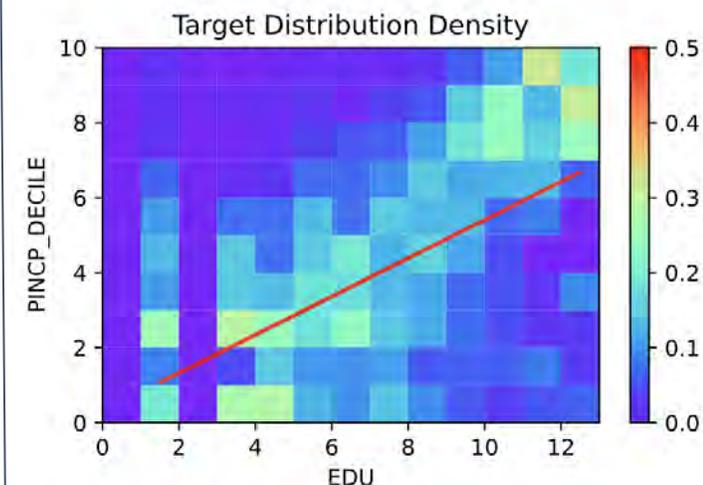
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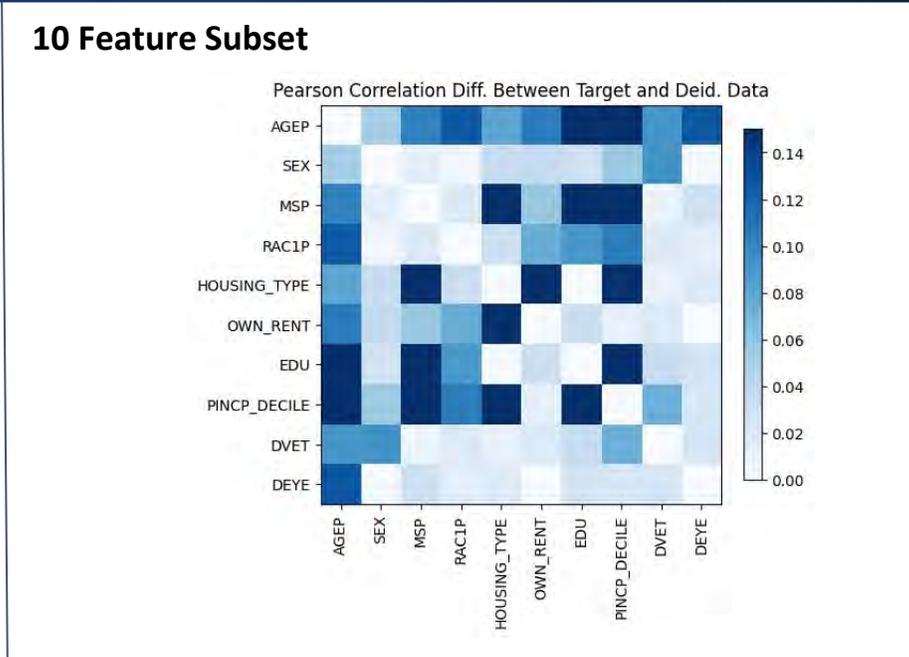
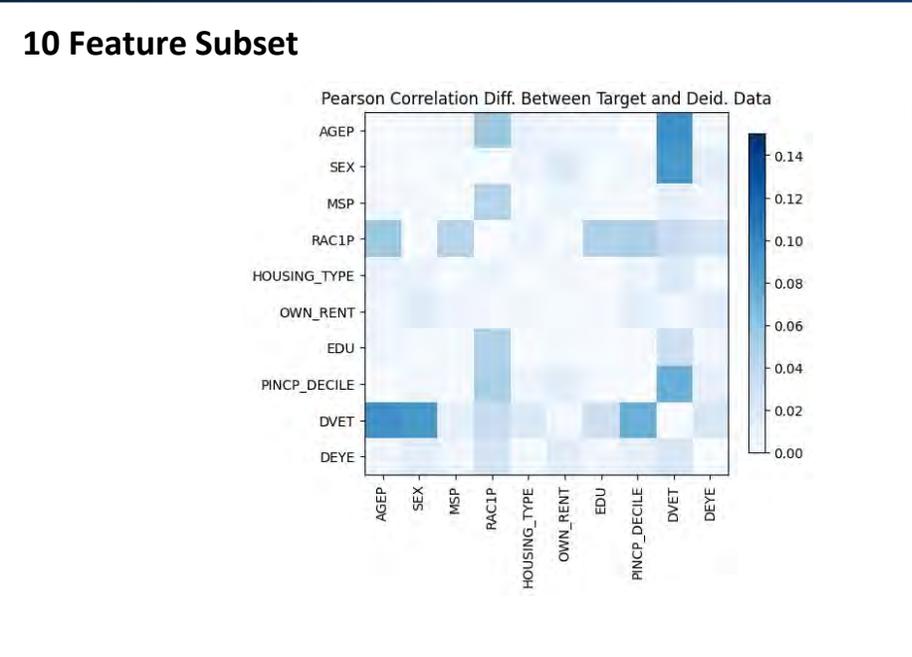
Cell Suppression ( $k = 6$ )



This data-specific metric looks at **linear regression** on adults (AGEP > 15) across two features: Income Decile and Educational Attainment. Higher values of EDU should lead to higher values of PINCP\_DECILE, however the relationship is different for different demographic subgroups.

Here we show how well the deidentified data preserves the distribution of black women, using a deviation heatmap: Purple indicates the deidentified data contains too few individuals in that area, brown indicates too many. The original target distribution is shown above in blue.

# What Happens on the Full Feature Set?: Pairwise Correlations



### 21 Features

**CART-model Synthesis (non-DP synthetic)**

### 21 Features

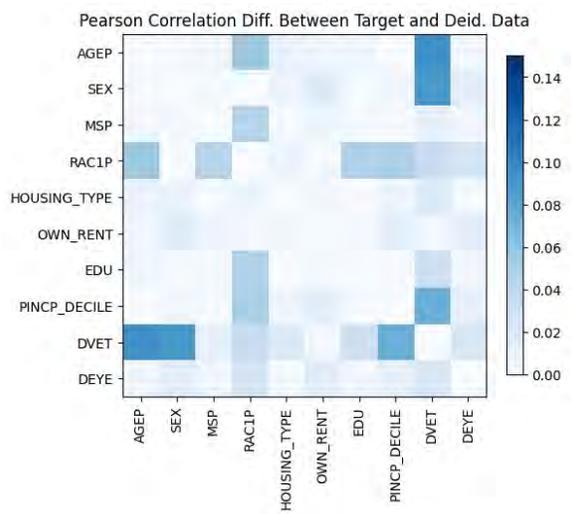
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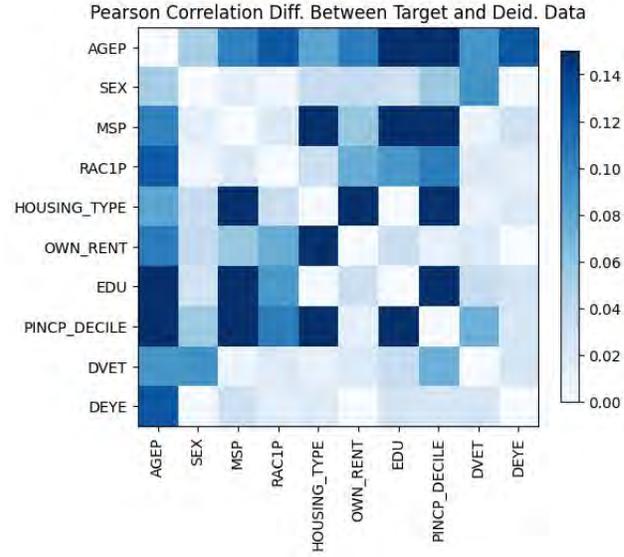
The [Pearson Correlation](#) difference was a popular utility metric during the [HLG-MOS Synthetic Data Test Drive](#). Note that darker highlighting indicates pairs of features whose correlations were not well preserved by the deidentified data.

# What Happens on the Full Feature Set?: Pairwise Correlations

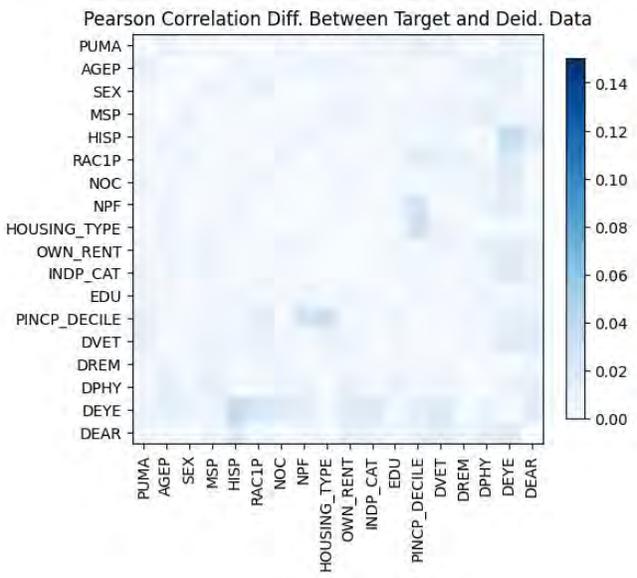
## 10 Feature Subset



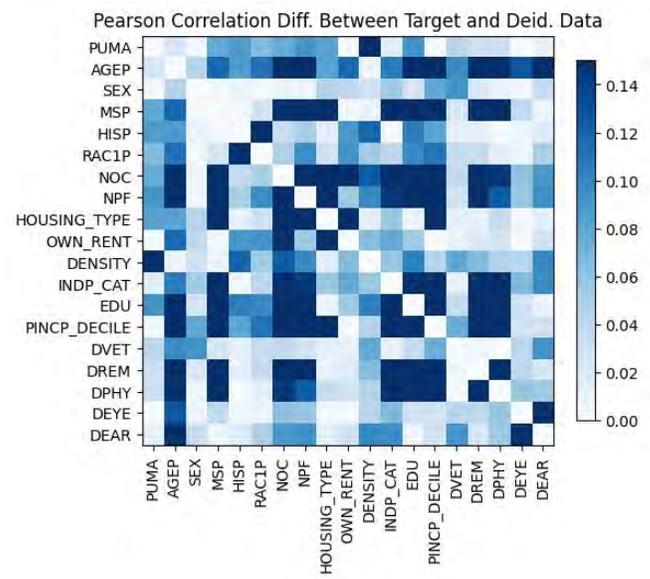
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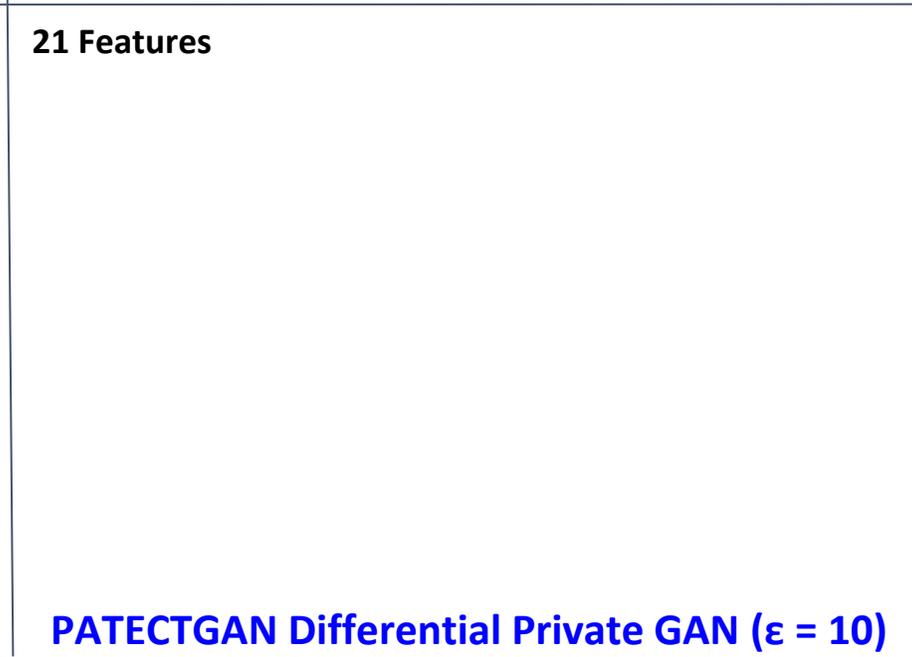
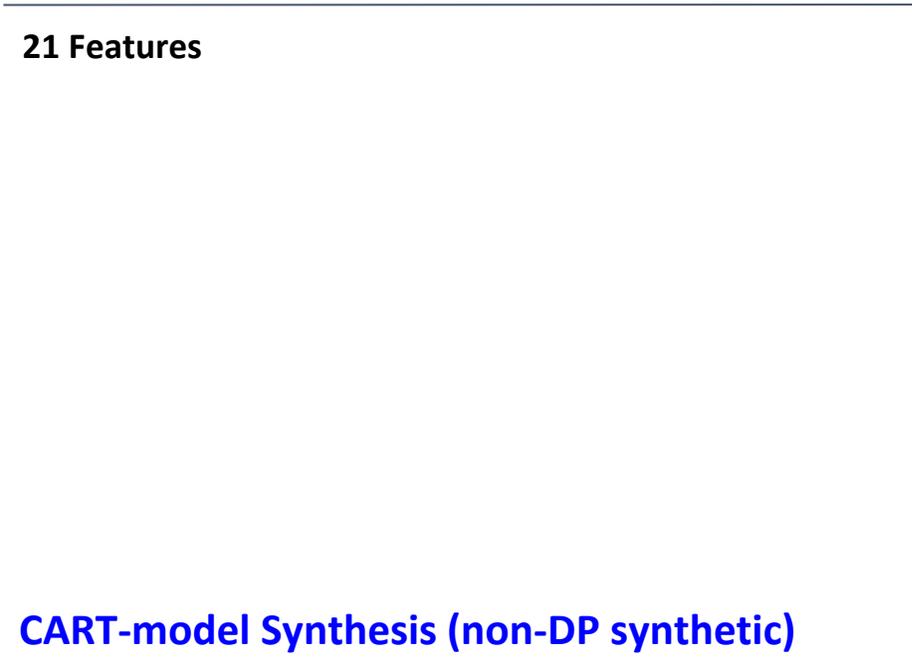
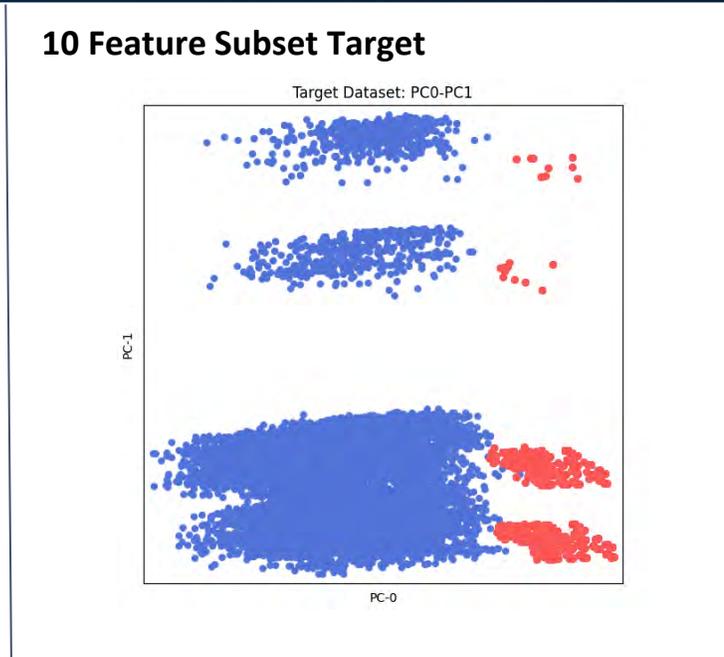
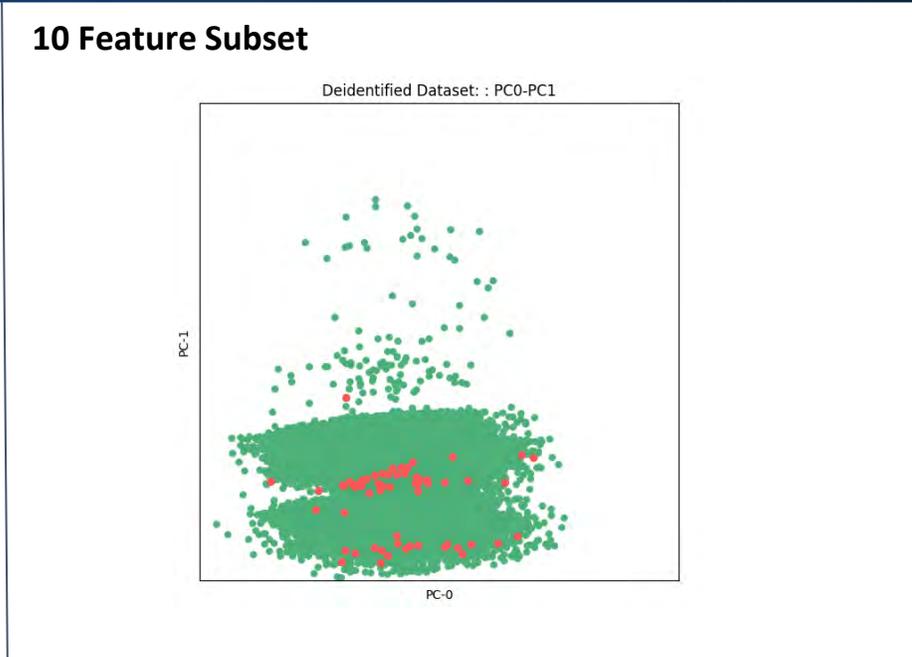
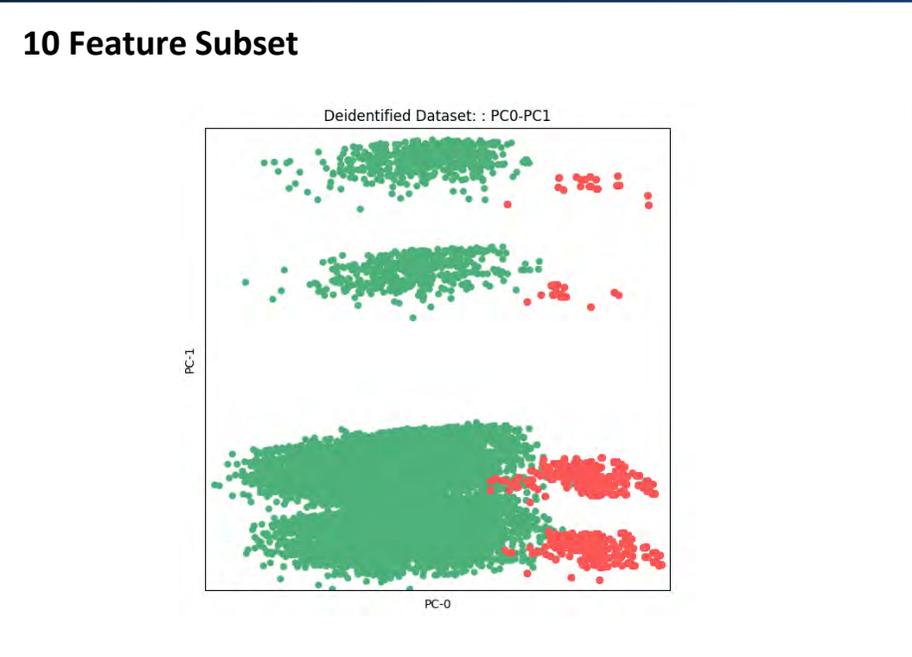
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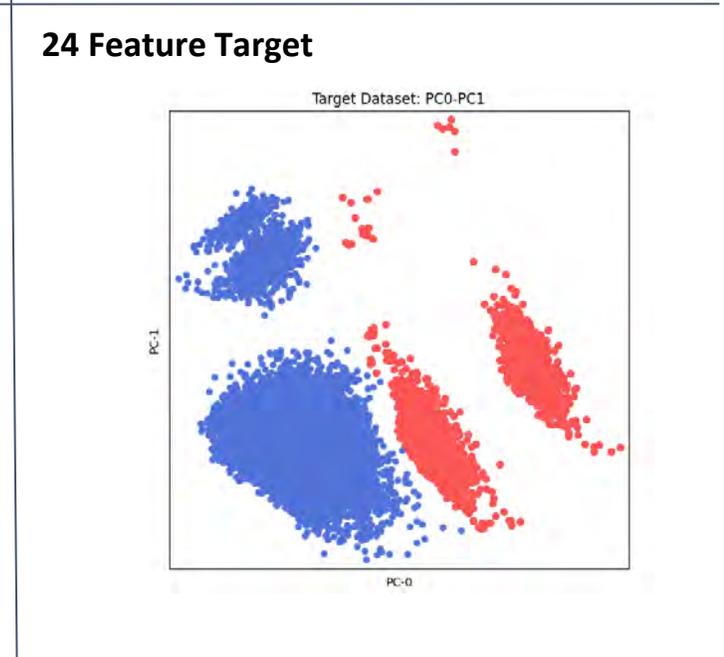
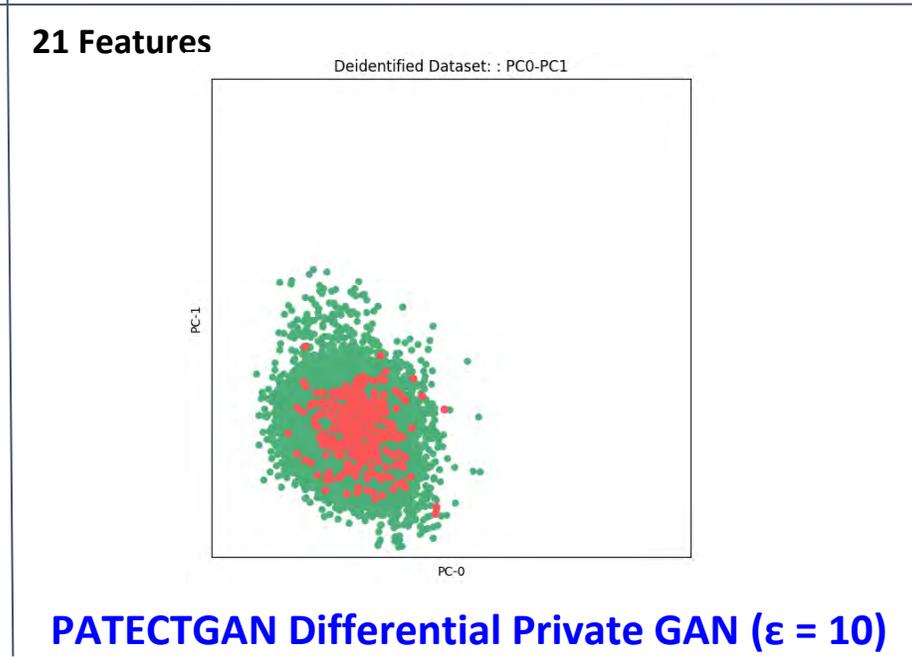
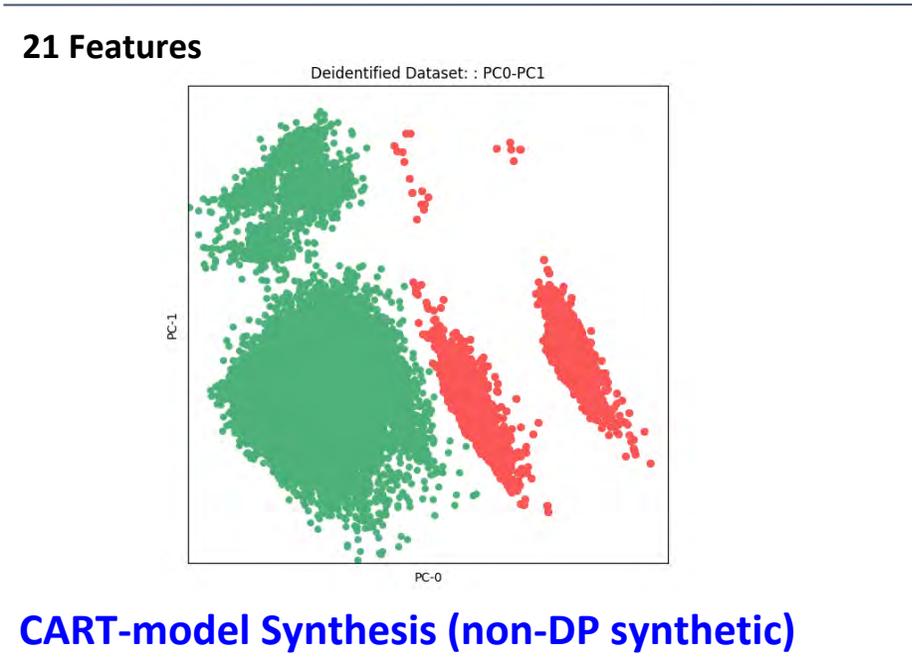
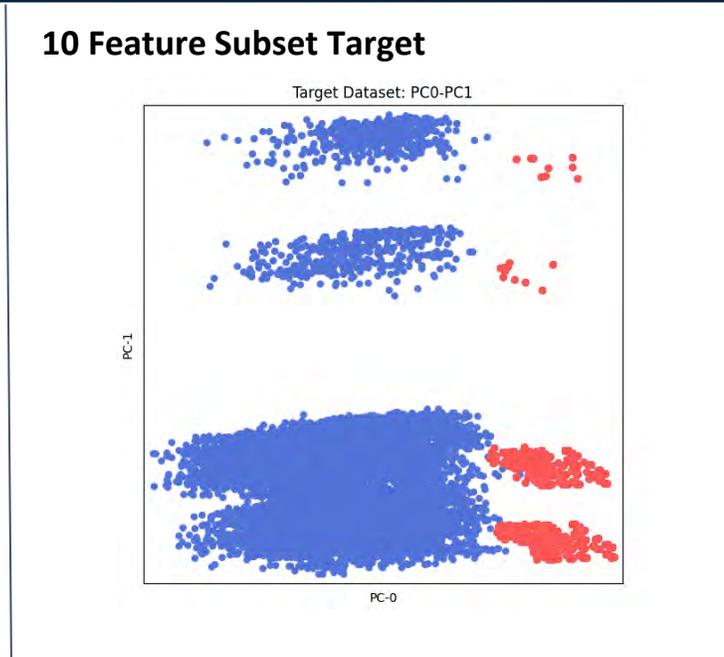
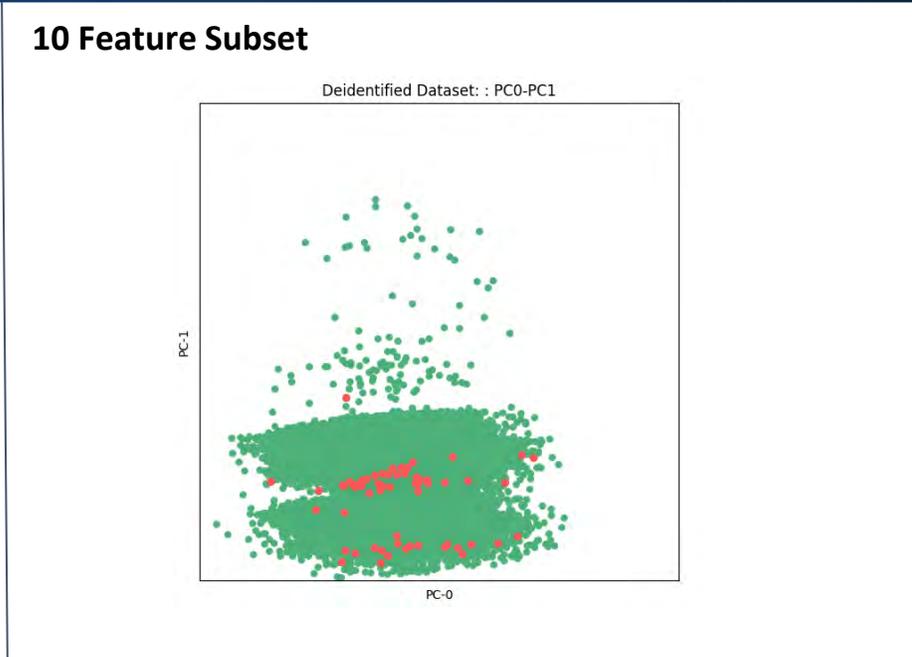
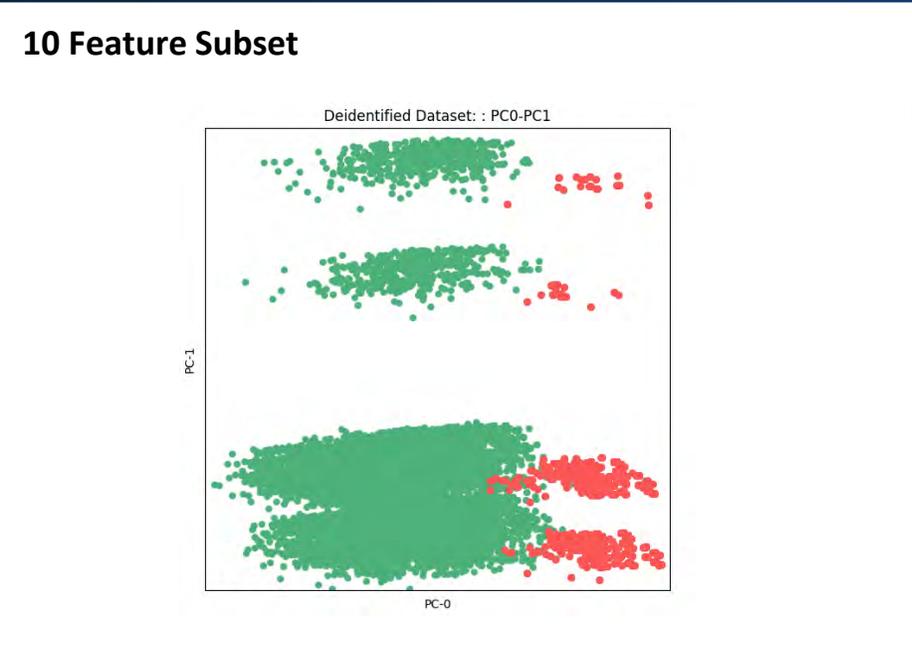
**Pairwise Correlations:** A key goal of deidentified data is to preserve the feature correlations from the target data, so that analyses performed on the deidentified data provide meaningful insight about the target population. Which correlations are the deidentified data preserving, and which are being altered?

The [Pearson Correlation](#) difference was a popular utility metric during the [HLG-MOS Synthetic Data Test Drive](#). Note that darker highlighting indicates pairs of features whose correlations were not well preserved by the deidentified data.

# What Happens on the Full 24 Feature Set?: Pairwise PCA



# What Happens on the Full 24 Feature Set?: Pairwise PCA



**CART-model Synthesis (non-DP synthetic)**

**PATECTGAN Differential Private GAN ( $\epsilon = 10$ )**

# What Happens on the Full 24 Feature Set?: UEM

|   |   |  |
|---|---|--|
| <p><b>10 Feature Subset</b></p> <p>Percent of unique Target Data records exactly matched in Deid. Data:<br/><b>20.32%</b></p>   | <p><b>10 Feature Subset</b></p> <p>Percent of unique Target Data records exactly matched in Deid. Data:<br/><b>7.1%</b></p>   | <p><b>Unique Exact Match Rate:</b><br/>This is a count of unique records in the target data that were exactly reproduced in the deidentified data. Because these records were unique outliers in the target data, and they still appear unchanged in the deidentified data, they are potentially vulnerable to reidentification.</p> |
| <p><b>21 Features</b></p> <p>Percent of unique Target Data records exactly matched in Deid. Data:<br/><b>2.4%</b></p> <p><b>CART-model Synthesis (non-DP synthetic)</b></p> | <p><b>21 Features</b></p> <p>Percent of unique Target Data records exactly matched in Deid. Data:<br/><b>0%</b></p> <p><b>PATECTGAN Differential Private GAN (<math>\epsilon = 10</math>)</b></p> |  |



[https://pages.nist.gov/privacy\\_collaborative\\_research\\_cycle/](https://pages.nist.gov/privacy_collaborative_research_cycle/)

The diagram illustrates the Collaborative Research Cycle as a continuous loop. At the top left is 'Research' with a magnifying glass icon. An arrow points to 'Engineering' at the top right with a gear icon. An arrow points to 'Engagement' at the bottom center with an icon of three people. An arrow points back to 'Research' from 'Engagement'. The background is a gradient from blue to green.

## Collaborative Research Cycle

Welcome to the homepage of the Collaborative Research Cycle (CRC), hosted by the [NIST Privacy Engineering Program](#)

- Home
- Participate
- Results Blog
- Techniques
- Archive & Tools
- How to Cite

# Collaborative Research Cycle

The CRC is an ongoing NIST program that provides resources for researching the behavior of deidentification (data privacy) on diverse populations.

Resources include:

- **Techniques Directory**
- Evaluation Reports
- Archive of Deidentified Data Samples

## Contents:

### Open Source:

- [SmartNoise MST](#)
- [SmartNoise MWEM](#)
- [SmartNoise PACSynth](#)
- [SmartNoise PATE-CTGAN](#)
- [RSynthpop-CART](#)
- [RSynthpop Catal](#)
- [RSynthpop IPF](#)
- [SDV Copula-GAN](#)
- [SDV CTGAN](#)
- [SDV TVAE](#)
- [SDV Gaussian Copula](#)
- [SDV FAST-ML](#)
- [Synthcity DPGAN](#)
- [Synthcity PATEGAN](#)
- [Synthcity adsgan](#)
- [Synthcity bayesian\\_network](#)
- [Synthcity privbayes](#)
- [Synthcity TVAE](#)
- [Sdcmicro PRAM](#)
- [Sdcmicro K-anonymity](#)

### Commercial Products:

- [MostlyAI-SD](#)
- [Sarus-SDG](#)

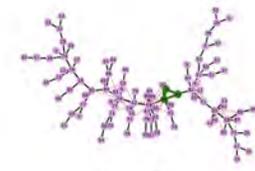
### SmartNoise MST

SmartNoise library implementation of MST, winner of the 2018 NIST Differential Privacy Synthetic Data Challenge. Data is generated from a differentially private PGM instantiated with noisy marginals. The structure of the PGM is a Maximum Spanning Tree (MST) capturing the most significant pair-wise feature correlations in the ground-truth data.

Library: [smartnoise-synth \(Python\)](#)  
Privacy: Differential Privacy

References:

- [SmartNoise MST Documentation](#)



[Mehanna 2019]

### SmartNoise MWEM

SmartNoise library implementation of MWEM. Algorithm initializes synthetic data with random values and then iteratively refines its distribution to mimic noisy query results on ground-truth data. The split\_factor parameter can be used to improve efficiency on larger feature sets. This approach satisfies differential privacy.

Library: [smartnoise-synth \(Python\)](#)  
Privacy: Differential Privacy

References:

- [SmartNoise MWEM Documentation](#)

**Inputs:** Data set  $D$  over a universe  $\mathcal{U}$ .  
Number of iterations  $T < \infty$ .  
Privacy parameter  $\epsilon > 0$ .

Let  $n$  denote  $|D|$ , the number of records in  $D$ .  
Let  $A_i$  denote a finite uniform distribution over  $D$ .  
For iteration  $t = 1, \dots, T$ :

1. **Exponential Mechanism:** Sample a query  $q$  in  $\mathcal{Q}$  using the Exponential Mechanism parameterized with equal value  $\frac{1}{2T}$  and the score function  $s(D, q) = \frac{1}{2T} \sum_{i=1}^n \mathbb{1}_{q(A_i)}$ .
2. **Laplace Mechanism:** Let measurement  $m_t = w(D) + \text{Lap}(T/\epsilon)$ .
3. **Multiplicative Weights:** Let  $A_t$  be a new finite distribution whose entries satisfy  $A_t(q) \propto A_i(q) \exp(q(D) + (m_t - q(A_i)) / (2\epsilon))$ .

**Output:**  $A = \text{mk}_{i=1}^T A_t$ .

[Hardt, Moritz and Liggett, Kalina and McSherry, Frank, 2014]

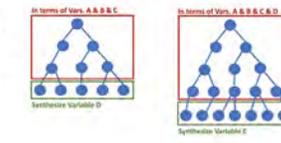
### RSynthpop CART

R Synthpop library implementation of fully conditional CART model-based synthesis (default synth function). New records are generated one feature at a time, using a sequence of decision trees that select plausible new values for each feature, based on the values synthesized for previous features. Data is synthetic, but not DP.

Library: [synthpop \(R\)](#)  
Privacy: Synthetic Data (Non-differentially Private)

References:

- [R Synthpop Documentation](#)



### RSynthpop Catal

Catal fits a saturated model by selecting a sample from a multinomial distribution with probabilities calculated from the complete cross-tabulation of all the variables in the data set. This is similar to DP-Histogram, but rather than using the noisy bin counts to directly generate the data, new records are sampled according to the probability distribution defined by the counts.

Library: [synthpop \(R\)](#)  
Privacy: Differential Privacy

References:

- [R Synthpop Catal Documentation](#)



# Collaborative Research Cycle

The CRC is an ongoing NIST program that provides resources for researching the behavior of deidentification (data privacy) on diverse populations.

Resources include:

- Techniques Directory
- **Evaluation Reports**
- Archive of Deidentified Data Samples

## Data Evaluation Report

Report created on: May 19, 2023 18:14:41

Created with [SDNIST v2.2.1](#)

### Data Description

#### Deidentified (Deid.) Data:

| Label Name     | Label Value             |
|----------------|-------------------------|
| Algorithm Name | pacsynth                |
| Library        | smartnoise-synth        |
| Feature Set    | family-focused          |
| Target Dataset | national2019            |
| Epsilon        | 10                      |
| Variant Label  | preprocessor-epsilon: 3 |
| Privacy        | Differential Privacy    |

| Property | Value                                |
|----------|--------------------------------------|
| Filename | pac_synth_e_10_family_focused_na2019 |
| Records  | 4579                                 |
| Features | 11                                   |

#### Target Data:

| Property | Value        |
|----------|--------------|
| Filename | national2019 |
| Records  | 27253        |
| Features | 24           |

# Collaborative Research Cycle

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## The NIST Collaborative Research Cycle (CRC) Research Acceleration Bundle v1.1

- [Direct download link for deidentified data and reports \(537 MB\)](#)
- [Direct download link for the metareports \(484 MB\)](#)

### Introduction

Welcome!

This repository contains deidentified data submitted to the CRC and their evaluation results as generated by SDNist v2.3.0. The [CRC homepage](#) provides more detailed information about the program, its goals, and how to participate.

In short, the CRC seeks to equip the research community with resources to explore, evaluate, and discuss deidentification approaches. The original data for this project are the [NIST Diverse Communities Excerpts](#), curated data drawn from the American Community Survey.

There are three ground truth partitions, corresponding to three geographic regions (Boston-area (ma), Dallas-Fort Worth Area (tx), and a national sample (national)). Submissions may include any or all of these partitions.

The original data contains 24 features. We also have a list of recommended reduced-size feature sets which can be found in the Excerpts Readme. Deidentified data may include any combination of feature set, though we have encouraged participants to use one of the recommended combinations to facilitate comparison of techniques.

### What do we have here?

This repository contains the results of the first round of submissions. Additional submissions will be added with the next drop (expected in July 2023). The repository contains the navigable structure for the entire bundle. You can find all of the compressed data in [Releases](#) or you can use the links at the top of this readme.

The `crc-data-and-metrics-bundle` file contains:

- All of the deidentified data submissions and their evaluation metric results in the current release of our archive,
- An `index.csv` file that tracks all submission metadata, algorithm properties and definitions,
- A comprehensive set of tutorial jupyter notebooks and utilities that teach users how to programmatically explore the archive using the index file, and

# Collaborative Research Cycle

The CRC is an ongoing NIST program that provides resources for researching the behavior of deidentification (data privacy) on diverse populations.

Resources include:

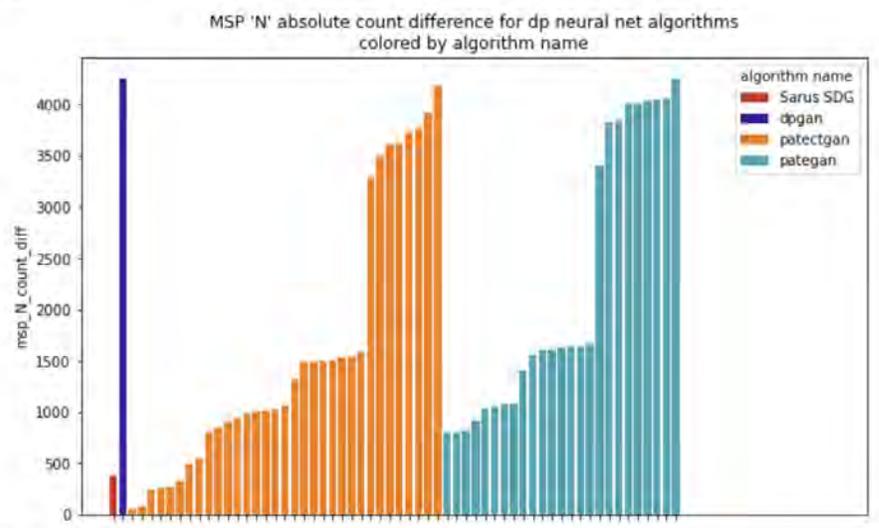
- Techniques Directory
- Evaluation Reports
- **Archive of Deidentified Data Samples**

| Library          | Algorithm        | Team                  | #Entries | #Feature sets | Avg. Feat. Space Size | $\epsilon$  | Utility: SsE | Privacy Leak: UEM |
|------------------|------------------|-----------------------|----------|---------------|-----------------------|-------------|--------------|-------------------|
| rsynthpop        | ipf_NonDP        | Rsynthpop-categorical | 1        | 1             | 3.405e+08             |             | 50.0         | 15.82             |
| rsynthpop        | catall_NonDP     | Rsynthpop-categorical | 1        | 1             | 2.270e+08             |             | 50.0         | 63.37             |
| subsample_40pcnt | subsample_40pcnt | CRC                   | 15       | 5             | 4.363e+25             |             | 40.67        | 39.93             |
| rsynthpop        | cart             | CRC                   | 12       | 4             | 3.457e+20             |             | 40.0         | 16.14             |
| sdcmicro         | pram             | CRC                   | 12       | 3             | 9.747e+10             |             | 38.33        | 56.27             |
| MostlyAI SD      | MostlyAI SD      | MOSTLY AI             | 6        | 1             | 1.891e+26             |             | 30.0         | 0.01              |
| rsynthpop        | catall           | Rsynthpop-categorical | 6        | 1             | 2.270e+08             | 1, 10, 100  | 22.33        | 47.24             |
| rsynthpop        | cart             | CBS-NL                | 3        | 1             | 2.270e+08             |             | 21.67        | 28.6              |
| tumult           | DPHist           | CRC                   | 5        | 2             | 5.732e+07             | 1, 2, 4, 10 | 18.8         | 92.14             |
| smartnoise-synth | mst              | CRC                   | 36       | 5             | 3.781e+25             | 1, 5, 10    | 14.03        | 6.8               |
| Genetic SD       | Genetic SD       | DataEvolution         | 19       | 2             | 9.454e+25             | 1, 10       | 11.84        | 0.11              |
| LostInTheNoise   | MWEM+PGM         | LostInTheNoise        | 1        | 1             | 5.178e+26             | 1           | 10.0         | 0.0               |
| synthcity        | bayesian_network | CRC                   | 12       | 4             | 5.672e+25             |             | 7.17         | 17.86             |
| subsample_5pcnt  | subsample_5pcnt  | CRC                   | 4        | 4             | 1.295e+26             |             | 5.0          | 4.97              |
| Sarus SDG        | Sarus SDG        | Sarus                 | 1        | 1             | 2.270e+08             | 10          | 5.0          | 13.99             |
| sdv              | ctgan            | CBS-NL                | 6        | 1             | 1.891e+26             |             | 4.33         | 0.0               |

# NIST Collaborative Research Cycle: Far more than four algorithms

Meta-analysis notebooks and tools available on the NIST CRC site make it easy to explore the archive

Introduction Tutorial:

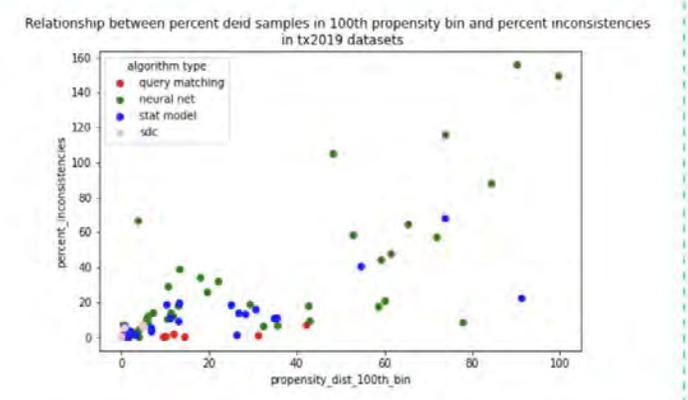


We teach all the [basics](#) for performing meta-analysis on the deidentified data archive:

1. Setup notebook.
2. Load deid datasets index file (index.csv).
3. Select specific deid. datasets from the index dataframe.
4. Working with the deidentified data csv files.
5. Working with the target data csv files.
6. Compare target and deid datasets.
7. Use index.csv to highlight plots by algorithm properties.
8. Access SDNIST evaluation reports.
9. Show relationship between two evaluation metrics.
10. Identify specific data samples of interest.
11. Show images from SDNist evaluation reports.
12. Get evaluation metrics for specific samples of interest.

Example Notebook 2: Imposter plot (propensity scores and inconsistencies).

We show how to collect the counts of individuals in the 100% confidence propensity bin (obviously synthetic records, 'imposters') across all deidentified data submissions. We then provide a scatterplot comparing imposter count with inconsistencies count. This notebook demonstrates accessing metrics in report.json files and metric result .csv files, and using the CRC plotting utility to make highlighted scatter plots.



Example Notebook 3: Race distribution

We show how to check deidentification impact on race distribution by directly counting individuals in the target and deidentified data csv files. We filter the index.csv metadata to print a data frame containing this score alongside relevant algorithm properties.

| library name | algorithm name   | algorithm type  | target dataset | privacy category | epsilon | feature set name | race_edit_distance_percent        |        |
|--------------|------------------|-----------------|----------------|------------------|---------|------------------|-----------------------------------|--------|
| 241          | syntholly        | sdgan           | neural net     | ma2019           | non_dp  | NaN              | industry-focused                  | 14.38  |
| 224          | subsample_40pct  | subsample_40pct | sdg            | national2019     | sdg     | NaN              | all-features                      | 0.61   |
| 67           | sdmetrics        | kanonymity      | sdg            | tx2019           | sdg     | NaN              | demographic-focused               | 24.56  |
| 178          | smartnoise-synth | piacynth        | query matching | tx2019           | dp      | 5.0              | demographic-focused               | 28.72  |
| 72           | sdmetrics        | kanonymity      | sdg            | tx2019           | sdg     | NaN              | industry-focused                  | 31.16  |
| 85           | sdv              | copula-gan      | neural net     | ma2019           | non_dp  | NaN              | custom-features-23                | 88.43  |
| 185          | smartnoise-synth | mieem           | query matching | national2019     | dp      | 10.0             | custom-features-12                | 1.09   |
| 274          | syntholly        | patagan         | neural net     | national2019     | dp      | 1.0              | all-features                      | 22.86  |
| 281          | syntholly        | patagan         | neural net     | tx2019           | dp      | 10.0             | all-features                      | 5.13   |
| 121          | smartnoise-synth | mst             | stat model     | ma2019           | dp      | 1.0              | demographic-focused               | 1.47   |
| 288          | syntholly        | privbyte        | stat model     | national2019     | dp      | 1.0              | demographic-focused               | 43.08  |
| 132          | smartnoise-synth | mst             | stat model     | national2019     | dp      | 10.0             | demographic-focused               | 0.05   |
| 320          | turnoff          | DPHfit          | histogram      | national2019     | dp      | 1.0              | demographic-focused-accept-AGESEX | 113.01 |
| 229          | subsample_40pct  | subsample_40pct | sdg            | tx2019           | sdg     | NaN              | all-features                      | 1.82   |
| 306          | syntholly        | privbyte        | stat model     | tx2019           | dp      | 1.0              | industry-focused                  | 0.86   |
| 8            | Genetic SD       | Genetic SD      | query matching | national2019     | dp      | 1.0              | all-features                      | 4.45   |
| 137          | smartnoise-synth | mst             | stat model     | national2019     | dp      | 10.0             | family-focused                    | 0.18   |

## Pair-wise PCA Inspection

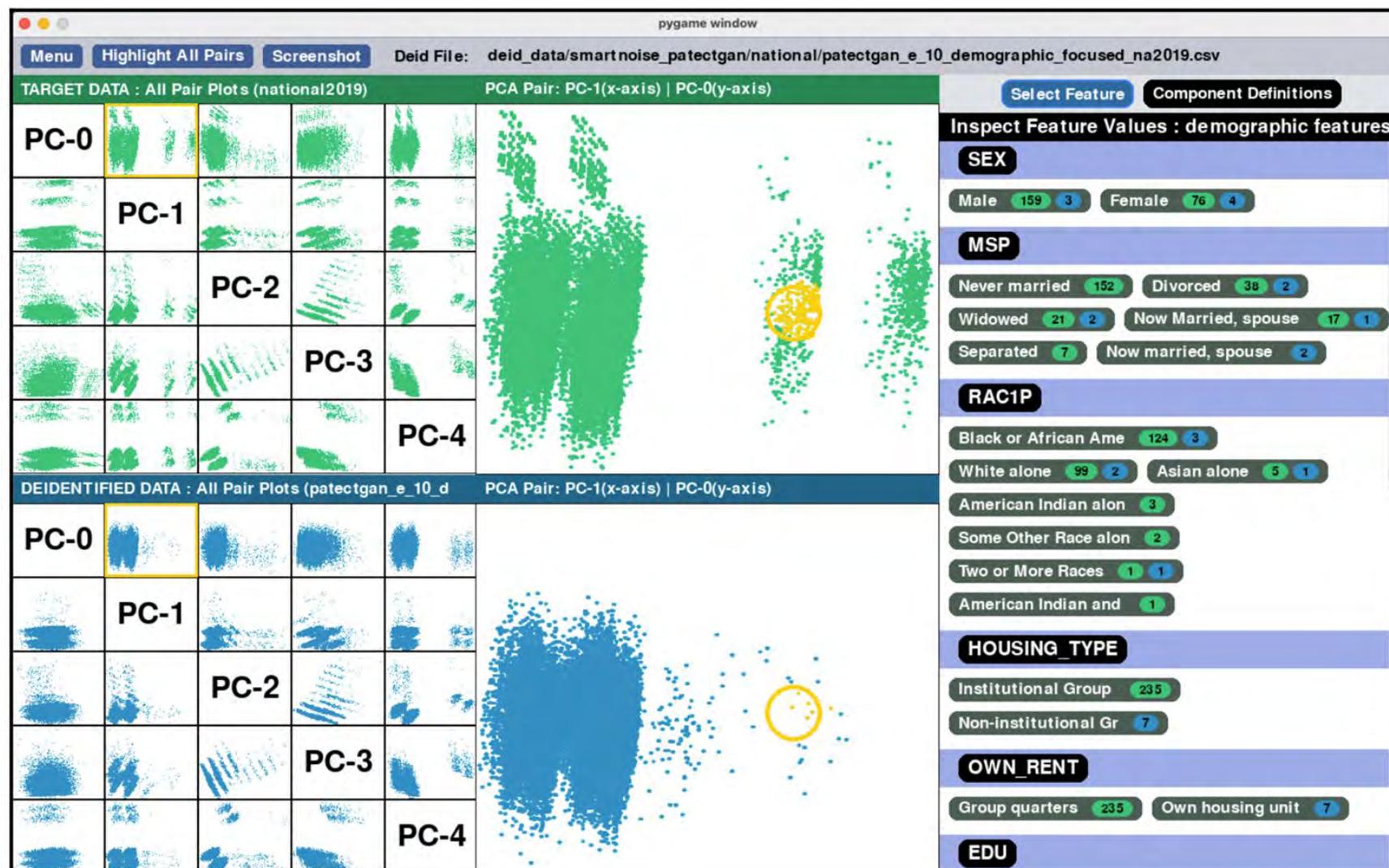
### Tool

Pairwise PCA is a relatively new visualization metric that was introduced by the [IPUMS International team](#) during the HLG-MOS Synthetic Data Test Drive.

It lets us look at the high dimensional data distribution using a set of 2D scatterplots along [principle component axes](#). The plots look at the deidentified data and target data from the same angle (ie, using axes from the target data), so we can directly see where their distributions differ from each other.

The pairwise PCA tool lets you interactively explore these plots using a GUI interface.

You can install it by following the directions here: [https://github.com/usnistgov/pair-wise\\_PCA](https://github.com/usnistgov/pair-wise_PCA)



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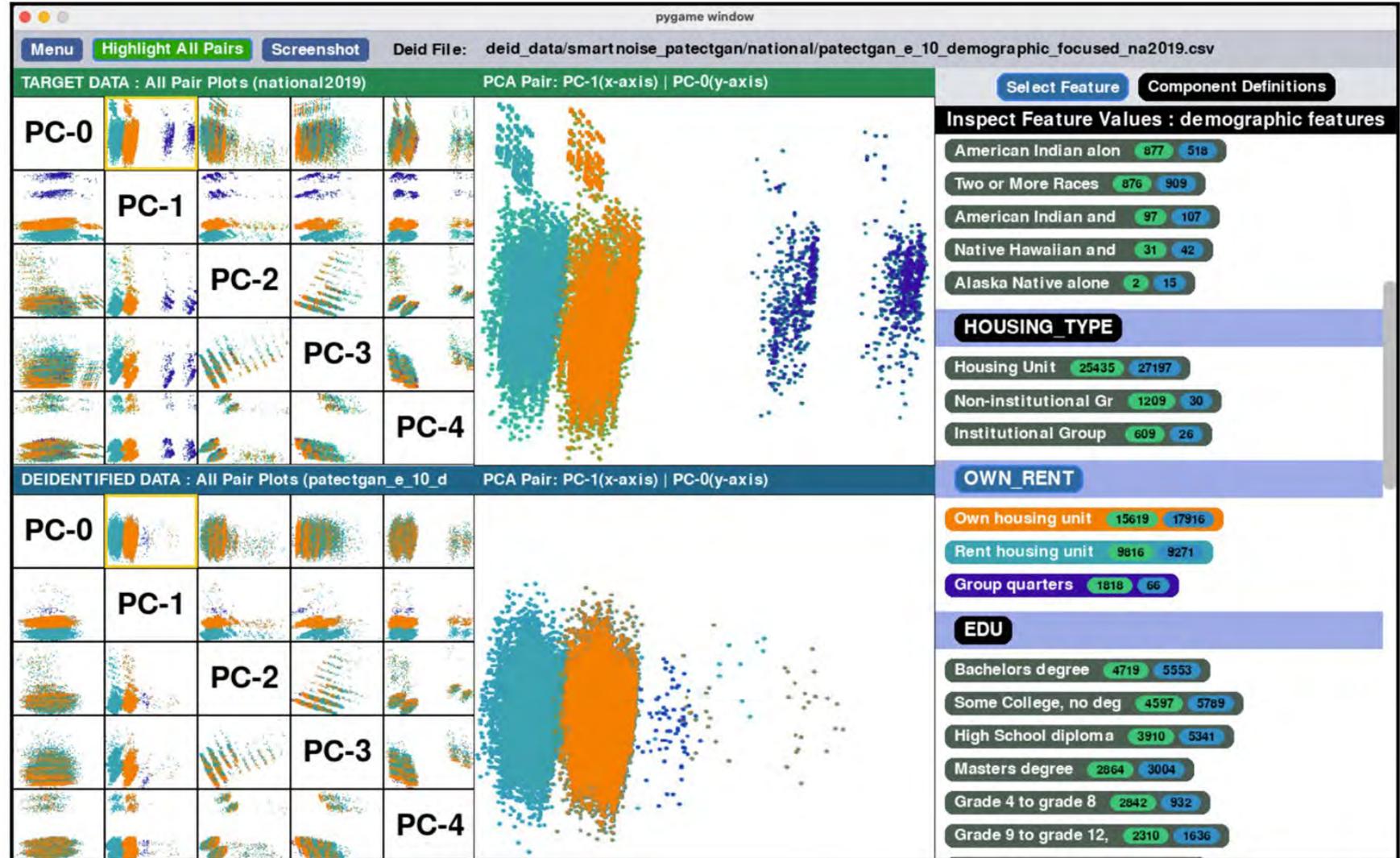
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# Collaborative Research Cycle (CRC) Strategy

- 12-month program that collects, disseminates, and analyzes synthetic data
- No prize money, low barrier to participation, emphasizes cooperation

## Exploratory Phase (Feb. 2023 - July. 2023)

- NIST releases Diverse Community Excerpt Data
- Participants submit de-identified data and abstract on techniques
- NIST releases machine readable analysis of submissions (*acceleration bundle*)

## Explanatory Phase (July. 2023 - Dec. 2023)

- Participants perform meta-analysis on the acceleration bundle.
- NIST hosts a seminar series and conducts outreach
- Participants submit papers on their analyses Nov 17th 2023
- NIST hosts conference Dec. 18 2023



# Thank you! Questions?

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google keywords: NIST collaborative research cycle  
or NIST CRC

