Epistemic Parity: Reproducibility as an Evaluation Metric for Differential Privacy

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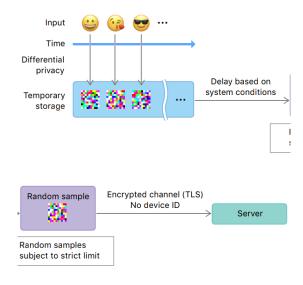


Pervasively Deployed DP Mechanisms

Big Tech Uses DP with all your data!

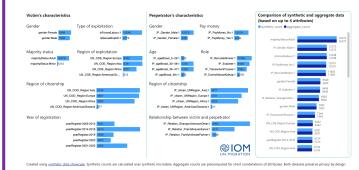


Emoji Suggestions + Health Type Usage



Microsoft

Global victim-perpetrator synthetic dataset

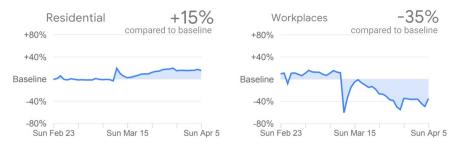


US Broadband Coverage Dataset

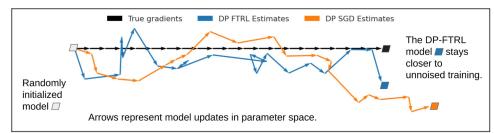




Community Mobility Reports



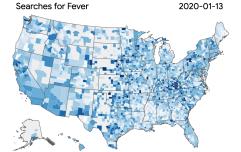
Next-word prediction model on Gboard



https://desfontain.es/privacy/real-world-differential-privacy.html

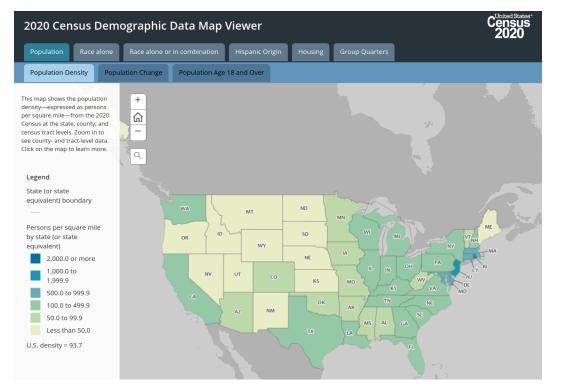


Search Trends Symptoms



Pervasively Deployed DP Mechanisms

And so does the U.S. Government...



2020 Census Redistricting Data

- A lot of these deployments rely on variations of **DP Synthetic Data**
- DP for the Census was met with resistance among many in the research community. They claim DP noise:
 - Affects demographic totals [Ruggles 2019]
 - Exacerbates underrepresentation of minorities [Ganev et. al 2021, Kenny et. al 2021]
- However, DP is still probably better than swapping in terms of the privacy/utility tradeoff [Christ et al 2022]



A Proposed Benchmark

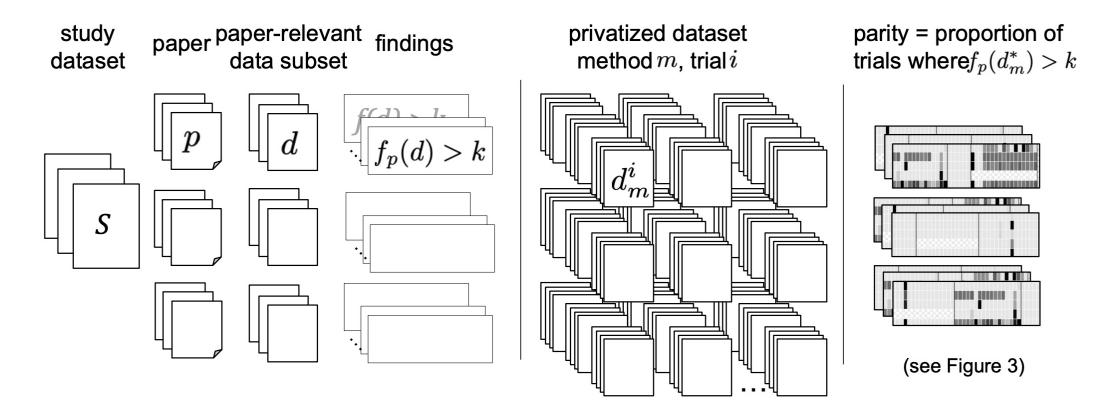
- Major challenge: **Evaluation!**
- How do we **convincingly** evaluate DP synthetic data?
 - Social scientists and practitioners don't trust *random linear query* workloads
 - Open questions: how do these synthesizers perform on a variety of data? What are their limitations?

• SynRD: An "Epistemic Parity" Benchmark

- 1. Avoid assumptions about the representativeness of proxy tasks!
- 2. Instead, measure likelihood that published conclusions (like those run on Census data) would *change had the authors used DP synthetic data*.
- 3. Make this an accessible benchmark and choose the "published conclusions" to be real, high-quality papers on impactful studies



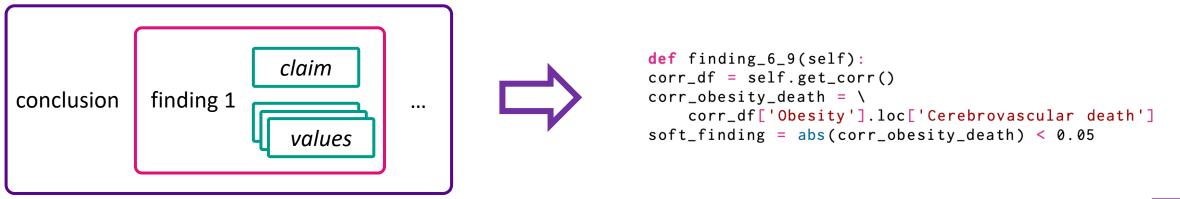
SynRD: Benchmark for Evaluating "Epistemic Parity"





Challenge: Taxonomy over findings

- Problem with operationalizing "Epistemic Parity:" many scientific findings/conclusions are semantic!
- Solution: principled taxonomy over language of scientific literature (inspired by Cohen et. al, 2018)
- Means we can realize taxonomy (we do this in python)





Challenge: significance of results

- Correctly done, experimental science relies on significance testing
- How does this work with DP synthetic data?
- Rubin's Rules for calculating uncertainty over results of synthetic data
 - (over estimated locations q_1, ...q_m and variances v_1, ...v_m)

$$\hat{q} = \frac{1}{m} \sum_{i=1}^{m} q_i$$

$$\hat{v} = \frac{1}{m} \sum_{i=1}^{m} v_i$$

$$b = \frac{1}{m-1} \sum_{i=1}^{m} (q_i - \hat{q})^2$$

$$T = \left(1 + \frac{1}{m}\right) b - \hat{v},$$

$$df = \left(1 - \frac{1}{1 + \frac{1}{m}} \frac{\hat{v}}{b}\right)^2 (m-1).$$

• Problem: Crucially relies on a normality assumption for each τ (X_i) = q_i

Solution: simplify finding statistics!

1. Findings are simply "reproduced or not"

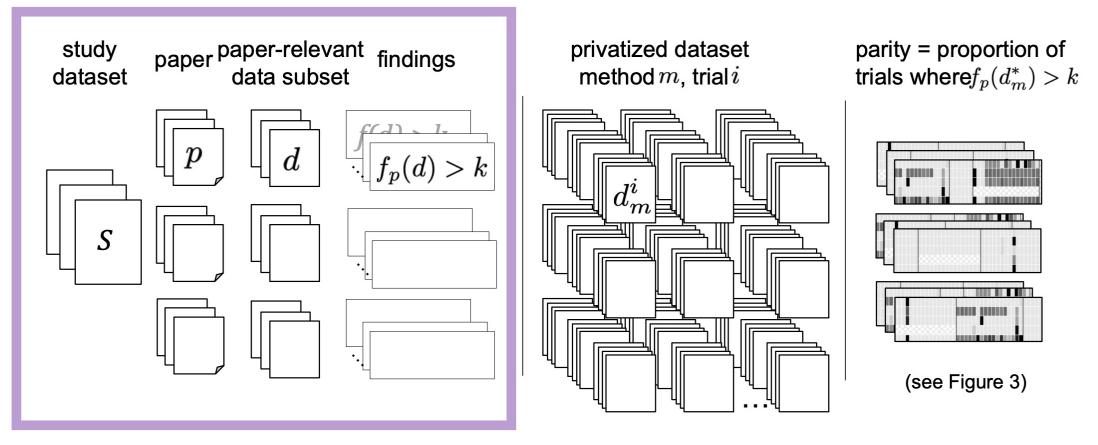
$$finding(\tau, q_i^{synth}, q_i^{real}) = \mathbb{1}[|\tau(q_i^{synth}) - \tau(q_i^{real})| \le \alpha]$$

- Source of randomness 1 Synthetic draw from fixed synthesizer
 Solution: Bootstrap over *B* samples from synthesizer (*B* is `big,' > 25).
- Source of randomness 2 fitting synthesizer (expensive!).
 Solution: Fit as many synthesizers as we can, aggregate and caveat that variance is underreported.

Thus, we report on the uncertainty relative to the real finding of the synthetic one, bootstrapping to estimate variance.



SynRD Composition





Four Studies => 8 Papers

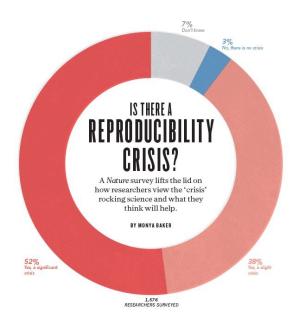
Studies

- HSLS:09 (High School Longitudinal Study)
- ACL (Americans Changing Lives Survey)
- AddHealth (National Study of Adolescent and Adult Health)
- **NSDUH** (National Survey on Drug Use and Health)

8 Papers (8 different journals)

- Variety of methodologies
- Strict criteria for selection
- Reproducibility is hard!

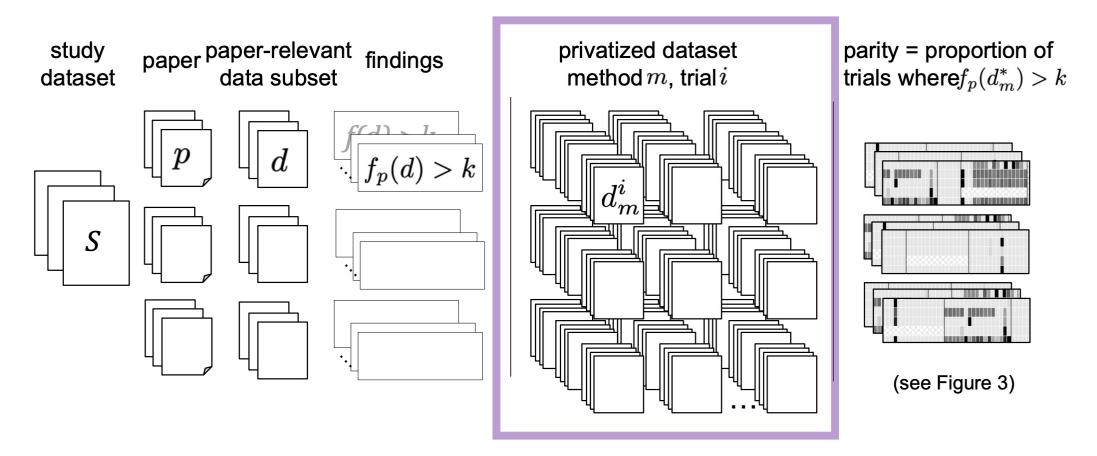
	Descriptive Statistics	8
Regression	Between-Coefficients	4
	Fixed Coefficient (Sign)	2
	Variability	1
Causal Paths	Interaction	1
	Coefficient Difference	19
Logistic Regression	PBR	2
	FNR	2
	FPR	2
	Accuracy	2
Mean Difference	Between-Class	24
	Temporal (FC)	26
Correlation	Pearson	12
Correlation	Spearman	1



Most scientists agree, reproducible science isn't as common as it should be (Baker, Nature 2016)



SynRD Composition





Five Synthesizers => 4 ϵ regimes

Synthesizers

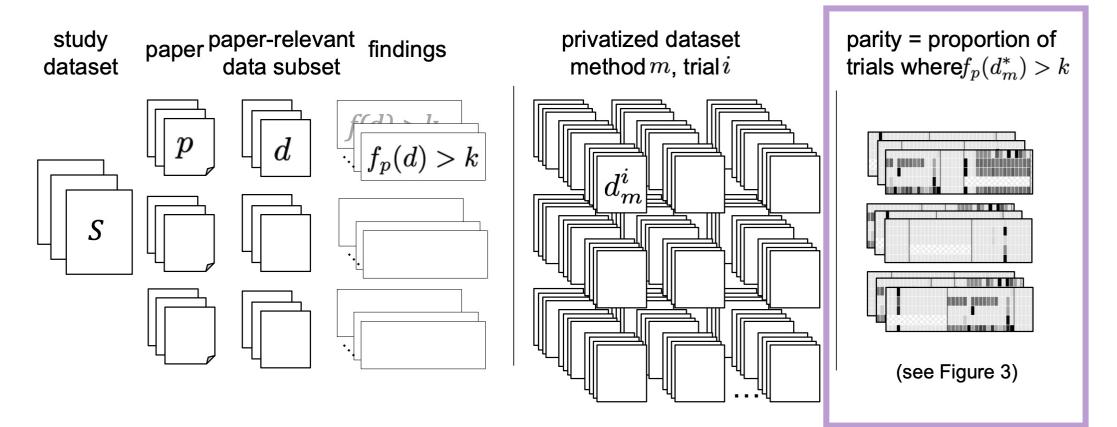
	Budget-aware	Workload-aware	Data- aware	Efficiency-aware	Type?
PrivBayes	\star		\star	\star	Bayesian
MST			\star	*	Marginal (PGM)
PATECTGAN	*		\star		GANs (Neural)
PrivMRF	*		\star	*	Marginal (PGM)
AIM	*	\star	*	*	Marginal (PGM)

ε = [e[^]-1, e[^]0, e[^]1, e[^]2]

- Here, e is scientific constant e (~2.72)
- Representative of "low to medium privacy" (informally)



SynRD Composition



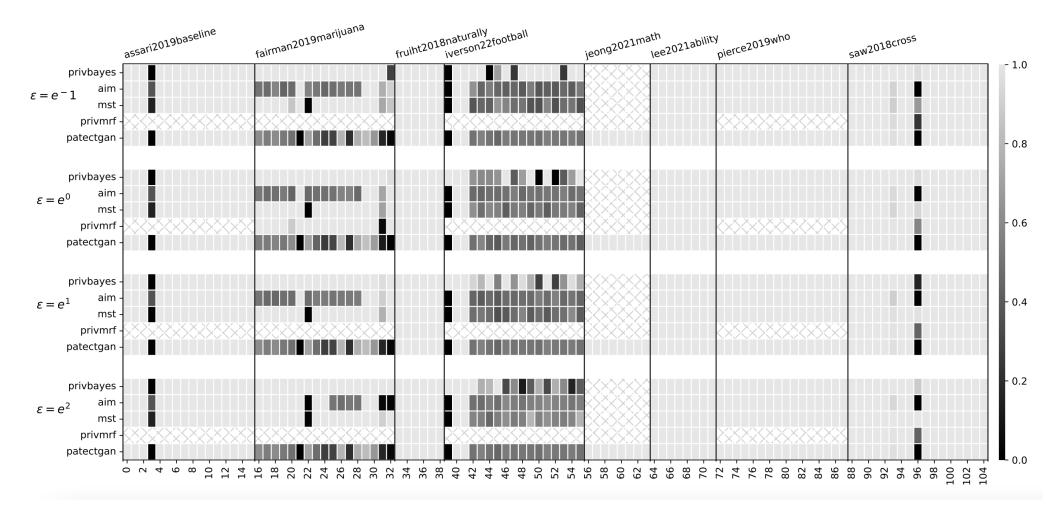


The benchmark!

```
from SynRD.papers import Saw2018Cross
from SynRD.benchmark import Benchmark
from SynRD.synthesizers import MSTSynthesizer
benchmark = Benchmark()
B = 25 # Bootstrap parameter
synth = MSTSynthesizer(epsilon=1.0)
papers = benchmark.initialize_papers([Saw2018Cross])
for paper in papers:
    synth.fit(paper.real_dataframe)
    dataset = synth.sample(len(paper.real_dataframe) * B)
    paper.set_synthetic_dataframe(dataset)
    benchmark.eval(paper, B=B)
```



Results





Results

- Overall performance of the synthesizers: impressive!
- Still, no synthesizer succeeded across all papers, and, remarkably, some findings were never reproduced by any of the synthesizers
- High number of findings across all our papers (even those that we were unable to replicate) relying only on 1- or 2-dimensional comparisons
- The low-dimensionality suggests that targeted improvements to the synthesizers may allow us to simultaneously support high utility for individual findings and their composition into broad conclusions



Future Work

- Improving reproducibility and replicability of scientific discovery.
 - File-drawer problem [29, 52] or publication bias researchers publish positive results, negative results "end up in the researcher's drawer."
 - Epistemic parity could be extended to quantify the effect of DP noise in producing findings—which may or may not be false positives—that would not have been identified from the original data
- Monte Carlo estimation of sample size for desired power for a particular finding



Questions?

