On the Responsible use of Pseudo-Random Number Generators in Scientific Research

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ECSR 2024

What is a PRNG?

“A pseudo-random number generator (PRNG) is an algorithm that generates a sequence of numbers approximating true randomness. However, unlike true random numbers, PRGNs are deterministic, meaning they rely on an initial value called a ‘seed’ and follow a predictable pattern. Though not truly random, they are widely used in comptuer simulations, cryptography, and games due to their efficiency and ability to produce long sequences of seemingly random numbers with minimal computational resources.“

`- GPT-4o, (2024).`

PRGNs are just one type of RNG!

	'RN'	'RN*' and 'Hardware'	'RN*' and 'Quantum'	'RN*' and 'Pseudo'	'RN*' and 'Quasi'
Health Sciences	0.406	0.000646	0.000407	0.00109	0.004201
Life Sciences	0.292	0.000516	0.001336	0.00179	0.001202
Physical Sciences	0.225	0.005430	0.007717	0.00726	0.003884
Social Sciences	0.092	0.000216	0.000242	0.00055	0.002420

A cursory scientometric analysis of Randon Numbers (RN*). Data comes from OpenAlex API. All numbers are % of the entire scientific record.

- More 'PRNG papers' in CS (4222) than others combined.
- %PRGN papers since 1970: 0.0008% $\rightarrow$ 0.0048%.

PRNGs occur <u>everywhere</u>.

Computational Sciences:

- Numerical Integration
- Cryptography
- Genetic Algorithms
- Signal Processing
- Deep Learning
- Weather Forecasting
- Procedural Content
- ...

'Applied' (Health/Social) Sciences:

- RCTs/Survey Sampling
- Bootstrapping
- Epidemiological Modeling
- Econometric Estimation
- Data Imputation
- Topic Modeling
- ABMs
- ...

MT64: ubiquitous PRNG implementation (R, Stata, Python, ...)

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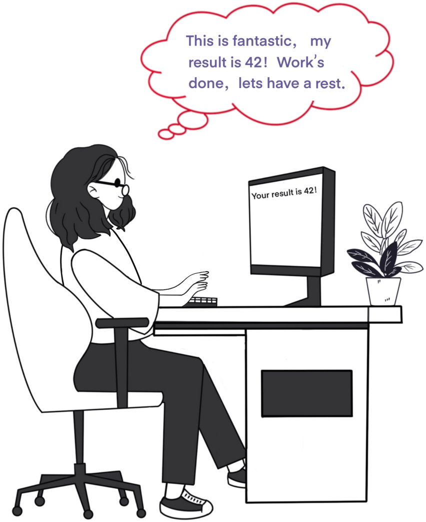
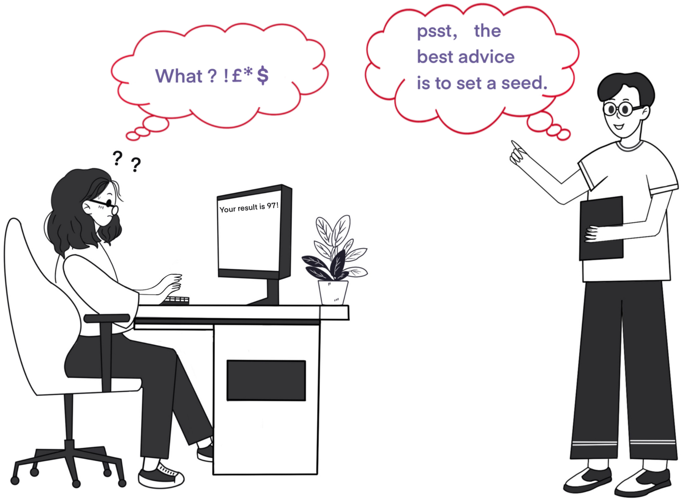
  - This seems to be the current 'best practice' advice.
- This is very well intentioned: it allows reproducibility. Yay!

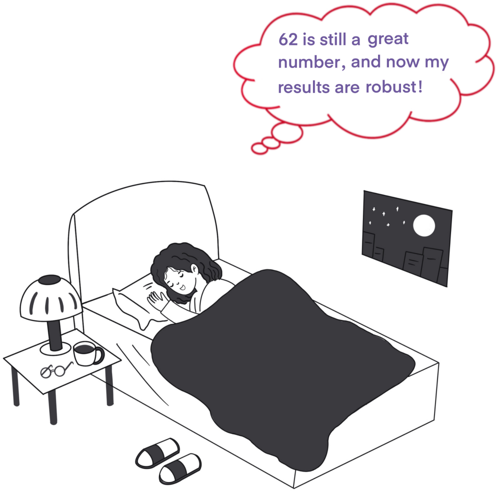

This is fantastic, my result is 42! Work's done, lets have a rest.
Your result is 42!

42 is such a great number
I'll surely be famous!

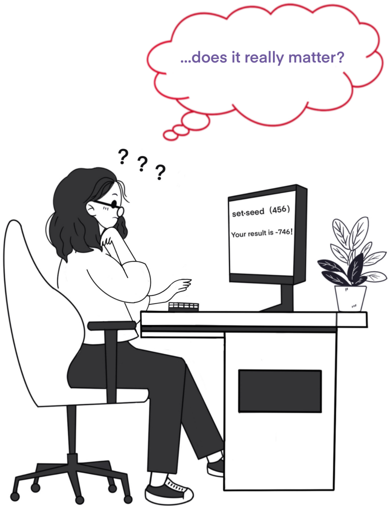
What ? ! £* $
? ?
Your result is 97!


What ? ! £* $
? ?
Your result is 97!
psst, the best advice is to set a seed.

OK, lets try 123, because he didn't say what seed to set...
? ?
set.seed(123)
Your result is 62!


62 is still a great number, and now my results are robust!

...does it really matter?
So how did you choose that seed?
set·seed(123)
Your result is 62!


...does it really matter?
? ? ?
set-seed (456)
Your result is -746!

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- Outside of these narrow fields, it's **severly** under-appreciated.
- The variation in estimand can be **huge** (as we'll show).
- We bring attention to this through multiple types of replications.
  - Simulations, machine learning, NLP, and inferential research.

"If any research design is susceptible to this kind of variation, there is a problem".

— Anonymous Colleague, Oxford (2019).

The General Premise

- **Problem Statement**: By setting **one** seed in applied algorithmic pipelines, we ignore the variation of our estimand as a function of how PRNGs were instantiated, This is computationally un-intensive, but scientifically dangerous.

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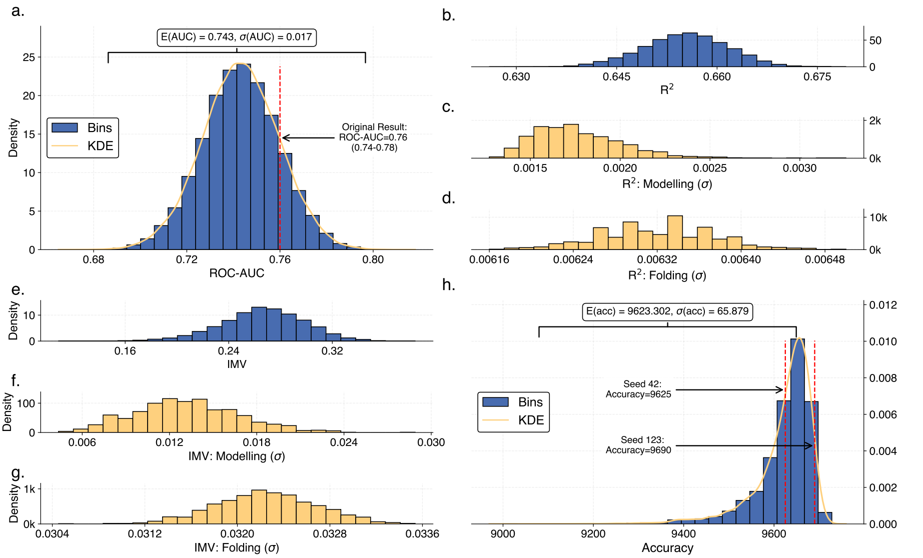
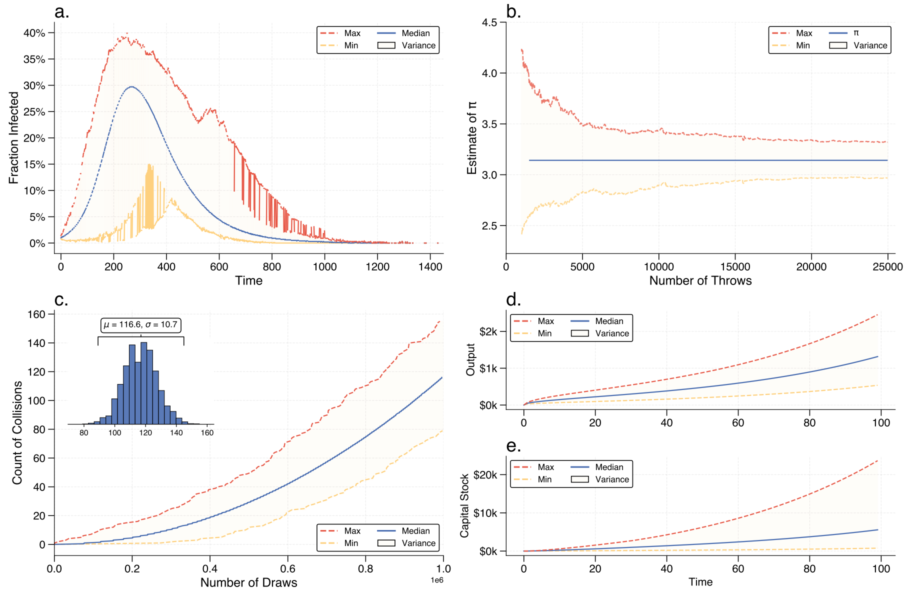
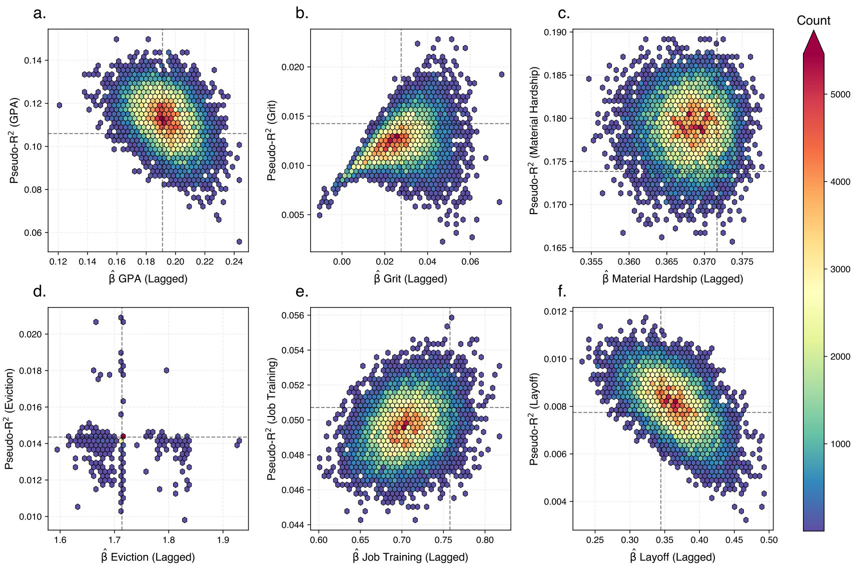
- **Problem Statement**: By setting **one** seed in applied algorithmic pipelines, we ignore the variation of our estimand as a function of how PRNGs were instantiated, This is computationally un-intensive, but scientifically dangerous.
- **Solution**: Visualize the outcome space of a **large number** (10k? 100k?) of seeds simultaneously. This is computationally intensive, but scientifically responsible.
- **Replication**: Similar to specification curves and p-hacking, we can retrospectively consider whether an original result is in the tail/IQR of the distribution of possible outcome space.


a.
E(AUC) = 0.743, σ(AUC) = 0.017
Original Result: ROC-AUC=0.76 (0.74-0.78)
Bins
KDE
Density
ROC-AUC
b.
R²
c.
R²: Modelling (σ)
d.
R²: Folding (σ)
e.
IMV
f.
IMV: Modelling (σ)
g.
IMV: Folding (σ)
h.
E(acc) = 9623.302, σ(acc) = 65.879
Seed 42: Accuracy=9625
Seed 123: Accuracy=9690
Accuracy


a.
Fraction Infected
Time
Max
Min
Median
Variance
b.
Estimate of π
Number of Throws
π
c.
Count of Collisions
Number of Draws
1e6
μ = 116.6, σ = 10.7
d.
Output
e.
Capital Stock
Time

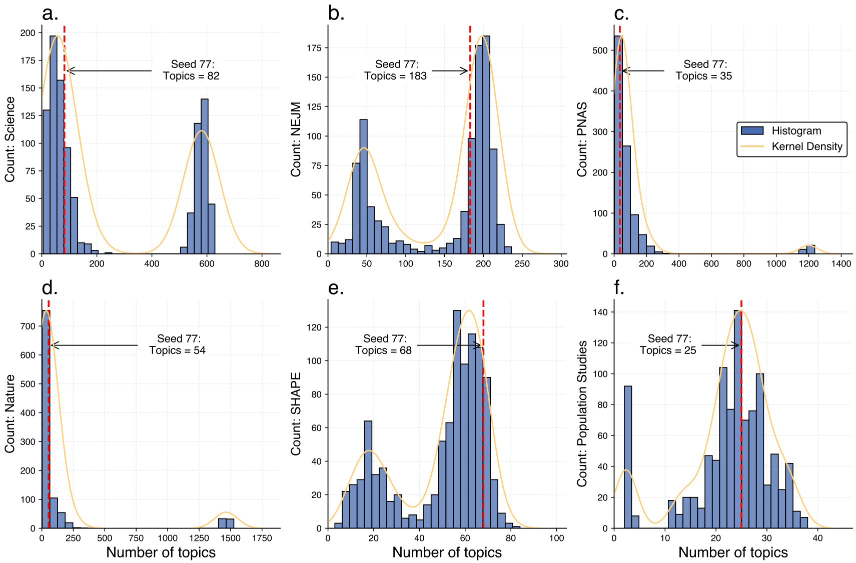
More Complex Replications

- Lets move into more complex and direct replications.
  - Major focus on the quantitative/computational social sciences.
    - Machine/Deep Learning
    - Sociology
    - Digital Humanities
    - Econometrics
    - Time Series Analysis
    - Urban Segregation
- Both recent and classical papers.
  - For each example, we'll give intuition as to what's going on.
- In total, this project replicates about 15 different papers.


a.
b.
c.
d.
e.
f.
Count
Pseudo-R^2 (GPA)
$\hat{\beta}$ GPA (Lagged)
Pseudo-R^2 (Grit)
$\hat{\beta}$ Grit (Lagged)
Pseudo-R^2 (Material Hardship)
$\hat{\beta}$ Material Hardship (Lagged)
Pseudo-R^2 (Eviction)
$\hat{\beta}$ Eviction (Lagged)
Pseudo-R^2 (Job Training)
$\hat{\beta}$ Job Training (Lagged)
Pseudo-R^2 (Layoff)
$\hat{\beta}$ Layoff (Lagged)
1000
2000
3000
4000
5000

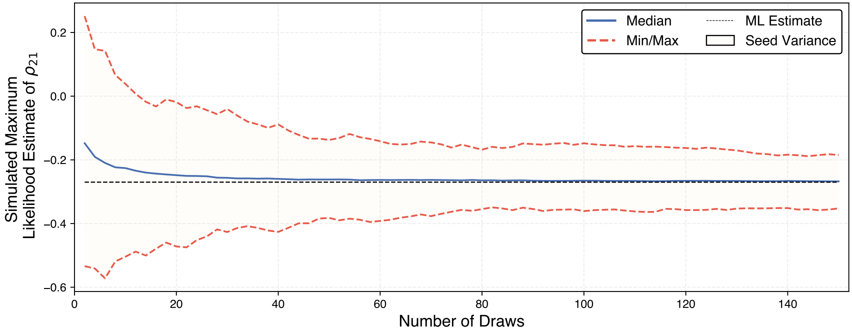
What's going on here?

- Amelia fills in missing data by drawing values from distributions.
- These distributions are based on observed data patterns.
- The imputed values reflect the uncertainty in the missing data.
- This is a form of Multiple Imputation.
- This results in entirely different models being built.
- This has implications for both inference and prediction.


a.
Seed 77:
Topics = 82
Count: Science
b.
Seed 77:
Topics = 183
Count: NEJM
c.
Seed 77:
Topics = 35
Count: PNAS
Histogram
Kernel Density
d.
Seed 77:
Topics = 54
Count: Nature
Number of topics
e.
Seed 77:
Topics = 68
Count: SHAPE
Number of topics
f.
Seed 77:
Topics = 25
Count: Population Studies
Number of topics

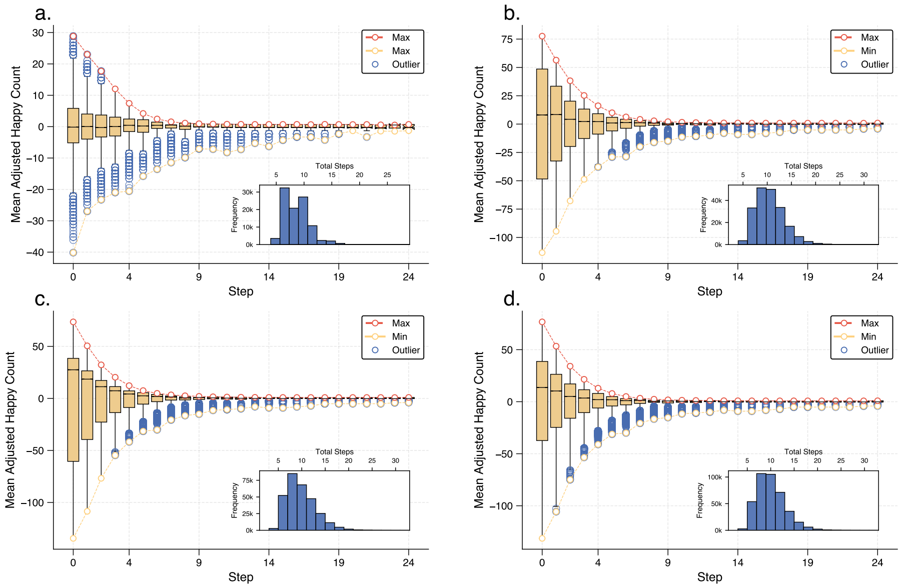
What’s going on here?

- BERTopic has many process: one particularly volatile to seeds.
- It commonly involves dimension reduction via UMAP.
  - **UMAP**: causes different low-dimensional embeddings.
- Note: CUML implementation of UMAP gives variable outputs for spectral initialisation *even when setting the seed*.
- If using HDBScan for clustering, no seed variability.
- In general here, the seed variance looks **enormous**.


Median
Min/Max
ML Estimate
Seed Variance
Simulated Maximum Likelihood Estimate of ρ_{21}
Number of Draws
0.2
0.0
−0.2
−0.4
−0.6
0
20
40
60
80
100
120
140

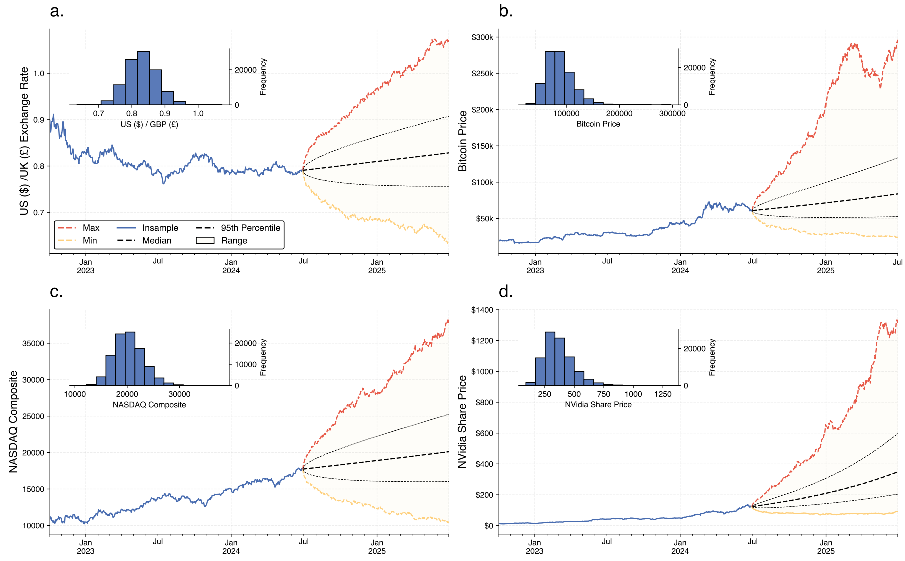
What's going on here?

- The `mvprobit` estimator requires evaluating M integrals jointly.
- This can be rewritten into a multivariate normal distributions.
  - Then, a sequence of normal distributions with certain properties.
- `mvprobit` samples from this to get at the underlying likelihood.
- Rewrite each individual normal to its CDF, which allows you to sample by just entering a uniform value between [0,1].
  - This random value is seed-dependent.
- Where CDF is steep on a small interval, seeds matter a lot.


a.
b.
c.
d.
Mean Adjusted Happy Count
Step
Max
Max
Min
Outlier
Total Steps
Frequency

What’s going on here?

- There are *multiple* (!) sources of PRNG in the Schelling Model:
  1. The initialisation of the agents on the grid.
  2. The shuffling of unhappy agents and empty cells.
- Agents might start more/less segregated from the beginning.
  - This affects the speed of total segregation over time.
- Even if the model reaches similar segregation, configuration of agents and trajectories will differ.
- As shown in the previous slide, parameterisation matters (a lot).


a.
b.
c.
d.
US ($) /UK (£) Exchange Rate
US ($) / GBP (£)
Bitcoin Price
NASDAQ Composite
NVidia Share Price
Frequency
Max
Min
Insample
Median
95th Percentile
Range
Jan 2023
Jul
Jan 2024
Jul
Jan 2025
Jul

What's going on here?

- Seeds modify sequences of PRNG draws, affecting y_t.
- Moments of previous changes (μ, $\sigma/2$) control magnitude.
- Draws of $\mathcal{N}(\mu, \sigma/2)$ impact asset price trajectory.
- The seed affects long-term trends by influencing both direction and size of early random steps.

This can be formally written as:

$$y_t = y_{t-1} + \epsilon_t \quad \text{where} \quad \epsilon_t \sim \mathcal{N}(\mu, \sigma/2) \tag{1}$$

- Previously thought that nothing outperforms RW for ForEx.
- RWs commonly used as a benchmark for structural models.

Concluding Thoughts (Part One)

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        - There are times when you can eliminate/reduce seed variability.
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  - **Reviewers:** Question papers you read – is there stochasticity?
    - Even well established results are susceptible.
  - **Editors:** Ubiquitous mandate for responsible use of PRNGs!

simple_seed_algorithm.py

```
import numpy as np # for randomisation
import matplotlib.pyplot as plt # for plotting

def analytical_function(input, seed):
        ''' Simple analytical function: can be anything'''
        np.random.seed(seed)
        return input*np.random.normal()

results = [] # store results
inputs = 42 # dataset, figure path, etc.

for seed in range(0, 100000): # simple loop; can be distributed
        results.append(analytical_function(inputs, seed))

plt.hist(results) # plot results
```

better_seed_algorithm.py

```python
import numpy as np # for randomisation
import matplotlib.pyplot as plt # for plotting

def analytical_function(input, seed):
        ''' Simple analytical function: can be anything'''
        np.random.seed(seed)
        return input*np.random.normal()

results = [] # store results
inputs = 42 # dataset, figure path, etc.

# Instead, use list of predefined, complex 'secret' seeds we provide
with open(os.path.join( '..', 'assets', 'seed_list.txt')) as f:
    seed_list = [int(line.rstrip('\n')) for line in f]

for seed in seed_list: # simple loop; can be distributed
        results.append(analytical_function(inputs, seed))

plt.hist(results) # plot results
```

Concluding Thoughts (Part Two)

- Ideally, we want to move towards <u>distributional</u> reproducibility.
- Moving foward, PRGNs <u>shouldn't</u> exist (QRNGs the norm).
- Does anyone have ideas for other types of seed variability?
- Can this be corrective? Index historical seed variability?
- Prospectively: we make available a list of seeds (replication materials), encouraging their use as a pre-specified set.
- **TLDR**: when variation can't be eliminated, should be visualised.

Thanks to my Coauthors!

Mark Verhagen

Jiani Yan

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Jiani Yan

And <u>thanks to you for your attention and attendance!</u>

Replication Materials

Naturally, all code available on GitHub at the QR code above