This form documents the artifacts associated with the article (i.e., the data and code supporting the computational findings) and describes how to reproduce the findings.

Part 1: Data

☐ This paper does not involve analysis of external data (i.e., no data are used or the only data are generated by the authors via simulation in their code).

☒ I certify that the author(s) of the manuscript have legitimate access to and permission to use the data used in this manuscript.

Abstract

The Mentoring dataset is a randomized controlled trial conducted on German adolescents. It contains baseline covariates of the following categories: demographics (age, gender, migrant status), home environment (books at home, parental support), academic grades (math, German, English), personality (Big Five scales), and socioeconomic status. Treatment is a binary indicator for assignment to a mentoring intervention. A standardized labor market outcome was measured for each child.

Availability

☒ Data **are** publicly available.
☐ Data **cannot be made** publicly available.

If the data are publicly available, see the *Publicly available data* section. Otherwise, see the *Non-publicly available data* section, below.

Publicly available data

☒ Data are available online at: https://dataverse.harvard.edu/dataset.xhtml?persistentId=doi:10.7910/DVN/IP98QW

☒ Data are available as part of the paper's supplementary material.

☐ Data are publicly available by request, following the process described here:

☐ Data are or will be made available through some other mechanism, described here:

Non-publicly available data

Description

File format(s)

☐ CSV or other plain text.
☒ Software-specific binary format (.Rda, Python pickle, etc.): pkcle
☐ Standardized binary format (e.g., netCDF, HDF5, etc.):
☐ Other (please specify):

Data dictionary

- ☐ Provided by authors in the following file(s):
- ☐ Data file(s) is(are) self-describing (e.g., netCDF files)
- ☒ Available at the following URL: https://dataverse.harvard.edu/dataset.xhtml?persistentId=doi:10.7910/DVN/IP98QW

Additional Information (optional)

Data can be accessed through the Harvard Dataverse, but for convenience is also attached in the data subfolder.

Part 2: Code

Abstract

The code is organized into three parts: R/replication_functions.R defines all relevant functions for analysis, then, two analysis scripts (scripts/generate_figures.R and scripts/generate_tables.R) call those functions to produce all figures and tables. The master script (scripts/run_analysis.R) activates the renv environment, creates the necessary output directories, and runs the figure and table scripts.

Description

Code format(s)

- ☒ Script files
  - ☒ R
  - ☐ Python
  - ☐ Matlab
  - ☐ Other:
- ☐ Package
  - ☐ R
  - ☐ Python
  - ☐ MATLAB toolbox
  - ☐ Other:
- ☐ Reproducible report
  - ☐ R Markdown
  - ☐ Jupyter notebook
  - ☐ Other:
- ☐ Shell script
- ☐ Other (please specify):

Supporting software requirements

Version of primary software used R version 4.4.2

Libraries and dependencies used by the code

- here (1.0.1)
- renv (0.18.0)
- dirmult (0.3.0)
- pracma (2.3.3)
- MASS (7.3-58)
- abind (1.4-5)
- reshape2 (1.4.4)
- ggplot2 (3.4.2)
- foreach (1.5.2)
- doParallel (1.0.18)
- parallel (base)
- stats (base)
- dplyr (1.1.1)
- haven (2.6.1)
- fastDummies (1.7.0)
- SuperLearner (2.0-30)
- gbm (2.1.8)
- glmnet (4.1-7)
- earth (5.5.1)
- ranger (0.14.1)

Supporting system/hardware requirements (optional)

Parallelization used

☐ No parallel code used
☒ Multi-core parallelization on a single machine/node
  – Number of cores used: 15
☐ Multi-machine/multi-node parallelization
  – Number of nodes and cores used:

License

☒ MIT License (default)
☐ BSD
☐ GPL v3.0
☐ Creative Commons
☐ Other: (please specify)

Additional information (optional)

Part 3: Reproducibility workflow

Scope

The provided workflow reproduces:

☒ Any numbers provided in text in the paper
☒ The computational method(s) presented in the paper (i.e., code is provided that implements the method(s))
☒ All tables and figures in the paper
☐ Selected tables and figures in the paper, as explained and justified below:

Workflow

Location

The workflow is available:

☐ As part of the paper's supplementary material.
☒ In this Git repository: https://anonymous.4open.science/r/rerandomization-quadratic-forms-3DAC
☐ Other (please specify):

Format(s)

☒ Single master code file
☒ Wrapper (shell) script(s)
☐ Self-contained R Markdown file, Jupyter notebook, or other literate programming approach
☒ Text file (e.g., a readme-style file) that documents workflow
☐ Makefile
☐ Other (more detail in *Instructions* below)

Instructions

To reproduce the full analysis, including Figures 1–3 and Table 2:

1. **Download and unzip the anonymized repository**

```
https://anonymous.4open.science/r/rerandomization-quadratic-forms-3DAC
```

2. **Restore R environment**

```
Rscript -e "install.packages('renv', repos='https://cloud.r-project.org')"
Rscript -e "renv::restore(repos='https://cloud.r-project.org')"
```

3. **Run master script**

```
Rscript scripts/run_analysis.R
```

Expected run-time

Approximate time needed to reproduce the analyses on a standard desktop machine:

- ☐ < 1 minute
- ☐ 1-10 minutes
- ☐ 10-60 minutes
- ☐ 1-8 hours
- ☒ > 8 hours
- ☒ Not feasible to run on a desktop machine, as described here: It is possible to run on a desktop machine, but it will take several days. Analysis from the paper was run in batches.

Additional information (optional)

None.

Notes (optional)

None.