Author Contributions Checklist Form

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 Medical Information Mart for Intensive Care is a database that contains information on critical care patients from Beth Israel Deaconess Medical Center in Boston, Massachusetts. The database includes information such as demographics, vital sign measurements made at the bedside, laboratory test results, procedures, medications, caregiver notes, imaging reports, and mortality. The data are freely available to researchers worldwide: https://mimic.mit.edu/.

## 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 dat*a section, below.

### Publicly available data

Data are available online at: https://mimic.mit.edu/

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

Discussion of lack of publicly available data:

## Description

### File format(s)

CSV or other plain text:

Software-specific binary format (.Rda, Python pickle, etc.):

Standardized binary format (e.g., netCDF, HDF5, etc.):

Other (described here):

The MIMIC database is publicly available at: <https://mimic.mit.edu/> ; however, accessing MIMIC requires additional steps. Please see <https://github.com/microsoft/mimic_sepsis> and <https://github.com/matthieukomorowski/AI_Clinician> for the details.

### Data dictionary

Provided by the authors in the following file(s):

Data file(s) is (are) self-describiing (e.g., netCDF files)

Available at the following URL:

https://mimic.mit.edu/docs/iii/

### Additional information (optional)

# Part 2: Code

## Abstract

The README.Rmd provides instructions on how to implement the code. The TWDIDP.R files implements the proposed two-way doubly inhomogeneous decision process; the target.R and the MCMC.R were used to calculate the true value function; the mixdata.R was used to generate the observed data. The mimic.R file contains code for doing analysis in the paper and the pre-processed MIMIC datasets. The fitted-q.R file is the competing method for the fitted-q evaluation. Finally, the cartpole.ipynb file illustrate how to generate data from the OpenAI Gym environment Cartpole.

## 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 (described here):

### **Supporting software requirements**

Version of primary software used

R version 4.2.2

Python 3.10.12

Libraries and dependencies used by the code

dplyr version 1.0.10

Gym version 0.26.1

Numpy version 1.25.2

Pandas version 1.5.3

### Supporting system/hardware requirements (optional)

### Parallelization used

No parallel code used

Multi-core parallelization on a single machine/node

Number of cores used:

Multi-machine/multi-node parallelization

Number of nodes and cores used:

### License

MIT License (default)

BSD

GPL v3.0

Creative Commons

Other (described here):

### 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 here:

Figure 3 in the main paper;

Figure S3 in the Supplemental Materials;

Figure S4 in the Supplemental Materials.

## Workflow details

### Location

The workflow is available:

As part of the paper’s supplementary material

In this Git repository: <https://anonymous.4open.science/r/JASA2023/README.md>

Other:

### 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

The detail of how to use code and reproduce our results can be found in README.md in our repository.

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:

### Additional documentation (optional)

# Notes (optional)