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 transNOAH breast cancer trial dataset (GSE50948), as described in Prat et al. (2014).

This data consists of gene expression profiling measurements from 156 patients. For our analysis, we use expression measurements of the gene probe 204531\_s\_at, associated with BRCA1, as the response variable Y.

## 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:

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 dataset is saved as Rdata format.

### Data dictionary

Provided by the authors in the following file(s): transNOAH.Rdata in the folder “Real Data Analysis”

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

Available at the following URL:

Using the following command:

if (!requireNamespace(“BiocManager”, quietly = TRUE))

install.packages(“BiocManager”)

BiocManager::install(“GEOquery”)

Sys.setenv(“VROOM\_CONNECTION\_SIZE” = 500000)

readr::local\_edition(1)

transNOAH = GEOquery::getGEO(“GSE50948”)

save(transNOAH, file = “transNOAH.RData”)

### Additional information (optional)

# Part 2: Code

## Abstract

All the codes of the simulation study and real data analysis are included in different folders based on their tasks. Details can refer to the illutration file in the folders.

## 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 4.2.1

Libraries and dependencies used by the code

Biobase version 2.58.0; BiocGenerics version 0.440; data.table version 1.14.8;

GEOquery version 2.66.0; glmnet version 4.1-7; ncvreg version 3.13.0; MASS version 7.3-58.1;

SIHR version 2.0.1; stringr version 1.5.0; tidyr version 1.3.0.

### 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: Number of nodes and cores used: 300 nodes and 300 cores

### 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:

## Workflow details

### Location

The workflow is available:

As part of the paper’s supplementary material

In this Git repository: https://github.com/anonymousci42/HdimLinearInference

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

Step 1: load the required R packages.

Step 2: Run the “NPE1.R” script to generate the results of the proposed method without power enhancement term JPE. We only provide a script with fixed parameters, the whole tasks cannot be done in a single local computer.

Step 3: Run the “PPE1.R” and “SIHR.R” to generate the results of two comparative methods.

Step 4: Run the “PE1.R” in the folder PE\_FULL, to reproduce the results of the proposed method with power enhancement term JPE.

Step 5: Run the “Data\_Analysis.R” to summarize all the output into different tables.

Step 6: Run the “Real\_Data\_Analysis.R” in the folder “Real Data Analysis” to reproduce the result of the transNOAH data.

Implementation details and illustration of outputs are provided in the README.md.

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)

Due to the large computational cost, We use the clusters of the University to finish all the tasks.

# Notes (optional)