Nonparametric Bayesian Deconvolution of a Symmetric Unimodal Density

**1 Code**

**1.1 Abstract**

We submitted all the R codes to output the simulation results including Figures and Tables in Section 5 of the submitted paper. The Figures will be output as .pdf files, and the numbers in the Tables will be printed on the R console screen.

**2.2 Description**

**2.2.1 How to Deliver**

We provide one R function and several supportive R functions to deliver the proposed method. In addition, we provide the R file to generate data, perform analysis and deliver the output. For specific use of the code to reproduce the simulation results in our submitted paper, see below.

**2.2.2 Permission and Licensing**

All the codes are free to use with a proper citation of the submitted paper.

**2.3 Optional Information**

**2.3.1 Hardware Requirements**

The code was tested on a Linux machine with the following specifications:

OS: CentOS Linux 7 (Core),

Kernel: 3.10.0-693.17.1.el7.x86\_64,

CPU: Intel(R) Xeon(R) CPU E5-2690 0 @ 2.90GHz.

**2.3.2 Software Requirements**

All the codes are tested under the base version of R 3.4.3. The following R packages need to be installed for running the code, coda, MCMCpack, evd, truncdist, Rcpp, RcppArmadillo, VGAM, batch.

**3 Introduction for Use**

**3.1 Reproducibility**

We have three types of codes, the R code for running one simulation on a specified seed and sample size, the batch R code for running the combinations of sample size and seed in parallel, the R code that outputs the Figure and numbers in the Table. There are other R files containing functions we used in the above R codes. The root folder “code\_for\_paper” containing all supporting R files and six sub folders with the main R codes for reproducing the Figures and Tables as indicated by the names of the sub folders.

The main workflow of our analyses:

1. Open the sub folder in the name format “FigureX\_TableX”. X can be 1, 2, 3, 4 or S3, S4 corresponding to the same indices in the submitted paper.

2. One can run the batch R code in the name format “run\_Parallel” + “true model” that will generate four folders whose name corresponds to the sample size. After running, each folder consists 100 csv files in the name format “seed” + “true model”. Each csv file stores the density estimates and goodness of fit metrics under the corresponding seed.

3. After 2, we can reproduce plots and numbers in the corresponding FigureX and TableX by running the R code in the name format “analyze\_result”+”true model”. The figure will be outputted to a .pdf file with the name format “sample size” + “true\_model”. The numbers in the Table can be found in R console. The R code will by default analyze the results when sample size is 5000. Users can vary the sample size to other choices (1000, 10,000 and 15,000) by changing the first line of the R code.

**3.2 Replication**

For other purposes than reproducing the Figures and Tables in the simulations we implemented, uses might also use our main function ddsc\_mcmc in the R file “ddsc\_mcmc\_prior1\_cpp” to conduct analysis on data in accordance to the description in the submitted paper to produce density estimator with unimodal and symmetric shape constraints. Refer to the R code starting with “Constrained\_Bayes” in the sub folders FigureX\_TableX as references or illustrating examples.