Guide to the data and codes used in "Marital matching, economies of scale and intrahousehold allocations"

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All the results shown in the paper and the supplementary online Appendix can be replicated using the files in folders `Data and codes_Main` and `Data and codes_Appendix`. With exception to the tables in Appendix F.1, F.3, F.4 and F.5, all the tables can be obtained using the files in the folder `Data and codes_Main`. Rest of the tables can be obtained using the files in folder `Data and codes_Appendix`.

Data

Our dataset is drawn from a sample of US based households data drawn from the 2013 wave of Panel Study of Income Dynamics. The selected sample in our main analysis contains 1322 couples (see sub-folder `1.Sample selection` in `Data and codes_Main` for more details on sample selection). In particular, the selected sample is stored in `psid_cleaned_onlycouples.dta` in folder `1.Sample selection`.

Programs

The programs for the paper are written in STATA (version 13.0) and MATLAB (version R2013b). The optimization programs in MATLAB use YALMIP (see Löfberg (2014)) and GUROBI optimization solver. YALMIP can be downloaded for free from here (Copyright owned by Johan Löfberg). After downloading YALMIP, one needs to adding its directories using the function 'addpath'. see this for more information. The optimization problems have been solved using the solver Gurobi (academic version of Gurobi is availabe for free to academic users here). For more information on how to install Gurobi, see this.

Folder: `Data and codes_Main`

- The results can be replicated from scratch in three steps.
  - First step-Sample selection: Processes the raw PSID data to obtain the selected sample used in the main analysis (see sub-folder: `1.Sample selection`),
  - Second step-Identification: Uses the selected sample to obtain bounds on economies of scale and individual RICEBs (see sub-folder: `2.Identification`) and,

  - Third step-Analysis: Uses the bounds obtained in second step for further analysis (see sub-folder: `3.Analysis`).

- Each folder contains a read-me file which provides further details.
- If someone is interested only in a particular step, they can directly start from the corresponding folder. The inputs from previous steps are already present in each sub-folder.

Folder: `Data and codes_Appendix`

- Results from Appendix F.1, F.3, F.4 and F.5 can be replicated using files in the corresponding sub-folders.
- The read-me files in each sub-folder will guide the users further.

References

[1] Löfberg, Johan. "YALMIP: A toolbox for modeling and optimization in MATLAB." *Computer Aided Control Systems Design, 2004 IEEE International Symposium on. IEEE*, 2004.