

### **Read Me**

This document provides information needed to replicate all of the results presented in Bursztyn et al., “Understanding Mechanisms Underlying Peer Effects: Evidence from a Field Experiment on Financial Decisions.”

The files needed for the replication are as follows:

1. do-file.do
2. Main\_Data.dta
3. Appendix\_Data.dta

### **Overview:**

The single .do file provided (“do-file.do”) reproduces all of the results presented in tables and figures, both in the main text of the paper and in the supplemental online appendix. The results presented in the paper, and nearly all of the results in the appendix are produced using the dataset “Main\_Data.dta”, which includes data on the experimental sample of 300 investors. In Appendix Table A.1, we compare the 300 investors in the experimental sample to the universe of investors in the main office of the brokerage with which we worked to conduct the experiment. The dataset “Appendix\_Data.dta” includes data on both the experimental sample and the broader set of clients of the brokerage needed to conduct this comparison.

The .do file is annotated; there are several notes that we highlight here. First, users should edit the .do file to set the directory to that in which they save the datasets for the .do file to run smoothly. Currently, the .do file has a comment (*\*cd "NAME OF DIRECTORY WHERE DATASETS ARE SAVED"*), which should be replaced with the command to set the directory appropriately. Second, in the replication of Appendix Tables A.5 and A.6, the .do file currently generates bootstrapped standard errors based on 100 replications, while in the appendix to the paper, we calculate standard errors based on 500 replications; this was done to allow the program to run more quickly. It is straightforward to change the number of replications in the .do file to exactly match the procedure used to produce the results in the appendix. Third, in the replication of Appendix Table A.8, the .do file currently generates p-values based on permutation tests with 1,000 reassignments of the treatment conditions, while in the appendix to the paper, we calculate p-values based on 10,000 reassignments; again, this was done to allow the program to run more quickly. Again, it is straightforward to change the number of reassignments in the .do file to exactly match the procedure used to produce the results in the appendix.