Replication package for "Impacts of natural resource traceability programs: evidence from the United States' Seafood Import Monitoring Program"
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There are four steps to replicate this paper. 1) Build the import database, 2) Prep data for analysis, 3) Run model selection on the ASU Sol Supercomputer, and 4) Generate forecasts and impact estimates for the main SIMP species, placebos, and subgroups.

Replication folder organization:
Order of code files:
- 01_Main_data_prep.R
- Supercomputer/02_Main_ModelSelect.R
- 03_Main_ImpactEst.R

All figures and tables will be output to "SIMP_price_impacts/Output/" unless otherwise specified in the files "01_Main_data_prep.R" and "03_Main_ImpactEst.R"

Steps to replicate:
First, the raw trade data must be cleaned and the database built.
- Download raw import data, available here: https://github.com/kaitlyn-c-lee/seafood-traceability-design
    - Navigate to "Source Data/NOAA_imports/"
    - Download the entire "NOAA_imports" folder to: "SIMP_price_impacts/Trade data/Source Data/"
- Run Trade data/00_Main_htstrade.R

Next, run "01_Main_data_prep.R" to prepare the data.
- Before running this file, you must request an API key from BLS and enter the key on line 11 in the file "Code files/13_Covariates_Get.R"
- Alternatively, the covariate data has been provided. The file "Code files/13_Covariates_Get.R" does not need to be run for replication of the paper results and can be skipped.

Next, the sub-folder "Supercomputer" was uploaded to the ASU Sol supercomputer to perform model selection. The number of cores can be specified in 02_Main_ModelSelect.R. For the paper run, the request was for 80 cores and 128 GB of memory. 50 cores were specified in the code.
- "Supercomputer/Output/" contains csv files output from running 02_Main_ModelSelect.R

Finally, run "03_Main_ImpactEst.R" to estimate impacts and output all tables and figures from the paper. Output location must be specified in this file before running.