Ordinal Variables for Blocking

January 5, 2021

Committee meeting May 21

- I thought my Table 2.2 shows evidence that OP is better than making things numeric. It doesn't. I am using a placebo treatment, i.e. there is no treatment, so the Group T2 coefficient should be zero. In other words: There would be differences with anything here, since it's just one single draw. I need evidence that OP works better
 - Evidence 1: Monte Carlo simulations
 - Evidence 2: Repeat the Table 2.2. estimations 100 times and show the distributions around zero
- Perform a test to check that OP assigns people correctly
- Write up the shiny survey environment in the appendix
- Emphasize machine learning in the write-up

shiny

- The only current option to design an online survey environment is through a provider like Qualtrics. You can randomize there, but only by clicking "Randomize". It is not possible to use blocking online. I create a survey environment which can do that
- I found the package ShinyPsych. It creates a survey environment with shiny (among other things)
 - Overview
 - How to create a survey
 - Specifications of .txt files for questions
- A survey environment is created by running the code in the file app.R in the package folder ShinyPsych/shiny-examples/Survey. This code reads in questions in .txt format from the package folder ShinyPsych/extdata. The .txt files need to be very specifically formatted (a question goes into one cell, all answer options go into one cell etc.). To adapt everything for my needs, I need to write my own questions as .txt files and I need to edit the code in app.R
- It's a pain to edit a .txt question file. It's much better to turn it into a .csv, edit that, then turn it back into a .txt
- I made a copy of app.R called shiny_psych_survey.R that I will continue to edit. Running shiny_psych_survey.R creates my survey environment setup. Running app.R creates the the original package example survey environment
- Questions as .txt files:
 - I copied an existing .txt file and edited it to contain an example of the questions
 I need. So far, I created the following files in /questions:
 - * code.txt
 - * education.txt
 - * goodbye.txt
 - * instructions.txt

* demographics.txt

And the following ones in /questions/treatment:

```
* mw.control.txt
* mw.m.opp.txt
* mw.m.supp.txt
* mw.p.opp.txt
* mw.p.supp.txt
* tb.control.txt
* tb.m.opp.txt
* tb.m.supp.txt
* tb.p.opp.txt
```

- I copied the code from app.R into shiny_psych_survey.R and adapted it to load my question files
- Crucial: The code to load the question files needs to include any file path and
 .txt as well as have defaulttxt = FALSE. Otherwise these external files will not
 be read in by the code
- Saving data
 - I can save locally and to Dropbox
 - Locally
 - * Use the saveData function from shinyPsych and set location = "local". That saves each response as a .csv in whatever outputDir is
 - Dropbox setup:
 - * Much more complicated
 - * Use the rdrop2 (link) and dplyr packages
 - * Setup things:
 - · Sign into my AU Dropbox in the browser
 - · Generate a Dropbox access token
 - · Pull and save the access token to the same folder where shiny_psych_survey is located:

```
library(rdrop2)
token <- drop_auth()
saveRDS(token, "droptoken.rds")</pre>
```

- * Create the function savedata to upload a .csv to Dropbox folder /block_data (instructions are here)
- * Create the function loaddata (instructions are here) to download all the .csv files from Dropbox /block_data, turn them into a list, then a data frame, then save that data frame in my local folder /block_data
- * savedata needs to be defined before the actual shiny code and is executed in the app code by adding savedata(data.list) instead of the original shinyPsych data saving code
- * loaddata is defined and executed from edit_package.R
- Randomly assigning respondents to one of five treatment groups
 - Took me a lot of experimenting, but the end result is very nice and simple
 - For each issue, create an R vector with the names of the group .txt files, then

- randomly sample one of those names and store it. Then paste that stored object name into the createPageList function and create the needed objects in the other sections
- Each input question in each treatment .txt needs to be labelled "treat", otherwise the data can't be read. With this generic labelling, it is not shown what group the respondent was assigned to in the resulting data frame. That's why I added the stored randomly sampled group name for each issue as a variable to the list of data saved in data.list

• edit_package.R:

- Code to edit question files
- Code to source shiny_psych_survey.R and run the app to test that the questions are properly loaded. Responses are saved to my AU Dropbox folder /block_data
- Code to re-deploy the app on my shiny server account
- Code to create function loaddata
- Code to execute loaddata
- Code to source ShinyPsych's app.R if I want to look up some things in the original version. Responses are saved locally under /package_data
- shiny_psych_survey.R:
 - Code to create function savedata
 - Code to create the setup of my app survey environment
 - No additional code for authentication with Dropbox needed. The original setup above is enough for use on my local machine
- Deployed app on my shiny server account: https://sheuberger.shinyapps.io/survey_experiment/
 - Everything is in /survey_experiment:
 - * app.R
 - · Code to create authentication with Dropbox (adapted from here, not needed locally but needed when deployed to create Dropbox authentication and save the data):
 - drop_auth(rdstoken = "droptoken.rds")
 - · Code to create function savedata
 - · All app code
 - · Data saved to AU Dropbox /block_data
 - · Randomized treatment questions for both issues
 - · Code set up so I have to adjust only the bare minimum
 - * questions/code.txt
 - * questions/education.txt
 - * questions/instructions.txt
 - * questions/demographics.txt
 - * questions/pid_foll_dem.txt
 - * questions/pid_foll_ind_else.txt
 - * questions/pid_foll_rep.txt
 - * questions/treatment/mw.control.txt
 - * questions/treatment/mw.m.opp.txt
 - * questions/treatment/mw.m.supp.txt
 - * questions/treatment/mw.p.opp.txt

- * questions/treatment/mw.p.supp.txt
- * questions/treatment/tb.control.txt
- * questions/treatment/tb.m.opp.txt
- * questions/treatment/tb.m.supp.txt
- * questions/treatment/tb.p.opp.txt
- * questions/treatment/tb.p.supp.txt
- * droptoken.rds
- shiny_psych_survey.R is for my local machine where I can test and make changes as I go along. app.R in /survey_experiment is the live survey on the server. If I make any code changes to shiny_psych_survey.R that I want to see in the deployed app, I need to manually copy it to app.R. This is for safety, so I don't accidentally overwrite it with stupid things
- The same goes for the questions. All question files are under /questions for my local machine. There are separate versions of them in /survey_experiment. Any changes need to be copied manually
- Over the course of development, I massively changed the original code in shiny_psych_survey.R so that I had to adjust only a minimum of things as I move forward (I had to keep going through and changing all the cases over and over again). I have commented things out and also saved the old version. In the current one, only the sampled questions need to be adjusted throughout (otherwise I would keep resampling). The rest is set once at the beginning of the document and then called with paste, assign etc.
- Include OPM function OPMord (from OPM above) in existing shiny environment
 - This is actually not necessary because the OPM does not need to be part of the shiny environment. Users run OPMord with data, DV, and EVs of their choice to obtain data-driven ordinal categories. These categories then replace the original categories in ordinal variable in the user's experimental data. She can then use these categories as the basis for sequential blocking. Basically, OPMord is run before anything in shiny and thus does not need to be included in it
- Modify shiny_psych_survey.R to include/run seqblock
 - Overall idea: Feed the user-selected category into seqblock(). If the MD code doesn't set in yet, the respondent is randomly assigned to a treatment group. If the MD code sets in, all previously assigned education data is loaded from Dropbox, and the code blocks the respondent into a treatment group. In both cases, the respective group is extracted, the respective treatment .txt is saved as mw.sample/tb.sample, and the newly updated assigned data is saved to Dropbox
 - seqblock() only works with .RData files and only stores the variables that are blocked on. So saving the seqblock data and saving all input data needs to be separate. seqblock data goes to Dropbox/seqblock, all input data goes to Dropblox/alldata. The seqblock data needs to be overwritten on Dropbox and within shiny, so it's one .RData file. The input data is one small .csv file for each user that I later download and combine on my laptop (so exactly the same as before)
 - seqblock() creates a .RData file for the first person. All following people are

- assigned based on that continuously updated file. The website code doesn't detect whether someone is the first person or not. As a work-around for now, I put in my education category a the first user by running seqblock() once before the shiny environment and uploading that .RData file
- I need a reaction when users click "Continue" on the education page (i.e. they select their category, then the blocking code sets in and draws/uploads stuff from/to Dropbox). Thats' done via observeEvent(). I also need to save an output for use in a later function when users click that button (i.e. the assigned treatment group, which determines which treatment page is shown). That's done via eventReactive(). I don't know how to combine them, so each issue has one observeEvent() and one eventReactive()
- Order of code
 - * sequpload()
 - · Function that uploads a .RData file to Dropbox/seqblock
 - * seqdownload()
 - · Function that downloads a .RData file from Dropbox/seqblock
 - * observeEvent() when hitting "Continue" on education page
 - · Download .RData (seqdownload)
 - · Load .RData
 - · Run seqblock() on user-selected category and loaded .RData
 - · Upload .RData (sequpload)
 - * eventReactive() when hitting "Continue" on education page
 - · Download .RData (seqdownload)
 - · Load .RData
 - · Save assigned treatment group to object for later use to display correct treatment page
- App is deployed and working. The whole .RData downloading/uploading works.
 It only causes a few split seconds of loading before the web page displays the next question. Except for the issue where I have to be the first user, I think this looks good
- Improve the code
 - Am I using the right variables in seqblock (I use exact.vars but there is also covar.vars)?
 - * Nope. exact.vars requires exact variables. So if an incoming person has a 2 but a treatment group is made up of 1s and 3s, it won't find anything to match
 - * I want covar.vars, which matches on the distribution
 - * I switched the code to covar.vars
 - Find a setup where I don't have to put in my own data to create the first person
 - * Done. I used the drop_exists function and wrapped it in if ... else. drop_exists tests whether a file exists in a Dropbox path
 - * If the mw .RData file exists on Dropbox/seqblock which means other respondents have been assigned before this current respondent the code now reads in that data, blocks on the data and the current respondent, then uploads the updated .RData to Dropbox/seqblock

- * If the mw .RData file doesn't exist which means the current respondent is the first respondent to fill in the survey the code now blocks only on the current respondent, then uploads the resulting .RData
- * Obviously the same repeated for any/all other issues
- * App is deployed and working
- Added pid to block on as an exact.vars
- Incorporate skip logic (if "Republican", give question "Strong or weak?") with eventReactive()
 - * I used the same technique I used for the two issues. I created separate question .txt files for the party ID follow-up questions (one for Dem, one for Rep, one for Ind/Something Else)
 - * Depending on the number that represents what the respondent selected, the code displays the corresponding follow-up .txt
- Test the blocking code with the Dropbox upload/download code
 - * I want to make sure that everything really does result in balance and that the Dropbox stuff doesn't mess things up somewhere somehow
 - * Ideally, I would like to get randomized survey responses. Ryan said there was a way to make the computer fill in responses randomly, but I couldn't find anything on that
 - * I don't think this test has to be in the finished survey. I want to simulate the blocking part including the uploading/downloading to Dropbox I can do that locally on Jeff's machine. I'm also including the .csv saving code. It should look identical to the .RData, but I just want to make sure there's nothing muddled up there
 - * I started doing that on Jeff's machine. It worked well for n = 1,000 for education and pid. So the Dropbox stuff doesn't mess anything up and we get balance
 - * One weird thing: The blocked education numbers have decimals. It's something to do with seqblock(). I printed a screenshot of the blocked bdata\$x
 - * Show Ryan bdata\$x with decimals and my code (all printed)
 - * For reasons I don't understand, bdata\$x includes a jitter() part, hence the decimals (or noise) around the values
 - * Change bdata\$x to bdata\$orig, which keeps the original values in shiny_psych_survey.R, the deployed app.R, and testing_blocking_dropbox.R. Then rerun the test for 1,000 simulations
 - * Reran test for 1,000 simulations everything looks good
- Work in redirects for Lucid
 - The Lucid folks need my survey to read in a respondent-based unique alphanumeric number (called RID) before anything is loaded. This number is created in their system when a respondent clicks on my survey link and added to the web link, creating an initial Lucid link. For the placeholder RID 123456-abc, the initial link is https://sheuberger.shinyapps.io/survey_experiment/?rid=123456-abc. My survey needs to read in 123456-abc from that link
 - The Lucid folks also need my survey to pass out the read-in RID. This means that
 my survey needs to redirect to a Lucid completion link with the RID in it once all

- questions have been answered. For the placeholder RID 123456-abc, the completion link is https://notch.insights.supply/cb?token=98b98d10-789d-42ec-ba71-a077 cbbd909c&RID=123456-abc
- It took a lot of emails and a Zoom meeting to figure out the above details. Here is what I did:
 - * I took out the GoodBye page (all the code plus the question files) and added a Thank You message on the Code page
 - * To read the RID in: shiny stores the current session data, which includes everything in the URL. In order to read in the RID, I needed to access the component of the URL in the session data with the RID in it. It turns out that this URL component is the query string, which is the stuff after the question mark (it's all described here). The shiny session location for that is session\$clientData\$url_search. To read that in, it needed to be wrapped into parseQueryString(). The resulting R object is a list, so it needed to be made a character with [[1]] (explained here and here). I set all that up
 - * I added the stored RID to the data.list I save on Dropbox, so I can see what is being initially read in
 - * To pass the RID out: I defined a Javascript function, called js\$browseURL, that automatically redirects respondents to a website (code taken from here). I set it so that respondents are automatically redirected to a specified website when they hit "Continue" after typing in the survey code. I set the specified website to Lucid's completion link, with the stored RID pasted in
 - * I also added two if...else() wrappers for the reading-in and the passingout code, so that the same code can be run if there is no query string (which is when I run it) and if there is a query string (which is when Lucid runs it). The background here is that the pulled-in list is empty if there is no query string, which means you can't subset it with [[1]] because it throws an error. So now the code stores the query string if there is one and stores "no.query.string" if there isn't. It also redirects to Lucid's completion page in the first case and to Google in the second
- Lucid successfully tested the reading-in and passing-out code on April 22. The technical setup is now ready for the launch with Lucid

ordered_outcomes_modeling

- Note: I don't have to invent new R code to block, either normally or sequentially, because OPM comes before blocking. Ryan already developed R code to block normally and sequentially (seqblock) using MD. seqblock is set up so that the MD blocking code doesn't set in for a specified 'first few people' to be assigned. They are assigned randomly. Then, at a code-specified point, the MD code sets in and takes over for everyone else. Use that and the 'normal' blocking function to block after OPM is applied
- Test OPM model
 - Block on the original 10 ANES education variables, then run OLS regression on some ANES outcome. Then do the same for the 5 re-estimated OPM categories and compare the differences in results. If there were no differences, this would

raise some doubts whether OPM is really necessary

- * opm_create_model.R loads the ANES variables, runs the OPM model, saves .csv, .pdf (I used both of these for the presentation), and .rds files
- * opm_test_model_100.Rmd loads the .rds files, blocks and runs OLS for 100 ANES observations. Outputs a regression table as a .pdf
- * opm_test_model_all_jeff.R does the same, but for all ANES observations. This is a separate .R file because I ran this on Jeff's computer (the loop takes a while on mine). Outputs another set of .rds files
- * opm_test_model_all.Rmd loads the extra set of .rds files. Outputs a regression table as a .pdf
- * Most EVs are the same for both regressions, which makes sense. They haven't been modified, so they shouldn't be different. The treatment group coefficient, however, is different. The groups were blocked on education, so that's definitely the effect of the different categories. I think this is different enough to justify OPM. Jeff agrees, so this is all good
- Set up an R function (or functions, whatever is better)
 - I set up opm_create_function.R, which creates the function OPMord, which:
 - * Applies polr() to specified training data, DV, EVs
 - * Attaches binned cases
 - * Creates a new DV with re-estimated categories
 - * Attaches new DV to the originally supplied data
 - * Saves several objects as outputs as a list, to be called with \$
 - I saved OPMord as OPMord.RData so I can load into any R session
 - The re-estimated levels outputted by OPMord can be used by block and seqblock for any data. In my case, I will block my data on the education levels that result from training the OPM on the ANES data. The OPM part stops after OPMord has been run and the re-estimated levels have been obtained
- Simulate things by including different groups as the EVS and see how that affects the estimated new number of categories
 - If run with only one variable as EV, these are the resulting number of categories:
 - * race: 4 estimated new categories
 - * income: 3
 - * occupation: 3
 - * gender: 2
 - * pid: 1
 - * age: 1
 - Using just one variable as EV is silly, but it gives a good indicator of the influence of each variable. I played around with a few different combinations, and that confirmed: You get the same 5 categories just with race, income, and occupation. The others don't affect the overall new number
- \$lp v. \$fitted.values
 - I'm using \$1p. Ryan said that I could also use \$fitted.values, which lists the probabilities of assignment for each observation for each education category
 - After investigating a bit, we found that \$1p gave 5 categories but \$fitted.values only 4

- I calculated the percentages of observations within each category (all in opm_create_model.R) and found the results very confusing. I sent them to Ryan. He didn't respond, and it's been ages, so I'm just going to leave this be
- Repeat and visualize Table 2.2
 - The table is created with a placebo treatment, i.e. there is no real treatment. That means Group T2 should be zero. The table is not evidence that the OP method is better
 - Repeat the estimations for Table 2.2 100 times and visualize the distribution of the Group T2 coefficients. This will show which category estimation is closer to zero, which is the true value of that coefficient
 - I set all this up in the opm_test_model_regression_100_obs and opm_test_model_regression_all_obs files
 - The setup works for 100 observations (to test it) and all observations
 - I ran 100 repeats for all observations
 - I ran 1,000 repeats for all observations
- Do Monte Carlo simulations
 - Resources Jeff sent me
 - * https://scholar.cu.edu.eg/sites/default/files/mohamed_abonazel/files/how_to_create_a_mon
 - * https://statweb.stanford.edu/ owen/mc/
 - * http://citeseerx.ist.psu.edu/viewdoc/download?doi=10.1.1.703.5878&rep=rep1&type=pdf
 - MVN data with some cross-correlations
 - I know the true treatment effect here
 - So when I then block on categories 1:15 and 1:5, I know which one performs better
 the one that's closer to the true treatment effect
 - Set up in opm_monte_carlo.Rmd
 - Still needs tweaking, though I'm not sure in which way(s)
 - Further space out theta and adjust rounding of theta.star to achieve greater difference (play around)
 - Sent it to Jeff
 - Space it out some more; play with the sample size; modify the covariate generation with more cross-correlation
 - * I spaced theta out in many different ways and played with the sample size barely any change
 - * Y is based on theta and X comes from the ANES correlation matrix
 - * I could manually change the correlation matrix, but then it wouldn't be the ANES correlations any more. Is that what he meant?
 - * How can I make Y correlate more strongly with X but still create Y from theta and X from the ANES?
 - * Try link Jeff sent me (first steps in R file)
 - * The results never really change, no matter what I do with the correlations
 - * I implemented exactly what was in the link; now Jeff tells me that this doesn't create realistic data and doesn't go anywhere. Then what was the point of the link?
 - I need to speak more with Jeff/Ryan to figure this out. I'll pick this up again when the comprehensive framing draft is done and ordinal missing has been signed off

on

- I emailed Jeff and Ryan the current chapter, where we are, what the next steps should be etc. and asked Eileen to set up a doodle for a zoom call
- I spoke with Jeff. Ryan never responded or filled in the Doodle

Simulations

- Use the ANES data and block it into 5 treatment groups, once with the ordered categories, once with the ANES categories. Calculate differing group means, within-group and between-group variances
- That's not a simulation at the moment, since I can only do that once. Jeff told me to do that, then we'll address the next steps
- I got the analysis and a great table with the group means. I also got all the output for the variances and put that into extensive tables as well
- I don't really know what to make of the output, but I sent everything to Jeff with my attempts at interpreting things
- Waiting for feedback from Jeff

Crispify writing

- 2.1 I'm missing an opportunity to bring in Covid here. A paragraph that says "what if we did this today?" would be good, about the human expectations connected with this. The Kahnemann example even talks about an Asian diseas, so make it relevant to today. Because everyone will think about Covid when they read about "Asian disease"
- Define Mahalanobis and Euclidian distance in mathematical terms (i.e. the algebraic formulas) (bottom of p. 10). I can move the MD formula up from a later page, but make it an equation (i.e. in the middle of the page, not in-line)
- Figure 2.2: Make the sections where the graphs overlap black (not grey). Add to the legend that the then-black sections show where randomized and blocked overlap (that wasn't clear to Jeff)
- I also need to talk more about figure 2.2 in the text. What does it mean that these distributions are different and imbalanced? I only have one sentence about this figure at the moment
- Discuss the ANES when I first mention it. Pretend that I'm talking to someone who's never heard of it before. Explain what it is etc.
- Not technical enough, not enough background maths in general. Put some algebra/formulas back in from Ryan (that I had originally taken out again), but put them in my own notation
- Make the chapter stand on its own by repeating things from the introduction a bit. "Recall that ...", "As noted in chapter 1 ..." etc.
- Table 2.1: Make the vertical bars bigger or bold. Line up the bars vertically. That can be done with the tabular command.
 - $\begin{tabular}{0{}} r0{\$}r0{\$} r0{\$} r0$
- 2.3.2 Add some stuff about what a placebo regression is, some background, some citations
- Figure 2.4: Come up with some bolder colors. Experiment with other colors that are stronger, more forceful. Leave overlapping part as it is (i.e. don't make that one black)