

# Evaluating the impact of HISP: Regression Discontinuity Designs (RDD)

In the design of HISP, the authorities targeted the program to low-income households using **the national poverty line**. The poverty line is based on a poverty index that assigns each household in the country a score between 20 and 100 based on its assets, housing conditions, and sociodemographic structure. **The poverty line has been officially set at 58**. This means that all households with a score of 58 or below are classified as poor, and all households with a score of more than 58 are considered to be nonpoor. Even in the treatment villages, only poor households are eligible to enroll in HISP.

We will conduct 4 steps to measure HISP with RDD:

- Step 1: Check data eligibility
- Step 2: Apply RDD
- Step 3: Set RDD robustness check point
- Step 4: Estimate treatment effect

## Set up

### Launching stata from the jupyter notebook

```
In [5]: %%capture
import stata_setup
import os
os.chdir('C:\Program Files\Stata17\utilities')
from pystata import config
config.init('mp');
```

### Initial set up of log file and load data

```
In [6]: %%capture
%%stata

clear
set more off, perm

# redirect to workplace
cd "C:\Users\USER\Desktop\Charlene\2022 Charlene at York\Evaluation of Health Policy\practical exercise"

# Load data
use "evaluation.dta", clear

# Limit sample to the cross section of post-treatment data
drop if round==0
```

### Create(rename) variable for treatment effect evaluation

```
In [7]: %%capture
%%stata

# create generic variable (y)
clonevar y=health_expenditures
label var y "out of pocket health expenditure pc/pa"
clonevar d=enrolled
label var d "Treatment"

# create potential outcome y0 and y1
clonevar y0=y
replace y0=. if d==1
clonevar y1=y
replace y1=. if d==0

# summarise outcome of the treated and control group
bysort d:summ y y0 y1
tabstat y y0 y1, by(d)

# Create global list of regressors
global xs "age_hh age_sp educ_hh educ_sp female_hh indigenous hhsize dirtfloor bathroom land hospital_distance"
```

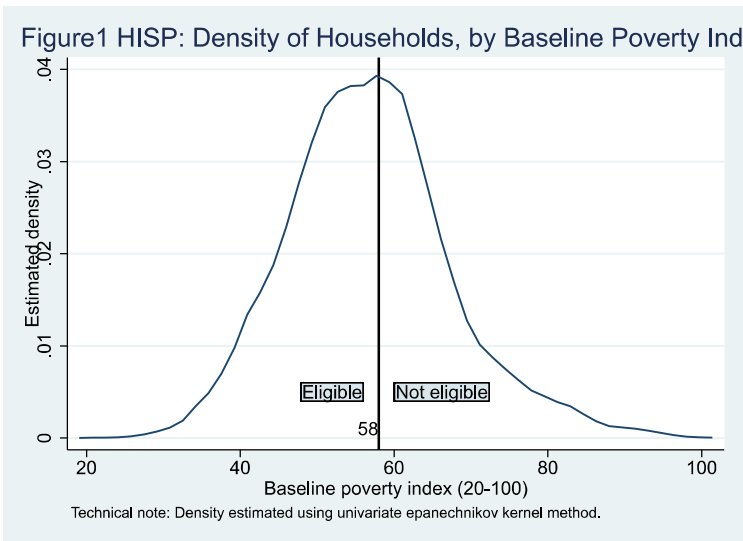
## Step1: Check Data Eligibility

Before carrying out the regression discontinuity design estimations, we shall check the data eligibility by answering:

- Whether there is any evidence of **manipulation of the eligibility index**?
- Whether **households respected their assignment to the treatment** and comparison groups on the basis of their eligibility score?

To answer the first question, I plot the percentage of households against the baseline poverty index (figure 1). The figure does not indicate any "bunching" of households right below the cutoff of 58.

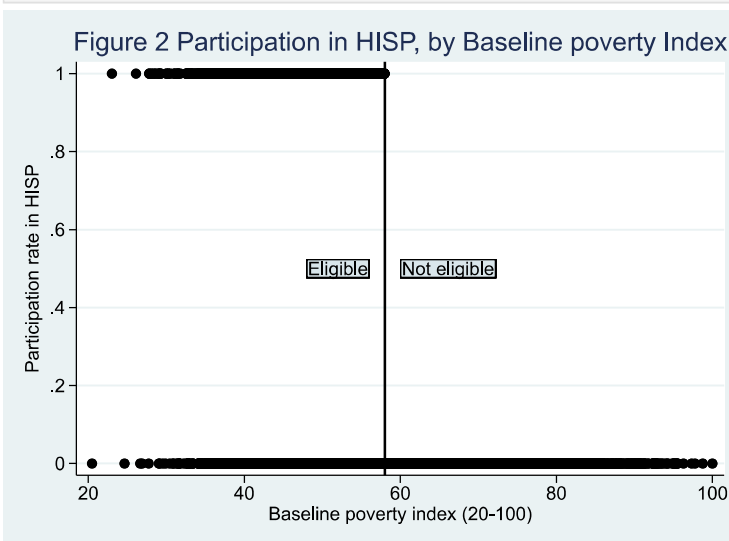
```
In [8]: %%stata
kdensity poverty_index, title("Figure1 HISP: Density of Households, by Baseline Poverty Index") ytitle("Estimated density") xt
```



Next, to answer the second question, I plot participation in the program against the baseline poverty index (figure 2). Figure 2 shown that two years after the start of the pilot, only households with a score of 58 or below (that is, to the left of the poverty line) have been allowed to enroll in HISP. In addition, all of the eligible households enrolled in HISP. In other words, here find full compliance and have a "sharp" RDD. (Two method show below: **rdplot** and **graph tw scatter**)

```
In [9]: %%capture
%%stata
qui rdplot enrolled poverty_index, c(58) lowerend(20) upperend(100) graph_options(title(RDD plot of treatment) xtitle(Poverty Index) ytitle(Enrollment))
```

```
In [10]: %%stata
graph twoway scatter enrolled poverty_index, title("Figure 2 Participation in HISP, by Baseline poverty Index") ylabel(0, .2, .4, .6, .8, 1) xline(58)
```



## Step 2: Apply RDD

Now I process to apply the RDD method to compute the impact of the program. Using follow-up data (treatment\_locality == 1), I again plot the relationship between the scores on the poverty index and predicted health expenditures and find the relation illustrated in figure 3.

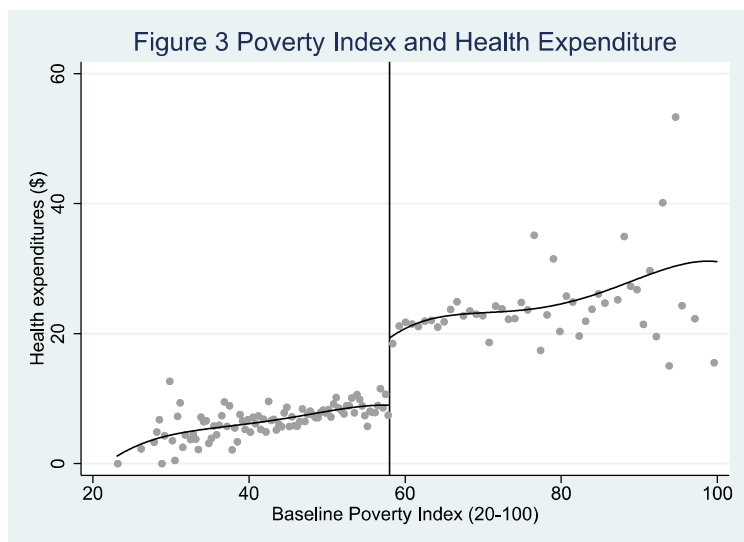
```
In [11]: %%capture
%%stata

# ssc install rdrobust

# clone the running/ forcing variable (rv)
clonevar rv = poverty_index

# restrict the sample to the relevant Locality
keep if treatment_locality == 1
```

```
In [12]: %%stata
qui rdplot y rv, c(58) lowerend(20) upperend(100) graph_options(title(Figure 3 Poverty Index and Health Expenditure) xtitle(Baseline poverty index) ytitle(Health expenditure))
```

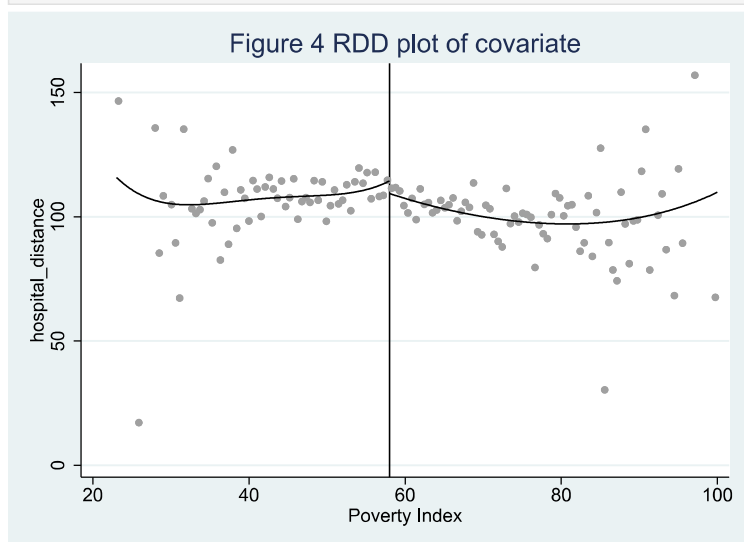


The discontinuity reflects a decrease in health expenditures for those households eligible to receive the program. Given that households on both sides of the cutoff score of 58 are very similar, the plausible explanation for the different level of health expenditures is that one group of households was eligible to enroll in the program and the other was not.

### Step 3: Set RDD Robustness Check

To make sure the running variable(poverty index) only react with our outcome(health expenditure). Here I plot a robustness check for the covariates(hospital\_distance) against the running variables(health expenditure) to make sure they are not with RDD trends. The result in figure 4 shown that the covariates did not response to the running variable.

```
In [13]: %%stata
          qui rdplot hospital_distance rv, c(58) lowerend(20) upperend(100) graph_options(title(Figure 4 RDD plot of covariate) xtitle(Poverty Index))
```



### Step 4: Estimate Treatment Effect

Now estimate the treatment effect using rdrobust

```
In [14]: %%stata
          rdrobust y rv $xs, c(58) h(10)
```

Sharp RD estimates using local polynomial regression.

```
Cutoff c = 58 | Left of c   Right of c           Number of obs =      496
> 0 -----+-----
> 1          Number of obs |      2965      1995          BW type      =      Manua
> r          Eff. Number of obs |      1887      1437          Kernel      = Triangula
> N          Order est. (p) |          1          1          VCE method  =          N
          Order bias (q) |          2          2
          BW est. (h) |     10.000     10.000
          BW bias (b) |     10.000     10.000
          rho (h/b) |      1.000      1.000
```

Outcome: y. Running variable: rv.

```
-----+-----
> -          Method |   Coef.   Std. Err.   z    P>|z|   [95% Conf. Interval
> ] -----+-----
> -          Conventional |  10.689   .74145   14.4170  0.000   9.23627   12.142
> 7          Robust |      -      -     9.0610  0.000   7.69788   11.947
> 3 -----+-----
> -
```

```
In [15]: %%stata
         rdrobust y rv $xs, c(58) h(10) kernel(uni)
```

Sharp RD estimates using local polynomial regression.

```
Cutoff c = 58 | Left of c   Right of c           Number of obs =      496
> 0 -----+-----
> 1          Number of obs |      2965      1995          BW type      =      Manua
> m          Eff. Number of obs |      1887      1437          Kernel      = Unifor
> N          Order est. (p) |          1          1          VCE method  =          N
          Order bias (q) |          2          2
          BW est. (h) |     10.000     10.000
          BW bias (b) |     10.000     10.000
          rho (h/b) |      1.000      1.000
```

Outcome: y. Running variable: rv.

```
-----+-----
> -          Method |   Coef.   Std. Err.   z    P>|z|   [95% Conf. Interval
> ] -----+-----
> -          Conventional |  10.799   .6872   15.7148  0.000   9.4523   12.146
> 1          Robust |      -      -    10.2192  0.000   8.47911   12.503
> 4 -----+-----
> -
```

## Is the result shown valid for all eligible households?

No, the RDD estimates represent the effects for households very close to the cutoff poverty index score. Intuitively, this is the region where eligible and ineligible households have most similar characteristics and as such can be compared.

## Compared with the impact estimated with the randomized assignment method, what does this result say about those households with a poverty index of just under 58?

This result says that households just under the poverty line have a slightly smaller reduction in health expenditures than the average eligible household (about \$1 less). Households with a poverty index just under 58 will spend on average 9.03 less on health as a result of the HISP. This is less than the result in randomized assignment, which was an average decrease in health expenditures of 10.

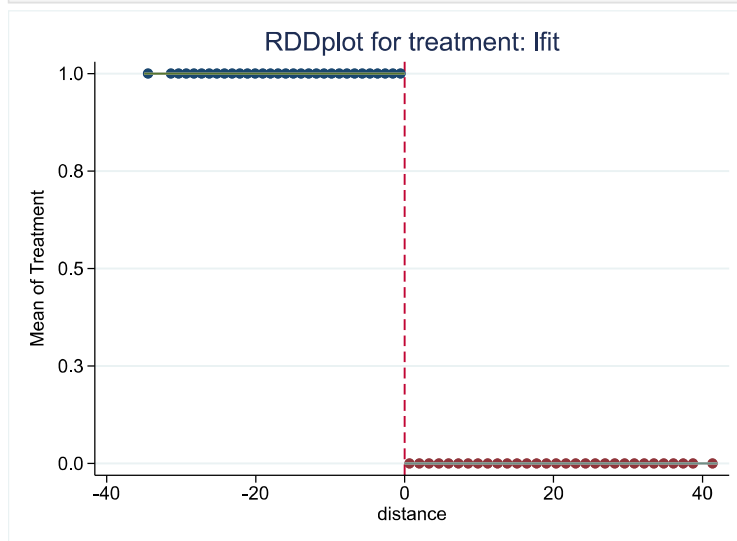
## Based on the RDD impact estimates, should the HISP be scaled up nationally?

No, based on this result, the HISP should not be scaled up nationally because it decreased health expenditures by less than the \$10 threshold level.

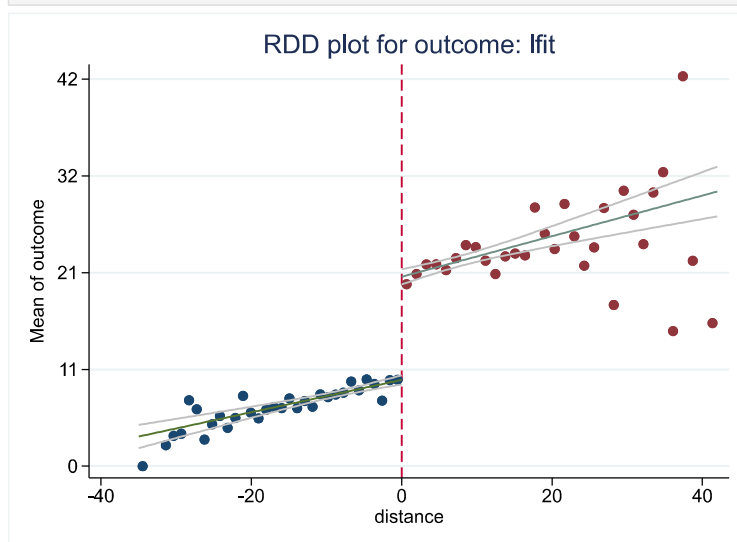
## Additional Method

```
In [16]: %%capture
%%stata
qui gen distance = rv-58
qui gen cutoff = distance > 0
```

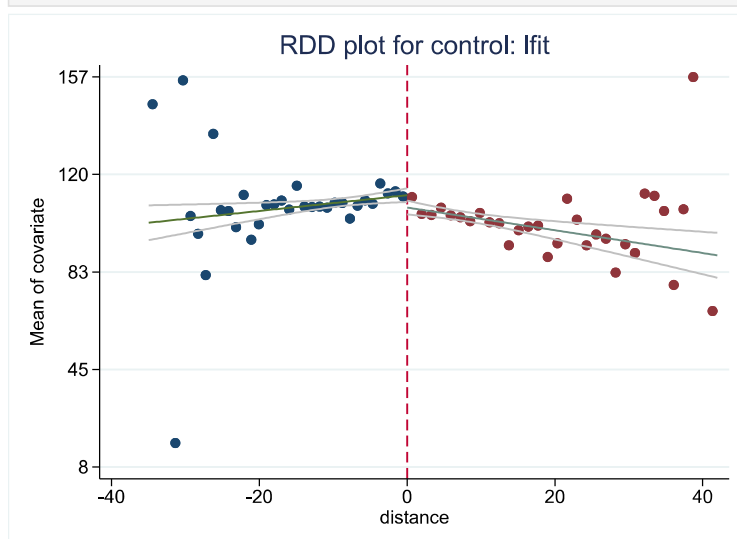
```
In [17]: %%stata
qui cmogram d distance, cut(0) scatter line(0) lfitci graphopts( ytitle(Mean of Treatment) ylabel(, angle(horizontal)) title(RDDplot for treatment: lfit
```



```
In [18]: %%stata
qui cmogram y distance, cut(0) scatter line(0) lfitci graphopts(ytitle(Mean of outcome) ylabel(, angle(horizontal)) title(RDD
```



```
In [19]: %%stata
qui cmogram hospital_distance distance, cut(0) scatter line(0) lfitci graphopts(ytitle(Mean of covariate) ylabel(, angle(horizontal)) title(RDD
```



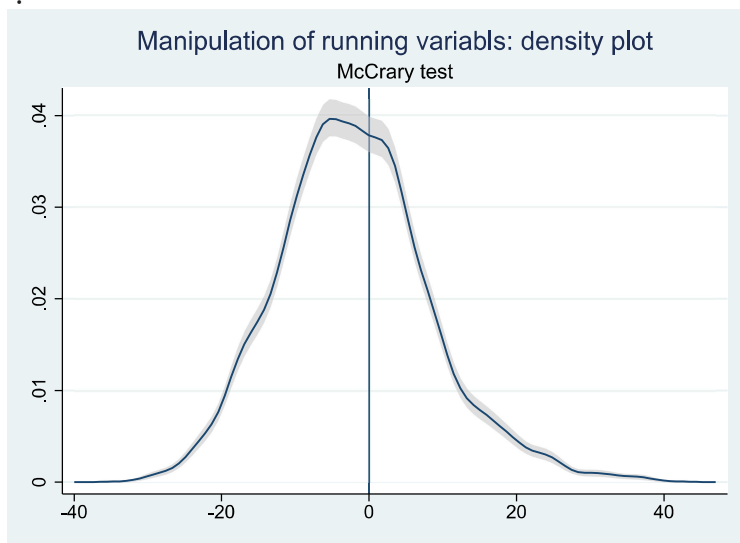
```
In [20]: %%stata
qui dstat density distance
dstat graph, title(Manipulation of running variables: density plot) subtitle(McCrary test) xline(0, lcol(navy) lwidth(medium))
```

```

. qui dstat density distance

. dstat graph, title(Manipulation of running variabls: density plot) subtitle(M
> cCrary test) xline(0, lcol(navy) lwidth(medium) lp(solid)) note($note) graphr
> egion(margin(r small))
(note: named style sma not found in class gsize, default attributes used)

```



In [ ]: