Week 10: Regression discontinuity designs

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Health Services Research Methods I
HSMP 7607
2020

Outline

- Review of RD design and assumptions
- Parametric estimation
- RDD and complete lack of overlap
- Examples
- Nonparametric estimation: -lpoly- and -rdrobust-
- Detour on instrumental variables (IV)
- Fuzzy RDD as IVs

Features

- The key feature of RDD is that there is a *continuous* variable X_i that determines who gets treatment, denoted by D_i (1 if treated). By convention X is called the **running variable**, the **assignment variable** or the **forcing variable**
- In **sharp RDD**, a unit is treated if $X_i >= c$ and not treated if $X_i < c$. That is, D_i is a deterministic function of X_i: $D_i = f(X_i)$. The running variable completely determines who gets treatment
- We must observe X and know the **cutoff** or **threshold** c
- In **fuzzy RDD**, we can think of D as a random variable given X, but $E[D_i|X_i = c]$ is known to be discontinuous at c. Note that $E[D_i|X_i = c] = Pr[D_i = 1|X_i = c]$
- In fuzzy RDD $f(X_i)$ is not a deterministic function of X_i; other variables affect treatment assignment, some of them could be *unobserved*
- Said another way, in fuzzy RDD X at c is a predictor of who gets treatment but it does not completely determines treatment assignment

Identification

- One assumption of RDD is that it requires the continuity of X for identification, although in practice some RDD studies have used discrete running variables. The continuity of X is required because identification is at the limit
- A comparison of $lim_{x \to c} E[Yi|Xi = x]$ and $lim_{x \leftarrow c} E[Yi|Xi = x]$ would provide an estimate of treatment effects (note the direction of the arrows)
- The above is equivalent to: $lim_{x \to c} E[Yi|Xi = x, D_i = 0]$ and $lim_{x \leftarrow c} E[Yi|Xi = x, D_i = 1]$ since in this example to right the right of c everybody gets treatment; to the left nobody does
- So:

  $lim_{x \to c} E[Yi|Xi = x] \approx E[Y_{0i}|X_i = c]$ and

  $lim_{x \leftarrow c} E[Yi|Xi = x] \approx E[Y_{1i}|X_i = c]$
- Remember that Y_{0i} and Y_{1i} is the potential outcome notation. See Hahn et al. (2001) for details

Assumptions

- The most important exclusion restriction assumption is the so-called **no-manipulation-with-precision** assumption
- The identification of treatment effects is based on X being like a "randomizer" around c. Imagine that X is a uniform random variable used to assign treatment. If $X >= c$, a unit receives treatment
- In RDD, X has the same role except that we don't assume that X is independent of the outcome Y. In most applications, X and Y are correlated in some form and must condition on it
- However, if c is not arbitrary or has a deterministic relationship to Y or if units could **–with precision–** determine their scores X and thus choose to receive treatment or not, then X around c is not like a randomizer anymore – there is some form of self-selection that could depend on unobservables
- In part, it is testable. Units wouldn't look similar close to c and there would be "heaping" close to c. However, we can't rule out manipulation with precision with data – we must argue for it with subject knowledge (it's an exclusion restriction)

Estimation

- One key issue with estimation in sharp RDD is that we have **complete lack of overlap**
- Remember, overlap requires that $0 < P(D_i = 1|\mathbf{X}_i) < 1$ for the domain of $\mathbf{X}_i$
- In the domain of the running variable X_i, this is clearly not satisfied. In sharp RDD, $P(D_i = 1|X_i < c) = 0$ and $P(D_i = 1|X >= c) = 1$
- Remember the issue with lack of overlap. **We rely on extrapolation to estimate treatment effects**
- Said another way, we may not be able to correctly estimate treatment effects if we get the functional form $Y_i = f(X_i)$ wrong
- The problem is we never know if we get it right or not, so model specification is a key issue in RDD estimation. The problem screams for a **nonparametric** estimation method
- We will use both, parametric and nonparametric methods (or semiparametric)

Estimation

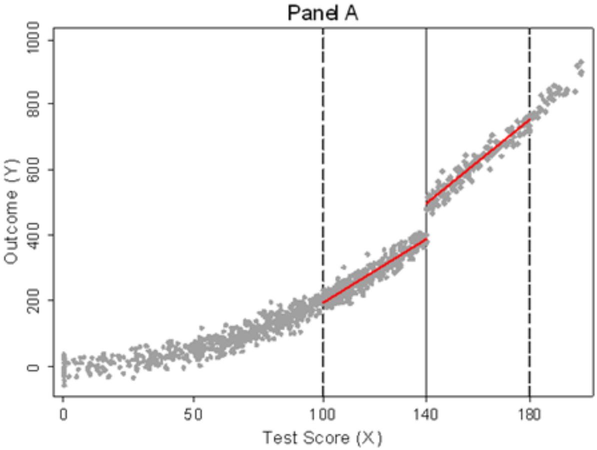
- The other key and related estimation issue is that the identification of treatment effects is at $X_i \to c$ (at the limit)
- The more observations we use far away from c on X the more we rely on extrapolation and functional form assumptions
- The closer we get to c the better, but then we may not have enough sample sizes
- It's a bias-variance trade-off: closer to c, less bias and more variance; farther way, more bias but less variance
- We will see some optimal bandwidth methods. The idea is to restrict the estimation to a window around $X_i = c$, which can be of different sizes to the left or the right

Interpretation

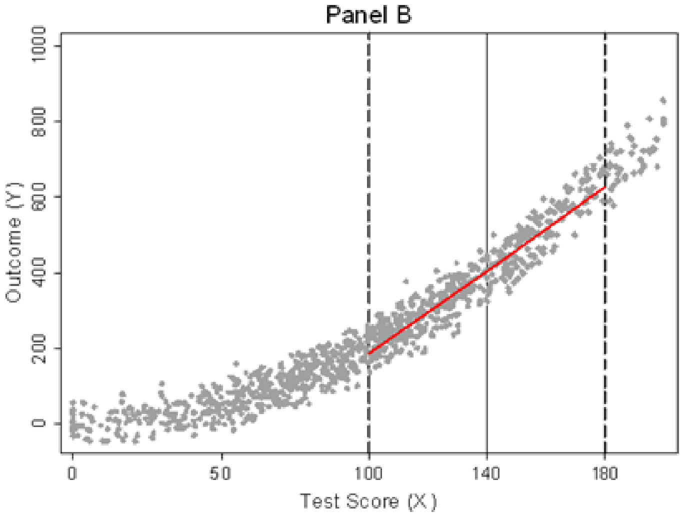
- In RDD, treatment effects are local average treatment effects or LATE
- We don't estimate the effect of getting the treatment, but rather the effect of getting the treatment for units that were close to c, not everybody in the sample (that's the "local" part)
- In a sense, this is the price we pay for being able to estimate treatment effects. However, in some applications, we might actually be interested in this particular group and not others
- In fuzzy RDD, we need to talk about the "complier" or the "marginal patient" or "marginal unit"

Example of positive treatment effect

- Simulated data with $c = 140$ and window $(100, 180)$



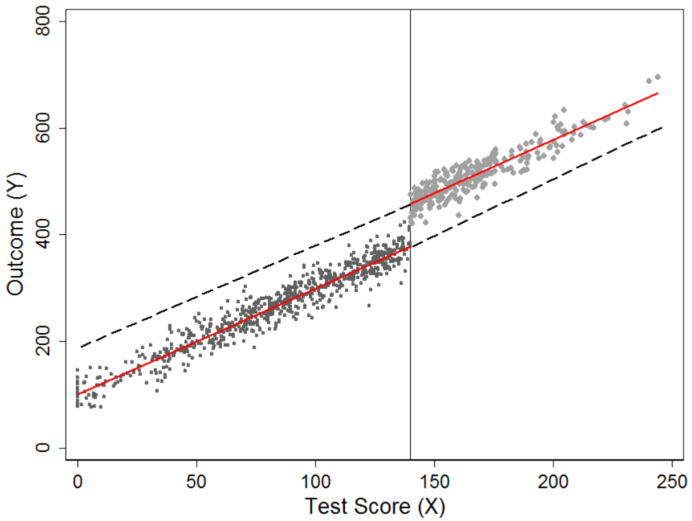
No effect



Panel B
Outcome (Y)
Test Score (X)
0
200
400
600
800
1000
0
50
100
140
180

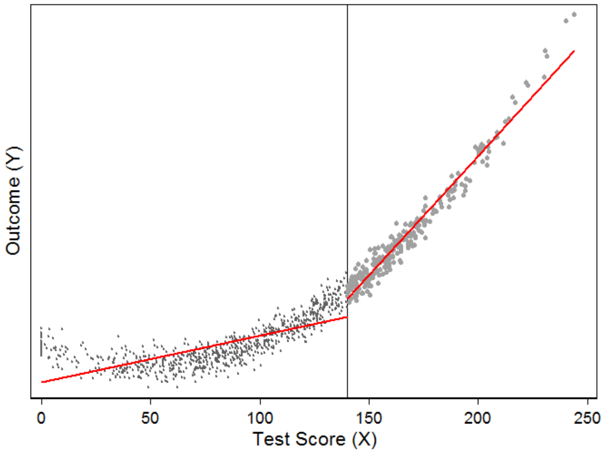
Extrapolation

Dashed lines are extrapolations. If real-life example were like this, life would be easier: perfect linear relationship, so extrapolation is not a problem



A bit more realistic

- True relationship is non-linear, but we use a linear model and incorrectly find a positive treatment effect



Parametric estimation

- Linear relationship between Y and X: $Y_i = \beta_0 + \beta_1 D_i + \beta_3 X_i + \epsilon_i$
- $D_i = 1$ if subject i received treatment and $D_i = 0$ otherwise. We can also write this as $D_i = \mathbf{1}(X_i \geq c)$ or $D_i = \mathbb{1}_{[X_i \geq c]}$
- We can center center the running variable at c:

$$Y_i = \beta_0 + \beta_1 D_i + \beta_3 (X_i - c) + \epsilon_i$$

- We have:

  $E[Y_i|D_i = 1, X_i = c] = \beta_0 + \beta_1$ and $E[Y_i|D_i = 0, X_i = c] = \beta_0$, so:

  $E[Y_i|D_i = 1, X = c] - E[Y_i|D_i = 0, X_i = c] = \beta_1$
- Note that in $Y_i = \beta_0 + \beta_1 D_i + \beta_3 X_i + \epsilon_i$ there is no interaction between X and D so the effect of D does not depend to the value of X. In the above models, β_1 is the same

Parametric estimation

- If we add an interaction, we have:
  $Y_i = \alpha_0 + \alpha_1 D_i + \alpha_2(X_i - c) + \alpha_3(X_i - c) \times D_i + \eta_i$
- Now α_1 is the treatment effect at $X_i = c$ since at $X_i = c$, $X_i - c = 0$. If $\alpha_3 \neq 0$, then the treatment effect at some other point could be different, but we care about the treatment effect at the discontinuity
- As we saw with some examples, the assumption of a linear relationship between Y and X is strong and limiting. We could relax it
- To keep the notation simpler, let $\tilde{X} \equiv (X - c)$. The model then becomes: $Y_i = \alpha_0 + \alpha_1 D_i + \alpha_2 \tilde{X}_i + \alpha_3 \tilde{X}_i \times D_i + \eta_i$
- We could add a quadratic term to relax the linear assumption: $Y_i = \alpha_0 + \alpha_1 D_i + \alpha_2 \tilde{X}_i + \alpha_3 \tilde{X}_i^2 + \alpha_4 \tilde{X}_i \times D_i + \alpha_5 \tilde{X}_i^2 \times D_i + \eta_i$
- We could add polynomials of higher order. That used to be the usual recommendation

Parametric estimation

- Gelman and Imbens (2019) pointed our several problems and recommend using only polynomials up to the second degree (quadratic)
- They justify the approach in three ways:
  - Polynomials impose "weights" that can be noisy with polynomials of higher order (the average treatment effect is a weighted function of X)
  - Estimates can be sensitive to the degree of the polynomial
  - Confidence intervals don't have good coverage with higher order polynomials
- See their article for more examples
- Of course, all these arguments are specification error type of arguments since a priori we do not know the correct functional form

Covariates

- If the assumptions of RDD hold, then all observed and unobserved covariates are balanced and we don't need to include them
- In practice, we often include the most relevant confounders. The model is then
- $Y_i = \alpha_0 + \alpha_1 D_i + \alpha_2 \tilde{X}_i + \alpha_3 \tilde{X}_i^2 + \alpha_4 \tilde{X}_i \times D_i + \alpha_5 \tilde{X}_i^2 \times D_i + \mathbf{Z}_i \gamma + \eta_i$
- It's also possible to extend the model to accommodate treatment heterogeneity by interacting D with one of the variables in $\mathbf{Z}$
- Of course, we don't need to assume that Y is normally distributed conditional on covariates. We can relax that assumption and estimate other type of models (any of the GLM models, for example)

Testing assumptions

- Besides checking that the balance around the cutoff point is good, there is another way of verifying that the assumptions are met
- **There shouldn't be any discontinuity on the covariates**
- So we can do the same RDD analysis for each of the *continuous baseline covariates* to verity that they are not discontinuous at $X_i = c$
- If we see a discontinuity in a covariate, that may imply that the discontinuity in the *outcome* is due to a discontinuity in a confounder and not a treatment effect
- Graphical presentations of this analysis are helpful. It's the same analysis we will below for the outcome, but we replace the outcome with each continuous covariate in $\mathbf{Z}$

Data

- We will start with an example from Lee, Moretti, and Butler (2004)
- Forcing variable is Democratic vote share. If $c > 50\%$ then the Democratic candidate wins. Outcome is a liberal voting score from the Americans for Democratic Action (ADA)
- Do candidates who are elected in close elections tend to moderate their congressional voting? In this example, LATE is what they authors wanted
- Nowadays the research question is kind of funny. Moderation is so last century

```
describe score demvoteshare age sex medianincome pcturban pctblack

              storage   display    value
variable name   type    format     label      variable label
------------------------------------------------------------------------------------------
score           float   %9.0g
demvoteshare    float   %9.0g
age             int     %8.0g
sex             byte    %10.0g     V9
medianincome    double  %12.0g                P107A001
pcturban        float   %9.0g
pctblack        float   %9.0g
```

Stats

- Some basics stats

```
* Treatment variable
gen     d = 1
replace d = 0 if demvoteshare < 0.5

sum demvoteshare age sex medianincome pcturban pctblack  if d==1

    Variable |        Obs        Mean    Std. Dev.       Min        Max
-------------+---------------------------------------------------------
demvoteshare |      8,097     .727859    .1670382   .5002307          1
         age |      8,068    51.85957    10.77453         26         88
         sex |      8,068    1.035821     .185854          1          2
medianincome |      5,659    11209.68    6305.193       1968      33404
    pcturban |      5,659    .7462079     .244452       .177   1.000002
-------------+---------------------------------------------------------
    pctblack |      5,659    .1341779    .1587711          0   .9205155

sum demvoteshare age sex medianincome pcturban pctblack  if d==0

    Variable |        Obs        Mean    Std. Dev.       Min        Max
-------------+---------------------------------------------------------
demvoteshare |      5,480    .3663305    .1064886          0    .499875
         age |      5,371    51.96518    10.02428         27         86
         sex |      5,375    1.035349    .1846771          1          2
medianincome |      3,599     12002.9    7014.439       2085      33404
    pcturban |      3,599    .6660516    .2154873       .171   1.000002
-------------+---------------------------------------------------------
    pctblack |      3,599    .0552526    .0764815          0    .542022
```

Closer to cutoff point

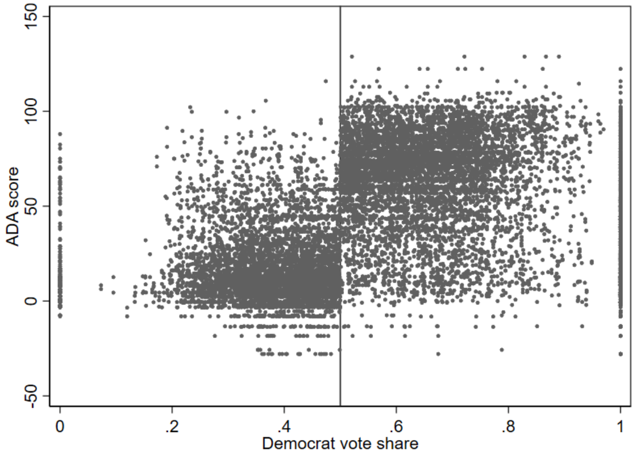
- See how the balance improves; notice some missing data. We could use standardized differences to check balance
- Balancing covariates close to cutoff point when one can argue no precise manipulation can be very convincing (not as propensity score "magic")

```
sum demvoteshare age sex medianincome pcturban pctblack if d==1 & (demvoteshare>.40 & d
> emvoteshare<.60)

    Variable |        Obs        Mean    Std. Dev.       Min        Max
-------------+---------------------------------------------------------
demvoteshare |      2,204    .5484703    .0288765   .5002307   .5997699
         age |      2,188    48.64762    10.40249         26         87
         sex |      2,188    1.031993    .1760208          1          2
medianincome |      1,460    10691.14    5931.001       2608      30726
    pcturban |      1,460    .7109719    .2302929       .193   1.000002
-------------+---------------------------------------------------------
    pctblack |      1,460    .0751407    .0914119          0    .889344

sum demvoteshare age sex medianincome pcturban pctblack if d==0 & (demvoteshare>.40 & d
> emvoteshare<.60)

    Variable |        Obs        Mean    Std. Dev.       Min        Max
-------------+---------------------------------------------------------
demvoteshare |      2,428    .4502578    .0283787   .4000038    .499875
         age |      2,354    51.34749     10.4509         27         83
         sex |      2,358    1.025869    .1587792          1          2
medianincome |      1,303    10335.45    5845.274       2085      29850
    pcturban |      1,303    .6469805     .212883       .171   1.000002
-------------+---------------------------------------------------------
    pctblack |      1,303    .0633695    .0849373          0    .542022
```

Scatterplot

- Note uncontested elections; see how the bulk of observations shifts after $c = 0.5$

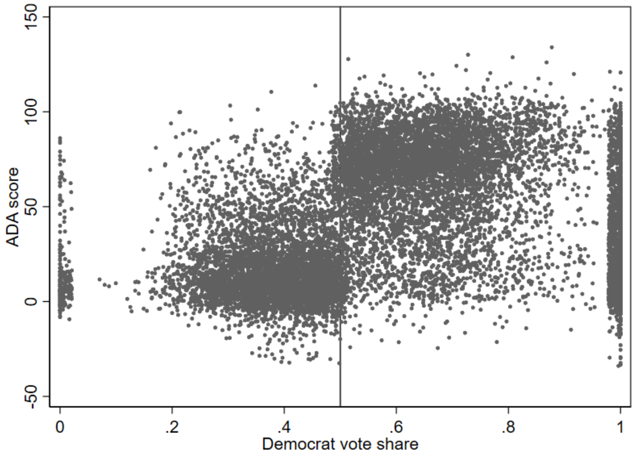
```
scatter score demvoteshare, msize(tiny) xline(0.5) xtitle("Democrat vote share") ytitle("ADA score")
graph export lee1.png, replace
```



Scatterplot with jittering

- When there are too many observations on top of each, jittering helps a lot

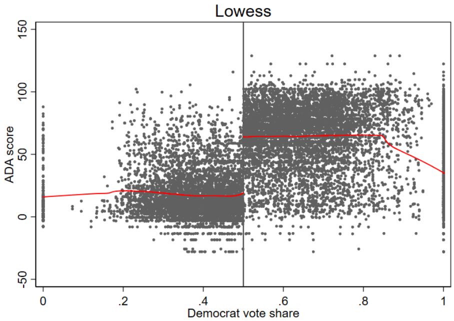
```
scatter score demvoteshare, msize(tiny) xline(0.5) xtitle("Democrat vote share") ///
  ytitle("ADA score") jitter(5)
graph export lee_j.png, replace
```



Smoothing

- Smoothing is helpful to see trends; in RDD we will use it later to estimate models (but not with lowess because of bad boundary properties)
- Remember, lowess is estimating a "local" conditional expectation $E[Y_i|X_i]$

```
capture drop lowess_y_d1 lowess_y_d0
lowess score demvoteshare if d ==1, gen (lowess_y_d1) nograph bw(0.5)
lowess score demvoteshare if d ==0, gen (lowess_y_d0) nograph bw(0.5)

scatter score demvoteshare, msize(tiny) xline(0.5) xtitle("Democrat vote share") ///
  ytitle("ADA score") || ///
  line lowess_y_d1 demvoteshare if democrat ==1, sort color(red) || ///
  line lowess_y_d0 demvoteshare if democrat ==0, sort color(red) legend(off) ///
  title("Lowess")
graph export lee_lowess.png, replace
```



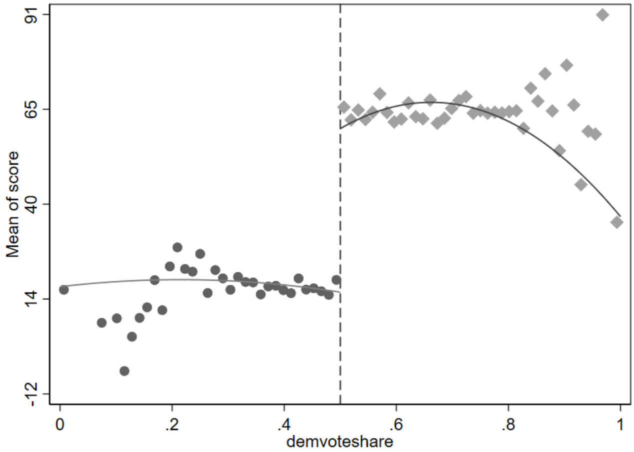
Things to note

- There is large effect at c, so whatever we do will probably result in a positive treatment effect
- Going back to the research question, in close elections, candidates do not moderate their vote. The authors concluded that voter chose "policies" rather than
- Around c, the function is flat, which suggests that not controlling for the running variable would fit well
- Sometimes researchers choose other ways of showing the raw data, in particular if there are a lot of data points
- I like to see the variability and all the data, but less common in published papers
- One option is to "bin" the data like in a histogram to calculate $E[Y_i|X_i]$ in bins defined by X_i values

cmogram

- User written command -cmogram- estimates “binned” $E[Y_i]$
- The lines are polynomials of second order estimated using the binned data (qfit option). Note that a flat line would be better, but we force the quadratic function. It’s an **assumption**

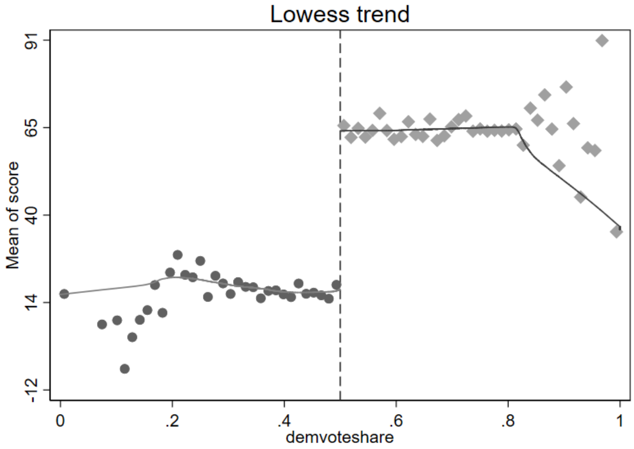
```
cmogram score demvoteshare, cut(.5) scatter line(.5) qfit
graph export lee_binned.png, replace
```



cmogram with lowess

- Now smoothed with lowess again. Remember, with parametric models, model specification is an assumption. Repeat after me...

```
qui cmogram score demvoteshare, cut(.5) scatter line(.5) lowess ///
    title("Lowess trend")
graph save cmlowes.gph, replace
```



Parametric model - linear $f(X)$ using all data

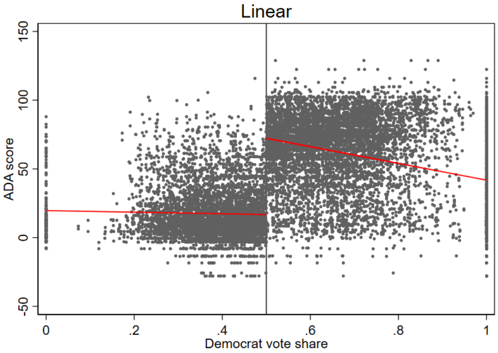
- Linear relationship between Y and X. Model is $Y_i = \alpha_0 + \alpha_1 D_i + \alpha_2(X_i - c) + \alpha_3(X_i - c) \times D_i + \eta_i$

```
reg score i.d##c.x_c, robust

Linear regression                               Number of obs     =     13,577
                                                F(3, 13573)       =    4160.73
                                                Prob > F          =     0.0000
                                                R-squared         =     0.4344
                                                Root MSE          =     24.544

------------------------------------------------------------------------------
             |               Robust
       score |      Coef.   Std. Err.      t    P>|t|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
         1.d |   55.43136   .6373768    86.97   0.000     54.18201    56.68071
         x_c |  -5.682785   2.609124    -2.18   0.029    -10.79703   -.5685406
             |
     d#c.x_c |
          1  |  -55.15188   3.217652   -17.14   0.000    -61.45893   -48.84484
             |
       _cons |   16.81598   .4184826    40.18   0.000      15.9957    17.63627
------------------------------------------------------------------------------
```

Parametric model - linear $f(X)$ using all data

- Always plot your models! Note how the estimated line depends on data away from c. Remember, the line is minimizing the error from each of the point (the sum of square errors)

```
predict double yhatm1 if e(sample)
scatter score demvoteshare, msize(tiny) xline(0.5) xtitle("Democrat vote share") ///
  ytitle("ADA score") || ///
  line yhatm1 demvoteshare if democrat ==1, sort color(red) || ///
  line yhatm1 demvoteshare if democrat ==0, sort color(red) legend(off) ///
  title("Linear")
graph export lee_xc.png, replace
```



Parametric model - quadratic $f(X)$ using all data

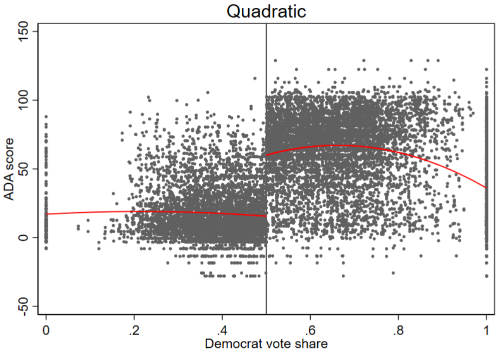
- $f(X)$ is now quadratic. Model is
$Y_i = \alpha_0 + \alpha_1 D_i + \alpha_2 \tilde{X}_i + \alpha_3 \tilde{X}_i^2 + \alpha_4 \tilde{X}_i \times D_i + \alpha_5 \tilde{X}_i^2 \times D_i + \eta_i$

```
reg score i.d##(c.x_c##c.x_c), robust

Linear regression                               Number of obs     =     13,577
                                                F(5, 13571)       =    2589.02
                                                Prob > F          =     0.0000
                                                R-squared         =     0.4559
                                                Root MSE          =     24.075

------------------------------------------------------------------------------
             |               Robust
       score |      Coef.   Std. Err.      t    P>|t|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
         1.d |   44.40229   .9086222    48.87   0.000     42.62126    46.18331
         x_c |   -23.8496   6.710943    -3.55   0.000    -37.00398   -10.69522
             |
 c.x_c#c.x_c |  -41.72917   14.67192    -2.84   0.004    -70.48817   -12.97018
             |
     d#c.x_c |
          1  |   111.8963   9.779383    11.44   0.000     92.72733    131.0652
             |
d#c.x_c#c.x_c |
          1  |  -229.9544   19.53577   -11.77   0.000    -268.2472   -191.6615
             |
       _cons |   15.60635   .5747061    27.16   0.000     14.47984    16.73285
------------------------------------------------------------------------------
```

Parametric model - quadratic $f(X)$ using all data

- Note that we force the curvature. Is this right? We do not know. We could compare fit using in the usual way (Wald test, BIC, etc). In the previous slide, quadratic seems to fit ok

```
predict double yhatm2 if e(sample)
scatter score demvoteshare, msize(tiny) xline(0.5) xtitle("Democrat vote share") ///
  ytitle("ADA score") || ///
  line yhatm2 demvoteshare if democrat ==1, sort color(red) || ///
  line yhatm2 demvoteshare if democrat ==0, sort color(red) legend(off) ///
  title("Quadratic")
graph export lee_xc2.png, replace
```



Parametric model - quadratic restricted to window

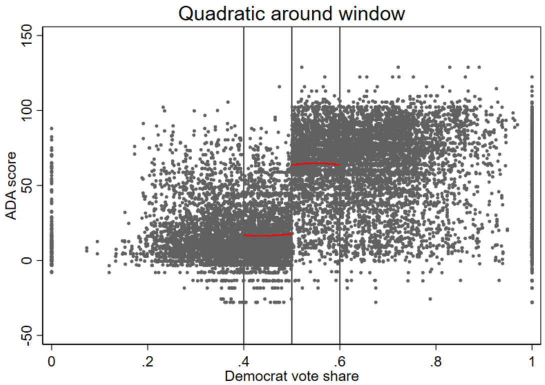
- We now do not use all data; we focus on a bandwidth *h* around *c* of 0.1. At this point, it's an arbitrary window, but it could be based on a comparison of balance for different windows

```
reg score i.d##(c.x_c##c.x_c) if (demvoteshare>.40 & demvoteshare<.60), robust
Linear regression                               Number of obs     =      4,632
                                                F(5, 4626)        =    1132.17
                                                Prob > F          =     0.0000
                                                R-squared         =     0.5549
                                                Root MSE          =     21.327
------------------------------------------------------------------------------
             |               Robust
       score |      Coef.   Std. Err.      t    P>|t|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
         1.d |    45.9283   1.851157    24.81   0.000     42.29915    49.55745
         x_c |   38.63987   54.10772     0.71   0.475    -67.43706    144.7168
             |
  c.x_c#c.x_c |   295.1722   513.8466     0.57   0.566    -712.2123    1302.557
             |
     d#c.x_c |
          1  |   6.507425    88.6282     0.07   0.941    -167.2461     180.261
             |
d#c.x_c#c.x_c |
          1  |  -744.0247   867.1782    -0.86   0.391    -2444.108    956.0581
             |
       _cons |   17.71198   1.183657    14.96   0.000     15.39145    20.03251
------------------------------------------------------------------------------
```

Parametric model - quadratic, bandwidth: $h = .10$

- Note that the curvature is not as noticeable since we don't use observations far away from c. Based on Wald tests, the quadratic terms are not necessary when restricted the estimation to this window

```
predict double yhatm2_w if e(sample)
scatter score demvoteshare, msize(tiny) xline(0.5 0.4 0.6) xtitle("Democrat vote share") ///
  ytitle("ADA score") || ///
  line yhatm2_w`' demvoteshare if democrat ==1, sort color(red) || ///
  line yhatm2_w demvoteshare if democrat ==0, sort color(red) legend(off) ///
  title("Quadratic around window")
graph export lee_xc2_w.png, replace
```



Parametric model - linear restricted to window

- Maybe not even linear? Drop the running variable? That's what the Wald tests suggest

```
reg score i.d##c.x_c if (demvoteshare>.40 & demvoteshare<.60), robust
Linear regression                               Number of obs     =      4,632
                                                F(3, 4628)        =    1886.70
                                                Prob > F          =     0.0000
                                                R-squared         =     0.5548
                                                Root MSE          =     21.324

------------------------------------------------------------------------------
             |               Robust
       score |      Coef.   Std. Err.      t    P>|t|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
         1.d |   47.15915   1.217625    38.73   0.000     44.77203    49.54628
         x_c |   9.421594   13.05183     0.72   0.470    -16.16621     35.0094
             |
     d#c.x_c |
          1  |  -9.127629   21.92807    -0.42   0.677     -52.1171    33.86184
             |
       _cons |   17.22656   .7556057    22.80   0.000     15.74521    18.70791
------------------------------------------------------------------------------
```

Parametric model - no running variable restricted to window

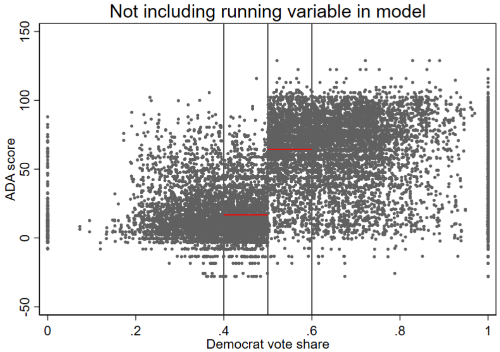
- Even if it seems strange, that's is the best fitting model, which agrees with the lowess graph
- Compare R^2 with the previous model

```
reg score i.d if (demvoteshare>.40 & demvoteshare<.60), robust
Linear regression                               Number of obs     =      4,632
                                                F(1, 4630)        =    5630.09
                                                Prob > F          =     0.0000
                                                R-squared         =     0.5548
                                                Root MSE          =      21.32

------------------------------------------------------------------------------
             |               Robust
       score |      Coef.   Std. Err.      t    P>|t|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
         1.d |   47.64205   .6349402    75.03   0.000     46.39727    48.88684
       _cons |   16.75791   .3765671    44.50   0.000     16.01966    17.49616
------------------------------------------------------------------------------
```

Parametric model - no running variable restricted to window

- Not including the running variable is the same as assuming a "flat" relationship between $E[Y]$ and X. In other words, $E[Y]$ is *mean independent* of X since $E[Y]=E[Y|X]$ for all values of X. Yes, it's an assumption

```
predict double yhatflat_w if e(sample)
scatter score demvoteshare, msize(tiny) xline(0.5 0.4 0.6) xtitle("Democrat vote share") ///
  ytitle("ADA score") || ///
  line yhatflat_w‘’ demvoteshare if democrat ==1, sort color(red) || ///
  line yhatflat_w demvoteshare if democrat ==0, sort color(red) legend(off) ///
  title("Not including running variable in model")
graph export lee_flat.png, replace
```



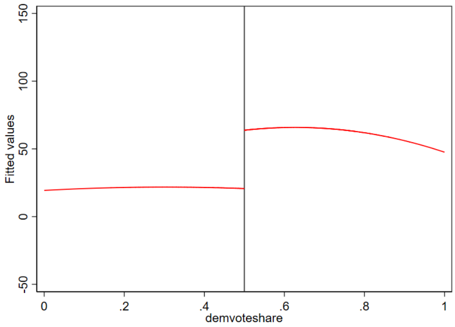
Big picture

- Any parametric model makes an assumption about the functional form between X and Y
- If we thought that other covariates $\mathbf{Z}_i$ should be added to the model, we could repeat this same exercise but then graphs would need to be adjusted
- Our final parametric model ended up being the simplest one
- The best model depends on whether we use all the observations or not
- **The window is of course a very important consideration**. We want to make sure that observed covariates are well balanced
- We should try other windows in sensitivity analyses, but we will see "optimal" windows as well
- You can imagine that with less robust results you can find different results depending on models

Example adding a covariate - adjusted graph

- -margins- a bit cumbersome here so we will do it “by hand”

```
reg score i.d##(c.demvoteshare##c.demvoteshare) pcturban, robust
* Save mean of pcturban
qui sum pcturban
scalar mu = r(mean)
preserve
   * Hold pcturban at mean
   replace pcturban = scalar(mu)
   predict  double yhatadj if e(sample)

   line yhatadj demvoteshare if democrat ==1, sort color(red) || ///
   line yhatadj demvoteshare if democrat ==0, sort color(red) legend(off) ///
        xline(0.5) ylabel(-50(50)150)
   graph export adj.png, replace
restore
```



Nonparametric

- Going back to the beginning. The issue with RDD estimation is that we need to get $f(X_i)$ right, but every single parametric model we try makes an assumption about the shape of $f(X_i)$
- So rather than making assumptions about $f(X_i)$ we could estimate models in which we don't assume a specific functional form – the data drives the shape, which is what lowess showed us
- Lowess has poor boundary properties. RDD estimation is at $X \rightarrow c$, and c is a boundary. We saw this in the first homework (or second?)
- We will use instead Kernel-weighted local polynomial smoothing (command -lpoly-) since it's easier to understand, but it has many limitation as it is
- We will then move to what has now become the standard implementation for RDD using the user-written -rdrobust- command, which estimates similar nonparametric models

Kernel-weighted local polynomial smoothing, lpoly

- With nonparametric methods, the idea is to let the data tell us the shape of $E[Y_i|X_i]$ rather than imposing specification assumptions like we did in the parametric version
- Say we have Y_i, X_i data usually represented as pairs $\{(x_1, y_1), ..., (x_n, y_n)\}$
- We want to estimate a model like $y_i = m(x_i) + \sigma(x_i)\epsilon_i$, but we do not want to assume any functional form for $m(x_i)$
- This is similar to linear regression. We can make $E[\epsilon_i] = 0$ and $var(\epsilon_i) = 1$ so we have that $E[y_i|x_i = x_0] = m(x_0)$, where x_0 is some point $\in X_i$
- Said in simpler terms, for each point x_0 we want to find the "smoothed" $E[y_i|x_i = x_0] = m(x_0)$, which is of course the conditional mean of y_i at $x_i = x_0$
- -lpoly-, like -lowess-, estimates $m(x_0)$ using a weighted polynomial regression

Kernel-weighted local polynomial smoothing, lpoly

- The "local" part is that for each point x_0 only data around x_0 is used defined by the bandwidth h
- The smoothed y_i is a prediction $\hat{y}_i$ resulting from this regression (the intercept)
- For intuition, forget about the weight/kernel for a second and imagine doing this:
  1. Choose a point x_0. Use only data around x_0, say x_{lb} and x_{ub}
  2. Run a polynomial linear regression, say, of degree 2: $y_i = \beta_0 + \beta_1(x_i - x_0) + \beta_2(x_i - x_0)^2 + \epsilon_i$ if $x_{lb} \leq x_i \leq x_{ub}$
  3. The smoothed $\hat{y}_i$ is $\hat{m}(x_0) = \hat{\beta}_0$ (it's the mean at x_0 since we center at x_0)
  4. Repeat for every single point in x. The result is not a parameter but rather a new grid or pairs $\{(x_1, \hat{y}_1), ...(x_n, \hat{y}_n)\}$
- This close to the idea behind lpoly, but it's the kernel that defines, based on the bandwdith, the observations used
- By default -lpoly- creates a new grid that is equally spaced like binning in cmogram. We can, and will, change this option to compute the smoothed treatment effect at $x_i = c$

Kernel-weighted local polynomial smoothing, lpoly

- The kernel part is that the regression in 2) is a weighted regression (like what we did with IPW)
- The weight is the kernel. The most commonly used kernel is the triangular kernel that gives more weight to points close to x_0. The rectangular kernel gives same weight to observations. The default is the Epanechnikov kernel
- The kernel is a function $K(\frac{x_i - x_0}{h})$. Let's define $z \equiv \frac{x_i - x_0}{h}$, so $K(z)$. The numerator is the distance from the point we want to smooth; the denominator is the bandwidth
- With a **rectangular kernel**, $K(z) = 1/2$ if $|z| < 1$ and 0 otherwise
- With a **triangular kernel**, $K(z) = 1 - |z|$ if $|z| < 1$ and 0 otherwise
- The bandwidth h determines which observations are used because if an observation is far away from x_0, the weight is zero
- With a rectangular kernel, the weight is always the same. With a triangular kernel, the weight is larger if closer to x_0
- With rectangular and triangular: if $\frac{|x_i - x_0|}{h} < 1$, the observation is included. So it is included if $|x_i - x_0| < h$, which defines x_{lb} and x_{ub}

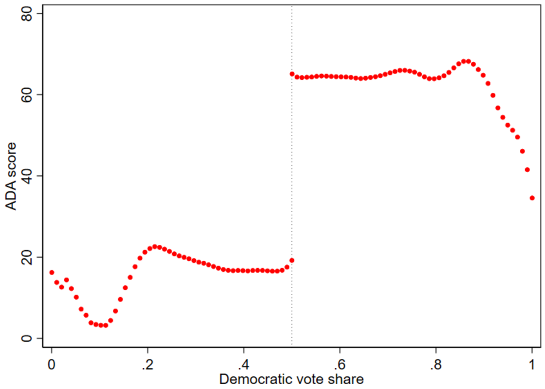
Kernel-weighted local polynomial smoothing, lpoly

- We can choose the order of polynomials
- Bandwidth selection procedures are automated using a Rule of Thumb (ROT) algorithm, but one can choose the bandwidth as well
- Larger bandwidth h produces a "smoother" curve since more observations are used
- **The bottom line is that we use n parametric, weighted regression models to obtain "smoothed" local predictions $\hat{y}_i = \hat{m}(x_i)$ that we call nonparametric estimates of** $E[y_i|x_i = x_0]$. The default is $n = min = (N, 50)$ regressions
- In RDD, we don't care about smoothing all data, we care about estimates at the cutoff point
- So we will use this method to estimate $E[y_i|x_i = c, D_i = 1]$ and $E[y_i|x_i = c, D_i = 0]$

lpoly example

- Smoothing with second degree polynomials
- **Check out the new grid variables x0, sdem0, x1, and sdem1** (see next slide)

```
lpoly score demvoteshare if democrat == 0, nograph kernel(triangle) gen(x0 sdem0)  ///
        bwidth(0.1) degree(2)
lpoly score demvoteshare if democrat == 1, nograph kernel(triangle) gen(x1 sdem1)  ///
        bwidth(0.1) degree(2)
scatter sdem1 x1, color(red) msize(small) msymbol(o) || scatter sdem0 x0, msize(small) msymbol(o) color(red) ///
     xline(0.5,lstyle(dot)) legend(off) xtitle("Democratic vote share") ytitle("ADA score")
graph export lee_lpoly.png, replace
```



lpoly example

- Remember, no parameter of interest is estimated even though we did used N parametric regressions to get $\hat{m}(x_i) = \hat{y}_i$
- The original data is $\{(x_1, y_1), ..., (x_n, y_n)\}$ and now we have a new grid $\{(x'_1, \hat{y}_1), ..., (x'_n, \hat{y}_n)\}$, where $\hat{y}_i$ is the smoothed y_i
- We saved the new grid using the gen() option in variables x0, sdem0, x0, and sdem0
- Remember, by default, lpoly uses an equally spaced grid to divide the x axis, much like cmogram:

```
. list  x0 sdem0  x1 sdem1 in 1/5

     +-----------------------------------------------+
     |        x0       sdem0          x1       sdem1 |
     |-----------------------------------------------|
  1. |         0   16.273488   .50023067   65.160334 |
  2. | .01020153   13.828991   .51043004   64.363744 |
  3. | .02040306   12.661728   .52062942    64.24728 |
  4. | .03060459   14.445168   .53082879   64.335256 |
  5. | .04080613   12.304093   .54102817   64.393172 |
     +-----------------------------------------------+
```

lpoly example

- We can obtain the treatment effect but saving the smoothed values at the cutoff point $x_i = c = 0.5$
- Again, by default lpoly builds an equally spaced grid to calculate $E[y_i|x_i]]$, but we can change that with the "at" option (we could, for example, ask -lpoly- to calculate $E[y_i|x_i]$ at each of the observed values)
- We need to define a variable with cutoff point (the "at" option takes a variable)

```
gen forat = 0.5 in 1
capture drop sdem0 sdem1
lpoly score demvoteshare if democrat == 0, nograph kernel(triangle) gen(sdem0) degree(2)  ///
       at(forat) bwidth(0.1)
lpoly score demvoteshare if democrat == 1, nograph kernel(triangle) gen(sdem1) degree(2) ///
       at(forat) bwidth(0.1)
gen dif = sdem1 - sdem0
list sdem1 sdem0 dif in 1/1
     +-----------------------------------+
     |     sdem1       sdem0        dif |
     |-----------------------------------|
  1. | 65.190977   19.275926   45.91505 |
     +-----------------------------------+
```

- So treatment effect at c is 45.91
- Think about this for a second. We are using all the data, but the estimate at c here is local because of h. So in this sense, we are not using data far away from c to estimate the treatment effect at $x_i = c$

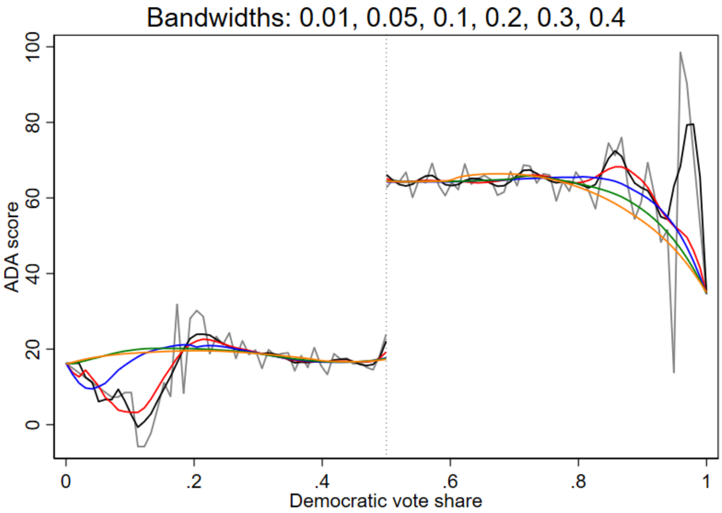
See how bandwidth matters

- Changing bandwidth, from 0.01 to 0.40. Polynomial degree 1. More curvature with higher degree polynomials
- In general, the choice of bandwidth *h* is more important (or makes more of a difference) than the choice of kernel and the order of the polynomial
- gray is the smallest *h*; orange the largest

```
capture drop smoothdem0* smoothdem1* x0* x1*
local co 0
foreach i in 0.01 0.05 0.1 0.20 0.30 0.40 {
   local co = ‘co’ +1
   lpoly score demvoteshare if democrat == 0, nograph kernel(triangle) gen(x0‘co’ smoothdem0‘co’)  ///
         bwidth(‘i’) degree(2)
   lpoly score demvoteshare if democrat == 1, nograph kernel(triangle) gen(x1‘co’ smoothdem1‘co’)  ///
         bwidth(‘i’) degree(2)
}

line smoothdem01 x01, msize(small) color(gray) sort || line smoothdem11 x11, sort color(gray) || ///
     line smoothdem02 x02, color(black) sort || line smoothdem12 x12, sort color(black) || ///
     line smoothdem03 x03, color(red) sort || line smoothdem13 x13, sort color(red) || ///
     line smoothdem04 x04, color(blue) sort || line smoothdem14 x14, sort color(blue) || ///
  line smoothdem05 x05, color(green)sort || line smoothdem15 x15, sort color(green)|| ///
  line smoothdem06 x06, color(orange) sort || line smoothdem16 x16, sort  color(orange) ///
     xline(0.5,lstyle(dot)) legend(off) xtitle("Democratic vote share") ytitle("ADA score") ///
  title("Bandwidths: 0.01, 0.05, 0.1, 0.2, 0.3, 0.4")
graph export lee_dif_bws.png, replace
```

Different bandwidths for the smoothing

- Think about how this would matter at *c* if the mass of points were not so stable



Big picture

- The above examples highlights how a nonparametric approach to estimating RDD works, but it's not that helpful beyond a graphical representation
- We need statistical inference, which means that we need a way to estimate standard errors that allow us to test hypotheses and build confidence intervals (we could get CIs with lpoly; by default the bandwidth is 1.5 larger to calculate SEs; $\rho = 1/1.5 = 0.667$). Since $\hat{m}(x_0)$ is the intercept, we actually do have SEs
- We would also want the capability to incorporate covariates so estimates of treatment effect could be more efficient
- One criticism of nonparametric methods is that we replace one set of assumptions (about model specification) for other assumptions: bandwidth? What degree of polynomials? Assumptions about SEs?
- Much of the work on nonparametric methods is about optimal ways of choosing bandwidths, smoothing parameters, and estimating SEs (variances)
- All these features are part of the -rdrobust- command described in Calonico, Cattaneo, Farrell, and Titiunik (2017)
- Plus -rdrobust- implemented a data-driven *RDD bandwidth* selection around $x_i = c$

rdrobust

```
rdrobust score demvoteshare, c(0.5) h(0.1) p(2)
Sharp RD estimates using local polynomial regression.

     Cutoff c = .5 | Left of c  Right of c            Number of obs =      13577
-------------------+----------------------            BW type       =     Manual
     Number of obs |       5480        8097            Kernel        = Triangular
Eff. Number of obs |       2428        2204            VCE method    =         NN
    Order est. (p) |          2           2
    Order bias (q) |          3           3
       BW est. (h) |      0.100       0.100
       BW bias (b) |      0.100       0.100
         rho (h/b) |      1.000       1.000

Outcome: score. Running variable: demvoteshare.
--------------------------------------------------------------------------------
            Method |   Coef.    Std. Err.    z     P>|z|    [95% Conf. Interval]
-------------------+------------------------------------------------------------
      Conventional |  45.915      1.717   26.7410  0.000    42.5497      49.2804
            Robust |     -          -     19.8261  0.000    40.9024      49.8766
--------------------------------------------------------------------------------
. count if (demvoteshare>.40 & demvoteshare<.60)
  4,632
. di 2428 + 2204
4632
```

- CIs are robust to heteroskedasticity and can accommodate clustering as well
- The default kernel is triangular. I used polynomials of degree 2 to smooth. Note that we obtain the same estimate of treatment effect (45.915) “by hand”
- rdrobust uses one bandwidth for the treatment effect and another for the robust variance, although now we are forcing it to use the same: 0.10, BW est.(b) and BW bias (b)

rdrobust

- We can ask rdrobust to find the optimal bandwidths that are data driven in the sense that they optimize the bias-variance trade-off (the mean square error to be more precise) given the data
- The default is the same bandwidth on each side of the cutoff point (could be different). Note that the optimal bandwidth, 0.13, is not that different than the one we have been using

```
rdrobust score demvoteshare, c(0.5) p(2) bwselect(mserd)
Mass points detected in the running variable.

Sharp RD estimates using local polynomial regression.

     Cutoff c = .5 | Left of c  Right of c            Number of obs =      13577
-------------------+----------------------            BW type       =      mserd
     Number of obs |      5480        8097            Kernel        = Triangular
Eff. Number of obs |      3197        2965            VCE method    =         NN
    Order est. (p) |         2           2
    Order bias (q) |         3           3
       BW est. (h) |     0.136       0.136
       BW bias (b) |     0.185       0.185
         rho (h/b) |     0.732       0.732
        Unique obs |      2770        3351

Outcome: score. Running variable: demvoteshare.
--------------------------------------------------------------------------------
            Method |   Coef.    Std. Err.    z     P>|z|    [95% Conf. Interval]
-------------------+------------------------------------------------------------
      Conventional |  46.227     1.4598   31.6675  0.000    43.3661      49.0882
            Robust |     -          -     27.5319  0.000    42.7683      49.3242
--------------------------------------------------------------------------------
Estimates adjusted for mass points in the running variable.
```

rdrobust

- The bandwidth depends on the smoothing model
- Now we use polynomial of degree 1 (linear). Bandwidth is now smaller, 0.086

```
. rdrobust score demvoteshare, c(0.5) bwselect(mserd)
Mass points detected in the running variable.

Sharp RD estimates using local polynomial regression.

     Cutoff c = .5 | Left of c  Right of c            Number of obs =      13577
-------------------+----------------------            BW type       =      mserd
     Number of obs |      5480        8097            Kernel        = Triangular
Eff. Number of obs |      2112        1895            VCE method    =         NN
    Order est. (p) |         1           1
    Order bias (q) |         2           2
       BW est. (h) |     0.086       0.086
       BW bias (b) |     0.141       0.141
         rho (h/b) |     0.609       0.609
        Unique obs |      2770        3351

Outcome: score. Running variable: demvoteshare.
--------------------------------------------------------------------------------
            Method |   Coef.    Std. Err.    z     P>|z|    [95% Conf. Interval]
-------------------+------------------------------------------------------------
      Conventional |  46.491     1.2405   37.4775  0.000     44.06       48.9227
            Robust |     -          -     31.4254  0.000    43.2929      49.0524
--------------------------------------------------------------------------------
Estimates adjusted for mass points in the running variable.
```

Plots

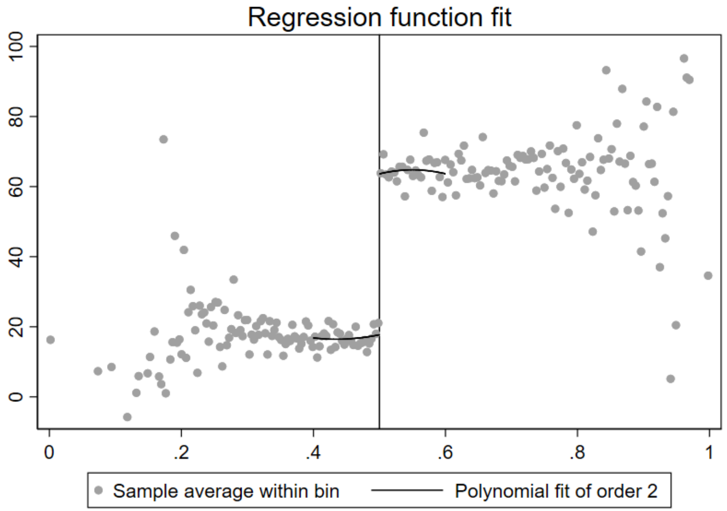
- rdrobust implement plots using a combination of tools we saw before
- It does create bins rather than plotting the raw data in the same way we did it with cmogram, but using a different algorithm
- The plots match the nonparametric treatment effect estimates and the smoothing model
- As usual, we can customize the plot (see graph_options()) but we will use the defaults here

rdplot

- Same syntax as rdrobust

```
rdplot score demvoteshare, c(0.5) h(0.10) p(2)
RD Plot with evenly spaced mimicking variance number of bins using spacings estimators.

        Cutoff c = .5 | Left of c  Right of c        Number of obs  =      13577
----------------------+----------------------        Kernel         =    Uniform
        Number of obs |      5480        8097
   Eff. Number of obs |      2428        2204
  Order poly. fit (p) |         2           2
     BW poly. fit (h) |     0.100       0.100
 Number of bins scale |     1.000       1.000

Outcome: score. Running variable: demvoteshare.
---------------------------------------------
                      | Left of c  Right of c
----------------------+----------------------
        Bins selected |       146         123
   Average bin length |     0.003       0.004
    Median bin length |     0.003       0.004
----------------------+----------------------
    IMSE-optimal bins |         9          26
  Mimicking Var. bins |       146         123
----------------------+----------------------
Rel. to IMSE-optimal: |
        Implied scale |    16.222       4.731
    WIMSE var. weight |     0.000       0.009
    WIMSE bias weight |     1.000       0.991
---------------------------------------------

graph export rdplot2.png, replace
```

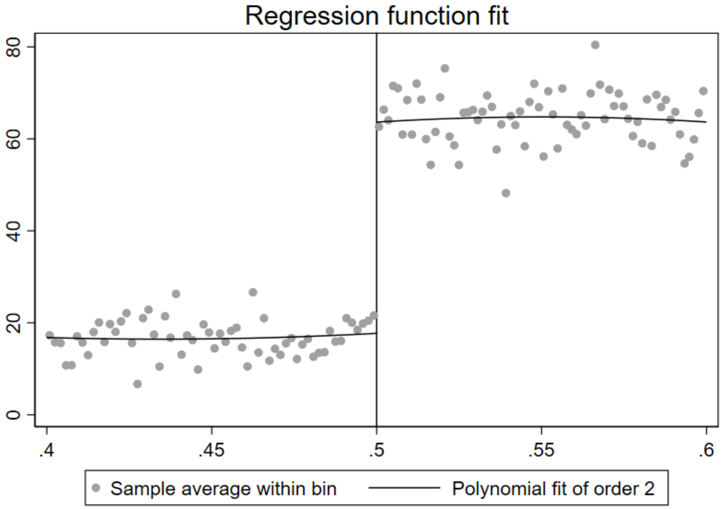
rdplot


Regression function fit
100
80
60
40
20
0
0
.2
.4
.6
.8
1
● Sample average within bin
Polynomial fit of order 2

rdplot

- Restrict to bandwidth

```
rdplot score demvoteshare if 0.4 <= demvoteshare & demvoteshare <= 0.6, c(0.5) h(0.1) p(2)
graph export rdplot2_1.png, replace
```



Covariates

- An important feature of the new -rdrobust- package is that covariates can be added
- Covariates should not change the estimate of treatment effects since they should be balanced (so not confounders), but estimation **could** be more efficient (smaller SEs) –could be noisier too
- Below, we add two and let rdrobust choose the optimal bandwidth. Again, the bandwidth is data driven so it depends on the smoothing model. Bandwidth happened to be 0.106

```
. rdrobust score demvoteshare, c(0.5) bwselect(mserd) covs(pcturban pctblack)
Mass points detected in the running variable.

Covariate-adjusted sharp RD estimates using local polynomial regression.

     Cutoff c = .5 | Left of c  Right of c            Number of obs =       9248
-------------------+----------------------            BW type       =      mserd
     Number of obs |      3599        5649            Kernel        = Triangular
Eff. Number of obs |      1347        1550            VCE method    =         NN
    Order est. (p) |         1           1
    Order bias (q) |         2           2
       BW est. (h) |     0.106       0.106
       BW bias (b) |     0.162       0.162
         rho (h/b) |     0.654       0.654
        Unique obs |      1728        2394

Outcome: score. Running variable: demvoteshare.
--------------------------------------------------------------------------------
            Method |   Coef.    Std. Err.    z     P>|z|    [95% Conf. Interval]
-------------------+------------------------------------------------------------
      Conventional |  45.229     1.4315   31.5952  0.000    42.4233      48.0348
            Robust |     -          -     26.1661  0.000     41.927      48.7166
--------------------------------------------------------------------------------
```

Matching other results

- We can match treatment effect estimates using lpoly and rdrobust. Both use polynomial of 1 degree (linear) now

```
capture drop sdem0 sdem1 forat dif
gen forat = 0.5 in 1
lpoly score demvoteshare if democrat == 0, nograph kernel(triangle) gen(sdem0) degree(1)  ///
       at(forat) bwidth(0.1)
lpoly score demvoteshare if democrat == 1, nograph kernel(triangle) gen(sdem1) degree(1) ///
       at(forat) bwidth(0.1)
gen dif = sdem1 - sdem0

list sdem1 sdem0 dif in 1/1
     +----------------------------------+
     |     sdem1       sdem0        dif |
     |----------------------------------|
  1. | 64.101309   17.415352   46.68596 |
     +----------------------------------+

rdrobust score demvoteshare, c(0.5) h(0.1) p(1)
...
...
--------------------------------------------------------------------------------
            Method |  Coef.    Std. Err.    z     P>|z|    [95% Conf. Interval]
-------------------+------------------------------------------------------------
      Conventional |  46.686     1.1428   40.8525  0.000    44.4461      48.9258
            Robust |     -          -     26.7410  0.000    42.5497      49.2804
--------------------------------------------------------------------------------
```

Matching other results II

- Same bandwidth for both. Below $h = 0.15$, so with triangular kernel obserbations with $|x_i - c| < h$ have nonzero weight

```
capture drop sdem0 sdem1 forat dif
lpoly score demvoteshare if democrat == 0, nograph kernel(triangle) gen(sdem0) degree(1)  ///
       at(forat) bwidth(0.15)
lpoly score demvoteshare if democrat == 1, nograph kernel(triangle) gen(sdem1) degree(1) ///
       at(forat) bwidth(0.15)
gen dif = sdem1 - sdem0
list sdem1 sdem0 dif in 1/1
     +----------------------------------+
     |     sdem1       sdem0        dif |
     |----------------------------------|
  1. | 64.312993   17.147009   47.16599 |
     +----------------------------------+

rdrobust score demvoteshare, c(0.5) h(0.15)
...
...

Outcome: score. Running variable: demvoteshare.
--------------------------------------------------------------------------------
           Method |   Coef.    Std. Err.    z     P>|z|    [95% Conf. Interval]
------------------+-------------------------------------------------------------
     Conventional |  47.166     .93435   50.4800  0.000    45.3347      48.9973
           Robust |     -          -     33.5370  0.000    43.7645      49.1974
--------------------------------------------------------------------------------
```

Important: rdrobust is really a parametric method given a bandwidth

- Given a bandwidth h, rdrobust is really a parametric model weighted by the kernel. To see this, let's use a rectangular kernel (uniform), which gives the same weight to all observations. See how results below match

```
rdrobust score demvoteshare, c(0.5) h(0.10) kernel(uniform) p(1)
...
...
Outcome: score. Running variable: demvoteshare.
--------------------------------------------------------------------------------
           Method |   Coef.    Std. Err.    z     P>|z|    [95% Conf. Interval]
------------------+-------------------------------------------------------------
     Conventional |  47.159     1.0432   45.2066  0.000    45.1145      49.2038
           Robust |     -          -     28.6039  0.000    42.7813      49.0753
--------------------------------------------------------------------------------

reg score i.d##c.x_c if demvoteshare >= (0.5-0.10) & demvoteshare <= (0.5+0.10), robust
...
...

------------------------------------------------------------------------------
             |               Robust
       score |      Coef.   Std. Err.      t    P>|t|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
         1.d |   47.15915   1.217625    38.73   0.000     44.77203    49.54628
         x_c |   9.421594   13.05183     0.72   0.470    -16.16621     35.0094
             |
     d#c.x_c |
          1  |  -9.127629   21.92807    -0.42   0.677     -52.1171    33.86184
             |
       _cons |   17.22656   .7556057    22.80   0.000     15.74521    18.70791
------------------------------------------------------------------------------
```

Important: rdrobust is really a parametric method given a bandwidth

- Same adding covariates

```
rdrobust score demvoteshare, c(0.5) h(0.10) kernel(uniform) p(1) covs(pcturban pctblack)
...
...
Outcome: score. Running variable: demvoteshare.
--------------------------------------------------------------------------------
            Method |   Coef.    Std. Err.    z     P>|z|    [95% Conf. Interval]
-------------------+------------------------------------------------------------
      Conventional |  44.869     1.3179   34.0464  0.000    42.2859      47.4518
            Robust |     -          -     22.1095  0.000    41.6342      49.7338
--------------------------------------------------------------------------------
Covariate-adjusted estimates. Additional covariates included: 2

reg score i.d##c.x_c pcturban pctblack if demvoteshare >= (0.5-0.10) & demvoteshare <= (0
> .5+0.10), robust
...
------------------------------------------------------------------------------
             |               Robust
       score |      Coef.   Std. Err.      t    P>|t|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
         1.d |   44.86885   1.532883    29.27   0.000     41.86313    47.87456
         x_c |  -2.511174   16.33057    -0.15   0.878    -34.53255    29.51021
             |
     d#c.x_c |
          1  |   27.79169   26.45986     1.05   0.294    -24.09145    79.67484
             |
    pcturban |   31.08685   1.791139    17.36   0.000     27.57474    34.59896
    pctblack |  -63.18889   5.592308   -11.30   0.000    -74.15443   -52.22335
       _cons |   2.106124   1.448386     1.45   0.146    -.7339069    4.946155
------------------------------------------------------------------------------
```

Limitations, other things

- Helpful to explore the sensitivity of estimates to model specification using nonparametric methods
- In this example, not much difference, **but in other situations it could be a world of difference** between parametric and nonparametric, which could mean model specification issues or just a lot of noise in the data
- When there is more noise than signal, different models will produce difference answers, in magnitude, direction, and statistical significance
- Nonparametric methods are not always better; they do have many underlying assumptions. They are less efficient when the parametric model is right. Problem is only in simulations we know for sure what is the "right" model
- No way to test for treatment heterogeniety with current nonparametric models. We could estimate stratified models, not as efficient as interactions
- **Summary is that we should try both and be concerned when results differ (and try to figure out why)**

Fuzzy RDD, instrumental variables detour

- If we randomize people into groups using a uniform random variable U, U is an *unconditional* randomizer. It works because U is uncorrelated in any functional form with any observed and unobserved covariate and also the outcome (it's random)
- In RDD the forcing variable X is like a *conditional* randomizer **but only close to cutoff point** c and we must condition for X. It's conditional because it's like the example of conditional randomization when we use the values of a variable –severity– to randomize people into treatments. The key difference is that RDD induces a discontinuity – every single person is given treatment if $X_i \geq c$
- The idea behind an **instrumental variable** approach is that the instrument Z acts like a psuedo "randomizer" in the sense that Z is a strong predictor of treatment but it must be conditional independent of the outcome
- The "conditional independent of the outcome" part is the exclusion restriction, or the assumption that must be argued and in practice is so difficult to determine with clarity

Encouragement design

- Let's go back to the example of an **encouragement design**. The idea is to randomly assign people into two groups and then **encourage** one group to receive a treatment or intervention (say, to receive regular preventive services)
- In this setting, randomization is about encouragement not actually receiving treatment. If we compare an outcome Y in both groups, we would obtain an estimate of encouraging people to do something, not an estimate of receiving the treatment. That is, intent-to-treat (ITT)
- You can imagine that there are different types of people. No matter what you do, some do not want to go to the doctor (**never-takers**), while other people are very concerned about their health and will get preventive services regardless of what you tell them (**always-takers**)
- Then there is a group of people whose behavior can be changed. After the encouragement, they decide to follow the recommendation. These are the **compliers**
- Finally, there could be contrarians: they do the opposite of what they are told. **We must rule them out**

Encouragement design

- **Randomization ensures that the distribution of the type of people is the same in the treatment and control group**
- Other than ITT, the estimate of treatment effect we could obtain is on the compliers, sometimes called the “complier average treatment effect” or the LATE
- Keep in mind that in this setting nothing prevents people in the control group to get preventive services. The always-takers will in fact get preventive services. The never-takers in the control group will not. But the compliers may not because we have not encourage them to do so, although some could do it anyway
- When we think about counterfactuals, the control group can only provide a conterfactual for the compliers: what would have happened if the treated had not been encouraged to be treated. That’s why we can only obtain LATE for the compliers
- In this example, the randomizer (instrument) was actually the random treatment assignment: it’s a strong predictor of receiving treatment and is uncorrelated with outcomes

Estimation

- Our target of estimation is not the effect of encouraging people to receive preventive services but rather the effect of receiving preventive services on an outcome Y, say a measure of health status
- We will denote prevention services as P (say preventive doctor visits). The causal, population model we care about is $Y_i = \beta_0 + \beta_1 P_i + \epsilon_i$
- In the above model, P and ϵ are correlated since we know that P is also correlated with being randomized into the encouragement group, which we denote with a dummy variable Z_i. What we don't observed are factors that explain who would follow the recommendation and go visit the doctor. This is the unobserved selection. If we add Z to the above model, its coefficient would be 0 because of randomization (this becomes important later)
- If we compare $E[Y_i|Z_i = 1] - E[Y_i|Z_i = 0]$ we would be estimating the average difference in health status between the group that was encouraged to received treatment and the group that was not encouraged (ITT)
- Intuitively, the piece that is missing is that in both groups people could have received preventive services, the actual treatment. So we could "weight" ITT by the (average) *difference* in preventive differences services received by each group: $E[P_i|Z_i = 1] - E[P_i|Z_i = 0]$

Estimation and intuition

- It turns out that this is actually the estimator we want:
  $\hat{\beta}_1 = \frac{E[Y_i|Z_i=1]-E[Y_i|Z_i=0]}{E[P_i|Z_i=1]-E[P_i|Z_i=0]}$
- The above estimator is called the Wald estimator (introduced in the context of measurement error models; see AP page 127)
- If in both groups prevention services received are the same, then the denominator is zero and the treatment effect is infinity
- With a small difference, $\hat{\beta}_1$ could get very large. In words, *being randomized into the encouragement group is not a strong predictor of receiving treatment* (this is what is called a **weak instrument**)
- If more people in the control group actually received treatment, then the treatment effect would flip signs
- If being randomized into the encouragement group makes a difference in receiving preventive services (strong predictor), the difference $E[P_i|Z_i = 1] - E[P_i|Z_i = 0]$ would be large. We "adjust" or weight the numerator by more
- Again, this new estimate only applies to the *compliers*, because the encouragement only worked on this "local" set of participants (hence, LATE)

Estimation, more general

- In a more general case without covariates and with a possibly continuous instrument Z, we can think of a system of equations:
  1. $P_i = \alpha_0 + \alpha_1 Z_i + \epsilon_i$
  2. $Y_i = \gamma_0 + \gamma_1 P_i + \eta_i$
- In the first equation, we estimate how the instrument Z predict the treatment P
- The second equation is the outcome equation, which we know we can't estimate as is because P is not random, there is selection (ignorability fails). We don't know what factor explain why people decided to get preventive services; these factors are likely unobserved
- What we do is exploit the fact that we know there is an external/exogenous/randomizer factor Z, which we called the instrument, that strongly predicts who gets prevention services and because it's a randomizer we assume it is not related to the outcome. Another way people say this is something like "we exploit the variability in P induced by Z"
- The system of equations can be estimated using two-stage least squares (2SLS) or using structural model equations (SEM). In 2SLS, predictions from model 1) are used to estimate model 2: $Y_i = \gamma_0 + \gamma_1 \hat{P}_i + \eta_i$

Assumptions

- Again, with the more general setting:
  1. $P_i = \alpha_0 + \alpha_1 Z_i + \epsilon_i$
  2. $Y_i = \gamma_0 + \gamma_1 P_i + \eta_i$
- One assumption is that the instrument Z must be uncorrelated with both ϵ and η, which amounts to assuming ignorability of the instrument and the exclusion restriction that says that the only way the instrument affects the outcome is through the treatment
- We are safe when the instrument is randomization since randomization is not related to the outcome (treatment assignment is random)
- It's very hard to come up with instruments in the wild. In some cases, controlling for variables could give us conditional ignorability and make the exclusion restriction hold (or hold "better"), so we would add a vector of variables **X** in both regressions

Estimation II

- Here is one way we could derive the instrument in the more general setting of Z continuous, following Gelman, Hill, and Vehtari (2020). We can rewrite:
  1. $P_i = \alpha_0 + \alpha_1 Z_i + \epsilon_i$
  2. $Y_i = \gamma_0 + \gamma_1 P_i + \gamma_2 Z_i + \eta_i$
- Since we assume the exclusion restriction, $\gamma_2 = 0$ in equation (2) (think about it, this is important. It's only zero if P is in the model). **Our goal is to obtain γ_1 accounting for selection on unobservables contained in η**
- Now plug in equation (1) into equation (2):

  $$Y_i = \gamma_0 + \gamma_1(\alpha_0 + \alpha_1 Z_i) + \gamma_2 Z_i + \eta_i = (\gamma_0 + \gamma_1\alpha_0) + (\alpha_1\gamma_1 + \gamma_2)Z_i + \eta_i \quad (3)$$
- We could rewrite (3) as $Y_i = \beta_1 + \beta_2 Z_i + e_i$, which we could estimate using the data. Here, $\beta_2 = (\alpha_1\gamma_1 + \gamma_2)$, which means $\gamma_1 = \frac{\beta_2 - \gamma_2}{\alpha_1}$
- Since we know $\gamma_2 = 0$ due to the exclusion restriction, we are left with $\gamma_1 = \frac{\beta_2}{\alpha_1}$
- And that's the 2SLS estimate, similar to the Wald estimate with a binary instrument. Note that α_1 is the coefficient of Z in (1). If close to zero, we have a weak instrument. β_2 is the ITT
- Note how we get a different estimate, $\gamma_1^{biased} = \frac{\beta_2}{\alpha_1} - \frac{\gamma_2}{\alpha_1}$, if the exclusion restriction in fact doesn't hold

Back to fuzzy RDD

- The connection with fuzzy RDD is straightforward
- The assignment variable X at the cutoff point c (the instrument) must be a strong predictor of receiving treatment; that's the first condition
- If the RDD assumptions hold, around $X_i = c$, conditioning on the running variable X_i, the exclusion restriction holds too: the only way the instrument affects the outcome is through the treatment
- In this sense, the assumptions of fuzzy RDD are milder than the assumptions of IV (see Hahn et al., 2001)
- Estimation follows IV in parametric approaches
- -rdrobust- estimates nonparametric fuzzy RDD with the option fuzzy()
- Remember that the key insight is that we are exploiting the fact that the discontinuity in $X_i = c$ is a strong predictor of treatment, which we must assume is not related to the outcome Y (only through treatment). Absence a treatment, there would have been continuity

There is much more to it

- More details next semester. The world of IV is vast...
- For an application of IVs when the instrument is randomization, see Baicker et al. (2013) describing Medicaid's Oregon experiment