Lecture Notes: Applied Econometrics 2

Claire Duquennois

Contents

1 Regression Discontinuity

Regression discontinuity research designs were introduced in other fields as far back as the 1960s but only gained popularity in economics in the past 20 years or so as economist became increasingly focused on causal inference and large administrative datasets became more widely available. This increased popularity is well deserved. When correctly applied, presented and explained, RD designs are very transparent in how they achieve causal identification which makes them very appealing.

RD designs tend to leverage the researchers knowledge of a rule or policy that determines treatment. Identification is then based on the idea that how some rules are applied can be quite arbitrary and that this arbitrary application generates the randomness we crave for the identification of causal effects.

RD designs come in two flavors: Sharp and fuzzy. I will start by disscussing general elements common to all RD designs, I will then cover sharp RD's and finally discuss how things change when things get fuzzy.

1.1 The set up

Suppose that we want to estimate the effect of some binary treatment D_i on an outcome Y_i. Using the potential outcomes framework, we write $Y_i(0)$ as the potential untreated outcome and $Y_i(1)$ as the potential treated outcome, with $Y_i = D_i Y_i(1) + (1 - D_i) Y_i(0)$. Now suppose that the value of D_i-i.e. whether or not an individual gets treated- is completely (or partially) determined by whether some predictor R_i lies above or below a certain threshold, c.

Figure 2.1: Conditional Probability of Receiving Treatment in Sharp RD Design
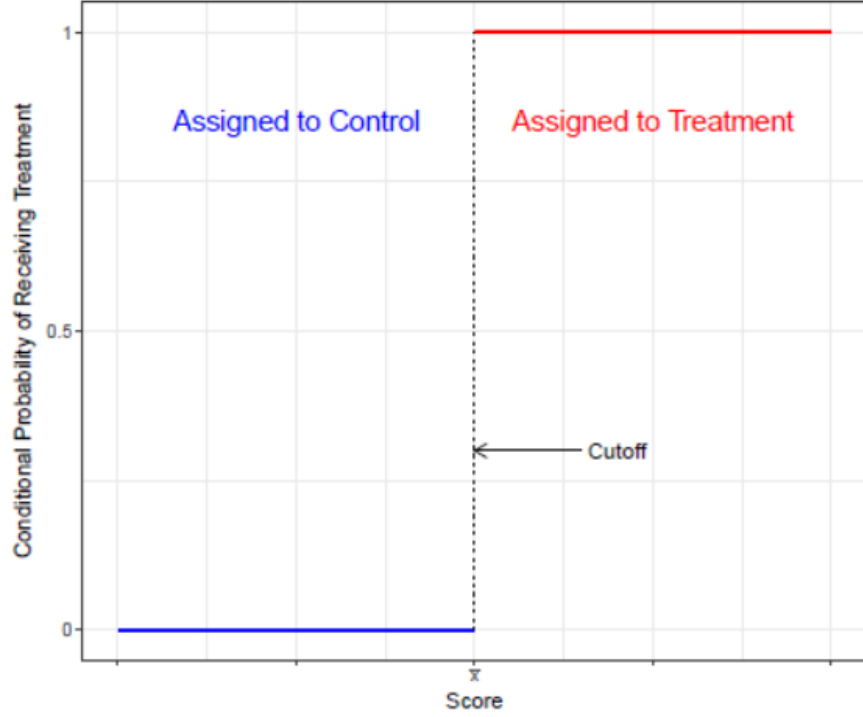
The predictor R_i need not be randomly assigned. In fact, we assume that it is related to the potential outcomes $Y_i(0)$ and $Y_i(1)$, but that this relationship is smooth, i.e. $Y_i(0)$ and $Y_i(1)$ do not jump discontinuously as R_i changes. Any discontinuous change in Y_i as R_i crosses c can thus be interpreted as a causal effect of D_i. We call R_i the "running variable".

RD designs often arise in administrative situations in which units are assigned a program, treatment or award based on a numerical index being above or below a certain threshold. For example, a politician may be elected if and only if the differential between the vote share that she receives and the vote share that her opponent receives exceeds 0. A student may be assigned to summer school if and only if his performance on a combination of tests falls below a certain threshold. A toxic waste site may receive cleanup funds if and only if it's hazard rating falls above a certain level. In these cases , individuals or units whose indices R lie directly below the threshold c are considered to be comparable to individuals or units whose indices R lie directly above the threshold c and we can estimate the treatment effect by taking a difference in mean outcomes for units directly above the threshold and units directly below the threshold.

1.2 The continuity assumption

To estimate the causal effect of D_i on some outcome Y_i, we can compare the outcomes of units directly above and below the threshold.

To justify this interpretation, we need it to be the case that $Y_i(0)$ and $Y_i(1)$ are smooth functions of R_i as R_i crosses c. We make this assumption in the form of a conditional expectation:

Assumption: The continuity assumption

$E[Y_i(0)|X_i = x]$ **and** $E[Y_i(1)|X_i = x]$ **are continuous in** x.
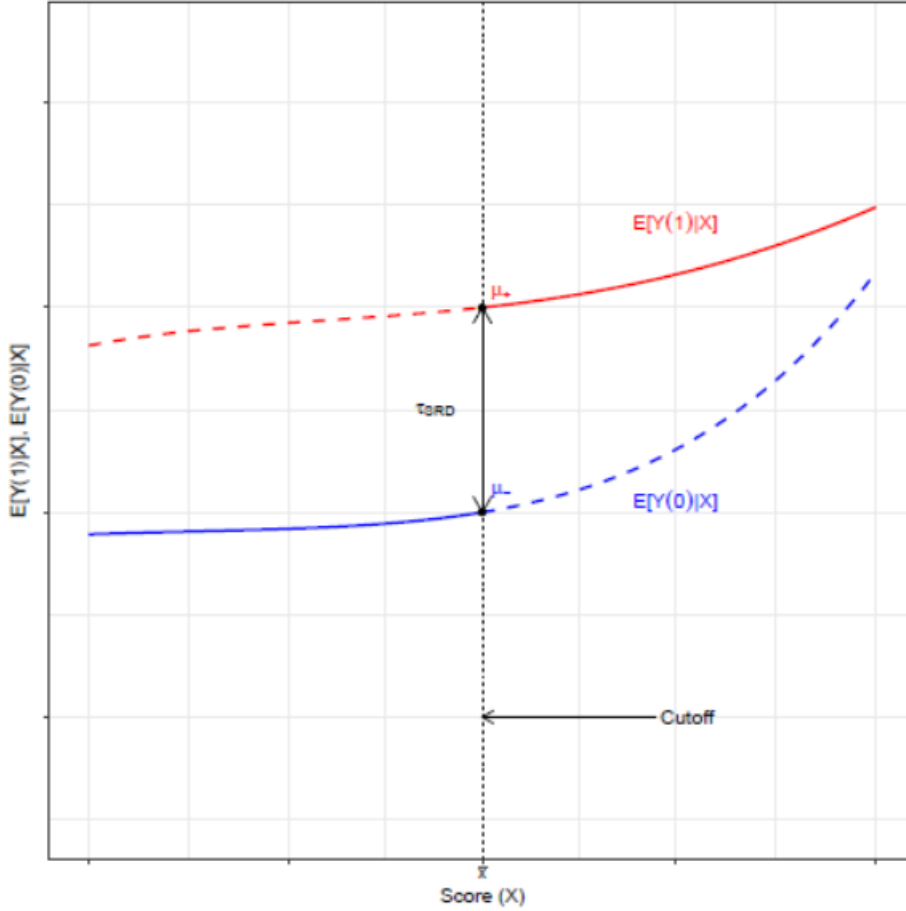
2

Figure 2.2: RD Treatment Effect in Sharp RD Design

In the image above, τ, the effect of receiving treatment, is estimated as the difference in the mean outcomes of those that are right above the cutoff (who are treated) and those right below the cutoff (who are untreated). This gap will correctly estimate the treatment effect if the continuity assumption holds: had they not received treatment, the treated groups outcomes would be represented by the dashed blue line, and had they received treatment, the untreated groups outcomes would have been the dashed red line.

1.3   The Graphs

At the heart of any good RD paper is the graphical analysis. The strength of the RD design is that the treatment assignment rule is known (or at least partially known). We should therefore be able to see discontinuous changes in the treatment and the outcome (if there is an effect) as the running variable crosses the threshold c. Any RD that fails to exhibit a visually perceptible break in treatment probability at the discontinuity threshold is basically not credible, regardless of the regression results. Conversely, a break that is visually perceptible will almost surely be statistically significant. So with RD papers, the statistical results really take a back seat to the graphical analysis.

There are several types of graphs that make appearances in RD analyses. All of them require some data preperation and design as a simple scatterplot of your data is unlikely to reveal the patterns you wish to illustrate. The main graphs of an RD design are basically a histogram-type plot that presents the average value of the outcome, treatment status and covariates as well as the density of the running variable at evenly spaced values of the running variables.

Generating these plots requires choosing two key parameters: the binwidth, h, and the number of bins shown to the left and right of the threshold value, K_0 and K_1. Once these choices are made, you construct $K_0 + K_1$ bins: K_0 evenly spaced bins of width h below the threshold value and K_1 evenly spaced bins of width h above the threshold value. Note, you should avoid having any bin crossing the threshold value c as this will make the discontinuities we hope to ovserve less easy to identify visually.

1.3.1   Treatment status

RD papers often include a graph that plots treatment by the running variable. We expect to see a visually perceptible discontinuity in the probability of treatment as the running variable crosses the threshold.

After constructing the bins described above, plotting this graph requires calculating, $\bar{D}_k$, the average treatment level in the bin

$$\bar{D}_k = \frac{1}{N_k} \sum_{i=1}^{N} D_i * \mathbf{1}(b_k < R_i \leq b_{k+1})$$

and plotting these values against the midpoint of each of the bins.

1.3.2   Outcomes

The main course of an RD paper is a plot of the outcome by the running variable. If there is a treatment effect, we would expect to see a discontinuity here too.

Plotting this graph requires calculating, $\bar{Y}_k$, the average outcome in each bin

$$\bar{Y}_k = \frac{1}{N_k} \sum_{i=1}^{N} Y_i * \mathbf{1}(b_k < R_i \leq b_{k+1})$$

and plotting these values against the midpoint of each of the bins.

A visual break at c implies that crossing the threshold has a significant effect on the outcome, which in turn implies (under our assumptions) that the treatment has a significant effect on the outcome.

In addition to inspecting the threshold for a discontinuity, you should also inspect whether there are any other discontinuities of similar (or greater) magnitude at other values of the running variable. If there are, and if there is not a clear a priori reason to expect these discontinuities, then the research design is called into question - effectively we have detected a violation of Assumption 1 (smoothness in expected potential outcomes).

1.3.3   Covariates

Using the same methodology as above, it is common to plot the average value of certain covariates that may be related to the outcome but should not be affected by the treatment. As above, we calculate $\bar{X}_i$ where

$$\bar{X}_k = \frac{1}{N_k} \sum_{i=1}^{N} X_i * \mathbf{1}(b_k < R_i \leq b_{k+1})$$

is plotted against the midpoint of each bin.

For the covariate graphs, if the research design is valid there should not be any discontinuity in $\bar{X}_k$ as the running variable crosses the threshold c. This plot allows us to determine whether the covariate is balances across the threshold- the equivalent of showing covariates are balanced in an RCT. As in an RCT, you are essentially checking that the treated and un-treated groups are similar along covariates which validates the argument that treatment is as good as randomly assigned within the bandwidth being studied.

1.3.4 Density of the Running Variable

Finally, it is also common to plot the density of the running variable. For each bin, you calculate

$$N_k = \sum_{i=1}^{N} \mathbf{1}(b_k < R_i \leq b_{k+1})$$

and plot these against the midpoint of the bin.

A major concern in RD designs is that individuals may "game" the assignment rule. That is to say, if individuals understand the assignment mechanism and can manipulate their value of the running variable, then they may be able to place themselves just above (or just below) the threshold c. In that case, the individuals just above the threshold will disproportionately consist of those gaming the rule and they will not be directly comparable to the individuals lying just below the threshold. For instance, consider a scholarship that activates only when scores on a test fall above a certain threshold c. Shrewd students could retake the test many times until they pass the threshold. If a researcher uses an individuals maximum test score as the running variable, motivated individuals who retake the test many times are more likely to fall just above the threshold, then just below it. Thus this group of observations is selected and no longer directly comparable to the observations that fall directly below the threshold.

To address this issue, you can inspect the density of the running variable as it crosses c. If units are manipulating their values of the running variable, to fall just above or below c, then we should observe a discontinuity in the distribution of the running variable as it crosses c. If the distribution of the running variable is smooth as it crosses c, then it's unlikely that individuals are gaming the assignment mechanism.
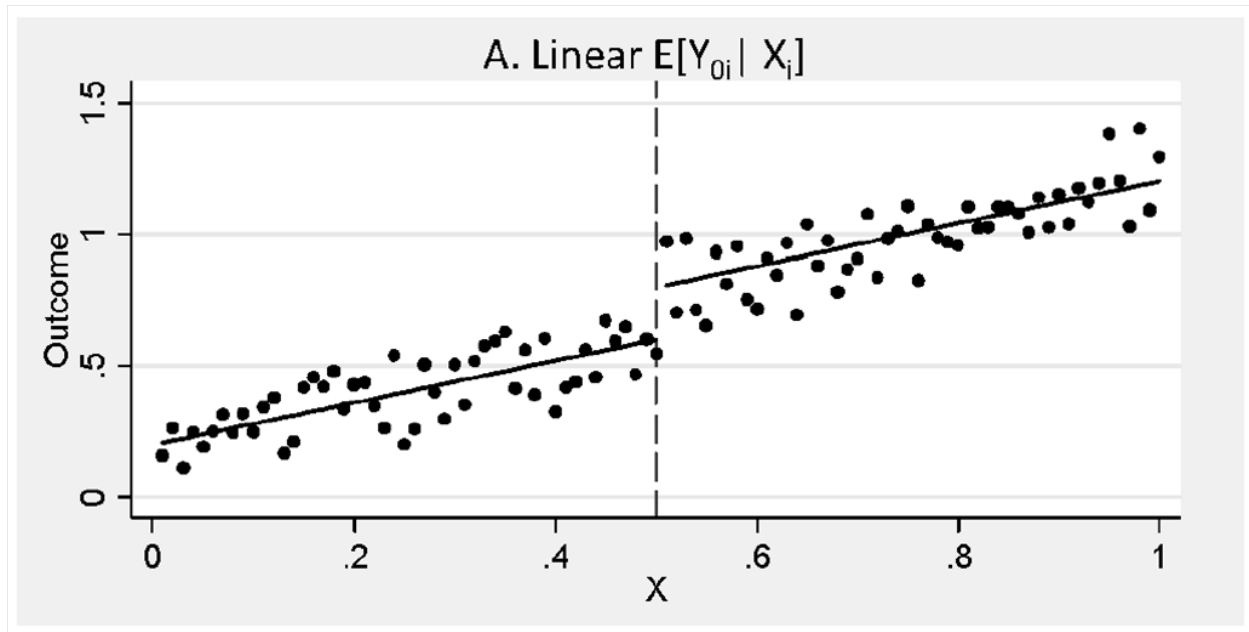
1.4 Estimation

RD estimations can be done quite easily in a regression framework. There are a couple things to keep in mind when it comes to RD estimation strategies: the choice of functional form and the choice of bandwidth.

1.4.1 Choosing a functional form

In RD projects, there is an underlying continuous relationship between the running variable and the outcome variable. The treatment effect is isolated by finding a "break" in this continuous realationship at the threshold. In order to correctly isolate the treatment effect, it is important that you have a good model of the underlying relationship between the running variable and the outcome.

When the underlying relatonship between the running variable and the outcome is linear, this can be done quite easily using simple linear regressions. As illustrated in figure A, a linear regression fits the data well and we can identify the treatment effect as the "jump" between the intercepts at the threshold value.

A. Linear $E[Y_{0i}|X_i]$

In figure B, the underlying relationship between the running varible and the outcome is no longer linear. To correctly model it will require the addition of higher order polynomial terms to our estimating equation. If we fit the data correctly, here too we can identify the treatment effect as the "jump" between the intercepts at the threshold value. If we do not fit the data correctly, the "jump" at the the threshold will not correctly estimate the treatment effect. Imagine if instead of fitting a polynomial to this relationship I fit a linear function. Using a linear function would return different intercepts at the threshold and thus a different (incorrect) estimate of the treatment effect.

B. Nonlinear $E[Y_{0i}|X_i]$
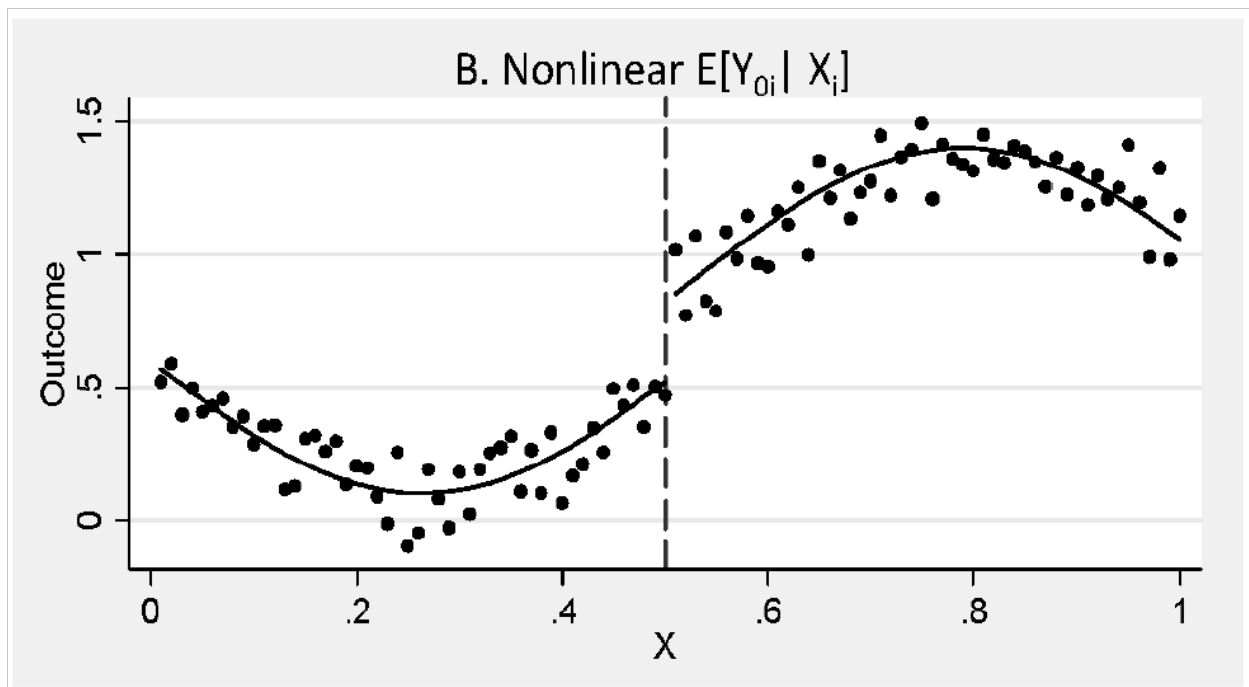
This problem can be particularly concerning in situations such as that represented in figure C. In figure C, the underlying relationship between the running varible and the outcome is not linear. If I model this underlying relationship correctly, I can see that there is no discontinuity at the threshold. If however I force my model to fit a linear regression to this data I will detect a discontinuity, concluding that there is a

treatment effect when if fact there is none.
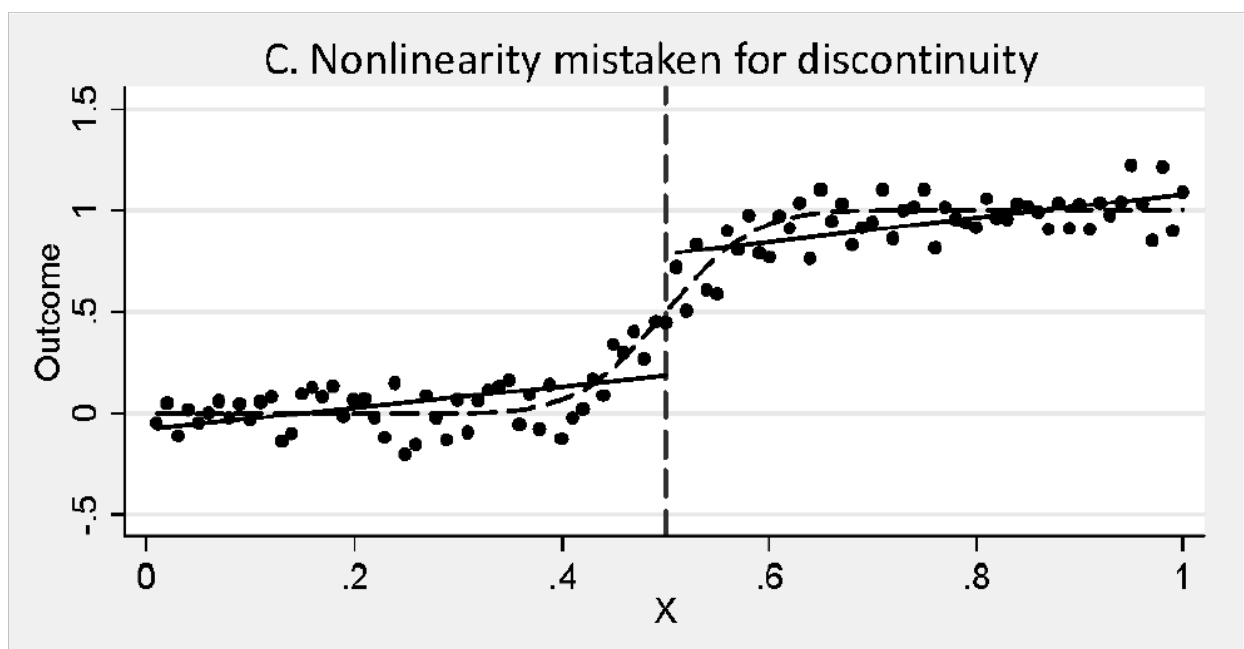
These issues are one of the reasons the graphs are so important in RD projects, as a good graph will alert you to figure C type stuations. Another way to avoid mistakes such as the one illustrated in figure C is to run specifications with higher order polynomials and check that your estimated treatment effect is not sensitive to their inclusion (or exclusion).

1.4.2 Choosing the bandwidth

In addition to thinking about the functional form in an RD project, thought should also be given to the bandwidth, h, that you will use. The bandwidth determines how close to the threshold an observation's running variable has to be to be a part of the regression sample. While there is an econometric literature that discusses methods to choose the optimal bandwidth if you wish to get technical, in practice this choice is more art than science and many papers make this choice fairly arbitrarily. The choice of bandwidth basically involves considering a tradeoff. With a large bandwidth, you will have a larger sample which can shrink your standard errors and improve the precision of your results. However there are two main drawbacks to a large bandwidth. First, with a very large bandwidth, it becomes more difficult to argue that observations on either side of the threshold are similar, since you are now including observations that fall quit far above and below the threshold in your comparison. Secondly, making sure you select the right functional form will be more important if you are working with a wide bandwidth. Consider the plot in figure C. The functional form becomes important if you are working with the ±0.5 bandwidth. If however you are working with a narrow bandwidth, such as ±0.1 , there simply isn't much variation in x. In this small range of x, a linear specification fits the data quite well. It is generally good practice to check that RD results are not sensitive to the choice of bandwidth.

The concerns behind the choice of functional form and the choice of bandwidth are the same for both sharp and fuzzy RD's. The details of how the estimation proceeds from this point will depend on whether you are in sharp or fuzzy land and will be discussed in the relevant section.

1.5 Sharp RD Designs

In a sharp RD design, the probability that $D = 1$ changes from 0 to 1 as the running variable crosses c. In other words, no one with $R < c$ gets treated and everyone with $R \geq c$ gets treated, thus, D_i is a deterministic

function of $R_i : D_i = 1$ if $(R_i \geq c)$. (Note: Here we assume that high values of the running variable get treated. For some RD set ups, the reverse will be true.)

Figure 2.1: Conditional Probability of Receiving Treatment in Sharp RD Design
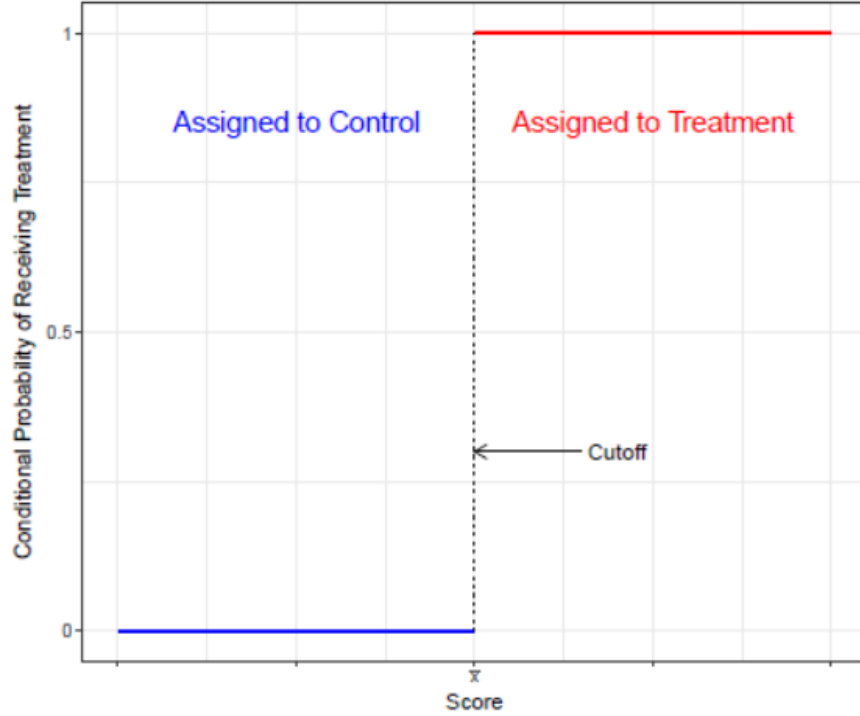
In the image above we see that that the probability of getting treated switches from 0 to 1 when an observation's running variable X crosses the threshold c.

To estimate the causal effect of D_i on some outcome Y_i, we simply take the difference in mean outcome on either side of c. Formally, we estimate

$$\lim_{r \to c} E[Y_i|R_i = r] - \lim_{r \leftarrow c} E[Y_i|R_i = r] = \lim_{r \to c} E[Y_i(1)|R_i = r] - \lim_{r \leftarrow c} E[Y_i(0)|R_i = r]$$

This represents the causal effect of D on some outcome Y for individuals with $R_i = c$. We will call this effect τ_{SRD}.

$$\tau_{SRD} = E[Y_i(1) - Y_i(0)|R_i = c]$$

To justify this interpretation, we need it to be the continuity assumption holds: $Y_i(0)$ and $Y_i(1)$ are smooth functions of R_i as R_i crosses c.

With the continuity assumption we can write

$$\tau_{SRD} = \lim_{r \to c} E[Y_i|R_i = r] - \lim_{r \leftarrow c} E[Y_i|R_i = r]$$

and estimate τ_{SRD} as the difference between the two regression functions estimated in the **neighborhood** of c.

Figure 2.2: RD Treatment Effect in Sharp RD Design
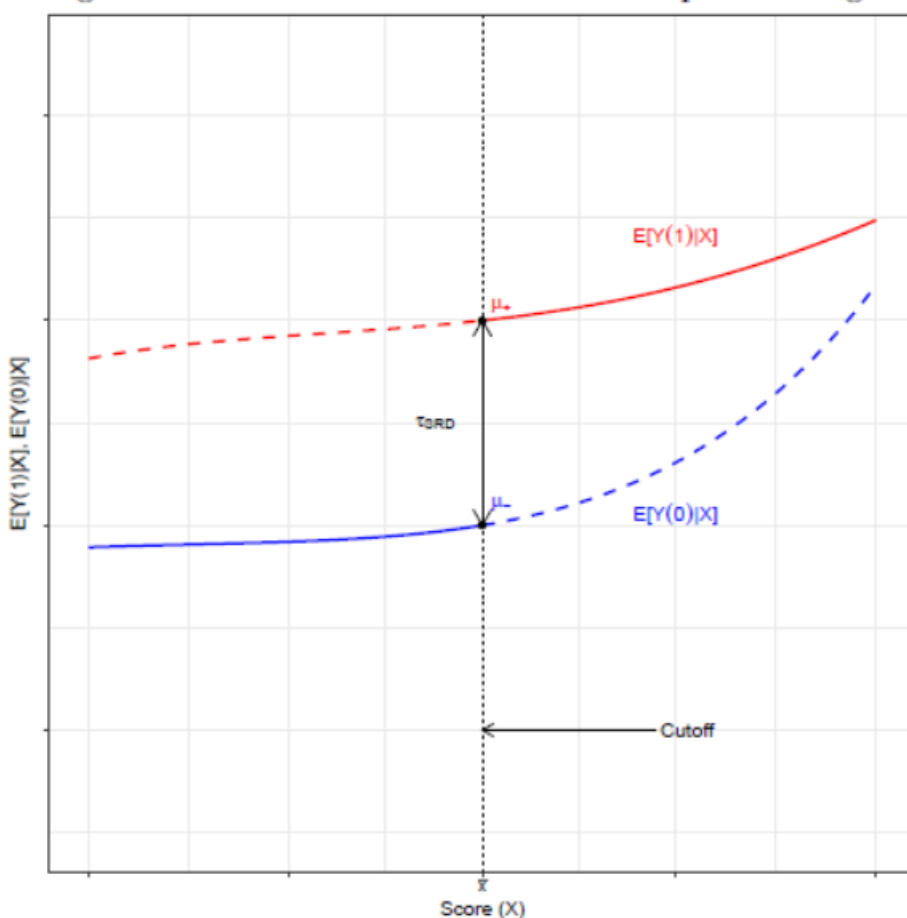
In the image above, τ_{SRD}, the effect of receiving treatment, is estimated as the difference in the mean outcomes of those that are right above the cutoff (who are treated) and those right below the cutoff (who are untreated). This gap will correctly estimate the treatment effect if the continuity assumption holds: had they not received treatment, the treated groups outcomes would be represented by the dashed blue line, and had they received treatment, the untreated groups outcomes would have been the dashed red line.

1.6   Sharp RD: Simulation

Suppose you are the superintendent of a large school district. Last year you made participation in small reading groups **mandatory** for all students whose 3rd grade reading score was 75 points or less. You would like to know how these reading groups affected student performance on their 4th grade reading tests. Your data includes the 3rd and 4th grade reading scores for all 5000 students in your school district.

```
set.seed(7000)

sharp <- rnorm(5000, mean = 80, sd = 5)
sharp <- as.data.frame(sharp)

names(sharp) <- c("read3")
sharp$error <- rnorm(5000, mean = 0, sd = 5)
sharp$pe3 <- rnorm(5000, mean = 90, sd = 4)
```

```r
sharp$height <- rnorm(5000, mean = 130, sd = 15)

sharp$treated <- 0
sharp$treated[sharp$read3 <= 75] <- 1


# the DGP
sharp$read4 <- (-6) + 0.8 * sharp$read3 + 10 * sharp$treated + sharp$error

sharp <- sharp[sharp$read3 < 78 & sharp$read3 > 72, ]
```

1.6.1 Sharp RD Simulation: Treatment status Graphs

Recall, it is common in RD designs to include a graph that plots treatment by the running variable. We expect to see a visually perceptible discontinuity in the probability of treatment as the running variable crosses the threshold.

After constructing the bins described above, plotting this graph requires calculating, $\bar{D}_k$, the average treatment level in the bin

$$\bar{D}_k = \frac{1}{N_k} \sum_{i=1}^{N} D_i * \mathbf{1}(b_k < R_i \leq b_{k+1}).$$

In a sharp RD, $\bar{D}_k$ should be either 0 or 1 depending on whether the bin is above or below the threshold. Thus this graph is not particularly interesting in a sharp RD (and is therefore sometimes relegated to the appendix), and primarily serves to validate the RD design.

```r
library(dplyr)
library(ggplot2)
# I will break up the data into 60 bins (30 above and 30 below the threshold)

cuts <- c(72, 72.1, 72.2, 72.3, 72.4, 72.5, 72.6, 72.7, 72.8, 72.9, 73, 73.1, 73.2,
    73.3, 73.4, 73.5, 73.6, 73.7, 73.8, 73.9, 74, 74.1, 74.2, 74.3, 74.4, 74.5, 74.6,
    74.7, 74.8, 74.9, 75, 75.1, 75.2, 75.3, 75.4, 75.5, 75.6, 75.7, 75.8, 75.9, 76,
    76.1, 76.2, 76.3, 76.4, 76.5, 76.6, 76.7, 76.8, 76.9, 77, 77.1, 77.2, 77.3, 77.4,
    77.5, 77.6, 77.7, 77.8, 77.9, 78)
midpoints <- cuts[2:61] - 0.05

sharp$bins <- cut(sharp$read3, breaks = cuts, include.lowest = TRUE, right = FALSE,
    labels = midpoints)


sharp_mean <- sharp %>%
    group_by(bins) %>%
    dplyr::summarize(outbinmean = mean(read4, na.rm = TRUE), treatbinmean = mean(treated,
        na.rm = TRUE), pebinmean = mean(pe3, na.rm = TRUE), heightbinmean = mean(height,
        na.rm = TRUE), numb = n())

sharp_mean$bins <- as.numeric(as.character(sharp_mean$bins))

plot1shp <- ggplot(sharp_mean, aes(x = bins, y = treatbinmean)) + geom_point() +
```
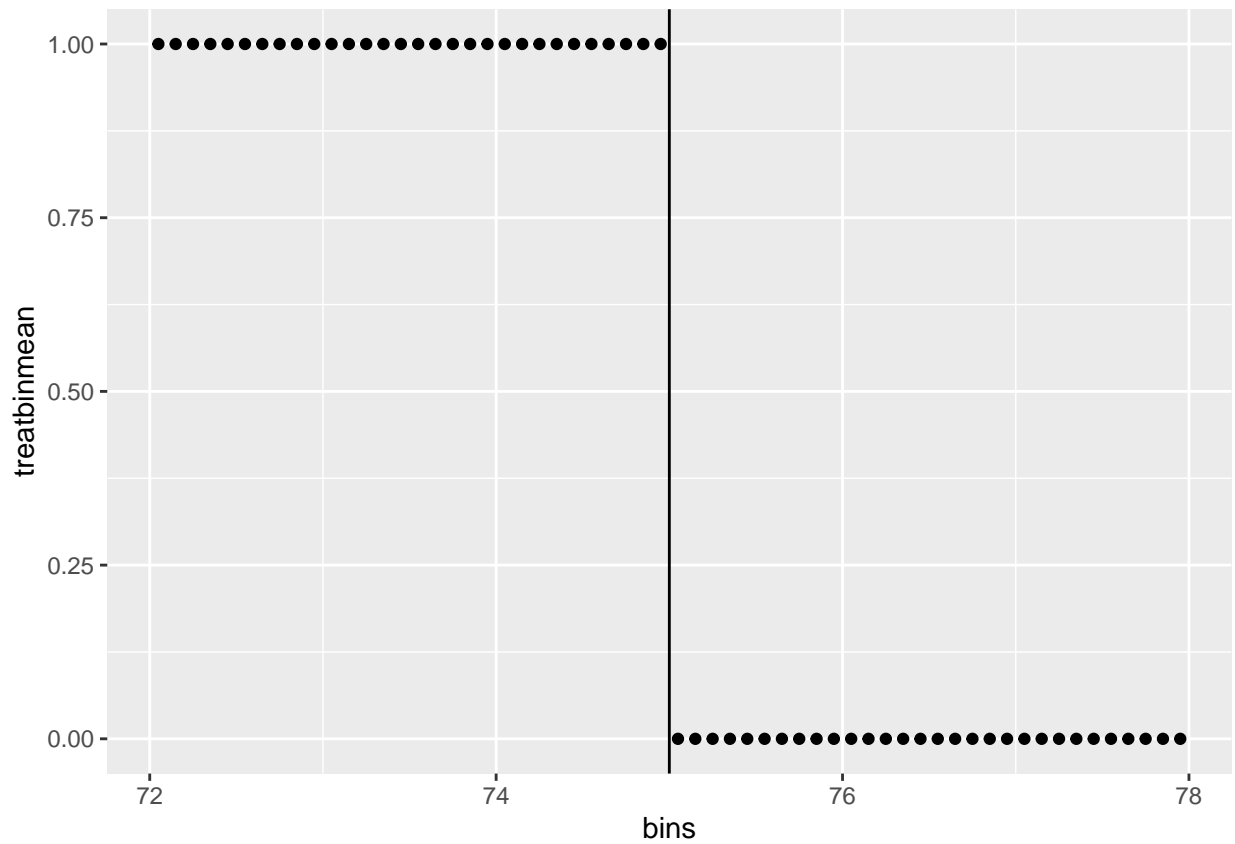
```
    geom_vline(xintercept = 75)
plot1shp
```


1.6.2   Sharp RD Simulation: Outcome Graphs

This is typically the most important element of RD projects. We calculate, $\bar{Y}_k$, the average outcome in each bin
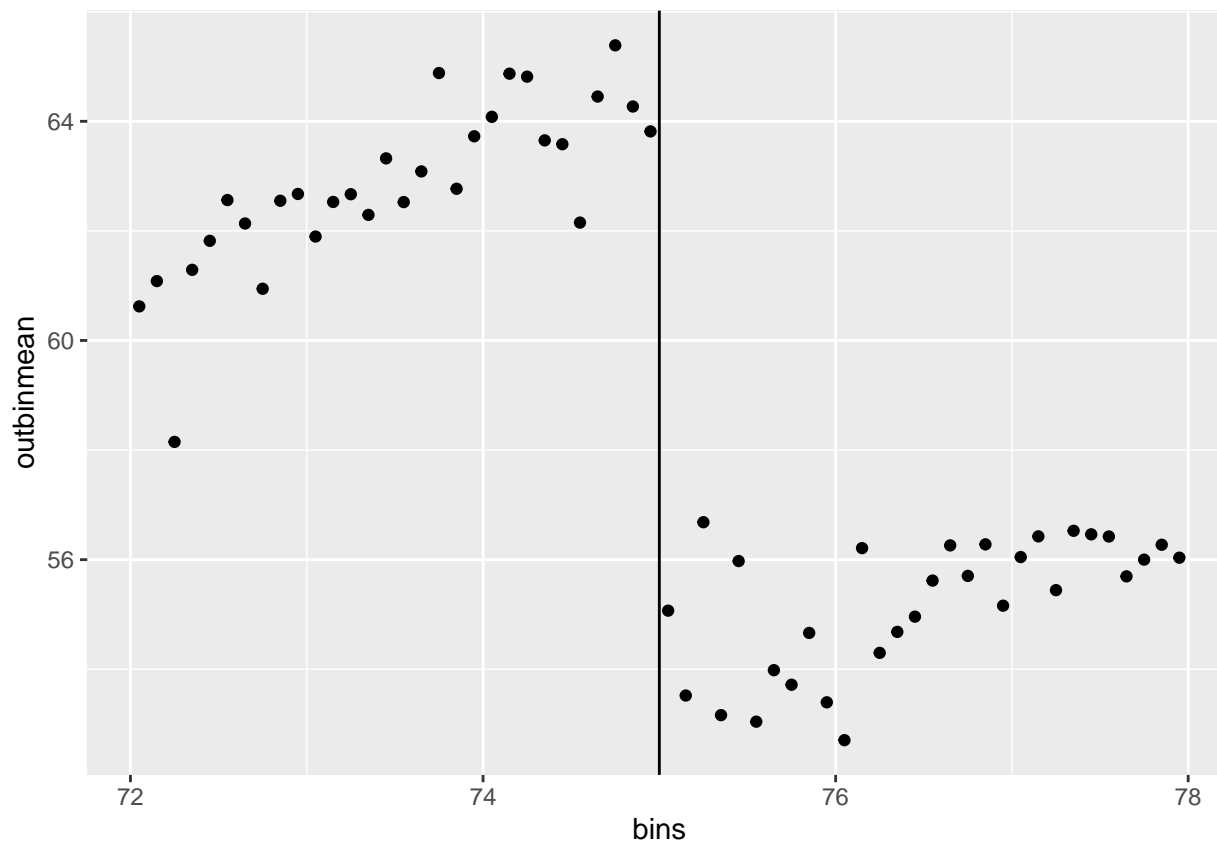
$$\bar{Y}_k = \frac{1}{N_k} \sum_{i=1}^{N} Y_i * \mathbf{1}(b_k < R_i \leq b_{k+1})$$

and plotting these values against the midpoint of each of the bins.

A visual break at c implies that crossing the threshold has a significant effect on the outcome, which in turn implies (under our assumptions) that the treatment has a significant effect on the outcome.

```
# using the values calculated in an earlier chunk

plot2shp <- ggplot(sharp_mean, aes(x = bins, y = outbinmean)) + geom_point() + geom_vline(xintercept =
plot2shp
```

1.6.3 Sharp RD Simulation: Covariate Graphs

We calculate $\bar{X}_i$ where

$$\bar{X}_k = \frac{1}{N_k} \sum_{i=1}^{N} X_i * \mathbf{1}(b_k < R_i \le b_{k+1})$$

is plotted against the midpoint of each bin.

This is a robustness test. We are esentially making sure that our treatment and control groups are similar, by checking that observation on either side of the threshold are comprable. This is similar conceptually to a balance test. We do not want to have a discontinuity here.

```
# using the values calculated in an earlier chunk
plot3shp <- ggplot(sharp_mean, aes(x = bins, y = pebinmean)) + geom_point() + geom_vline(xintercept = 75
plot3shp
```
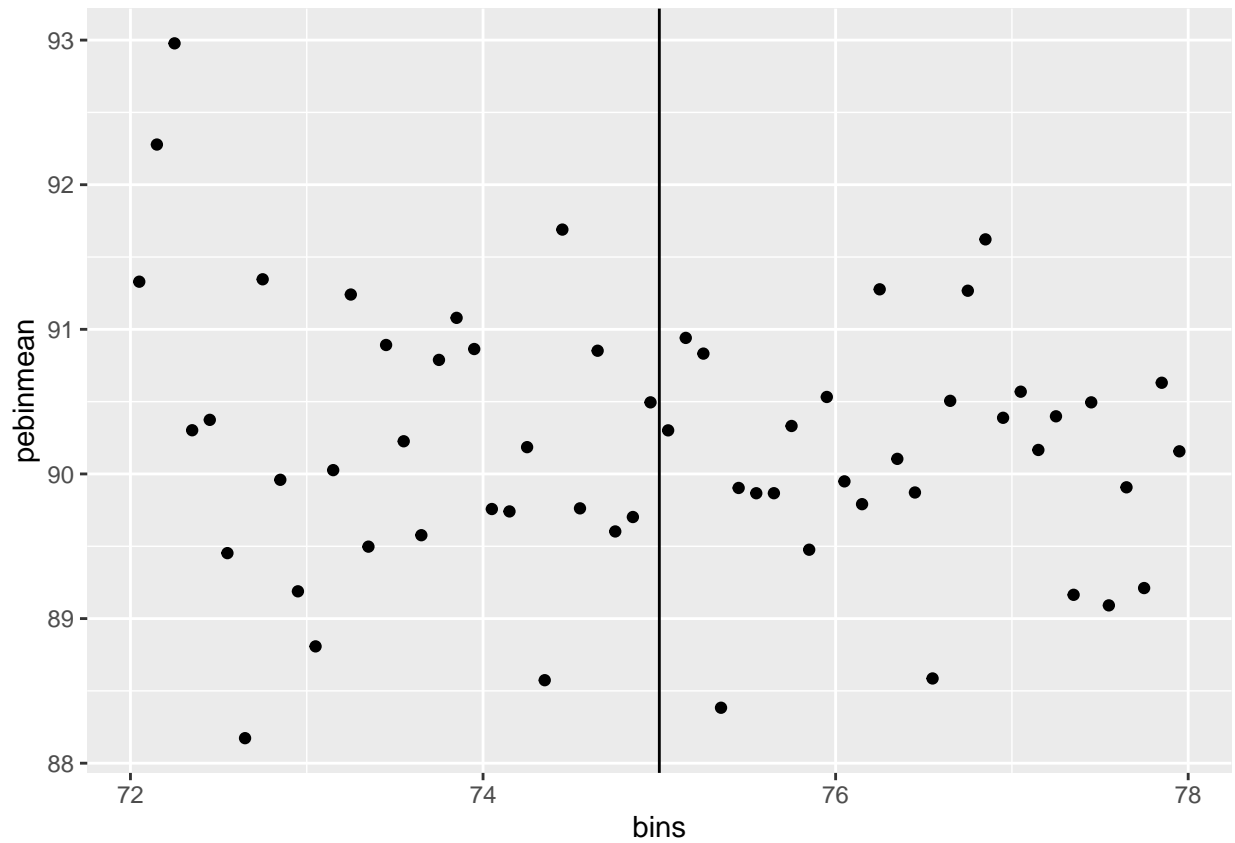
```
plot4shp <- ggplot(sharp_mean, aes(x = bins, y = heightbinmean)) + geom_point() +
    geom_vline(xintercept = 75)
plot4shp
```
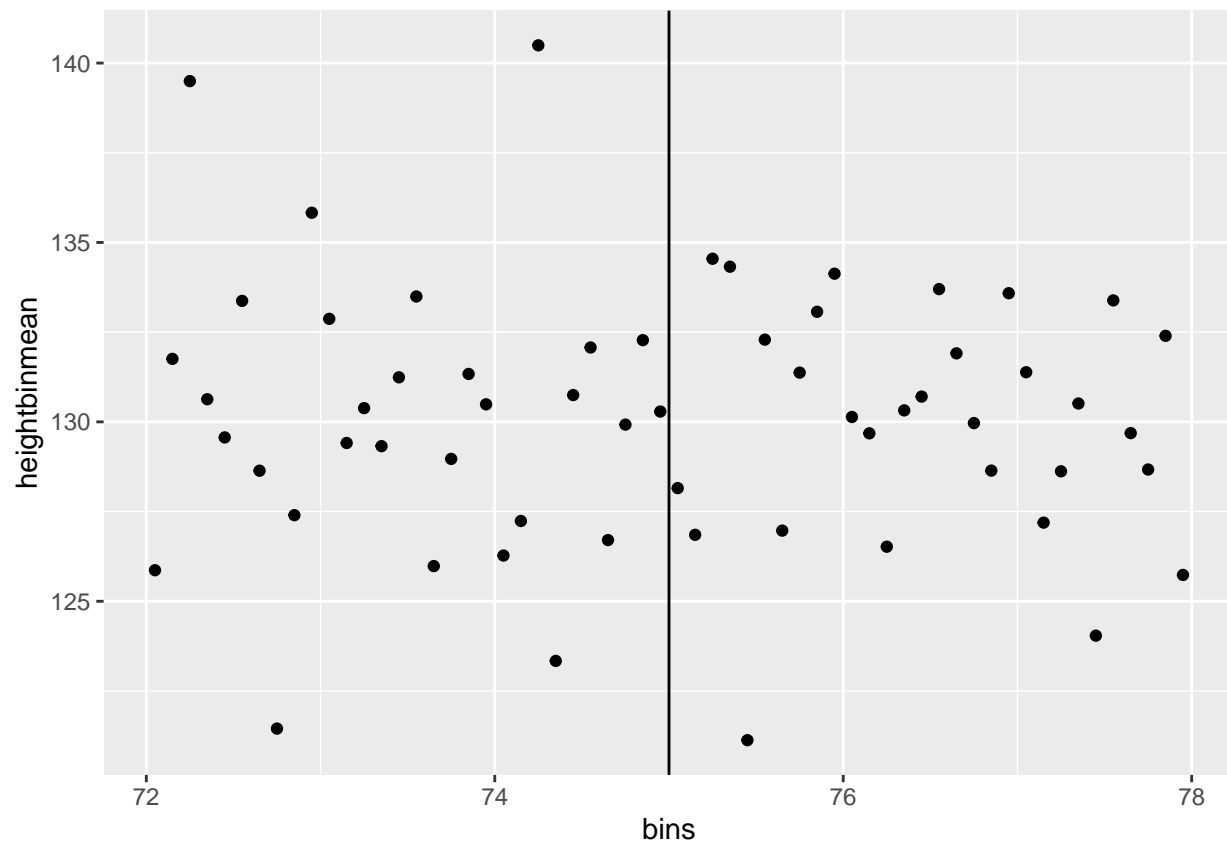
### 1.6.4 Sharp RD Simulation: Density of the running variable

We calculate

$$N_k = \sum_{i=1}^{N} \mathbf{1}(b_k < R_i \leq b_{k+1})$$

and plot these against the midpoint of the bin.

We want to make sure that there is no evidence that observations were able to move their R_i accross the threshold as a response to incentives to receive (or avoid) treatment.

```
# using the values calculated in an earlier chunk

plot5shp <- ggplot(sharp_mean, aes(x = bins, y = numb)) + geom_point() + geom_vline(xintercept = 75)
plot5shp
```
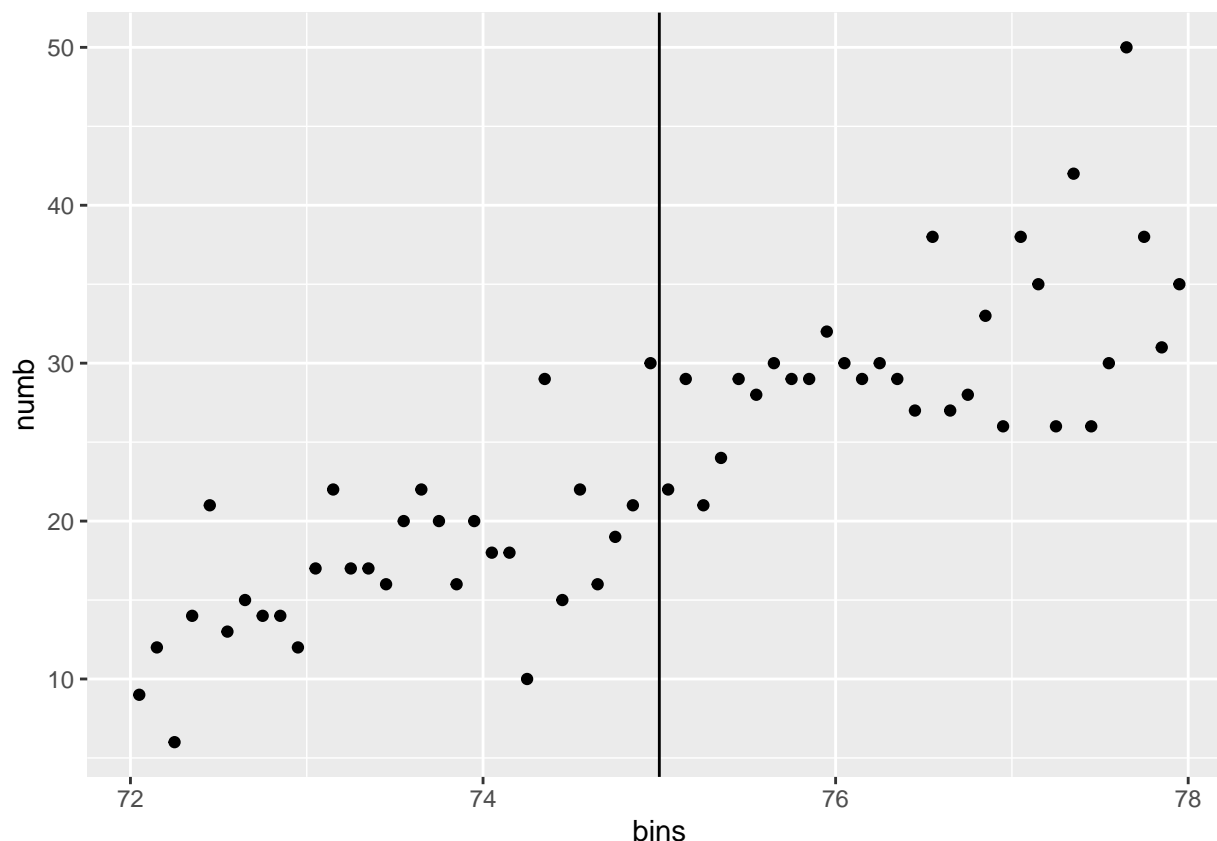
1.7 Sharp RD Estimation

To generate treatment estimate for a sharp RD we fit a linear regression on either side of the threshold point for the samples with $R_i \in (c-h, c)$ and $R_i[c, c+h)]$. This can be done by estimating some version (you can include covariates) of the following specification,

$$Y_i = \alpha + \tau D_i + \beta(R_i - c) + \gamma(R_i - c) * D_i + u_i \text{ for } c - h < R_i \leq c + h.$$

With this estimation strategy, $\hat{\tau}_{SRD}$ will estimate the treatment effect for units right at the threshold.

```
sharp$runminc <- sharp$read3 - 75
shpestim <- felm(read4 ~ treated + runminc + treated * runminc, sharp)

stargazer(shpestim, type = "latex")
```

% Table created by stargazer v.5.2.2 by Marek Hlavac, Harvard University. E-mail: hlavac at fas.harvard.edu
% Date and time: Thu, Mar 30, 2023 - 10:49:03 AM

It is helpful to see how the coefficients estimated above translate to the RD graph.

```
sharp_mean$runminc <- sharp_mean$bins - 75

plot6shp <- ggplot(sharp_mean, aes(x = runminc, y = outbinmean)) + geom_point() +
    geom_vline(xintercept = 0) + geom_segment(aes(x = 0, xend = 3, y = shpestim$coefficients[1],
    yend = shpestim$coefficients[1] + 3 * shpestim$coefficients[3])) + geom_segment(aes(x = -3,
```

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Table 1:

	Dependent variable:
	read4
treated	10.764***
	(0.555)
runminc	0.880***
	(0.197)
treated:runminc	0.304
	(0.333)
Constant	53.868***
	(0.356)
Observations	1,436
R^2	0.358
Adjusted R^2	0.356
Residual Std. Error	5.128 (df = 1432)
Note:	*p<0.1; **p<0.05; ***p<0.01

```
    xend = 0, y = shpestim$coefficients[1] + shpestim$coefficients[2] + (-3 * (shpestim$coefficients[3]
        shpestim$coefficients[4])), yend = shpestim$coefficients[1] + shpestim$coefficients[2])) +
    # adding some labeling for course notes:
annotate("text", x = 0.75, y = 64.8, label = "Intercept~is~alpha~+~tau", parse = TRUE) +
    annotate("text", x = -0.6, y = 54, label = "Intercept~is~alpha", parse = TRUE) +
    annotate("text", x = -2, y = 64, label = "Slope~is~beta~+~gamma", parse = TRUE) +
    annotate("text", x = 2, y = 54, label = "Slope~is~beta", parse = TRUE)
plot6shp
```
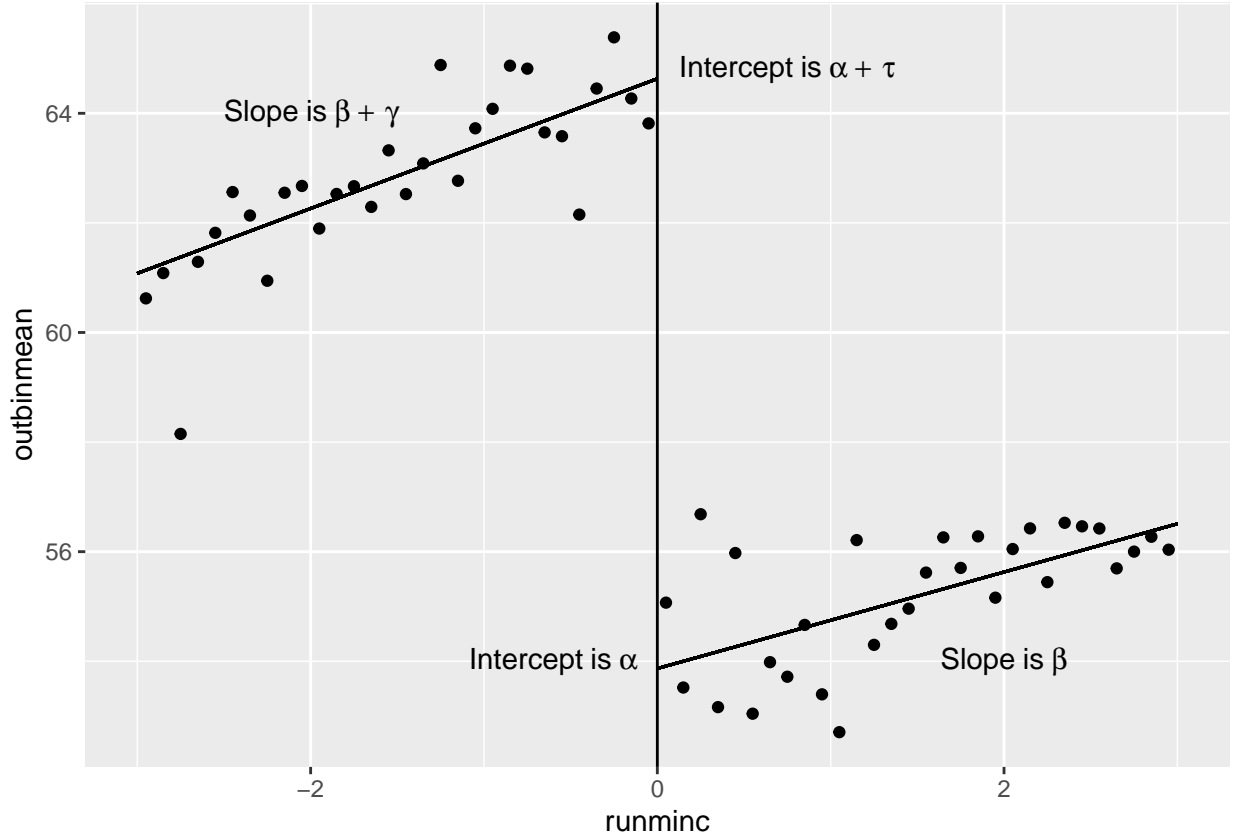
1.8 Fuzzy RD Designs

The fuzzy RD design (FRD) is similar in concept to the sharp RD except that D_i is no longer a deterministic function of R_i. Instead, the probability of treatment changes by some nonzero amount as the running variable crosses the threshold c, but this change in probability is less than 100 percentage points.

Formally we have that

$$0 < \lim_{r \to c} P(D_i = 1 | R_i = r) - \lim_{x \leftarrow c} P(D_i = 1 | R_i = r) < 1$$

This scenario is potentially more common than the sharp RD scenario as most things in life are determined by multiple factors and the influence of the running variable as it crosses the threshold c may be just one of these factors. In the fuzzy RD designs, there are now two causal effects to be estimated: the effect of crossing the threshold on the probability of treatment (which is 1 in the sharp RD) and the effect of crossing the threshold on the outcome. Formally, the fuzzy RD estimator is

$$\tau_{FRD} = \frac{\lim_{r \to c} E[Y_i | R_i = r] - \lim_{r \leftarrow c} E[Y_i | R_i = r]}{\lim_{r \to c} E[D_i | R_i = r] - \lim_{r \leftarrow c} E[D_i | R_i = r]}.$$

If this looks familiar, that's because it should. It's the direct analog of an IV estimator in which the instrument is an indicator for whether R_i lies directly above c. The way the IV estimator is being used, and should be interpreted here is very similar to how the IV estimator allowed us to recover the LATE estimate in an RCT.

In a fuzzy RD there is the intend-to-treat group (say who have $R_i \geq c$ for example) and the control group ($R_i < c$). Because we are in fuzzy land, just because you are in the intend-to-treat group does not necessarily mean you get treated (there are never takers) and similarly, some in the control get treated (always takers). But there is a group of observations, the compliers, whose treatment status would change if they went from control to intend-to-treat (ie if they were moved across the threshold). This is analogous to an RCT with never and always takers. Thus, just like in the RCT context, if I just compare the outcomes of those that are above and below the threshold ($\lim_{r \to c} E[Y_i|R_i = r] - \lim_{r \leftarrow c} E[Y_i|R_i = r]$) the effect is "diluted" by the fact that for many observations, crossing the threshold has no effect (since they are always or never takers). Therefore, just as we were able to recover the local average treatment effect (LATE) effect in the RCT by scaling the average treatment effect by the change in the probability of treatment, here too we scale our estimate by the change in probability of receiving treatment ($\lim_{r \to c} E[D_i|R_i = r] - \lim_{r \leftarrow c} E[D_i|R_i = r]$). Thus, intuitively, the fuzzy RD design measures the average treatment effect for RD compliers at the threshold,

$$\tau_{FRD} = E[Y_i(1) - Y_i(0)|\text{unit } i \text{ is a complier and } R_i = c].$$

1.9 Fuzzy RD: Simulation

Suppose you are the superintendent of a large school district. Last year you **strongly encouraged** students to participate in small reading groups if their 3rd grade reading score fell below 75 points. You would like to know how these reading groups affected student performance on their 4th grade reading tests. Your data includes the 3rd and 4th grade reading scores for all 5000 students in your school district and whether or not a student participated in the small reading groups.

```
set.seed(2000)

fuzzy <- rnorm(5000, mean = 80, sd = 5)
fuzzy <- as.data.frame(fuzzy)

names(fuzzy) <- c("read3")
fuzzy$error <- rnorm(5000, mean = 0, sd = 5)
fuzzy$pe3 <- rnorm(5000, mean = 90, sd = 4)
fuzzy$height <- rnorm(5000, mean = 130, sd = 15)


fuzzy$lowprob <- rbinom(5000, 1, 0.3)
fuzzy$highprob <- rbinom(5000, 1, 0.8)
fuzzy$treated <- NA
fuzzy$treated[fuzzy$read3 > 75] <- fuzzy$lowprob[fuzzy$read3 > 75]
fuzzy$treated[fuzzy$read3 <= 75] <- fuzzy$highprob[fuzzy$read3 <= 75]




# the DGP
fuzzy$read4 <- (-6) + 0.8 * fuzzy$read3 + 10 * fuzzy$treated + fuzzy$error

fuzzy <- fuzzy[fuzzy$read3 < 78 & fuzzy$read3 > 72, ]
```

1.9.1 Fuzzy RD Simulation: Treatment status Graphs

As described in earlier sections, calculate, $\bar{D}_k$, the average treatment level in the bin

$$\bar{D}_k = \frac{1}{N_k} \sum_{i=1}^{N} D_i * \mathbf{1}(b_k < R_i \leq b_{k+1}).$$

In a fuzzy RD, $\bar{D}_k$ can take on many possible values. This plot should show that there is a visual discontinuity in the probability of getting treated at the threshold c. A visual break implies that crossing the threshold has a significant effect on the probability of treatment. In fuzzy RD designs, this graph is equivalent to the first stage in an IV analysis. It shows that we have found a tool that generates some random variation we can leverage to estimate unbiased treatment effects.

```r
library(dplyr)
library(ggplot2)
# I will break up the data into 60 bins (30 above and 30 below the threshold)

cuts <- c(72, 72.1, 72.2, 72.3, 72.4, 72.5, 72.6, 72.7, 72.8, 72.9, 73, 73.1, 73.2,
    73.3, 73.4, 73.5, 73.6, 73.7, 73.8, 73.9, 74, 74.1, 74.2, 74.3, 74.4, 74.5, 74.6,
    74.7, 74.8, 74.9, 75, 75.1, 75.2, 75.3, 75.4, 75.5, 75.6, 75.7, 75.8, 75.9, 76,
    76.1, 76.2, 76.3, 76.4, 76.5, 76.6, 76.7, 76.8, 76.9, 77, 77.1, 77.2, 77.3, 77.4,
    77.5, 77.6, 77.7, 77.8, 77.9, 78)
midpoints <- cuts[2:61] - 0.05

fuzzy$bins <- cut(fuzzy$read3, breaks = cuts, include.lowest = TRUE, right = FALSE,
    labels = midpoints)


fuzzy_mean <- fuzzy %>%
    group_by(bins) %>%
    dplyr::summarize(outbinmean = mean(read4, na.rm = TRUE), treatbinmean = mean(treated,
        na.rm = TRUE), pebinmean = mean(pe3, na.rm = TRUE), heightbinmean = mean(height,
        na.rm = TRUE), numb = n())

fuzzy_mean$bins <- as.numeric(as.character(fuzzy_mean$bins))

plot1fuz <- ggplot(fuzzy_mean, aes(x = bins, y = treatbinmean)) + geom_point() +
    geom_vline(xintercept = 75)
plot1fuz
```
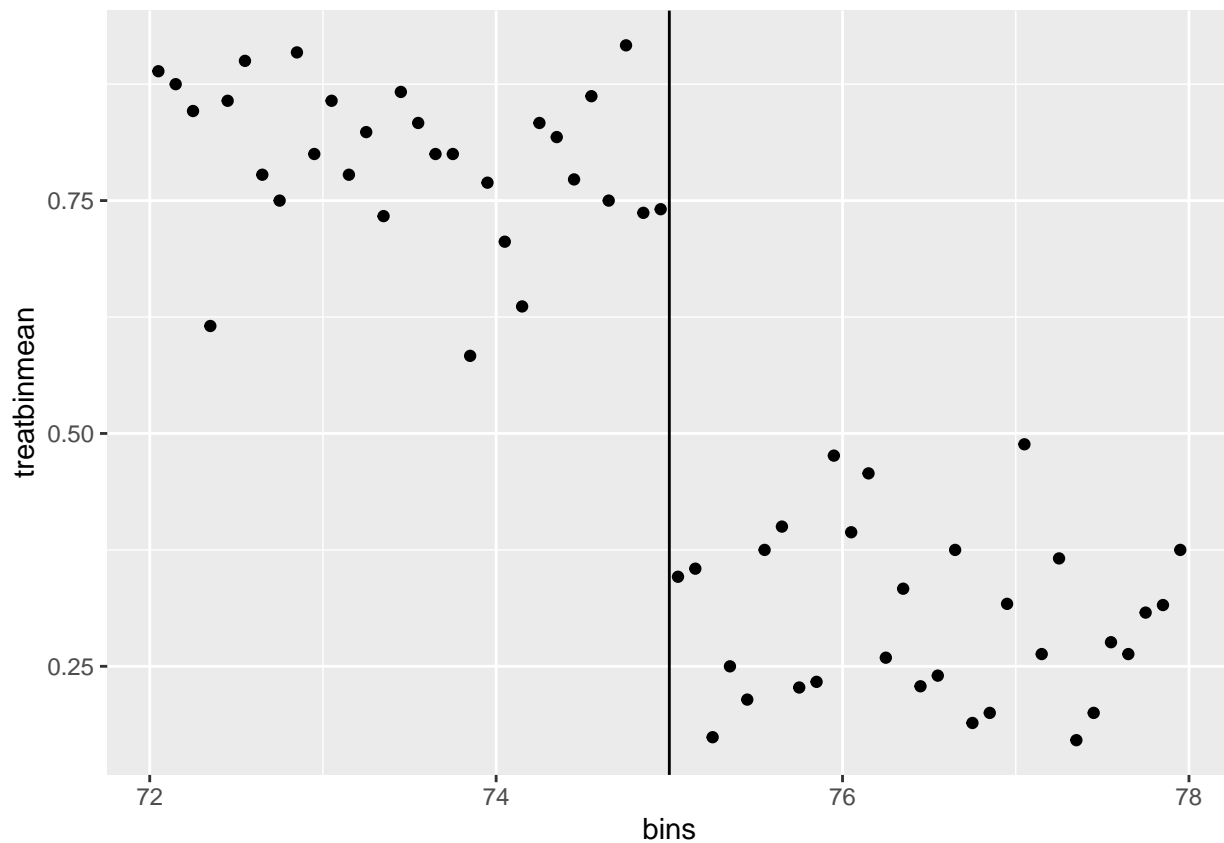
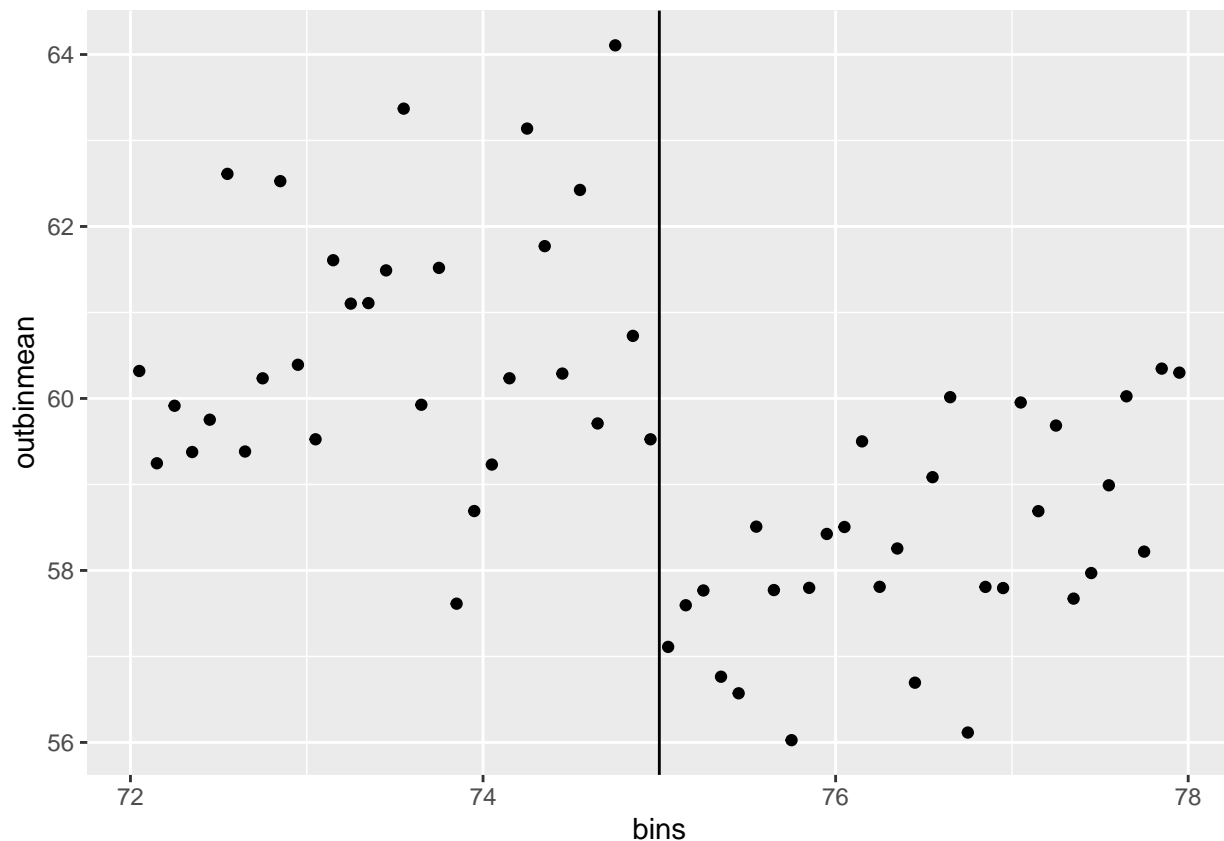### 1.9.2 Fuzzy RD Simulation: Treatment status Graphs

We calculate, $\bar{Y}_k$, the average outcome in each bin

$$\bar{Y}_k = \frac{1}{N_k} \sum_{i=1}^{N} Y_i * \mathbf{1}(b_k < R_i \leq b_{k+1})$$

and plotting these values against the midpoint of each of the bins.

```
# using the values calculated in an earlier chunk

plot2fuz <- ggplot(fuzzy_mean, aes(x = bins, y = outbinmean)) + geom_point() + geom_vline(xintercept = 
plot2fuz
```

### 1.9.3 Fuzzy RD Simulation: Covariate Graphs

We calculate $\bar{X}_i$ where

$$\bar{X}_k = \frac{1}{N_k} \sum_{i=1}^{N} X_i * \mathbf{1}(b_k < R_i \leq b_{k+1})$$

is plotted against the midpoint of each bin.

As above, we want to check that assignment to treatment is "as good as random" by making sure the treated and control groups are comprable along observable characteristics.

```
# using the values calculated in an earlier chunk

plot3fuz <- ggplot(fuzzy_mean, aes(x = bins, y = pebinmean)) + geom_point() + geom_vline(xintercept = 75
plot3fuz
```
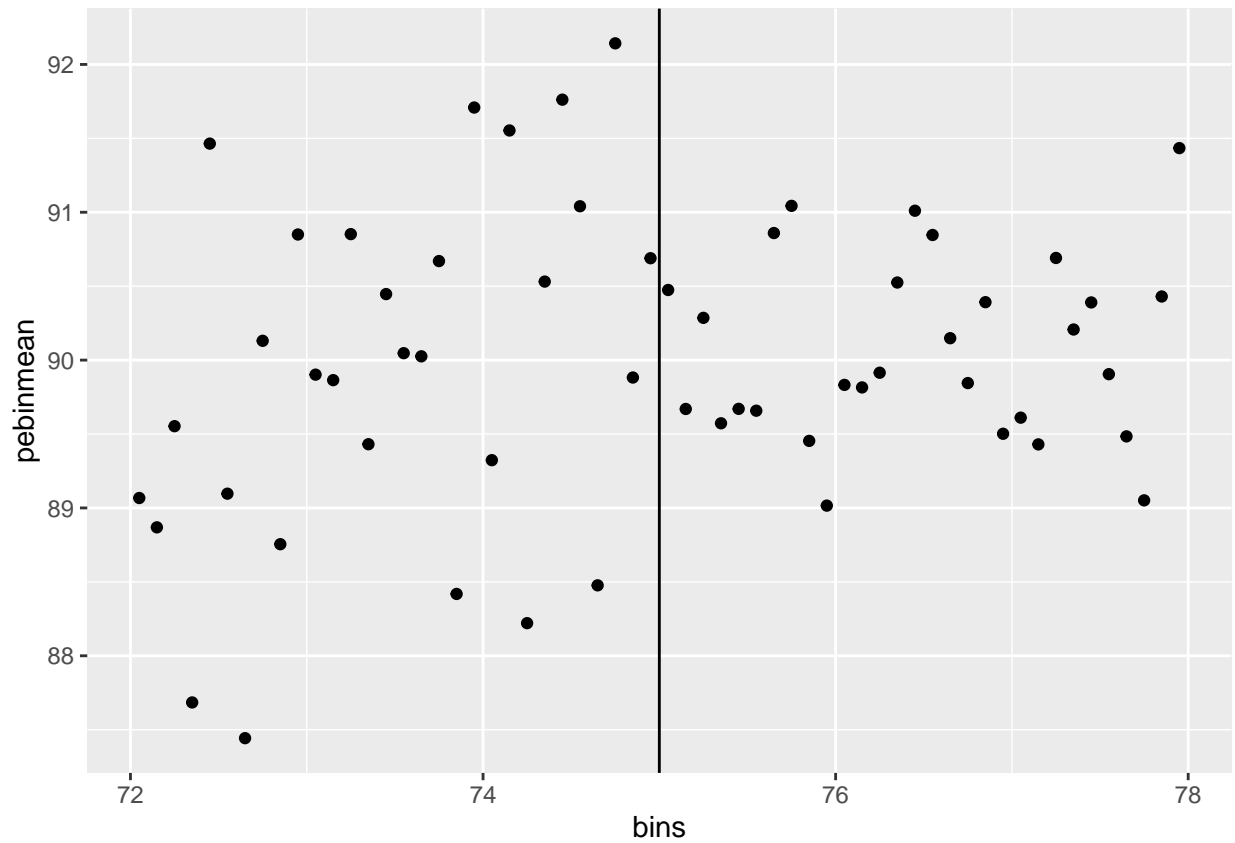
```
plot4fuz <- ggplot(fuzzy_mean, aes(x = bins, y = heightbinmean)) + geom_point() +
    geom_vline(xintercept = 75)
plot4fuz
```
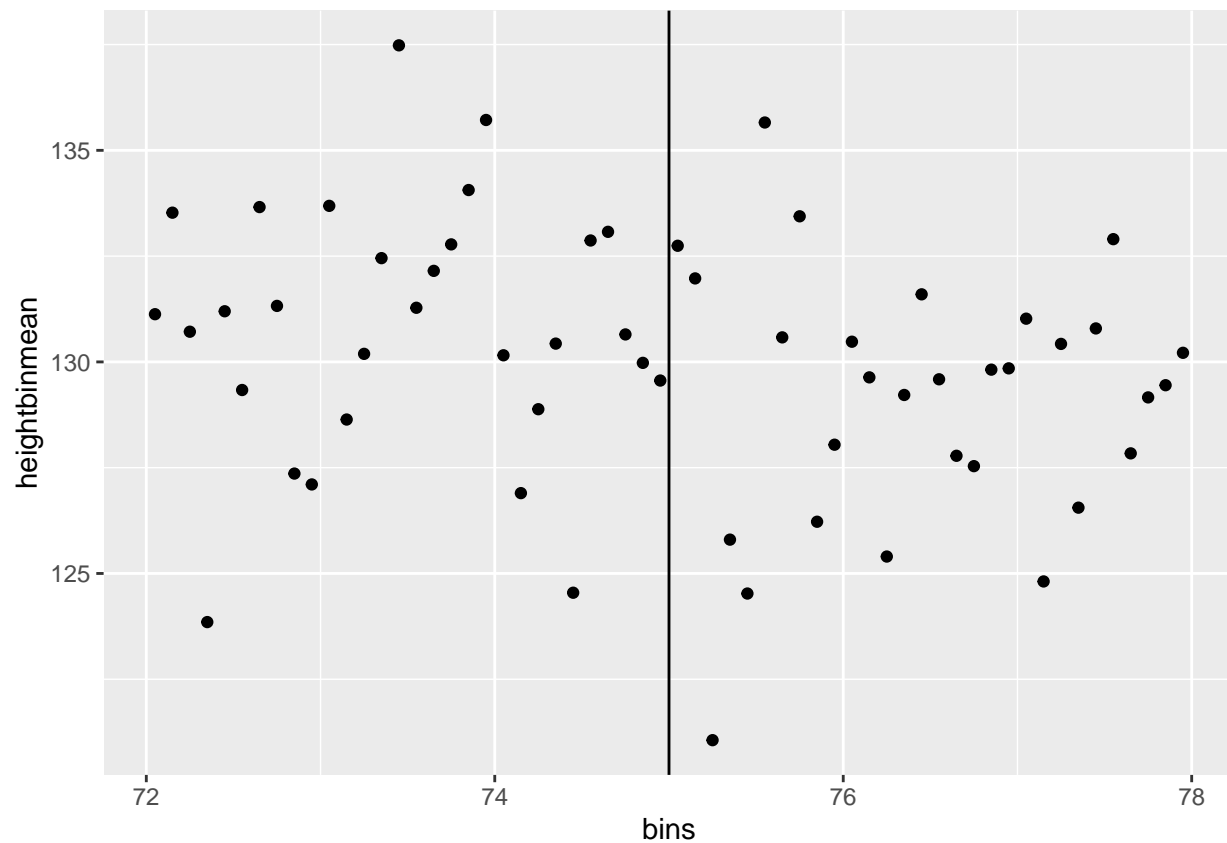
### 1.9.4 Fuzzy RD Simulation: Density of the running variable

We calculate

$$N_k = \sum_{i=1}^{N} \mathbf{1}(b_k < R_i \le b_{k+1})$$

and plot these against the midpoint of the bin.

We want to make sure that there is no evidence that observations were able to move their R_i accross the threshold as a response to incentives to receive (or avoid) treatment.

```
# using the values calculated in an earlier chunk

plot5fuz <- ggplot(fuzzy_mean, aes(x = bins, y = numb)) + geom_point() + geom_vline(xintercept = 75)
plot5fuz
```
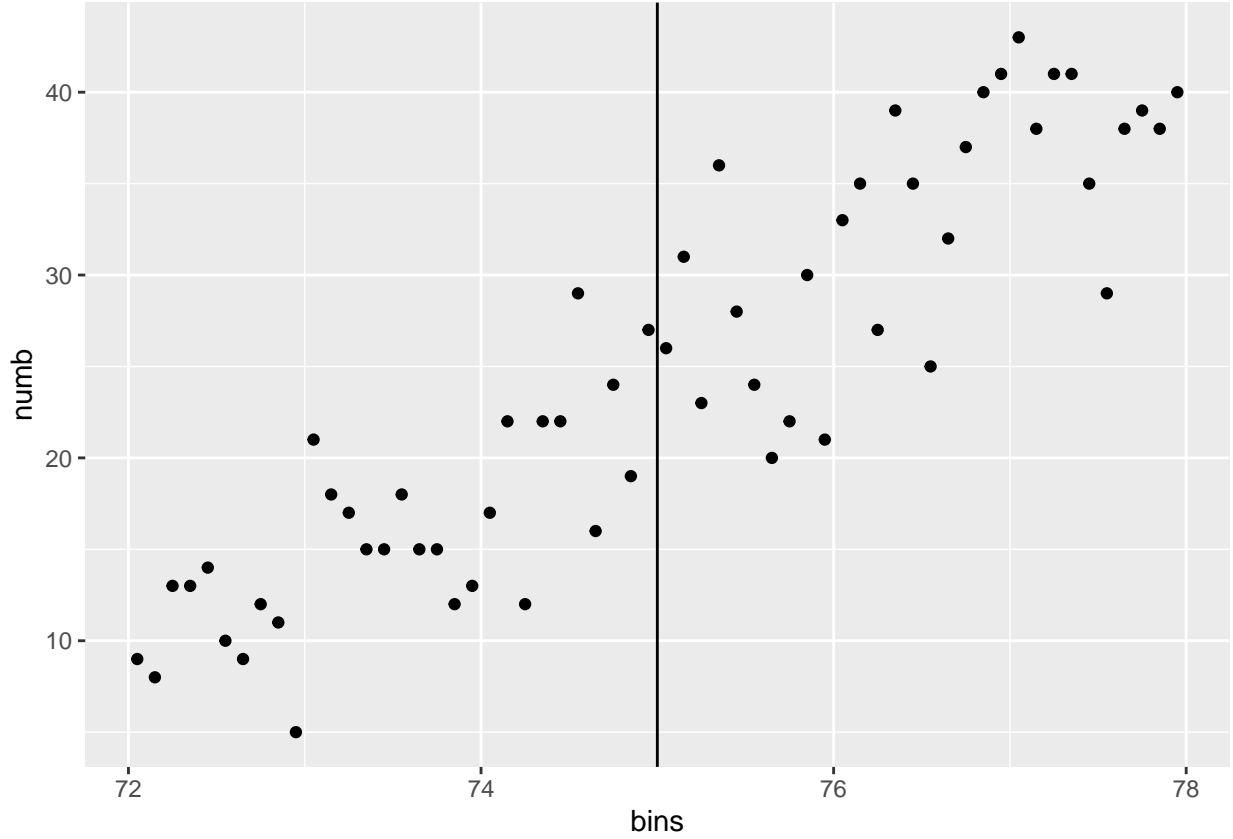
1.10 Fuzzy RD Estimation

In the fuzzy RD design, we have two effects to estimate: the effect of crossing the threshold on the treatment (the "first stage") and the effect of crossing the threshold on the outcome (the "reduced form"). As you might expect, we apply the same methodology as in earlier IV's to estimate the effect of crossing the threshold on Y_i and the effect of crossing the threshold on D_i. For the sample with $c - h < R_i \leq c + h$ we run some version (you can include covariates) of the following regressions,

$$Y_i = \pi_0 + \pi_1 Z_i + \pi_2 (R_i - c) + \pi_3 (R_i - c) * Z_i + u_i$$

and

$$D_i = \gamma_0 + \gamma_1 Z_i + \gamma_2 (R_i - c) + \gamma_3 (R_i - c) * Z_i + v_i$$

where $Z_i = \mathbf{1}(R_i \geq c)$. The fuzzy RD estimator is then

$$\hat{\tau}_{FRD} = \frac{\hat{\pi}_1}{\hat{\gamma}_1}.$$

In other words, the FRD estimator is simply the ratio of the reduced form and the first stage estimates (the IV estimator), i.e. the effect of crossing the discontinuity threshold on the outcome, scaled by the effect of crossing the discontinuity threshold on the probability of treatment.

```
fuzzy$runminc <- fuzzy$read3 - 75

# first stage
fuzzy$ittgroup <- 0
fuzzy$ittgroup[fuzzy$read3 <= 75] <- 1

fuzfs <- felm(treated ~ ittgroup + runminc + ittgroup * runminc, fuzzy)

# reduced form
fuzrf <- felm(read4 ~ ittgroup + runminc + ittgroup * runminc, fuzzy)


fuzzy$interedog <- fuzzy$treated * fuzzy$runminc
fuzzy$interinst <- fuzzy$ittgroup * fuzzy$runminc
# IV
fuziv <- felm(read4 ~ runminc | 0 | (treated | interedog ~ ittgroup + runminc + interinst),
    fuzzy)


## Warning in chol.default(mat, pivot = TRUE, tol = tol): the matrix is either
## rank-deficient or indefinite

stargazer(fuzfs, fuzrf, fuziv, type = "latex")
```

% Table created by stargazer v.5.2.2 by Marek Hlavac, Harvard University. E-mail: hlavac at fas.harvard.edu
% Date and time: Thu, Mar 30, 2023 - 10:49:04 AM

In a fuzzy RD, you will not be able to plot and represent visually the "scaled" treatment effect as the graphs are limited to the graphical equivalent of the first stage and the reduced form estimates.

1.11   External Validity

Our treatment estimator for a sharp RD is given by

$$\tau_{SRD} = E[Y_i(1) - Y_i(0)|R_i = c].$$

Our treatment estimator for a fuzzy RD is given by

$$\tau_{FRD} = E[Y_i(1) - Y_i(0)|\text{unit } i \text{ is a complier and } R_i = c].$$

The conditioning in the equation above does suggest that there are limitation to the applicability of RD estimates. First of all, we focus on observations that are in the neighborhood of the threshold since observations that are far below and far above the threshold likely differ from each other in many observable and unobservable ways. In an RD design, we are implicitly assuming that whether an observation fell just above or just below the threshold is effectively arbitrary and these observations are identical in all observable and non-observable characteristics and conditions, except for their treatment status. In this case we can measure a Local Average Treatment Effect (LATE) that is valid around the threshold. What this means is that RD estimates are inherently localized since the effects are estimated for a sub population where their R_i is in the neighborhood of c. Because of this, even though RD estimates have a relatively high degree of internal validity, it is important to think about their external validity since treatment effects could be quite different for observation where R_i is quite different from c. When we are considering a fuzzy RD, we must also be aware that we are estimating effects on compliers, which is yet another further subsample of the population.

Table 2:

	treated	read4	
Dependent variable:			
	(1)	(2)	(3)
ittgroup	0.464***	4.253***	
	(0.048)	(0.722)	
runminc	−0.004	0.821***	1.057***
	(0.017)	(0.251)	(0.332)
ittgroup:runminc	−0.013	−0.479	
	(0.029)	(0.441)	
'treated(fit)'			9.201***
			(1.162)
'interedog(fit)'			−0.685
			(0.631)
Constant	0.308***	57.010***	54.182***
	(0.030)	(0.460)	(0.640)
Observations	1,460	1,460	1,460
R^2	0.213	0.037	0.454
Adjusted R^2	0.211	0.035	0.453
Residual Std. Error (df = 1456)	0.443	6.728	5.065

Note: *p<0.1; **p<0.05; ***p<0.01