Regression discontinuity design

CMED6040 – Session 3

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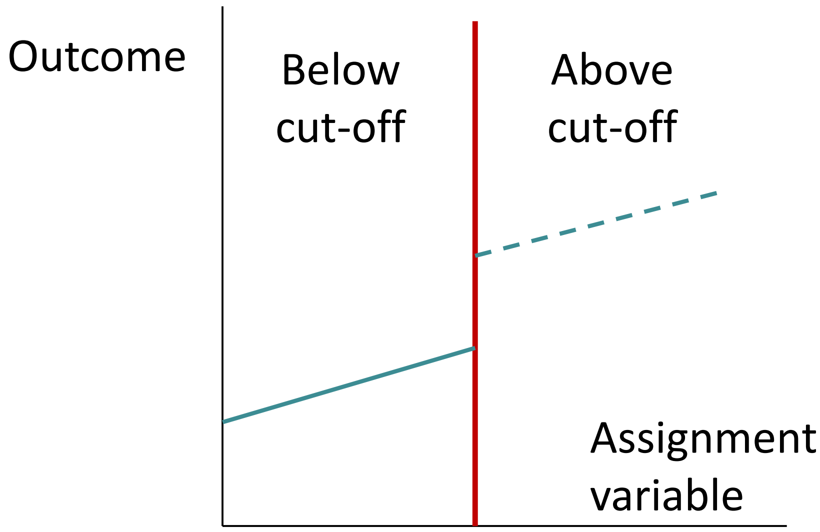
Session 3 learning objectives

After this session, students should be able to

- Understand the rationale and assumptions of regression discontinuity design
- Recognize situations where regression discontinuity design can be used to estimate causal effect
- Estimate and interpret the treatment effect under regression discontinuity design

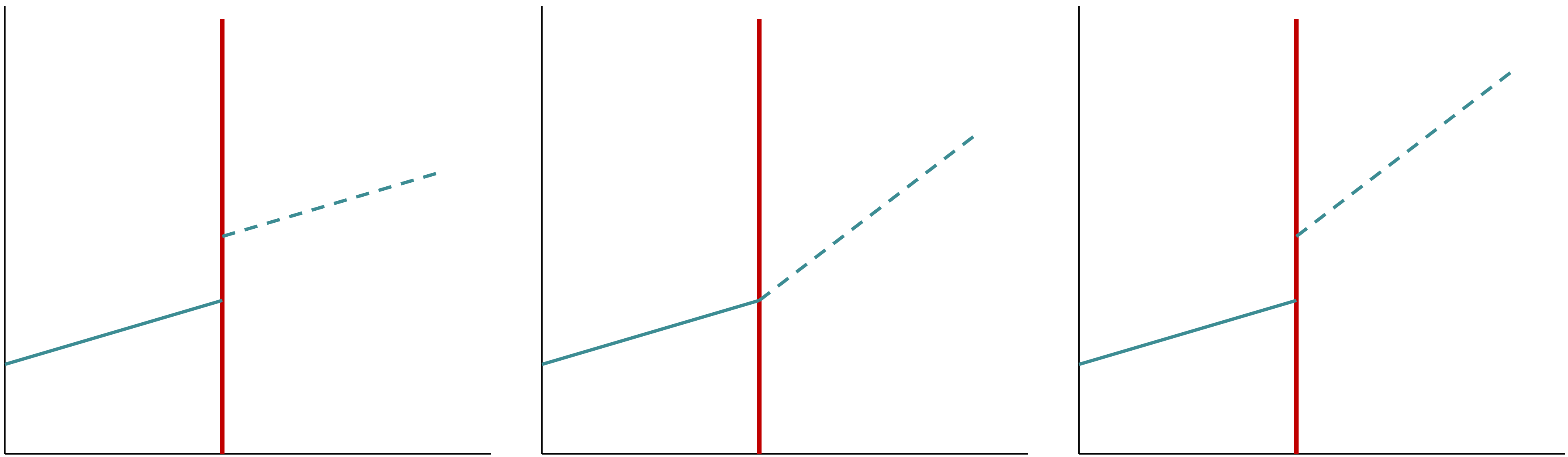
Regression discontinuity design (RDD)

- Non-randomized / quasi-experimental design
- Pre-post test design
- Suitable for program evaluation
- Widely used in economics, politics, getting more attention from medicine, epidemiology and education
- Simplest case: two groups – treatment (X = 1) and control (X = 0)



Possible forms of discontinuity

Change in intercept | Change in slope | Change in intercept and slope



Assumptions for RDD

- Known and universal principle for treatment assignment
  - e.g. start antiretroviral therapy (ART) when CD4 count ≤ 200 cells/mm^3 for HIV patients
- Assignment criteria measured prior to treatment
- There is an interval variable (assignment / forcing variable) in which a cut-off, or discontinuity, defines the assignment of subjects
  - Deterministic: Sharp RD
  - Probabilistic: Fuzzy RD
- Many units fall on either side of the cut-off
- Continuity in potential outcomes at the cut-off
  - Satisfied if there is random measurement error in the assignment variable ('local randomization')

Example 1 – RDD assumptions

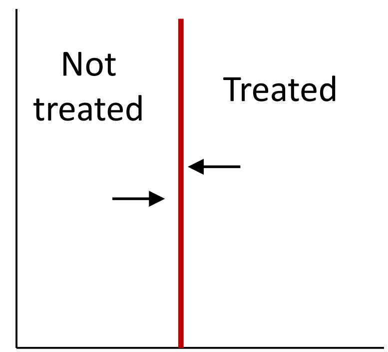
- HPV vaccine is offered to grade 8 girls. The objective is to estimate the effect of HPV vaccination program on risky sexual behaviour (Smith et al., 2015)
  - Assignment variable: birth year
- Assignment criteria measured prior to treatment (birth year)
- There is an interval variable (assignment / forcing variable) in which a cut-off, or discontinuity, defines the assignment of subjects (birth year)
- Many units fall on either side of the cut-off (girls at different birth year)
- Continuity in potential outcomes at the cut-off (similar risky sexual behaviour for girls just below or above grade 8)

Example 2 – RDD assumptions

- Patients eligible for ART if their CD4 count < 200 cells/µL or with stage IV AIDS-defining illness. The objective is to estimate the effect of ART initiation on mortality (Bor et al., 2014)
  - Assignment variable: CD4 count
- Assignment criteria measured prior to treatment (CD4 count)
- There is an interval variable (assignment / forcing variable) in which a cut-off, or discontinuity, defines the assignment of subjects (CD4 count)
- Many units fall on either side of the cut-off (patients with different levels of CD4 count)
- Continuity in potential outcomes at the cut-off (no discontinuity in mortality around CD4 count = 200 cells/µL; random measurement error in CD4 count)

Causal interpretation for RDD

- If the assumptions are satisfied, we can infer the difference in outcome as the causal effect of treatment / assignment
- Estimate local average treatment effect (LATE)
  - Strong assumption on the functional form is needed to estimate the global average treatment effect
- Consider two groups of patients
  - Those below the cut-off but approaching from below
  - Those above the cut-off but approaching from above
  - These two groups of patients are becoming more alike in both their observed and unobserved characteristics / confounders



- In a small interval around the cut-off, the only difference is the treatment assignment

Estimation of the treatment effect

- When treatment is a deterministic function of the assignment variable:

$$ACE_{SRD} = \lim_{z \to c} E[Y_i(1)|Z_i = z] - \lim_{z \to c} E[Y_i(0)|Z_i = z]$$
$$= E[Y_i(1) - Y_i(0)|Z_i = c]$$

ACE – average causal effect; SRD – sharp regression design

where Z_i is the assignment variable; *c* is the cut-off

- The corresponding linear regression model can be specified by:

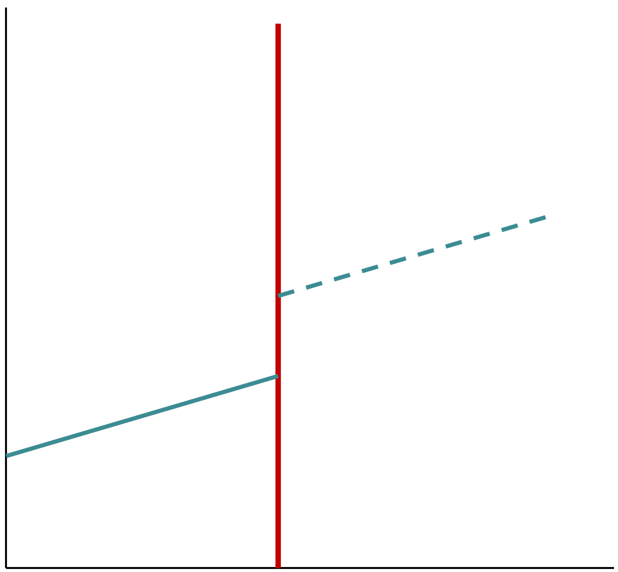
$$Y_i = \alpha + \beta_1 I(Z_i > c) + \beta_2 (Z_i - c) +$$
$$\beta_3 I(Z_i > c)(Z_i - c) + \varepsilon_i$$

where $I(Z_i > c)$ is a binary variable with value 1 when $Z_i > c$, 0 otherwise

- Note that the cut-off is usually subtracted from the assignment variable (i.e. $Z_i - c$)

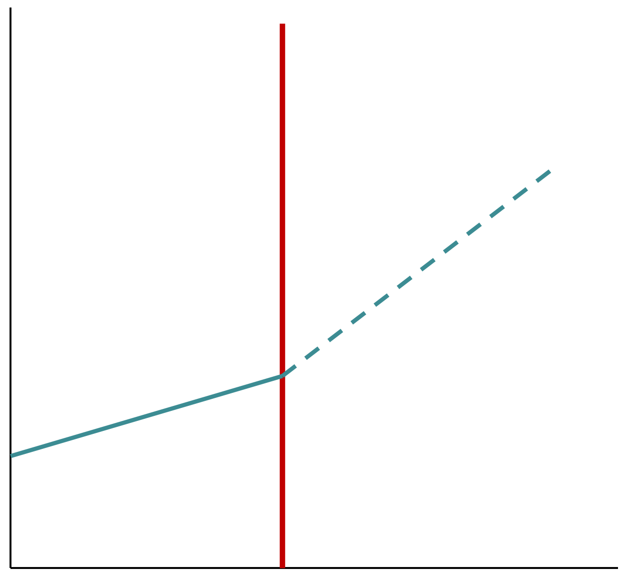
Possible forms of discontinuity

Change in intercept



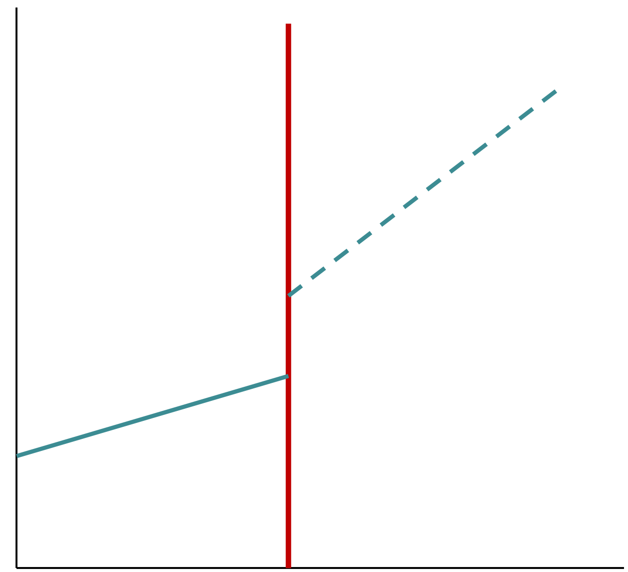
$\beta_1 > 0, \beta_3 = 0$

Change in slope



$\beta_1 = 0, \beta_3 > 0$

Change in intercept and slope



$\beta_1 > 0, \beta_3 > 0$

$$Y_i = \alpha + \beta_1 I(Z_i > c) + \beta_2 (Z_i - c) + \beta_3 I(Z_i > c)(Z_i - c) + \varepsilon_i,$$

$\beta_2 > 0$

Estimation strategy

- Parametric / global approach
  - Use all observations to help define the global function for estimating effect at cut-off
  - Different functional forms (e.g. linear, quadratic, cubic, and interactions with treatment) can be used to minimize bias
- Nonparametric / local approach
  - Limit analysis to observations near the cut-off (within the ‘bandwidth’)
  - In the local region, linear relation can be a good approximation

- Global approach: bias ↑ precision ↑
- Local approach: bias ↓ precision ↓

Example – alcohol-related suicide

- Saved in 'examplealcohol.csv'
- To test the effect of minimum legal drinking age (MLDA) on alcohol-related suicides (per 1,000 hospital episodes)
- Based on administrative records on inpatients and from emergency department
- In this case, age is the assignment variable

Example – alcohol-related suicide

- Suppose we hypothesize that there could be intercept and slope change due to MLDA
- Fit a model for regression discontinuity design (global approach):

$$suicide_i = \alpha + \beta_1 MLDA_i + \beta_2 month_i + \beta_3 MLDA_i \times month_i + \varepsilon_i$$

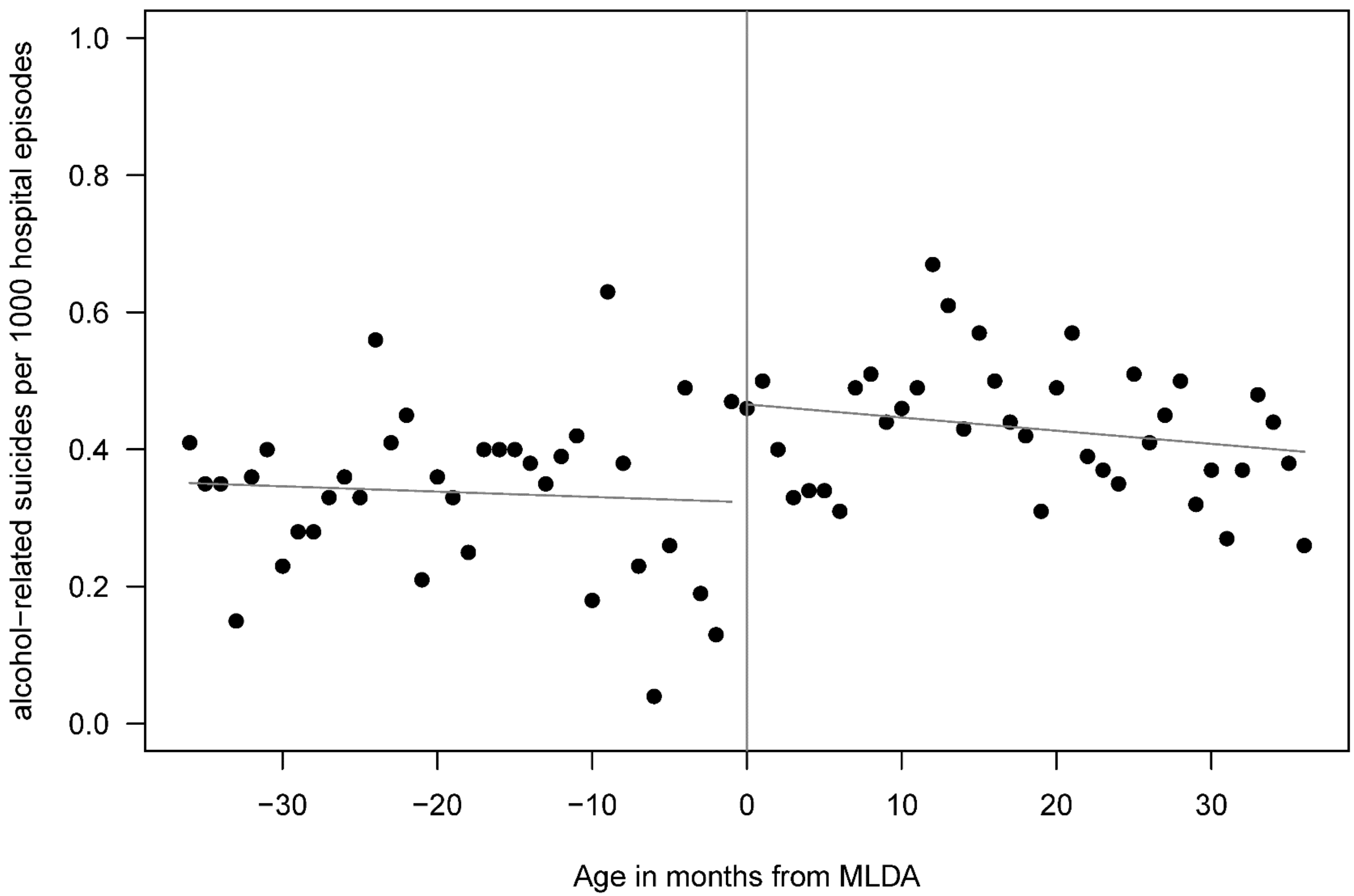
```
alc <- read.csv('examplealcohol.csv')
alc$MLDA <- 1*(alc$month>=0)
rd1 <- lm(alc.suicide ~ MLDA + month + MLDA*month, data=alc)
```

Example – alcohol-related suicide

```
summary(rd1)

Coefficients:
              Estimate Std. Error t value Pr(>|t|)
(Intercept)  0.3228889  0.0366951   8.799 6.92e-13 ***
MLDA         0.1427157  0.0505295   2.824  0.00619 **
month       -0.0007748  0.0017295  -0.448  0.65557
MLDA:month  -0.0011432  0.0023971  -0.477  0.63494
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

- There was a 0.14 (95% CI 0.04–0.24) excess alcohol-related suicide per 1000 hospital episodes among youths just older than MLDA

Figure: alcohol-related suicide



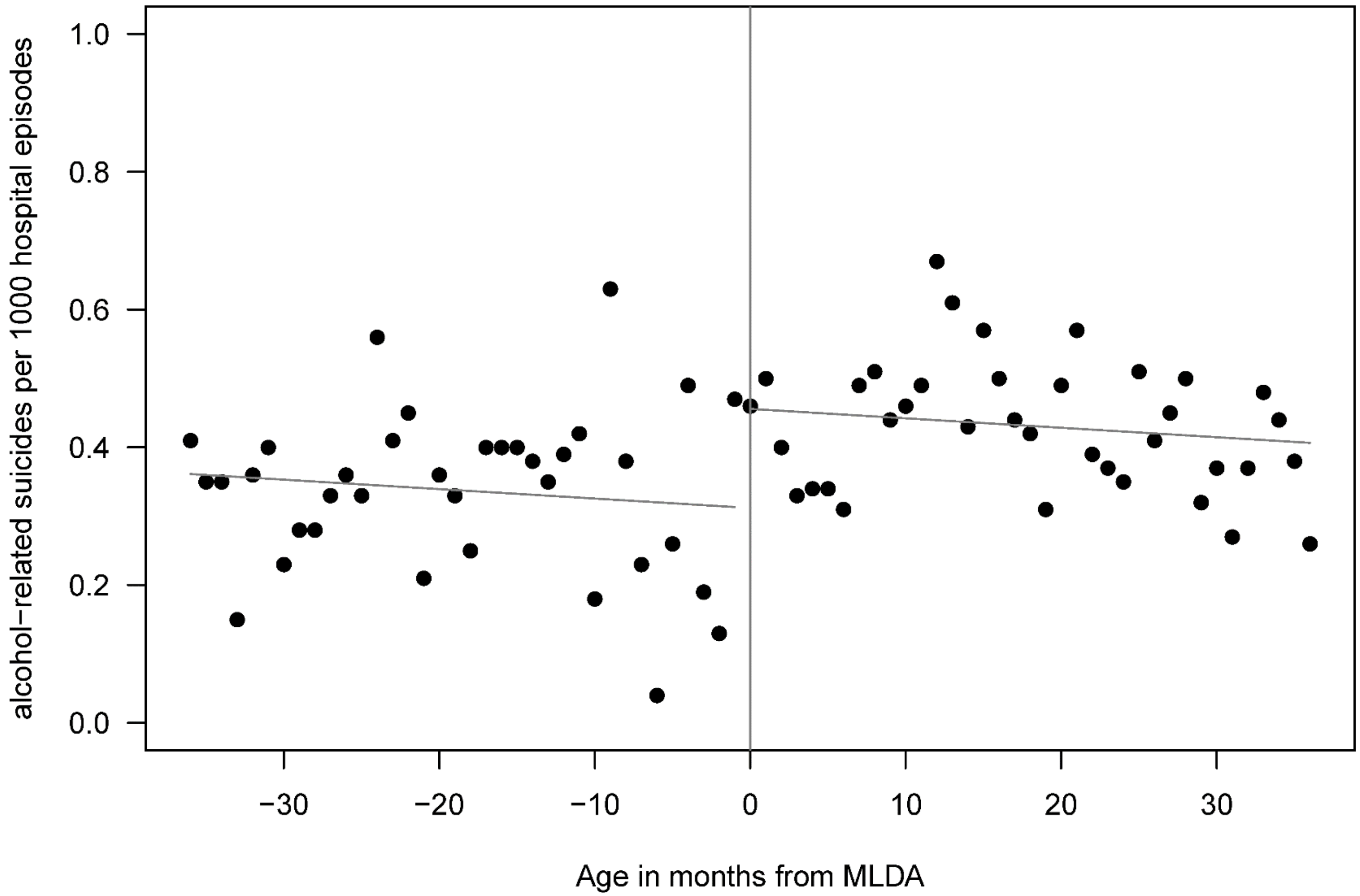
Example – alcohol-related suicide

- The is no significant change in slope and the interaction term can be dropped
- Revised model:

$$suicide_i = \alpha + \beta_1 MLDA_i + \beta_2 month_i + \varepsilon_i$$

```
rd1b <- lm(alc.suicide ~ MLDA + month, data=alc)
summary(rd1b)
Coefficients:
             Estimate Std. Error t value Pr(>|t|)
(Intercept)  0.311880   0.028366  10.995  < 2e-16 ***
MLDA         0.143859   0.050193   2.866  0.00548 **
month       -0.001370   0.001191  -1.150  0.25395
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Figure: alcohol-related suicide



Model specification

- Correct specification of the functional form is needed to obtain unbiased estimate of the treatment effect
- Curvilinear relationship could have explained the discontinuity
- Full data (global approach)
  - Models with polynomial term for comparison
- Local data (local approach)
  - With adequate data, just compare means around cut-off (model free)
  - Local regression
- A tradeoff between bias and precision

Example – alcohol-related suicide

- Test for potential polynomial relation (up to cubic order)
- Revised model:

$$suicide_i = \alpha + \beta_1 MLDA_i + \beta_2 month_i + \beta_3 month_i^2 + \beta_4 month_i^3 + \varepsilon_i$$

```
rd1c <- lm(alc.suicide ~ MLDA + month + I(month^2) + I(month^3),
data=alc)
```

OR

```
rd1c <- lm(alc.suicide ~ MLDA + poly(month, degree=3), data=alc)
```

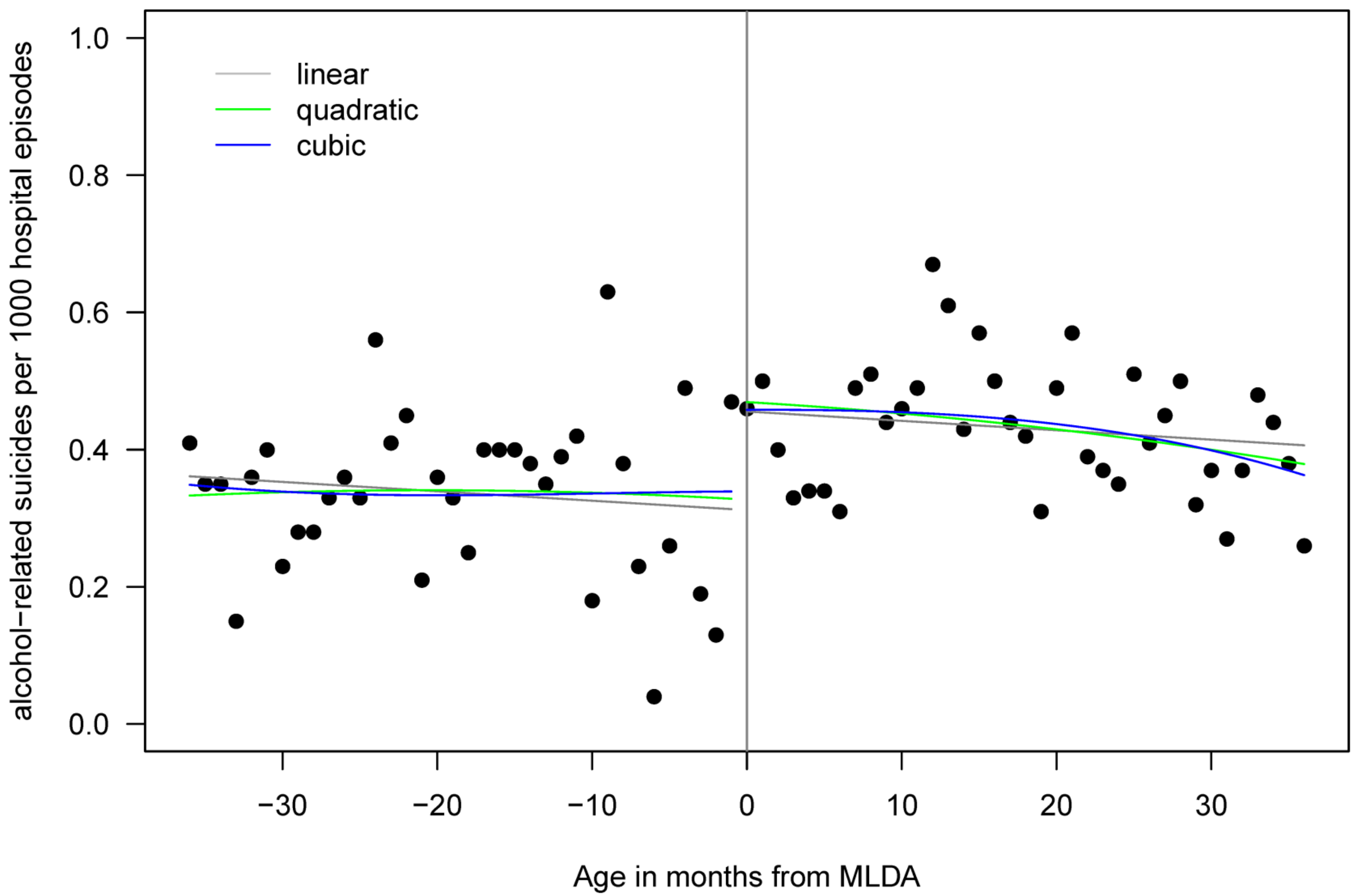
- I(): treat variables 'as is'; to differentiate from formula operators
- poly(): compute orthogonal polynomials to avoid multicollinearity

Example – alcohol-related suicide

```
summary(rd1c)


Coefficients:
                  Estimate Std. Error t value Pr(>|t|)
(Intercept)        0.32457    0.03636   8.927 4.57e-13 ***
MLDA               0.11883    0.06728   1.766   0.0818 .
poly(month, 3)1 -0.15403    0.27120  -0.568   0.5719
poly(month, 3)2 -0.11199    0.10781  -1.039   0.3026
poly(month, 3)3 -0.07566    0.14363  -0.527   0.6000
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

- The estimate changed slightly from 0.14 to 0.12 excess alcohol-related suicide per 1000 hospital episodes among youths just older than MLDA (though less precise)

Figure: alcohol-related suicide



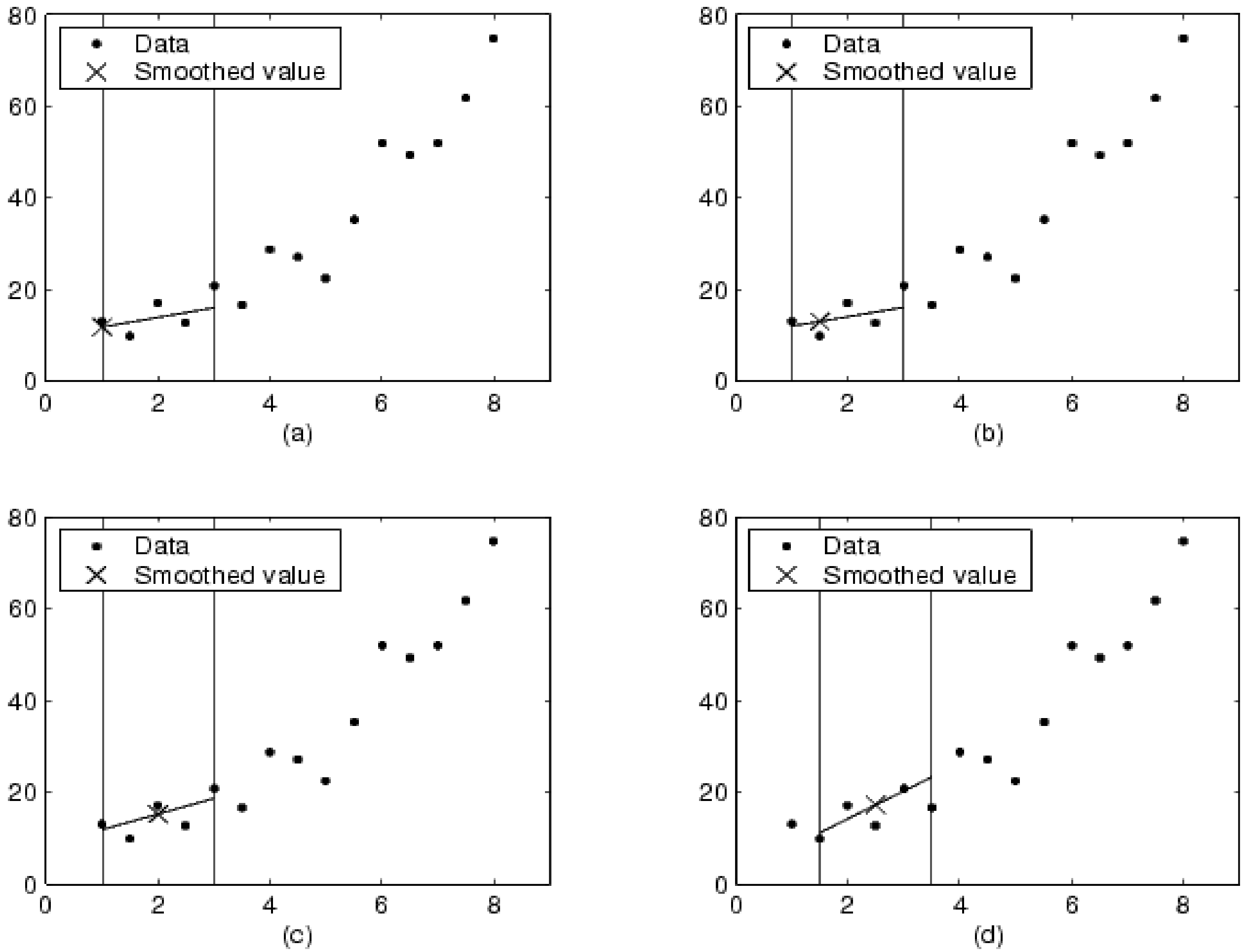
Local linear regression

- A technique to estimate a smoothing function
- Use local observations to fit linear regression
- Fit a regression model for each observation
- Reduce bias by giving up some precision
- At each observation x_0, minimize

$$\sum_i K_h(x_0, x_i)(y_i - \alpha - \beta x_i)^2$$

  where K_h is a kernel (weighting) function with bandwidth h
- Bandwidth controls how much neighboring observations are included
- Can be extended as local polynomial regression

Local linear regression

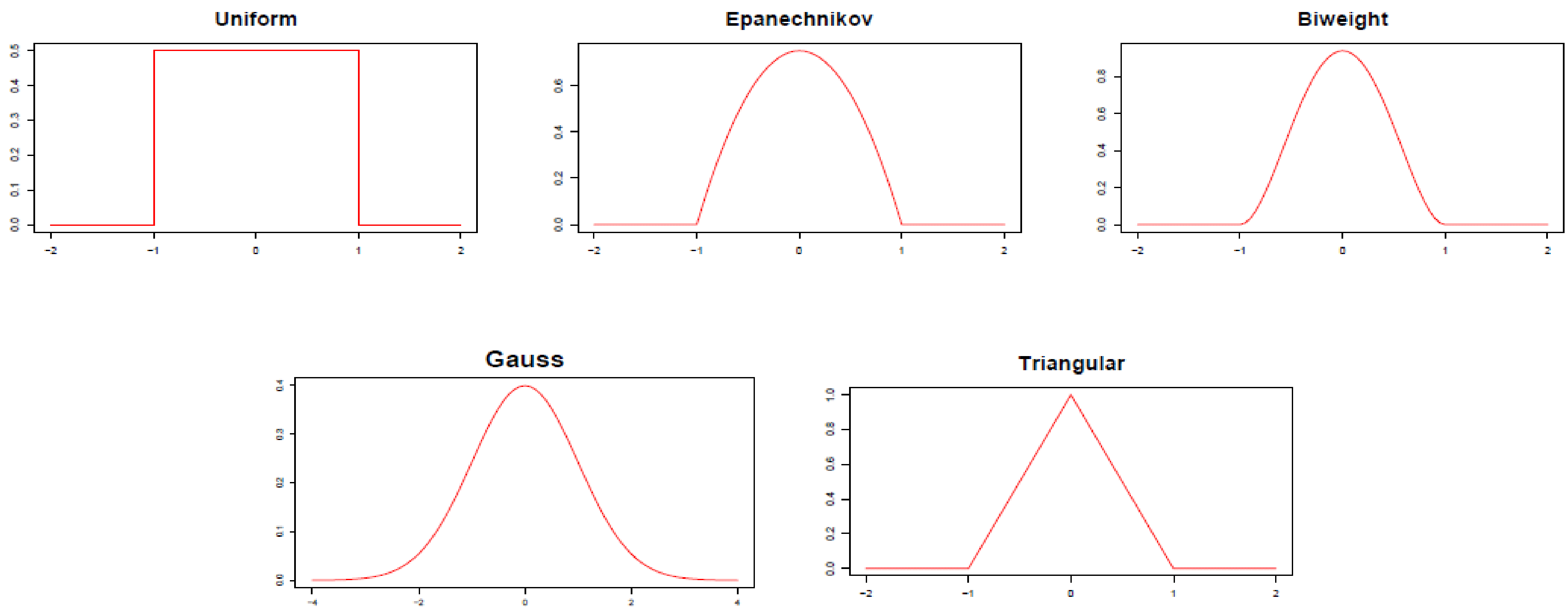


h = 2

Kernel smoothing

- Smoothing data to identify patterns
- Non-parametric method which does not assume a particular parametric form (e.g. linear, quadratic, sinusoidal) for the data
- Weighting are applied to neighbor data points, specified by the kernel function
  - Sum of the weighting equals to 1
- Bandwidth controls how many neighboring data points are included

Kernel functions



Choice of bandwidths

- Wider bandwidth
  - smoother plot
  - less accurate
  - may lose some of the features if bandwidths is too wide
- A balance between variability and bias
  - wider bandwidth: variability ↓, bias ↑
- Choice of bandwidth is more important than choice of kernel functions

- Use 'plug-in' (theoretically optimized) or cross-validation method to choose bandwidth

Local polynomial regression in R

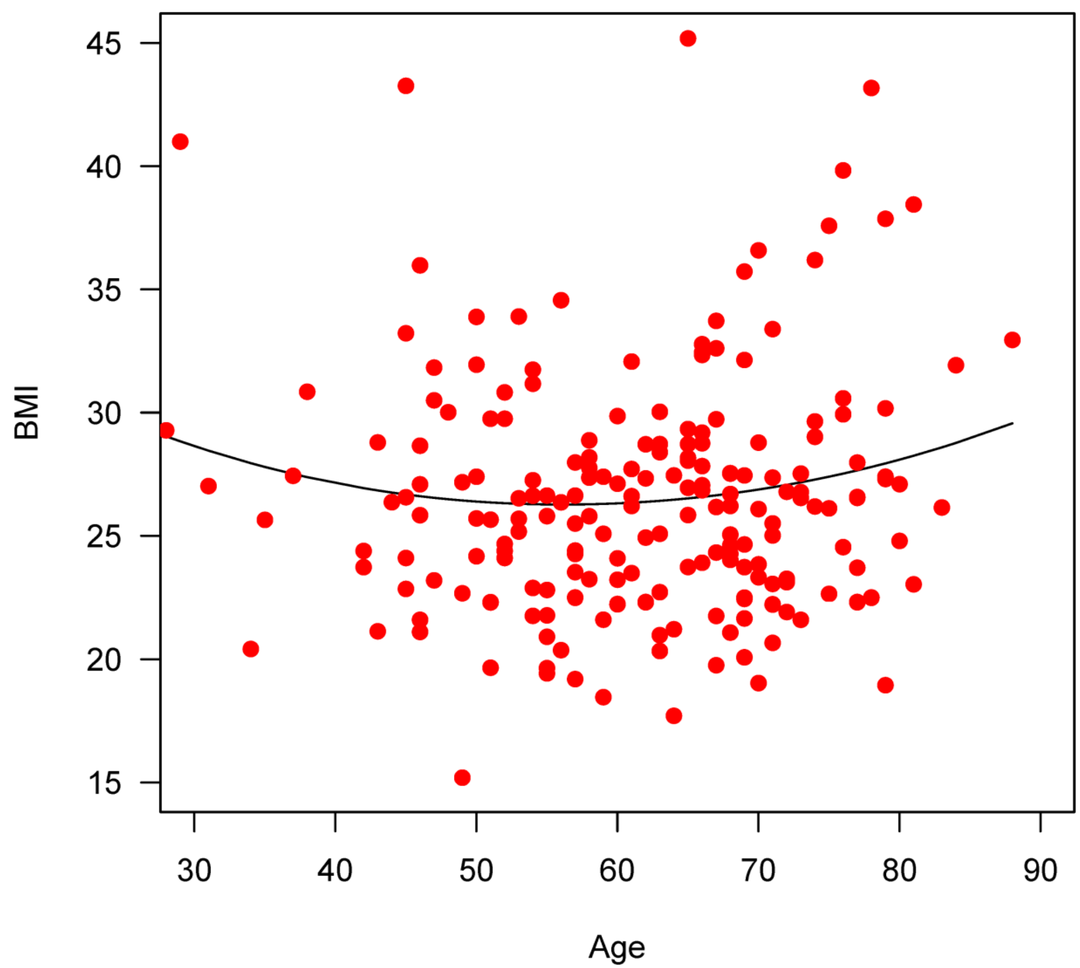
- Package: np
- Usually involve two steps: (1) computing the bandwidth; (2) fitting the local polynomial regression model
- npregbw(*y ~ x*, *bws*, *ckertype*, *regtype*, *bandwidth.compute=T, data*)
  - *x* are the explanatory variables
  - *bws* specifies pre-determined bandwidth
  - *ckertype* specifies the continuous kernel type, e.g. ‘gaussian’, ‘epanechnikov’, ‘uniform’
  - *regtype* = ‘ll’ generates a local linear estimator; ‘lc’ for local constant estimator
  - *bandwidth.compute = TRUE* to search for suitable bandwidths
- npreg(bws)
  - *bws* is the bandwidth specification from npregbw()

Local polynomial regression example – BMI and age

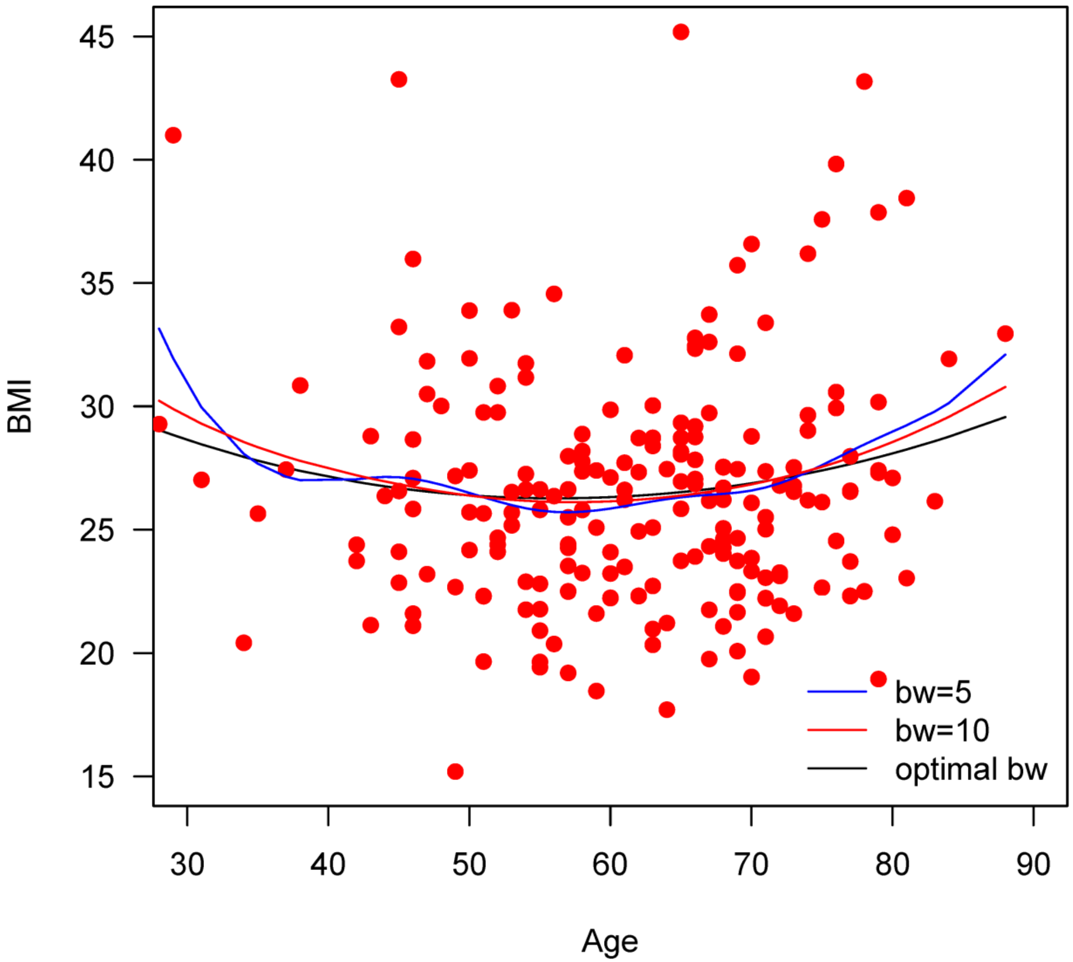
- Fit a simple local linear regression model for bmi on age

```
require(np)

data <- read.csv ("digoxin.csv")

plot(data$age, data$bmi, type="p", xlab="Age", ylab="BMI", las=1)


bmi.bw <- npregbw(bmi~age, bandwidth.compute=TRUE,
ckertype="gaussian", regtype="ll", data=data)

bmi.lp <- npreg(bws = bmi.bw)


with(data, plot(age[order(age)], predict(bmi.lp)[order(age)],
type='l', las=1, xlab="Age", ylab="BMI", xlim=c(30,90),
ylim=c(15,45)))

with(data, points(age, bmi, pch=19, col="red"))
```

Local polynomial regression example – BMI and age



Different smoothness



- bandwidth = 5 and 10 produce fitted curve with spurious bumps
- optimal bandwidth = 15.5 achieves adequate smoothness

RDD with local regression in R

- Package: rdrobust
- rdrobust(*y*, x, c = 0, p = 1, h = NULL, kernel = "tri", bwselect = "mserd", all = FALSE)
  - *y, x* are the outcome and assignment variables respectively
  - *c* specifies the cut-off in *x*
  - *p* is the order of the local polynomial, *p* = 1 refers to local linear regression
  - *h* specifies the bandwidth. If not specified, the bandwidth will be selected by *bwselect*
  - *kernel* selection the kernel function (e.g. ‘triangular’, ‘epanechnikov’ or ‘uniform’)
  - *bwselect* specifies the algorithm to select bandwidth, “mserd” minimizes the mean squared error (MSE)
  - *all = TRUE* to show conventional and bias-corrected / robust estimates

Local regression – alcohol-related suicide

```
rd.l <- rdrobust(alc$alc.suicide, alc$month, all=T)
rd.l

Number of Obs.                    73
BW type                        mserd
Kernel                    Triangular
VCE method                        NN

Number of Obs.                   36          37
Eff. Number of Obs.               9          10
Order est. (p)                    1           1
Order bias  (q)                   2           2
BW est. (h)                   9.240       9.240
BW bias (b)                  14.336      14.336
rho (h/b)                     0.645       0.645
Unique Obs.                      36          37
```

Local regression – alcohol-related suicide

Estimates:

Method	Coef.	Std. Err.	z	P>|z|	[95% C.I.]
Conventional	0.098	0.156	0.632	0.528	[-0.207 , 0.403]
Bias-Corrected	0.078	0.156	0.501	0.616	[-0.227 , 0.383]
Robust	0.078	0.194	0.402	0.687	[-0.302 , 0.458]

- There was an estimated 0.08 (95% CI -0.30–0.46) excess alcohol-related suicide per 1000 hospital episodes among youths just older than MLDA
- Bias correction is needed due to the bandwidth selection.
- Note the wide 95% CI
- Selected bandwidth was about h = 9 which significantly reduced the sample size

Practice – alcohol-related suicide

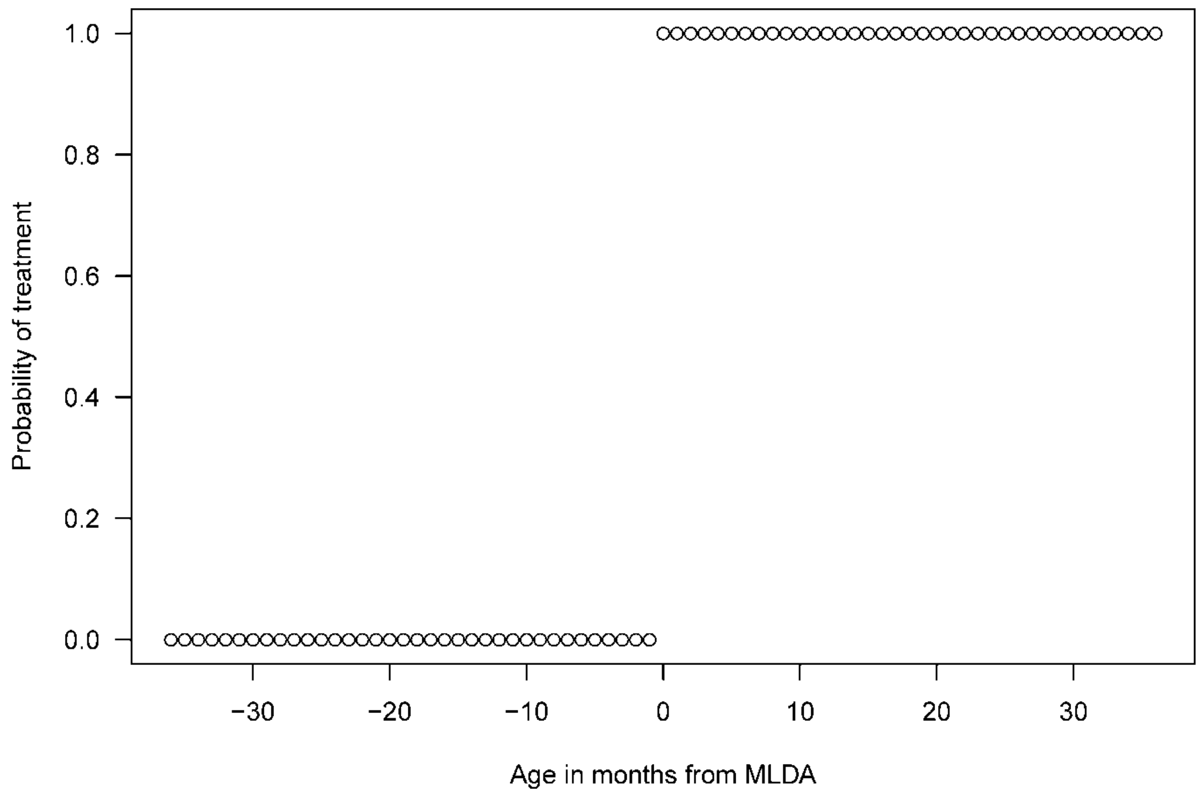
- Using the function rdrobust(), estimate the effect of MLDA using a global approach

```
rd.g <- rdrobust(alc$alc.suicide, alc$month, h=100, kernel='uniform', all=T)
rd.g
Estimates:
                Coef   Std. Err. z      P>|z|  CI Lower CI Upper
Conventional    0.1427 0.0635    2.2475 0.0246 0.0183   0.2672
Bias-Corrected  0.1268 0.0635    1.9971 0.0458 0.0024   0.2513
Robust          0.1268 0.1015    1.2497 0.2114 -0.0721  0.3257
```

- The estimated effect is 0.14 (95% CI = 0.02–0.27), the bias is caused by the bandwidth selection, therefore conventional approach could be used when the bandwidth is pre-defined.

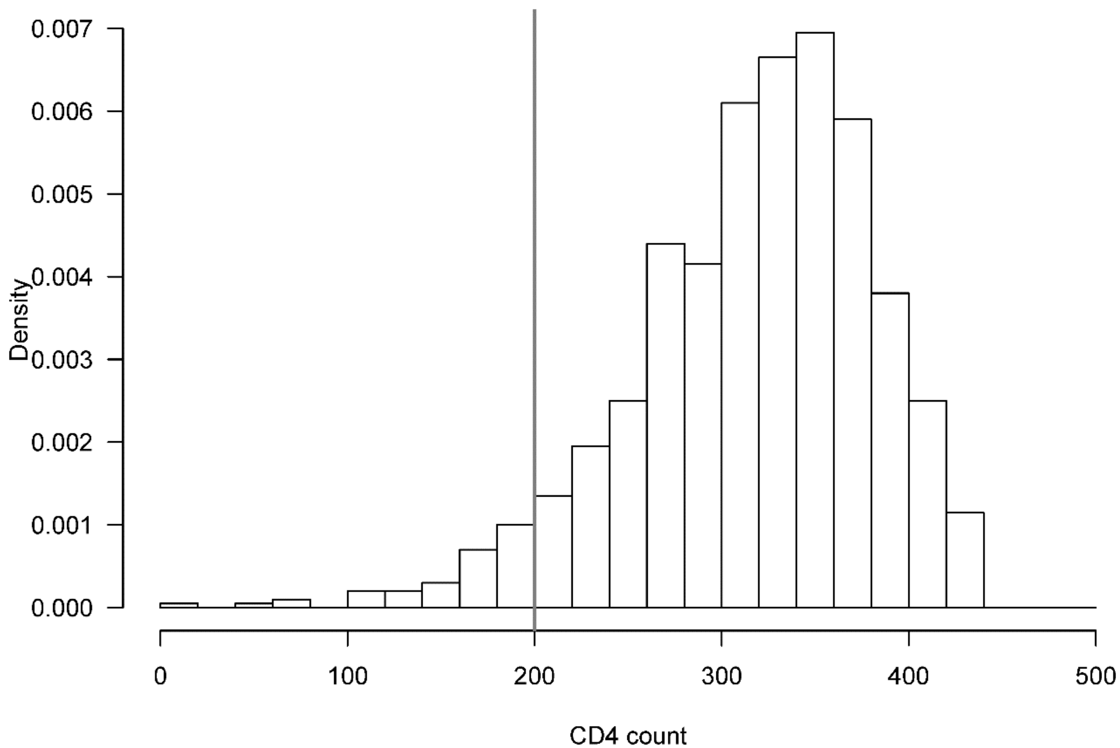
Assessing assumptions of RDD

- Known and universal principle for treatment assignment
  - Plot assignment/forcing variable against treatment status



Assessing assumptions of RDD

- Universal principle for treatment assignment
  - Make sure no manipulation of treatment status (no ‘bunching’)
  - Can be assessed by plotting the distribution of the assignment / forcing variable
  - Also by plotting the distribution of other covariates across the cut-off



Assessing assumptions of RDD

- Continuity in potential outcomes at the cut-off
  - Balance (continuity) of covariate
  - Subject characteristics similar on each side of the cut-off
  - Assess how the cut-off was established (should not be determined by discontinuity in the relation between Z and Y)
  - e.g. if the MLDA cut-off was determined to match the initiation timing of a national wide psychological health program
- Plot the outcome against assignment variable
  - Visual inspection will inform the model choice
  - An obvious ‘jump’ is expected if there is significant treatment effect
- Correct specification of the model
  - Sensitivity analysis by allowing curvilinear relation / local regression

Fuzzy regression discontinuity

- Some subjects may not receive the assigned treatment
- So treatment was partially defined by the assignment variable
- Treatment effect can be estimated by two-stage least square (2SLS) method:

(1st stage regression) $T_i = \alpha_i + \gamma_i D_i + f_1(Z_i - c) + \varepsilon_i$

(2nd stage regression) $Y_i = \alpha + \beta_1 \hat{T}_i + f_2(Z_i - c) + \mu_i$

where T_i, D_i are the observed treatment status and assigned treatment according to the assignment variable

- The assignment variable as instrumental variable
- Can be fitted using the *fuzzy* option in rdrobust

RDD example – HPV vaccine on sexual behaviour

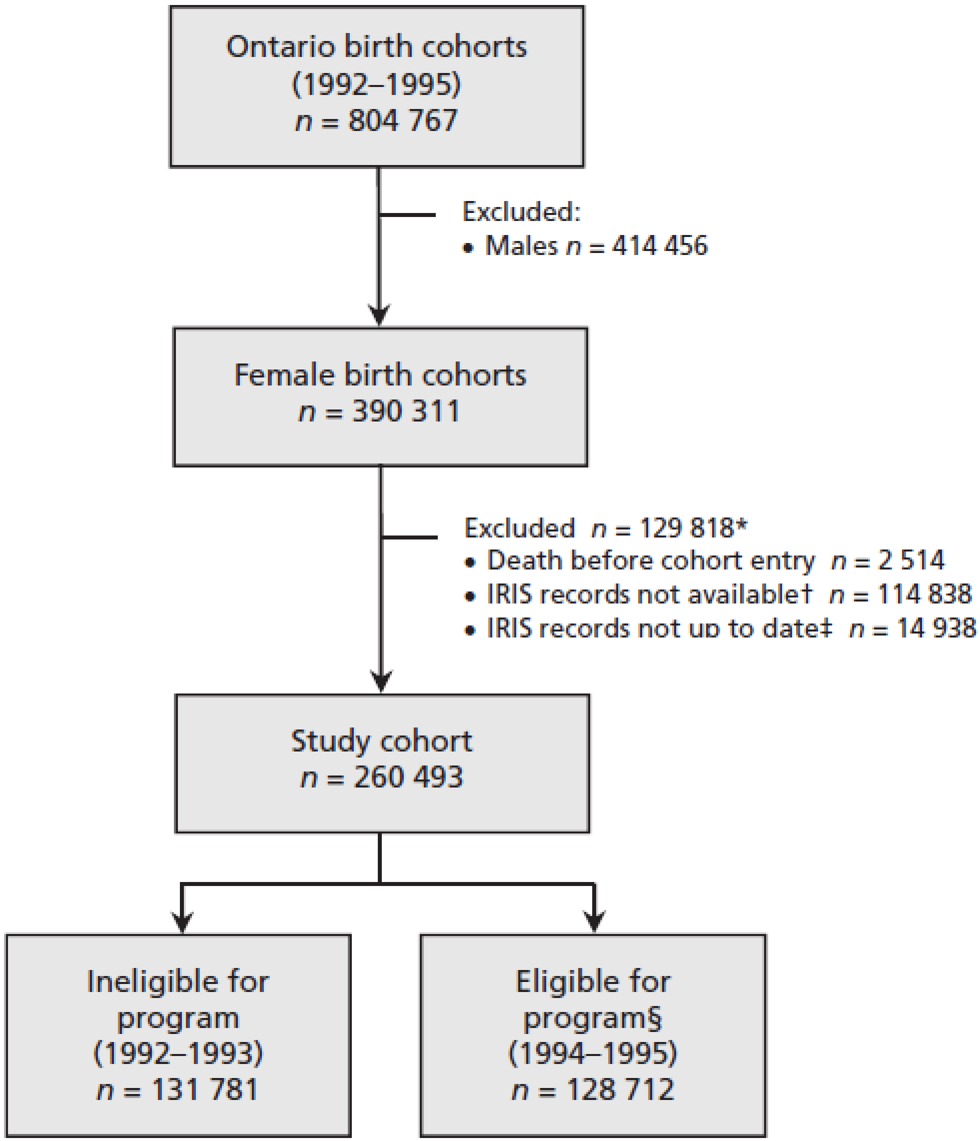
- Smith et al., CMAJ 2015
- Objective: to assess if HPV vaccine may increase risky sexual behaviour
- Regression discontinuity design

RESEARCH CMAJ

Effect of human papillomavirus (HPV) vaccination on clinical indicators of sexual behaviour among adolescent girls: the Ontario Grade 8 HPV Vaccine Cohort Study

Leah M. Smith MSc, Jay S. Kaufman PhD, Erin C. Strumpf PhD, Linda E. Lévesque PhD

RDD example – HPV vaccine on sexual behaviour



- HPV vaccination program began in 2007/08
- Using Ontario's administrative database
- n = 260, 493 grade 8 girls
- Assignment variable is birth year quarter

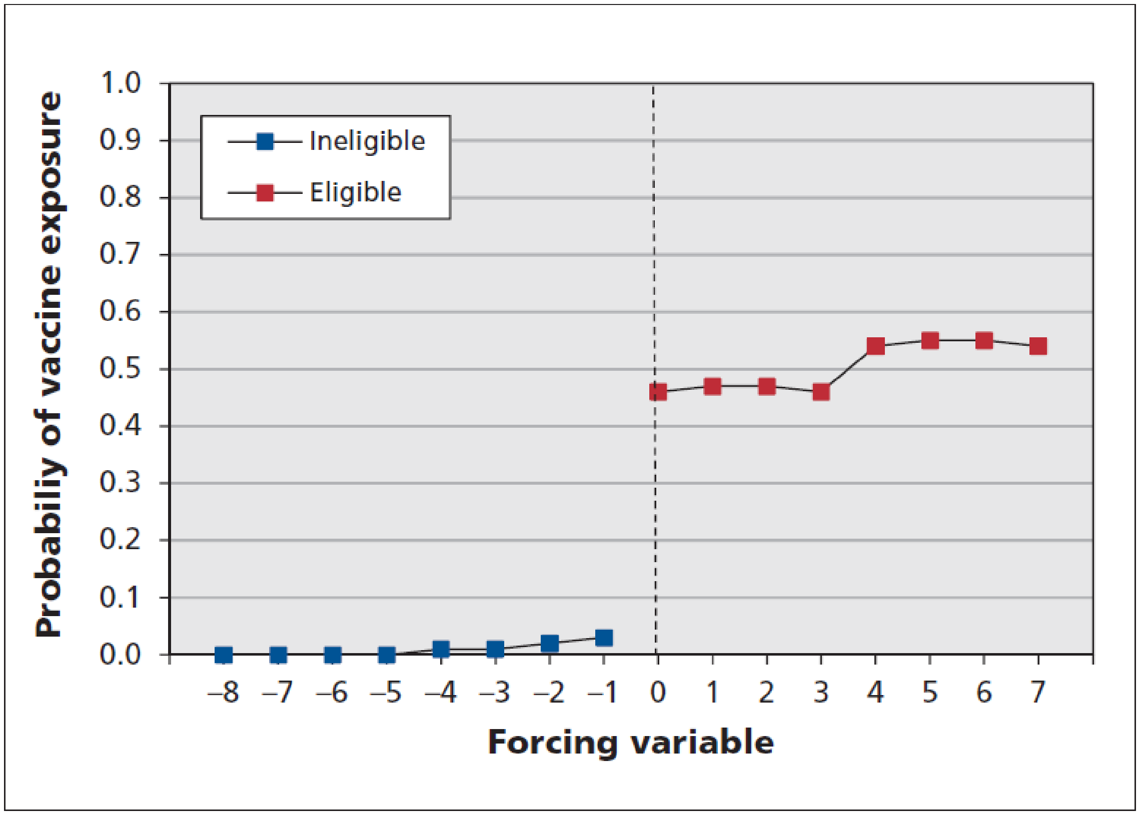
Comparing subjects characteristics around the cut-off

Table 1: Baseline characteristics of the eligibility groups in the study cohort

Characteristic	Program eligibility group; % of eligibility group*		Characteristic	Program eligibility group; % of eligibility group*	
	Ineligible (*n* = 131 781)	Eligible (*n* = 128 712)		Ineligible (*n* = 131 781)	Eligible (*n* = 128 712)
Sociodemographic†			**Health services use**††**		
Age, yr, mean ± SD	13.17 ± 0.28	13.17 ± 0.28	Hospital admission		
Birth quarter			0	98.0	98.2
Jan.–Mar.	24.3	24.2	≥ 1	2.0	1.8
Apr.–June	26.1	26.1	LOS, d, mean ± SD	7.4 ± 15.6	8.0 ± 18.2
July–Sept.	25.7	25.8	Same-day surgery		
Oct.–Dec.	23.9	23.9	0	97.7	97.8
Residency			≥ 1	2.4	2.2
Urban	85.3	85.8	Emergency department visits		
Rural	14.0	13.5	0	70.7	71.1
Missing‡	0.7	0.6	1	18.1	17.8
Income quintile			≥ 2	11.2	11.1
1 (lowest)	16.6	15.0	Outpatient visits		
2	18.4	17.8	0 or 1	22.6	22.8
3	20.6	21.1	2–5	27.4	26.9
4	22.0	23.1	6–12	25.1	24.5
5 (highest)	21.4	22.1	≥ 13	25.0	25.8
Missing‡	1.0	0.9	**Medical history**		
Vaccination history§			Cancer**	0.7	0.7
Measles–mumps–rubella¶	97.9	98.2	Mental health diagnosis**	9.5	9.7
Diphtheria, tetanus and pertussis¶	98.0	98.3	Sexual health indicators**‡‡	0.7	0.7
Hepatitis B¶	84.1	82.0	Down syndrome	0.5	0.5
All 3 vaccines	83.0	81.1	Congenital malformations	12.4	11.8
			Intellectual disability§	0.7	0.7

Assessing assignment variable and actual assignment

- Fuzzy regression design – eligible subjects has higher probability to receive vaccine



treat" estimate of vaccination. To evaluate the effect of the vaccine, actual receipt of vaccine was also taken into account; this was defined as receipt of all 3 doses between cohort entry and Aug. 31 of grade 9. In this analysis, we used 2-stage linear regression to estimate the association between program eligibility and vaccine exposure, in addition to the association between program eligibility and outcome. Analogously, we applied 1- and

RDD example – HPV vaccine on sexual behaviour

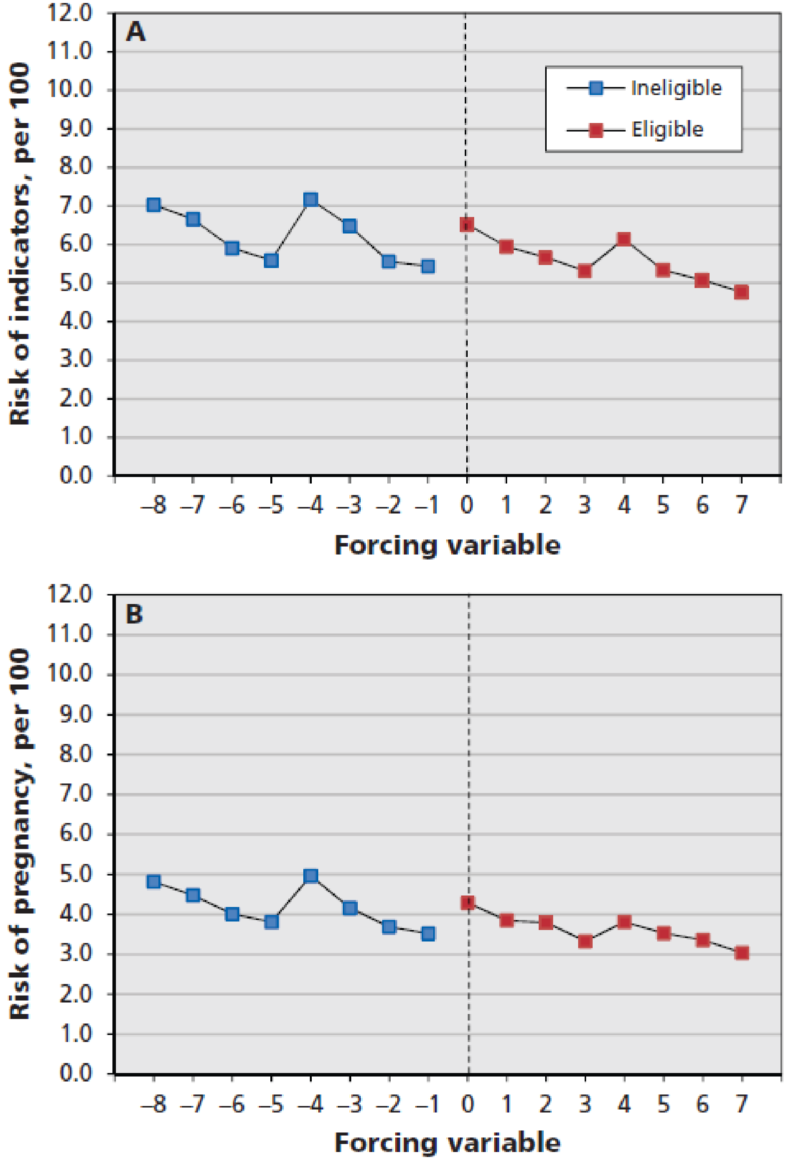


Table 3: Effect of quadrivalent human papillomavirus vaccination on clinical indicators of sexual behaviour*

Outcome	No. of excess cases per 1000 girls (95% CI)	RR (95% CI)	Adjusted† RR (95% CI)
Effect of vaccine			
Composite outcome	–0.61 (–10.71 to 9.49)	0.96 (0.81 to 1.14)	0.98 (0.84 to 1.14)
Pregnancy	0.70 (–7.57 to 8.97)	0.99 (0.79 to 1.23)	1.00 (0.83 to 1.21)
STIs	–4.92 (–11.49 to 1.65)	0.81 (0.62 to 1.05)	0.81 (0.63 to 1.04)
Effect of program			
Composite outcome	–0.25 (–4.35 to 3.85)	0.99 (0.93 to 1.06)	1.00 (0.93 to 1.07)
Pregnancy	0.29 (–3.07 to 3.64)	1.00 (0.92 to 1.09)	1.01 (0.93 to 1.10)
STIs	–2.00 (–4.67 to 0.67)	0.92 (0.83 to 1.03)	0.92 (0.83 to 1.03)

- No significant effect of HPV vaccine on various sexual behaviour
- Sensitivity analyses were also carried out

Review of RDD

Strengths

- Required relatively weak assumptions compared to other quasi-experimental design
- Provide strong evidence of causal effect if assumptions are satisfied
- Key assumptions can be supported by the study data

Limitations

- Need correctly specified model to obtain unbiased estimate
- Need larger sample size than RCT
- Curvilinearity may explain discontinuity if the model is misspecified
- Results generalizable around the cut-off but not globally unless strong assumptions are made