# STAT 545A Class meeting #12 (The End) Wednesday, October 17, 2012

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### Review of last class

Demonstrated the bootstrap approach to "two groups" testing on the yeast growth data.

Got bootstrap p-values for a non-standard test statistic and also for classical test statistics. Results very compatible.

Saw some tricks for bootstrapping or, for that matter, any resampling or simulation type of work. Explicit loop avoidance techniques include [1] generating the data at once and [2] apply-type functions for computing bootstrap statistics. set.seed() useful for making stochastic work repeatable, which can be invaluable for debugging.

### Review of last class (cont'd)

Tried out some robust regression techniques using the life expectancy data for Rwanda in the Gapminder dataset.

MM estimation is probably best general purpose option, implemented in Imrob() in robustbase package.

Revisited bootstrap for checking applicability of asymptotic standard errors and distribution. Results reassuring.

Brief remarks on data reshaping. Tips on avoiding it and on giving in and doing it "by hand" or with fancier functions and packages.

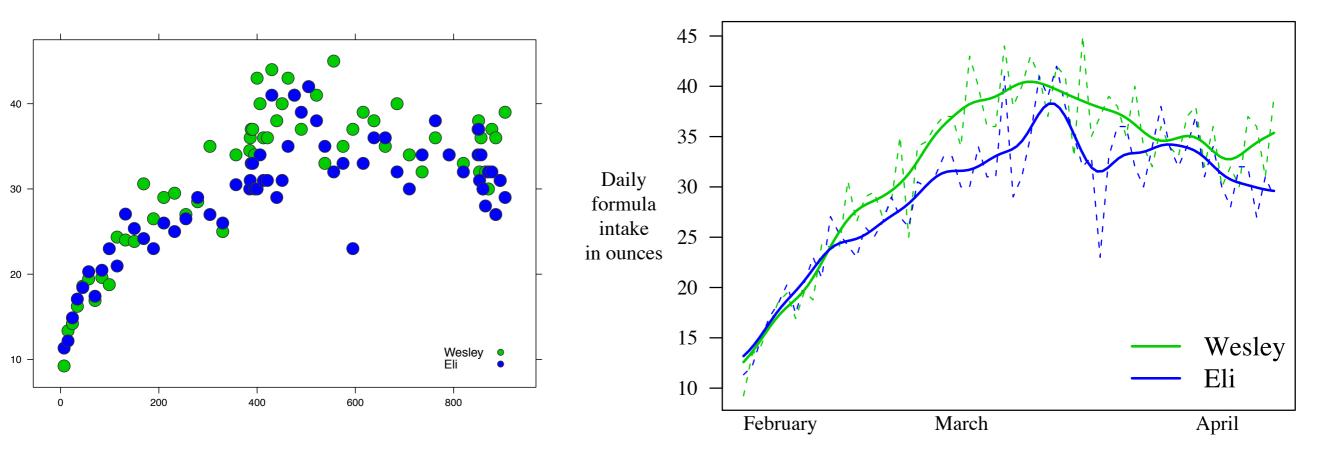
#### smoothing





#### Facilitate comparisons, identify trends.

Managing Inputs ... Nicer than Outputs



### Two quantitative variables: X and Y

- X ... 'independent variable', 'covariate', 'predictor', 'explanatory variable'
- Y ... 'dependent variable', 'response', 'outcome'
- Regression  $\approx$  study of the conditional expectation of Y given X=x

$$y_i = f(x_i) + \mathcal{E}_i$$

- Our focus: We believe f is smooth, but don't wish to specify much else about f.
  - Nonparametric regression, smoothing, etc.

### Two quantitative variables: X and Y

- X ... quantitative, often called the 'independent variable', 'covariate', 'predictor', 'explanatory variable'
- Y ... quantitative, often called the 'dependent variable', 'response', 'outcome'
- Regression refers generally to the study of the conditional distribution -- or, often, just the conditional expectation -- of Y given that X=x

$$Y \mid X = x \sim F_{\theta,\delta}$$

 Some parameters, referred to here as θ, are of direct interest. Others, referred to here as δ, are of secondary or no interest at all ("nuisance parameter").

### Nature of the parameter space

- The nature of the parameter  $(\theta, \delta)$  is one of the defining characteristics of the regression model
  - $(\theta, \delta) \in \mathbb{R}^p \Rightarrow \text{parametric model}$
  - (θ, δ) ∈ R<sup>p</sup> ⊗ (sthg complicated, such as a function space) ⇒ semi-parametric model
  - $(\theta, \delta) \in (\text{sthg complicated}) \Rightarrow \text{nonparametric model}$
- Examples of the 'complicated' spaces above: all possible distributions, all possible distributions with mean zero, etc.

## Narrowing focus to expectation

- Next half-course covers generalized linear models, so I will not.
- Frees us to focus on the conditional expectation of Y given X = x

$$Y_{X=x} = f(x;\beta) + \varepsilon_x, E(\varepsilon_x) = 0$$

- Common scenario: parameter  $\beta$  is of primary interest and parameter(s) relating to the distribution of the error term  $\varepsilon$  are a nuisance.
- It is very common for β ∈ R<sup>p</sup>, in which case assumptions about ε will determine whether the model is parametric or semi-parametric.

### Nature of the regression function

- The nature of the regression function  $f(x; \beta)$  is one of the defining characteristics of the regression model
  - f linear in  $\beta \Rightarrow$  linear model
  - f not linear in  $\beta \Rightarrow$  nonlinear model

$$y = \beta_0 + \beta_1 x + \beta_2 x^2 + \varepsilon$$
  
Note: this IS a linear model.

## Nonlinear regression

• Consider the case where the regression function -- the conditional expectation of Y given X = x -- is nonlinear in the parameter  $\beta$ :

$$Y_{X=x} = f(x;\beta) + \varepsilon_x, E(\varepsilon_x) = 0$$

- 'Nonlinear regression' is a huge area. Helpful to distinguish at least two broad classes within that:
  - Parametric nonlinear regression, e.g.  $f(x_i) = \beta_0 + \beta_1 x_i^{\beta_2}$
  - Nonparametric regression, aka 'smoothing'

# Smoothing methods / nonparametric regression

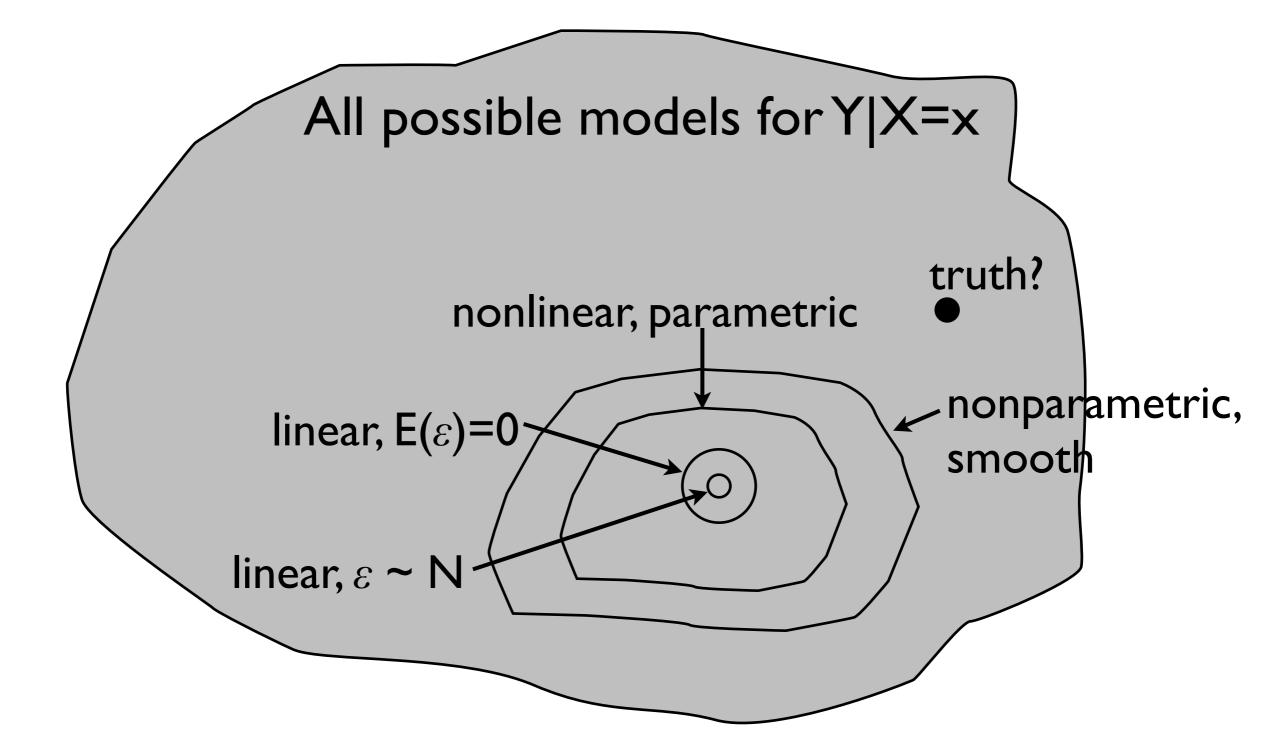
- Kernel-based methods
  - will tie in nicely to kernel-based density estimation
- Local polynomials (e.g. loess)
- Splines -- WILL NOT COVER

 $y_i = x_i \beta + \varepsilon_i$ 

linear model so plain yet so useful why must I move on?

 $y_i = f(x_i) + \mathcal{E}_i$ 

nonlinear *f* my head hurts already what's in it for me?



Nonlinear models allow us to explore a larger portion of the space of 'all possible models' and, therefore, increase the chance that we'll study a model that's 'close enough' to the truth to actually learn something useful.

## Some pros and cons

	Parametric regression function	Nonparametric regression function
Pros	Easy to write down Easy to fit Efficient, if model correct Parameters often have meaning Can easily incorporate prior/ external info	So flexible! Less biased, most of the time Leads to appealing figures accessible to many
Cons	Almost certainly doesn't contain true data-generating model	Hard to store, communicate, utilize the fitted result Path to inference not so clear

♦Please note: Broad generalities but their usefulness seems to outweigh any potential harm.

my husband, Jim weight loss bet w/ friend Craig late August 2011 to New Year's Eve 2011 winner = he who loses most as a percentage of starting weight Craig won, by the way :( data collection continues ....

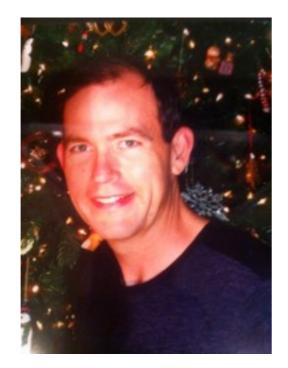
#### before



#### during

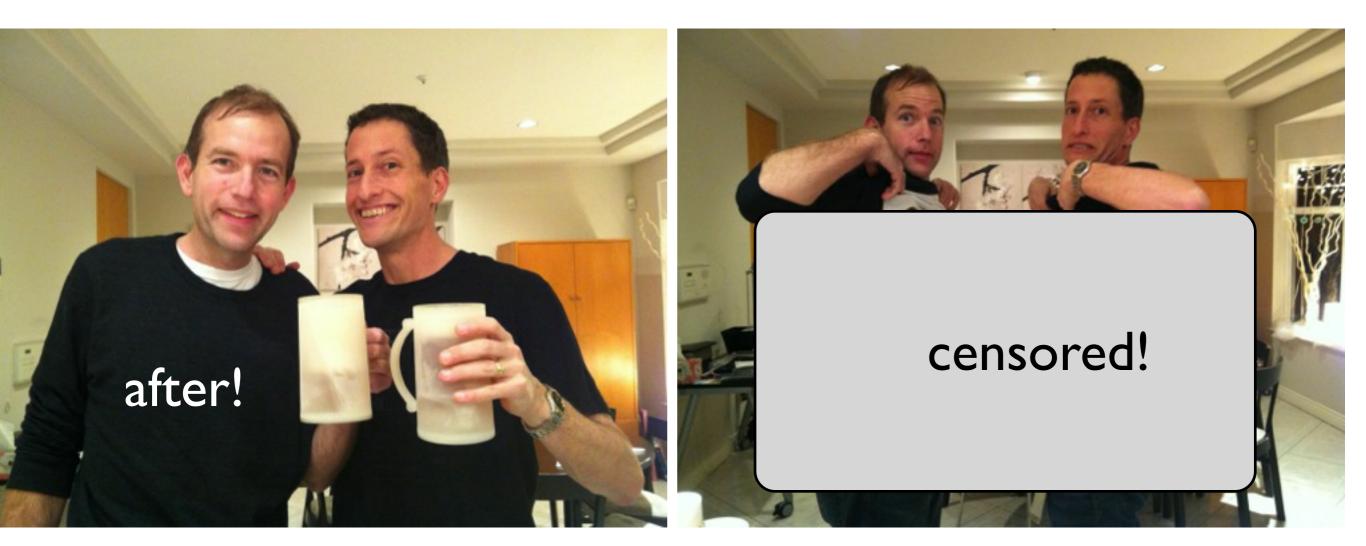












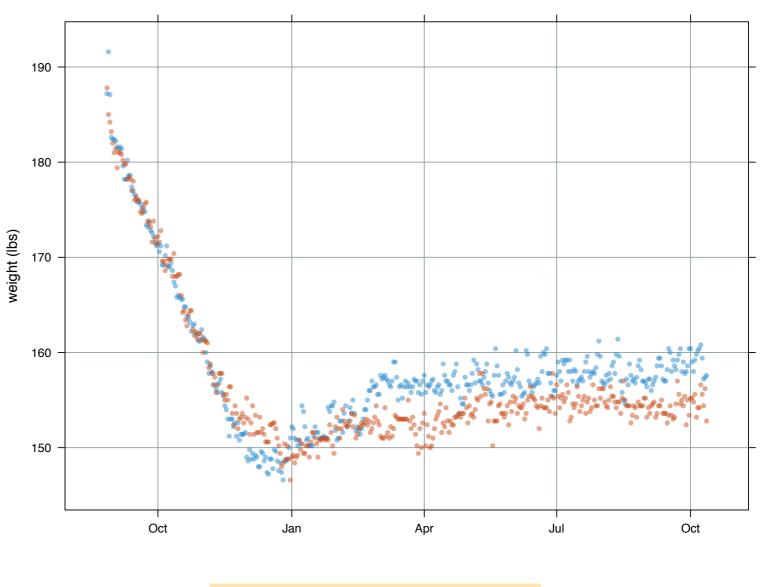
craig jim •

> peek(wDat)

date jim craig 55 2011-10-20 163.4 164.8 105 2011-12-09 151.6 148.0 131 2012-01-04 149.0 150.8 170 2012-02-12 152.2 155.0 174 2012-02-16 152.0 151.8 233 2012-04-15 152.2 157.6 249 2012-05-01 152.6 156.6

> dim(wDat) [1] 413 3

> most natural way to record the data is ... short and fat



xyplot(craig + jim ~ date, wDat, grid = TRUE, auto.key = TRUE, xlab = jXlab, ylab = jYlab)

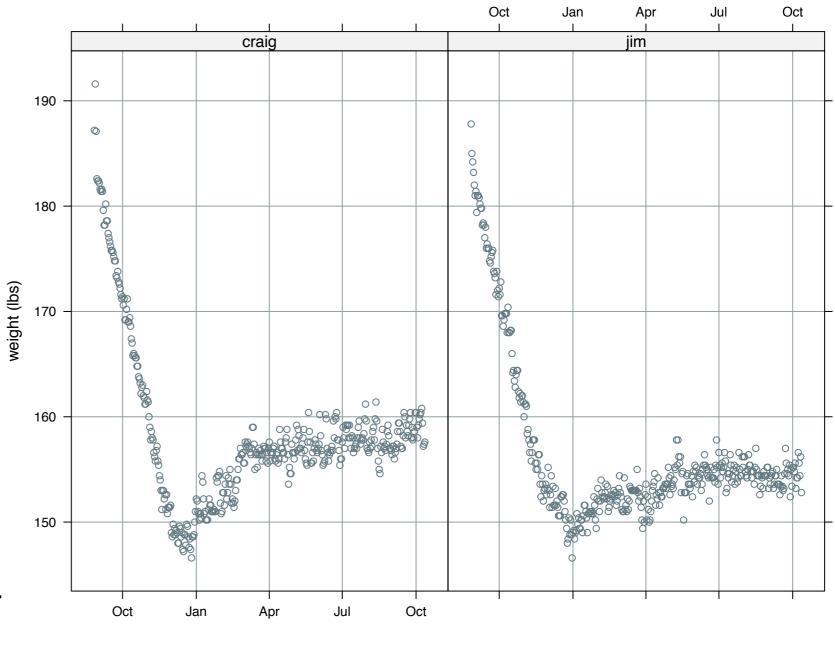
"extended formula interface" in lattice lets us do fake grouping / superposition

> peek(wDat)

date jim craig 55 2011-10-20 163.4 164.8 105 2011-12-09 151.6 148.0 131 2012-01-04 149.0 150.8 170 2012-02-12 152.2 155.0 174 2012-02-16 152.0 151.8 233 2012-04-15 152.2 157.6 249 2012-05-01 152.6 156.6

[1] 413 3

most natural way to record the data is ... short and fat



xyplot(craig + jim ~ date, wDat, grid = TRUE, auto.key = TRUE, outer = TRUE, xlab = jXlab, ylab = jYlab, pch = 1)

"extended formula interface" in lattice lets us do fake multi-panel conditioning too

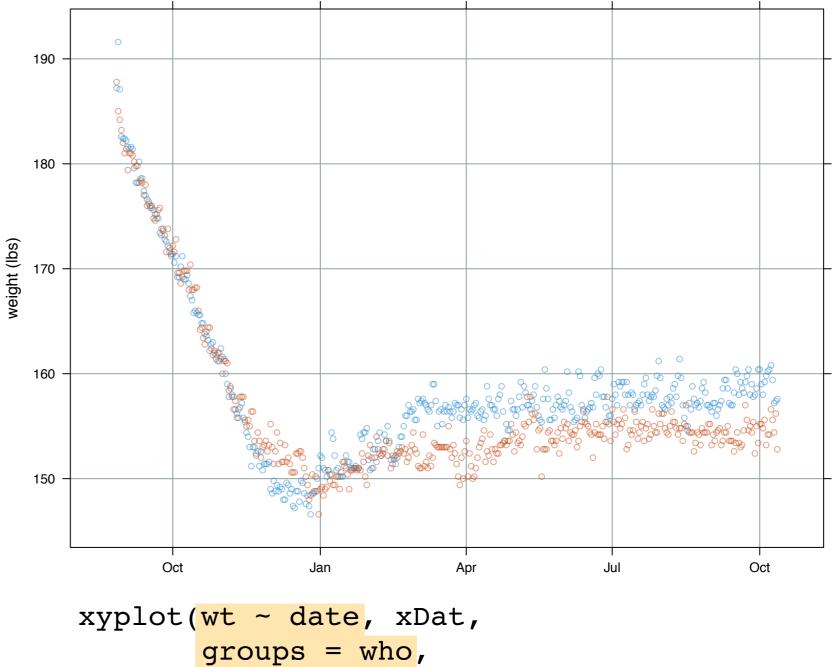
```
> peek(wDat)
                 jim craig
          date
55 2011-10-20 163.4 164.8
105 2011-12-09 151.6 148.0
                                            low-tech 'manual' data
131 2012-01-04 149.0 150.8
170 2012-02-12 152.2 155.0
                                            reshaping
174 2012-02-16 152.0 151.8
233 2012-04-15 152.2 157.6
249 2012-05-01 152.6 156.6
> dim(wDat)
[1] 413
          3
                        ## reshape the data
                        xDat <- with(wDat,</pre>
                                     data.frame(date = date,
                                                wt = c(jim, craig),
                                                who = factor(rep(c("jim", "craig"),
                                                              each = nrow(wDat)))))
> peek(xDat)
          date
                        who
                  wt
   2011-11-19 156.4
85
                        jim
235 2012-04-17 152.8
                        jim
243 2012-04-25 153.6
                        jim
                        jim
276 2012-05-28 154.4
359 2012-08-19 154.4
                        jim
555 2012-01-15 150.2 craig
773 2012-08-20 158.8 craig
> dim(xDat)
[1] 826
          3
```

> peek(xDat)

date who wt 2011-11-19 156.4 85 jim 235 2012-04-17 152.8 jim jim 243 2012-04-25 153.6 jim 276 2012-05-28 154.4 359 2012-08-19 154.4 jim 555 2012-01-15 150.2 craig 773 2012-08-20 158.8 craig

> dim(xDat)
[1] 826 3

store tall in tall and skinny format to facilitate data aggregation and visualization



grid = TRUE, auto.key = TRUE, xlab = jXlab, ylab = jYlab, pch = 1)

proper grouping / superposition via 'groups'

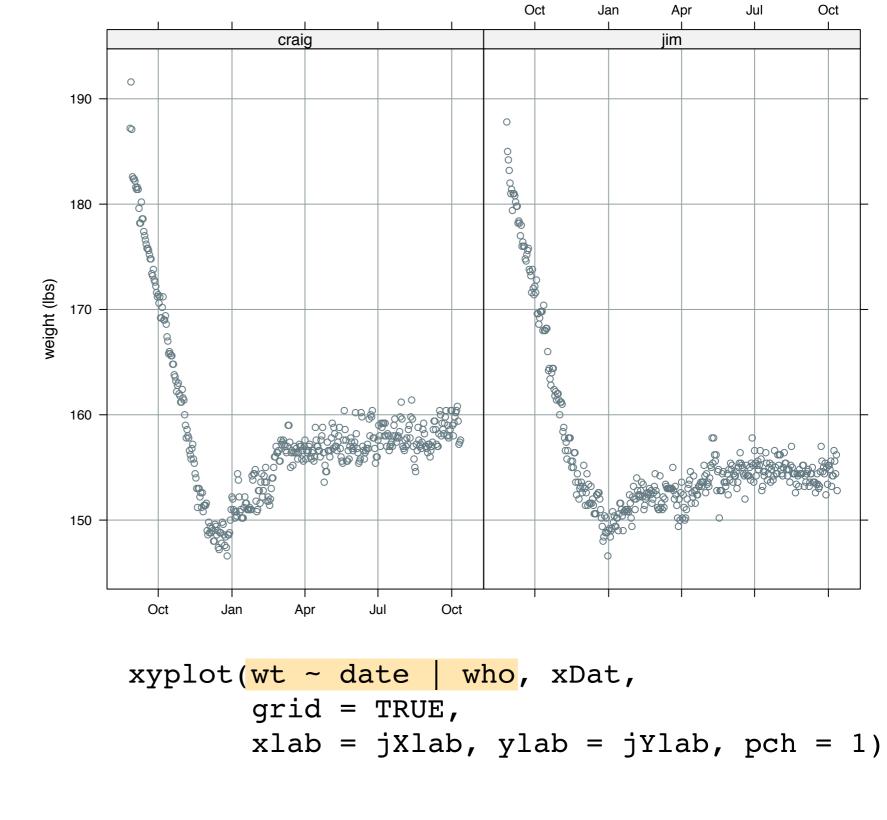
> peek(xDat)

[1] 826

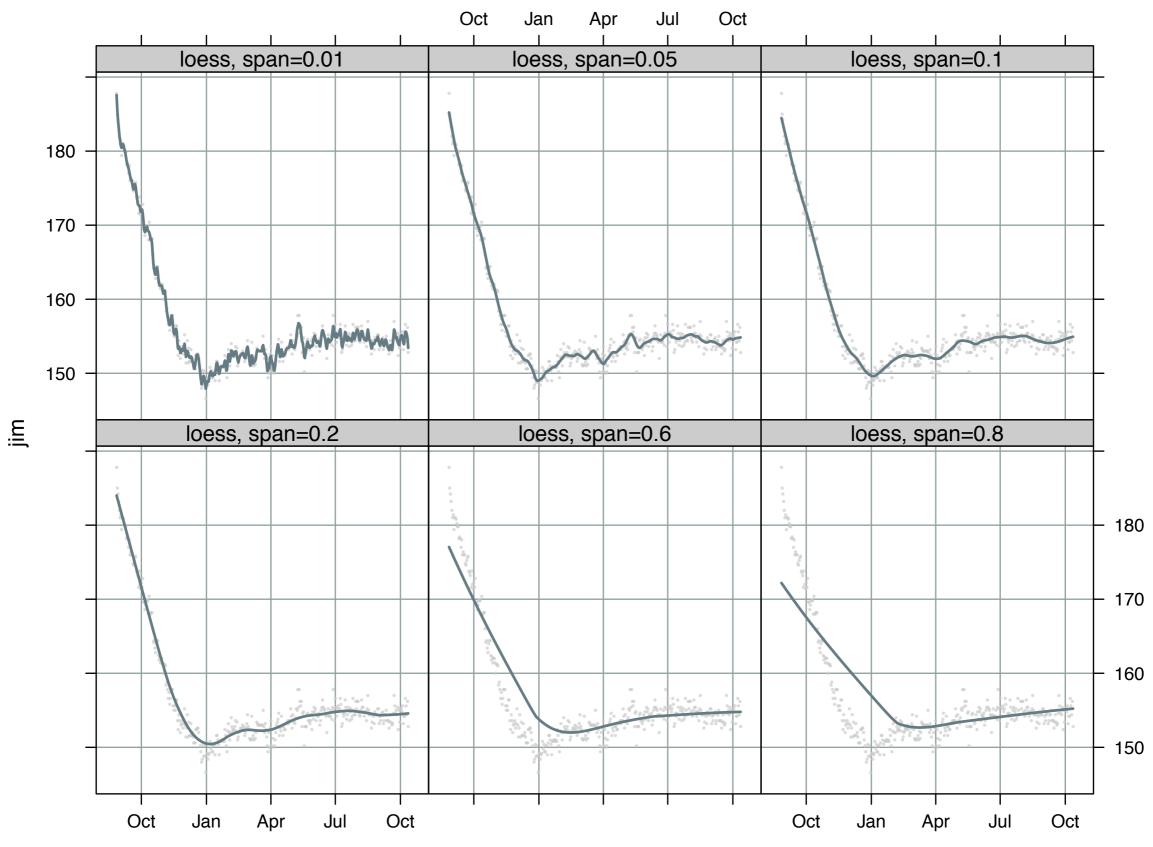
date who wt 2011-11-19 156.4 85 jim 235 2012-04-17 152.8 jim jim 243 2012-04-25 153.6 276 2012-05-28 154.4 jim 359 2012-08-19 154.4 jim 555 2012-01-15 150.2 craig 773 2012-08-20 158.8 craig > dim(xDat)

3

store tall in tall and skinny format to facilitate data aggregation and visualization

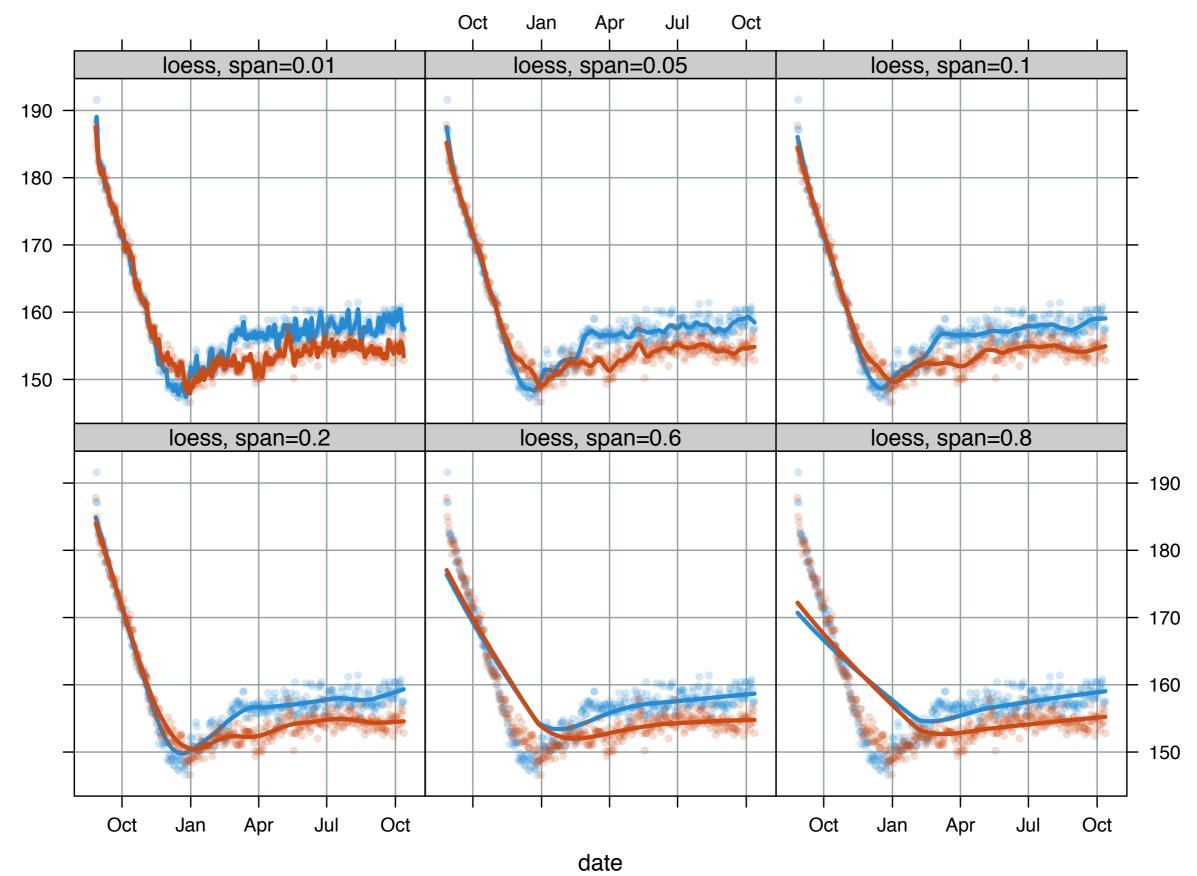


proper multi-panel conditioning via 'y  $\sim x \mid z'$ 



date

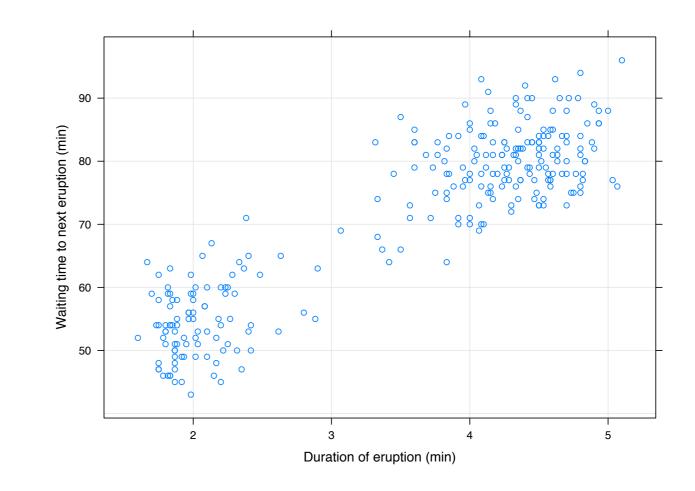
craig jim



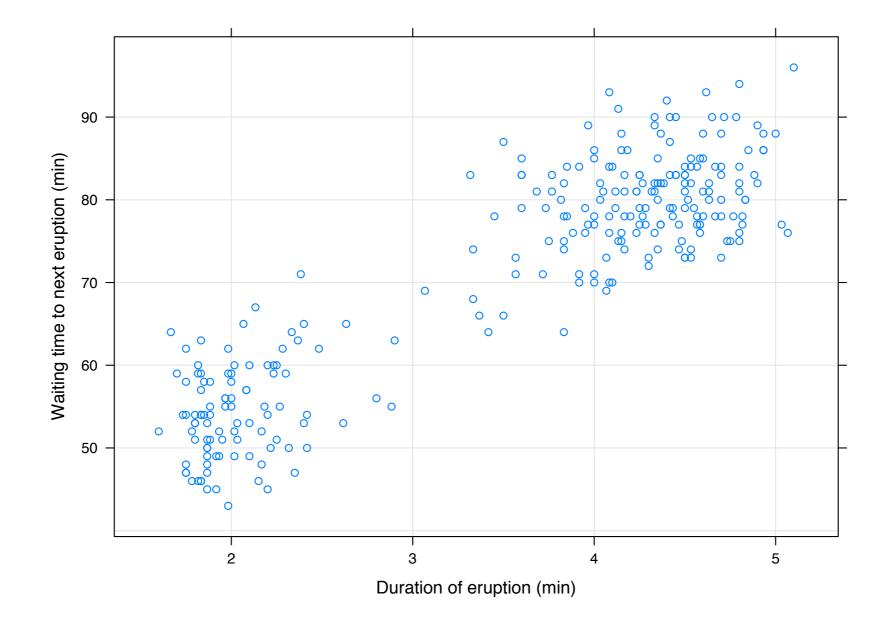
٧t

# Selected methods for smoothing / nonparametric regression

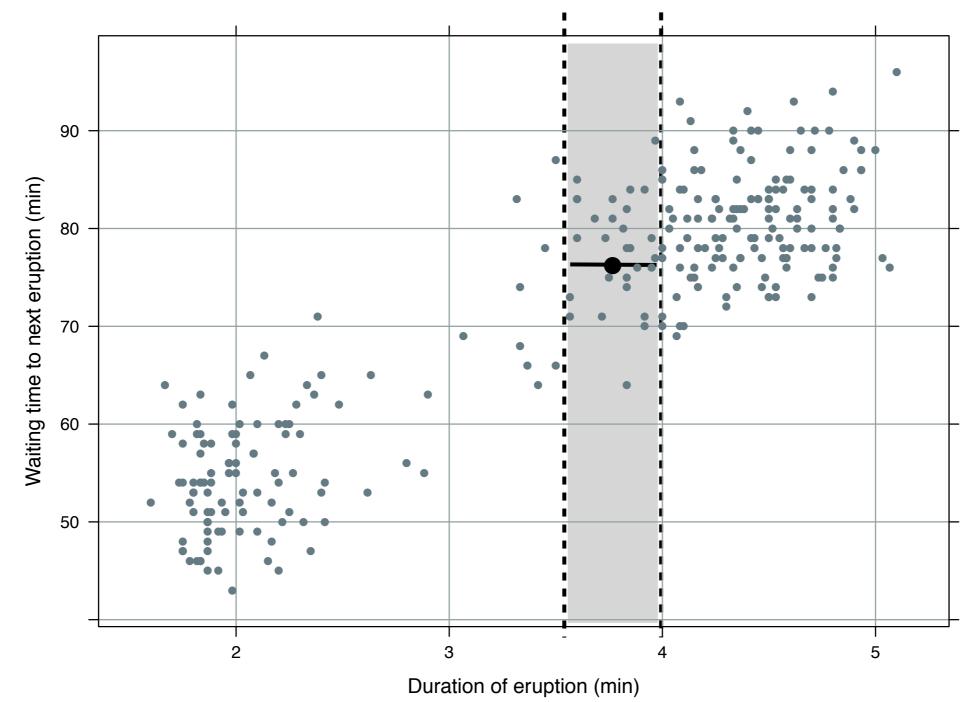
- Kernel-based methods
- Local polynomials (e.g. loess)
- (Splines)



### Old Faithful geyser data (faithful)



Key concept: Moving or running average  $\hat{f}(x_0) = avg$  of y's from all observations with x's falling in a window around  $x_0$  (e.g. nearest 10 observations or obs where  $x \in x_0 \pm sthg$ )



Old Faithful geyser data (faithful)

Key innovation for <u>kernel smoothing</u>: Use a <u>weighted</u> moving average. The kernel specifies the weights. The weight of a point close  $x_0$  is generally greater than that of a point that is far.

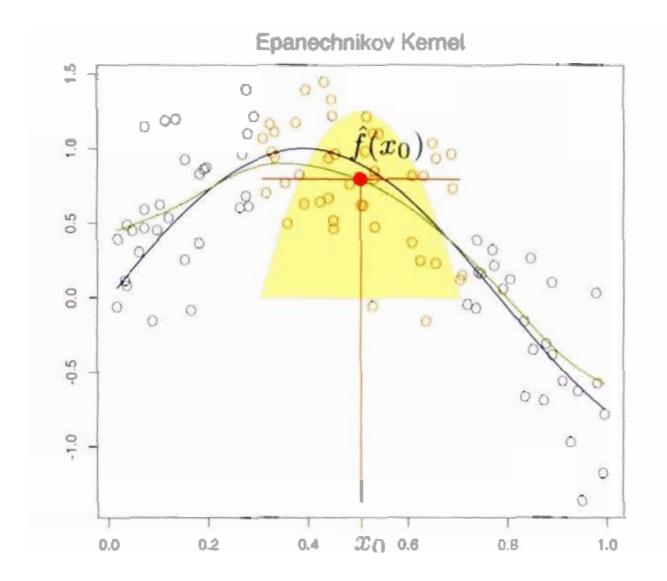


Figure from "The Elements of Statistical Learning", by by Hastie, Tibshirani, and Friedman (2001), Springer-Verlag.

http://compdiag.molgen.mpg.de/docs/talk\_05\_01\_04\_stefanie.pdf

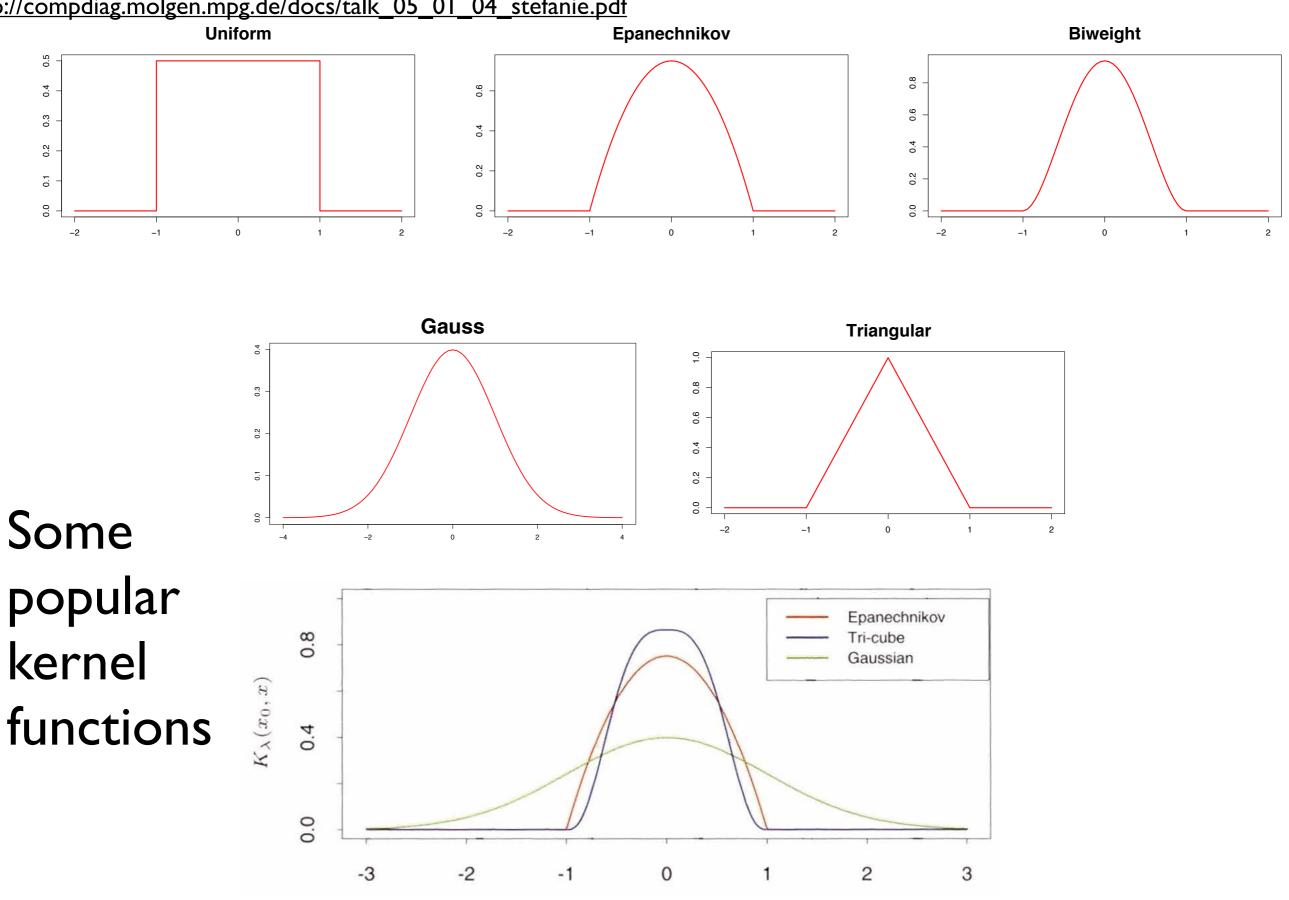


Figure from "The Elements of Statistical Learning", by by Hastie, Tibshirani, and Friedman (2001), Springer-Verlag.

#### Recall kernel density estimation?

$$\hat{f}_b(x) = \frac{1}{nb} \sum_i K\left(\frac{x - x_i}{b}\right) = \frac{1}{n} \sum_i w_i$$

f is a density

where the weight  $w_i$  is given by

$$w_i = \frac{1}{b} K \left( \frac{x - x_i}{b} \right)$$

#### Well, here's a kernel smoother:

$$\hat{f}_b(x) = \frac{1}{nb} \sum_i K\left(\frac{x - x_i}{b}\right) y_i = \frac{1}{n} \sum_i w_i y_i$$

f is the regression function

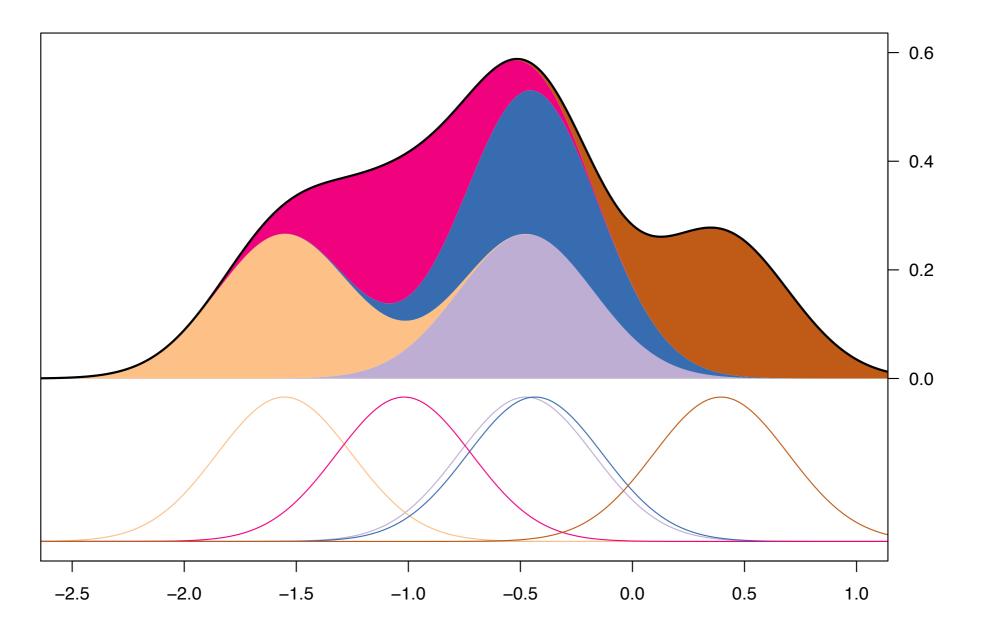
where the weight  $w_i$  is given by

$$w_i = \frac{1}{b} K \left( \frac{x - x_i}{b} \right)$$

### Themes of kernel-based methods

- A kernel density estimator is a glorified histogram.
- A kernel smoother is a glorified 'moving average'.
- Key concept: instead of the 'hard' contribution made by each point in a histogram or moving average (two options: contributes / does not contribute), contribution of each point to the density estimate or regression function varies with distance, i.e. is high in neighborhood of the point and low elsewhere
  - The kernel function describes exactly how this contribution varies with distance.
  - Introduces a smoothing parameter, denoted b earlier.
     Often called the bandwidth in this context.

#### Illustration of kernel density estimation



#### Produced from <u>code at the R graph gallery</u>

### Kernel smoother

- Moving average corresponds to a rectangular or nearestneighbor kernel.
- Qualities we often like in a kernel
  - Compact support: Otherwise every point makes a contribution to the regression function everywhere.
  - Smooth.
- Far more crucial than choice of kernel is ... choice of bandwidth.
  - Subjective method: eye ball it!
  - Cross validation -- and even the bootstrap -- can be extremely useful here.

### Nadaraya-Watson estimator

$$\hat{f}_b(x) = \frac{\sum_i w_i y_i}{\sum_i w_i}$$

Modifies the 'moving average' estimator to make it a more truly a moving average. When forming the estimate at x, the effective weights will sum to one.

Using this modification, here's the typical kernel smoother, again:

$$\hat{f}_b(x) = \frac{\sum_i K_b(x, x_i) y_i}{\sum_i K_b(x, x_i)}$$
  
where  $K_b(x, x_i) = K\left(\frac{x - x_i}{b}\right)$ 

### Epanechnikov kernel

$$K(z_i) = \begin{cases} \frac{3}{4}(1-z^2) \text{ if } |z| < 1\\ 0 \text{ otherwise} \end{cases}$$

Optimal choice under some standard assumptions. Minimizes asymptotic mean integrated squared error.

\*Despite its optimality, in R it is much easier to find software for Gaussian kernel.

Packages and functions for kernel smoothing

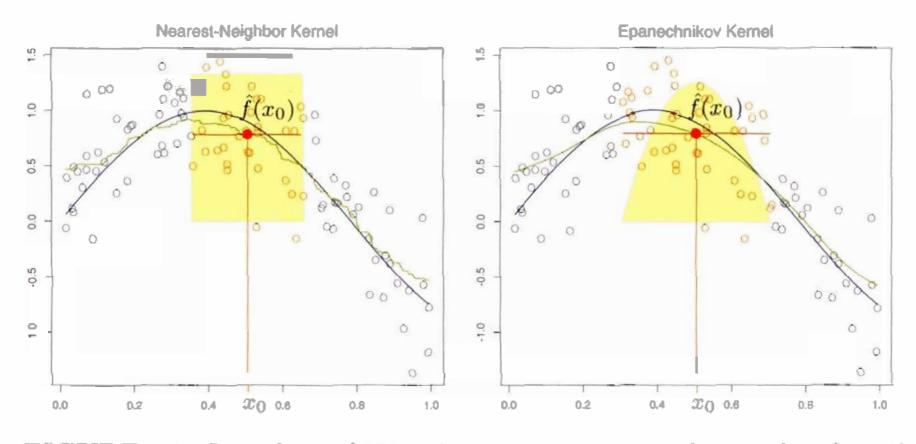
ksmooth, a really basic function, only does rectangular and Gaussian kernel. Don't use this. Even the help file says that!

KernSmooth package (only seems to offer Gaussian kernel).

sm package (only seems to offer Gaussian kernel).

Ipridge package offers Epanechnikov kernel.

#### 6. Kernel Methods



**FIGURE 6.1.** In each panel 100 pairs  $x_i$ ,  $y_i$  are generated at random from the blue curve with Gaussian errors:  $Y = \sin(4X) + \varepsilon$ ,  $X \sim U[0,1]$ ,  $\varepsilon \sim N(0,1/3)$ . In the left panel the green curve is the result of a 30-nearest-neighbor running-mean smoother. The red point is the fitted constant  $\hat{f}(x_0)$ , and the orange shaded circles indicate those observations contributing to the fit at  $x_0$ . The solid orange region indicates the weights assigned to observations. In the right panel, the green curve is the kernel-weighted average, using an Epanechnikov kernel with (half) window width  $\lambda = 0.2$ .

```
> ## trying ksmooth out for first time
> jSmooth <-
+ ksmooth(faithful$eruptions, faithful$waiting,
+ kernel = "normal", bandwidth = 1)
> str(jSmooth)
List of 2
$ x: num [1:272] 1.60 1.61 1.63 1.64 1.65 ...
$ y: num [1:272] 53.6 53.6 53.6 53.6 53.6 ...
```

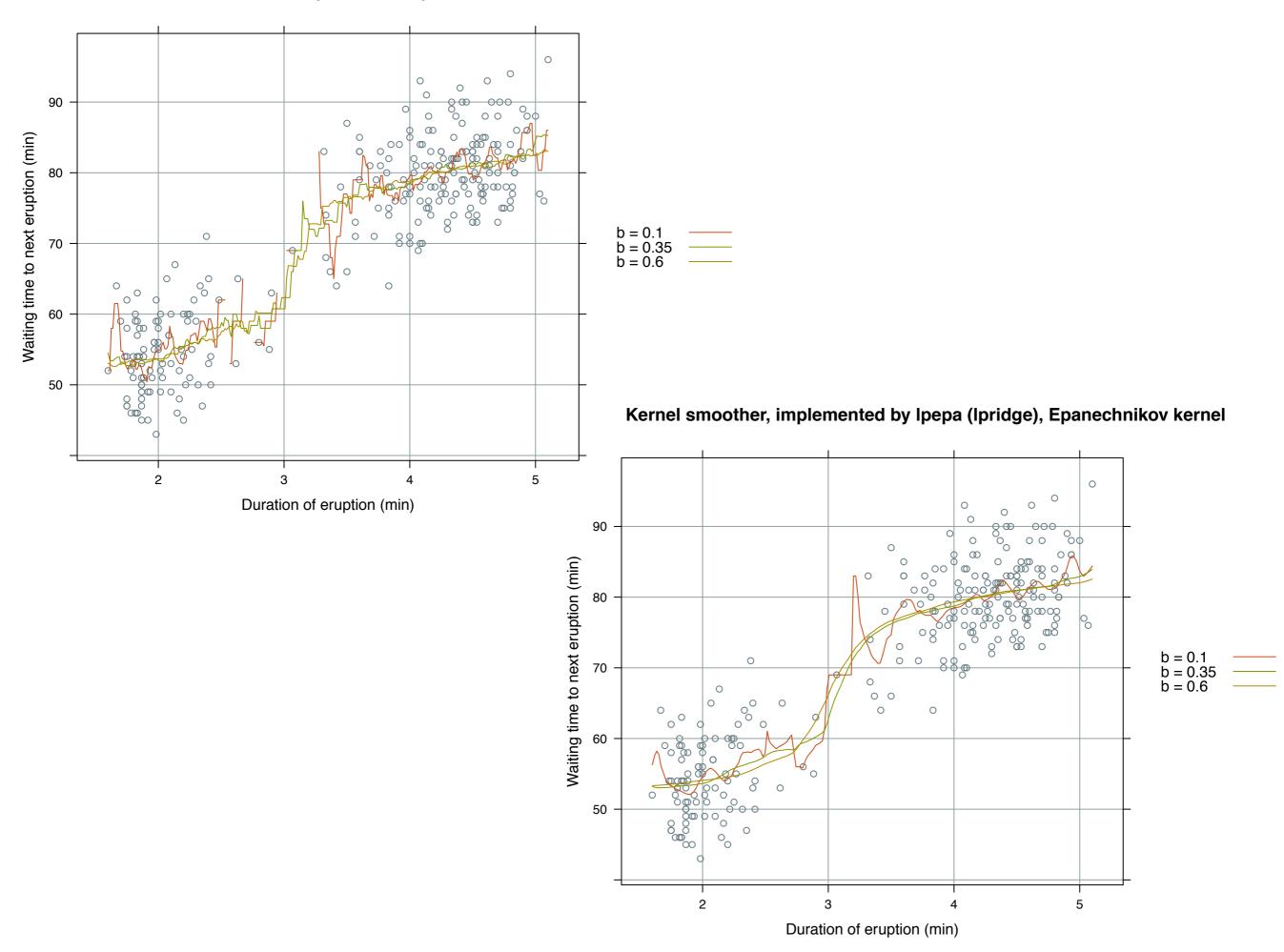
#### Kernel smoother, implemented by ksmooth, Gaussian kernel Ο 0 90 0 Waiting time to next eruption (min) 80 0 0 0 70 0 Ο 0 0 0 0 60 50 2 3 5 Δ

Duration of eruption (min)

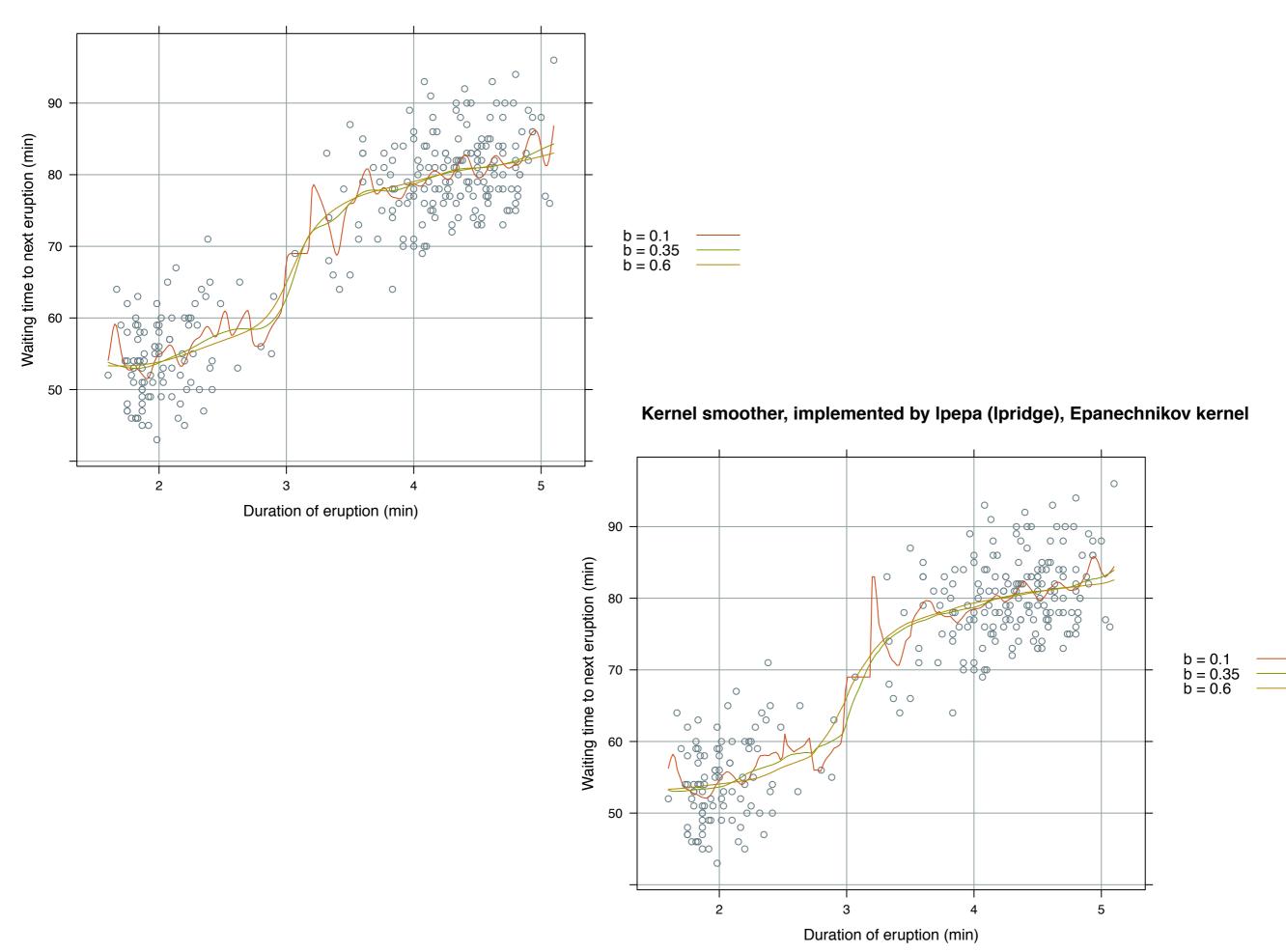
```
xyplot(waiting ~ eruptions, faithful,
       xlab = "Duration of eruption (min)",
       ylab = "Waiting time to next eruption (min)",
       main = "Kernel smoother, ...",
       panel = function(x, y, \dots) {
         panel.grid(h = -1, v = -1)
         panel.xyplot(x, y, ...)
         for(i in seq along(jBand)) {
           jSmooth <- ksmooth(x, y, kernel = "normal",</pre>
                               bandwidth = jBand[i])
           panel.lines(jSmooth$x, jSmooth$y,
                       col.line = jCols[i], ...)
         }
       },
       key = list(space = "right",
         text = list(paste("b =", jBand)),
         lines = list(col = jCols[1:length(jBand)]))
       )
```

```
b = 0.1
b = 0.35
b = 0.6
```

#### Kernel smoother, implemented by ksmooth, 'box' kernel

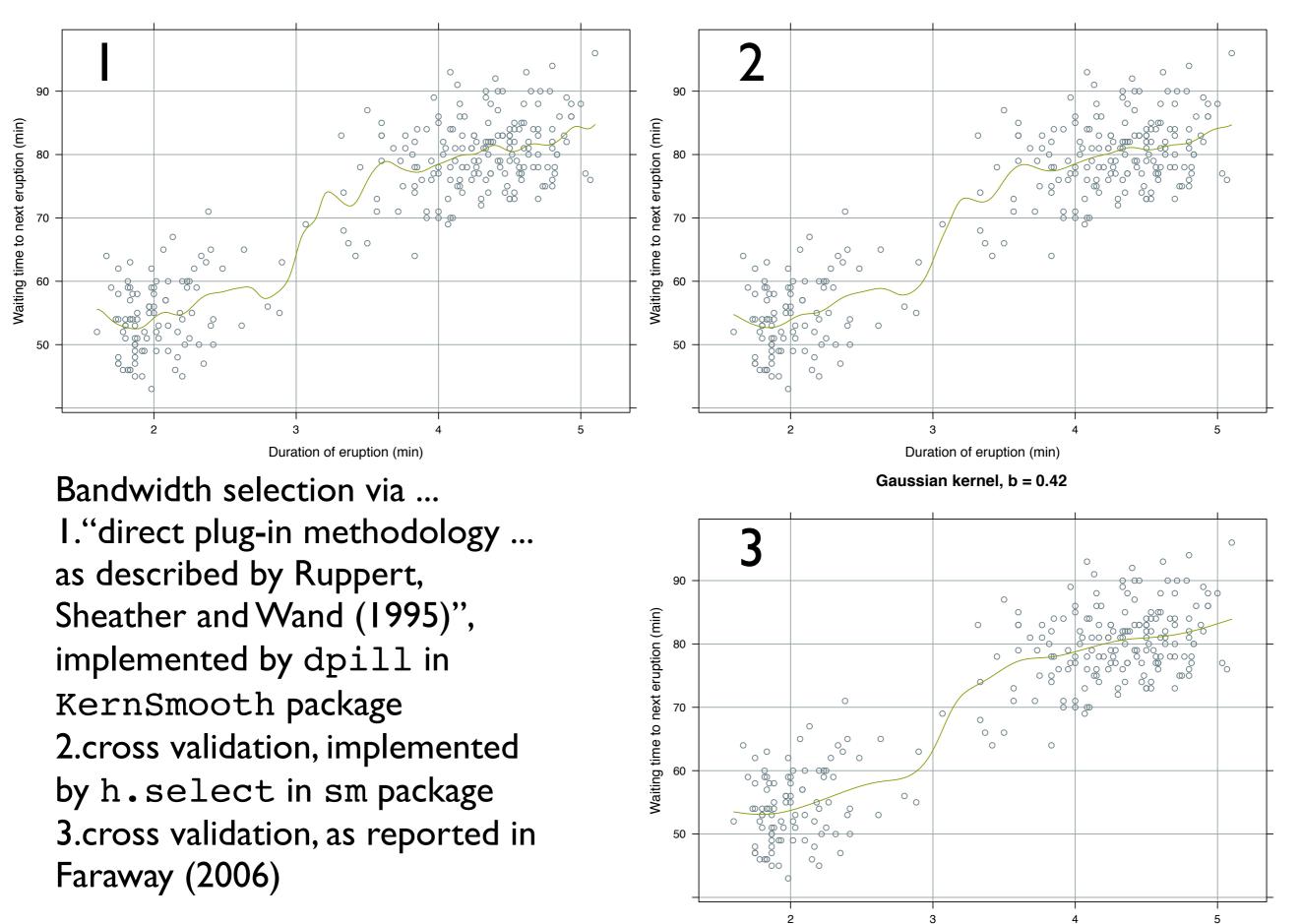


#### Kernel smoother, implemented by ksmooth, Gaussian kernel



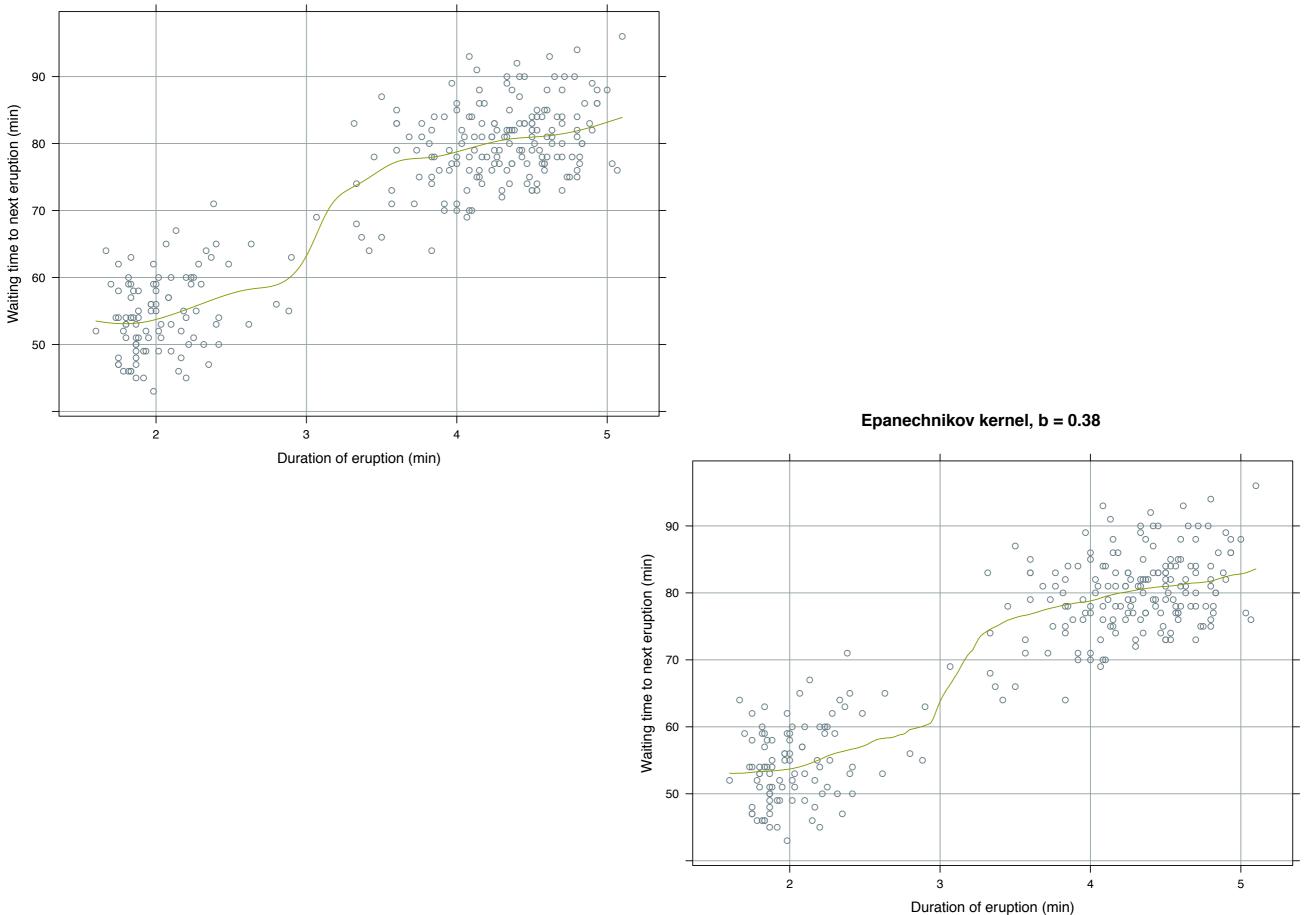
Gaussian kernel, b = 0.19

Gaussian kernel, b = 0.25



Duration of eruption (min)

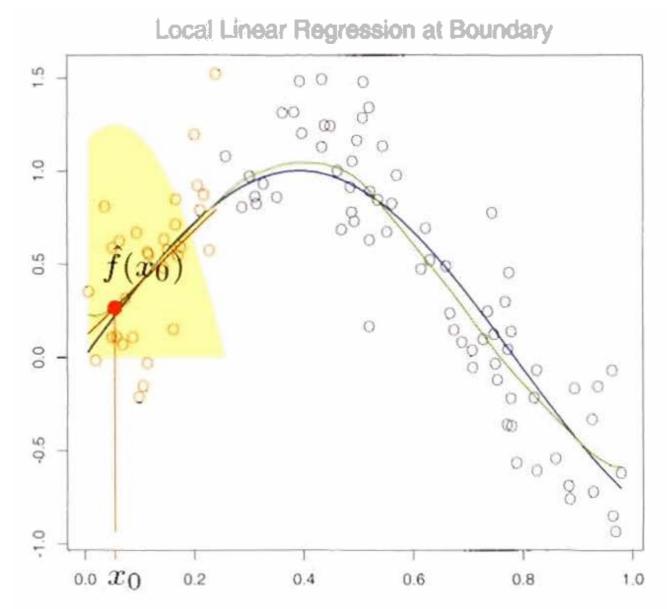
Gaussian kernel, b = 0.42



## Local constant →local polynomial

- Kernel smoother fits a local constant.
- Why not fit local lines or polynomials?
  - Built-in function loess does this
  - Packages KernSmooth and locfit also fit local polynomials
  - The weighting of observations via a kernel function persists in most of these local regression approaches
  - Robust local regression is also a nice add-on

Key innovation for <u>local polynomials</u>: Use the predicted y from <u>fitting a linear or quadratic function</u> to the (x,y)'s in the "neighborhood" of  $x_0$ . Often a kernel is used to weight the observations. Sometimes a robust procedure is used to fit the regression.



# Local polynomials

- Kernel smoothers can be quite biased near the edges
- Local linear fits work much better here
- Local linear fits are sometimes biased in the interior, in areas of curvature ("trimming the hills, filling the valleys")
   -- local quadratic fits can do better here
- Bias-variance trade-off
  - lower degree polynomials more biased, less variable
  - higher degree are less biased, more variable
- Proposal: default to local linear, use higher degrees with good reason.

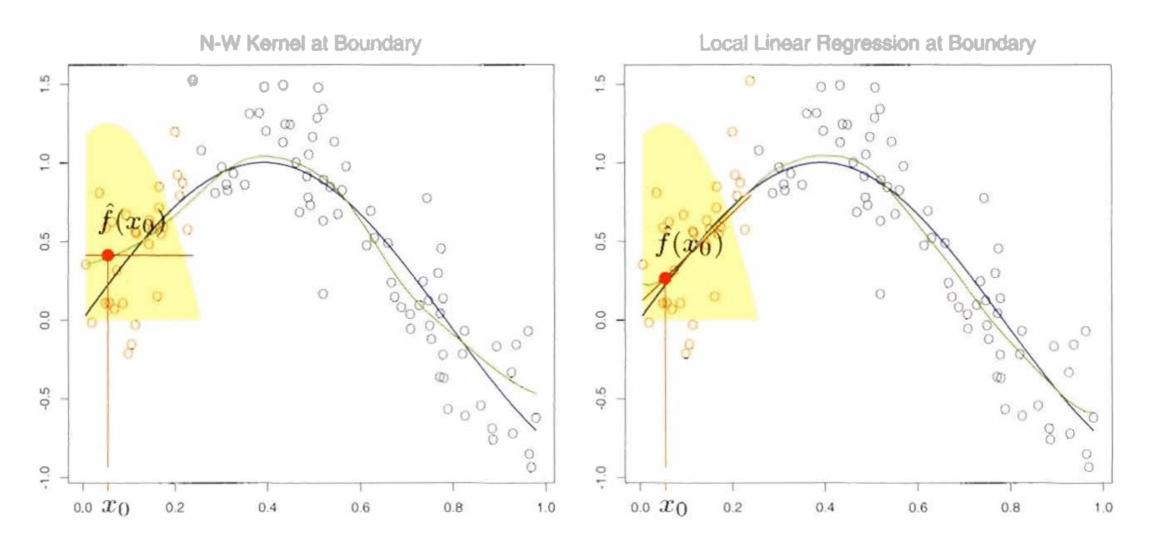
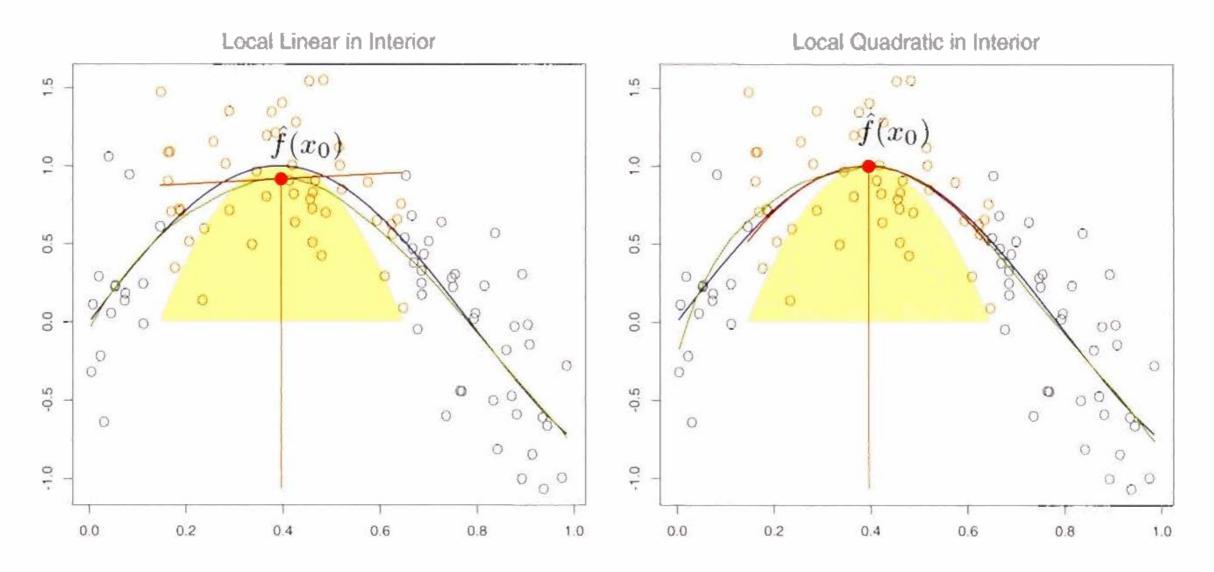
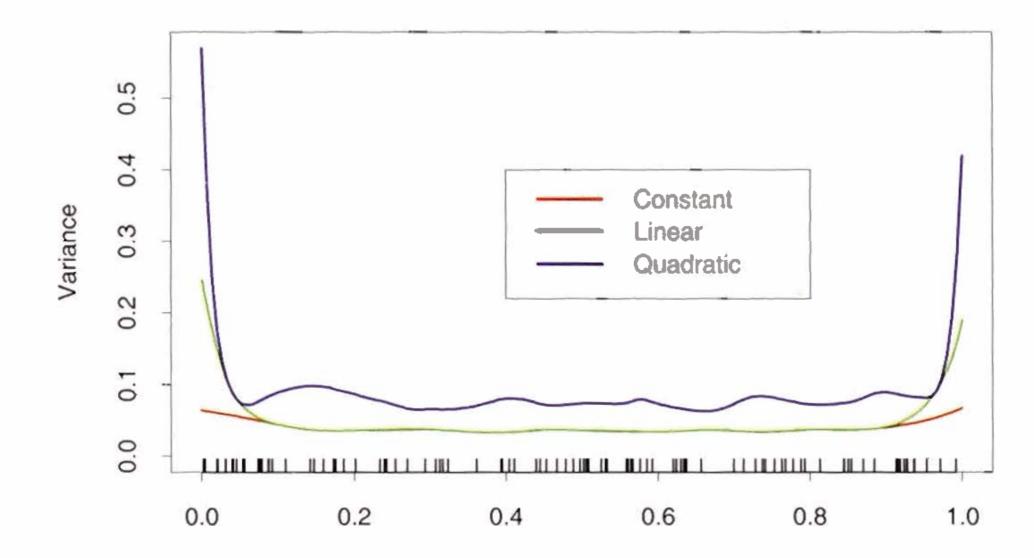


FIGURE 6.3. The locally weighted average has bias problems at or near the boundaries of the domain. The true function is approximately linear here, but most of the observations in the neighborhood have a higher mean than the target point, so despite weighting, their mean will be biased upwards. By fitting a locally weighted linear regression (right panel), this bias is removed to first order



**FIGURE 6.5.** Local linear fits exhibit bias in regions of curvature of the true function. Local quadratic fits tend to eliminate this bias.



**FIGURE 6.6.** The variances functions  $||l(x)||^2$  for local constant, linear and quadratic regression, for a metric bandwidth ( $\lambda = 0.2$ ) tri-cube kernel.

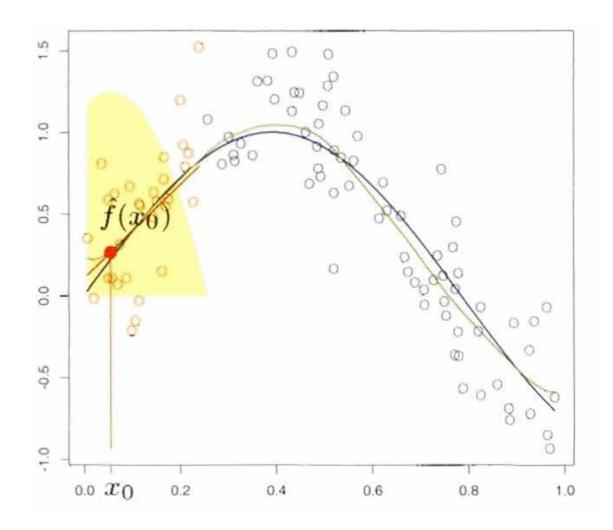
### Local polynomial approach (using least squares)

$$\hat{\boldsymbol{\beta}}(x) = \min^{-1} \sum_{i} K_b(x, x_i) (y_i - X\boldsymbol{\beta})^2$$

where the *i*-th row of X might be  $\begin{pmatrix} 1 & x_i \end{pmatrix}$  or  $\begin{pmatrix} 1 & x_i & x_i^2 \end{pmatrix}$ 

 $\hat{f}_b(x) = \tilde{x}\hat{\beta}(x)$ 

where  $\tilde{x}$  is an appropriately defined row vector, such as  $\begin{pmatrix} 1 & x \end{pmatrix}$  or  $\begin{pmatrix} 1 & x & x^2 \end{pmatrix}$ 



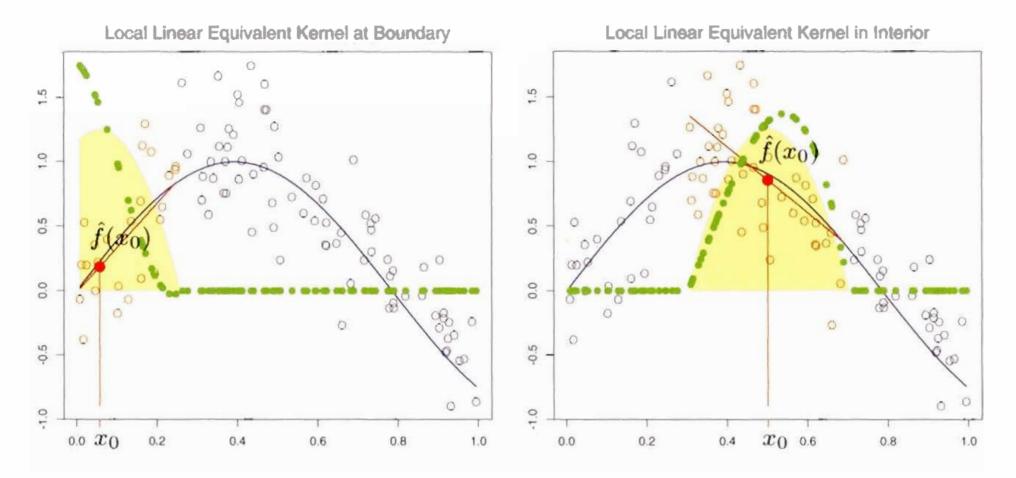
### Local polynomial approach (using least squares)

Let  $z = \begin{pmatrix} 1 & x \end{pmatrix}$  or  $\begin{pmatrix} 1 & x & x^2 \end{pmatrix}$ , i.e. the 'regression ready' predictor for the point x. Let Z be the n by 2 or 3 design matrix, with ith row  $\begin{pmatrix} 1 & x_i \end{pmatrix}$  or  $\begin{pmatrix} 1 & x_i & x_i^2 \end{pmatrix}$ . Let W(x) be the n by n diagonal matrix with ith diagonal element  $K_b(x, x_i)$ . Then the local polynomial fit at x can be written as:

$$\hat{f}_b(x) = z(Z^T W(x)Z)^{-1}Z^T W(x)y = \sum_i l_i(x)y_i$$
  
weighted least linear in the observed  
squares regression response  $y_i$ 

The weights  $l_i(x)$  combine the weighting from the kernel function with that from the least squares fitting approach. Sometimes called the <u>equivalent kernel</u>.

### 6. Kernel Methods



**FIGURE 6.4.** The green points show the equivalent kernel  $l_i(x_0)$  for local regression. These are the weights in  $\hat{f}(x_0) = \sum_{i=1}^{N} l_i(x_0)y_i$ , plotted against their corresponding  $x_i$ . For display purposes, these have been rescaled, since in fact they sum to 1. Since the orange shaded region is the (rescaled) equivalent kernel for the Nadaraya-Watson local average, we see how local regression automatically modifies the weighting kernel to correct for biases due to asymmetry in the smoothing window.

Local polynomial approach (using least squares)

$$\hat{f}_b(x) = z(Z^T W(x)Z)^{-1} Z^T W(x) y = \sum_i l_i(x) y_i$$
$$\hat{f} = S_b y$$
 "smoother matrix"

fitted values in a plain vanilla linear mod

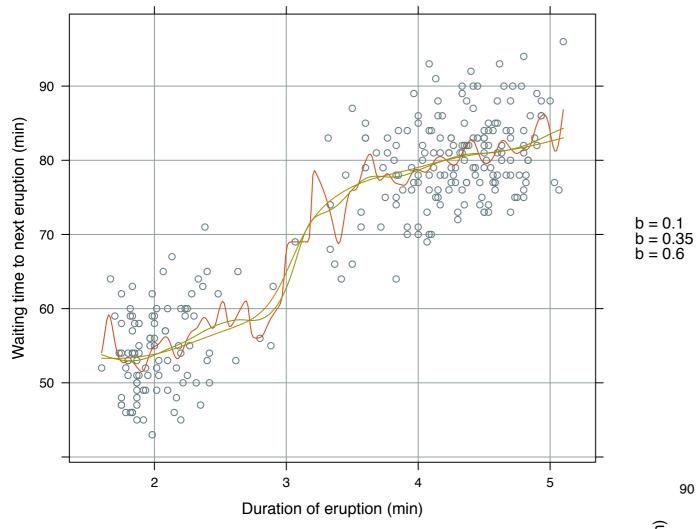
$$\hat{y} = \underbrace{X(X^T X)^{-1} X^T}_{\text{the "hat matrix"}}$$

The trace of the smoother matrix is used as the 'effective degrees of freedom' for the smoother. Recall that the trace of the analogous 'hat' matrix in linear regression is p = the number of parameters. (A similar smoother matrix arises with splines as well.) This 'pseudo degrees of freedom' can be used to calibrate different smoothers or as an alternative way to specify the amount of smoothing.

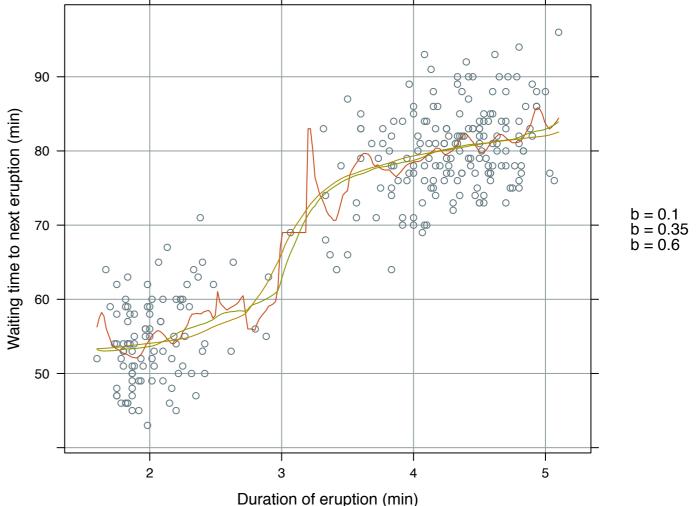
## **loess** (and lowess)

- Local, weighted polynomial regression
- Require specification of a span = proportion of points that influence fit at any given point
- Use tricubic weighting
- lowess: an older function that provides a local linear (or constant) fit, superceded by loess
- loess: local linear or quadratic fit, can work with multiple predictors, can use some predictors globally, local fits can be least squares or something more robust,

#### Kernel smoother, implemented by ksmooth, Gaussian kernel

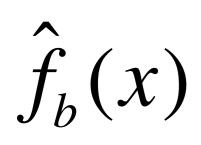


In contrast, the choice of bandwidth -- or whatever tuning parameter controls the amount of smoothing -**is** quite critical. Usually, choice of kernel is not terribly interesting / crucial from the perspective of exploratory figures.



Kernel smoother, implemented by Ipepa (Ipridge), Epanechnikov kernel

approach	tuning parameter(s) that controls smoothness	some leads on actual functions or packages		
kernel smoother	bandwidth sd (or some other measure of spread) of the kernel	ksmooth() KernSmooth sm Ipridge		
local polynomial regression	effective degrees of freedom trace of the smoother matrix span degree of polynomial	loess() locfit package		



Nonparametric regression estimate of  $\hat{f}_h(x) = E(Y|X=x)$  for smoothing parameter value h

### How to choose b?

We'd like to set b to minimize prediction error:

$$PE = E(Y - \hat{f}_b(X))^2$$

In practice, it is tempting to estimate PE with this simple-to-compute empirical quantity:

$$\frac{1}{n}\sum_{i}(y_i - \hat{f}_b(x_i))^2$$

However, this is too naive.

Average squared residual error will be too "optimistic".

Average squared residual error will tend to underestimate prediction error.

Circular logic: use the observed data to build the predictor THEN use the same data to evaluate the performance of the predictor.

If we pick the amount of smoothing to minimize avg residual error, we will "connect the dots" (i.e. do *no* smoothing) and get a value of zero, which is just silly.

Oops!

What we want:  $E(Y - \hat{f}_b(X))^2$  What we might settle for:

$$\frac{1}{n}\sum_{i}(y_i-\hat{f}_b(x_i))^2$$

Fundamental issue:

We need to use some data to build the predictor and other data to characterize its performance.

"Training vs. test"

<u>Cross validation</u> is an attractive approach.

What we want:  $E(Y - \hat{f}_b(X))^2$ What we almost settled for:  $\frac{1}{n} \sum_i (y_i - \hat{f}_b(x_i))^2$ 

Cross validation estimate of prediction error:

$$\frac{1}{n} \sum_{i} (y_i - \hat{f}_b^{-k(i)}(x_i))^2$$

prediction for obs *i*, based on a regression estimate that excluded the k(i)th part of the data Cross validation estimate of prediction error:

$$\frac{1}{n} \sum_{i} (y_i - \hat{f}_b^{-k(i)}(x_i))^2$$

prediction for obs *i*, based on a regression estimate that excluded the *k(i)*th part of the data

What's the deal with the "k(i)th" part of the data?

If k(i) = i, we get "leave one out" cross validation. If k(i) = a sub-sample of the dataset, of size ~ n/K, we get "K-fold" cross validation, e.g. "10-fold cross validation." Cross validation estimate of prediction error associated with smoothing parameter value b:

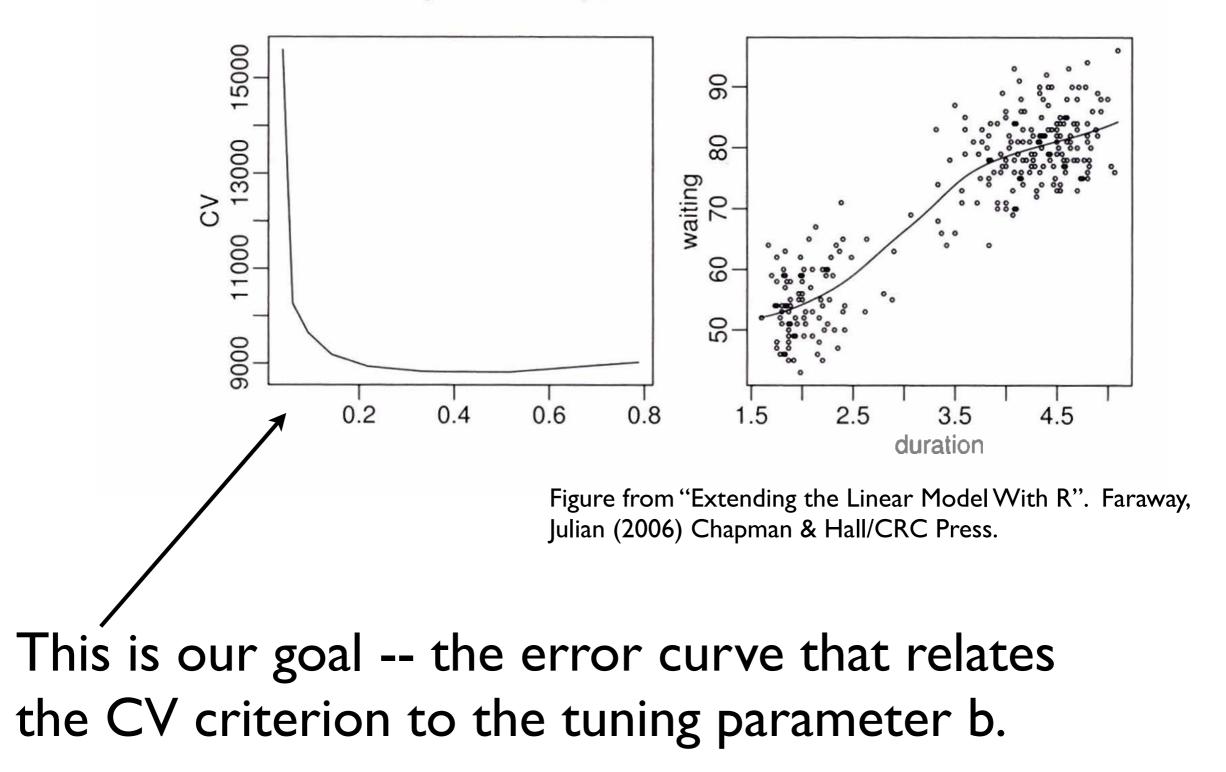
$$CV(b) = \frac{1}{n} \sum_{i} (y_i - \hat{f}_b^{-k(i)}(x_i))^2$$

Compute CV(b) for many values of b.

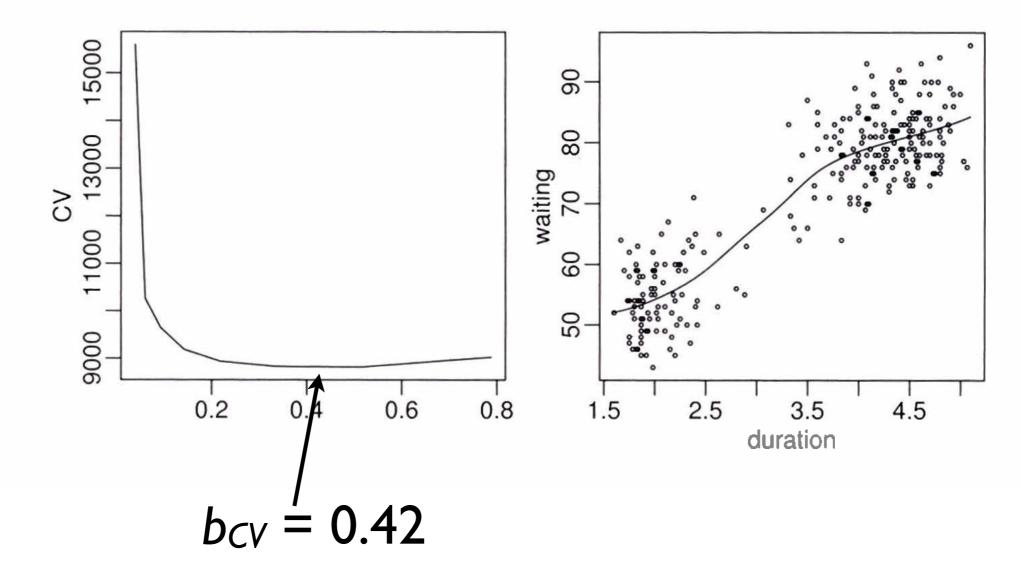
You should probably plot this.

The *b* value that minimizes CV(b), call it  $b_{CV}$ , should receive serious consideration as the "best" value of *b*.

> sm.regression(faithful\$duration,faithful\$waiting,h=hm, xlab="duration",ylab="waiting")



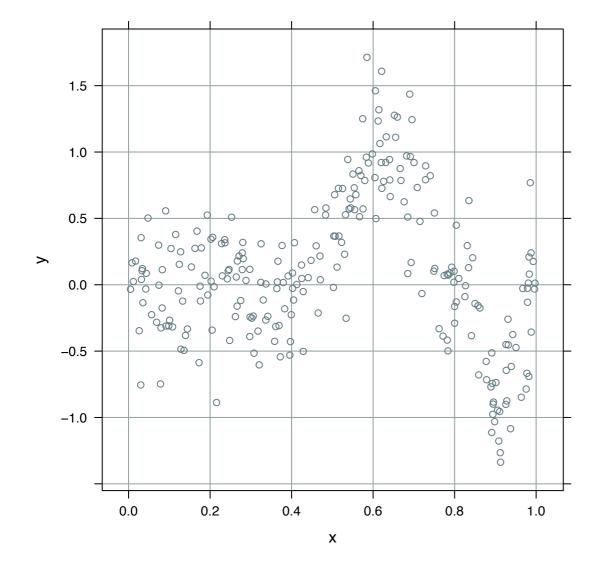
> sm.regression(faithful\$duration,faithful\$waiting,h=hm, xlab="duration",ylab="waiting")

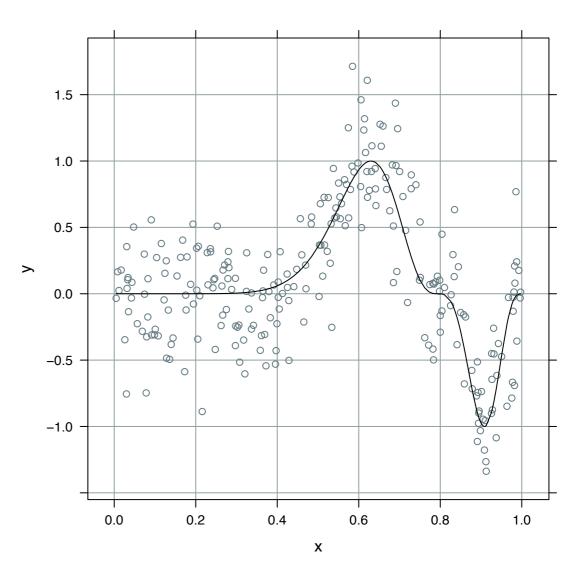


### But also note how flat that curve is ... many values of b perform about the same.

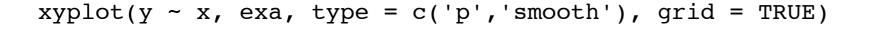
Figure from "Extending the Linear Model With R". Faraway, Julian (2006) Chapman & Hall/CRC Press.

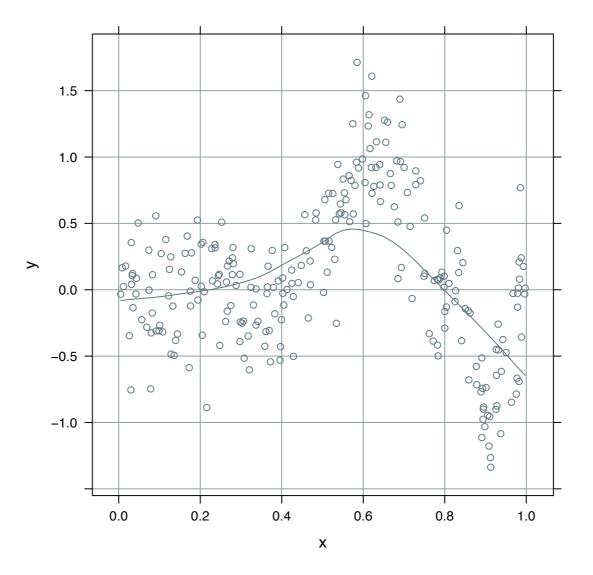
### Synthetic dataset from Faraway (2006).



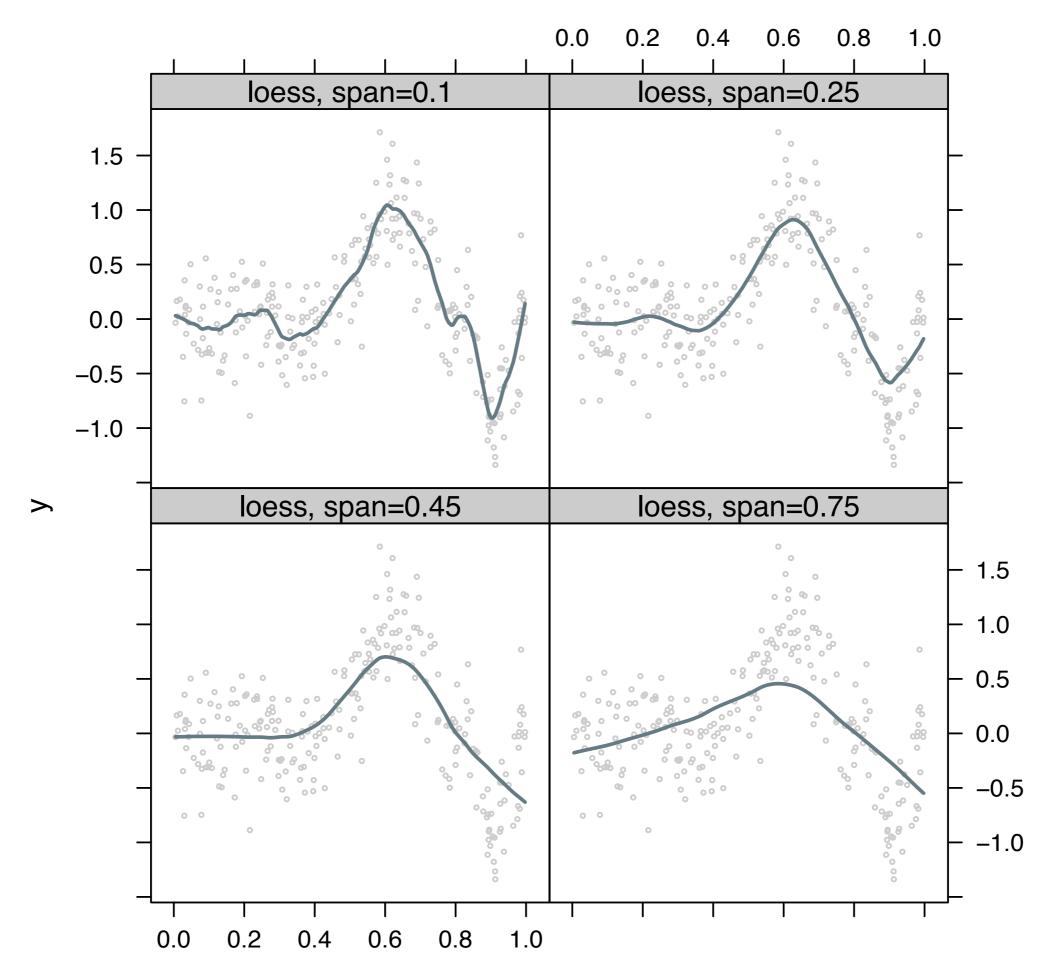


black line is the data-generating truth





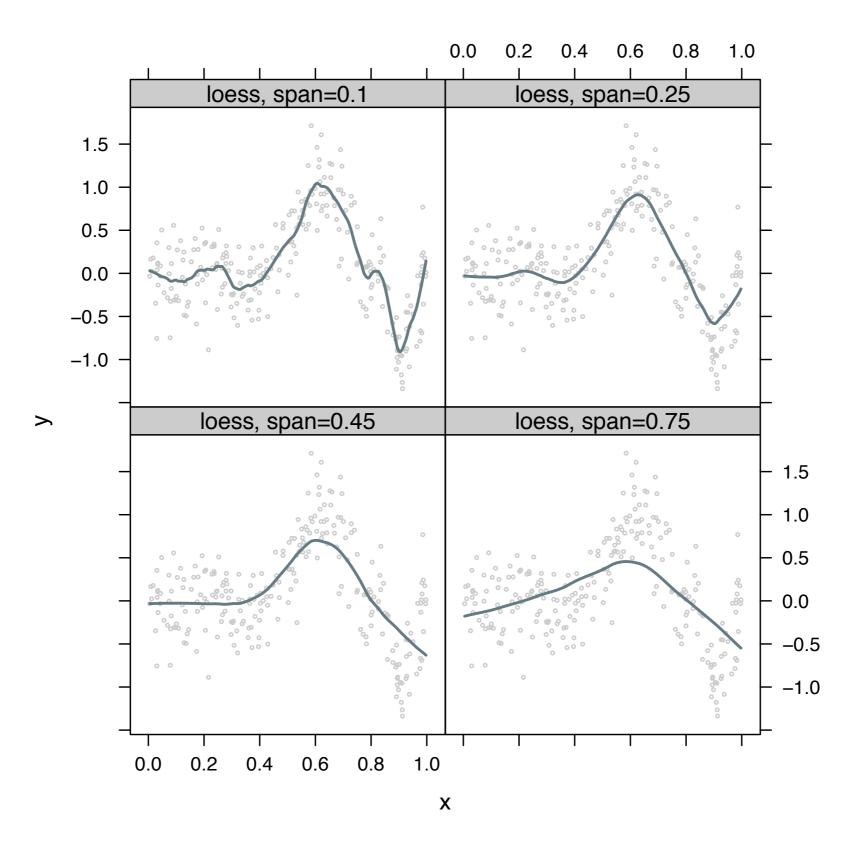
loess is the smoother used by lattice when type includes "smooth", so it's easy to get loess fit at the default settings (span = 0.75). Doesn't this seem *too* smooth, though?



Х

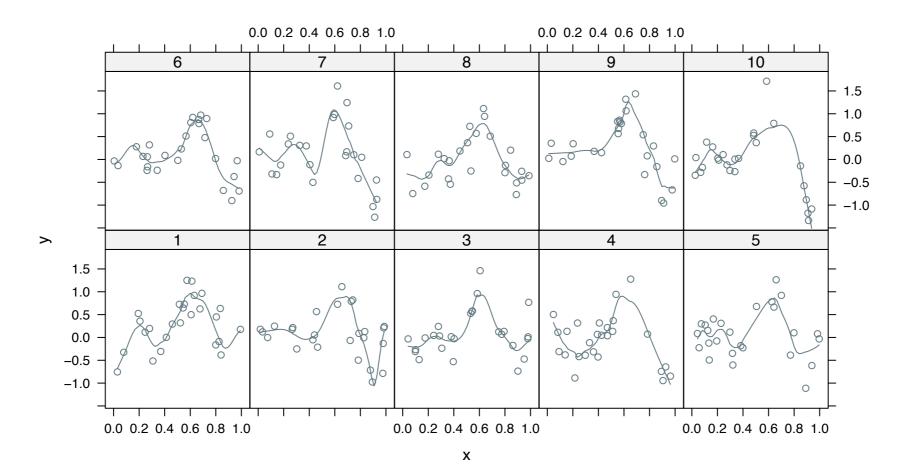
 $\begin{array}{l} \text{degree} = 1 \\ \text{degree} = 2 \end{array}$ 0 0 1.5 -D 0 0 0 Ø 0 000 1.0 -00 Ο 0 700 \ 0 0 <u>08</u> 0 0 00 0 0.5 Ο D Ο 0 0 þ Ο 0 Ο  $\succ$ 0 0 0 6 0.0 Ο 0 00 80 000 Ο 0 ଡ ے بر 00 0 0 0 Ø 000 Ο 8 0 0 Π -0.5 0 3 09 0 @ 00 S 0 0 0 -1.0 -0.0 0.2 0.4 0.6 0.8 1.0

Χ



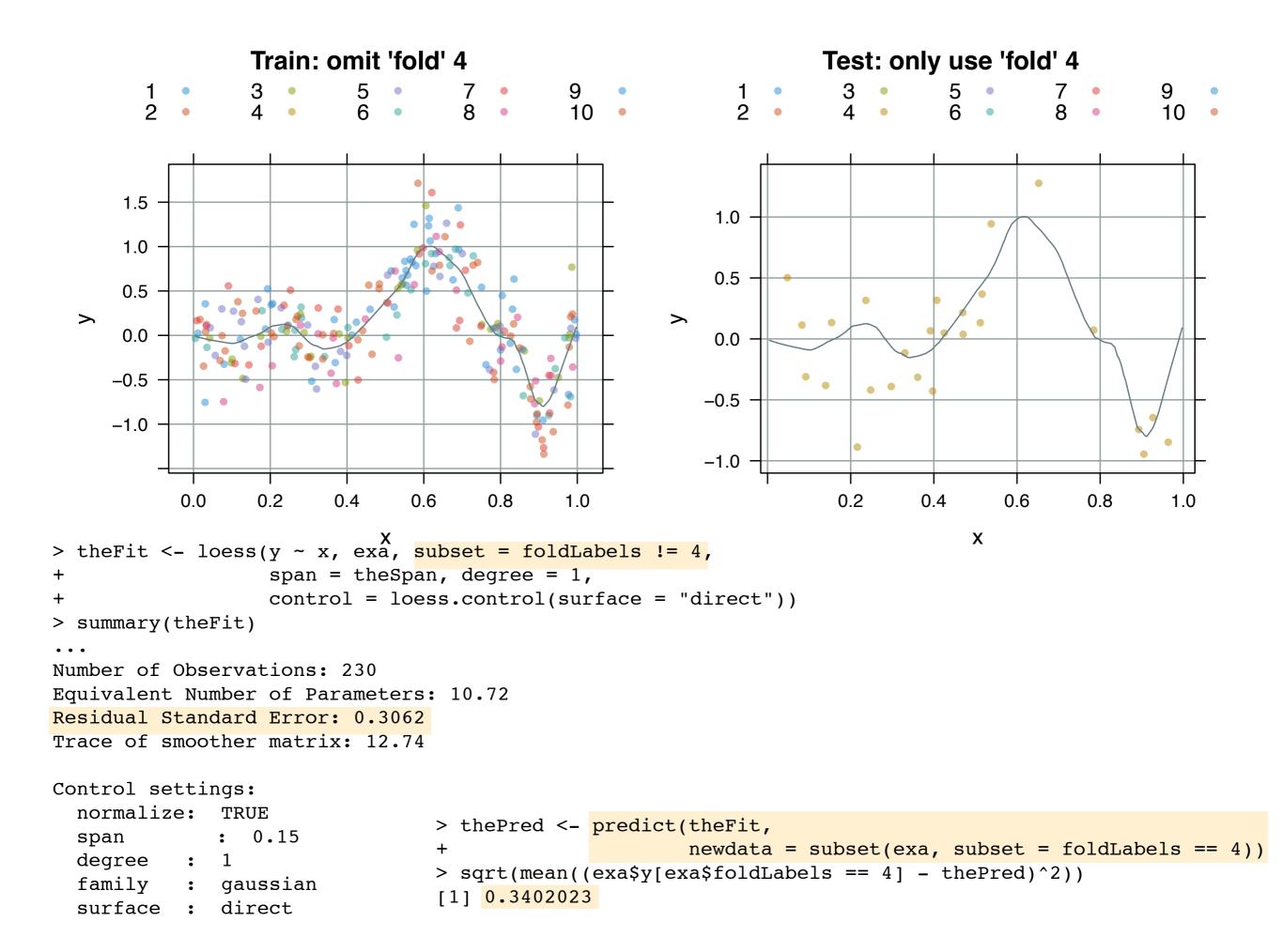
Let's implement the use of cross-validation to select the span.

```
K-fold: randomly divide
                                          # 256
> (n <- nrow(exa))</pre>
[1] 256
                                                              data into K parts
> K <- 10
> set.seed(88)
> exa$foldLabels <- sample(rep(1:K, length = n), n, replace = FALSE)</pre>
> table(exa$foldLabels)
    2
 1
                         9 10
       3
                6
26 26 26 26 26 26 25 25 25 25
> xyplot(y ~ x | factor(foldLabels), exa,
        type = c('p', 'smooth'), span = 0.3,
+
         layout = c(5, 2))
+
```



I	2	3	4	5	6	7	8	9	10
	2	3	4	5	6	7	8	9	10
Ι	2	3	4	5	6	7	8	9	10
I	2	3	4	5	6	7	8	9	10
I	2	3	4	5	6	7	8	9	10
	2	3	4	5	6	7	8	9	10
Ι	2	3	4	5	6	7	8	9	10
I	2	3	4	5	6	7	8	9	10
I	2	3	4	5	6	7	8	9	10
	2	3	4	5	6	7	8	9	10

train	test
-------	------



```
> cvSquaredErrors <-</pre>
    sapply(1:K, function(k) {
+
      cat(paste("fold =", k, "\n"))
+
      theFit <- loess(y ~ x, exa, subset = foldLabels != k,</pre>
+
                      span = theSpan, degree = 1,
+
                      control = loess.control(surface = "direct"))
+
+
      thePred <-
+
        predict(theFit,
+
                newdata = subset(exa, subset = foldLabels == k))
+
      theSquaredError <- (exa$y[exa$foldLabels == k] - thePred)^2</pre>
      return(theSquaredError)
+
+
   })
fold = 1
fold = 2
fold = 3
fold = 4
fold = 5
fold = 6
fold = 7
fold = 8
fold = 9
fold = 10
> sapply(cvSquaredErrors, mean)  # avg sq err by fold
 [1] 0.11730766 0.09362097 0.07410273 0.11573757 0.08207289 0.06686242
 [7] 0.15973350 0.12620991 0.07783665 0.09710683
> sqrt(sapply(cvSquaredErrors, mean))  # sqrt(avg sq err by fold)
 [1] 0.3425021 0.3059754 0.2722182 0.3402023 0.2864837 0.2585777 0.3996667
 [8] 0.3552603 0.2789922 0.3116197
> (cvCrit <- mean(unlist(cvSquaredErrors)))</pre>
[1] 0.1008378
> sqrt(cvCrit)
[1] 0.3175497
```

```
## pkg one CV as a function
cvFun <- function(jDat, span) {</pre>
  K <- length(unique(jDat$foldLabels))</pre>
  cvSquaredErrors <-
    sapply(1:K, function(k) {
      cat(paste("fold =", k, "\n"))
      theFit <- loess(y ~ x, jDat, subset = foldLabels != k,
                        span = span, degree = 1,
                        control = loess.control(surface = "direct"))
      thePred <-
        predict(theFit,
                 newdata = subset(jDat, subset = foldLabels == k))
      return((exa$y[exa$foldLabels == k] - thePred)^2)
                                                                              loess, degree = 1
    })
  return(mean(unlist(cvSquaredErrors)))
}
jSpan <- seq(from = 0.05, to = 0.2, length = 10)
cvCrit <- sapply(seq along(jSpan), function(i) {</pre>
                                                               0.106
  cat(paste("span =", jSpan[i], "\n"))
  return(cvFun(exa, jSpan[i]))
                                                            CV criterion
})
                                                               0.104
xyplot(cvCrit ~ jSpan, type = 'b',
       xlab = 'span', ylab = 'CV criterion',
       main = 'loess, degree = 1')
                                                               0.102
                                                               0.100
                                                                    0.05
                                                                                0.10
                                                                                           0.15
```

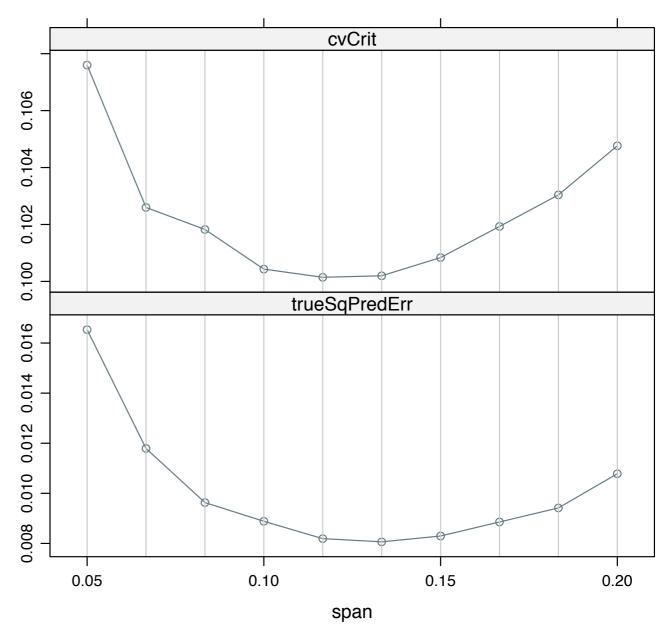
0.20

span

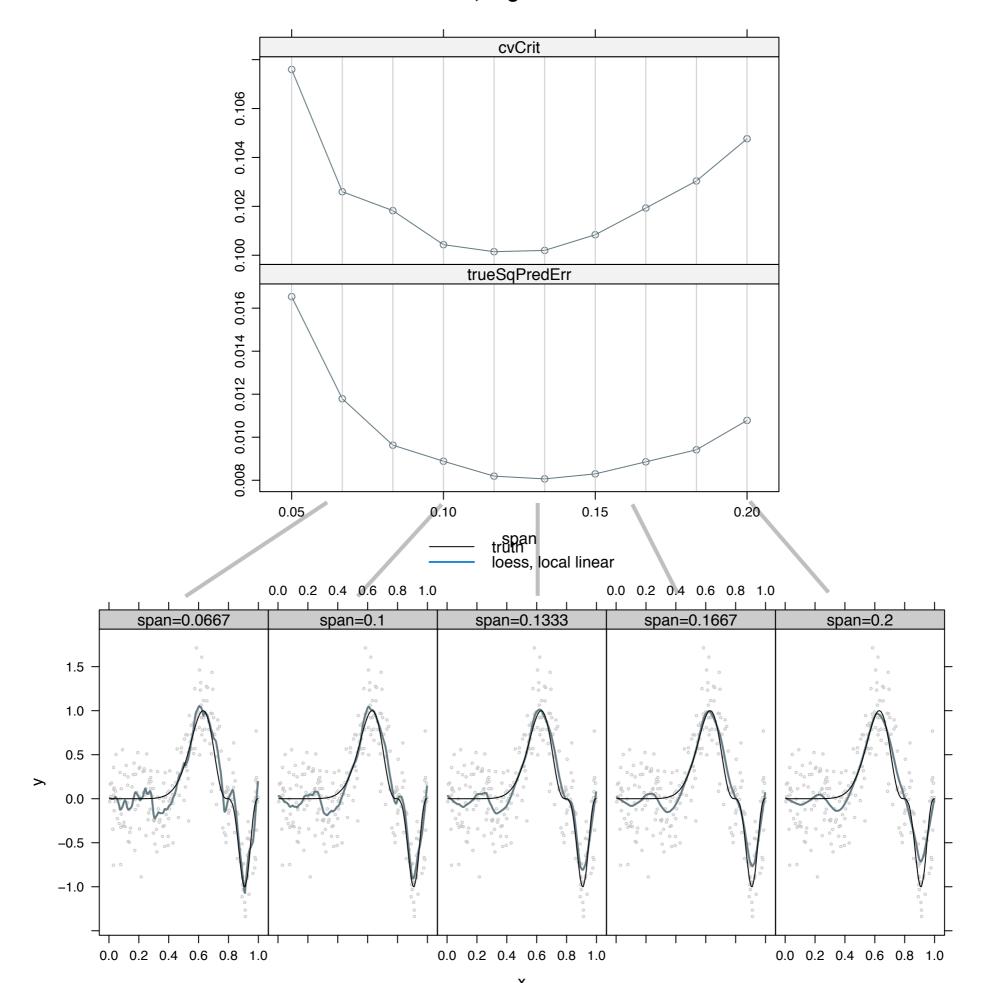
```
loess, degree = 1
```

```
xyplot(trueSqPredErr + cvCrit ~ jSpan, type = 'b',
    scales = list(y = list(relation = 'free')),
    xlab = 'span', ylab = '', layout = c(1, 2),
    main = 'loess, degree = 1', outer = TRUE,
    panel = function(x, y, ...) {
        panel.xyplot(x, y, ...)
        panel.abline(v = jSpan, col = jGray)
    })
```

Minimizer of CV criterion also is the minimizer of true squared prediction error. Illustrates the key idea of CV.



loess, degree = 1



## In defense of eyeball-o-metrics

- Methods that are more formal, more mathematical almost always make very specific assumptions.
- These assumptions are often quite inappropriate.
- So, you can assume a nice but wrong model, in order to permit you to Do The Math.
- Or, you can use common sense, years of experience, etc. to make a subjective choice.
- Both approaches are undoubtedly wrong and subjective. In general, we cannot say which one is more wrong.
- Theoretical solutions are incredibly valuable for offering constructive insight into how/why a system works (or doesn't!) but there is still a big role for judgement and common sense in real applications.

## Summary on smoothing

Kernel smoothing is an extension of kernel density estimation; histogram --> kernel density estimate, moving average --> kernel smoother

Local polynomials are an extension of kernel smoothers

In the absence of any other direction, use loess to get a local linear fit

## Summary on smoothing

Cross validation provides a good way to select tuning parameters; feel free to use pre-packaged CV implementations

Don't let yourself completely off the hook for choosing the amount of smoothing that is appropriate to your goals; use your own brain and eyeballs

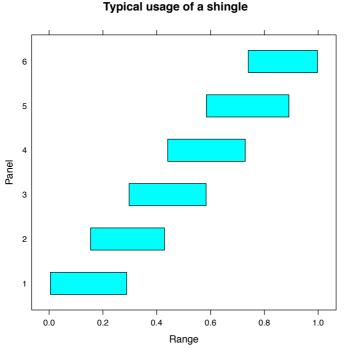
Note that CV is also used to estimate prediction error (as opposed to 'model selection' as done here, where we just seek to find the tuning parameter value that minimizes it) and there are some differences

## References for smoothing, CV

- Faraway, Julian. Extending the Linear Model With R. Chapman & Hall/CRC 2006. Available via <u>MyiLibrary</u>.
- Hastie, T., Tibshirani, R., Friedman, J. The Elements of Statistical Learning. Springer 2001. Available via <u>SpringerLink</u>.
- Efron, B., Tibshirani, R. An Introduction to the Bootstrap. Chapman & Hall/CRC 1998.

### "Mechanics" Sidebar

# How to 'trick' lattice into exploring a tuning parameter ... degenerate shingles



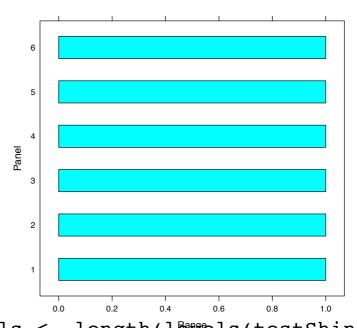
> testShingle1 <- equal.count(exa\$x)
> summary(testShingle1)

#### Intervals:

	min	max	count
1	0.00475	0.28815	73
2	0.15405	0.42875	73
3	0.29735	0.58345	73
4	0.44065	0.72895	73
5	0.58475	0.89115	73
6	0.74025	0.99725	73

```
Overlap between adjacent intervals:
[1] 36 37 36 37 36
> plot(testShingle1,
```

```
+ main = "Typical usage of a shingle")
```



Degenerate shingle

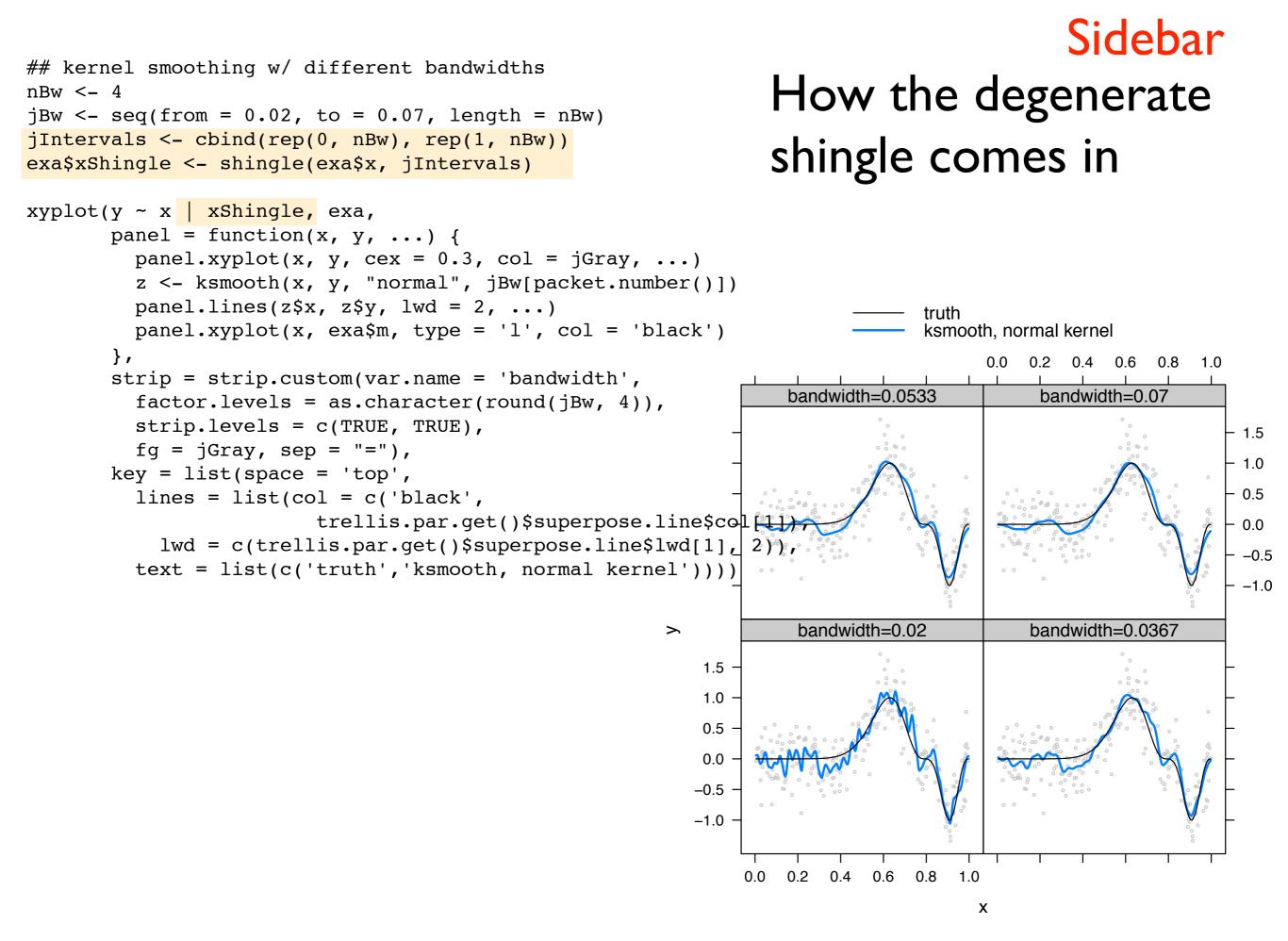
> nLevels <- length(levels(testShingle1))
> jIntervals <- cbind(rep(0, nLevels), rep(1, nLevels))</pre>

```
> testShingle2 <- shingle(exa$x, jIntervals)
> summary(testShingle2)
```

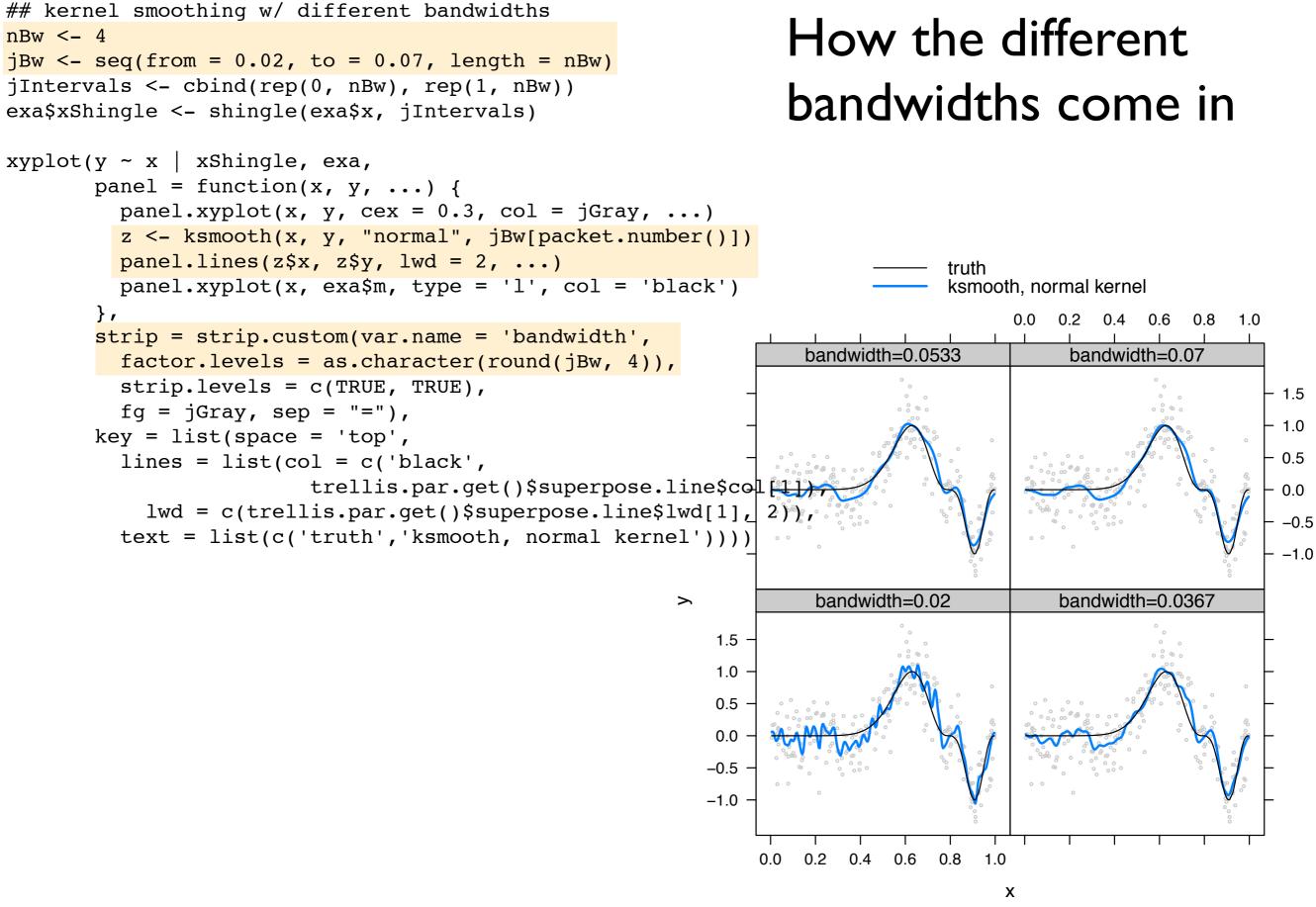
```
Intervals:
  min max count
1
    0
         1
              256
2
              256
     0
         1
3
    0
         1
              256
4
    0
              256
         1
              256
5
     0
         1
6
     0
              256
         1
Overlap between adjacent intervals:
```

```
[1] 256 256 256 256 256
```

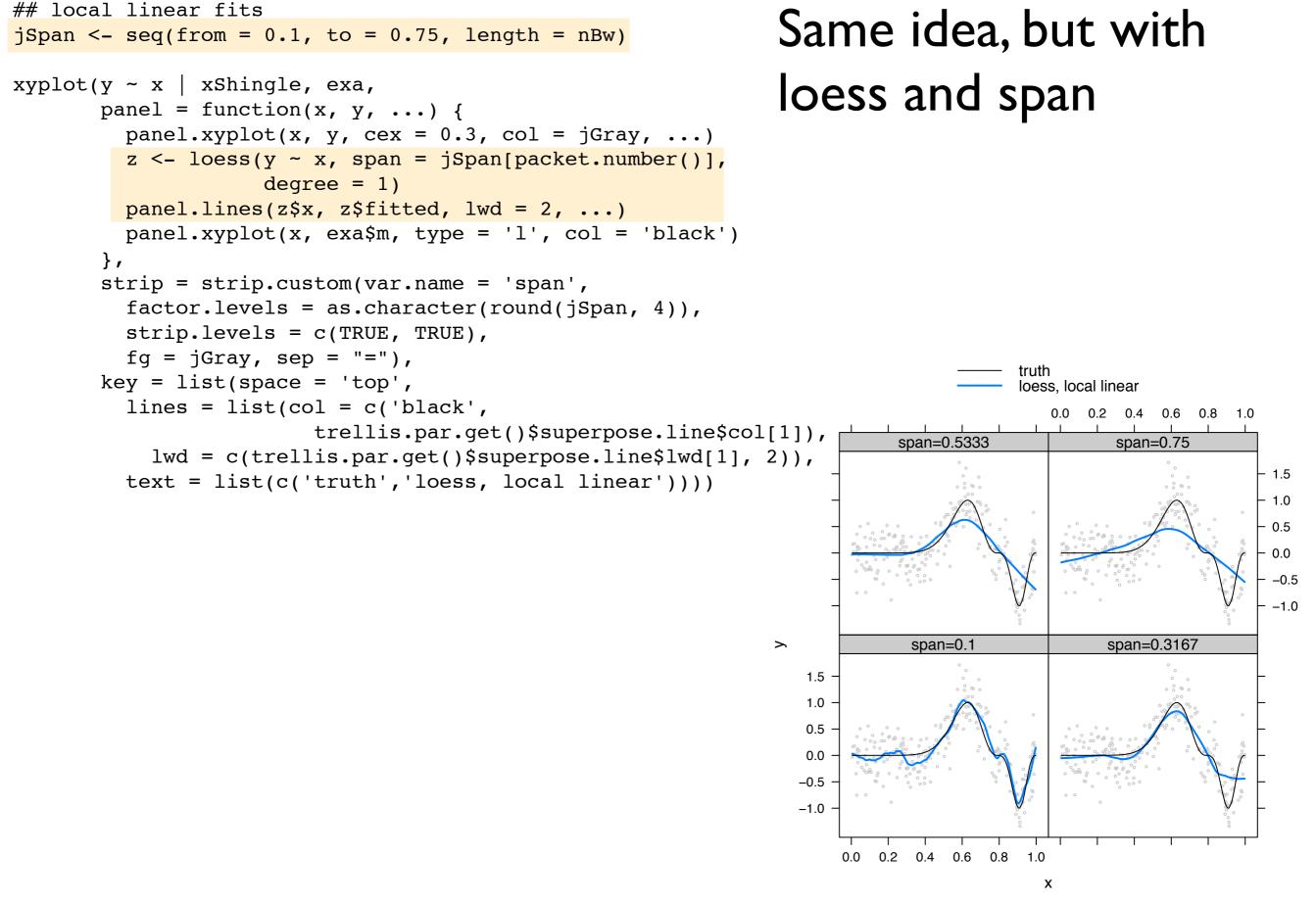
```
> plot(testShingle2, main = "Degenerate shingle")
```

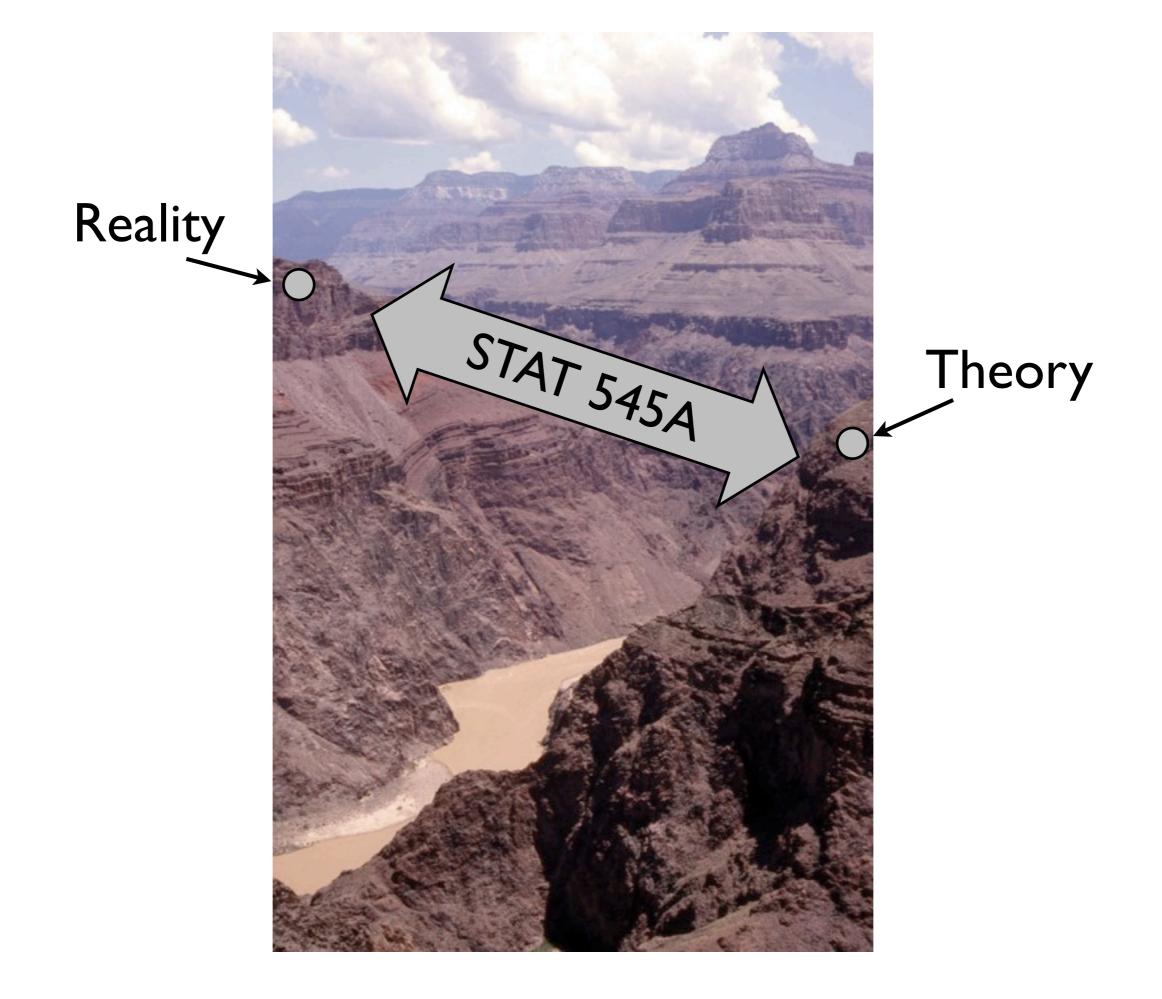


### Sidebar



### Sidebar





## Two inter-related goals

- Foster your development of a personal philosophy on data analysis, especially exploratory analysis.
- Strengthen your data analysis skills.

My hope:

You'll leave this course with (at least the beginnings of) a confident, deliberate attitude about how to approach data analysis and a base level of practical skills to put your attitude into action.