# Robust Regression

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## Motivation

- Least squares regression is sensitive to violation of assumptions
- Individual high-leverage points can substantially influence inference
- Specifically, least squares is vulnerable when error distribution is heavy-tailed
- We have considered one possible remedy: detect influential observations
- This has several drawbacks:
  - We cannot realistically expect users to always screen the data
  - The binary decision to keep/reject suspicious observations seems extreme; we may instead prefer to downweight such observations
  - Finding outliers may be difficult in multivariate or structured data
  - Rejecting outliers changes the sampling distribution of estimates; we should but usually do not make adjustments.
- Another alternative is to consider procedures that systematically guard against outliers

## Motivation: Location and scale

- A more familiar example before considering the regression problem:

$$X_1, \dots, X_n \sim N(\mu, \sigma^2)$$

```
(x <- rnorm(10, mean = 5, sd = 3))
```

```
 [1]  4.2967261  0.8741864  7.7031483 -0.0853126  2.5003953  5.6141429  8.6149780 11.0482167 -1.9215526
```

- Want to estimate location $\mu$ (as well as scale $\sigma$)
- Common estimators of location $\mu$:

| | | |
|---|---|---|
| Mean | `mean(x)` | 3.8344398 |
| Median | `median(x)` | 3.3985607 |
| Trimmed mean | `mean(x, trim = 0.25)` | 3.4838811 |

## Robust estimation of location

- How do these behave when data is "contaminated"?
- We know that
  - Mean can be changed by an arbitrary amount by changing a single observation
  - Median can be changed arbitrarily only by changing more than 50% observations

- But there is a cost: median is less "efficient"!
- Let us try to make these ideas formal

## Relative efficiency

- Consider two estimators $T_1$ and $T_2$
- Define the relative efficiency of $T_1$ w.r.t. $T_2$ (for a given underlying distribution) as

$$RE(T_1; T_2) = \frac{V(T_2)}{V(T_1)}$$

- For biased estimators, variance could be replaced by MSE
- $T_2$ is usually taken to be the optimal estimator, if one is available
- What are relative efficiencies of median and trimmed mean?
- Instead of trying to obtain variances theoretically (which is often difficult), we could use simulation to get a rough idea

```
sampling.variance <- function(estimator, rfun, n, NREP = 10000)
{
    var(replicate(NREP, estimator(rfun(n))))
}
trim.mean <- function(x) mean(x, trim = 0.25)
rdist <- function(n) rnorm(n, mean = 5, sd = 3)
var.mean <- sampling.variance(mean, rdist, n = 10)
var.median <- sampling.variance(median, rdist, n = 10)
var.tmean <- sampling.variance(trim.mean, rdist, n = 10)
round(100 * var.mean / var.median)
```

```
[1] 74
```

```
round(100 * var.mean / var.tmean)
```

```
[1] 91
```

## Asymptotic relative efficiency

$ARE(T_1; T_2)$ is the limiting value of relative efficiency as $n \to \infty$

```
rdist <- function(n) rnorm(n, mean = 5, sd = 3)
var.mean <- sampling.variance(mean, rdist, n = 5000)
var.median <- sampling.variance(median, rdist, n = 5000)
var.tmean <- sampling.variance(trim.mean, rdist, n = 5000)
round(100 * var.mean / var.median)
```

```
[1] 63
```

```
round(100 * var.mean / var.tmean)
```

```
[1] 84
```

- For comparison, the exact $ARE$ of the median is $\frac{2}{\pi} = 63.6\%$
- This is when the data comes from a normal distribution

### Relative efficiency for heavier tails

- Suppose errors are instead from $t$ with 5 degrees of freedom

```
rdist <- function(n) 5 + 3 * rt(n, df = 5)
var.mean <- sampling.variance(mean, rdist, n = 5000)
var.median <- sampling.variance(median, rdist, n = 5000)
var.tmean <- sampling.variance(trim.mean, rdist, n = 5000)
round(100 * var.mean / var.median)
```

```
[1] 96
```

```
round(100 * var.mean / var.tmean)
```

```
[1] 121
```

### Winsorized trimmed mean

- Similar to trimmed mean, but replaces trimmed observations by nearest untrimmed observation

```
win.mean <- function(x, trim = 0.25)
{
    q <- quantile(x, c(trim, 1-trim))
    x[x < q[1]] <- q[1]
    x[x > q[2]] <- q[2]
    mean(x)
}
rdist <- function(n) rnorm(n, mean = 5, sd = 3) # normal
var.mean <- sampling.variance(mean, rdist, n = 5000)
var.win.mean <- sampling.variance(win.mean, rdist, n = 5000)
round(100 * var.mean / var.win.mean)
```

```
[1] 91
```

```
rdist <- function(n) 5 + 3 * rt(n, df = 5) # t_5
var.mean <- sampling.variance(mean, rdist, n = 5000)
var.win.mean <- sampling.variance(win.mean, rdist, n = 5000)
round(100 * var.mean / var.win.mean)
```

```
[1] 117
```

### Relative efficiency for contamination

- Another "departure" model: contamination
- Suppose data is a mixture of $N(\mu, \sigma^2)$ with probability $1 - \epsilon$ and $N(\mu, 9\sigma^2)$ with probability $\epsilon$

```
rdist <- function(n) rnorm(n, mean = 5, sd = ifelse(runif(n) < 0.01, 3, 1)) # 1% contamination
var.mean <- sampling.variance(mean, rdist, n = 5000)
var.median <- sampling.variance(median, rdist, n = 5000)
var.tmean <- sampling.variance(trim.mean, rdist, n = 5000)
round(100 * var.mean / c(median = var.median, trim.mean = var.tmean))
```

```
   median trim.mean
       69        92
```

```
rdist <- function(n) rnorm(n, mean = 5, sd = ifelse(runif(n) < 0.05, 3, 1)) # 5% contamination
var.mean <- sampling.variance(mean, rdist, n = 5000)
```

```r
var.median <- sampling.variance(median, rdist, n = 5000)
var.tmean <- sampling.variance(trim.mean, rdist, n = 5000)
round(100 * var.mean / c(median = var.median, trim.mean = var.tmean))
```

```
   median trim.mean 
       82       108 
```

## Sensitivity / influence function

- How much does changing one observation change the estimate $T$?
- This is measured by the *empirical influence function* or *sensitivity curve*

$$SC(x; x_1, \ldots, x_{n-1}, T) = \frac{T(x_1, \ldots, x_{n-1}, x) - T(x_1, \ldots, x_{n-1})}{1/n}$$

- We are usually interested in limiting behaviour as $n \to \infty$
- The population version, independent of the sample $x_1, \ldots, x_{n-1}$, is known as the *influence function*

$$IF(x; F, T) = \lim_{\epsilon \to 0} \frac{T((1-\epsilon)F + \epsilon\delta_x) - T(F)}{\epsilon}$$

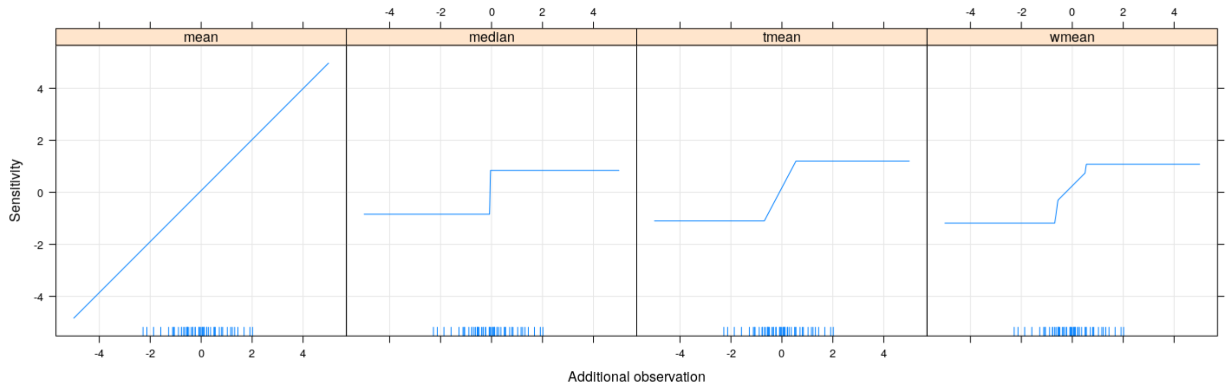
- Here $\delta_x$ is a point mass at $x$
- How does `mean(c(x, xnew))` change as function of `xnew`?
- How do other estimates change?

```r
n <- 50
x <- rnorm(n, mean = 0, sd = 1)
summary(x)
```

```
    Min.  1st Qu.   Median     Mean  3rd Qu.     Max. 
-2.28099 -0.61800 -0.06070 -0.06727  0.51522  2.01596 
```

```r
xx <- seq(-5, 5, 0.01)
sensitivity <-
    data.frame(xx = xx,
               mean = n * (sapply(xx, function(xnew) mean(c(x, xnew))) - mean(x)),
               median = n * (sapply(xx, function(xnew) median(c(x, xnew))) - median(x)),
               tmean = n * (sapply(xx, function(xnew) trim.mean(c(x, xnew))) - trim.mean(x)),
               wmean = n * (sapply(xx, function(xnew) win.mean(c(x, xnew))) - win.mean(x)))
```

```r
xyplot(mean + median + tmean + wmean ~ xx, sensitivity, type = "l", outer = TRUE,
       xlab = "Additional observation", ylab = "Sensitivity", grid = TRUE) +
    layer(panel.rug(x = .GlobalEnv$x))
```




### Breakdown point

- Defined as the proportion of the sample size that must be perturbed to make the estimate unbounded
- 50% is the best we can hope for
- For location, mean has 0% breakdown point (one out of $n$), median has 50%.

### Estimators of scale

- We can similarly consider estimators of scale $\sigma$
- Common estimators:
  - Sample standard deviation (`sd` in R)
  - Mean absolute deviation from mean
  - Median absolute deviation (MAD) from median (`mad` in R)
  - Inter-quartile range (`IQR` in R)
- May need scaling for normal distribution:

```
T1 <- sd
T2 <- function(x, ...) mean(abs(x - mean(x))) / sqrt(2/pi)
T3 <- function(x, ...) median(abs(x - median(x))) / sqrt(qchisq(0.5, df = 1))
T4 <- function(x, ...) IQR(x) / diff(qnorm(c(0.25, 0.75)))
```

### Relative efficiency for estimators of scale

```
rdist <- function(n) rnorm(n, mean = 5)                # Normal
var.T1 <- sampling.variance(T1, rdist, n = 5000)
var.T2 <- sampling.variance(T2, rdist, n = 5000)
var.T3 <- sampling.variance(T3, rdist, n = 5000)
var.T4 <- sampling.variance(T4, rdist, n = 5000)
round(100 * var.T1 / c(mean.abs.dev = var.T2, median.abs.dev = var.T3, iqr = var.T4))
```

```
  mean.abs.dev median.abs.dev            iqr
            89             38             38
```

```
rdist <- function(n) rnorm(n, mean = 5, sd = ifelse(runif(n) < 0.01, 3, 1)) # 1% Contamination
var.T1 <- sampling.variance(T1, rdist, n = 5000)
```

```
var.T2 <- sampling.variance(T2, rdist, n = 5000)
var.T3 <- sampling.variance(T3, rdist, n = 5000)
var.T4 <- sampling.variance(T4, rdist, n = 5000)
round(100 * var.T1 / c(mean.abs.dev = var.T2, median.abs.dev = var.T3, iqr = var.T4))
```

```
  mean.abs.dev median.abs.dev            iqr 
           152             70             70 
```

## M-estimators

- Most common location estimators can be expressed as M-estimators (MLE-like)

$$T(x_1, \ldots, x_n) = \arg\min_{\theta} \sum_{i=1}^{n} \rho(x_i, \theta)$$

- For MLE, $\rho(x_i, \theta)$ is the negative log-density, but $\rho$ need not correspond to a likelihood
- If $\psi(x_i, \theta) = \frac{d}{d\theta}\rho(x_i, \theta)$ exists, then $T$ is the solution to the *score equation*

$$\sum_{i=1}^{n} \psi(x_i, \theta) = 0$$

- We usually consider loss functions of the form $\rho(x - \theta)$
- Corresponding $\psi$ function is $\psi(x - \theta) = \rho'(x - \theta)$ (disregarding change in sign)
- This easily generalizes to vector parameters
- Mean

$$\rho(x - \theta) = (x - \theta)^2, \quad \psi(x - \theta) = 2(x - \theta)$$

- Median (ignoring non-differentiability of $|x|$ at 0)

$$\rho(x - \theta) = |x - \theta|, \quad \psi(x - \theta) = \text{sign}(x - \theta)$$

- Trimmed mean (for some $c$, ignoring dependence of $c$ on the data)

$$\rho(x - \theta) = \begin{cases} (x - \theta)^2 & |x - \theta| \leq c \\ c^2 & \text{otherwise} \end{cases}$$

$$\psi(x - \theta) = \begin{cases} 2(x - \theta) & |x - \theta| \leq c \\ 0 & \text{otherwise} \end{cases}$$

- Huber loss (similar to Winsorized trimmed mean)

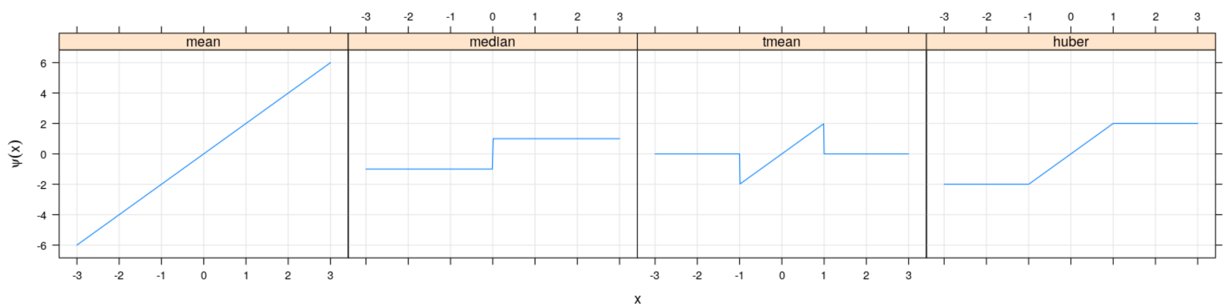
$$\rho(x - \theta) = \begin{cases} (x - \theta)^2 & |x - \theta| \leq c \\ c(2|x - \theta| - c) & \text{otherwise} \end{cases}$$

$$\psi(x - \theta) = \begin{cases} -2c & x - \theta < -c \\ 2(x - \theta) & |x - \theta| \leq c \\ 2c & x - \theta > c \end{cases}$$

- Can be thought of compromise between mean (squared error) and median (absolute error)
- Estimator reduces to mean as $c \to \infty$, median as $c \to 0$
- $\rho$ is differentiable everywhere
- Exercise: What do plots of $\rho$ and $\psi$ look like?

### Influence function revisited

```
xx <- seq(-3, 3, 0.01)
sensitivity <-
    data.frame(xx = xx,
               mean = 2 * xx,
               median = sign(xx),
               tmean = ifelse(abs(xx) < 1, 2 * xx, 0),
               huber = ifelse(abs(xx) < 1, 2 * xx, 2 * sign(xx)))
xyplot(mean + median + tmean + huber ~ xx, sensitivity, type = "l", outer = TRUE,
       xlab = "x", ylab = expression(psi(x)), grid = TRUE)
```




- Turns out that the corresponding influence functions have the same shape (but will not discuss why)

### M-estimation: general approach for location

- Choose function $\psi(x - \theta)$
- Find $T$ by solving (for $\theta$)

$$\sum_{i=1}^{n} \psi(x_i - \theta) = 0$$

- We can rewrite this as

$$\sum_{i=1}^{n} \frac{\psi(x_i - \theta)}{(x_i - \theta)}(x_i - \theta) = 0$$

- This suggests an iterative approach using weighted least squares in each step:
    1. Start with initial estimate $\hat{\theta}$
    2. Obtain current weights $w_i = \frac{\psi(x_i - \hat{\theta})}{(x_i - \hat{\theta})}$
    3. Obtain new estimate of $\theta$ by solving $\sum_i w_i(x_i - \theta) = 0 \implies \hat{\theta} = \sum_i w_i x_i / \sum_i w_i$
- Of course, a black-box numerical optimizer (e.g., `optim()`) can also be used instead

## Common robust loss function derivatives

- Absolute deviation $\psi(x) = \text{sign}(x)$
- Huber (same as Winsorized trimmed mean)

$$\psi(x) = \begin{cases} -c & x < c \\ x & |x| \leq c \\ c & x > c \end{cases}$$

- Trimmed mean

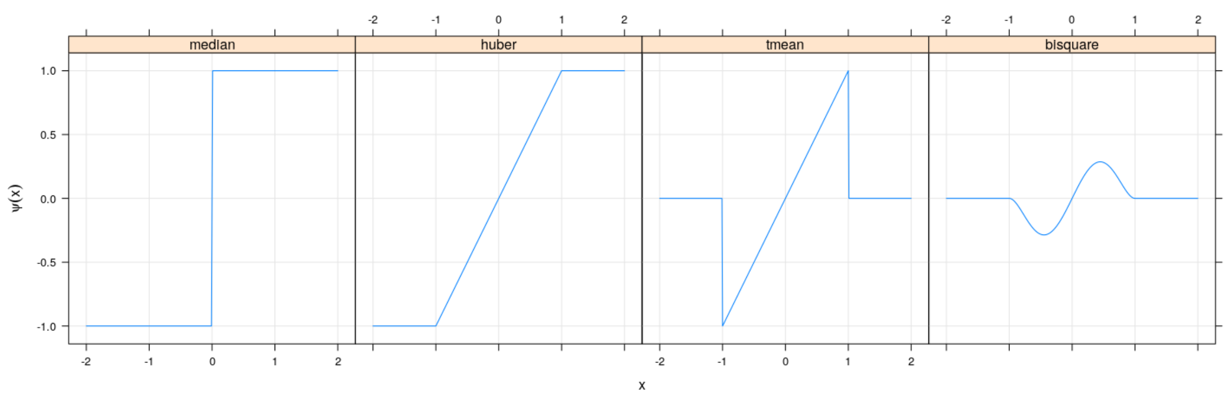
$$\psi(x) = \begin{cases} x & |x| \leq c \\ 0 & \text{otherwise} \end{cases}$$

- Tukey bisquare

$$\psi(x) = x\left[1 - (x/R)^2\right]_+^2 \qquad \text{for } \rho(x) = \begin{cases} R^2\left[1 - (1 - (x/R)^2)\right]^3 & |x| \leq R \\ R^2 & \text{otherwise} \end{cases}$$

- For the last three, choice of scale ($c$, $R$) is a tuning parameter

```
xx <- seq(-2, 2, 0.01)
c <- 1; R <- 1
psi <-
    data.frame(xx = xx,
               median = sign(xx),
               huber = ifelse(abs(xx) <= c, xx, c * sign(xx)),
               tmean = ifelse(abs(xx) <= c, xx, 0),
               bisquare = xx * pmax(0, (1 - (xx/R)^2))^2)
xyplot(median + huber + tmean + bisquare ~ xx, psi, type = "l", outer = TRUE,
       ylab = expression(psi(x)), xlab = "x", grid = TRUE)
```



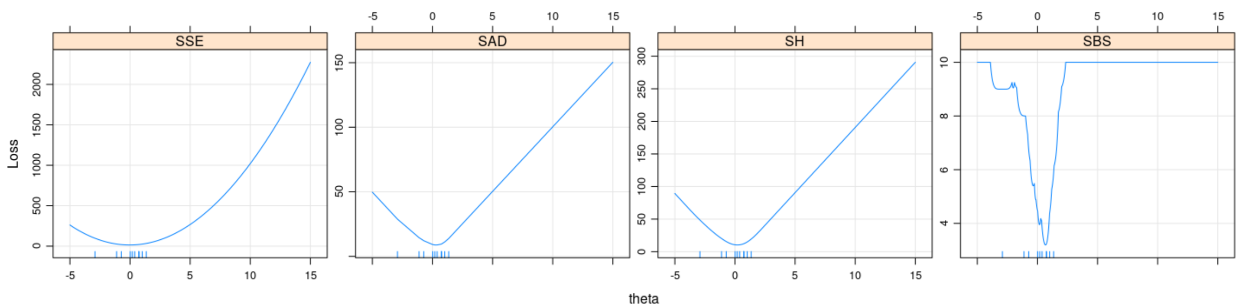

- The last two functions are examples of "redescending" influence functions
- Corresponding loss function $\rho$ becomes flat beyond a threshold
- In effect, beyond this threshold, extreme observations are *completely discounted*
- In other words, they have zero/constant contribution to the total loss
- However, this does make the objective function (to be minimized) non-convex

- Let us see what the objective function looks like for various loss functions

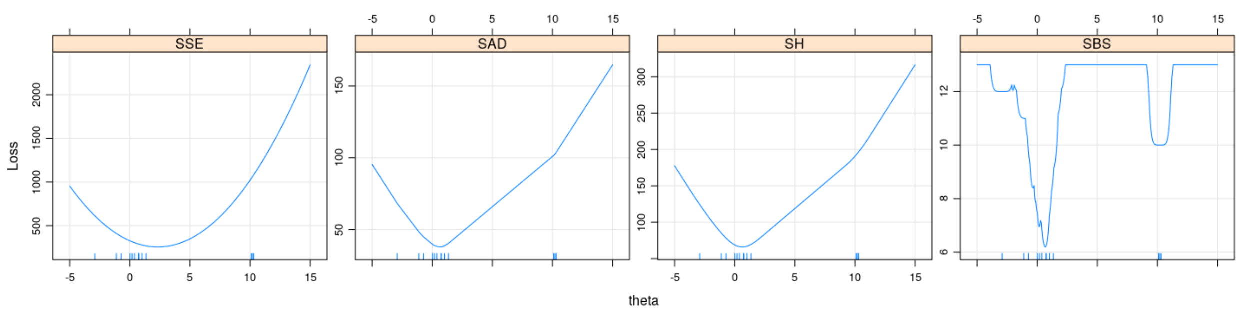
```
huber.loss <- function(x, c = 1) ifelse(abs(x) < c, x^2, c * (2 * abs(x) - c))
bisquare.loss <- function(x, R = 1) ifelse(abs(x) < R, R^2 * (1 - (1 - (x/R)^2))^3, R^2)
x <- rnorm(10)
y <- c(x, 10.1, 10.2, 10.3) # add three extreme observations to x
t <- seq(-5, 15, 0.01)
```

### Example: loss functions

```
SSE <- sapply(t, function(theta) sum((x - theta)^2))
SAD <- sapply(t, function(theta) sum(abs(x - theta)))
SH <- sapply(t, function(theta) sum(huber.loss(x - theta, c = 1)))
SBS <- sapply(t, function(theta) sum(bisquare.loss(x - theta, R = 1)))
xyplot(SSE + SAD + SH + SBS ~ t, type = "l", outer = TRUE,
       ylab = "Loss", xlab = "theta", grid = TRUE, scales = list(y = "free")) +
    layer(panel.rug(x = .GlobalEnv$x))
```




```
SSE <- sapply(t, function(theta) sum((y - theta)^2))
SAD <- sapply(t, function(theta) sum(abs(y - theta)))
SH <- sapply(t, function(theta) sum(huber.loss(y - theta, c = 1)))
SBS <- sapply(t, function(theta) sum(bisquare.loss(y - theta, R = 1)))
xyplot(SSE + SAD + SH + SBS ~ t, type = "l", outer = TRUE,
       ylab = "Loss", xlab = "theta", grid = TRUE, scales = list(y = "free")) +
    layer(panel.rug(x = .GlobalEnv$y))
```




- For non-convex loss functions, important to have good starting estimates

## Other practical considerations

- Tuning parameters are arbitrary
- Natural to express tuning parameter in terms of scale $\sigma$ (unknown) — scale invariance
- Common to take $\hat{\sigma}$ to be a multiple of the median absolute deviation (MAD) from the median
- Tuning parameter can then be chosen to achieve some target asymptotic relative efficiency under normality
- For example, Huber loss function with $c = 1.345\sigma$ would give 95% $ARE$ if $\sigma$ was known

## Standard errors

- M-estimators are consistent and asymptotically normal with variance $\tau\sigma^2/n$, where

$$\tau = \frac{E(\psi^2(X))}{[E(\psi'(X))]^2}$$

- Could be estimated by replacing $X$ by fitted (standardized) residuals

$$\hat{\tau} = \frac{\frac{1}{n}\sum_i \psi^2(e_i/\hat{\sigma})}{[\frac{1}{n}\sum_i \psi'(e_i/\hat{\sigma})]^2}$$

- Not necessarily reliable in small samples

## M-estimation for regression

- The ideas described above translate directly to linear regression
- Instead of minimizing least squared errors, minimize

$$\sum_{i=1}^{n} \rho(y_i - \mathbf{x}_i^T \beta)$$

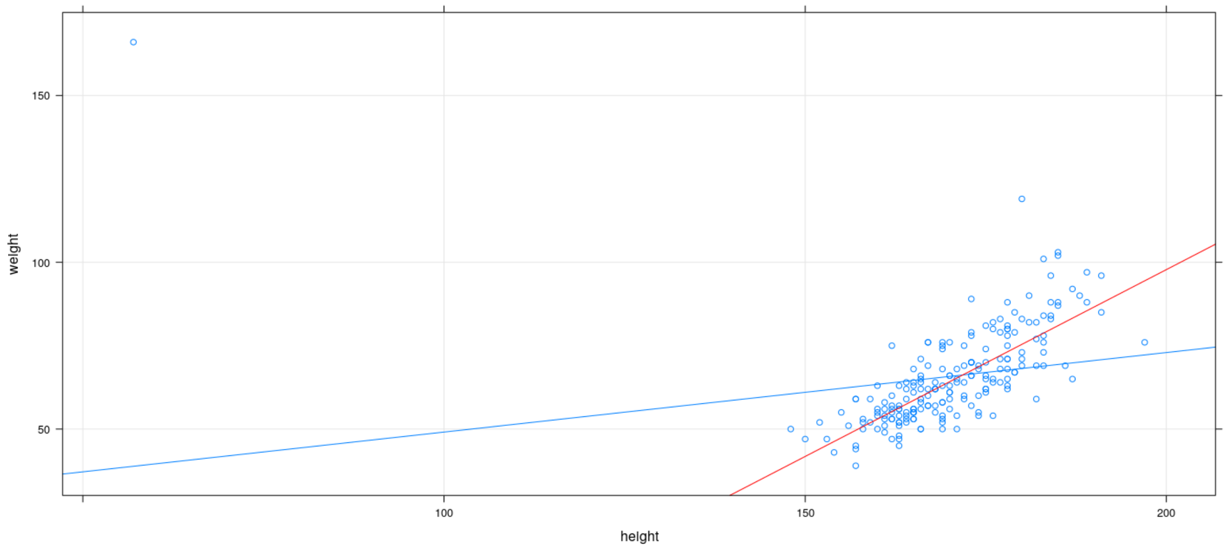
- Simple estimation approach: Iteratively (Re)Weighted Least Squares (IWLS / IRLS) with weights

$$w_i^{(t+1)} = \frac{\psi\left(y_i - \mathbf{x}_i^T \hat{\beta}^{(t)}\right)}{y_i - \mathbf{x}_i^T \hat{\beta}^{(t)}} = \frac{\psi(e_i^{(t)})}{e_i^{(t)}} > 0$$

- Implemented in the `rlm()` function (in the `MASS` package) among others
- By default, scale is estimated using MAD of residuals (updated for each iteration)

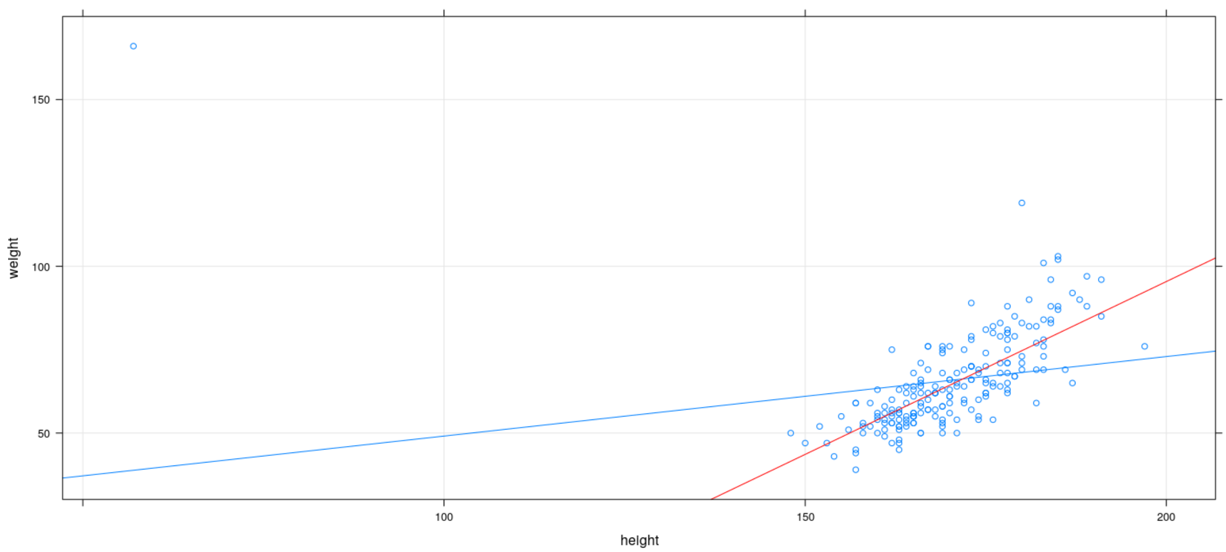
## M-estimation example: Bisquare

```
library(MASS)
fm <- rlm(weight ~ height, data = Davis, psi = psi.bisquare)
xyplot(weight ~ height, Davis, type = c("p", "r"), grid = TRUE) + layer(panel.abline(fm, col = "red"))
```



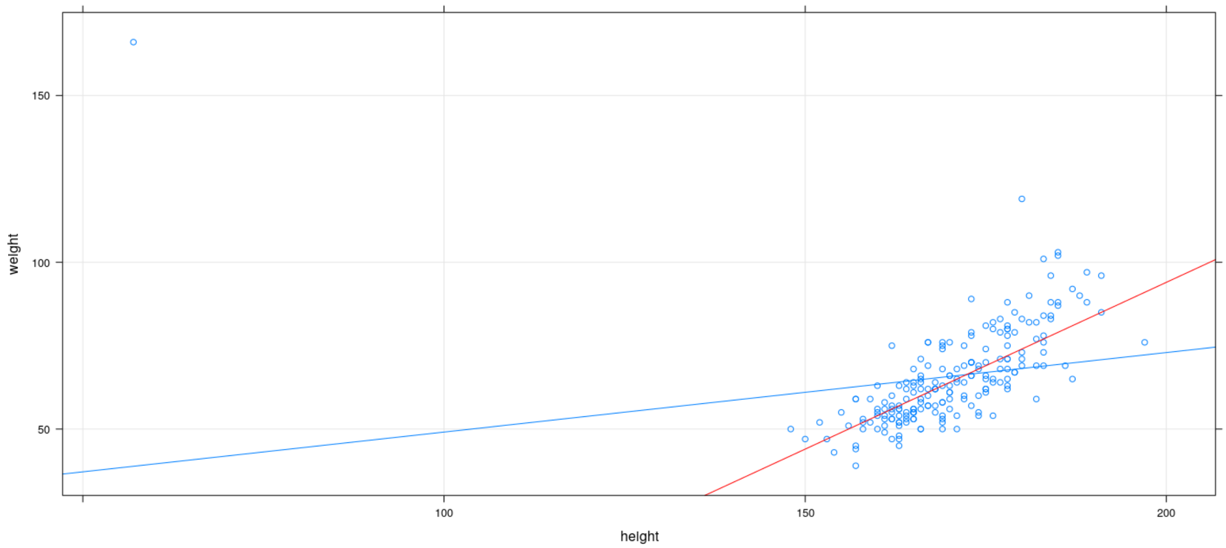

## M-estimation example: Huber

```
library(MASS)
fm <- rlm(weight ~ height, data = Davis, psi = psi.huber)
xyplot(weight ~ height, Davis, type = c("p", "r"), grid = TRUE) + layer(panel.abline(fm, col = "red"))
```




## M-estimation example: Least absolute deviation (using optim())

```
L <- function(p) with(Davis, sum(abs(weight - p[1] - p[2] * height)))
bhat <- optim(coef(fm), L)$par
xyplot(weight ~ height, Davis, type = c("p", "r"), grid = TRUE) + layer(panel.abline(bhat, col = "red"))
```




## M-estimation example: multiple regression

```
fm1 <- lm(prestige ~ income + education, data = Duncan, na.action = na.exclude)
fm2 <- rlm(prestige ~ income + education, data = Duncan, psi = psi.bisquare, na.action = na.exclude)
fm3 <- rlm(prestige ~ income + education, data = Duncan, psi = psi.huber, na.action = na.exclude)
coefficients(summary(fm1))
```

```
              Estimate Std. Error   t value     Pr(>|t|)
(Intercept) -6.0646629 4.27194117 -1.419650 1.630896e-01
income       0.5987328 0.11966735  5.003310 1.053184e-05
education    0.5458339 0.09825264  5.555412 1.727192e-06
```

```
coefficients(summary(fm2))
```

```
                 Value Std. Error   t value
(Intercept) -7.4121192 3.87702087 -1.911808
income       0.7902166 0.10860468  7.276082
education    0.4185775 0.08916966  4.694169
```

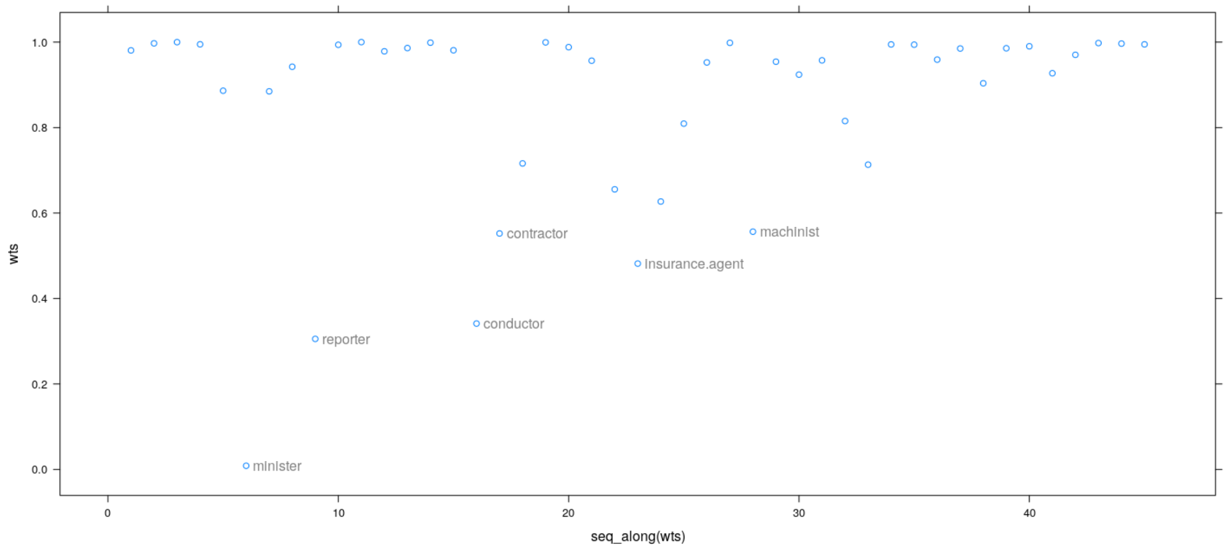
```
coefficients(summary(fm3))
```

```
                 Value Std. Error   t value
(Intercept) -7.1107028 3.88131509 -1.832034
income       0.7014493 0.10872497  6.451593
education    0.4854390 0.08926842  5.437970
```

## M-estimation example: weights as diagnostics

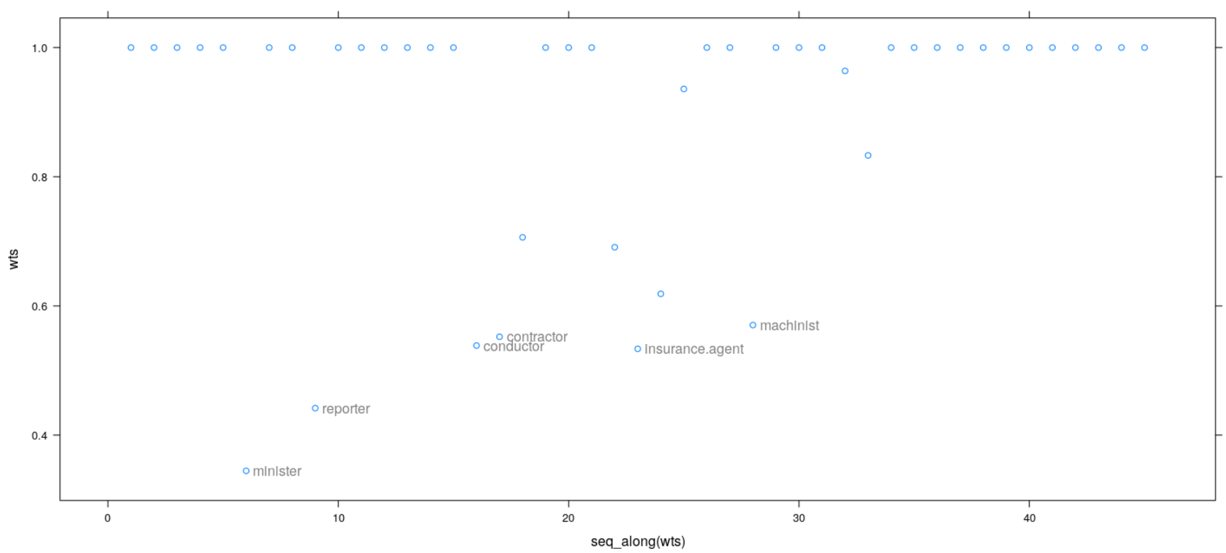
- IWLS weights give an alternative measure of influence

```
wts <- fm2$w # bisquare
id <- which(wts < 0.6)
xyplot(wts ~ seq_along(wts)) +
    layer(panel.text(x[id], y[id], labels = rownames(Duncan)[id], pos = 4, col = "grey50"))
```




- IWLS weights give an alternative measure of influence

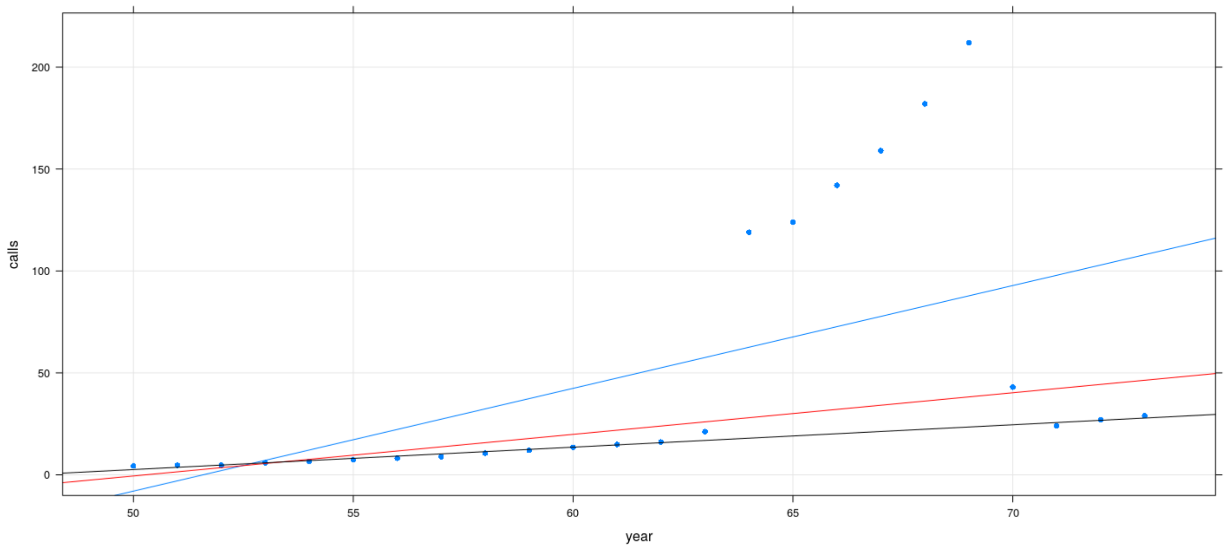
```
wts <- fm3$w # Huber
id <- which(wts < 0.6)
xyplot(wts ~ seq_along(wts)) +
    layer(panel.text(x[id], y[id], labels = rownames(Duncan)[id], pos = 4, col = "grey50"))
```




## Does M-estimation ensure high breakdown point?

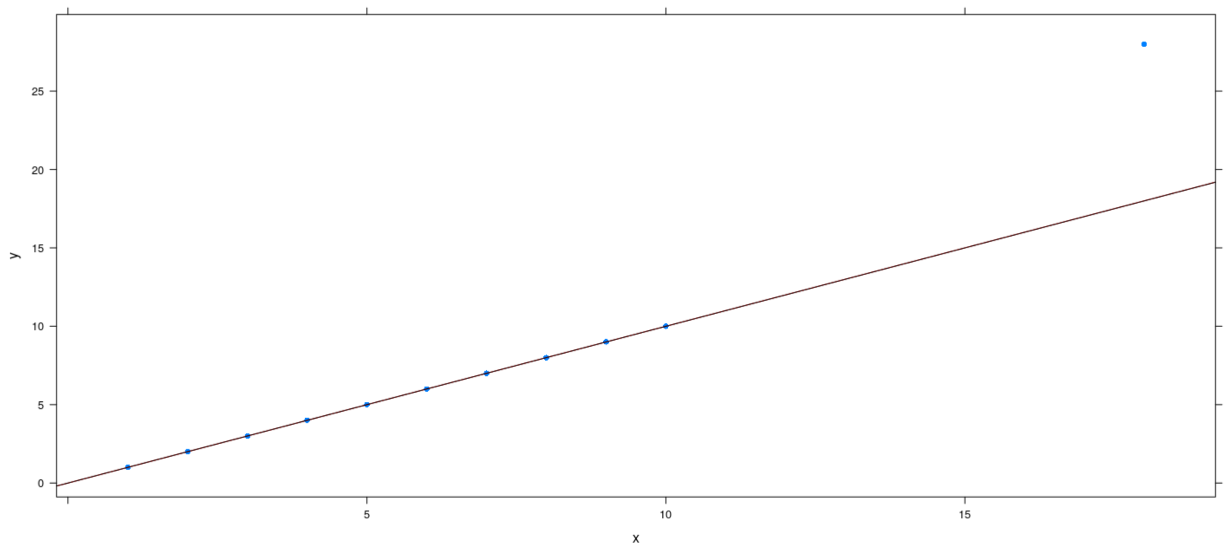
- Example: Number of phone calls (in millions) in Belgium
- Data available in the `MASS` package
- For 1964–1969, length of calls (in minutes) had been recorded instead of number

```r
data(phones, package = "MASS")
fm2 <- rlm(calls ~ year, data = phones, psi = psi.huber, maxit = 100)
fm3 <- rlm(calls ~ year, data = phones, psi = psi.bisquare)
xyplot(calls ~ year, data = phones, grid = TRUE, type = c("p", "r"), pch = 16) +
    layer(panel.abline(fm2, col = "red")) + layer(panel.abline(fm3, col = "black"))
```

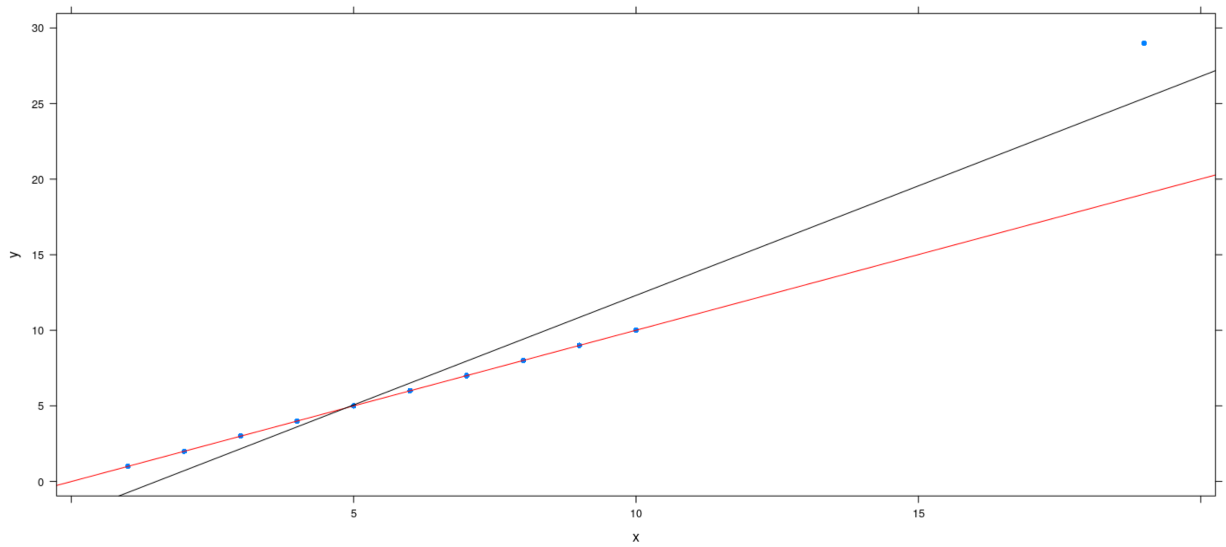



## An artificial example

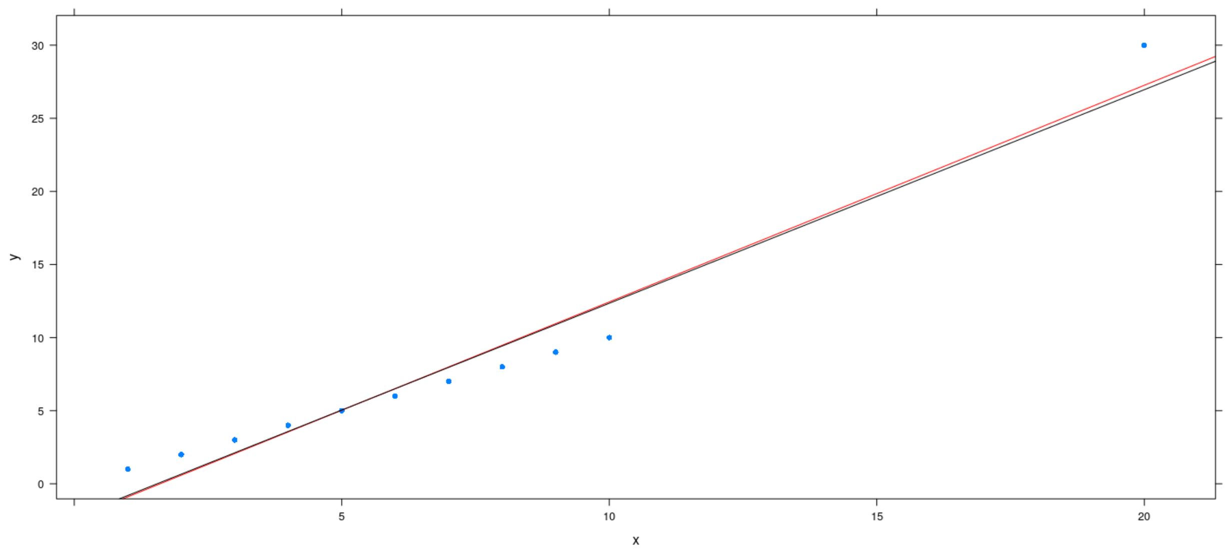
```r
x <- c(1:10, 18)
y <- c(1:10, 18 + 10)
fm.h <- rlm(y ~ x, psi = psi.huber, maxit = 100)
fm.bs <- rlm(y ~ x, psi = psi.bisquare)
xyplot(y ~ x, pch = 16) + layer(panel.abline(fm.h, col = "red")) + layer(panel.abline(fm.bs, col = "bla
```



```
x <- c(1:10, 19)
y <- c(1:10, 19 + 10)
fm.h <- rlm(y ~ x, psi = psi.huber, maxit = 200)
fm.bs <- rlm(y ~ x, psi = psi.bisquare, maxit = 200)
xyplot(y ~ x, pch = 16) + layer(panel.abline(fm.h, col = "red")) + layer(panel.abline(fm.bs, col = "blac
```



```
x <- c(1:10, 20)
y <- c(1:10, 20 + 10)
fm.h <- rlm(y ~ x, psi = psi.huber, maxit = 100)
fm.bs <- rlm(y ~ x, psi = psi.bisquare)
xyplot(y ~ x, pch = 16) + layer(panel.abline(fm.h, col = "red")) + layer(panel.abline(fm.bs, col = "blac
```



## Why does this happen?

- M-estimation approach can ensure high breakdown point for univariate location estimation
- This is not automatically true for regression
- Increasing loss function (LAD, Huber): sufficiently high-leverage outlier can always attract optimum line
- Loss functions that flatten out (Bisquare): result depends on choice of $c$ (which is estimated)
- In general, no guarantee that M-estimation approach has bounded influence in regression

## Resistant regression

- Resistant alternatives exist, but are much more difficult to fit computationally
- We will mention two examples: LMS and LTS regression
- Least Median of Squares (LMS) regression: Find $\hat{\beta}$ as

$$\arg\min_{\beta} \text{median} \left\{ (y_i - \mathbf{x}_i^T \beta)^2; i = 1, \dots, n \right\}$$

- More generally, LQS minimizes some quantile of the squared errors
- Least Trimmed Squares (LTS) regression: Find $\hat{\beta}$ as

$$\arg\min_{\beta} \sum_{i=1}^{q} (y_i - \mathbf{x}_i^T \beta)^2_{(i)}$$

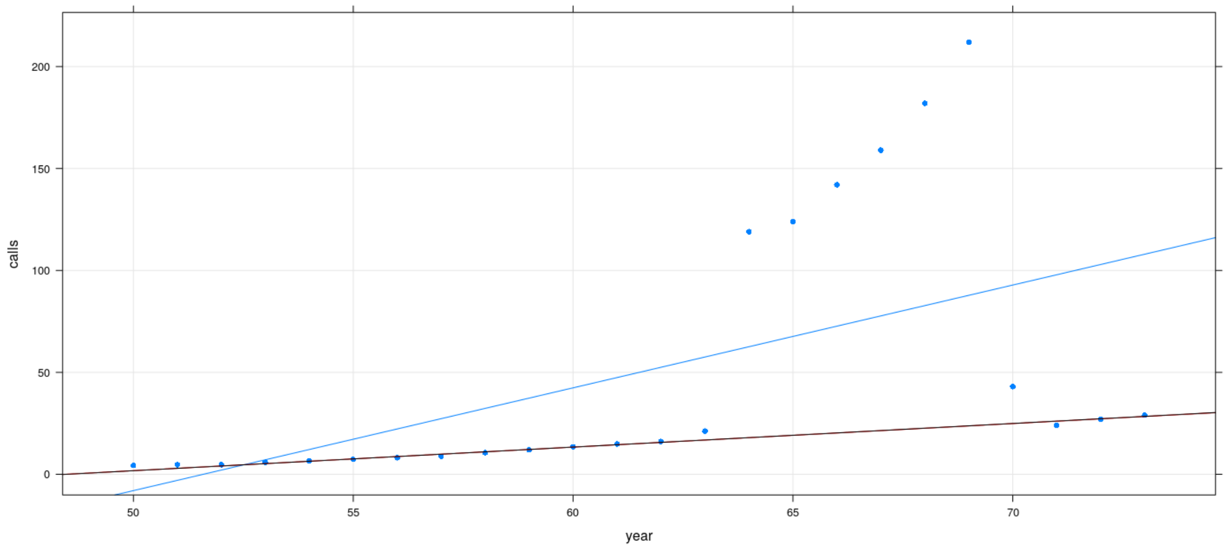
- Here the objective is the sum of the $q$ smallest error terms
- The recommended value of $q$ is $\lfloor (n + p + 1)/2 \rfloor$

## Resistant regression: LMS and LTS

- Both LMS/LQS and LTS have high resistance (breakdown point) but low efficiency
- LMS/LQS has lower efficiency than LTS, and there is no reason to prefer LMS over LTS
- Computation of both are difficult
- The `MASS` package provides one implementation in `lmsreg()` and `ltsreg()`

## Example: Number of phone calls (in millions) in Belgium

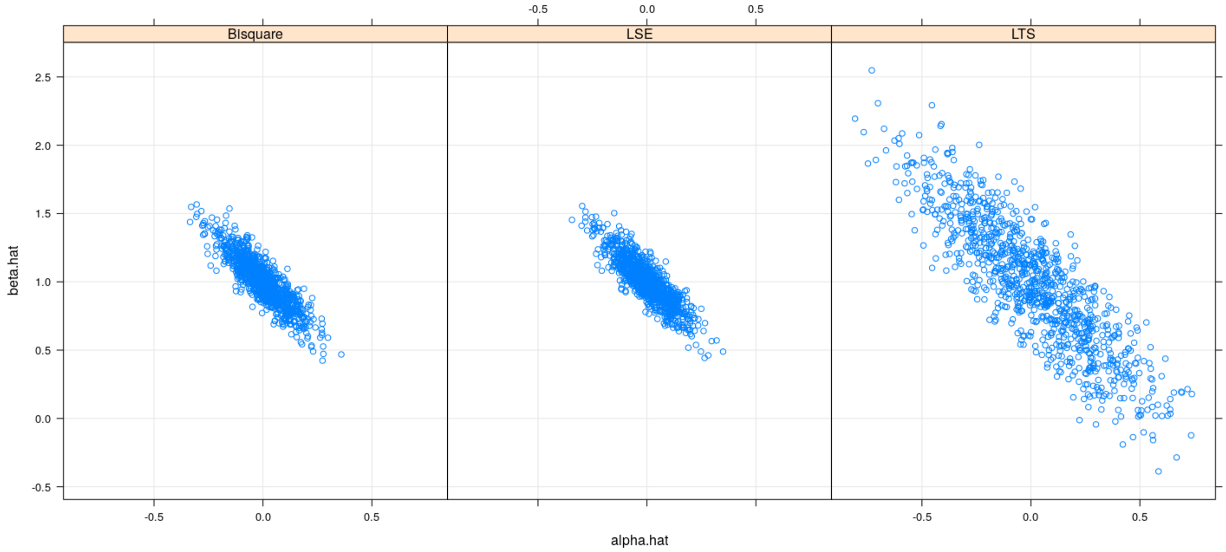
```
data(phones, package = "MASS")
fm2 <- lmsreg(calls ~ year, data = phones)
fm3 <- ltsreg(calls ~ year, data = phones)
xyplot(calls ~ year, data = phones, grid = TRUE, type = c("p", "r"), pch = 16) +
    layer(panel.abline(fm2, col = "red")) + layer(panel.abline(fm3, col = "black"))
```




## Efficiency comparison: simulation study (normal)

```
simulateCoefN <- function(n)
{
    x <- runif(n, 0, 1)
    y <- x + 0.5 * rnorm(n)
    fm1 <- lm(y ~ x)
    fm2 <- rlm(y ~ x, psi = psi.bisquare)
    fm3 <- ltsreg(y ~ x)
    data.frame(rbind(coef(fm1), coef(fm2), coef(fm3)),
               model = c("LSE", "Bisquare", "LTS"))
}
sim.coefsn <- replicate(1000, simulateCoefN(100), simplify = FALSE)
sim.coefsn.df <- do.call(rbind, sim.coefsn)
names(sim.coefsn.df) <- c("alpha.hat", "beta.hat", "model")
```

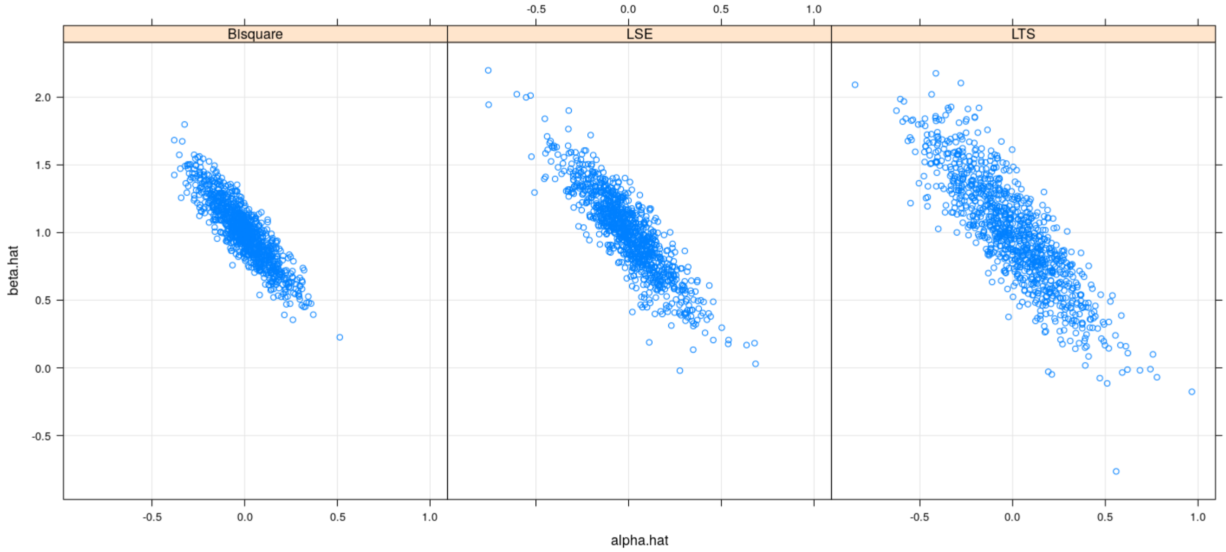
```
xyplot(beta.hat ~ alpha.hat | model, data = sim.coefsn.df, grid = TRUE)
```




## Efficiency comparison: simulation study ($t_3$)

```
simulateCoefT <- function(n)
{
    x <- runif(n, 0, 1)
    y <- x + 0.5 * rt(n, df = 3)
    fm1 <- lm(y ~ x)
    fm2 <- rlm(y ~ x, psi = psi.bisquare)
    fm3 <- ltsreg(y ~ x)
    data.frame(rbind(coef(fm1), coef(fm2), coef(fm3)),
               model = c("LSE", "Bisquare", "LTS"))
}
sim.coefst <- replicate(1000, simulateCoefT(100), simplify = FALSE)
sim.coefst.df <- do.call(rbind, sim.coefst)
names(sim.coefst.df) <- c("alpha.hat", "beta.hat", "model")
```

```
xyplot(beta.hat ~ alpha.hat | model, data = sim.coefst.df, grid = TRUE)
```



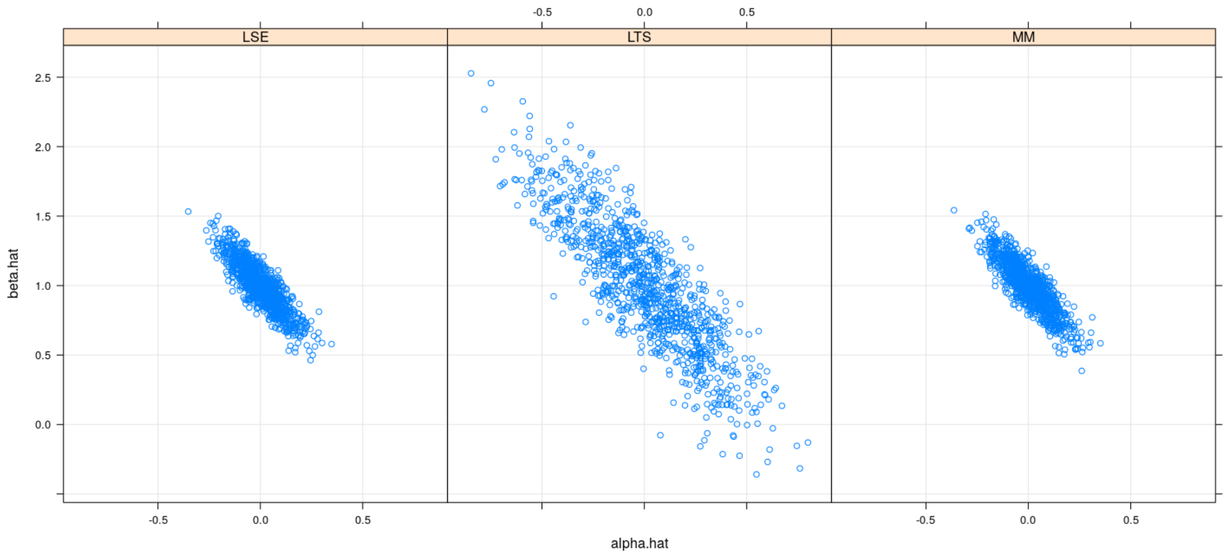

## MM-estimation

- M-estimation with Bisquare error has reasonable efficiency
- Should have high breakdown point if scale is "correctly" estimated
- High breakdown potentially fails if initial scale estimate is too high
- MM-estimation tries to ensure high breakdown point with high efficiency of Bisquare loss
- First step is to obtain a better scale estimate using S-estimation (will not discuss)
- This is followed by M-estimation with Bisquare loss function calibrated by estimated scale
- Implemented in `rlm()` with `method = "MM"`

## Efficiency comparison: simulation study (normal)

```
simulateCoefMM <- function(n)
{
    x <- runif(n, 0, 1)
    y <- x + 0.5 * rnorm(n)
    fm1 <- lm(y ~ x)
    fm2 <- rlm(y ~ x, method = "MM")
    fm3 <- ltsreg(y ~ x)
    data.frame(rbind(coef(fm1), coef(fm2), coef(fm3)),
               model = c("LSE", "MM", "LTS"))
}
sim.coefsmm <- replicate(1000, simulateCoefMM(100), simplify = FALSE)
sim.coefsmm.df <- do.call(rbind, sim.coefsmm)
names(sim.coefsmm.df) <- c("alpha.hat", "beta.hat", "model")
```

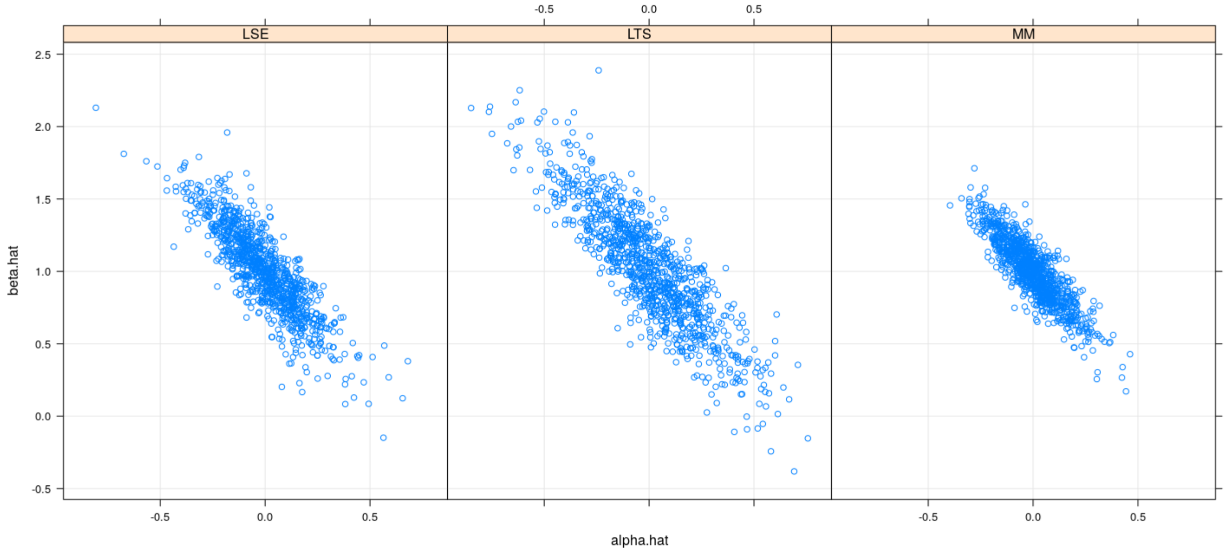
```
xyplot(beta.hat ~ alpha.hat | model, data = sim.coefsmm.df, grid = TRUE)
```




## Efficiency comparison: simulation study ($t_3$)

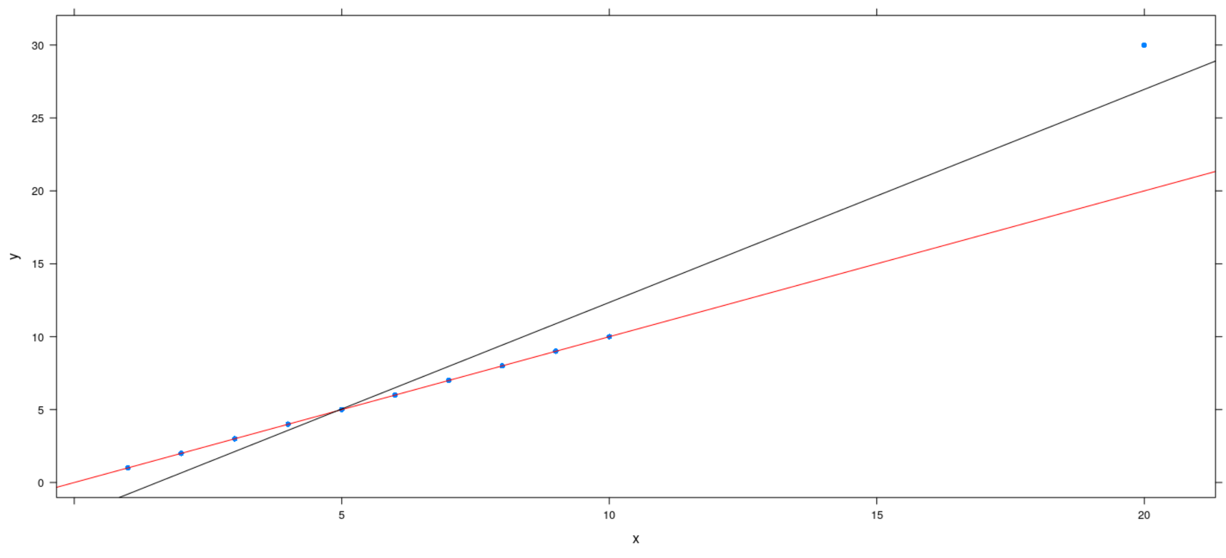
```
simulateCoefMMt <- function(n)
{
    x <- runif(n, 0, 1)
    y <- x + 0.5 * rt(n, df = 3)
    fm1 <- lm(y ~ x)
    fm2 <- rlm(y ~ x, method = "MM")
    fm3 <- ltsreg(y ~ x)
    data.frame(rbind(coef(fm1), coef(fm2), coef(fm3)),
               model = c("LSE", "MM", "LTS"))
}
sim.coefsmmt <- replicate(1000, simulateCoefMMt(100), simplify = FALSE)
sim.coefsmmt.df <- do.call(rbind, sim.coefsmmt)
names(sim.coefsmmt.df) <- c("alpha.hat", "beta.hat", "model")
```

```
xyplot(beta.hat ~ alpha.hat | model, data = sim.coefsmmt.df, grid = TRUE)
```




## Artificial example revisited

```
x <- c(1:10, 20)
y <- c(1:10 + rnorm(10, sd = 0.00001), 20 + 10)
fm.mm <- rlm(y ~ x, method = "MM")
fm.bs <- rlm(y ~ x, psi = psi.bisquare)
xyplot(y ~ x, pch = 16) + layer(panel.abline(fm.mm, col = "red")) + layer(panel.abline(fm.bs, col = "bla
```



## Software implementations in R

- The `MASS` package implements basic robust regression approaches

- For more comprehensive implementations, see the Robust Statistical Methods Task View on CRAN