

## Simple Linear regression

## Checking the model

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The assumptions.

Independent errors?

Predicted values and residuals.

Do the errors have the same distribution?

Normal errors?

Two examples, where the model is not valid.

Leverage: a measure of influence.

Standardized residuals.

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## Simple linear regression: The model

Let  $Y_i$  and  $x_i$  be the data for the  $i$ th person.

$$Y_i = \beta_0 + \beta_1 \cdot x_i + E_i \quad E_i \sim N(0, \sigma^2)$$

This model is based on the assumptions:

1. The expected value of  $Y$  is a linear function of  $x$ .
2. The unexplained random deviations are independent.
3. The unexplained random deviations have the same distributions.
4. This distribution is normal.

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## Checking the model: Independent errors ?

**Assumption no. 2:** the errors should be independent, is mainly checked by considering how the data was collected.

The assumption is violated if

- some of the persons are relatives (and some are not) and the dependent variable have some genetic component.
- some of the persons were measured using one instrument and others using another.
- in general if the persons were sampled in clusters.

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## Predicted values and residuals

$$Y_i = \beta_0 + \beta_1 \cdot x_i + E_i \quad E_i \sim N(0, \sigma^2)$$

Based on the estimates we can calculate the predicted (fitted) values and the residuals:

Predicted value:  $\hat{y}_i = \hat{\beta}_0 + \hat{\beta}_1 \cdot x_i$ Residual:  $r_i = y_i - \hat{y}_i = y_i - (\hat{\beta}_0 + \hat{\beta}_1 \cdot x_i)$ The predicted value is the best guess of  $y_i$  (based on the estimates) for the  $i$ th person.The residual is a guess of  $E_i$  (based on the estimates) for the  $i$ th person.STATA: 

```
predict PEFR_hat if e(sample), xb
predict PEFR_res if e(sample), resid
```

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**Checking the model:  
Linearity and identical distributed errors**

**Assumption no. 1:**

The **expected** value of  $Y$  is a linear function of  $x$ .

**Assumption no. 3:**

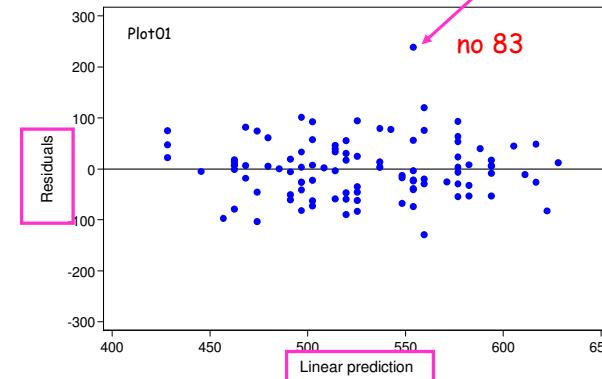
The unexplained random deviations have the **same** distributions.

These are checked by inspecting the following plots of:

- **Residuals versus predicted**
- **Residuals versus  $x$**

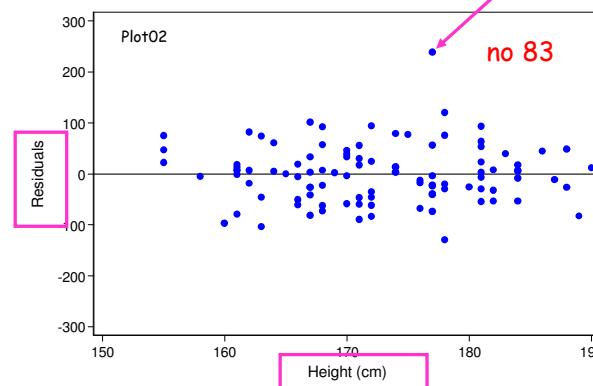
**Checking the model:  
Linearity and identical distributed errors**

No problems! Except this outlier



**Checking the model:  
Linearity and identical distributed errors**

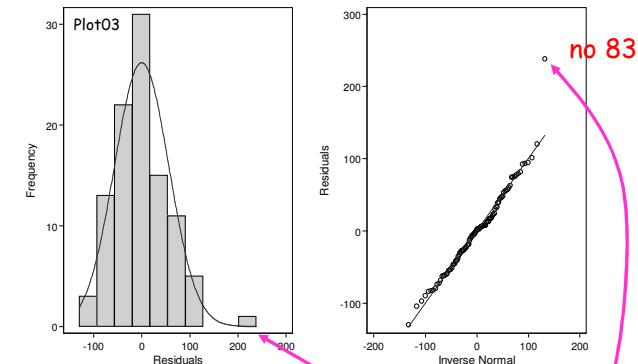
No problems! Except this outlier



**Checking the model: Normal errors ?**

**Assumption no. 4:** the errors should be **normal distributed**.

This is checked by making histograms or qq-plots of the residuals:

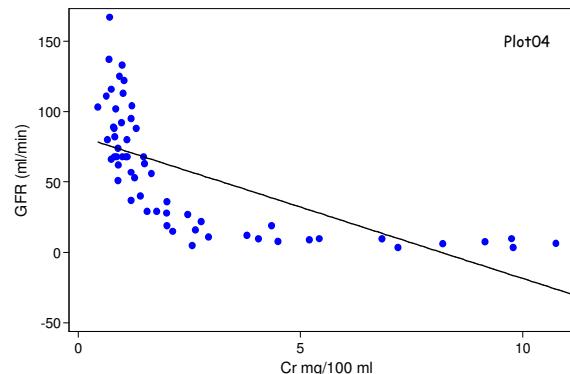


Not perfect, a bit skew.

Notice this point

**Assumptions violated: Example 2**

The relation between GFR and Serum Creatinine

**Clearly non-linear!**

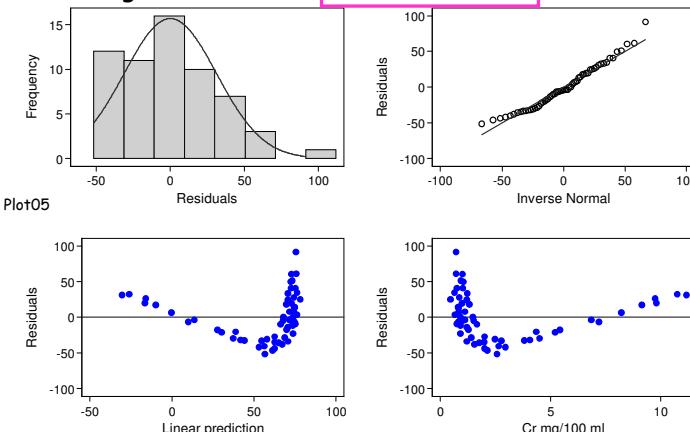
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**Assumptions violated: Example 2**

Checking the model

**Close to normal****Clearly not constant mean!**

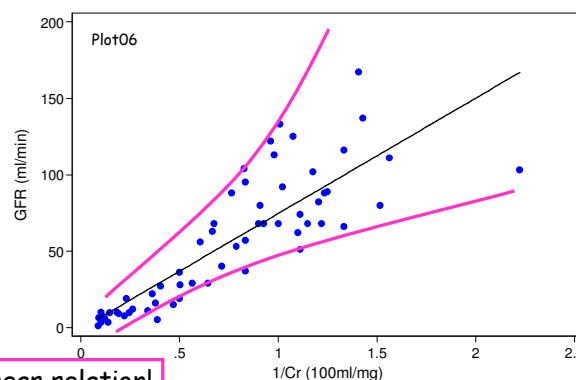
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**Assumptions violated: Example 3**

The relation between GFR and 1/Serum Creatinine

**A linear relation!****Increasing variation!**

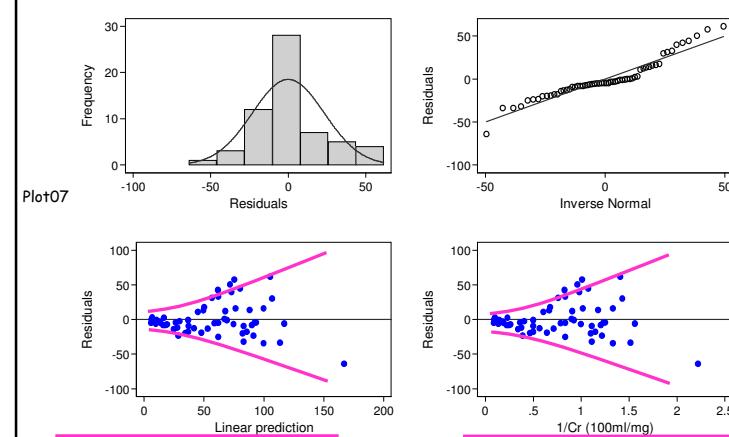
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**Assumptions violated: Example 3**

Checking the model

**Close to normal****Increasing variation!**

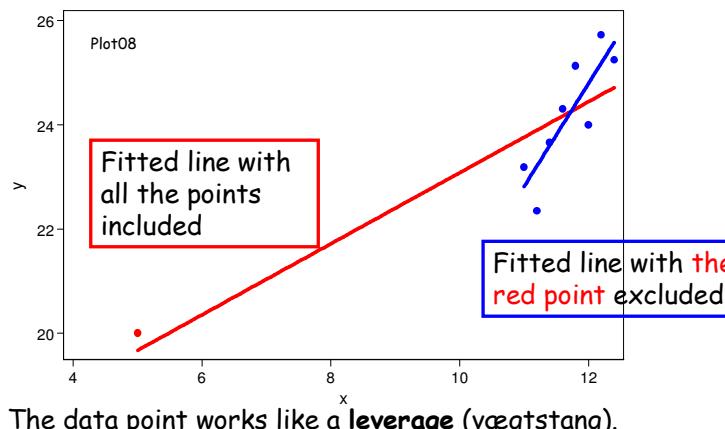
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### Influential data points: Example 4

Not all data points have the same influence on the estimates:



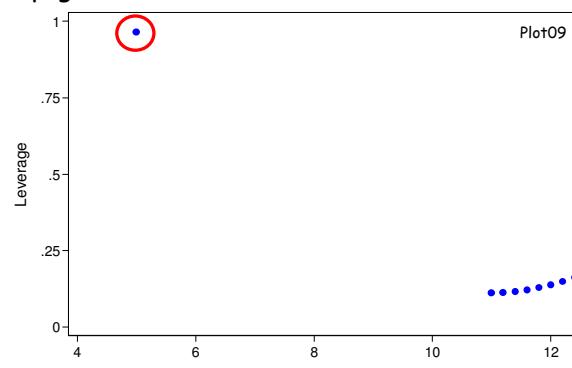
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### Influential data points Leverage

A leverage versus independent variable for the example on page 13.



The data point with the 'extreme'  $x$  value has very high leverage - as expected.

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### Influential data points: Leverage

The influence of a data point is sometimes measured by its leverage:

$$h_i = \frac{1}{n} + \frac{(x_i - \bar{x})^2}{\sum_{j=1}^n (x_j - \bar{x})^2}$$

Large values imply that the estimates and/or the standard errors is highly influenced by this observation.

$$0 \leq h_i \leq 1$$

Notice, it is a function only of the independent variable,  $x$  and the sample size.

The leverage for a given data point depends on how far away its independent variable is from the average value.

STATA: `predict PEFR_lev if e(sample), leverage`

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### Types of residuals: Standardized residuals

The (unstandardized) residual:  $r_i = y_i - (\hat{\beta}_0 + \hat{\beta}_1 \cdot x_i)$

Has mean zero but non-constant variance:  $sd(r_i) = \sigma \sqrt{1 - h_i}$

I. e. residuals from points with high leverage have smaller variance, than residuals from points with small leverage.

Due to this one often use the standardized residual:

$$z_i = \frac{r_i}{\hat{\sigma} \sqrt{1 - h_i}}$$

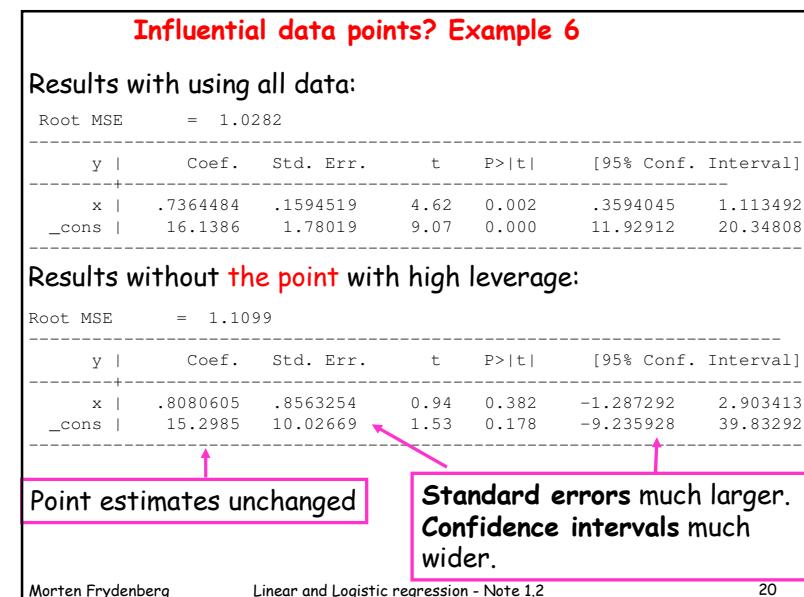
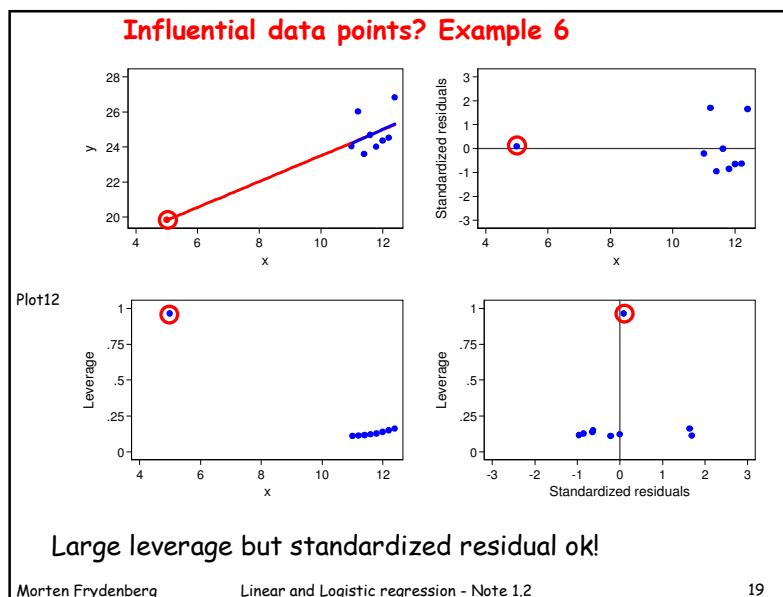
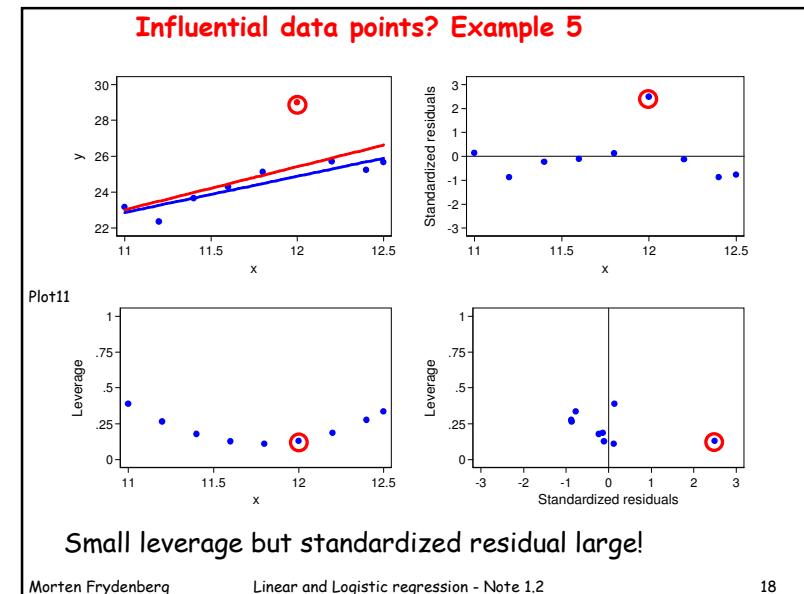
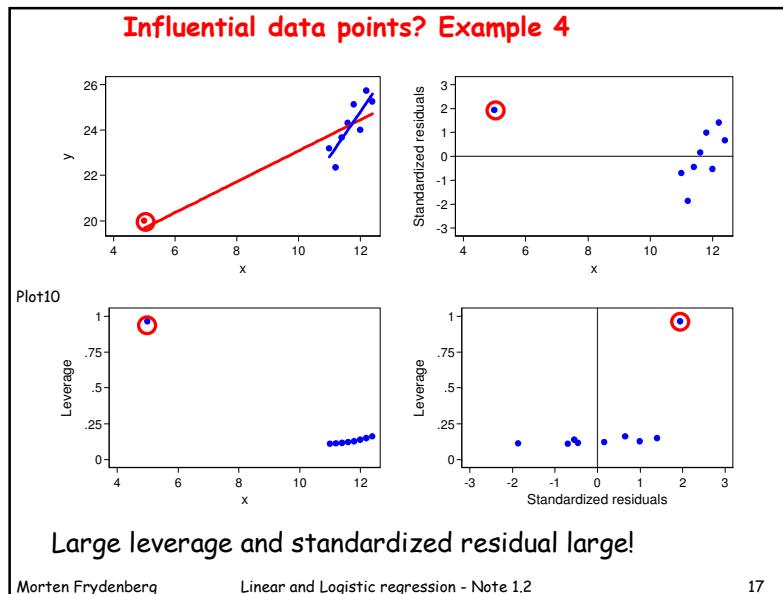
This will have variance 1, if the model is true.

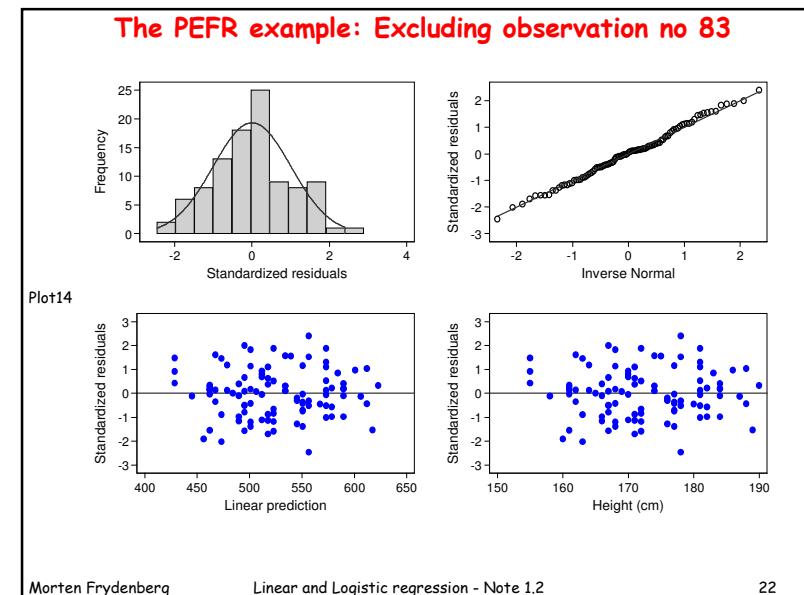
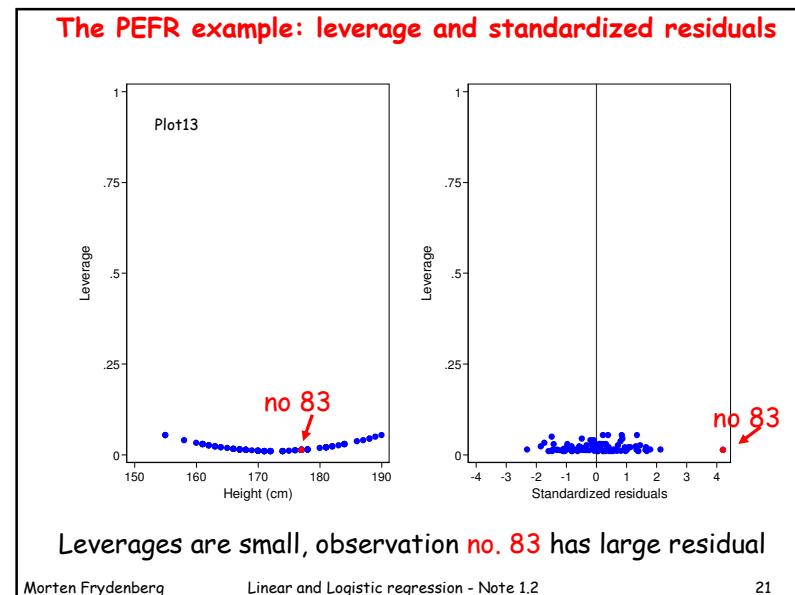
STATA: `predict PEFR_zres if e(sample), rstandard`

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**Some comments on checking a (simple) linear regression**

Always consider the design: **How was the data collected?**  
This has implications for the validity of the **statistical model**.  
And it has implications for the **interpretation** of the results.  
Observations with **high leverages** have 'extreme' values of the **independent variable**.  
These observations will have **high impact** on the results, but might not be 'representative'.  
Sometimes it is best to **exclude** these from the analysis.  
Observation with **large residuals**, that is observed **y** value far away from expected, should be **checked for errors**.

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**Prediction interval for future value**

The **true line** is given as :  $y = \beta_0 + \beta_1 \cdot x$   
and **estimated** by plugging in the estimates  $\hat{y} = \hat{\beta}_0 + \hat{\beta}_1 \cdot x$   
The standard **deviation** for a **new observation** is given by:  

$$sd(\hat{\beta}_0 + \hat{\beta}_1 \cdot x + E) = \hat{\sigma} \sqrt{1 + \frac{1}{n} + \frac{(x - \bar{x})^2}{\sum (x_i - \bar{x})^2}}$$
with the 95% (pointwise) **prediction interval**  

$$\hat{\beta}_0 + \hat{\beta}_1 \cdot x \pm t_{n-2}^{0.975} \cdot sd(\hat{\beta}_0 + \hat{\beta}_1 \cdot x + E)$$
Many programs can make a plot with the fitted line and its prediction limits.  
In STATA its done by the `lfitci` and `graph` command, the option `stdf`

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