Regression analysis Two variables

(Montgomery and Runger: ch 11 Brani Vidakovic: ch 14)

Reminder

Covariance Defined

Covariance is a number qunatifying average dependence between two random variables.

The covariance between the random variables X and Y, denoted as cov(X,Y) or σ_{XY} is

$$\sigma_{XY} = E\left[\left(X - \mu_X\right)\left(Y - \mu_Y\right)\right] = E\left(XY\right) - \mu_X \mu_Y \tag{5-14}$$

The units of σ_{XY} are units of X times units of Y.

Unlike the range of variance, $-\infty < \sigma_{xy} < \infty$.

Correlation is "normalized covariance"

Also called:
 Pearson correlation
 coefficient

 $\rho_{XY} = \sigma_{XY} / \sigma_X \sigma_Y$ is the covariance normalized to be $-1 \le \rho_{XY} \le 1$



Karl Pearson (1852–1936) English mathematician and biostatistician

Covariance and Scatter Patterns

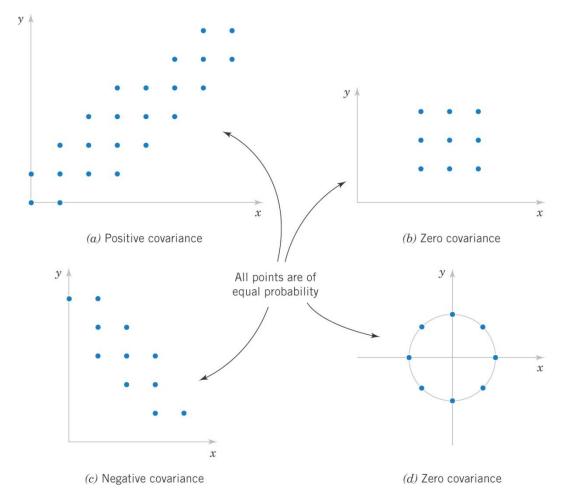


Figure 5-13 Joint probability distributions and the sign of cov(X, Y). Note that covariance is a measure of linear relationship. Variables with non-zero covariance are correlated.

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Credit: XKCD comics

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WHY AREN'T THERE GUNS IN HARRY POTTER

WHY ARE THERE

SQUIRRELS

WHY ARE THERE **GHOSTS**

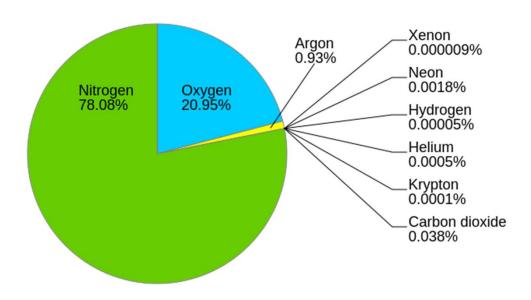
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Regression analysis

- Many problems in engineering and science involve sample in which two or more variables were measured
- Regression analysis is a statistical technique that is very useful for these types of problems
- Everyday example: in most samples height and weight of people are related to each other
- Biological example: in a cell sorting experiment the copy number of a protein may be measured alongside its volume
- Regression analysis uses a sample to build a model to predict protein copy number given a cell volume

Two variable samples



Oxygen can be distilled from the air

- Hydrocarbons need to be filtered out or the whole thing would go kaboom!!!
- The more hydrocarbons were removed the cleaner is the remaining oxygen
- Except we don't know how dirty was the air to begin with

Table 11-1 Oxygen and Hydrocarbon Levels

Observation Number	Hydrocarbon Level $x(\%)$	Purity y(%)
1	0.99	90.01
2	1.02	89.05
3	1.15	91.43
4	1.29	93.74
5	1.46	96.73
6	1.36	94.45
7	0.87	87.59
8	1.23	91.77
9	1.55	99.42
10	1.40	93.65
11	1.19	93.54
12	1.15	92.52
13	0.98	90.56
14	1.01	89.54
15	1.11	89.85
16	1.20	90.39
17	1.26	93.25
18	1.32	93.41
19	1.43	94.98
20	0.95	87.33

Scatter plot to visually detect trends Red line is called linear regression

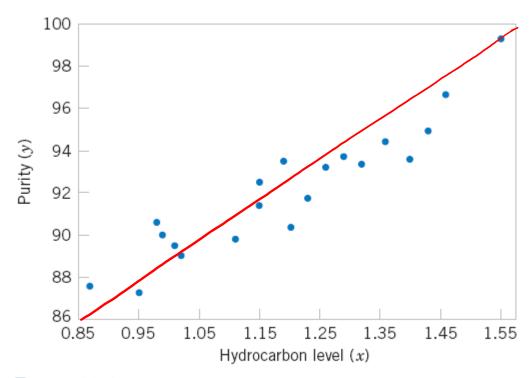
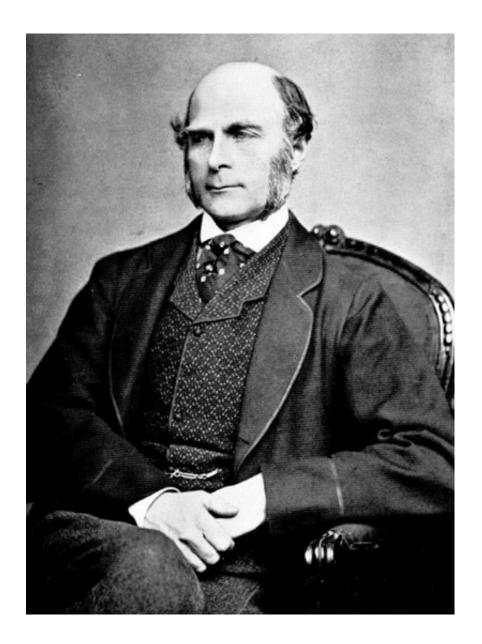


Figure 11-1 Scatter diagram of oxygen purity versus hydrocarbon level from Table 11-1.



Sir Francis Galton, (1822 -1911) was an English statistician, anthropologist, proto-geneticist, psychometrician, eugenicist, ("Nature vs Nurture", inheritance of intelligence), tropical explorer, geographer, inventor (Galton Whistle to test hearing), meteorologist (weather map, anticyclone).

Invented both correlation and regression analysis when studied heights of fathers and sons

Found that fathers with height above average tend to have sons with height also above average but closer to the average. Hence "regression" to the mean



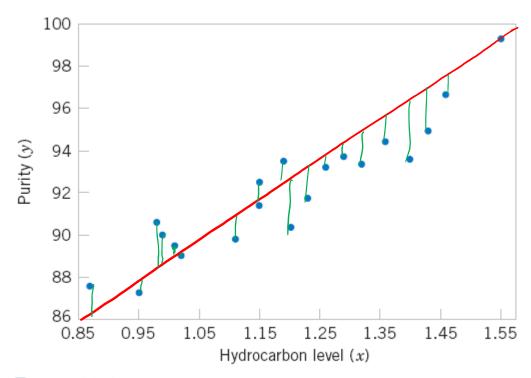


Figure 11-1 Scatter diagram of oxygen purity versus hydrocarbon level from Table 11-1.

$$Y = \beta_0 + \beta_1 \times + \epsilon$$

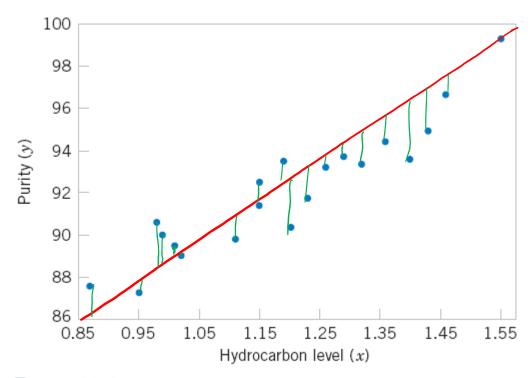


Figure 11-1 Scatter diagram of oxygen purity versus hydrocarbon level from Table 11-1.

Linear regression

The simple linear regression model is given by

$$Y = \beta_0 + \beta_1 X + \varepsilon$$

ε is the random error term

slope β_1 and intercept β_0 of the line are called regression coefficients

Note: Y, X and ε are random variables The minimal assumption: $E(\varepsilon \mid x) = 0 \rightarrow E(Y \mid x) = \beta_0 + \beta_1 x + E(\varepsilon \mid x) = \beta_0 + \beta_1 x$

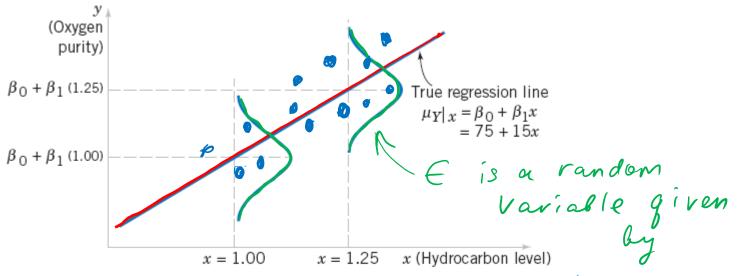


Figure 11-2 The distribution of Y for a given value of x for the expression oxygen purity—hydrocarbon data.

$$E(e|x) = 0$$
 for all x

Y=
$$\beta_0 + \beta_1 \times + \epsilon$$
; $E(\epsilon|x)=0$ $\forall x$
How does one find $\beta_0 k \beta_1$?
 $Cov(Y,X) = Cov((\beta_0 + \beta_1 \times + \epsilon), \xi)$:
 $= Cov(\beta_0,X) + \beta_1 Cov(X,X) + Cov(\xi,X)$
 $Cov(\beta_0,X)=0$ Since β_0 is constant
 $Cov(X,X)=E(X^2)-E(X)^2=Vax(X)$
 $Cov(\xi,X)=E(\epsilon \cdot X)-E(\xi)\cdot E(X)=$
 $= E(\epsilon \cdot X)=\sum_{\alpha \neq i,x} x \cdot E(\xi \mid x)=0$
Thus $\beta_1 = \frac{Cov(X,V)}{Var(X)}$, $\beta_0 = E(Y)-\beta_1 E(X)$

Method of least squares

• The method of least squares is used to estimate the parameters, β_0 and β_1 by minimizing the sum of the squares of the vertical deviations in

Figure 11-3.

Figure 11-3 Deviations of the data from the estimated regression model.

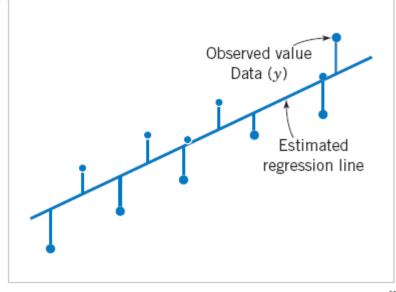


Figure 11-3 Deviations of the data from the estimated regression model.

Traditional notation

Definition

The **least squares estimates** of the intercept and slope in the simple linear regression model are

$$\hat{\beta}_0 = \overline{y} - \hat{\beta}_1 \overline{x} \tag{11-7}$$

$$\hat{\beta}_{1} = \frac{\sum_{i=1}^{n} y_{i} x_{i} - \frac{\left(\sum_{i=1}^{n} y_{i}\right) \left(\sum_{i=1}^{n} x_{i}\right)}{n}}{\sum_{i=1}^{n} x_{i}^{2} - \frac{\left(\sum_{i=1}^{n} x_{i}\right)^{2}}{n}} = \frac{\sum_{i=1}^{n} y_{i} x_{i} - \frac{\sum_{i=1}^{n} x_{i}}{n}}{\sum_{i=1}^{n} x_{i}^{2} - \frac{\sum_{i=1}^{n} x_{i}}{n}}$$
(11-8)

where $\overline{y} = (1/n) \sum_{i=1}^{n} y_i$ and $\overline{x} = (1/n) \sum_{i=1}^{n} x_i$.

11-2: Simple Linear Regression

Definition

The **least squares estimates** of the intercept and slope in the simple linear regression model are

$$\hat{\beta}_{0} = \overline{y} - \hat{\beta}_{1}\overline{x}$$

$$\hat{\beta}_{1} = \frac{\sum_{i=1}^{n} y_{i} x_{i}}{\sum_{i=1}^{n} y_{i}} - \frac{\left(\sum_{i=1}^{n} y_{i}\right)\left(\sum_{i=1}^{n} x_{i}\right)}{n^{2}} = \frac{Cov\left(X,Y\right)}{\sqrt{gv\left(X\right)}}$$

$$\sum_{i=1}^{n} x_{i}^{2} - \frac{\left(\sum_{i=1}^{n} x_{i}\right)^{2}}{n^{2}} = \frac{Vgv\left(X\right)}{\sqrt{gv\left(X\right)}}$$
(11-8)

where $\overline{y} = (1/n) \sum_{i=1}^{n} y_i$ and $\overline{x} = (1/n) \sum_{i=1}^{n} x_i$.

11-4.2 Analysis of Variance Approach to Test Significance of Regression

The analysis of variance identity is

$$\sum_{i=1}^{n} (y_i - \overline{y})^2 = \sum_{i=1}^{n} (\hat{y}_i - \overline{y})^2 + \sum_{i=1}^{n} (y_i - \hat{y}_i)^2$$
 (11-24)

Symbolically,

$$SS_T = SS_R + SS_E ag{11-25}$$

11-7: Adequacy of the Regression Model

11-7.2 Coefficient of Determination (R²) <u>VERY USEFUL</u>

• The quantity

$$R^2 = \frac{SS_R}{SS_T} = 1 - \frac{SS_E}{SS_T}$$

is called the **coefficient of determination** and is often used to judge the adequacy of a regression model.

- $0 \le R^2 \le 1$;
- We often refer (loosely) to R² as the amount of variability in the data explained or accounted for by the regression model.

11-7: Adequacy of the Regression Model

11-7.2 Coefficient of Determination (R²)

• For the oxygen purity regression model,

$$R^2 = SS_R/SS_T$$

= 152.13/173.38
= 0.877

• Thus, the model accounts for 87.7% of the variability in the data.

11-2: Simple Linear Regression

Estimating σ_{ϵ}^2

The error sum of squares is

$$SS_E = \sum_{i=1}^n e_i^2 = \sum_{i=1}^n (y_i - \hat{y}_i)^2 = (N - 2) \frac{1}{6} e^{-\frac{1}{2}}$$

11-3: Properties of the Least Squares Estimators

Slope Properties

$$E(\hat{\beta}_1) = \beta_1$$

• Intercept Properties

$$V(\hat{\beta}_1) = \frac{\sigma^2}{S_{xx}} = \frac{\delta_{\epsilon}^2}{n \delta_{x}^2}$$

$$Large \quad n \rightarrow Small \\ variance \\ of \beta_1$$

$$E(\hat{\beta}_0) = \beta_0 \quad \text{and} \quad V(\hat{\beta}_0) = \sigma^2 \left[\frac{1}{n} + \frac{\bar{x}^2}{S_{xx}} \right] =$$

$$= \hat{S}_2^2 \left[1 + \frac{V^2}{S_x^2} \right]^{-1}$$

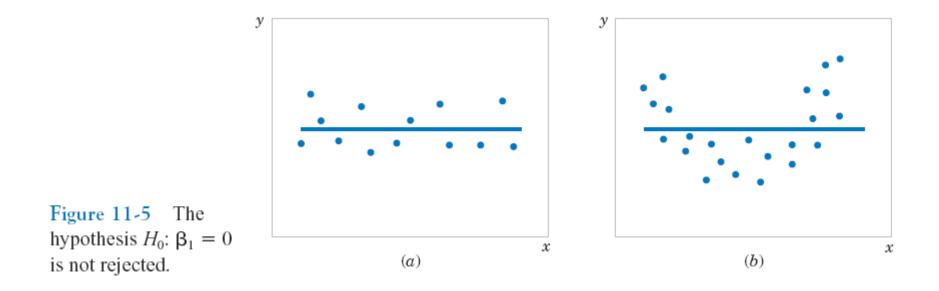


Figure 11-5 The null hypothesis H_0 : $\beta_1 = 0$ is accepted.

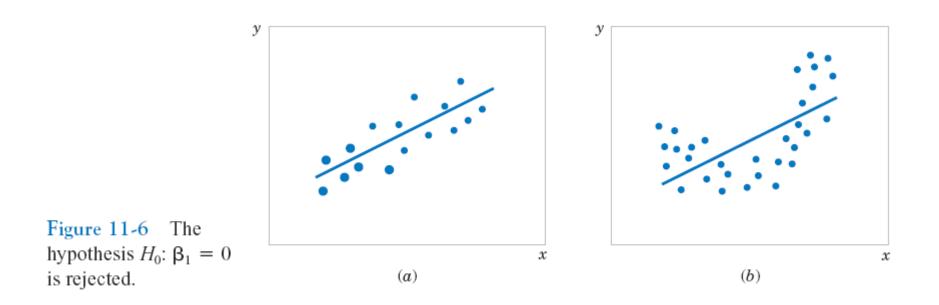


Figure 11-6 The null hypothesis H_0 : $\beta_1 = 0$ is rejected.

11-4.1 Use of *t*-Tests

An important special case of the hypotheses of Equation 11-18 is

$$H_0: \beta_1 = 0$$

$$H_1: \beta_1 \neq 0$$

These hypotheses relate to the **significance of regression**. *Failure* to reject H_0 is equivalent to concluding that there is no linear relationship between X and Y.

$$H_{0}: \beta_{1} = 0 \qquad \text{Choose d}$$

$$H_{1}: \beta_{1} \neq 0 \qquad \text{(e.g. d=5\%)}$$

$$\text{for 95\%}$$

$$\text{confidence}$$

$$\text{In rejecting}$$

$$H_{0})$$

$$\text{For d=5\%}$$

$$\text{Reject H_{0} -f $|Z$} > Z_{2/2}^{-1.96}$$

T-cell expression data

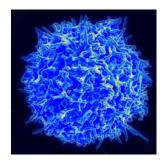
- The matrix contains 47 expression samples from Lukk et al,
 Nature Biotechnology 2011
- All samples are from <u>T cells in different individuals</u>
- Only the top 3000 genes with the largest variability were used
- The value is log2 of gene's expression level in a given sample as measured by the microarray technology

A global map of human gene expression

Margus Lukk, Misha Kapushesky, Janne Nikkilä, Helen Parkinson, Angela Goncalves, Wolfgang Huber, Esko Ukkonen & Alvis Brazma

Affiliations | Corresponding author

Nature Biotechnology 28, 322-324 (2010) | doi:10.1038/nbt0410-322



Although there is only one human genome sequence, different genes are expressed in many different cell types and tissues, as well as in different developmental stages or diseases. The structure of this 'expression space' is still largely unknown, as most transcriptomics experiments focus on sampling small regions. We have constructed a global gene expression map by integrating microarray data from 5,372 human samples representing 369 different cell and tissue types, disease states and cell lines. These have been compiled in an online resource (http://www.ebi.ac.uk/gxa/array/U133A) that allows the user to search for a gene of interest and

Gene Expression "Wheel of Fortune"

- Each group gets a pair of genes that are known to be correlated.
- Each group will also get a random pair of genes selected by the "Wheel of Fortune". They may or may not be correlated
- Download (log-transformed) expression_table.mat
- Run command fitlm(x,y) on assigned and random pairs
- Record β_0 , β_1 , R^2 , P-value of the slope β_1 and write them on the blackboard
- Validate Matlab result for R² using your own calculations
- Look up gene names (see gene_description)
 and write down a brief description of
 biological functions of genes. Does
 their correlation make biological sense?



Correlated pairs

2907	2881
1994	188
2274	1597
2982	1353
2872	1269
1321	10
2935	1654
2745	1695
886	819
2138	1364

Random pairs

```
>> g1=floor(3000.*rand)+1; g2=floor(3000.*rand)+1;
disp([g1,g2]);
>> g1=floor(3000.*rand)+1; g2=floor(3000.*rand)+1;
disp([g1,g2]);
>> g1=floor(3000.*rand)+1; g2=floor(3000.*rand)+1;
disp([g1,g2]);
>> g1=floor(3000.*rand)+1; g2=floor(3000.*rand)+1;
disp([g1,g2]);
```

Matlab code

```
    load expression table.mat

• g1=2907; g2=288;
x=exp(g1,:)'; y=exp(g2,:)';
figure; plot(x,y,'ko');
lm=fitlm(x,y)
y fit=lm.Fitted;
hold on; plot(x,lm.Fitted,'r-');

    SST=sum((y-mean(y)).^2);

SSR=sum((y fit-mean(y)).^2);

    SSE=sum((y-y fit).^2);

    R2=SSR./SST

disp([gene names(g1), gene_names(g2)]);
```

disp(gene description(g1)); disp(gene description (g2));

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