

Lecture 8:

Statistics for Data Science



Markus Hohle
University California, Berkeley

Numerical Methods for Computational Science



Numerical Methods for Computational Science

Course Map

Week 1: Introduction to Scientific Computing and Python Libraries

Week 2: Linear Algebra Fundamentals

Week 3: Vector Calculus

Week 4: Numerical Differentiation and Integration

Week 5: Solving Nonlinear Equations

Week 6: Probability Theory Basics

Week 7: Random Variables and Distributions

Week 8: Statistics for Data Science

Week 9: Eigenvalues and Eigenvectors

Week 10: Simulation and Monte Carlo Method

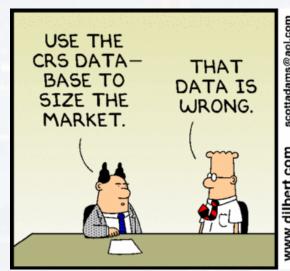
Week 11: Data Fitting and Regression

Week 12: Optimization Techniques

Week 13: Machine Learning Fundamentals

<u>Outline</u>

- Expectation, Variance, and Covariance
- Hypothesis Testing
- Confidence Intervals

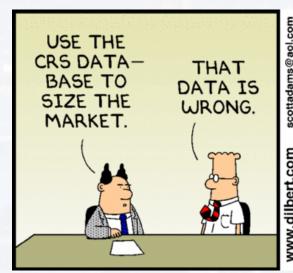


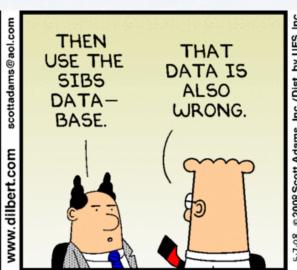




Outline

- Expectation, Variance, and Covariance
- Hypothesis Testing
- Confidence Intervals







the mean μ

the variance σ^2

(barycenter)

(natural scatter)

$$\mu = E(x) = \sum_{i} x_i \, p(x_i)$$

$$\sigma^2 = var(x) = \sum_i (x_i - \mu)^2 p(x_i)$$

$$\mu = E(x) = \int x \, p(x) \, dx$$

$$\sigma^2 = var(x) = \int (x - \mu)^2 p(x) dx$$

$$\mu = E(x) = \int x \, p(x) \, dx$$

$$\sigma^2 = var(x) = \int (x - \mu)^2 p(x) dx$$

$$var(x) = \int (x - \mu)^2 p(x) dx = E([x - \mu]^2)$$

variance can be interpreted as mean of $[x - \mu]^2$

$$= E(x^{2} - 2x\mu + \mu^{2})$$

$$= \int [x^{2} - 2x\mu + \mu^{2}] p(x) dx$$

$$= \int x^{2} p(x) dx - 2\mu \int x p(x) dx + \mu^{2} \int p(x) dx$$

$$= E(x^{2}) - 2\mu E(x) + \mu^{2} E(1)$$

$$= E(x^{2}) - 2\mu E(x) + \mu^{2}$$

$$= E(x^{2}) - 2\mu E(x) + \mu^{2}$$

$$= \mu = E(x)$$

$$\sigma^2 = E(x^2) - E(x)^2$$

$$\sigma^2 = E(x^2) - E(x)^2$$

plotting two sets of random number: x_1 and x_2

$$x1 = np.random.normal(0,2,(1000,))$$

x2 = np.random.normal(0,2,(1000,))

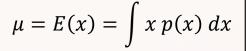
plt.scatter(x1, x2, color = 'k', alpha = 0.1, edgecolor = 'none')

plt.xlabel('\$x_1\$')

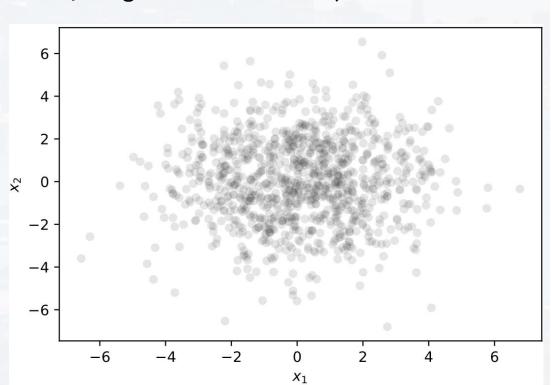
plt.ylabel('\$x_2\$')

 x_1 and x_2 are unrelated and mutually **independent**

→ featureless data cloud



$$\sigma^2 = var(x) = \int (x - \mu)^2 p(x) dx$$



$$\sigma^2 = E(x^2) - E(x)^2$$

plotting two sets of random number: x_1 and x_2

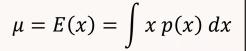
x1 = np.random.normal(0,2,(1000,))

x2 = np.random.normal(0, 20, (1000,))

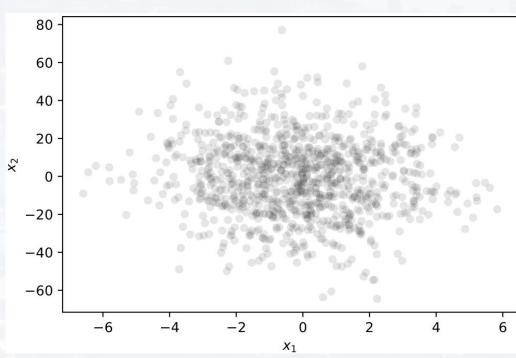
plt.scatter(x1, x2, color = 'k', alpha = 0.1, edgecolor = 'none')

plt.xlabel('\$x_1\$')
plt.ylabel('\$x_2\$')

 x_1 and x_2 are unrelated and mutually **independent** \rightarrow featureless data cloud



$$\sigma^2 = var(x) = \int (x - \mu)^2 p(x) dx$$



 $\mu = E(x) = \int x \, p(x) \, dx$

 $\sigma^2 = var(x) = \int (x - \mu)^2 p(x) dx$

Berkeley Statistics for Data Science:

$$\sigma^2 = E(x^2) - E(x)^2$$

plotting two sets of random number: x_1 and x_2

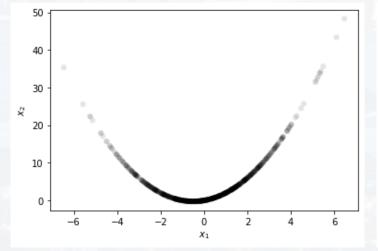
$$x1 = np.random.normal(0,2,(1000,))$$

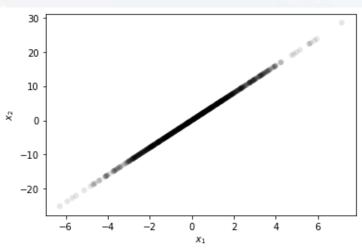
 $x2 = x1**2 + x1$
 $\#x2 = 4*x1$

```
plt.scatter(x1, x2, color = 'k', alpha = 0.1, edgecolor = 'none')
plt.xlabel('$x_1$')
plt.ylabel('$x_2$')
```

based on the shape of the data cloud

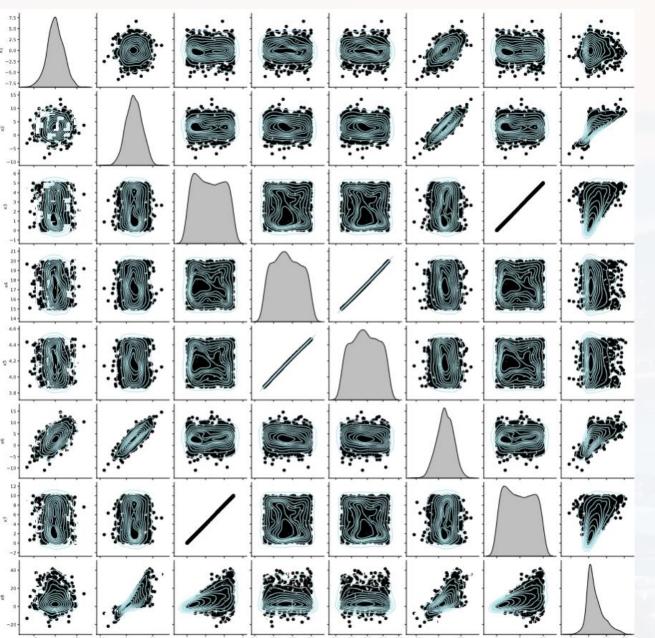
 \rightarrow prediction how x_1 and x_2 are related, i. e. how they **correlate**





```
\mu = E(x) = \int x \, p(x) \, dx
|\sigma^2 = E(x^2) - E(x)^2|
x1 = np.random.normal(0,2,(1000,))
                                                            \sigma^2 = var(x) = \int (x - \mu)^2 p(x) dx
x2 = np.random.normal(3,3,(1000,))
x3 = np.random.uniform(0,5,(1000,))
x4 = 5*np.random.uniform(3,4,(1000,))
x5 = np.sqrt(x4)
x6 = x1 + x2
x7 = 2*x3
x8 = x3*x2
All = np.vstack((x1, x2, x3, x4, x5, x6, x7, x8))
data = pd.DataFrame(All.transpose(),
                      columns = ['x1', 'x2', 'x3', 'x4', 'x5', 'x6', 'x7', 'x8']
out = sns.pairplot(data, kind = "kde", \
                         plot kws = {'color':[176/255, 224/255, 230/255]}, \
                         diag kws = {'color':'black'})
out.map_offdiag(plt.scatter, color = 'black')
```





$$\mu = E(x) = \int x \, p(x) \, dx$$

$$\sigma^2 = var(x) = \int (x - \mu)^2 p(x) dx$$

based on the shape of the data cloud

- \rightarrow prediction how x_1 and x_2 are related, i. e. how they **correlate**
- → how to quantify?

Expectation, Variance, and Covariance

a, b = const

$$\sigma^2 = E(x^2) - E(x)^2$$

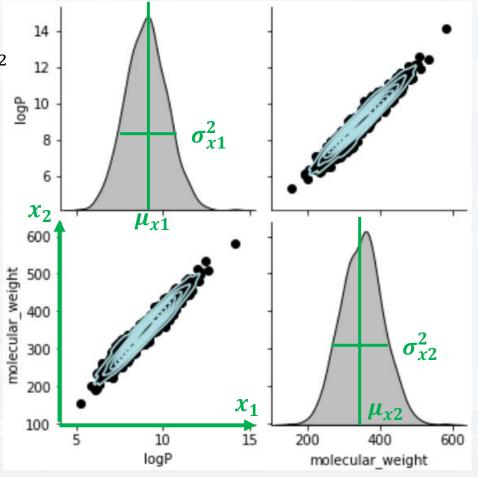
$$\mu = E(x) = \int x \, p(x) \, dx$$

$$var([a x_1 + b x_2]) = E([a x_1 + b x_2]^2) - E(a x_1 + b x_2)^2$$

$$\sigma^2 = var(x) = \int (x - \mu)^2 p(x) dx$$

$$= E(a^2 x_1^2 + 2ab x_1 x_2 + b^2 x_2^2) - E(a x_1 + b x_2)^2$$

$$= a^{2}E(x_{1}^{2}) + 2ab E(x_{1}x_{2}) + b^{2} E(x_{2}^{2}) - E(a x_{1} + b x_{2})^{2}$$



$$\sigma^2 = E(x^2) - E(x)^2$$

$$\mu = E(x) = \int x \, p(x) \, dx$$

$$var([a x_1 + b x_2]) = E([a x_1 + b x_2]^2) - E(a x_1 + b x_2)^2$$

$$\sigma^2 = var(x) = \int (x - \mu)^2 p(x) dx$$

$$= E(a^2 x_1^2 + 2ab x_1 x_2 + b^2 x_2^2) - E(a x_1 + b x_2)^2$$

$$= a^{2}E(x_{1}^{2}) + 2ab E(x_{1}x_{2}) + b^{2} E(x_{2}^{2}) - E(a x_{1} + b x_{2})^{2}$$

$$= a^{2}E(x_{1}^{2}) + 2ab E(x_{1}x_{2}) + b^{2} E(x_{2}^{2}) - [aE(x_{1}) + b E(x_{2})]^{2}$$

$$= a^{2}E(x_{1}^{2}) - a^{2}E(x_{1})^{2} + b^{2}E(x_{2}^{2}) - b^{2}E(x_{2})^{2} + 2ab E(x_{1}x_{2}) - 2abE(x_{1})E(x_{2})$$

$$a^{2} var(x_{1})$$

$$b^{2} var(x_{2})$$

$$2ab cov(x_{1}, x_{2})$$

$$= a^2 var(x_1) + b^2 var(x_2) + 2ab cov(x_1, x_2)$$

$$cov(x_1, x_2) = cov(x_2, x_1) = E(x_1x_2) - E(x_1)E(x_2)$$

covariance

$$cov(x_1, x_2) = cov(x_2, x_1) = E(x_1x_2) - E(x_1)E(x_2)$$

What does the covariance tell us?

- 1) geometrical interpretation \rightarrow next lecture
- 2) arithmetical interpretation

$$\mu = E(x) = \int x \, p(x) \, dx$$

$$\mu = E(x) = \int x p(x) dx$$

$$\sigma^2 = var(x) = \int (x - \mu)^2 p(x) dx$$

$$cov(x_1, x_2) = cov(x_2, x_1) = E(x_1x_2) - E(x_1)E(x_2)$$

What does the covariance tell us?

- 1) geometrical interpretation → next lecture
- 2) arithmetical interpretation
- a) x_1 and x_2 are independent

$$E(x_1x_2) - E(x_1)E(x_2)$$

$$= \iint x_1 x_2 \, p(x_1) \, p(x_2) \, dx_1 dx_2 \, - \int x_1 \, p(x_1) \, dx_1 \int x_2 \, p(x_2) \, dx_2$$

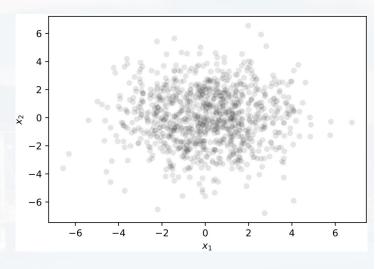
 x_1 and x_2 are independent:

 x_1 is not a function of x_2 and vise verse x_1 cannot be predicted by x_2 and vise verse

$$= \int x_1 p(x_1) dx_1 \int x_2 p(x_2) dx_2 - \int x_1 p(x_1) dx_1 \int x_2 p(x_2) dx_2 = 0$$

$$\mu = E(x) = \int x \, p(x) \, dx$$

$$\sigma^2 = var(x) = \int (x - \mu)^2 p(x) dx$$



Covariance equals **zero** if samples are **independent**!

$$cov(x_1, x_2) = cov(x_2, x_1) = E(x_1x_2) - E(x_1)E(x_2)$$

What does the covariance tell us?

- 1) geometrical interpretation → next lecture
- 2) arithmetical interpretation
- b) x_1 and x_2 are **not** independent

$$E(x_1x_2) - E(x_1)E(x_2)$$

$$= \iint x_1 x_2 \, p(x_1) \, p(x_2) \, dx_1 dx_2 \, - \int x_1 \, p(x_1) \, dx_1 \int x_2 \, p(x_2) \, dx_2$$

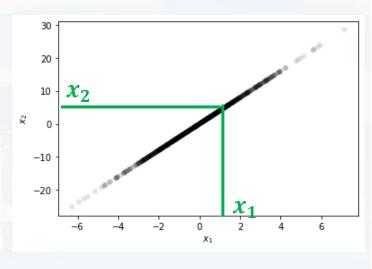
 x_1 and x_2 are **not** independent:

 x_1 is a function of x_2 and vise verse x_1 can be predicted by x_2 to certain degree and vise verse

$$= \iint x_1 \, p(x_1) \, x_2(x_1) \, p(x_2(x_1)) \, dx_1 dx_2(x_1) - \int x_1 \, p(x_1) \, dx_1 \int x_2 \, p(x_2) \, dx_2$$

$$\mu = E(x) = \int x \, p(x) \, dx$$

$$\sigma^2 = var(x) = \int (x - \mu)^2 p(x) dx$$



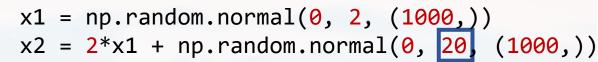
Covariance does not equal zero!

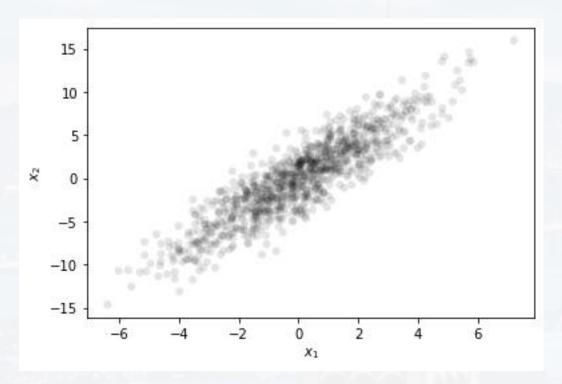
$$cov(x_1, x_2) = cov(x_2, x_1) = E(x_1x_2) - E(x_1)E(x_2)$$

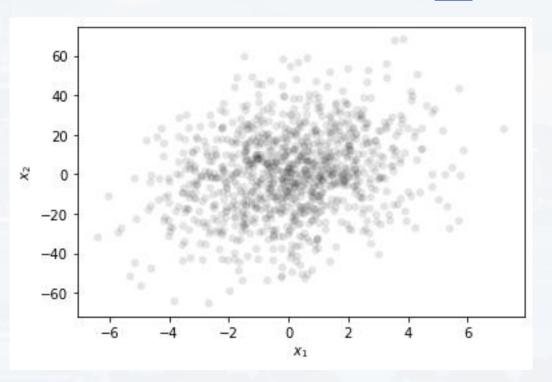
covariance

$$x1 = np.random.normal(0, 2, (1000,))$$

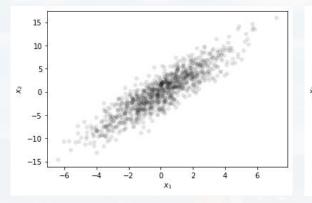
 $x2 = 2*x1 + np.random.normal(0, 2, (1000,))$

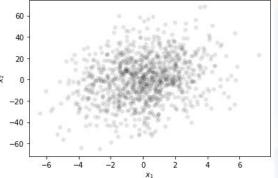






$$cov(x_1, x_2) = cov(x_2, x_1) = E(x_1x_2) - E(x_1)E(x_2)$$





covariance

Same dependency, but different variance!

Need to scale for the variance!

Pearson's correlation coefficient

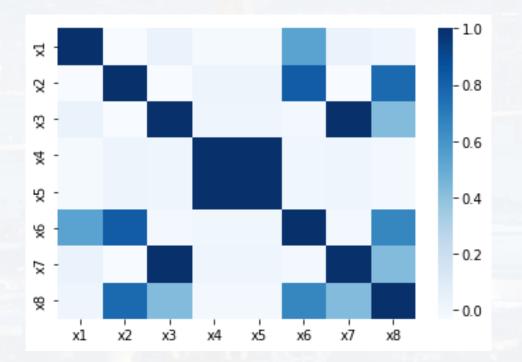
$$\rho(x_1, x_2) = \frac{cov(x_1, x_2)}{\sqrt{\sigma_1^2 \sigma_2^2}}$$

$$\rho(x_1, x_2)$$
:

- ranges from -1 to +1
- zero: no correlation(completely independent)
- -1: max anti correlation
- +1: max correlation

$$cov(x_1, x_2) = cov(x_2, x_1) = E(x_1x_2) - E(x_1)E(x_2)$$

$$\rho(x_1, x_2) = \frac{cov(x_1, x_2)}{\sqrt{\sigma_1^2 \sigma_2^2}}$$



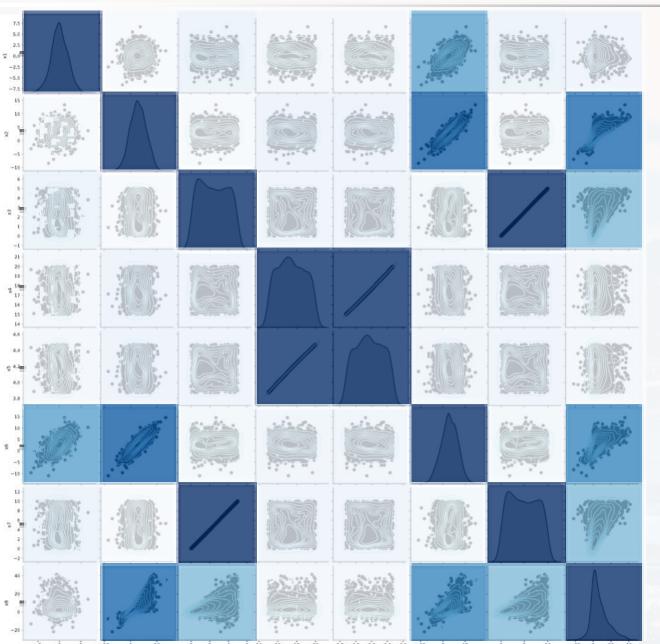
covariance

Pearson's correlation coefficient

$\rho(x_1, x_2)$:

- ranges from -1 to +1
- zero: no correlation(completely independent)
- -1: max anti correlation
- +1: max correlation





$\rho(x_1, x_2)$:

- ranges from -1 to +1
- zero: no correlation (completely independent)
- -1: max anti correlation
- +1: max correlation

Important quantities you should know:

mean

$$\mu = E(x) = \int x \, p(x) \, dx$$

variance

$$\sigma^2 = var(x) = \int (x - \mu)^2 p(x) dx$$

$$\sigma^2 = E(x^2) - E(x)^2$$

$$\sigma_{tot}^2 = \sigma_1^2 + \sigma_2^2 + 2 cov(x_1, x_2)$$

covariance

$$cov(x_1, x_2) = E(x_1x_2) - E(x_1)E(x_2)$$

correlation coefficient

$$\rho(x_1, x_2) = \frac{cov(x_1, x_2)}{\sqrt{\sigma_1^2 \sigma_2^2}}$$

median
$$m$$

$$\int_{a}^{m} p(x) dx = \frac{1}{2}$$

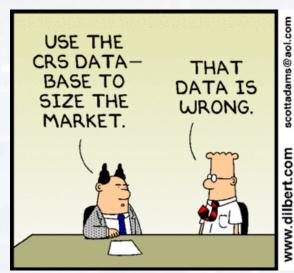
note:

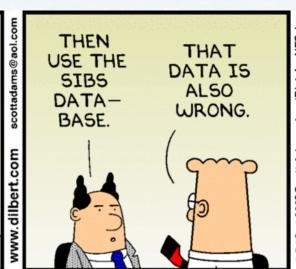
$$\int (x-\mu)^n p(x) dx$$

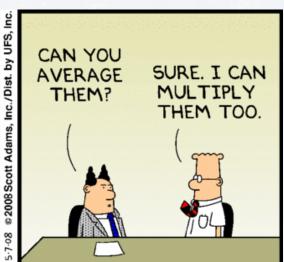
called n-th moment of a pdf

<u>Outline</u>

- Expectation, Variance, and Covariance
- Hypothesis Testing
- Confidence Intervals







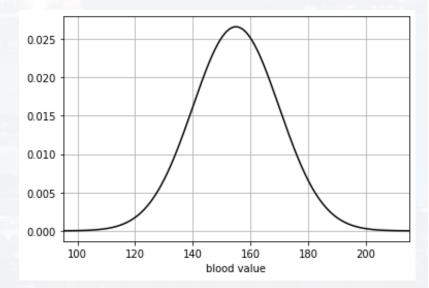
standard frequentist way (not Bayesian):

- 1) assume a likelihood function L as your model, aka null hypothesis H_0
- 2) take a datapoint x_0
- 3) calculate the *probability P* given L i. e. given H_0 is true, that x_0 has this value or a more extreme value
- 4) accepting or rejecting H_0 based on P and the threshold α

example:

1) a healthy person has a blood value that follows a normal distribution with

$$\mu = 155$$
, $\sigma = 15$, i. e. H_0 : $N(\mu = 155, \sigma = 15)$



standard frequentist way (not Bayesian):

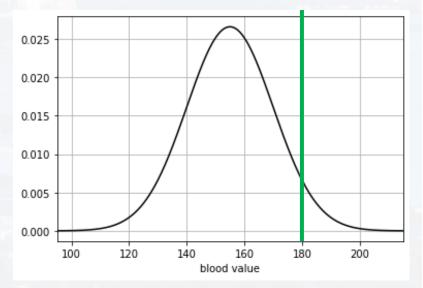
- 1) assume a likelihood function L as your model, aka null hypothesis H_0
- 2) take a datapoint x_0
- 3) calculate the *probability P* given L i. e. given H_0 is true, that x_0 has this value or a more extreme value
- 4) accepting or rejecting H_0 based on P and the threshold α

example:

1) a healthy person has a blood value that follows a normal distribution with

$$\mu = 155$$
, $\sigma = 15$, i. e. H_0 : $N(\mu = 155, \sigma = 15)$

2) a patient has the value $x_0 = 180$





standard frequentist way (not Bayesian):

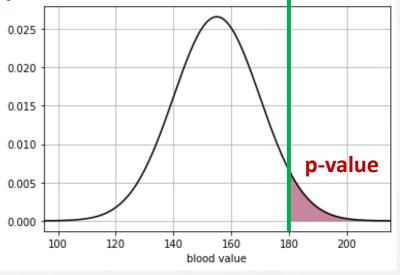
- 1) assume a likelihood function L as your model, aka null hypothesis H_0
- 2) take a datapoint x_0
- 3) calculate the *probability P* given L i. e. given H_0 is true, that x_0 has this value or a more extreme value
- 4) accepting or rejecting H_0 based on P and the threshold α

example:

1) a healthy person has a blood value that follows a normal distribution with

$$\mu = 155$$
, $\sigma = 15$, i. e. H_0 : $N(\mu = 155, \sigma = 15)$

- 2) a patient has the value $x_0 = 180$
- 3) probability $P(x \ge 180|H_0) = 0.048$ called p-value



standard frequentist way (not Bayesian):

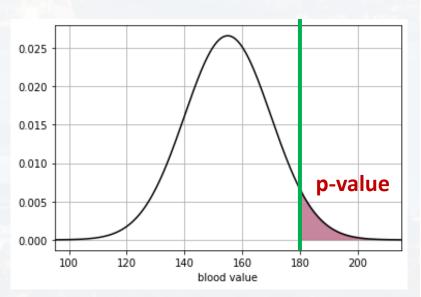
- 1) assume a likelihood function L as your model, aka null hypothesis H_0
- 2) take a datapoint x_0
- 3) calculate the *probability P* given L i. e. given H_0 is true, that x_0 has this value or a more extreme value
- 4) accepting or rejecting H_0 based on P and the threshold α

example:

1) a healthy person has a blood value that follows a normal distribution with

$$\mu = 155$$
, $\sigma = 15$, i. e. H_0 : $N(\mu = 155, \sigma = 15)$

- 2) a patient has the value $x_0 = 180$
- 3) probability $P(x \ge 180|H_0) = 0.048$ called p-value
- 4) for α = 0.05, H_0 is rejected, i. e. patient is not healthy
- \rightarrow alternative hypothesis H_1 : not healthy



example:

1) a healthy person has a blood value that follows a normal distribution with

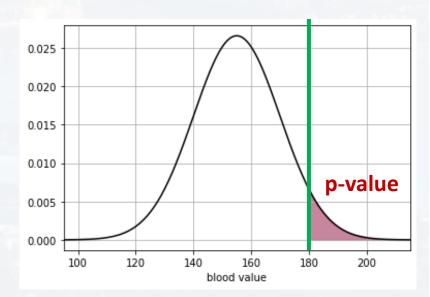
$$\mu = 155$$
, $\sigma = 15$, i. e. H_0 : $N(\mu = 155, \sigma = 15)$

- 2) a patient has the value $x_0 = 180$
- 3) probability $P(x \ge 180|H_0) = 0.048$ called p-value
- 4) for α = 0.05, H_0 is **rejected**, i. e. patient is

not healthy

 \rightarrow alternative hypothesis H_1 : not healthy

We just performed a so-called Z – Test (comparing one value to a normal distribution)



standard frequentist way (not Bayesian):

- 1) assume a likelihood function L as your model, aka null hypothesis H_0
- 2) take a datapoint x_0
- 3) calculate the *probability P* given L i. e. given H_0 is true, that x_0 has this value or a more extreme value
- 4) accepting or rejecting H_0 based on P and the threshold α

caveats:

- the model \boldsymbol{L} for $\boldsymbol{H_0}$ has to **be known**
- the p-value $P(x \ge x_0 | H_0)$ does not tell if H_0 is true or not
- the p-value $P(x \ge x_0 | H_0)$ does not tell which hypothesis is more likely
- the p-value just gives $P(x \ge x_0 | H_0)$
- the threshold α for accepting/rejecting H_0 is arbitrary
- we are aiming on disproving a hypothesis, by assuming it is true,
 without leading to a contradiction



- data point x versus normal
- $H_0: x \in N(\mu, \sigma)$

Z-test

0.025 0.020 0.015 0.010 0.005 0.000 100 120 140 160 180 200 blood value

- normal versus another normal
- two samples of sizes n_1 and n_2

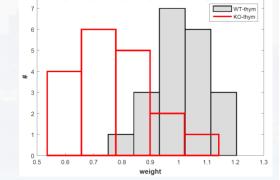
- two tail $H_0: \mu_1 = \mu_2, H_1: \mu_1 \neq \mu_2$

- right tail $H_0: \mu_1 < \mu_2, H_1: \mu_1 > \mu_2$

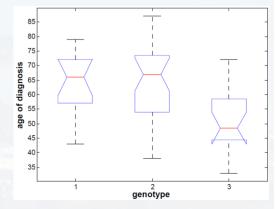
- left tail $H_0: \mu_1 > \mu_2, H_1: \mu_1 < \mu_2$

t-test

ANalysis Of VAriance



- N normal dist.
- N samples of sizes n_i
- H_0 : $\mu_i = \mu_j \ \forall \ i,j$, H_1 : $\mu_i \neq \mu_j$ for at least one pair i, j

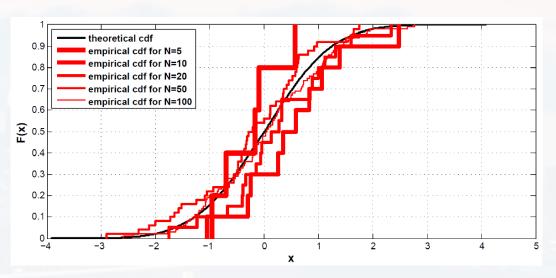


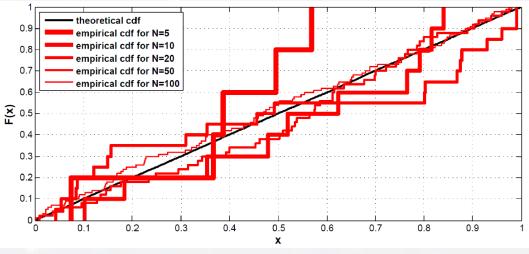
testing if a data set follows a particular distribution

Kolmogorov – **S**mirnov – test (KS test)

example: normal distribution:

example: uniform distribution:





testing if a data set follows a particular distribution

ranking tests (Wilcoxon)

...and many more...

They all generate a test statistic:

Z-value, t-value, F-value etc

→ from that: calculating a p-value

Hypothesis Testing

ranking tests (Wilcoxon)

alue

paired data, or redesign data in samples experiment Independent? repeated measures? yes yes calculate descriptive statistics (mean and standard deviation); construct histograms of data samples approximately normal may try data transformation, especially with similar variances? if data are proportions, ratios, or counts, yes transformed data approximately repeated normal with similar variances measures? , no Friedman repeated yes 2 samples? measures? yes 2 samples? **ANOVA** same? yes Kruskal-Wallis paired? paired? done no means (Mann-Whitney paired t test variances equal? no same? no yes t test assuming t test assuming Wilcoxon done unequal variances or signed rank or equal variances Mann-Whitney test sign test nonparametric parametric multiple comparisons multiple comparisons parametric tests nonparametric tests

Berkeley Statistics for D

testing if a data s

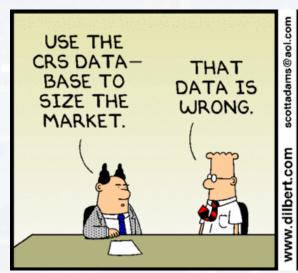
...and many more

They all generate

Current Protocols in Molecular Biology (1998) A.3I.1-A.3I.22

<u>Outline</u>

- Expectation, Variance, and Covariance
- Hypothesis Testing
- Confidence Intervals



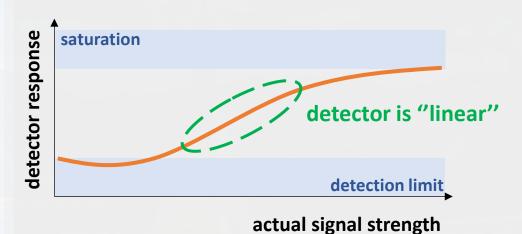




How sure can we be about a measured value?

two kinds of errors

systematic errors: calibration, non-linearity of the detector

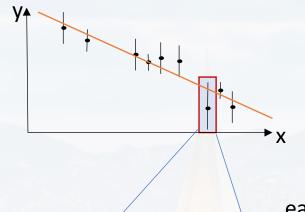


statistical errors: limited precision, natural variance of the data

→ spread of the data around an average value

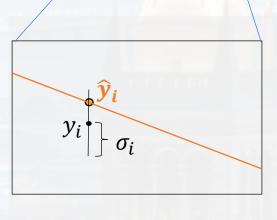
assumption: far from the detection limit and saturation:

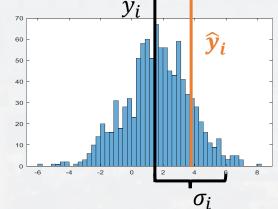
the spread follows approximately a normal distribution.



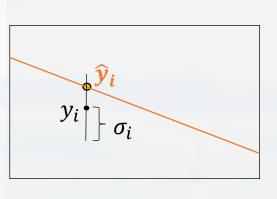
fitting a model (\hat{y}_i) , orange line) to data points (x_i, y_i) each with an error bar σ_i

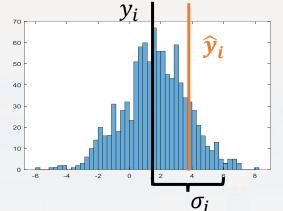
each data point x_i has been drawn from $N(\mu_i = y_i, \sigma_i)$



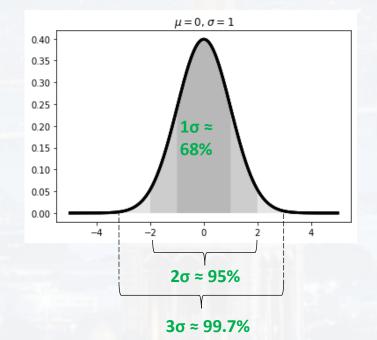


$$p_i(y_i|\hat{\mathbf{y}_i}, \sigma_i) = \frac{1}{\sqrt{2\pi}\sigma_i} exp\left[-\frac{1}{2} \frac{(y_i - \hat{\mathbf{y}_i})^2}{\sigma_i^2}\right]$$





$$p_i(y_i|\hat{\mathbf{y}_i}, \sigma_i) = \frac{1}{\sqrt{2\pi}\sigma_i} exp\left[-\frac{1}{2} \frac{(y_i - \hat{\mathbf{y}_i})^2}{\sigma_i^2}\right]$$



for large (> 50...100) N (number of data points):

 \approx 2/3 of the data points should be consistent with the model within their 1 σ error bars

≈ 95% of the data points should be consistent with the model within their 2σ error bars

 \approx 99.7% of the data points should be consistent with the model within their 3σ error bars



$$p_i(y_i|\hat{\mathbf{y}_i}, \sigma_i) = \frac{1}{\sqrt{2\pi}\sigma_i} exp\left[-\frac{1}{2} \frac{(y_i - \hat{\mathbf{y}_i})^2}{\sigma_i^2}\right]$$

based on this model: reduced chi square

$$\chi_{red}^2 = \frac{1}{df} \sum_{i=1}^{N} \left(\frac{y_i - \hat{y}_i}{\sigma_i} \right)^2 df = N - p - 1$$

given a fitted model: χ^2_{red} is a measure of the fit quality!

N: number of data points p: number of fit parameter (model)

$$p_i(y_i|\hat{\mathbf{y}_i}, \sigma_i) = \frac{1}{\sqrt{2\pi}\sigma_i} exp\left[-\frac{1}{2} \frac{(y_i - \hat{\mathbf{y}_i})^2}{\sigma_i^2}\right]$$

based on this model: reduced chi square

$$\chi_{red}^2 = \frac{1}{df} \sum_{i=1}^{N} \left(\frac{y_i - \hat{y}_i}{\sigma_i} \right)^2 \qquad df = N - p - 1$$

$$df = N - p - 1$$

N: number of data points p: number of fit parameter (model)

given a fitted model: χ^2_{red} is a measure of the fit quality!

example

good fit: $y_i - \hat{y}_i$ should be within σ_i for 2/3 of all data points, see $N(\mu_i = y_i, \sigma_i)$

therefore
$$\frac{y_i - \hat{y}_i}{\sigma_i} \approx 1$$

therefore
$$\sum_{i=1}^{N} \left(\frac{y_i - \hat{y}_i}{\sigma_i} \right)^2 \approx N$$

N should be much larger than p, therefore df $\approx N$

hence,
$$\chi^2_{red} \approx 1$$

$$p_i(y_i|\hat{\mathbf{y}_i}, \sigma_i) = \frac{1}{\sqrt{2\pi}\sigma_i} exp\left[-\frac{1}{2} \frac{(y_i - \hat{\mathbf{y}_i})^2}{\sigma_i^2}\right]$$

based on this model: reduced chi square

$$\chi_{red}^2 = \frac{1}{df} \sum_{i=1}^{N} \left(\frac{y_i - \hat{y}_i}{\sigma_i} \right)^2$$

$$df = N - p - 1$$

N: number of data points
p: number of fit parameter (model)

given a fitted model: χ^2_{red} is a measure of the fit quality

for large (> 50...100) N (number of data points):

≈ 2/3 of the data points should be consistent with the model within their 1σ error bars

 \approx 95% of the data points should be consistent with the model within their 2 σ error bars

 \approx 99.7% of the data points should be consistent with the model within their 3σ error bars



$$p_i(y_i|\hat{\mathbf{y}_i}, \sigma_i) = \frac{1}{\sqrt{2\pi}\sigma_i} exp\left[-\frac{1}{2} \frac{(y_i - \hat{\mathbf{y}_i})^2}{\sigma_i^2}\right]$$

based on this model: reduced chi square

$$\chi_{red}^2 = \frac{1}{df} \sum_{i=1}^{N} \left(\frac{y_i - \hat{y}_i}{\sigma_i} \right)^2$$

$$df = N - p - 1$$

N : number of data points
p: number of fit parameter (model)

given a fitted model: χ^2_{red} is a measure of the fit quality

for large (> 50...100) N (number of data points):

 \approx 2/3 of the data points should be consistent with the model within their 1σ error bars

 \approx 95% of the data points should be consistent with the model within their 2 σ error bars

 \approx 99.7% of the data points should be consistent with the model within their 3σ error bars

$$\chi^2_{red} \approx$$

1.0 excellent fit

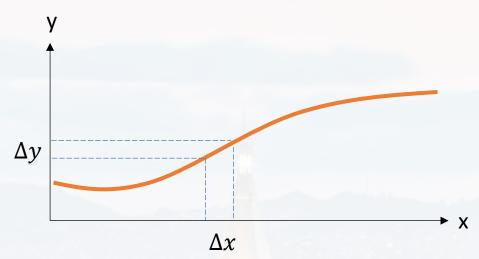
1.0...1.5 acceptable fit

1.5...1.7 bad fit

>2.0 not acceptable

<<1.0 suspicious, errors are overestimated!

error propagation



$$\frac{dy}{dx} \approx \frac{\Delta y}{\Delta x}$$

for
$$\Delta x \ll x$$

$$\Delta x \left| \frac{dy}{dx} \right| \approx \Delta y$$

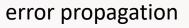
example:

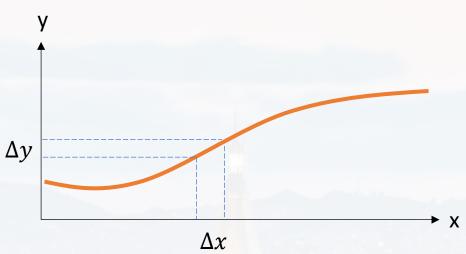
$$V = \frac{4}{3} \pi r^3$$
 $\Delta V = ?$ given Δr

$$\Delta V = \frac{dV}{dr} \Delta r = 4 \pi r^2 \Delta r$$

$$\frac{\Delta V}{V} = 3 \frac{\Delta r}{r}$$

$$\Delta r, \Delta V \approx 1\sigma$$





$$\frac{\Delta V}{V} = 3\frac{\Delta r}{r}$$

$$\Delta r$$
, $\Delta V \approx 1\sigma$

$$\Delta V = \frac{dV}{dr} \Delta r = 4 \pi r^2 \Delta r$$

radius:

$$r = 1.0 \mu m$$

$$\Delta r =$$

 $0.1\mu m$

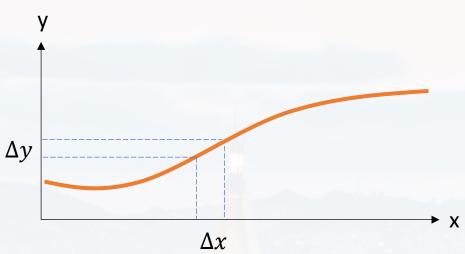
$$V = \frac{4}{3} \pi (1.0 \mu \text{m})^3 = 4.18879020.. \mu \text{m}^3$$

$$\Delta V = 4 \pi r^2 \Delta r = 4 \pi (1.0 \mu \text{m})^2 0.1 \mu \text{m}$$

$$= 1.2566370614359172 \mu m^3$$







$$V = (4.2 \pm 1.3) \mu m^3$$

$$\frac{\Delta V}{V} = 3\frac{\Delta r}{r}$$

$$\Delta r$$
, $\Delta V \approx 1\sigma$

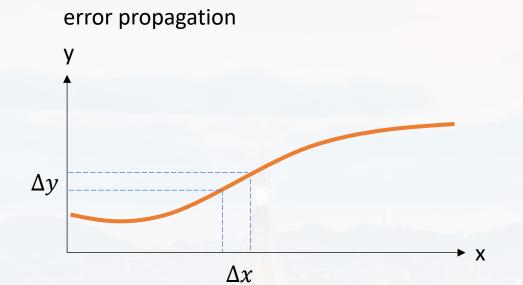
$$\Delta V = \frac{dV}{dr} \Delta r = 4 \pi r^2 \Delta r$$

radius: $r = 1.0 \mu m$ $\Delta r = 0.1 \mu m$

$$V = \frac{4}{3} \pi (1.0 \mu \text{m})^3 = 4.18879020.. \mu \text{m}^3$$

$$\Delta V = 4 \pi r^2 \Delta r = 4 \pi (1.0 \mu \text{m})^2 0.1 \mu \text{m}$$

=
$$1.2566370614359172 \mu m^3$$



general:

$$\Delta f(max) = \sum_{i=1}^{I} \left| \frac{\partial f}{\partial x_i} \right| \Delta x_i$$
 maximum error estimation

if x_i do not correlate, i. e. are mutually independent:

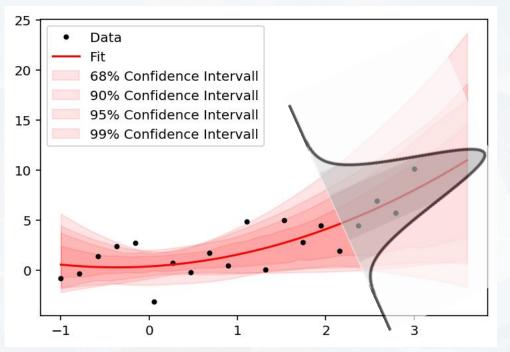
$$\Delta f^2 = \sum_{i=1}^{I} \left| \frac{\partial f}{\partial x_i} \right|^2 (\Delta x_i)^2$$

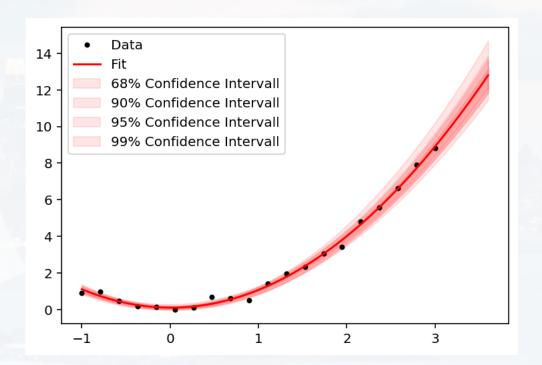
Note:
$$\Delta f(max)^2 > \Delta f^2$$
 because of the mixed terms $\left| \frac{\partial f}{\partial x_i} \right| \left| \frac{\partial f}{\partial x_j} \right| \Delta x_i \Delta x_j$ in $\Delta f(max)^2$



curve fitting (Module 11)

noisy data





Thank you very much for you attention!

