

Method validation & correlation

Johannes Müller

With material from

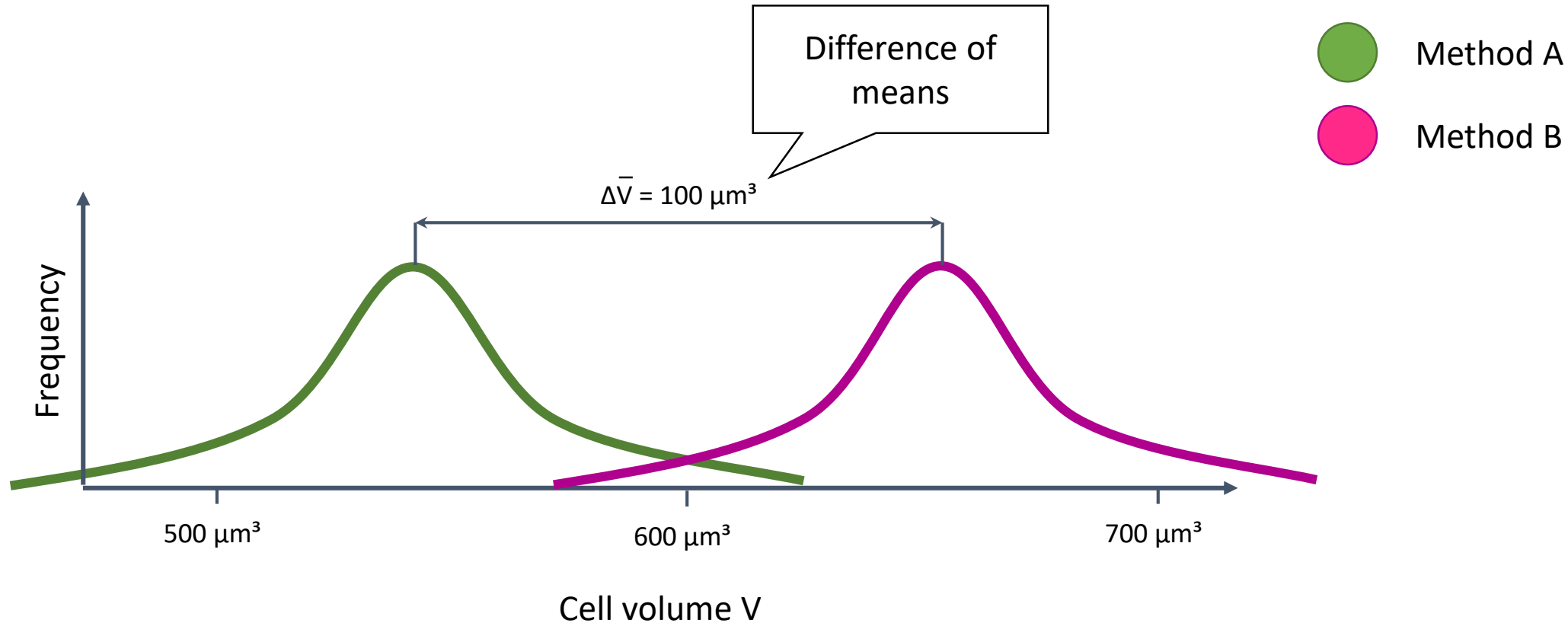
Robert Haase

Anna Poetsch

Martin J. Bland

Douglas G. Altman

- Comparing mean measurements appears reasonable on the first view.



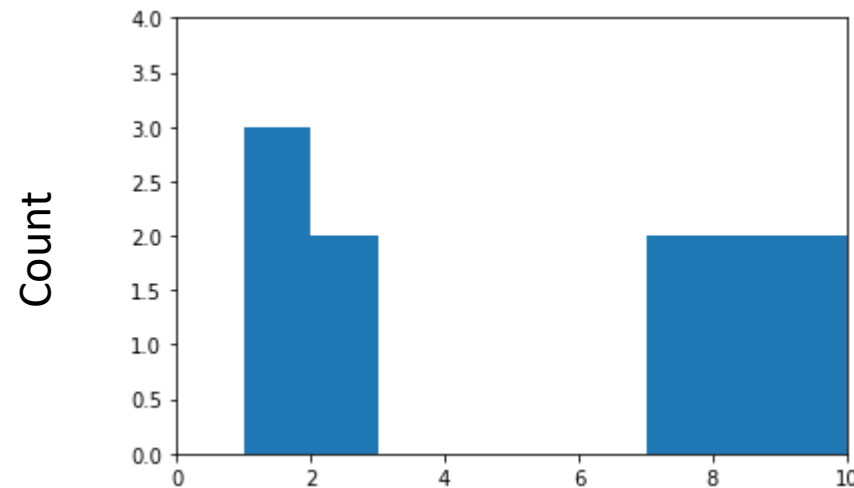
- Are two methods doing the same if their mean measurement is similar?

A	B
1	4
9	5
7	5
1	7
2	4
8	5
9	4
2	6
1	6
7	5
8	4

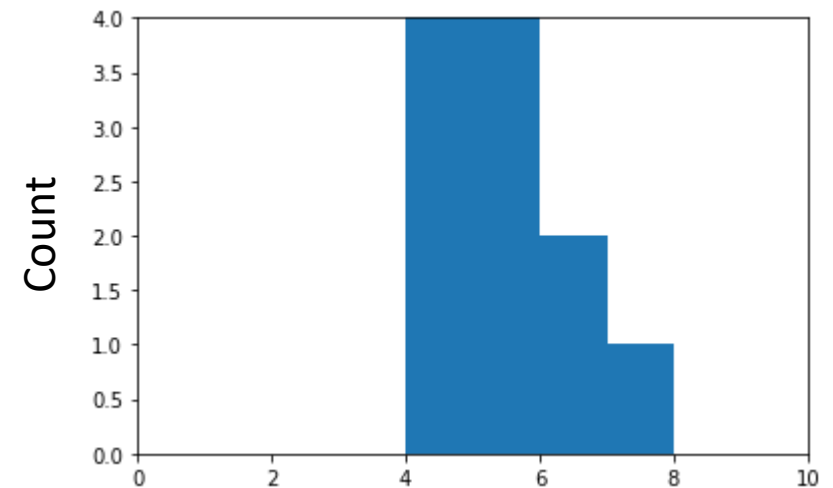
$$\text{Mean}(A) = 5.0$$

$$\text{Mean}(B) = 5.0$$

- Draw histograms! How can two methods do the same if histograms from their measurements are different?



Measurement A



Measurement B

Similar means is a necessary condition, but it is NOT sufficient!

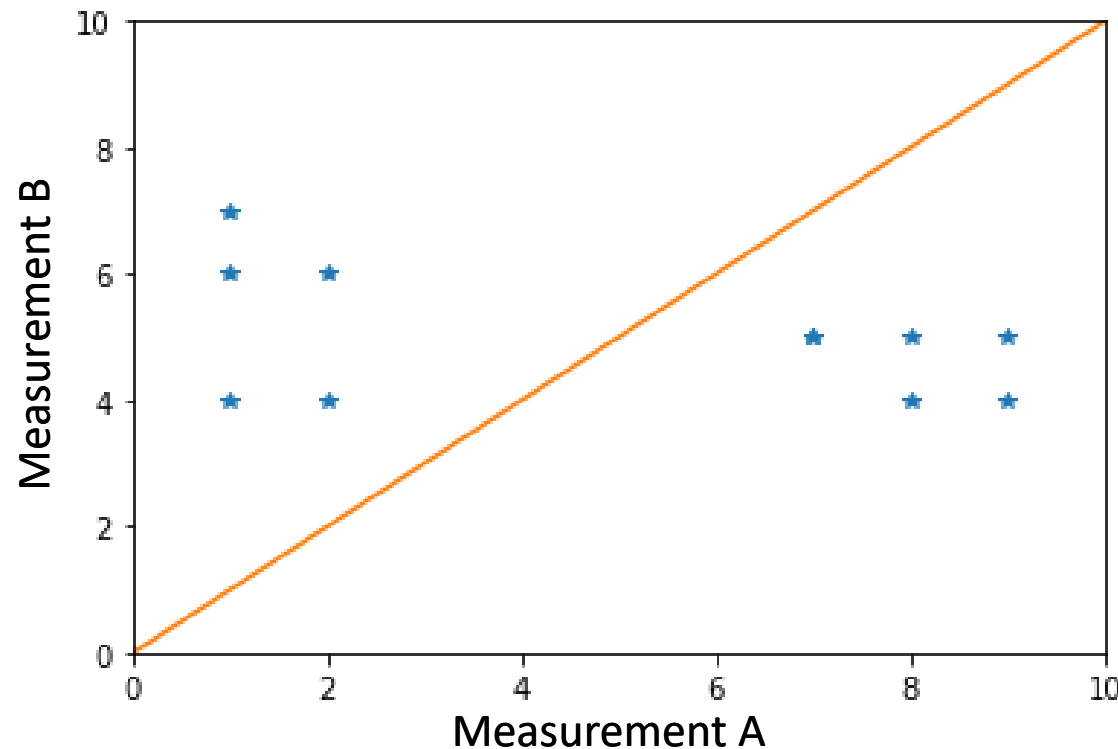
- Are two methods doing the same if their mean measurement is similar?

A	B
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1	6
7	5
8	4

$$\text{Mean}(A) = 5.0$$

$$\text{Mean}(B) = 5.0$$

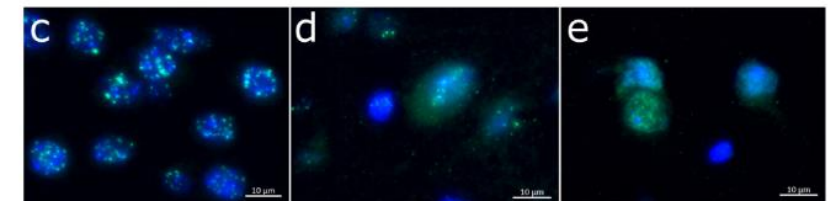
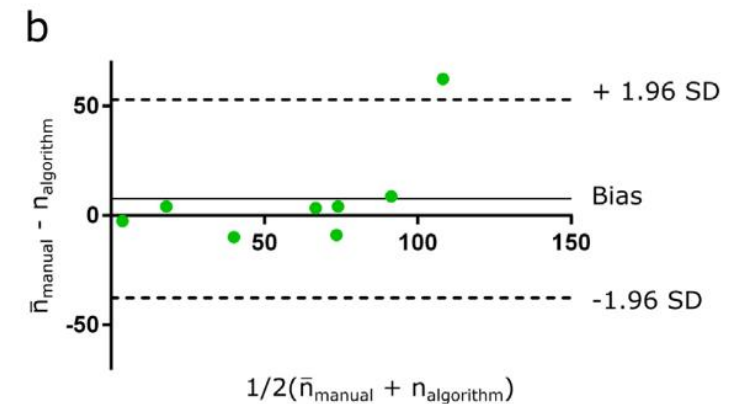
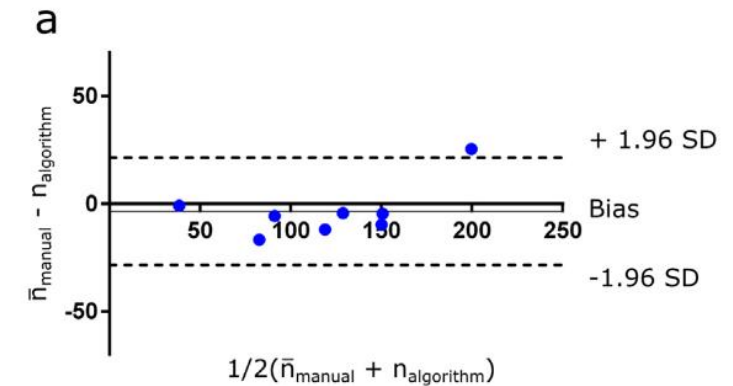
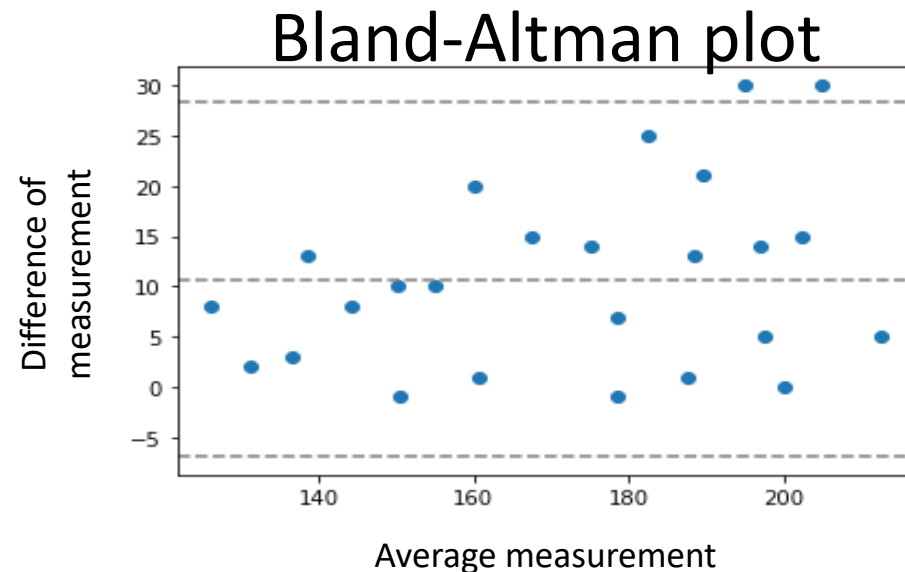
- Plot the measurements against each other. What does it mean if they lie on a straight line? What if not?



The “criterion of agreement was that the two methods gave the same mean measurement; ‘the same’ appears to stand for ‘not significantly different’. Clearly, this approach tells us very little about the accuracy of the methods.”¹

- **Practical application:**

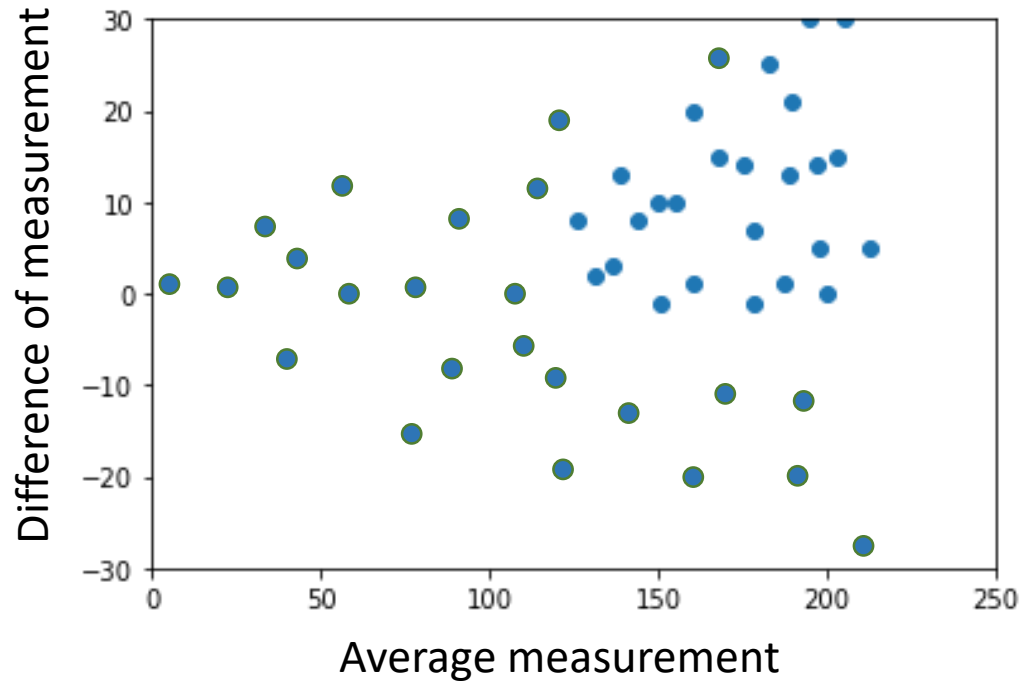
- Script counts cell damage (gH2AX expression) in **nucleus**
- **Damage** and **nuclei** are counted independently and require settings some parameters
- Bland-Altman analysis used to validate parameters



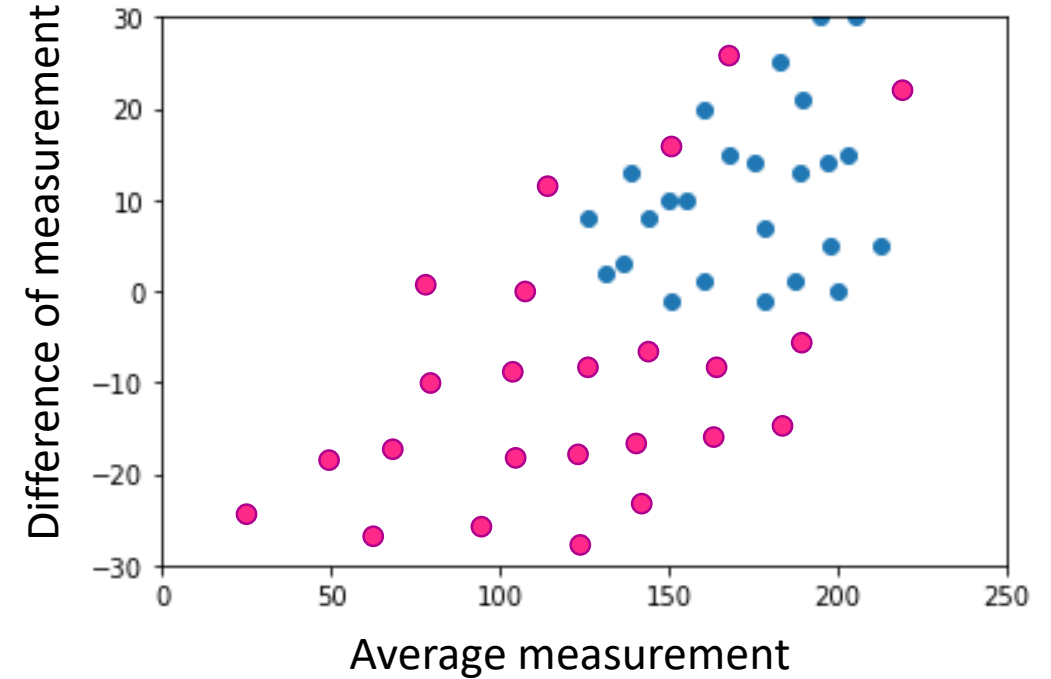
Suckert, Beyreuther, Müller et al. Rad. Onc. (2020)

- Bland-Altman plots allow us to differentiate various kinds of bias.

Agreement with random relative error

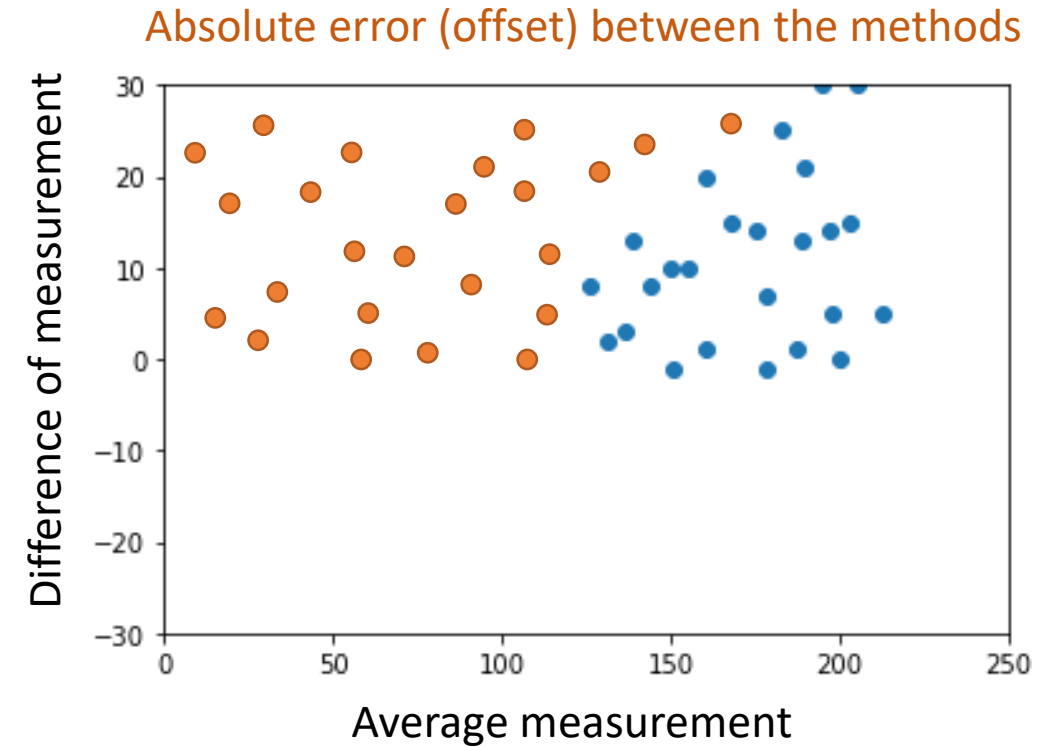
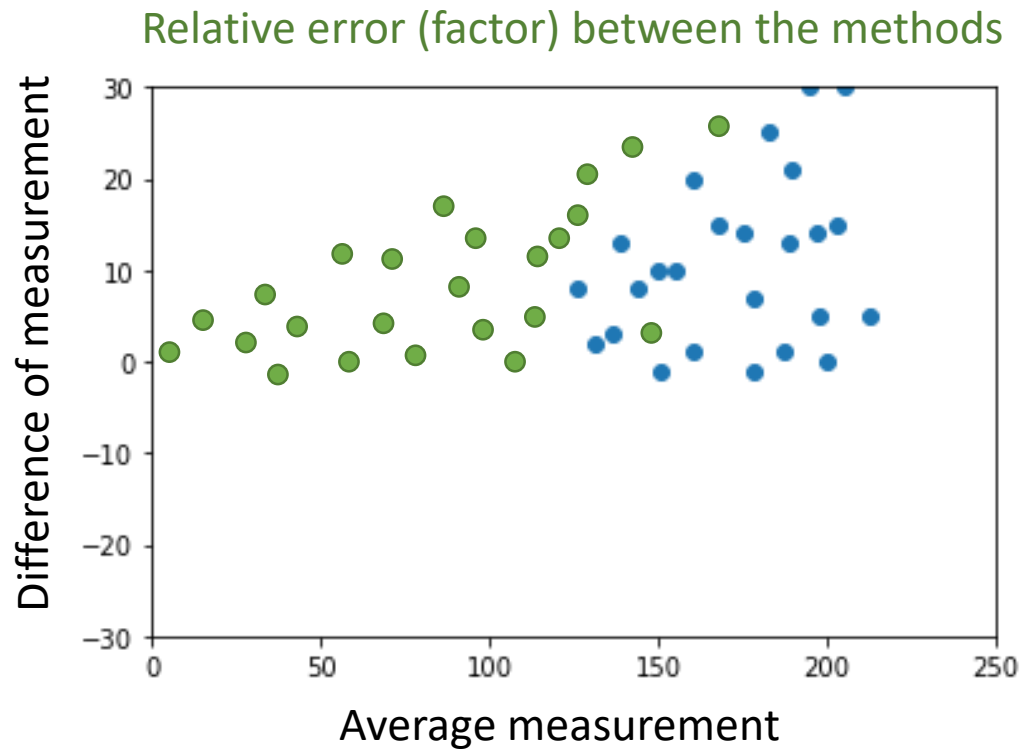


Systematic bias



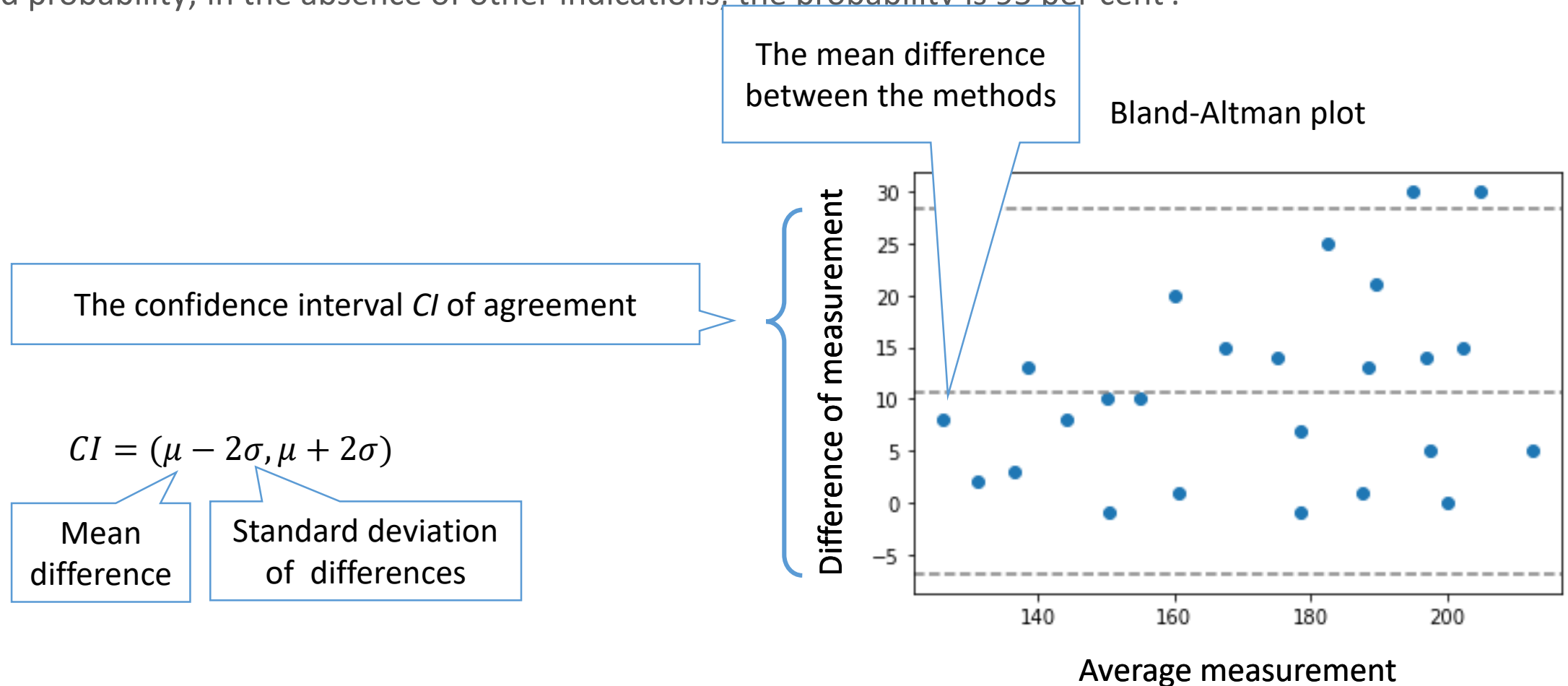
- Both distributions could have the same mean difference and confidence interval.

- Bland-Altman plots allow us to differentiate various kinds of bias.



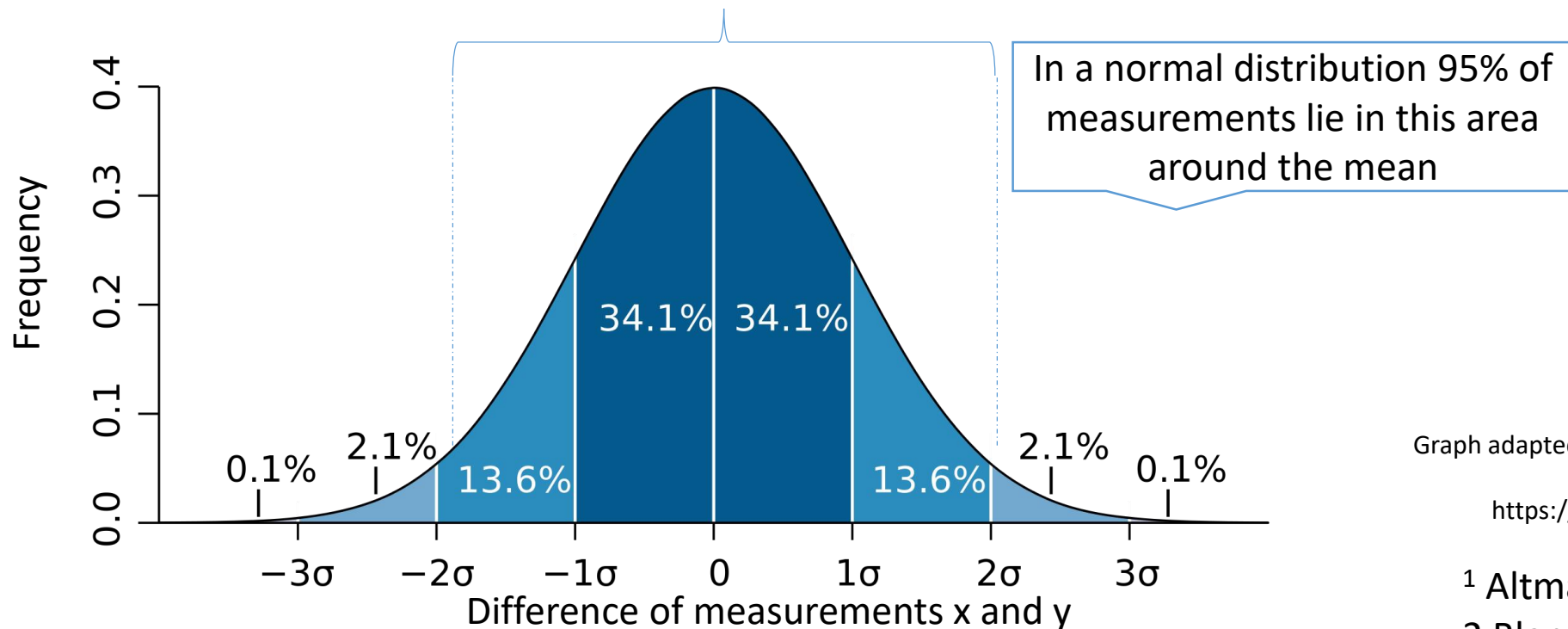
- Both effects can be corrected by calibration.

- “The British Standards Institution (1979) define a coefficient of repeatability as ‘the value below which the difference between two single test results ... may be expected to lie with a specified probability; in the absence of other indications, the probability is 95 per cent’.”¹



The confidence interval & the coefficient of repeatability.

- “The British Standards Institution (1979) define a coefficient of repeatability as ‘the value below which the difference between two single test results ... may be expected to lie with a specified probability; in the absence of other indications, the probability is 95 per cent’.”¹
- If the two measurements come from the same method which just repeated twice, we can assume that the mean difference is zero. The coefficient of repeatability *CR* can then be estimated: It’s the standard deviation of differences.²

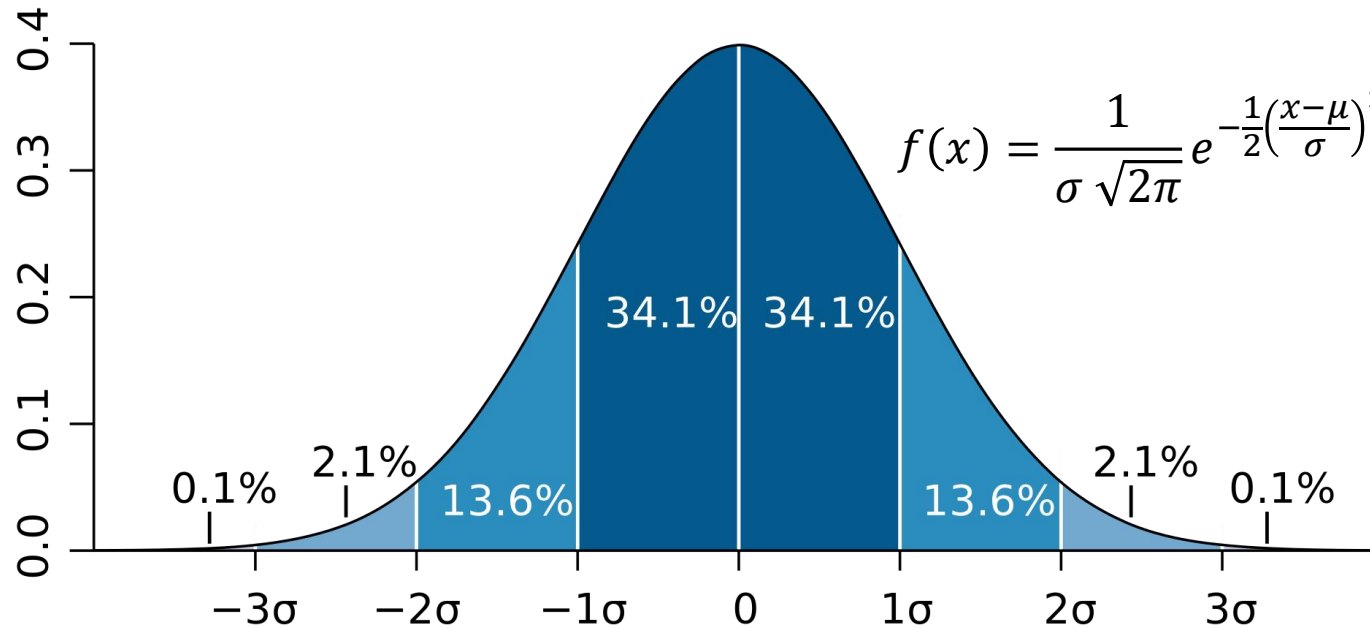


$$CR(X, Y) = \sqrt{\sum_{x \in X, y \in Y} \frac{(x - y)^2}{n}}$$

Graph adapted from: M. W. Toews - Own work, based (in concept) on figure by Jeremy Kemp, on 2005-02-09, CC BY 2.5, <https://commons.wikimedia.org/w/index.php?curid=1903871>

¹ Altman & Bland, The Statistician 32, 1983

² Bland & Altman, Lancet , 1986



Normal distribution:

- Can be completely described by mean μ and standard deviation σ
- Allows comparing distributions (e.g., with two-sided/paired t-test)

Ranked distribution:

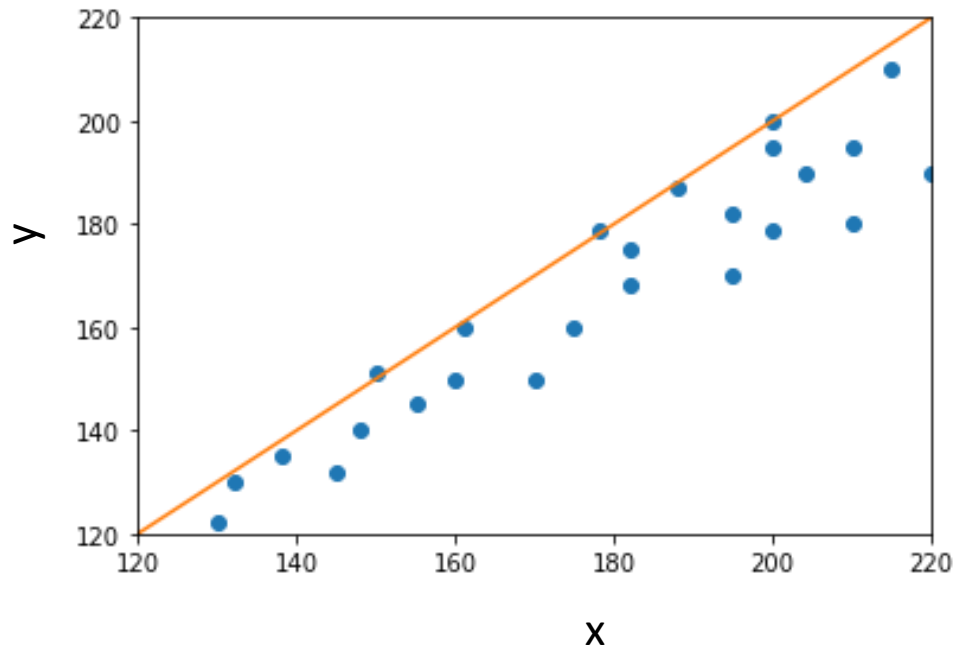
- Replace each value with its “rank”
- Rank = index of value in sorted list
- Robust to outliers
- Independent on underlying distribution

Value	Rank
10	1
15	2
3	0
97	3

Graph adapted from: M. W. Toews - Own work, based (in concept) on figure by Jeremy Kemp, on 2005-02-09, CC BY 2.5, <https://commons.wikimedia.org/w/index.php?curid=1903871>

- Are two methods doing the same if they correlate?
 - Correlation: Any kind of relationship.
 - Measurable; e.g. using Pearson's Correlation Coefficient r enumerated linear correlation.

Comparison of two methods of measuring systolic blood pressure (Data from 1)



Expectation E

Mean average μ

$$r(X, Y) = \frac{E[(X - \mu_X)(Y - \mu_Y)]}{\sigma_X \sigma_Y}$$

Standard deviation σ
→ Unit independence

Disclosure: Mean and standard deviation must be obtained from the whole population or from a sample set which is sufficiently large.

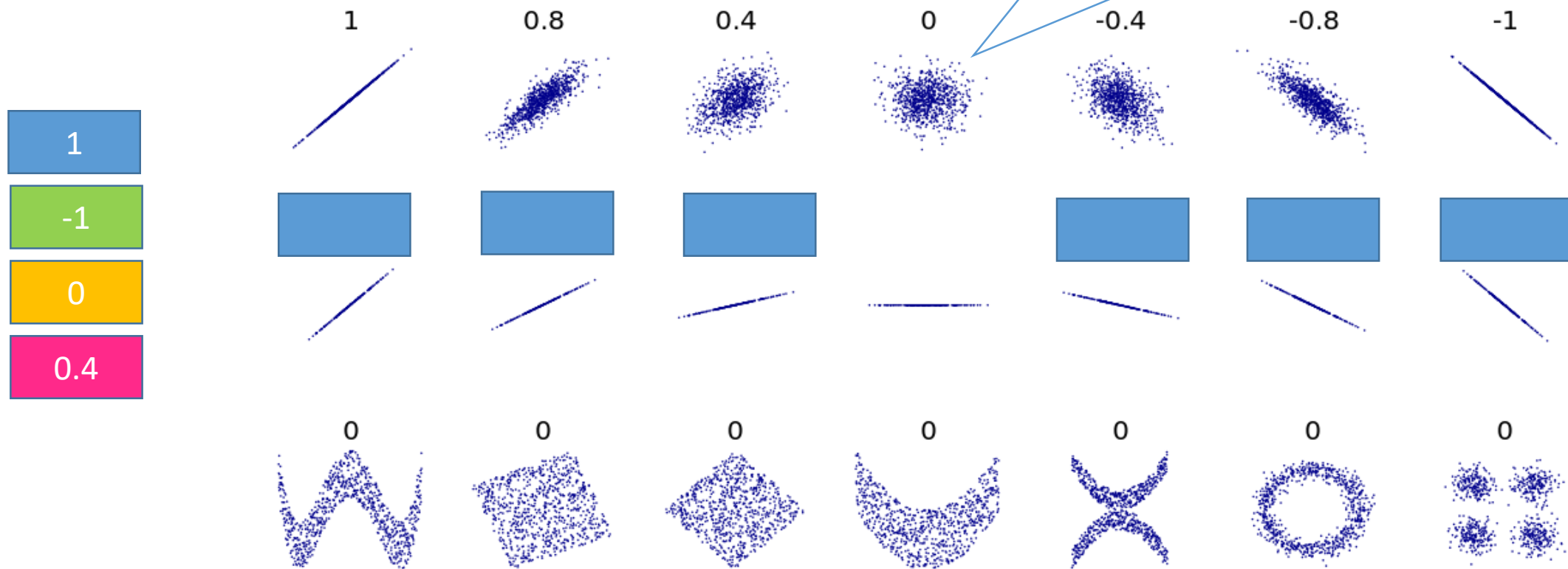
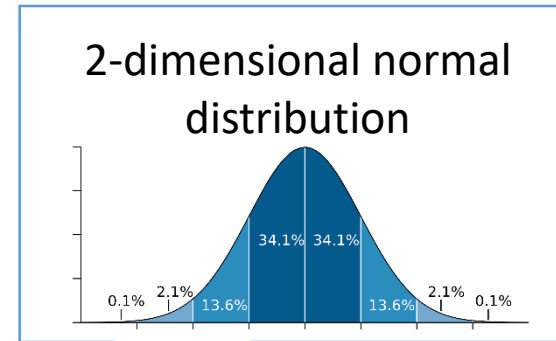
In practice E is the weighted sum:

$$r(X, Y) = \frac{\sum_{x \in X, y \in Y} \frac{(x - \mu_X)(y - \mu_Y)}{n}}{\sigma_X \sigma_Y}$$

Number of measurements n

Correlation: Pearson's r

- Pearson's r lies between -1 and 1
 - 1: Positive linear correlation
 - 0: No linear correlation
 - 1: Negative linear correlation



Value x	Rank x'
10	1
15	2
3	0
97	3
...	...

- Spearman's r lies between -1 and 1
 - 1: Positive **monotonous** correlation
 - 0: No monotonous correlation
 - -1: Negative monotonous correlation

Expectation E

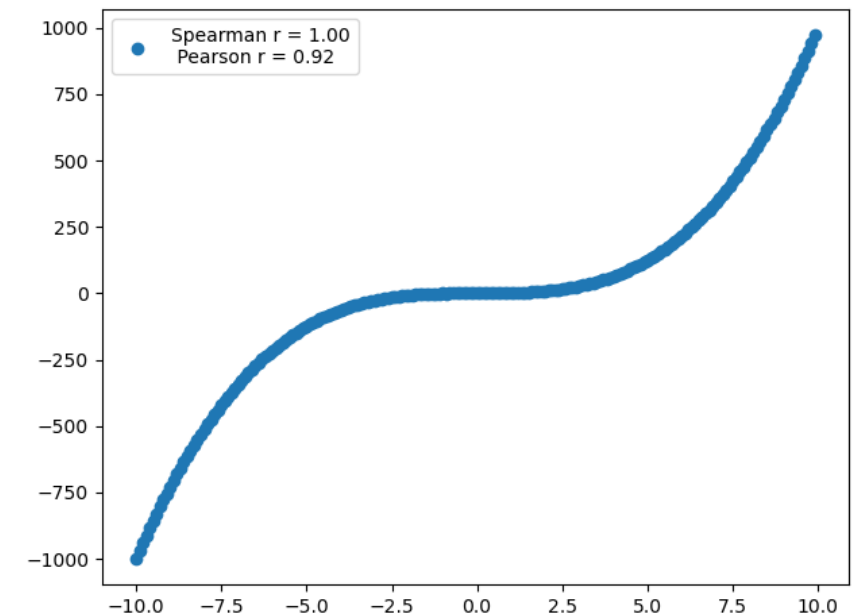
Mean average μ

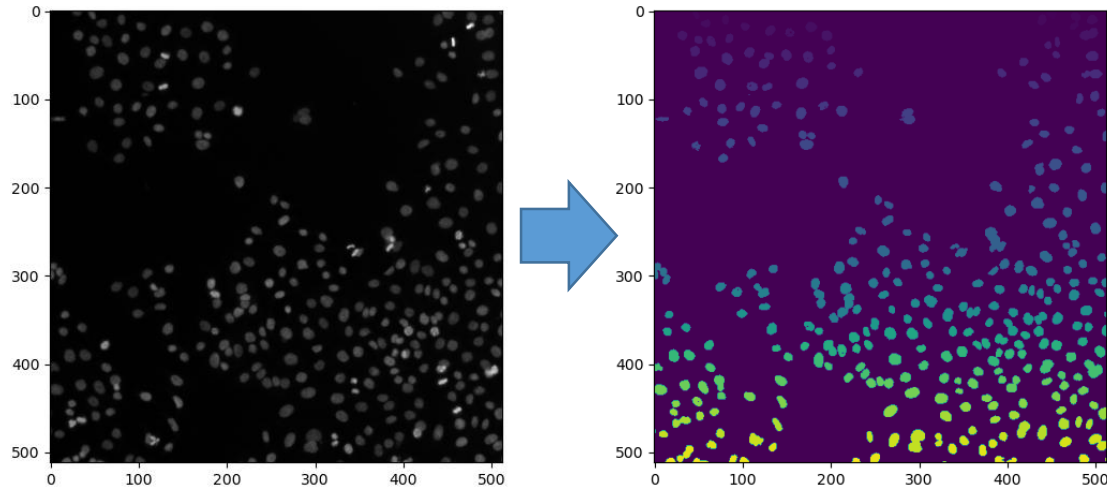
$$r_{\text{Spearman}}(X, Y) = \frac{E[(X' - \mu_{x'})(Y' - \mu_{y'})]}{\sigma_{x'}\sigma_{y'}}$$

Standard deviation σ

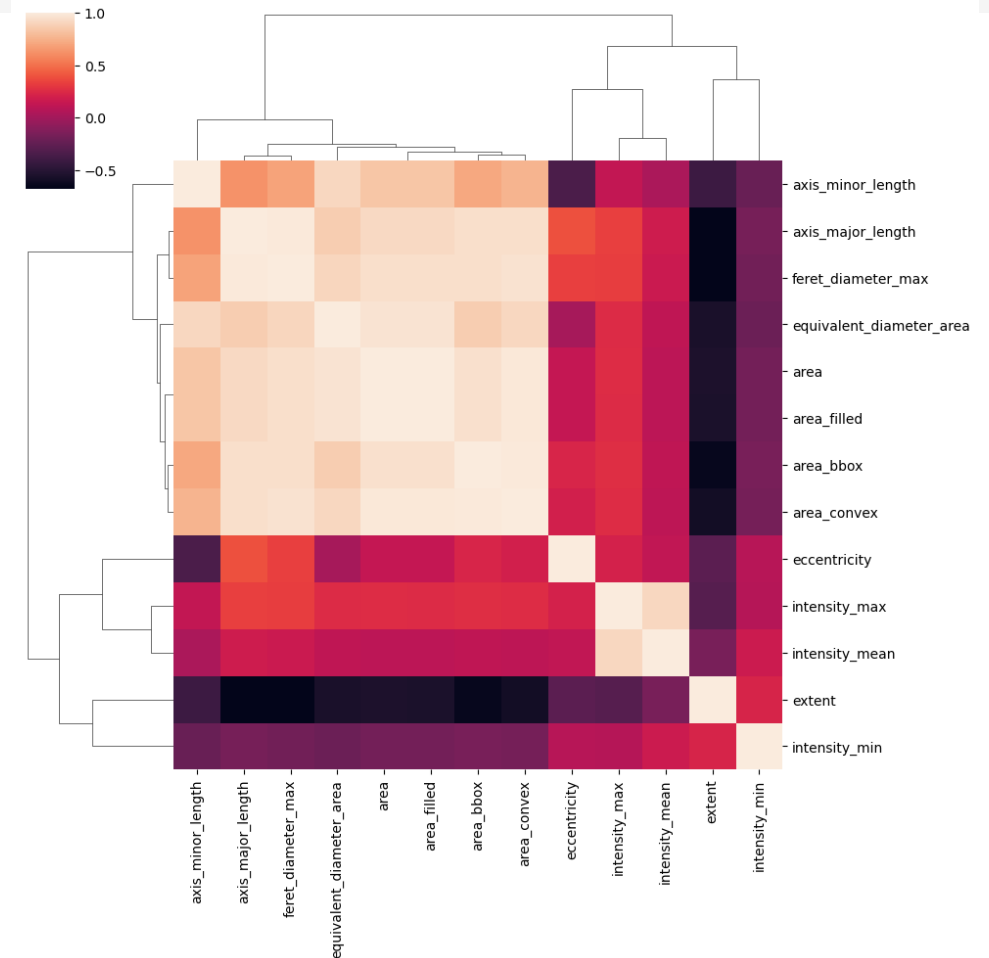
Spearman's r is equivalent to using Pearson's r on ranked data:

- μ_x : Mean of Samples in X
- μ_x : Mean of ranks of samples in X





```
properties=['area', 'area_bbox', 'area_convex',  
            'area_filled', 'axis_major_length',  
            'axis_minor_length', 'eccentricity',  
            'equivalent_diameter_area', 'extent',  
            'feret_diameter_max', 'intensity_max',  
            'intensity_mean', 'intensity_min']
```



Feature selection: Measuring many features usually brings along some redundancies

- Use the correlation coefficient to remove or group such features
 - Create meta-feature (linear combination, mean, etc.) from correlating features (scaling!)
 - Pick one
- Downstream analysis works better with fewer, relevant features

Hypothesis testing

Johannes Müller

With material from
Anna Poetsch

```
result = stats.pearsonr(x,y)  
result
```

```
PearsonRResult(statistic=-0.8868881579356616, pvalue=2.595689084498263e-14)
```



P-values: Probability that the **null hypothesis H_0** is true, but rejected by chance

General: It is (usually) much easier to falsify a statement than proving it true

Example 1: $x^n + y^n = z^n$ for $n \geq 3$ and $x, y, z \in \mathbb{Z}$

→ this took 358 years to prove – If we could have found just a single combination of x, y & z , we would immediately be done

Example 2: Albert Hammond (1972): *It never rains in southern california*

→ Very hard to prove – very easy to disprove

H_0 hypothesis: A treatment agent is ineffective/There is no difference between two groups/Cell fate is not correlated to feature_x

https://en.wikipedia.org/wiki/Fermat%27s_Last_Theorem


```
result = stats.pearsonr(x,y)
result
```

```
PearsonRResult(statistic=-0.8868881579356613, pvalue=2.595689084498263e-14)
```

H₀ hypothesis: correlation coefficient $r=0$

In scipy: **alternative** : {'two-sided', 'less', 'greater'}, optional

Defines the alternative hypothesis. Default is 'two-sided'. The following options are available:

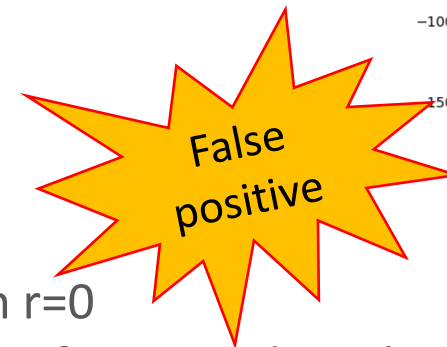
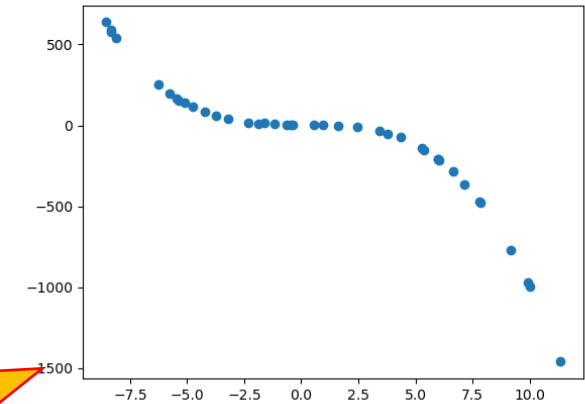
- 'two-sided': the correlation is nonzero H_0 ?
- 'less': the correlation is negative (less than zero) H_0 ?
- 'greater': the correlation is positive (greater than zero) H_0 ?

P-value: Probability that correlation coefficient $r \neq 0$ although $r=0$

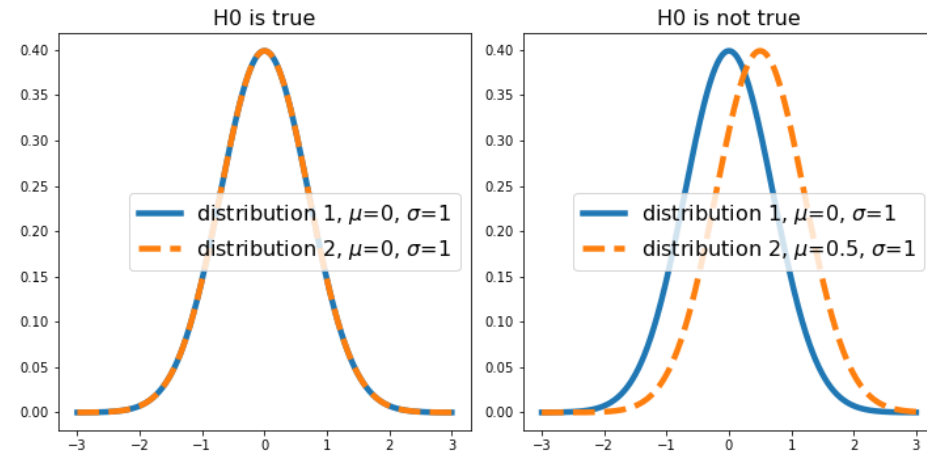
"We just happened to draw an unfortunate selection of points from our data that looked like correlation – the odds of this happening was p "

How small should the p-value be to confidently reject H_0 ? → alpha-value

- Don't set a threshold – just report
- Some pleasant number (0.05, 0.001, etc.)
- A common value in the field (0.05, 5σ , etc.)



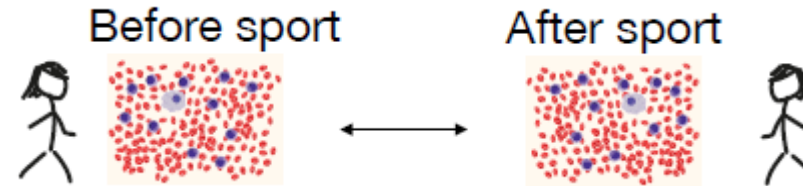
P-VALUE	INTERPRETATION
0.001	HIGHLY SIGNIFICANT
0.01	
0.02	
0.03	
0.04	SIGNIFICANT
0.049	
0.050	OH CRAP. REDO CALCULATIONS.
0.051	ON THE EDGE OF SIGNIFICANCE
0.06	
0.07	HIGHLY SUGGESTIVE, SIGNIFICANT AT THE $P < 0.10$ LEVEL
0.08	
0.09	
0.099	HEY, LOOK AT THIS INTERESTING SUBGROUP ANALYSIS
≥ 0.1	



Comparing two (normal) distributions

→ Unpaired t-test (H_0 : The means are different)

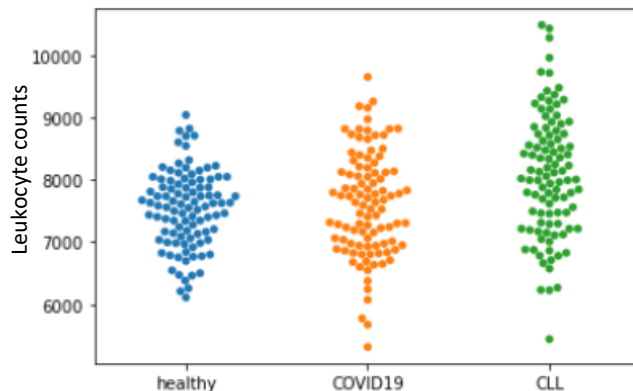
→ Paired t-test (H_0 : $X_{\text{after}} - X_{\text{before}} = 0$)



Alternative: Wilcoxon-Mann-Whitney-Test if assumptions are violated

Many observations don't follow normal distributions

- (Cell) count data: Poisson distribution
- Binary outcomes (e.g., coin flip): Binomial distribution
- Each provides appropriate tests



Comparing multiple groups:

- ANOVA (analysis of variances), H_0 : No differences between distributions
- Requires “post-hoc” tests to find out which groups are different

Data skewed by outliers:

- Consider comparing ranks rather than raw data

Multiple testing: More tests \rightarrow more type I errors (false positives)

Strategies:

1. Control family-wise error rate $\text{FWER} = P(n_{\text{false positives}} \geq 1) = 1 - (1 - \alpha)^N$

Bonferroni correction: $\alpha_{\text{adj}} = \frac{\alpha}{N}$

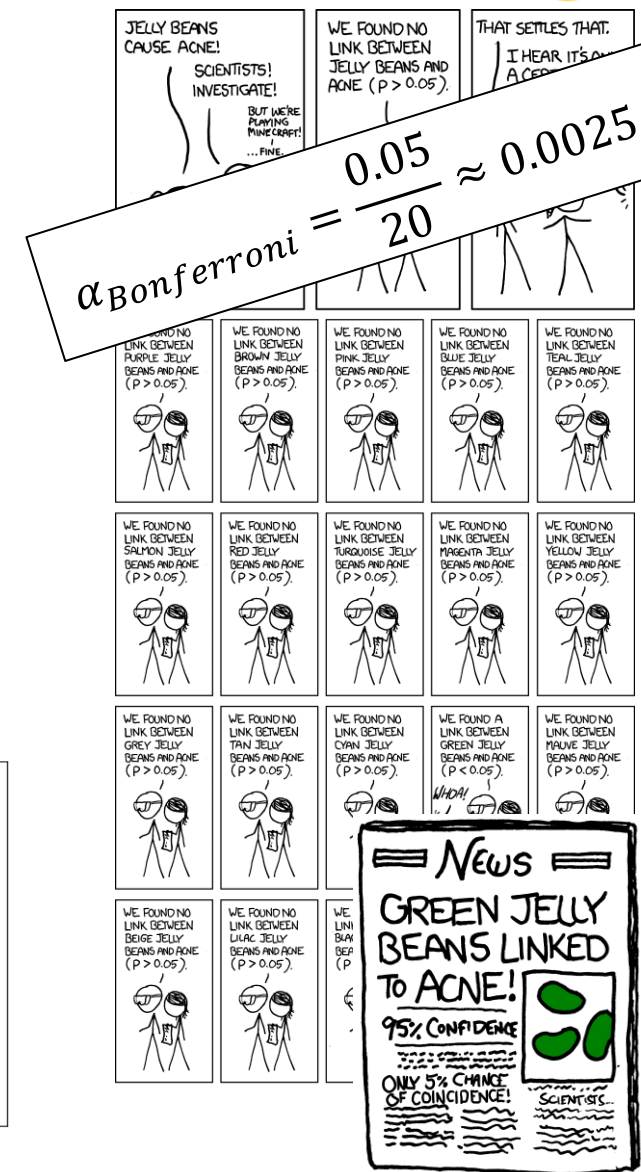
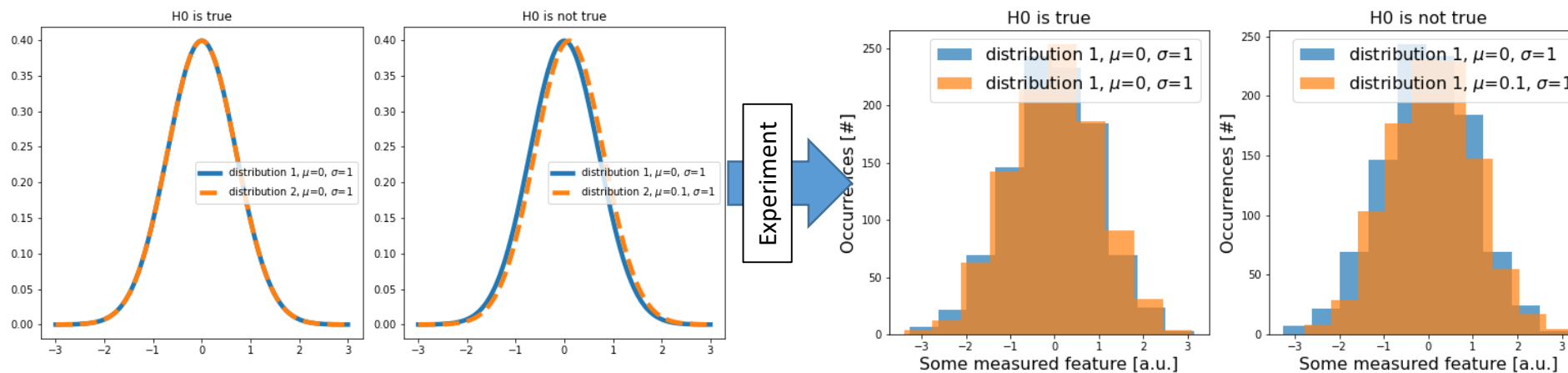
\rightarrow Prevents false positives (type I error)

\rightarrow Introduces false negatives (type II error)

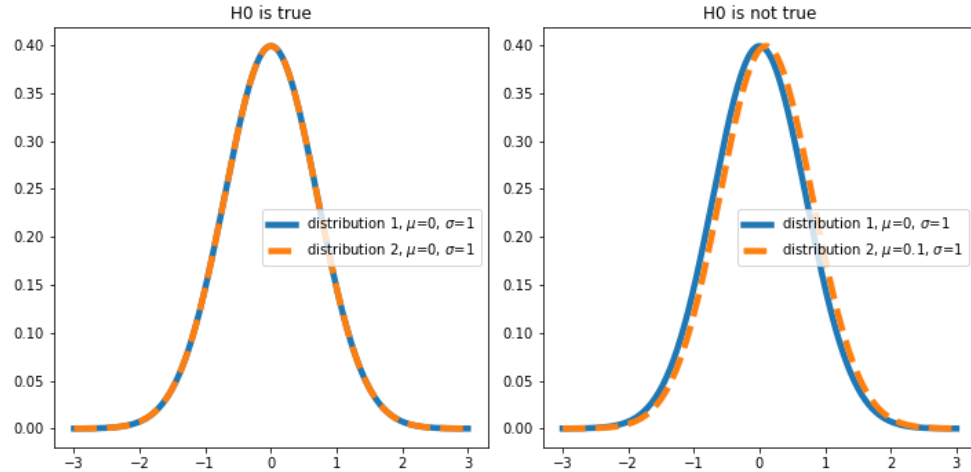
2. *Benjamini-Hochberg adjustment*: Control false discovery rate $\text{FDR} = \frac{\text{FP}}{\text{FP} + \text{TP}}$

\rightarrow Find largest k so that $p_k \leq \frac{k}{m} \alpha$ (p_k : p-value of rank k)

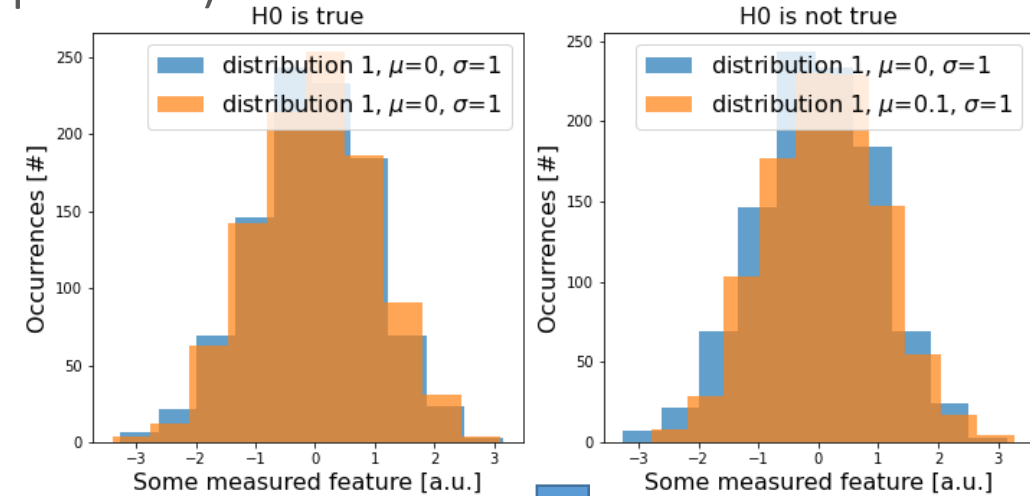
3. Tukey range test: Typically done after ANOVA, controls type I errors



Multiple testing: More tests \rightarrow more type I errors (false positives)



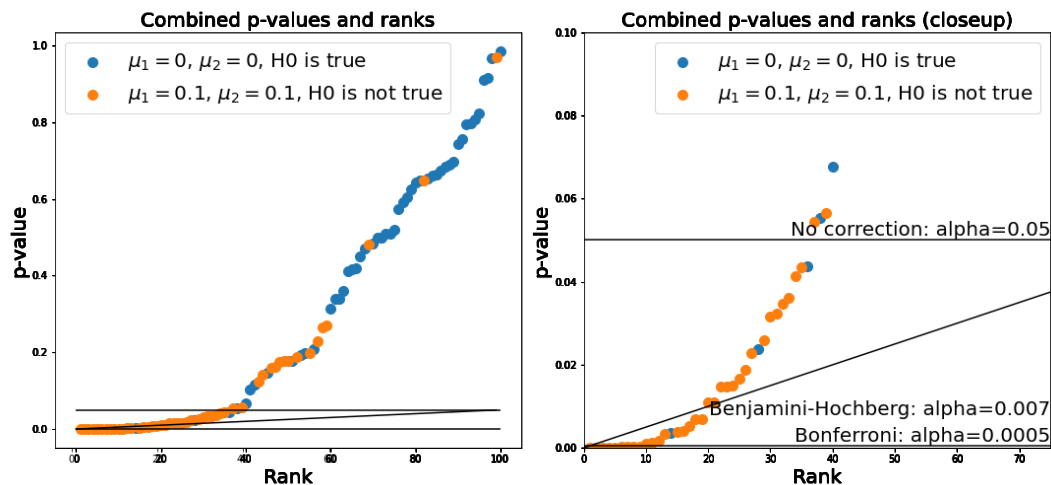
Experiment \rightarrow



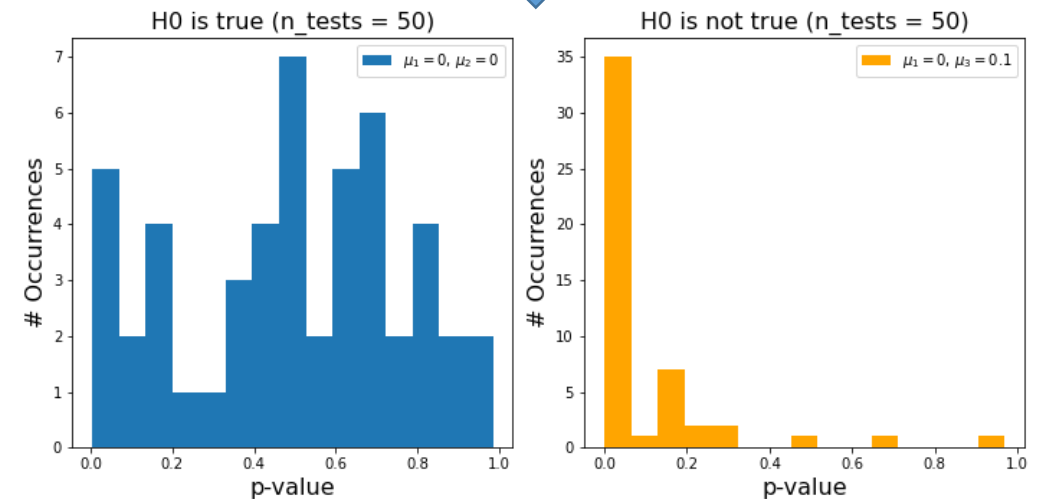
100 Experiments \downarrow

Multiple testing correction:

Separate cases (H0 true/false) in this plot:



Rank p-values \leftarrow



Multiple testing: More tests → more type I errors (false positives)

Distribution type: T-test assumes normal distribution of data

- Some data may follow different distributions (Poisson, binomial, etc.)
- The equivalent for a t-test exists for all other distributions, too!
- Less strict test types exist – ask your statistician!

Sample size: Do not perform statistical test with small ($n < 10$) sample sizes.

- If you work in this region (experiments expensive, animals, etc): Consult your local statistician!

Sample independence:

- T-tests are only valid if samples are independent: *“Two events are independent [...] if [...] the occurrence of one does not affect the probability of occurrence of the other”*

Examples:

Histological slices from same animal: Not independent

Same blood test derived from two patients: Independent

A small p-value indicates....

A big difference
between datasets

Small probability of
false positives

Small standard
deviations of the
compared groups

CURVE-FITTING METHODS AND THE MESSAGES THEY SEND

