



University of  
Zurich<sup>UZH</sup>

10  
01  
101

0101 10

functional genomics center zurich

01 01  
101 10  
010 01  
10 00  
01 11

# Exploratory Data Analysis

Hubert Rehrauer

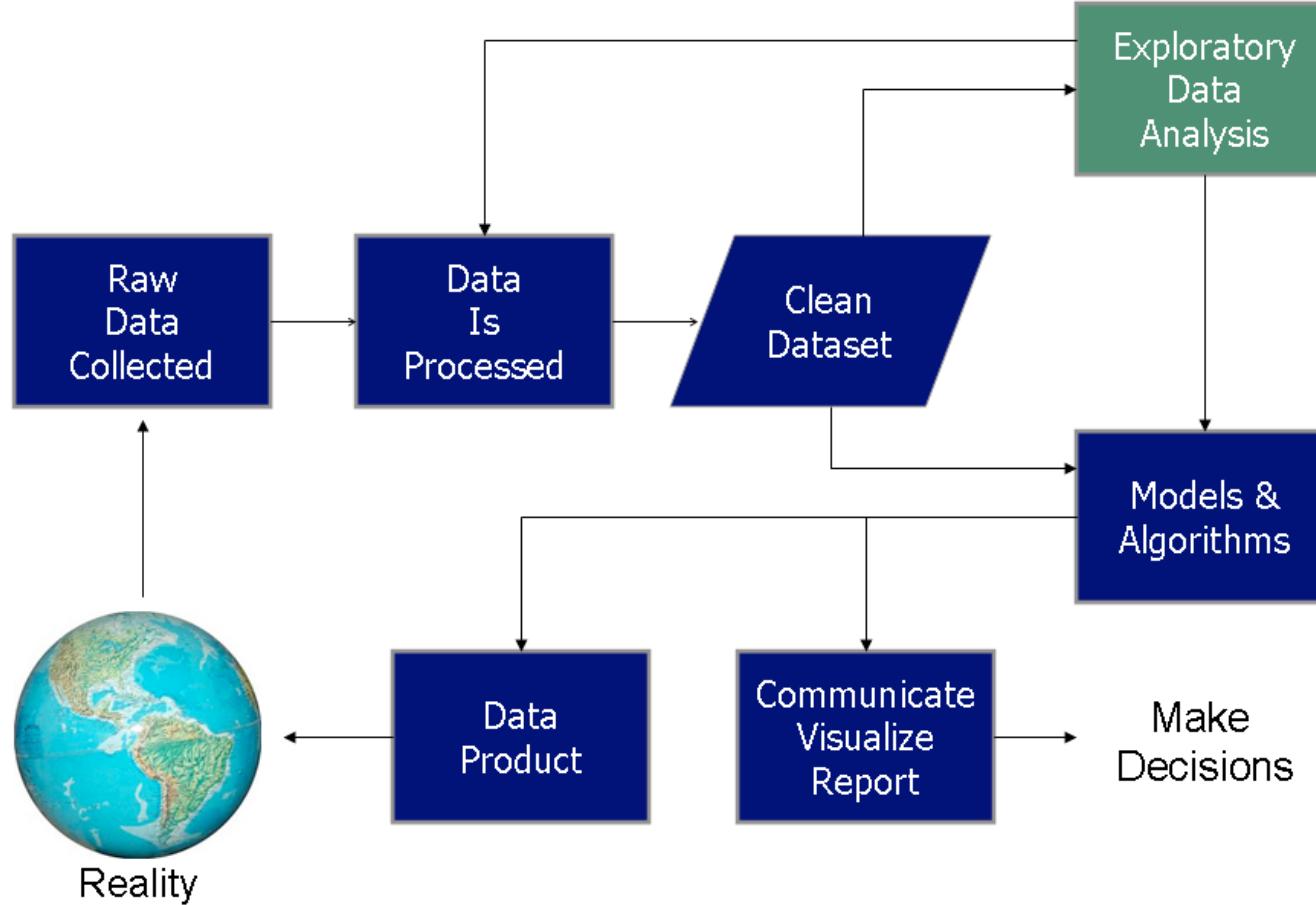


University of  
Zurich<sup>UZH</sup>

**ETH**

Eidgenössische Technische Hochschule Zürich  
Swiss Federal Institute of Technology Zurich

## Data Science Process



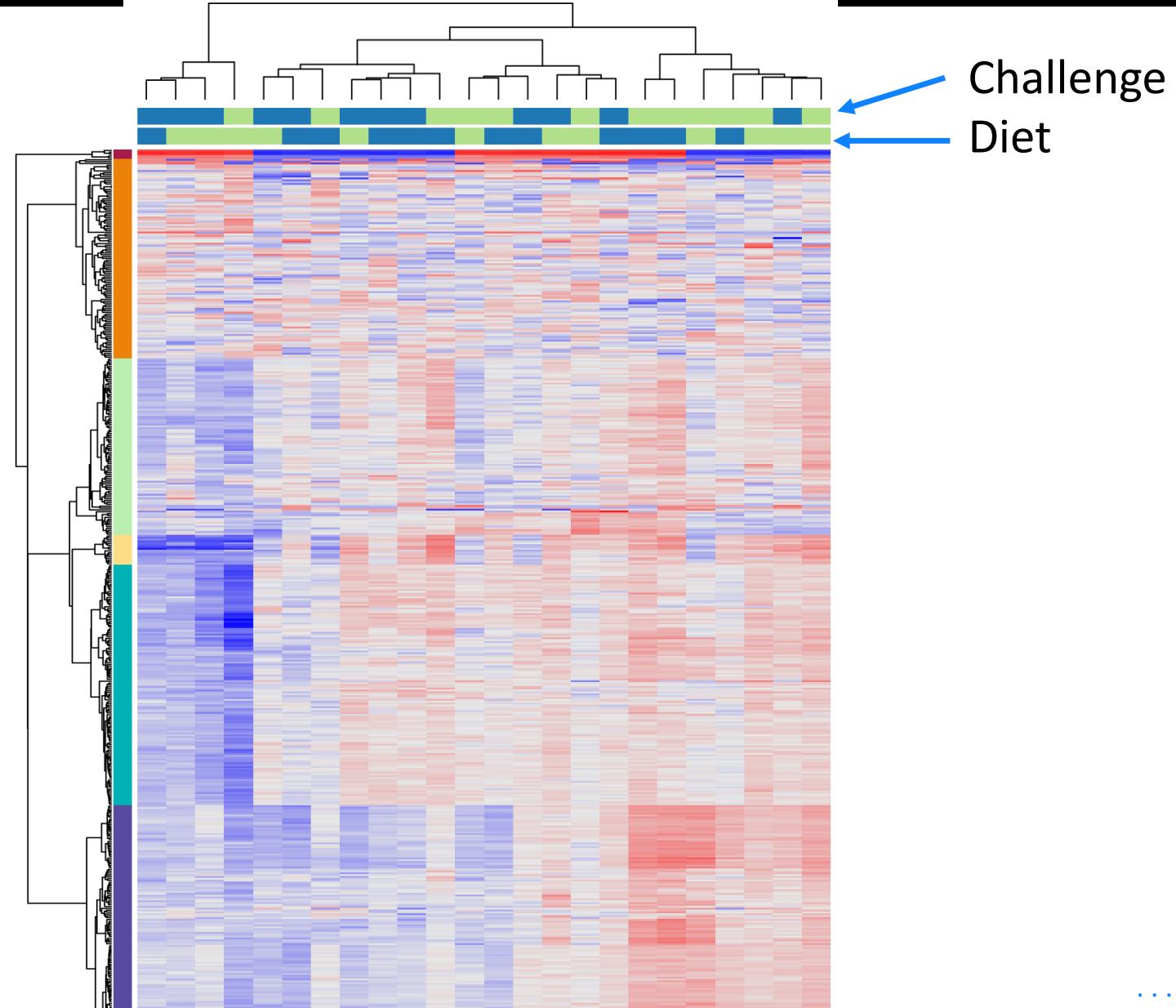
- summarize
- visualize
- characterize
- ...
- search for patterns

10  
01  
101

Columns are individuals  
Rows are genes

Individuals with the  
same Challenge and  
Diet are replicates.

Explanations???



10  
01  
101101 1  
010 0  
0101 1001 1  
01 0  
10 00 1  
0 0  
10 1  
01 1

## Dot map of cholera cases



John Snow, 1850, Source: <https://devopedia.org/exploratory-data-analysis>

# Periodic Table

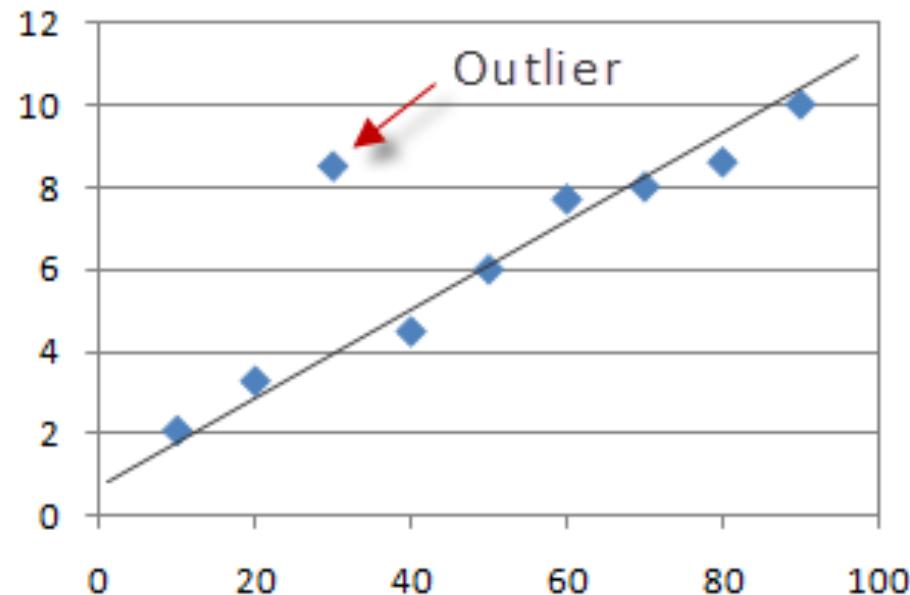
- made periodic structure apparent
- discovery of missing elements
- discovery of underlying principles

Group → 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18  
↓  
Period

1 H																	2 He	
3 Li	4 Be																	
11 Na	12 Mg																	
19 K	20 Ca	21 Sc	22 Ti	23 V	24 Cr	25 Mn	26 Fe	27 Co	28 Ni	29 Cu	30 Zn	31 Ga	32 Ge	33 As	34 Se	35 Br	36 Kr	
37 Rb	38 Sr	39 Y	40 Zr	41 Nb	42 Mo	43 Tc	44 Ru	45 Rh	46 Pd	47 Ag	48 Cd	49 In	50 Sn	51 Sb	52 Te	53 I	54 Xe	
55 Cs	56 Ba	57 La	*	72 Hf	73 Ta	74 W	75 Re	76 Os	77 Ir	78 Pt	79 Au	80 Hg	81 Tl	82 Pb	83 Bi	84 Po	85 At	86 Rn
87 Fr	88 Ra	89 Ac	*	104 Rf	105 Db	106 Sg	107 Bh	108 Hs	109 Mt	110 Ds	111 Rg	112 Cn	113 Nh	114 Fl	115 Mc	116 Lv	117 Ts	118 Og
*	58 Ce	59 Pr	60 Nd	61 Pm	62 Sm	63 Eu	64 Gd	65 Tb	66 Dy	67 Ho	68 Er	69 Tm	70 Yb	71 Lu				
*	90 Th	91 Pa	92 U	93 Np	94 Pu	95 Am	96 Cm	97 Bk	98 Cf	99 Es	100 Fm	101 Md	102 No	103 Lr				

10  
01  
101functional genomics center zurich  
010 01  
101 10  
010 01  
010 01  
f g c z  
10 00  
01 11  
01 10

## Simple visualization to find outliers



10  
01  
101

# Goals and methods of EDA

## Goals:

- Discover Patterns and Spot Anomalies
  - detection of trends but also mistakes
- Frame Hypothesis
  - assess direction and rough size of relationships between explanatory and outcome variables
- Check Assumptions
  - noise characteristics
  - preliminary selection of appropriate models

## Methods:

- **Visualize raw data**
- **Visualize statistics**
  - Visualize distributions
  - Visualize measures of central tendency (mean, median, mode)
  - Visualize measures of dispersion (range, standard deviation, ...)
- **Visualize relationships**

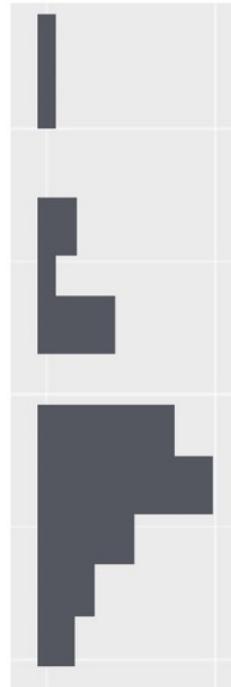


# Visualizing a single variable: Example of misleading boxplot

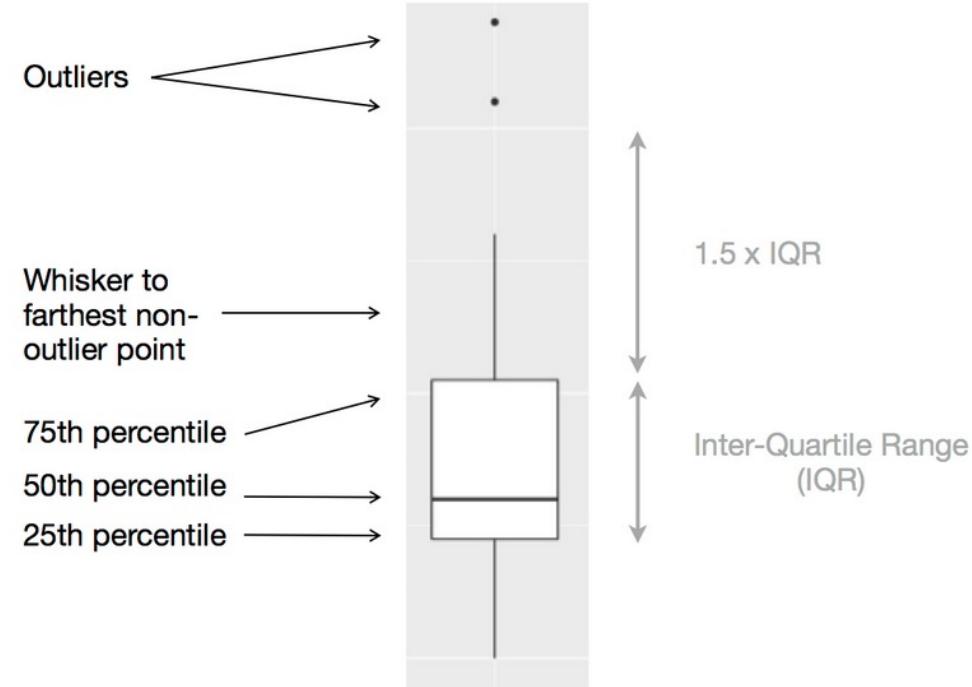
The actual values in a distribution



How a histogram would display the values (rotated)

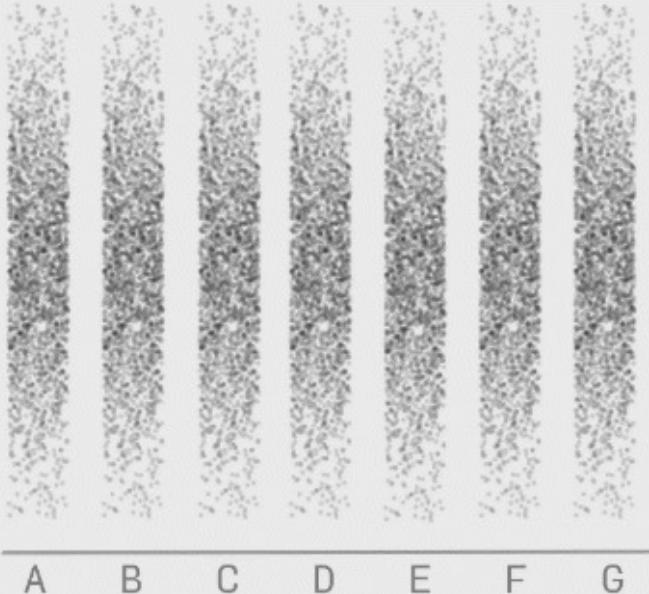


How a boxplot would display the values

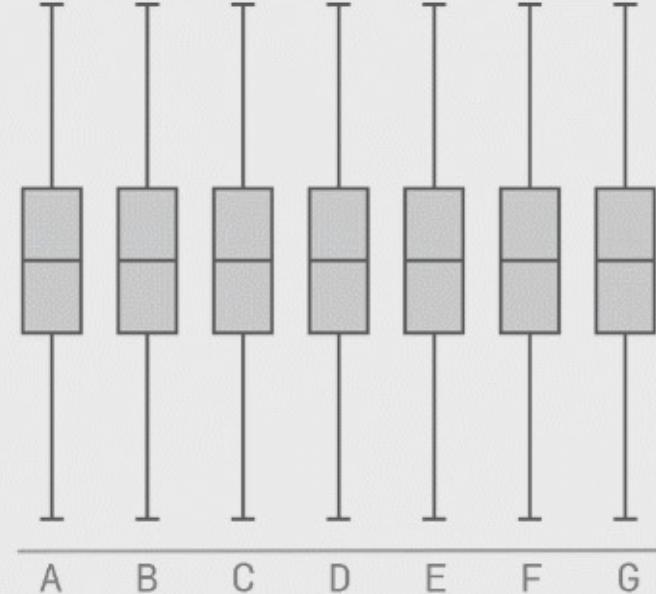


10  
01  
101functional genomics center zurich  
01 1  
01 01  
101 10  
010 01  
010 10  
f g c z  
10 01  
01 1

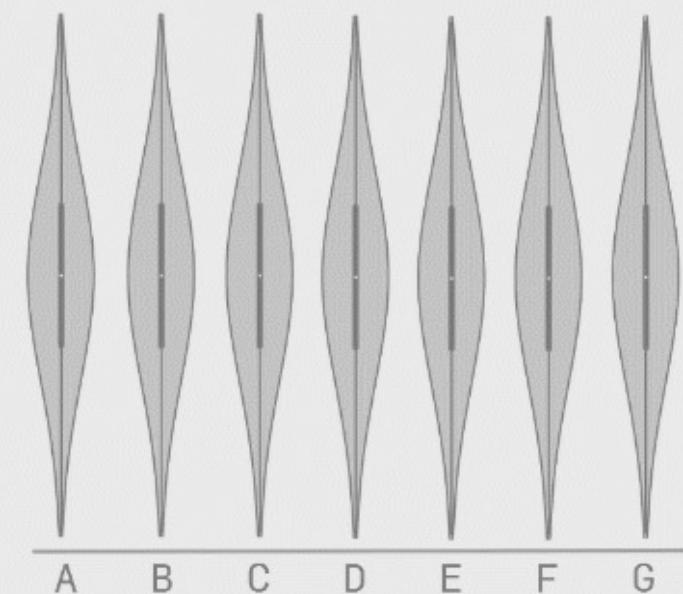
Raw Data



Box-plot of the Data



Violin-plot of the Data

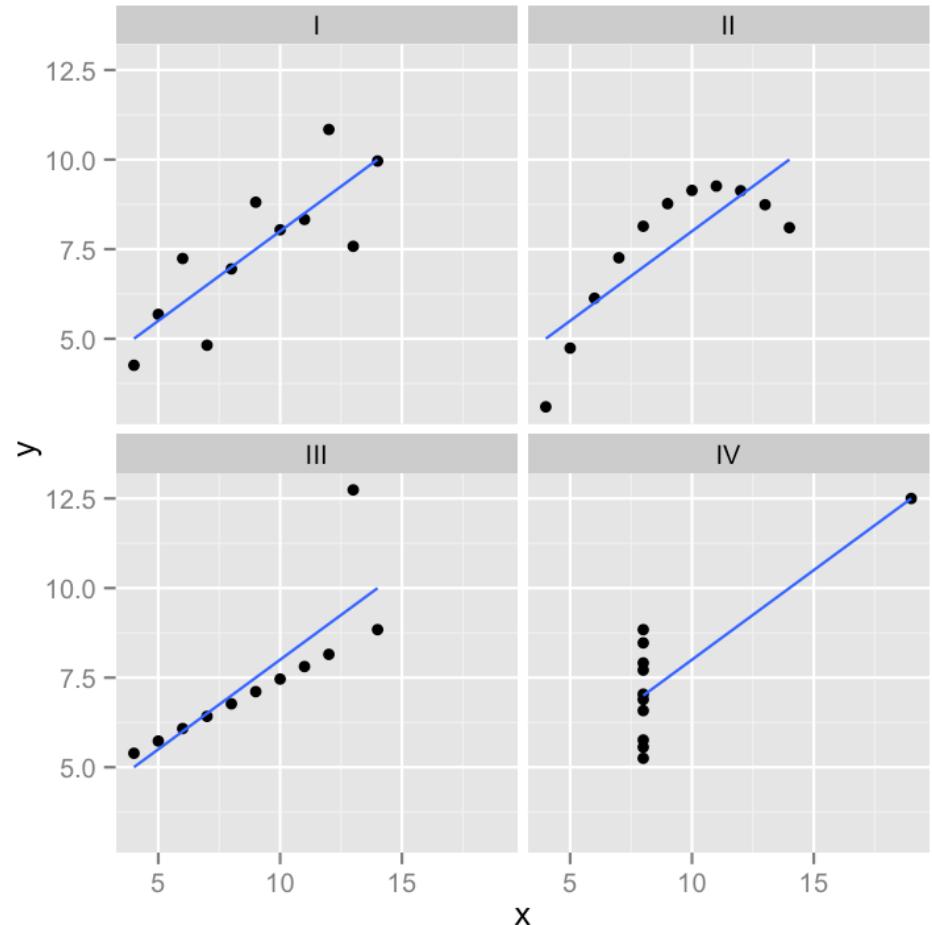


- never use boxplots!
- use violin, add data points if number is low (~50)



## Visualizing two variables: Anscombe's quartet

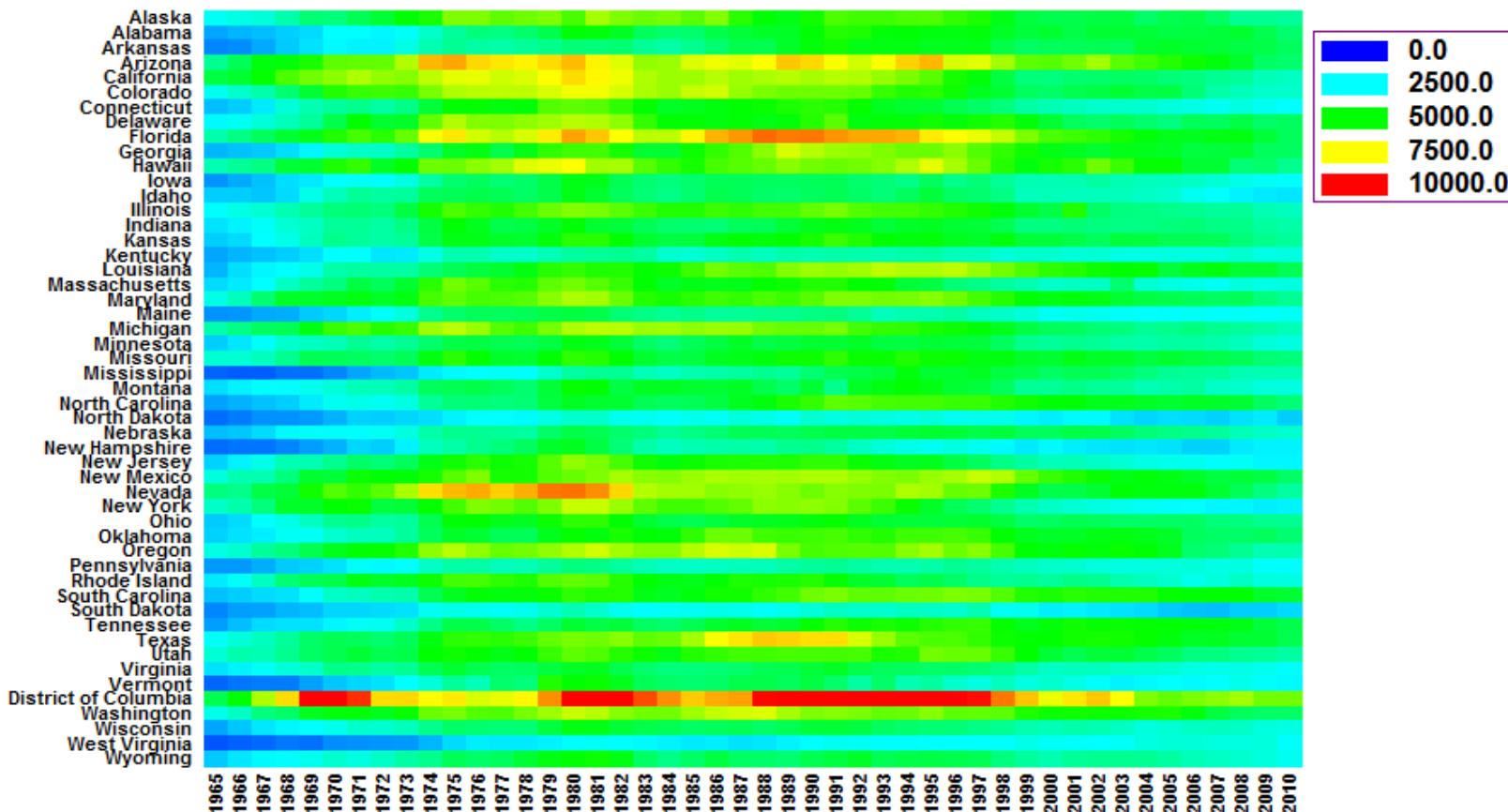
- All 4 datasets have nearly identical
  - mean
  - standard deviation
  - skewness & kurtosis
- Summarizing the data is not enough
- You have to visualize!





# Visualizing three variables

## Heat Map for Total Crime Rate





10

01

101

00

..

..

..

..

..

..

..

..

..

..

..

..

..

..

..

..

..

..

..

..

..

..

..

..

..

..

..

..

..

..

..

..

..

..

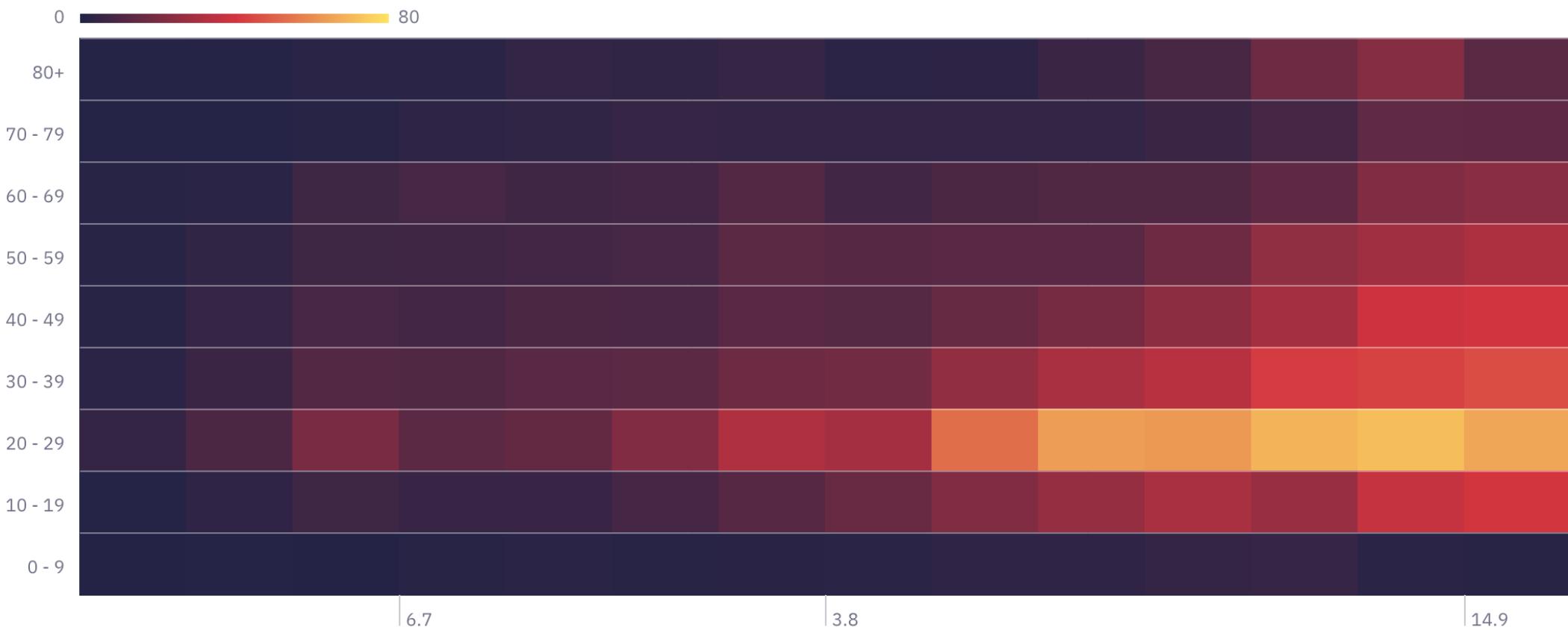
..

..

..

..

## Age distribution of COVID cases over time (2020)





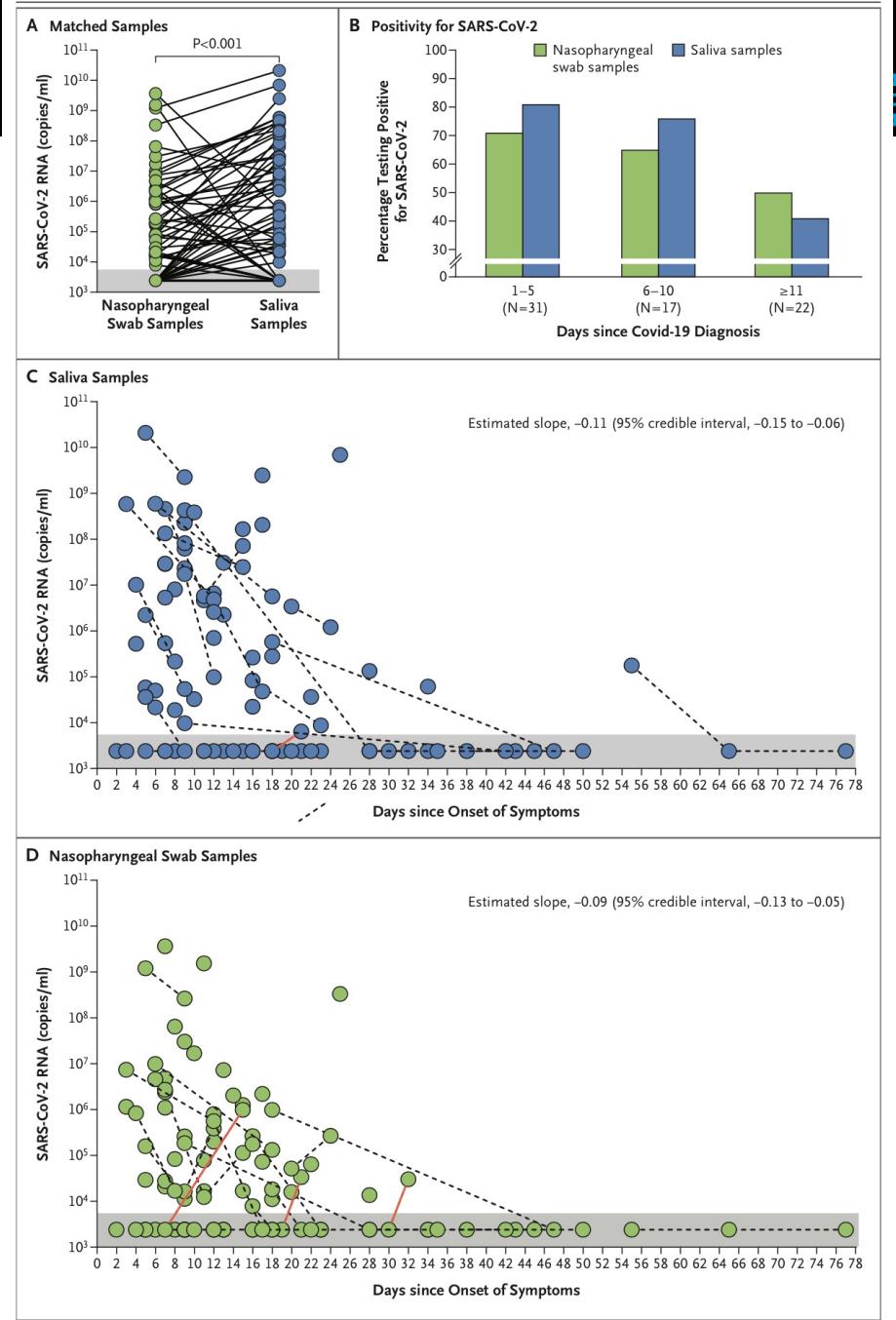
## Age distribution of COVID cases over time (2020)





# Covid: Nasal swabs vs saliva

- Can SARS-CoV2 be detected in Saliva?
- Both methods detect the virus
- Plot A triggers a data exploration question: Why are there so many subjects where the two methods disagree so strongly?



10  
01  
101functional genomics center zurich  
01 1  
0 0  
101 10  
010 01  
101 10  
010 01  
01 1  
10 0  
01 1

# Mutations in Vitamin D Receptor and sex hormone levels in elderly people

Attribute name	Description
AGE	age in years
HEIGHT	height given in [cm]
WEIGHT	weight in [kg]
WAISTLINE	waistline given in [cm]
HIP.GIRTH	hip girth given in [cm]
BMI	the body to mass index [ $\text{kg}/\text{m}^2$ ]
FAT	Amount of body fat as percentage of body weight [%]
CHOL.HDL	Cholesterol serum level—High Density Lipoprotein [mg/dl]
CHOL.LDL	cholesterol serum level—Ligh Density Lipoprotein [mg/dl]
CHOL.TOTAL	total level of cholesterol [mg/dl]
TGC	serum level of triglycerides [mg/dl]
GLUCOSE	Serum Glucose level [mg/dl]
INS	serum level of insulin [ $\mu\text{IU}/\text{ml}$ ]
TESTOSTERONE	serum level of testosterone [nmol/l]
ESTRADIOL	serum level of Estradiol [pmol/l]
DHEA.S	serum level of Dehydroepiandrosteron [ng/dl]
SHGB	serum level of sex hormone binding globulin [pmol/l]
FAI	Free Androgen Index defined as the ratio of total testosterone to SHBG $\times 100$ [19]
FEI	Free Estradiol Index defined as the ratio of total estradiol to SHBG $\times 100$ [19]
FSH	Serum Follicle-Stimulating Hormone level [IU/l]
ICTP	serum level of carboxy-terminal cross-linked telopeptide of type I collagen [mg/l]
OPG	serum level of osteoprotegerin [pmol/l]
VITAMIN.D	serum level of Vitamin D [ng/ml]

<https://doi.org/10.1371/journal.pone.0201950.t001>

Attribute name	Description
AGE.GROUP	age in discretized groups (5 year bins)
CG1.IDENTIFIED.DIABETES.YES	binary; 1 if observed
CITY.SIZE	city size bins: countryside, population < 20 thousand, 20–50 thousand, 50–100 thousand, 100–500 thousand, > 500 thousand
HYPERANDROGENISM.YES	binary; 1 if observed
HYPERTENSION.YES	binary; 1 if observed
INSOLATION.YES	binary; 1 if in summer and spring
MACROREGION	6 binary attributes: ‘north’, ‘east’, ‘south’, ‘central’, ‘north-west’, ‘south-east’
OBESTIY_PHENO_FLMHO	binary; obesity phenotype—metabolic healthy obesity [20]
OBESTIY_PHENO_FLMONW	binary; obesity phenotype—methabolic obesity normal weight [21]
OBESTIY_PHENO_FLOMWD	binary; obesity phenotype—obesity methabolic weist disease [20]
OBSETITY_PHENOOBZM	binary; obesity phenotype—adjustment of FLMHO for Polish population
OBSETITY_PHENOOZZM	binary; obesity phenotype—adjustment of FLMONW for Polish population
YEAR_SEASON	4 binary attributes: ‘winter’, ‘spring’, ‘summer’, ‘autumn’

<https://doi.org/10.1371/journal.pone.0201950.t002>

<https://journals.plos.org/plosone/article?id=10.1371/journal.pone.0201950>



# Mutations in Vitamin D Receptor and sex hormone levels in elderly people

- 515 participants
- 44 attributes



Subjects  
Explanatory variables

- Which attributes have an impact on the hormone levels?
- Are there attributes that are correlate with the receptor mutations? If yes, these are confounding factors

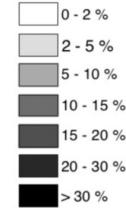
	AGE	SHGB	FSH	TESTOSTERONE	ESTRADIOL	DHEA.S	FAI	FEI	HEIGHT	WEIGHT	FAT	WAISTLINE	HIP.GIRTH	BMI	C
1	92	117.8	53	0.12	4.4	300	0.353174	0.0137	151	41.1	25.7	94	90	18.025525	
3	58	67.2	76.5	0.15	3.7	656	0.773883	0.0202	170	69	34	92	102	23.875432	
5	67	53.7	94.9	0.2	4	109	1.291247	0.0273	143	60.1	33.9	106	90	29.39019	
6	75	51.6	9.6	3.31	10.2	609	22.23986	0.0725	174	74.1	29	100	104	24.474832	
8	59	34.5	46.8	0.32	3.6	565	3.215768	0.0383	164	70	38	89	103	26.026175	
9	83	55.5	56.3	0.17	3.9	750	1.061963	0.0257	152	61.2	31.3	87	99.5	26.48892	
10	77	73.8	21.5	7.56	19.7	1298	35.51560	0.0979	162	54.9	17.3	80	96	20.919067	
13	57	102.4	116.9	0.41	5.8	632	1.388154	0.0207	154	61.5	33.8	83	104	25.93186	

```

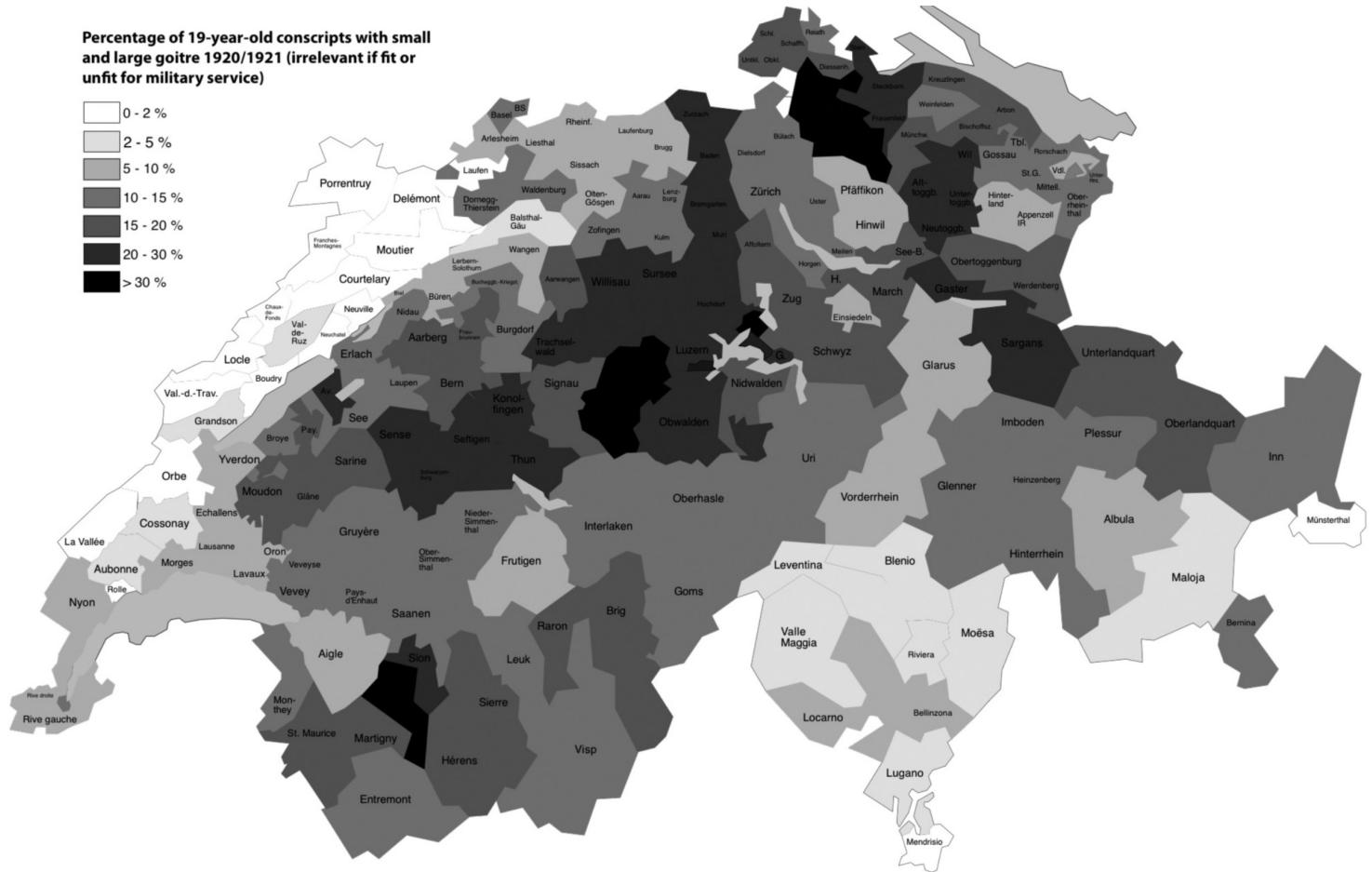
    10
    01
    101
    101 1
    010 0
    0101 10
    0101 10
    010 01
    101 10
    010 01
    101 10
    01 1
    01 0
    10 0
    01 1
  
```

# goiter – thyroid disease

Percentage of 19-year-old conscripts with small and large goitre 1920/1921 (irrelevant if fit or unfit for military service)



- caused by lack of iodine in nutrition



Source: RCC Perspectives , No. 3, Sickness, Hunger, War, and Religion: Multidisciplinary Perspectives (2012), pp. 75-90

# Quantitative Omics Data

- Gene expression data:
  - Quantification of relative mRNA abundance in cells/tissues
- Protein expression data
  - Quantification of relative protein abundance in cells/tissue
- Methylation status
- ...
- 10s – 100s subjects
- 1 – 10s attributes
- Additional:
- ~25'000 genes as explanatory variables

gene_name	Untreated_00	Untreated_00	Untreated_00	TSA_001	TSA_002	TSA_003	TFNA_001	TFNA_002	TFNA_003	DMSO_001	DMSO_002	DMSO_003
Actb	893495	837711	832581	1472528	981134	1120678	991944	1101636	1229135	1139451	1051921	1207426
Cd74	995494	787673	875016	949493	825139	818025	779110	901570	890373	875348	797970	746900
Psap	208993	174402	271321	327882	329209	287670	328943	345473	316682	443061	422382	375204
H2-Ab1	426933	343484	417642	449921	392453	392767	393112	439128	425410	414268	385411	344702
Wdfy4	179716	159346	203653	247430	204304	232487	207341	233608	226601	180468	192222	206202
Eef1a1	199487	170600	184701	237333	203035	214763	187098	236834	225352	204775	182308	199842
H2-Eb1	216846	199178	230637	265651	229147	227300	215171	255286	242801	238764	218298	192494
Tmsb4x	173784	146600	178973	254074	193715	218451	183551	212768	222196	184576	177274	183352

# Data Generation Workflow

Experiment



Omics method



Raw “machine” data



Raw quantitative  
data



- Normalization
- Transformation
- Visualization
- Quality Control
- Outlier Detection



- Quantitative sample differences



- Characteristics
  - obtained after analog signal transduction and amplification
  - not calibrated; no physical units
  - thousands or millions of measurements
  - measurements are at molecular scale



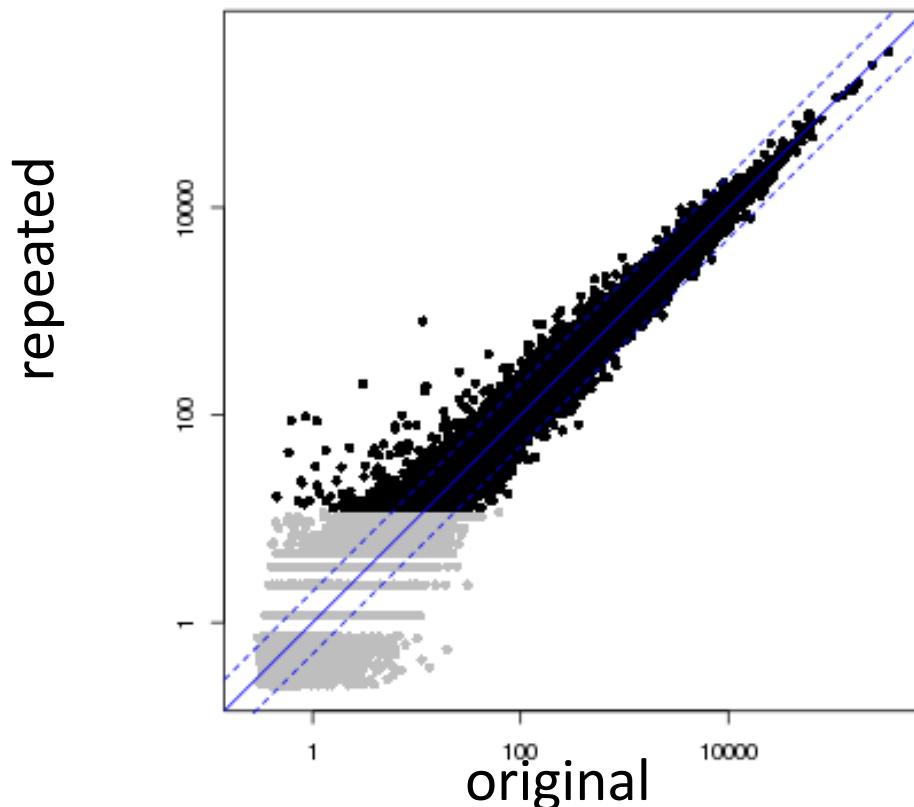
## Technical characteristics

- Dynamic Range
  - $\sim 10^4$  to  $10^6$ : largest value can be a million times higher than lowest values
  - non-linearity of measurement device
- Zero Measurements
  - additive background signal
  - zero value can have different explanations
    - technical failure to detect
    - value is truly zero
- Variability
  - Non-Gaussian noise

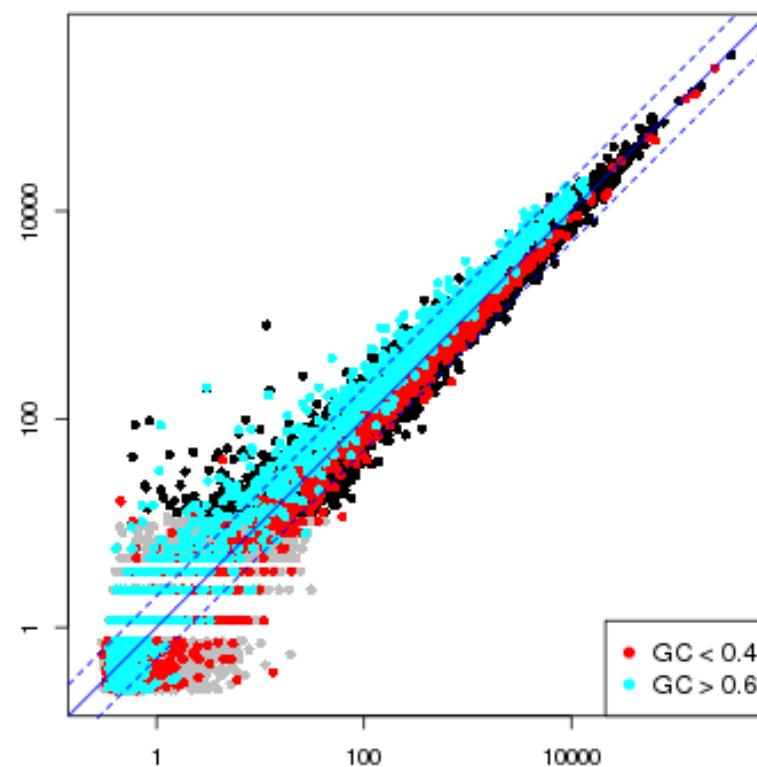
10  
01  
101

## Example of Quantitative Data

Comparison of a repeated experiment



Systematic effect of GC content on quantitative values



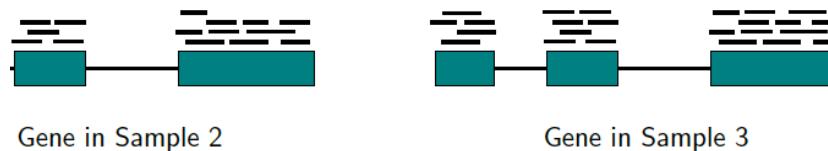
## Number of reads ≠ Expression level

	Sample 1	Sample 2	Sample 3
Gene A	5	3	8
Gene B	17	23	42
Gene C	10	13	27
Gene D	752	615	1203
Gene E	1507	1225	2455

- Gene D in the sample 3 has about twice as many reads aligned to it as in sample 2



- The gene is two times more expressed in sample 3 than in sample 2
- Difference in sequencing depth between samples – sequencing depth
- Longer isoform was expressed in sample 3 – transcript length



# Normalization & Transformation

- Scale samples so that all samples have the same total sum of expression values
  - We will cover more sophisticated methods later  
  - Methods that assume that the majority of genes has no expression change are usually more accurate



# Transformation

- Because of the large dynamic range of the expression values, the data should always be visualized at the log-scale  
→ Log Transform with an additive constant



## Data Exploration of RNA-seq data

- How similar are the expression profiles of the samples?
- Do the similarities match the experimental design and the anticipated effect sizes?
- Are samples within an experimental condition more similar than across conditions?
- Are there outliers?
- Distance measures for two expression profiles X und Y:
  - $1 - \text{correlation}(X, Y)$
  - Euclidian distance
  - ...
- Most frequently the correlation is used

10  
01  
10101 1  
01 0  
10 10  
010 01  
101 10  
010 01  
10 0  
01 1

## Euclidean Distance

Euclidean distance of two profiles  $\mathbf{x}$  and  $\mathbf{y}$  with  $p$  genes

$$d(\mathbf{x}, \mathbf{y}) = \sqrt{\sum_{i=1}^p (x_i - y_i)^2}$$

Note: Expression values should be at log scale



## Correlation measure

Correlation of two profiles with  $p$  genes:

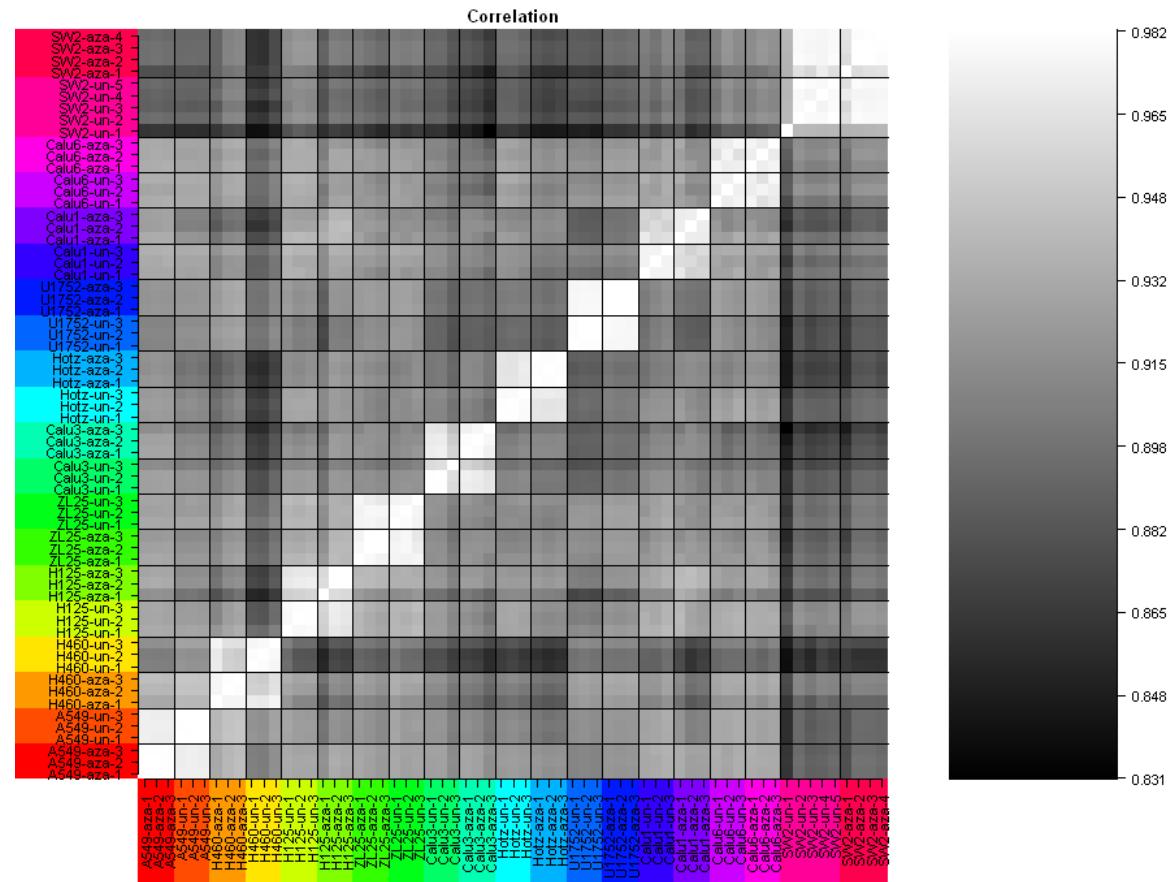
$$s(x, y) = \frac{\sum_{i=1}^p (x_i - \bar{x})(y_i - \bar{y})}{\sqrt{\sum_{i=1}^p (x_i - \bar{x})^2 \times \sum_{i=1}^p (y_i - \bar{y})^2}}$$

averages:  $\bar{x} = \frac{1}{p} \sum_{i=1}^p x_i$  and  $\bar{y} = \frac{1}{p} \sum_{i=1}^p y_i$ .

## Correlation matrix for samples

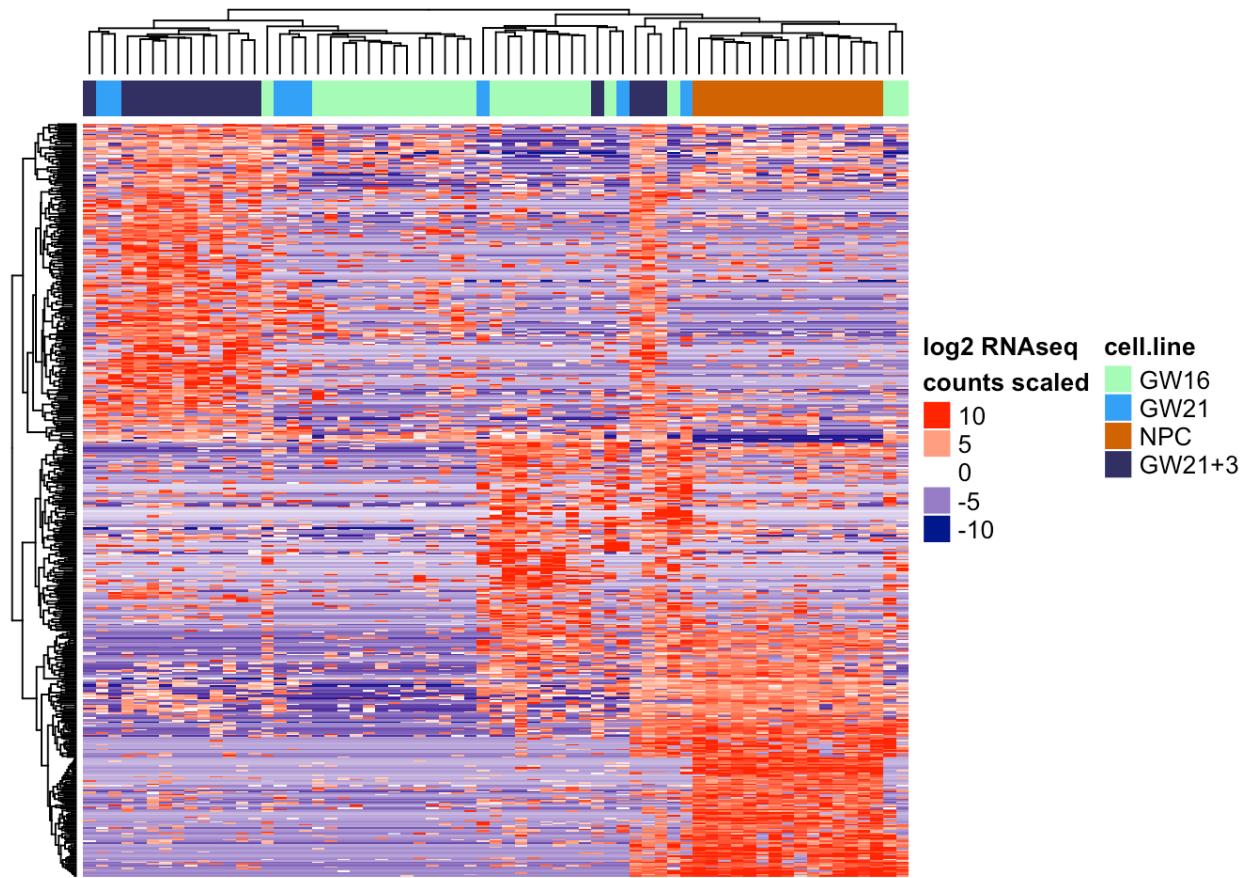
The matrix shows the correlation for all sample pairs.

This gives a quick overview on the presence of outliers.





## Example: Identifying Outlier Samples and Expression Structure



[https://rpubs.com/crazyhottommy/heatmap\\_demystified](https://rpubs.com/crazyhottommy/heatmap_demystified)



10

01

101

..

..

..

..

..

..

..

..

..

..

..

..

..

..

..

..

010

01

101

10

01

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01

10

01



# Hierarchical Clustering

## Goal

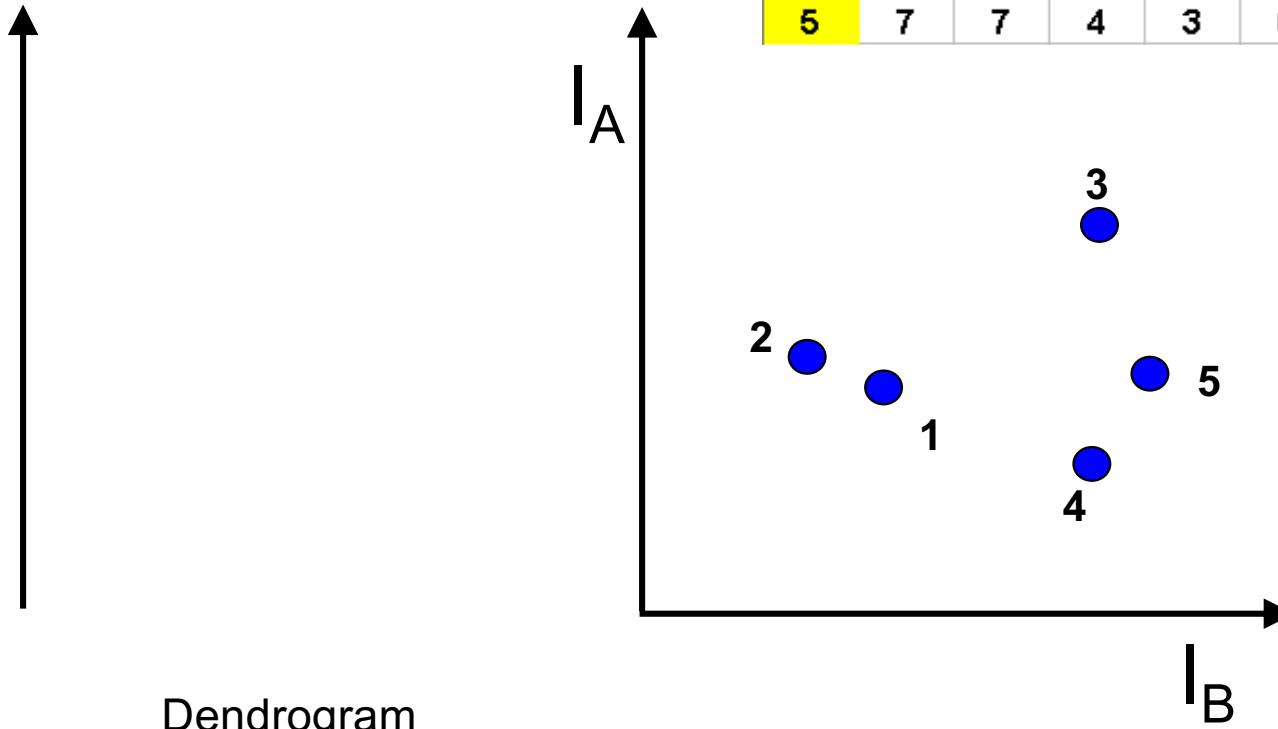
- Grouping of samples according to similarity

## Procedure

- Initialization
  - Every sample is a cluster
- Iteration:
  - Recursive joining of the most similar clusters

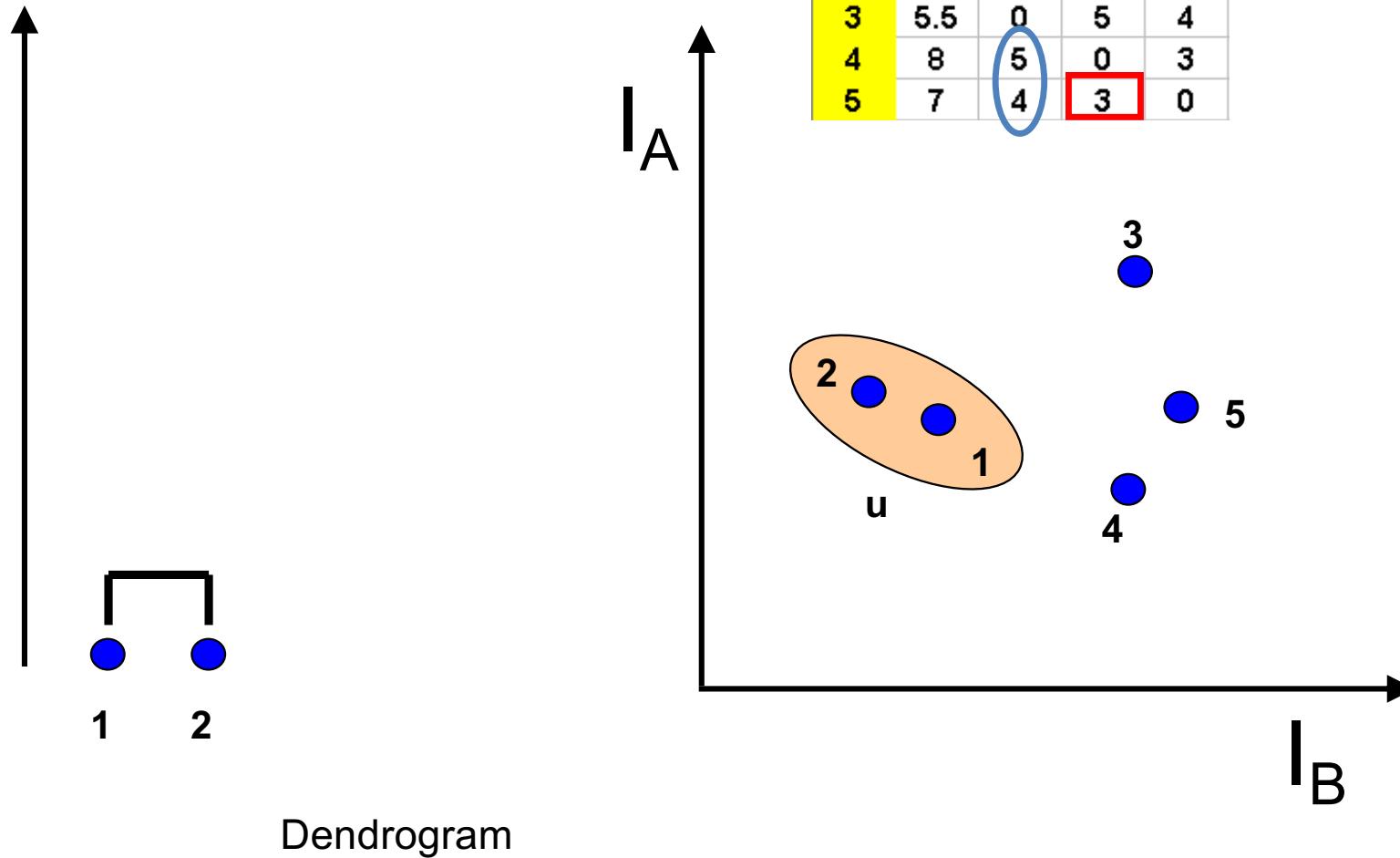
## Example

Cluster distances



# Example

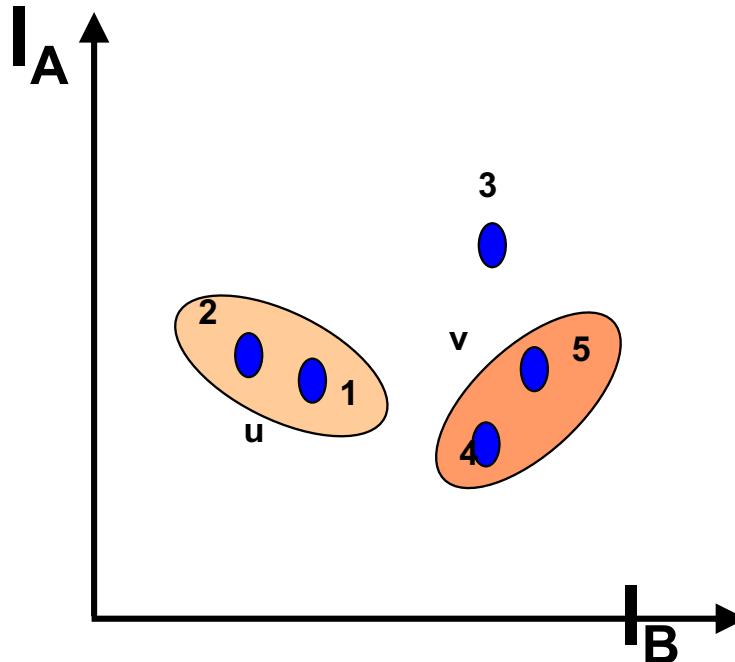
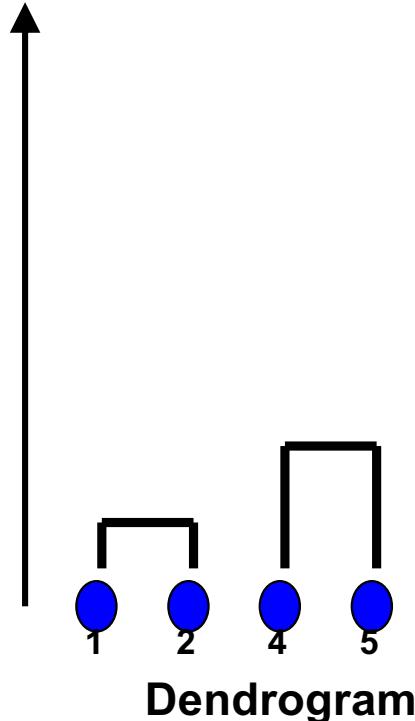
## Cluster distances



## Example

### Cluster distances

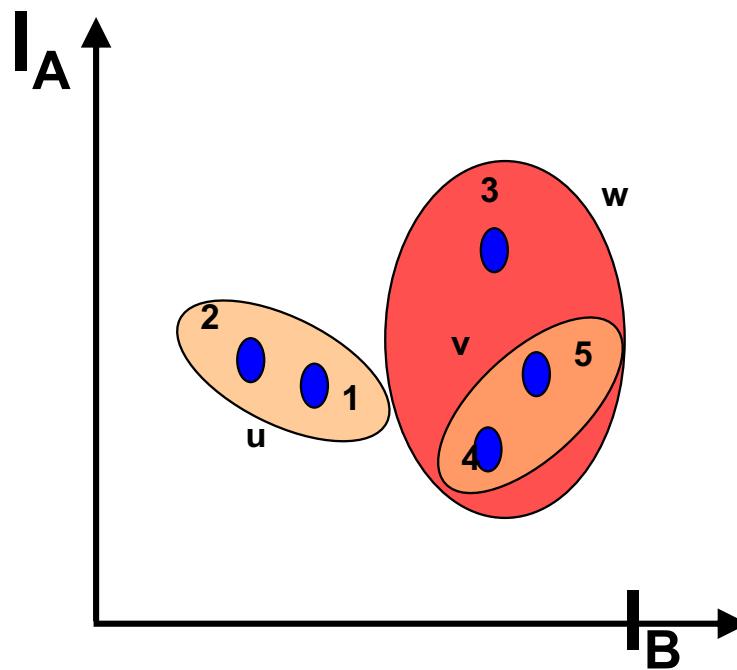
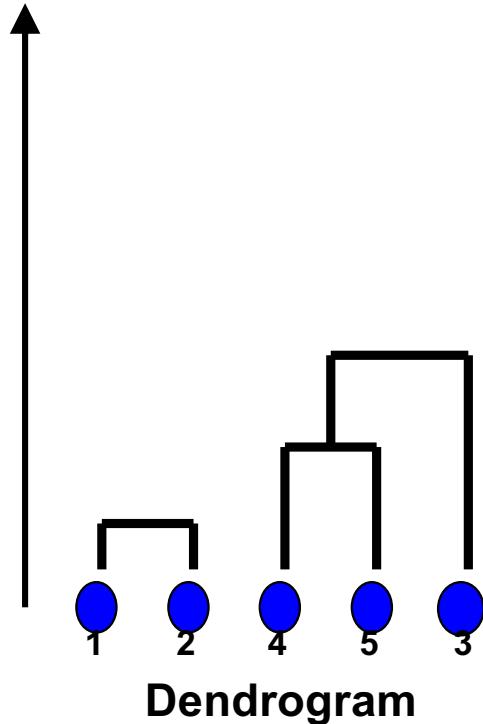
$d(ij)$	u	3	v
u	0	5.5	7.6
3	5.5	0	4.5
v	7.5	4.5	0



## Example

## Cluster distances

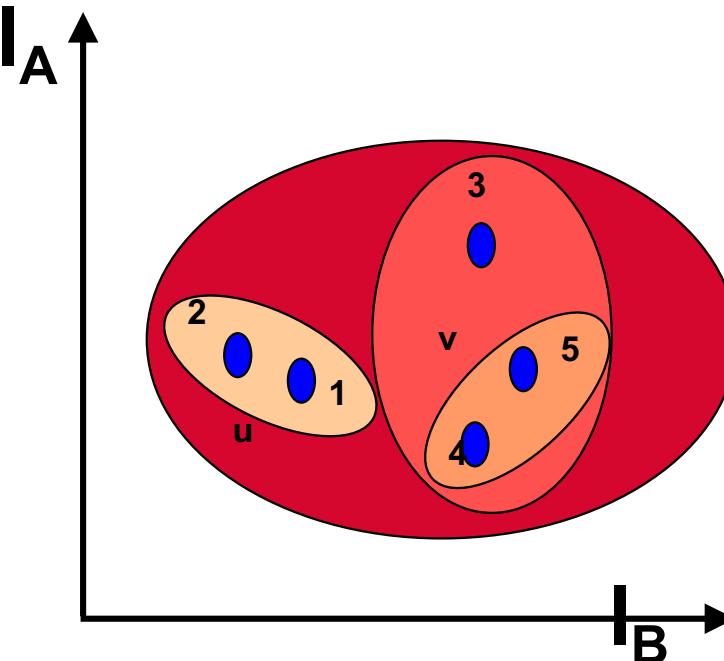
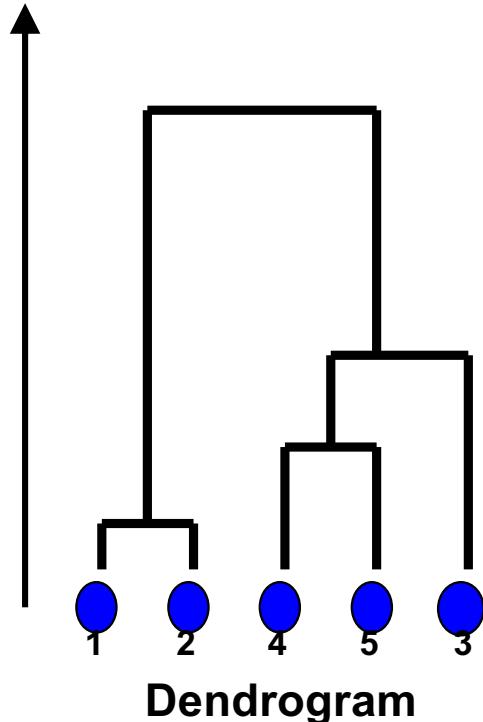
$d(ij)$	$u$	$w$
$u$	0	6.5
$w$	6.5	0





## Example

### Cluster distances





# Hierarchical Clustering: Algorithm

## Algorithm

1. Compute matrix of pair-wise distances
2. Find pair with minimal distance and merge them
3. Update distance matrix
4. Continue with step 2 until a single cluster is left

## Parameters:

- Distance measure for individual samples
  - For gene expression this is typically the correlation
- Distance measure for clusters of samples (linkage rule)



## Hierarchical Clustering

Linkage Rules:

How to compute the distance of two clusters (groups of samples)

- Single linkage: minimal distance of two members
- Complete linkage: maximal distance of two members
- Average linkage: average distance of all members
- Ward's linkage: minimal increase in intra-cluster variance
- ...

Hint:

- The above cluster distances can be derived directly from the distance matrix of the samples
- Cluster algorithm only needs the distance matrix as input not the measurements of the individual samples



## K-means Clustering

1. Initialization: Randomly assign each sample to a cluster
2. Compute the cluster centers as the average of the assigned samples
3. Assign each sample to the closest cluster center
4. Repeat steps 2 and 3 until convergence or maximum number of steps is reached

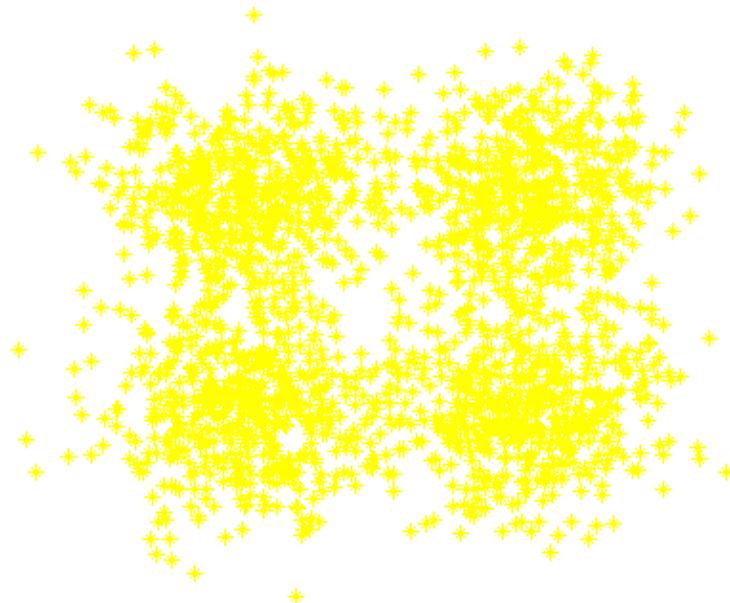
Characteristics:

- Finds clusters that minimize intra-cluster variance

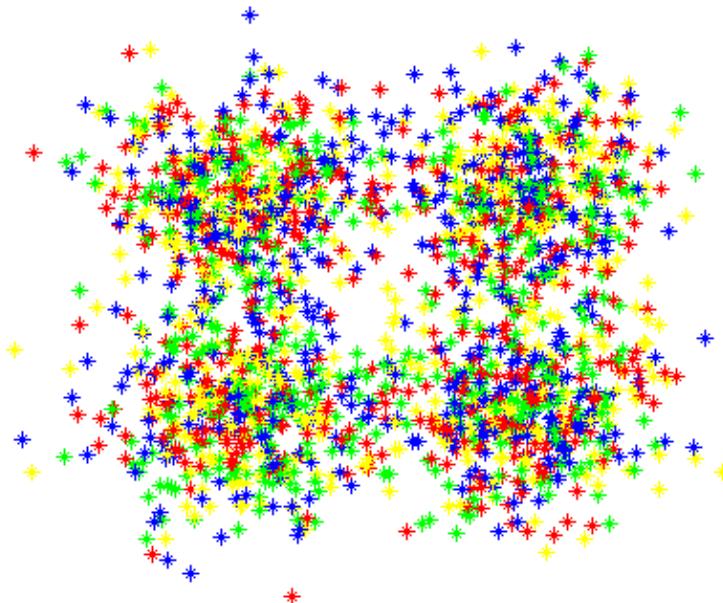
Parameters:

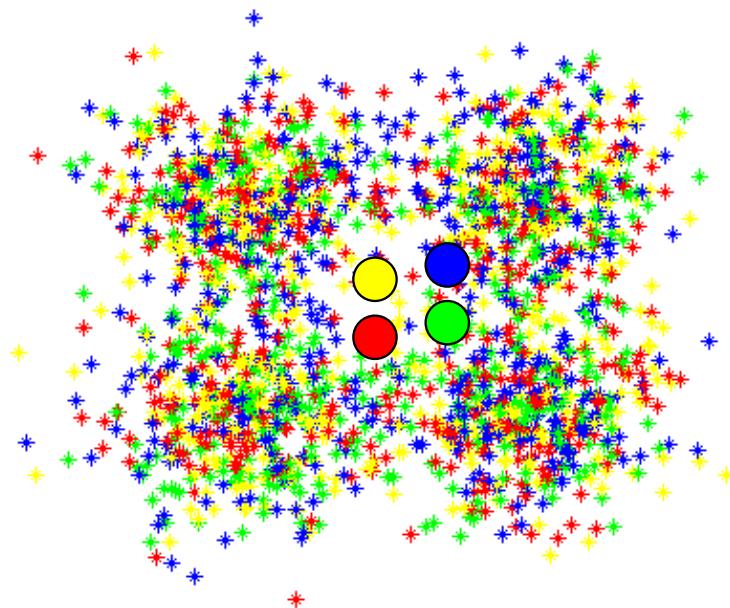
- number of clusters
- distance measure

## K-means Example



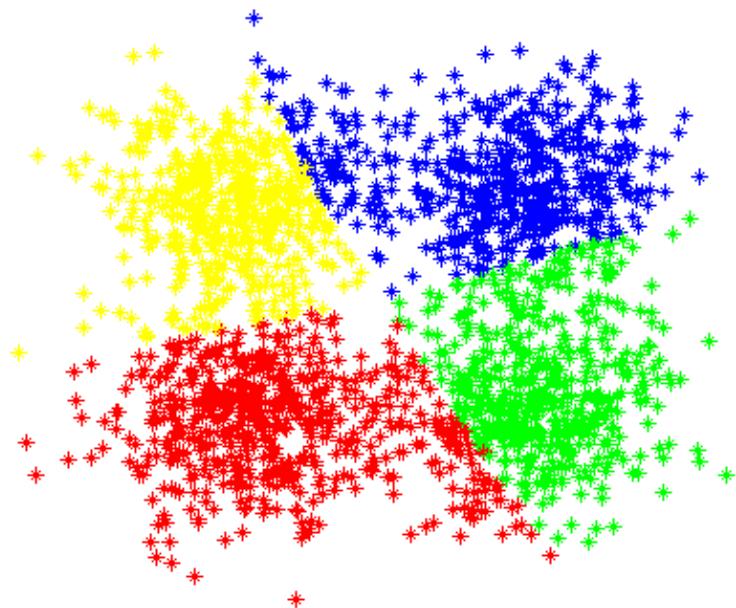
## K-means: Initialization







## K-means: Reassignment of points





# Comparison of Clustering Methods

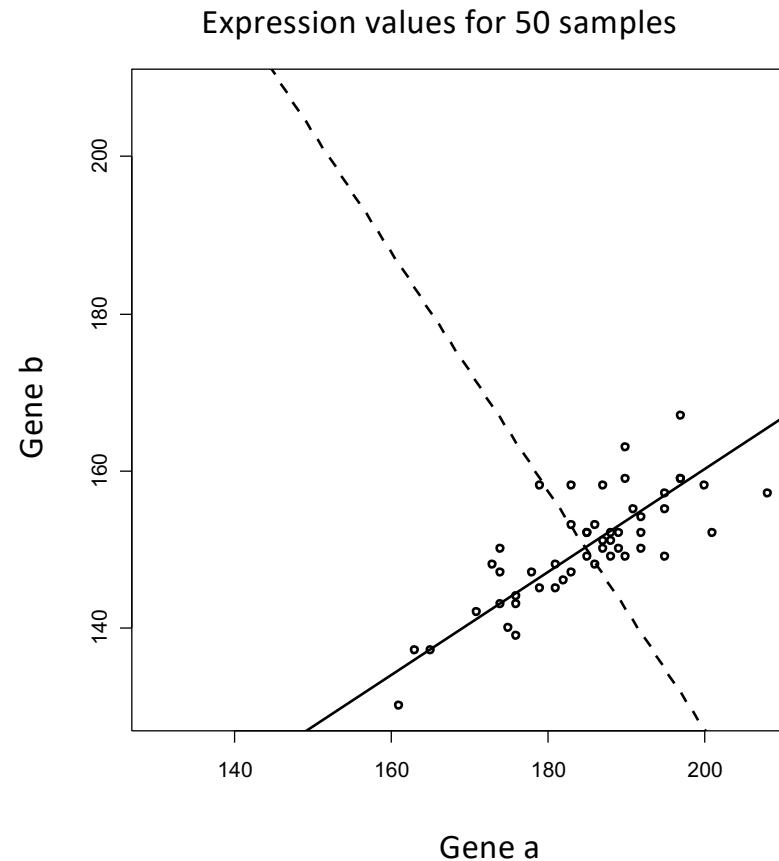
- Computing time:
- Hierarchical clustering
  - $O( n^2 \log(n) )$
- K-means clustering
  - t: number of iterations
  - k: number of clusters
  - $O( k t n )$
- Memory requirements:
- Hierarchical clustering
  - $O( n^2 )$
- K-means clustering
  - $O( kn )$

Note:

When clustering large numbers of genes ( $>1e4$ , hierarchical clustering becomes resource intensive)

# Principal Component Analysis

- An expression profile characterizes the state of a sample with ~25 000 genes (variables)
  - Can we get a representation that uses less variables?  
Reduction of dimensionality?
  - Yes, genes that are highly correlated can be summarized without major loss of information content
  - Goal is to represent the samples in a low-dimensional space where the distance relationships of the samples are similar to the relationships in the full space





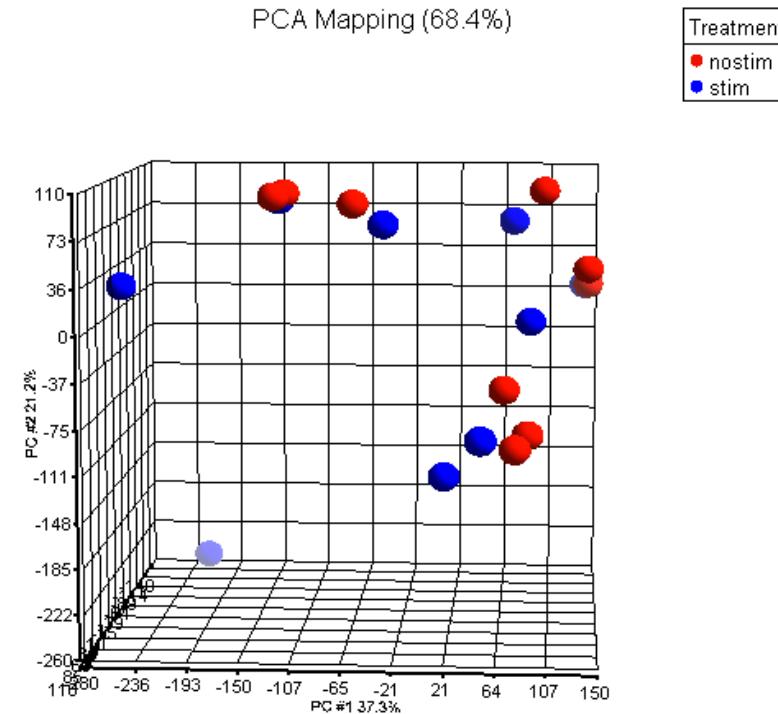
## Principal Component Analysis

Procedure:

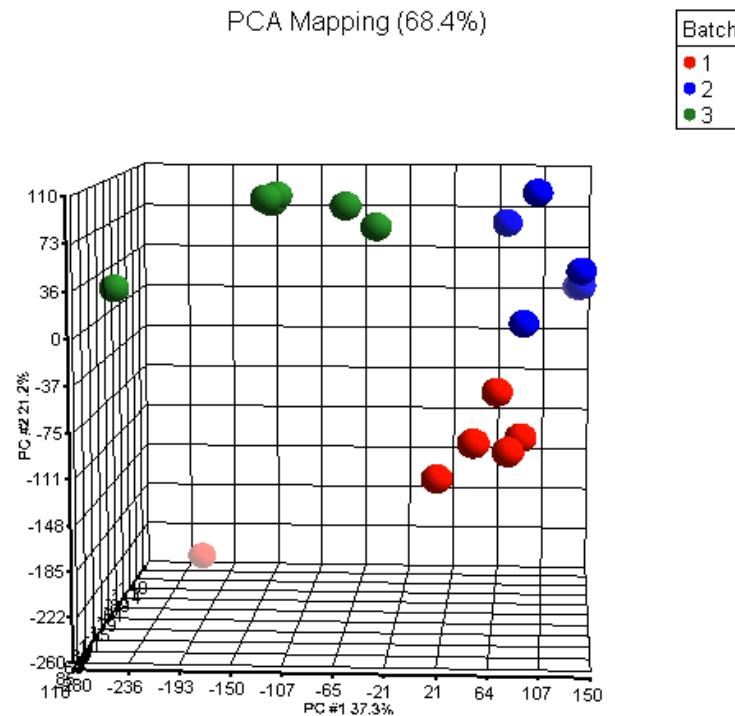
- Center the matrix: Subtract average
- Compute covariance matrix of the centered matrix (gives an  $n \times n$  Matrix)
- Compute Eigenvalues and Eigenvectors of the covariance matrix
- Sort Eigenvectors according to the magnitude of the associated Eigenvalues
- Transform to the E eigenspace
- Only show the first  $k$  variables in the E eigenspace

# Example: Stimulation experiment

- Plot showing the 18 samples in the PCA coordinates
  - Coloring by treatment of the samples
    - stimulated
    - not stimulated
  - The samples do not separate
  - There are two outliers on the left

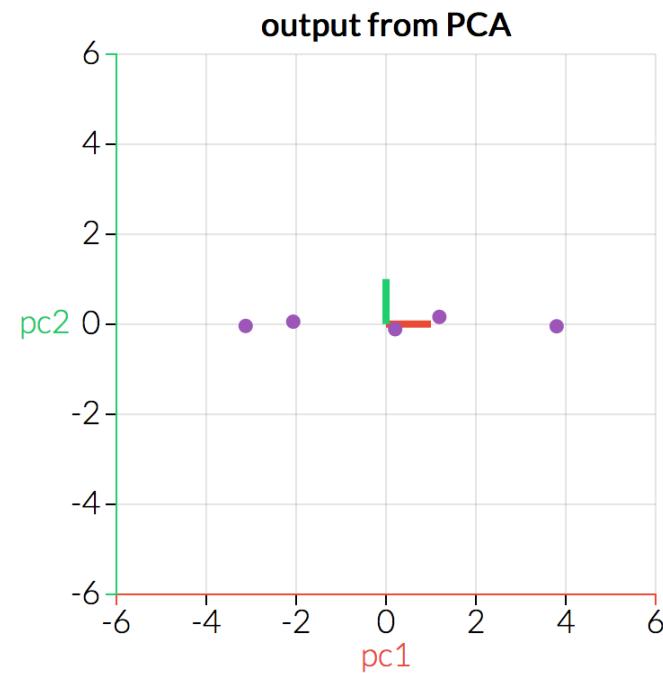
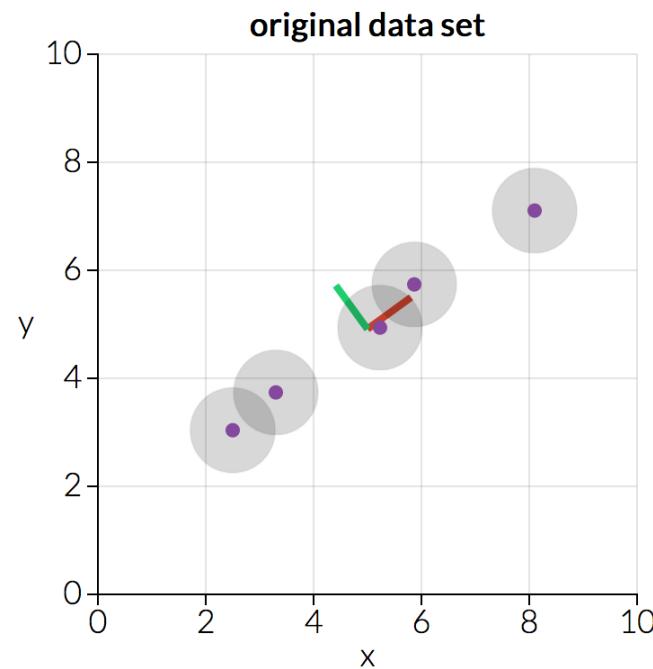


- Coloring by batch shows that the major effect is the batch effect
  - Global expression profile is majorily determined by the batch
  - Stimulation leads only to a minor modulation of the expression profile



## PCA Explained Visually

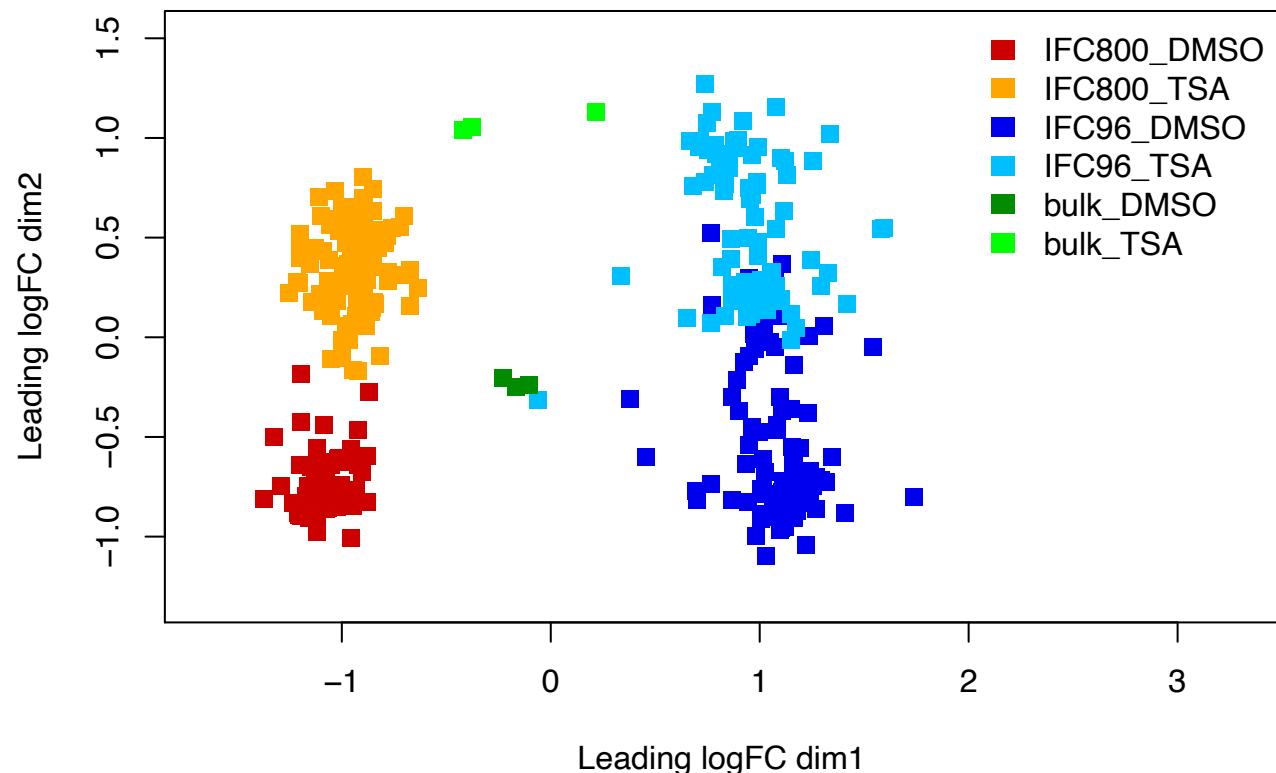
- <http://setosa.io/ev/principal-component-analysis/>





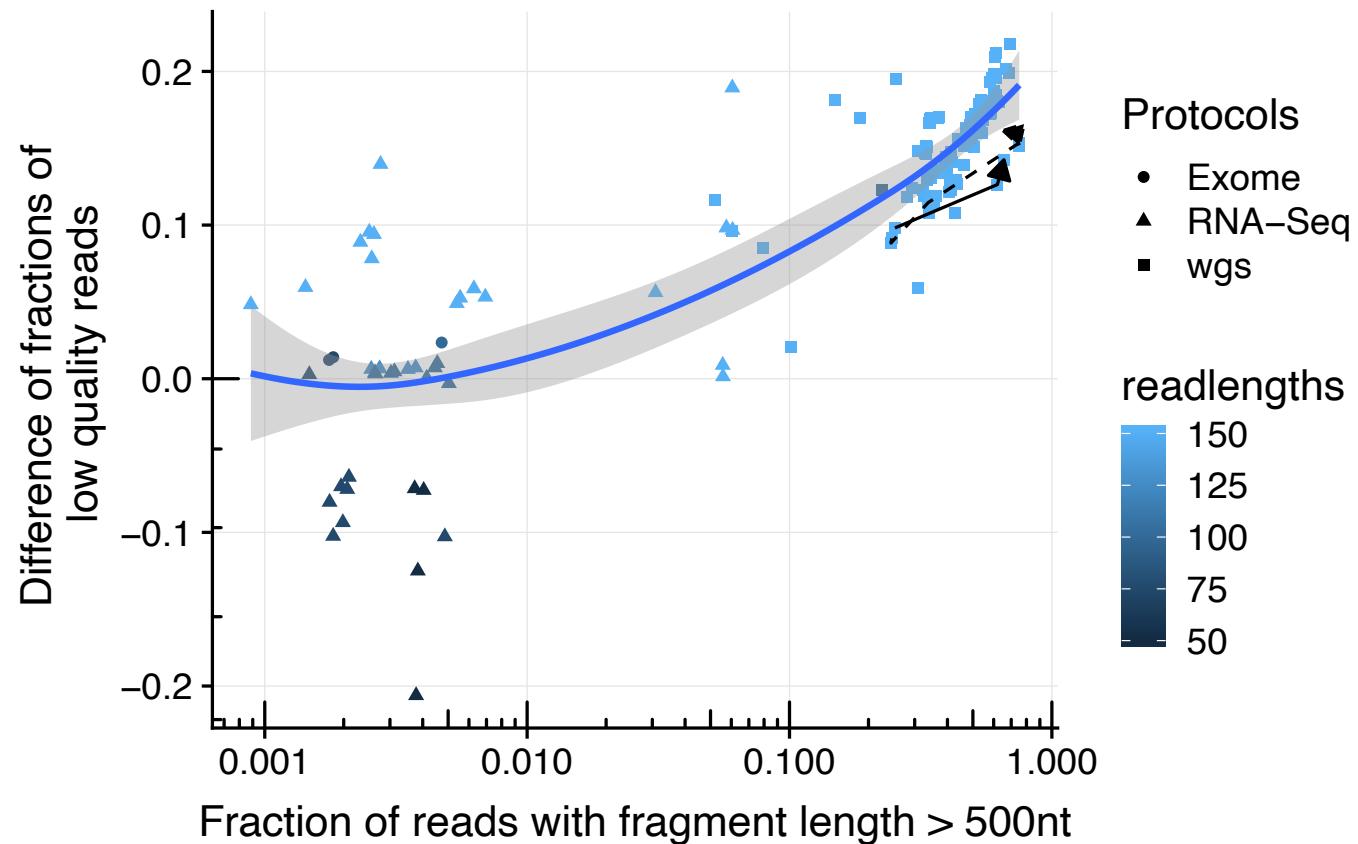
## Example of multi-dimensional scaling

- Samples treated with two compounds: TSA and DMSO
- Samples measured with three approaches: IFC800, IFC96, and bulk
- What do we learn about effect sizes?



# Example of exploratory analysis

- Fraction of low-quality reads increased in some sequencing results
  - What is the driving factor?
    - Sequencer
    - Sample preparation protocol
    - Readlength
    - Input amount
    - ....
  - Factors are correlated:
    - Key driving source: presence of long fragments





## Summary

- Always visualize all characteristics of your data
  - range, distribution, NA values, ...
- Be creative about potential correlations or associations that could exist, think of ways to visualize them
- Look for unexpected patterns!
  - Keep in mind at this stage you're on the exploratory trail not on the inference route! This aspect of your study is observational.