

More about QSAR and Similarity Searching

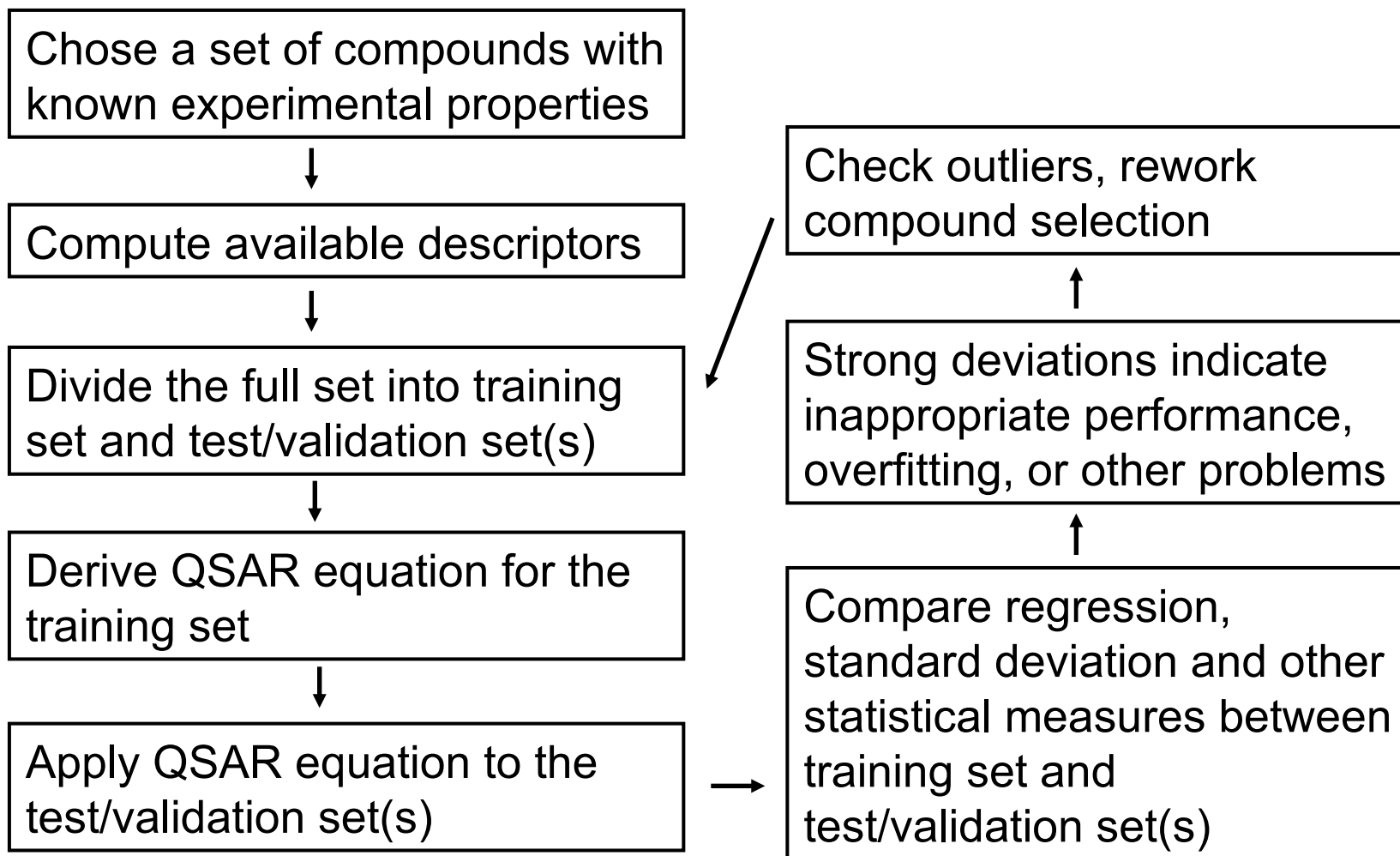
QSAR equations form a quantitative connection between chemical structure and (biological) activity.

$$\log(1/C) = k_1 \cdot P_1 + k_2 \cdot P_2 + \dots + k_n \cdot P_n$$

Problems:

- Which and how many descriptors to use?
- How reliable are the predictions (applicability domain)?
- How to test/validate QSAR equations
(continued from lecture 5)

Setting up and testing QSAR equations



Evaluating QSAR equations (1)

The most important **statistical measures** to evaluate QSAR equations are (preferred values given in parenthesis):

Correlation coefficient r (in squared from $r^2 > 0.75$)

Standard deviation se (small as possible, $se < 0.4$ units)

Fisher value F (level of statistical significance. Also a measure for the portability of the QSAR equation onto another set of data. Should be high, but decreases with increasing number of used variables/descriptors). Therefore only comparable for QSAR equations containing the same number of descriptors

t -test to derive the

probability value p of a single variable/descriptor.

Is a measure for coincidental correlation

$p < 0.05$ = 95% significance

$p < 0.01$ = 99%

$p < 0.001$ = 99.9%

$p < 0.0001$ = 99.99%

Evaluating QSAR equations (2)

Example output from OpenStat:

R	R2 r^2	F	Prob.>F	DF1	DF2
0.844	0.712	70.721	0.000	3	86

Adjusted R Squared = 0.702

Std. Error of Estimate =

0.427 se

Variable	Beta	B	Std.Error	t	Prob.>t
hbdon	-0.738	-0.517	0.042	-12.366	0.000
dipdens	-0.263	-21.360	4.849	-4.405	0.000
chbba	0.120	0.020	0.010	2.020	0.047

Constant =

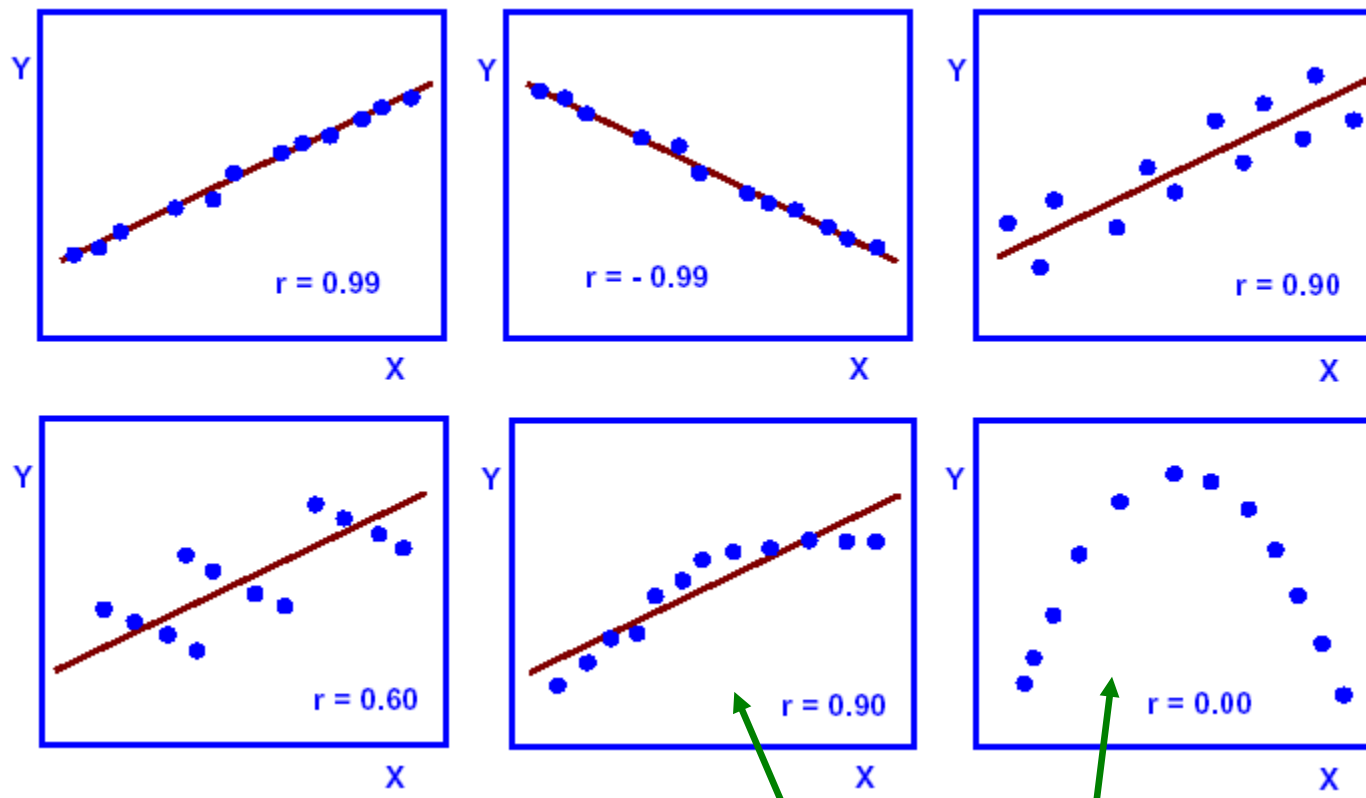
0.621

$$\log(1/C) = -0.517 \cdot \text{hbdon} - 21.360 \cdot \text{dipdens} + 0.020 \cdot \text{chbba} + 0.621$$

Lit: William „Bill“ G. Miller, OpenStat Reference Handbook

Evaluating QSAR equations (3)

A plot tells more than numbers:



Shape of curve indicates non-linear correlation

Source: H. Kubinyi, Lectures of the drug design course

<http://www.kubinyi.de/index-d.html>

For more examples see

https://en.wikipedia.org/wiki/Pearson_correlation_coefficient

Evaluating QSAR equations (4)

Examples where statistical measures between training set and test set strongly deviate:

Training set $n=15$, $r^2=0.91$, $se=0.27$ (5 descriptors used)

Test set $n=5$, $r^2=0.69$, $se=0.42$

Obvious reason: too many descriptors used in QSAR eq. Therefore the training set becomes overfitted, correlation breaks down for the test set.
→ Limit number of used descriptors in the QSAR equation to three.

Training set $n=26$, $r^2=0.88$, $se=0.32$, $F=110.7$ (3 descriptors used)

Test set $n=7$, $r^2=0.75$, $se=0.38$, $F=66.5$

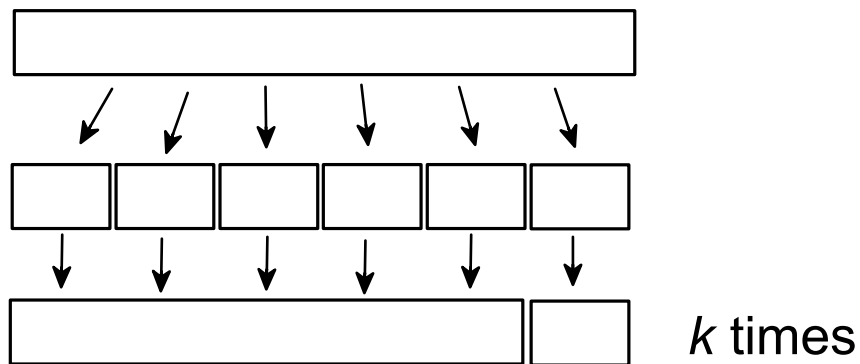
Possible reason: Compounds in the test set are too different compared to those in the training set.

→ Check compounds (and descriptor ranges) for similarity, redo compound selection for training and test set e.g. using cluster analysis

Evaluating QSAR equations (5)

(Simple) k -fold cross validation:

Partition your data set that consists of N data points into k subsets ($k < N$).



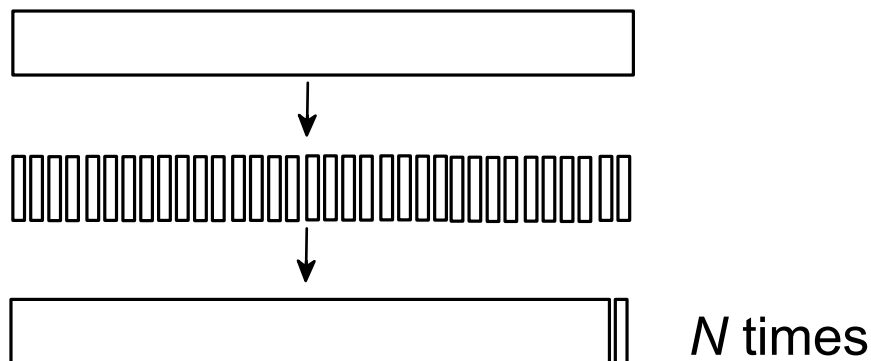
Generate k QSAR equations using a subset as test set and the remaining $k-1$ subsets as training set respectively. This gives you an average error from the k QSAR equations.

In practise $k = 5$ or $k = 10$ has shown to be reasonable (refers to 5-fold or 10-fold cross validation, respectively)

Evaluating QSAR equations (6)

Leave one out cross validation:

Partition your data set that consists of N data points into k subsets ($k = N$).



Disadvantages:

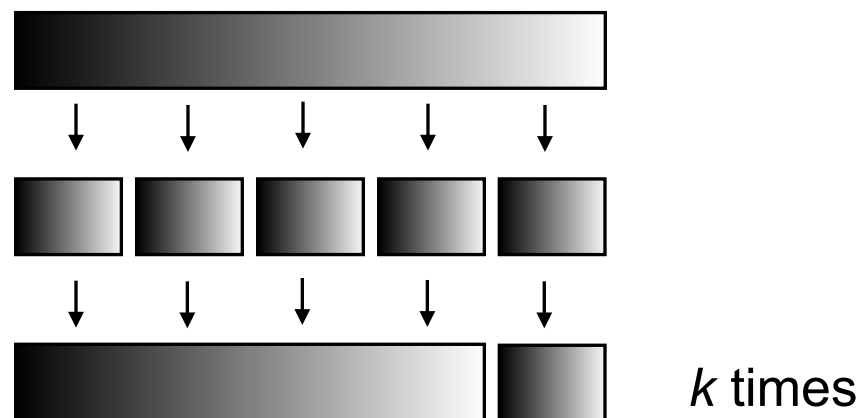
- Computationally expensive
- Partitioning into training and test set is more or less by random, thus the resulting (average) error can be way off in extreme cases.

Solution: (feature) distribution within the training and test sets should be identical or similar

Evaluating QSAR equations (7)

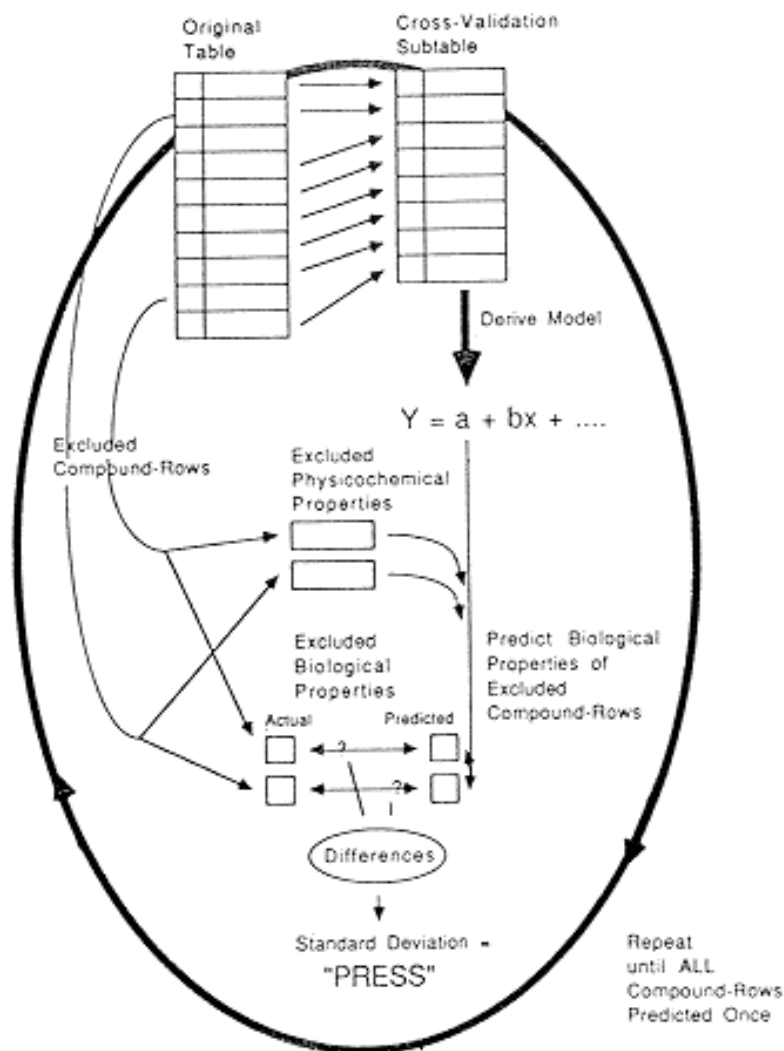
Stratified cross validation:

Same as k -fold cross validation but each of the k subsets has a similar (feature) distribution as the training set.



The resulting average error is thus more prone against errors due to equal distribution of features between training set and the test sets.

Evaluating QSAR equations (8)



alternative
Cross-validation and
leave one out (LOO)
schemes

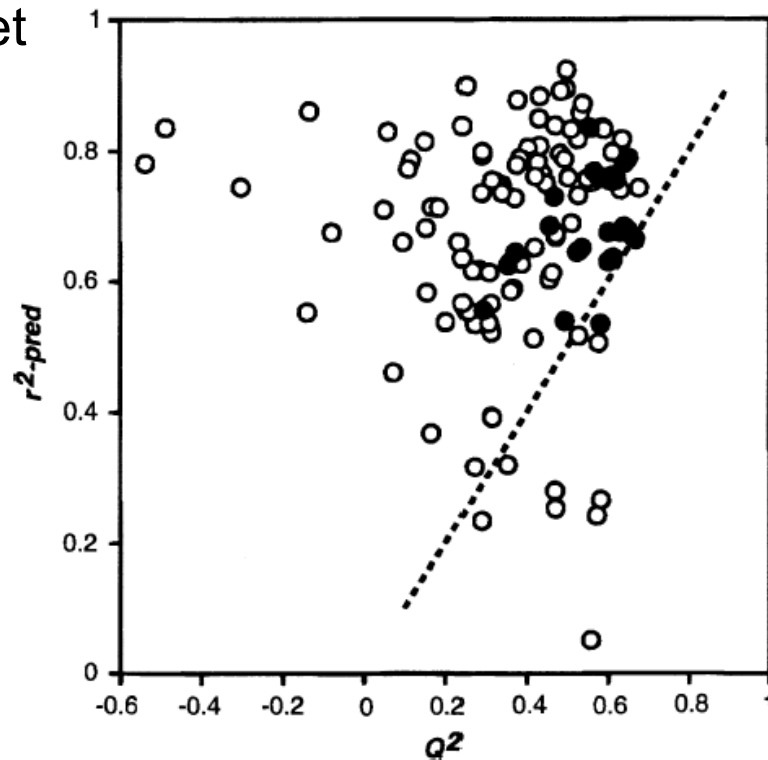
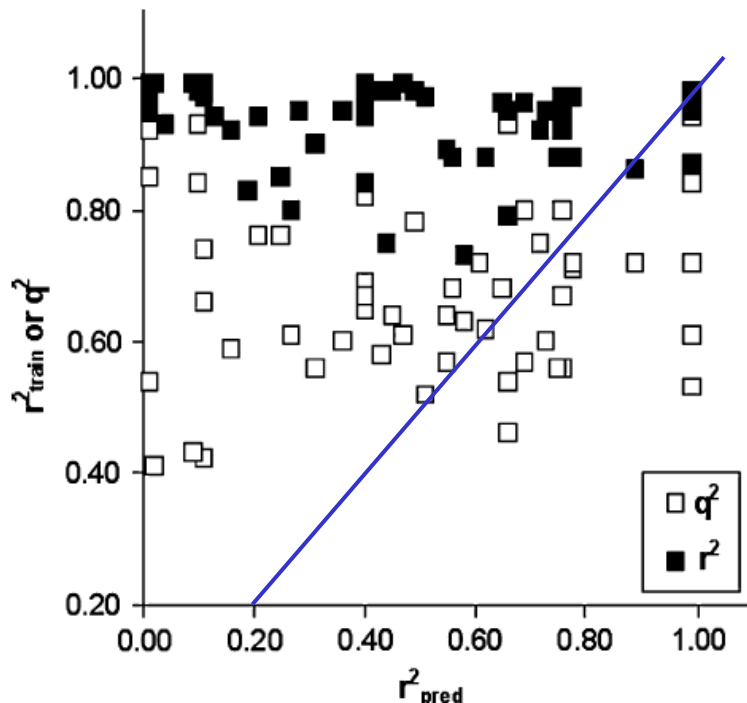
Leaving out one or more descriptors from the derived equation results in the cross-validated correlation coefficient q^2 .

This value is of course lower than the original r^2 .
 q^2 being much lower than r^2 indicates problems...

Evaluating QSAR equations (9)

Problems associated with q^2 and *leave one out* (LOO)

→ There is no correlation between q^2 and test set predictivity, q^2 is related to r^2 of the training set



Kubinyi's paradoxon: Most r^2 of test sets are higher than q^2 of the corresponding training sets [due to manual selection?]

Lit: A.M.Doweyko *J.Comput.-Aided Mol.Des.* **22** (2008) 81-89.

Evaluating QSAR equations (10)

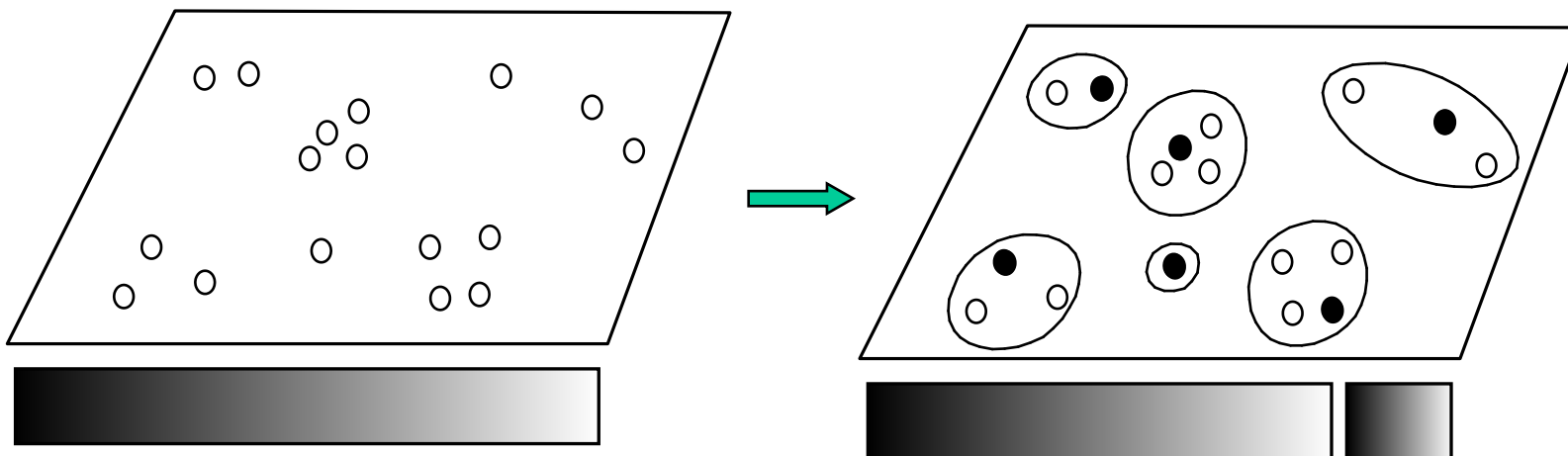
One of most reliable ways to test the performance of a QSAR equation is to apply an external test set.

→ partition your complete set of data into training set (2/3) and test set (1/3 of all compounds, ideally)

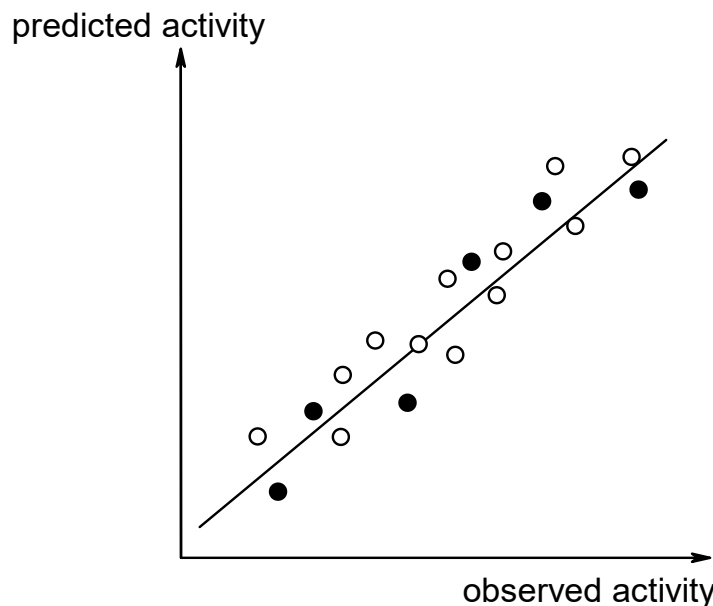
Compounds of the test set should be representative (confers to a 1-fold stratified cross validation)

→ Cluster analysis using the descriptor values of each compound plus their activities.

→ Use cluster centroids as test set and the remaining compounds for the training set (these account for the diversity)

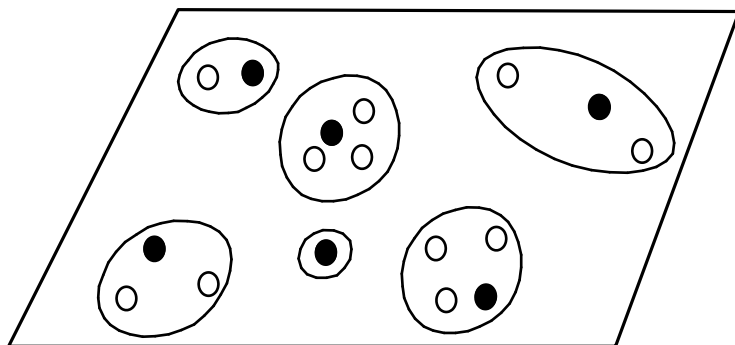


Evaluating QSAR equations (11)



Compounds of the test set must cover the same activity range as those of the training set

- Training set
- Test set



Evaluating QSAR equations (12)

Estimating the error (range) of predicted values is difficult.

Approaches to give a confidence range (as in statistics) or determining the applicability domain of the model:

- Distance based: similar to *k*-nearest neighbor; where is the predicted compound located in the descriptor space?

Close to one group or rather in between clusters?

Large training sets can be split into a further calibration set that is used for estimating the error of unseen data based on their similarity.

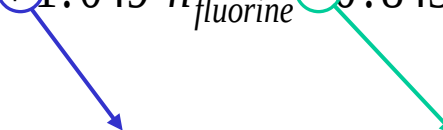
- Are there consistent outliers in the data set?
→ These are either too dissimilar or are likely to contain experimental errors.

Lit: K. Roy et al. *Chemomet. Intell. Lab. Sys.* **145** (2015) 22-29.

Interpretation of QSAR equations

The kind of applied variables/descriptors should enable us to

- draw conclusions about the underlying physico-chemical processes
- derive guidelines for the design of new molecules by interpolation

$$\log(1/K_i) = +1.049 \cdot n_{\text{fluorine}} - 0.843 \cdot n_{\text{OH}} + 5.768$$


Higher affinity requires **more** fluorine, **less** OH groups

Some descriptors give information about the biological mode of action:

- A dependence of $(\log P)^2$ indicates a transport process of the drug to its receptor.
- Dependence from E_{LUMO} or E_{HOMO} indicates a chemical reaction

Evaluating QSAR equations (13)

Reduce the number of available descriptors before performing a regression analysis:

- More descriptors cause longer run times
- More descriptors raise the likelihood of accidental correlation (see also slides further below)
- Descriptors might be correlated to each other and thus do not provide more information
- Can you interpret what your descriptors mean?

→ get rid of the „garbage“



Correlation of descriptors

Other approaches to handle correlated descriptors and/or a wealth of descriptors:

Transforming descriptors to uncorrelated variables by

- *principal component analysis* (PCA)
- *partial least square* (PLS)

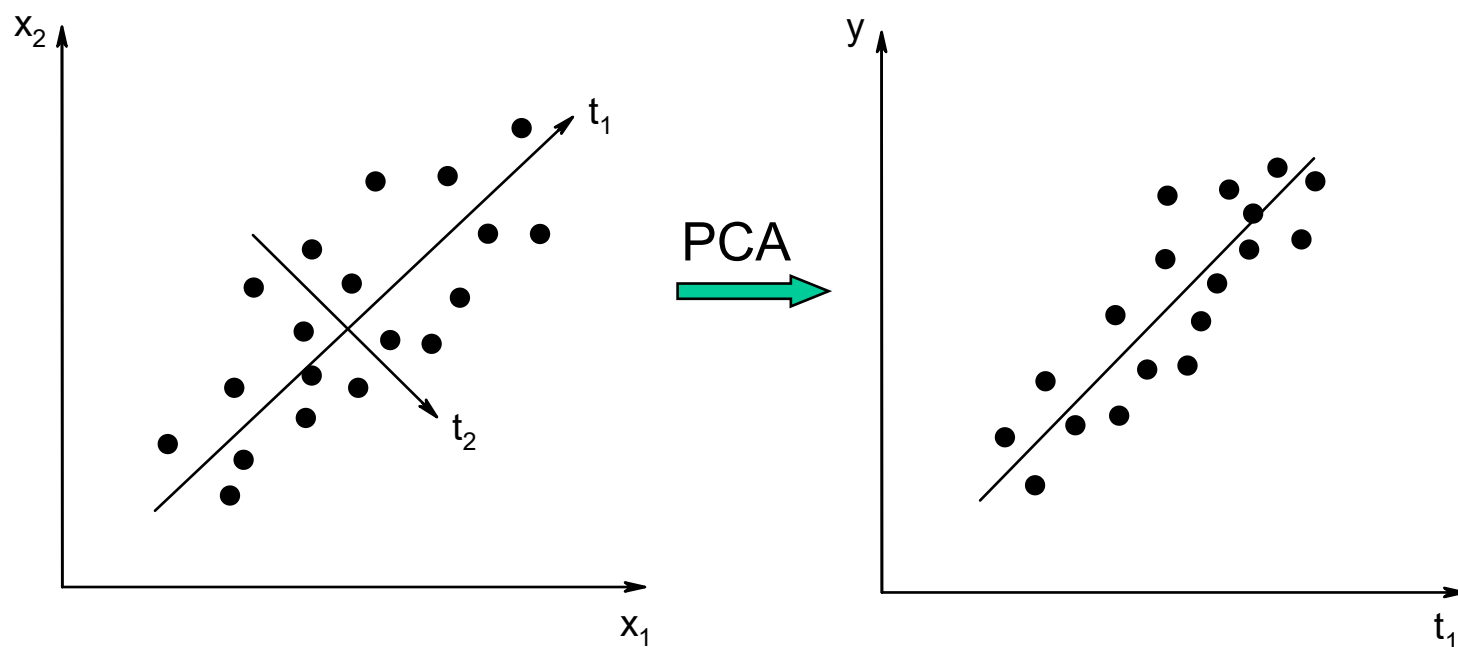
for example applied in *comparative molecular field analysis* (CoMFA), see below

Methods that intrinsically handle correlated variables

- *neural networks*, especially *deep learning networks*

Partial least square (I)

The idea is to construct a small set of latent variables t_i (that are orthogonal to each other and therefore uncorrelated) from the pool of inter-correlated descriptors x_i .



In this case t_1 and t_2 result as the normal modes of x_1 and x_2 where t_1 shows the larger variance.

Partial least square (II)

The predicted term y is then a QSAR equation using the latent variables t_i

$$y = b_1 t_1 + b_2 t_2 + b_3 t_3 + \dots + b_m t_m$$

where

$$t_1 = c_{11} x_1 + c_{12} x_2 + \dots + c_{1n} x_n$$

$$t_2 = c_{21} x_1 + c_{22} x_2 + \dots + c_{2n} x_n$$

$$\cdot \quad \cdot \quad \cdot \quad \cdot$$

$$t_m = c_{m1} x_1 + c_{m2} x_2 + \dots + c_{mn} x_n$$

The number of latent variables t_i is chosen to be (much) smaller than that of the original descriptors x_i .

But, how many latent variables are reasonable?

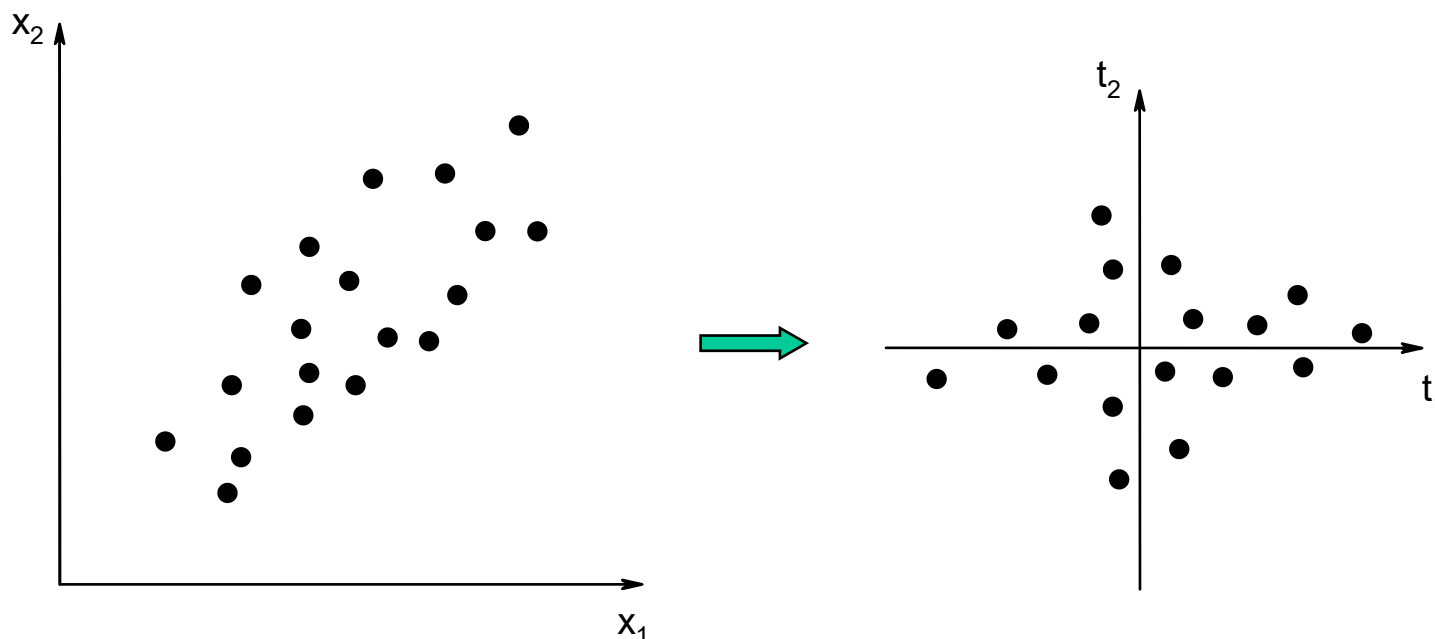
→ plot r^2 , se , q^2 and their fluctuations against the number of latent variables and identify the minimal number of latent variables.

Principal Component Analysis PCA (I)

Problem: Which are the (decisive) „significant“ descriptors?

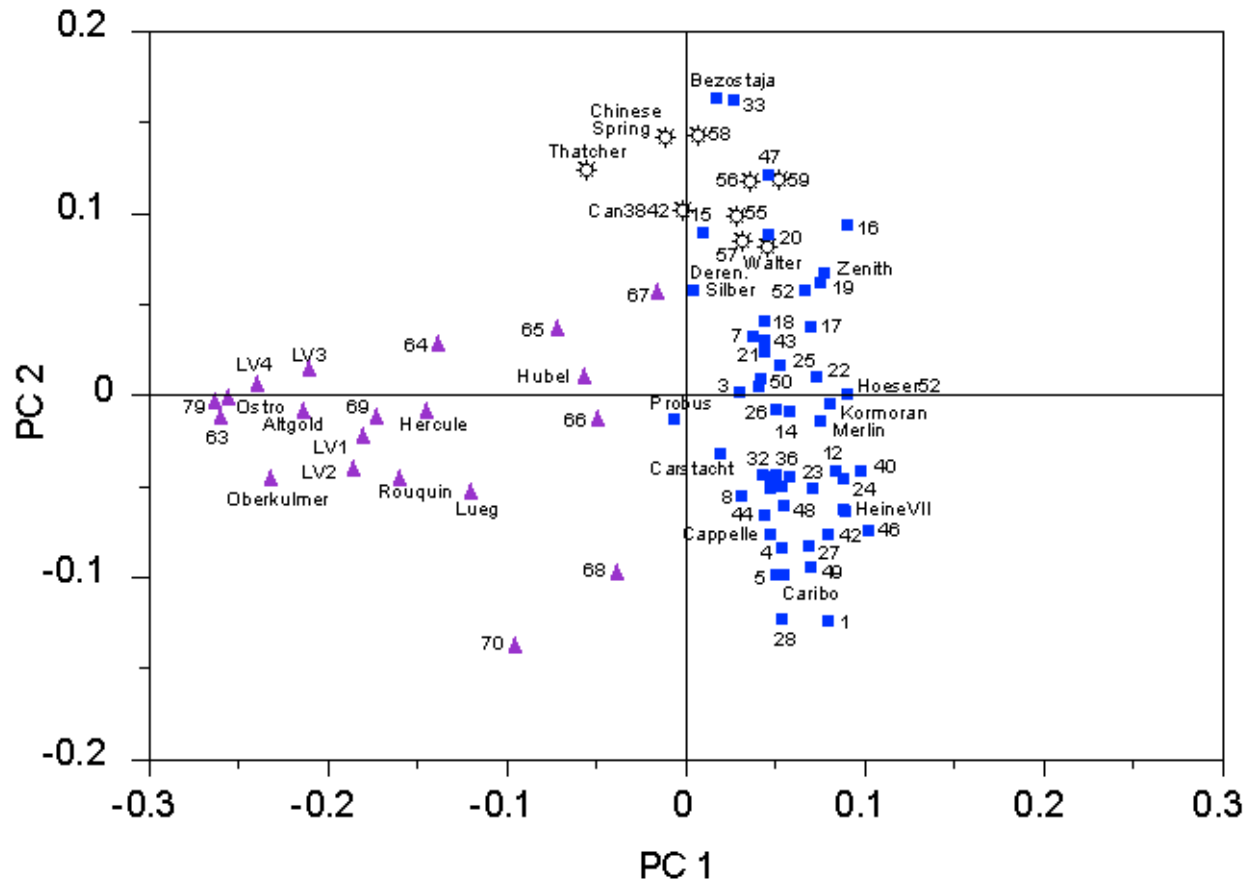
Principal component analysis determines the normal modes from a set of descriptors/variables.

This is achieved by a coordinate transformation resulting in new axes. The first principal component then shows the largest variance of the data. The second and further normal components are orthogonal to each other.



Principal Component Analysis PCA (II)

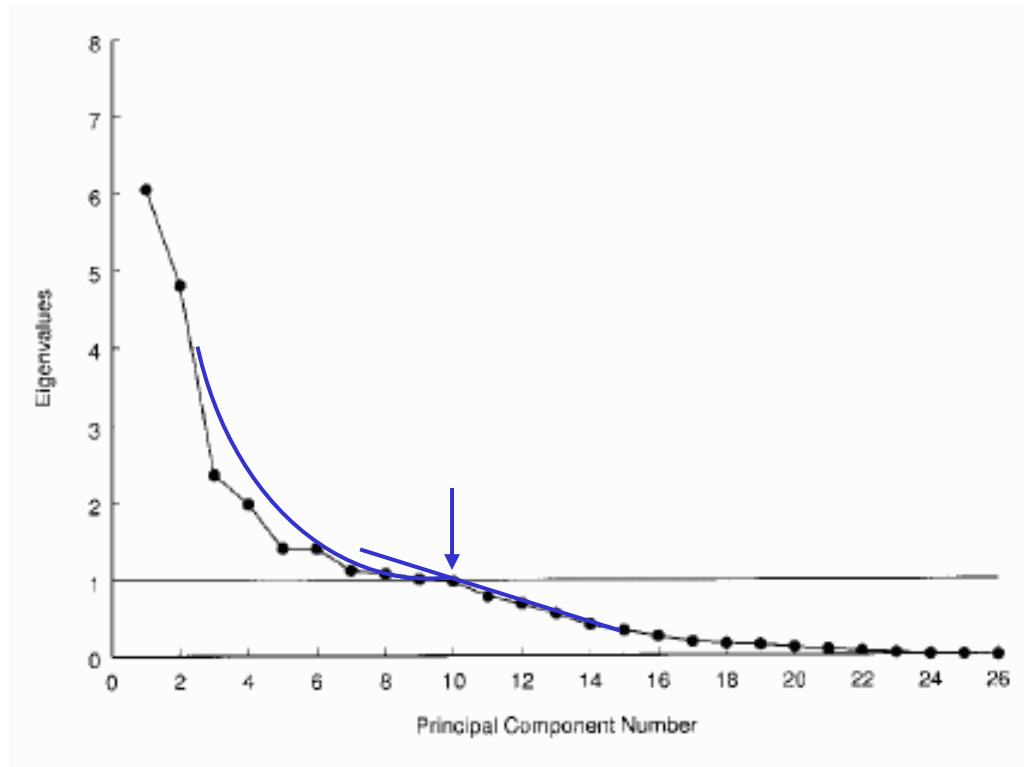
The first component (pc1) shows the largest variance, the second component the second largest variance, and so on.



Lit: E.C. Pielou: *The Interpretation of Ecological Data*, Wiley, New York, 1984

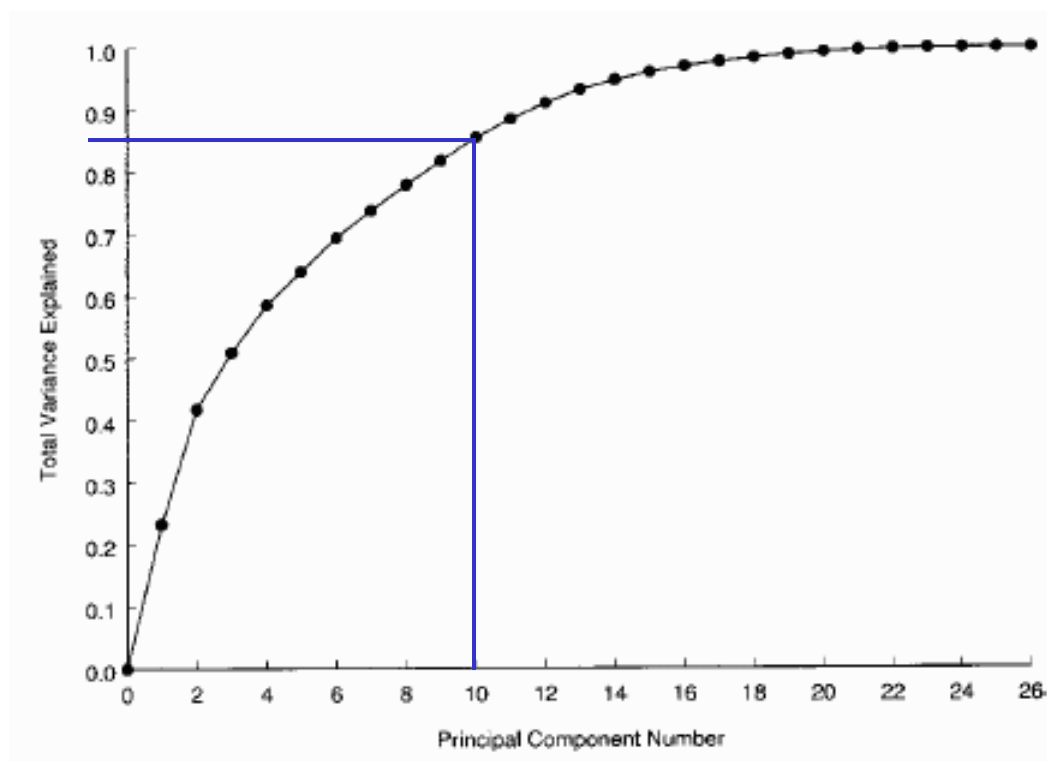
Principal Component Analysis PCA (III)

The significant principal components usually have an Eigen value >1 (Kaiser-Guttman criterion). Frequently there is also a kink that separates the less relevant components (Scree test)



Principal Component Analysis PCA (IV)

The obtained principal components should account for more than 80% of the total variance.

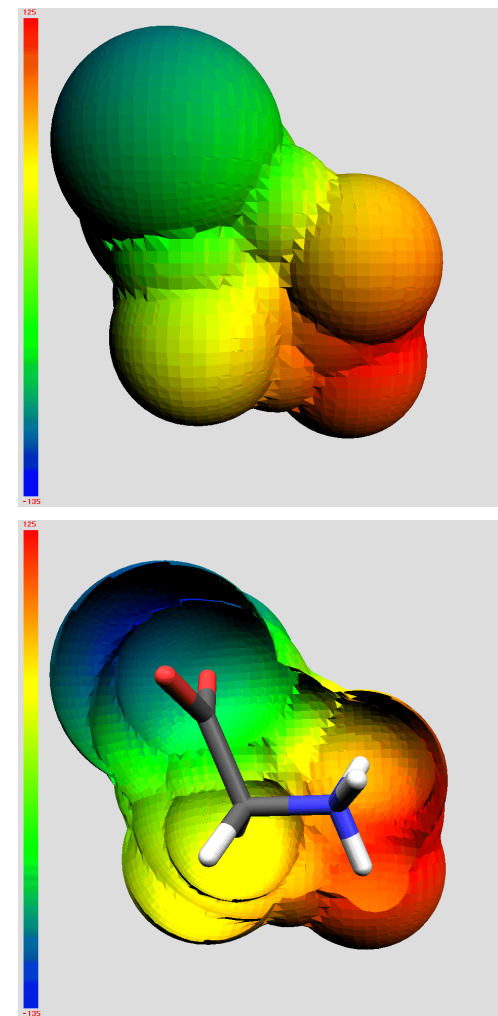


Principal Component Analysis (V)

Example: What descriptors determine the logP?

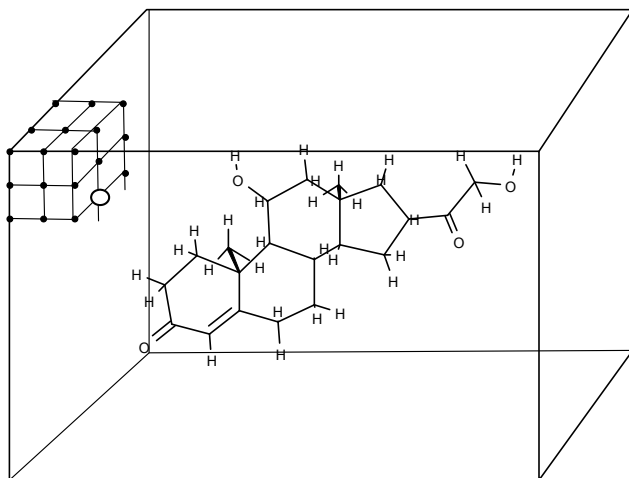
property	pc1	pc2	pc3
dipole moment	0.353		
polarizability		0.504	
mean of +ESP	0.397	-0.175	0.151
mean of -ESP	-0.389	0.104	0.160
variance of ESP	0.403	-0.244	
minimum ESP	-0.239	-0.149	0.548
maximum ESP	0.422		0.170
molecular volume		0.506	0.106
surface	0.519	0.115	
fraction of total variance	28%	22%	10%

Lit: T.Clark et al. *J.Mol.Model.* **3** (1997) 142



Comparative Molecular Field Analysis (I)

The molecules are placed into a 3D grid and at each grid point the steric and electronic interaction with a probe atom is calculated (force field parameters)



For this purpose the GRID program can be used:

P.J. Goodford
J.Med.Chem. **28** (1985) 849.

Problems: „active conformation“ of the molecules needed
All molecule must be superimposed (aligned according to their common scaffold)

Lit: R.D. Cramer et al. *J.Am.Chem.Soc.* **110** (1988) 5959.

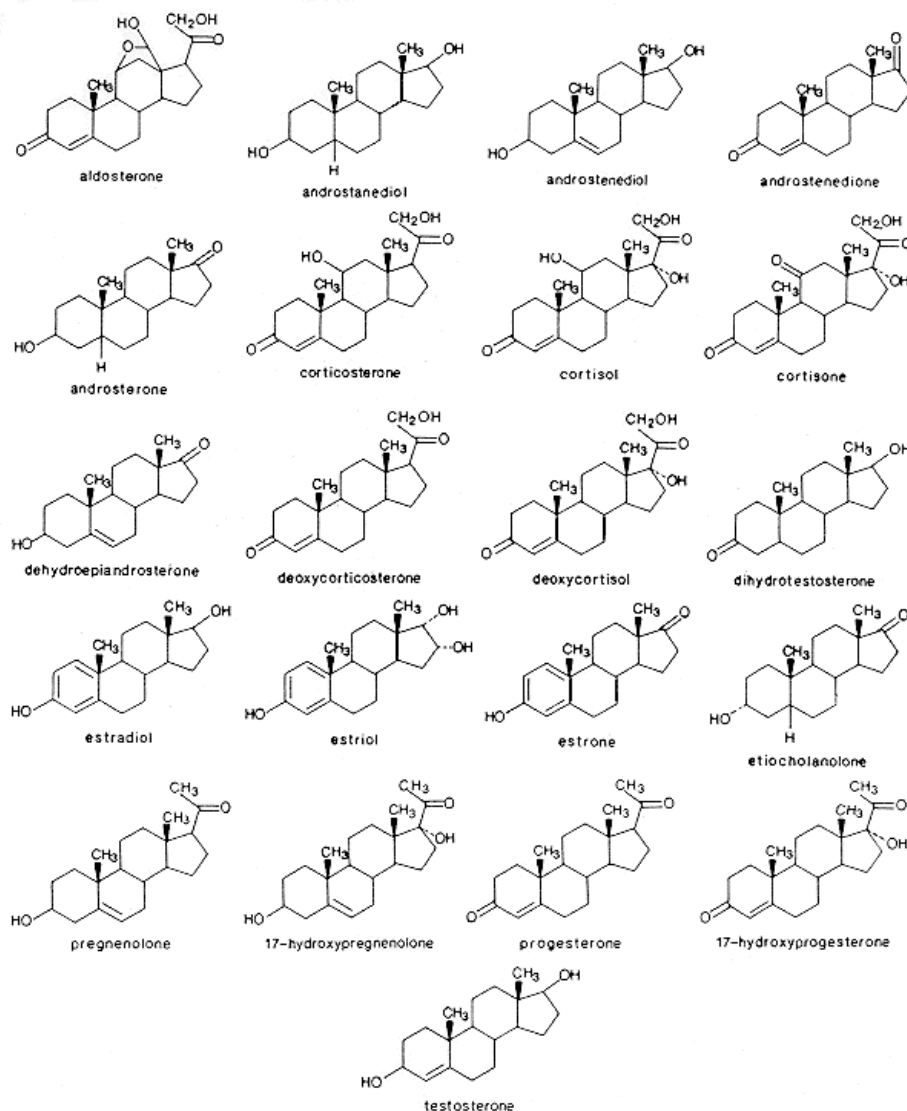
Comparative Molecular Field Analysis (II)

The resulting coefficients for the matrix S (N grid points, P probe atoms) have to be determined using a PLS analysis.

compound	log (1/C)	S1	S2	S3	...	P1	P2	P3	...
steroid1	4.15								
steroid2	5.74								
steroid3	8.83								
steroid4	7.6								
...									

$$\Downarrow$$
$$\log(1/C) = \text{const} + \sum_{i=1}^N \sum_{j=1}^P c_{ij} S_{ij}$$

Comparative Molecular Field Analysis (III)

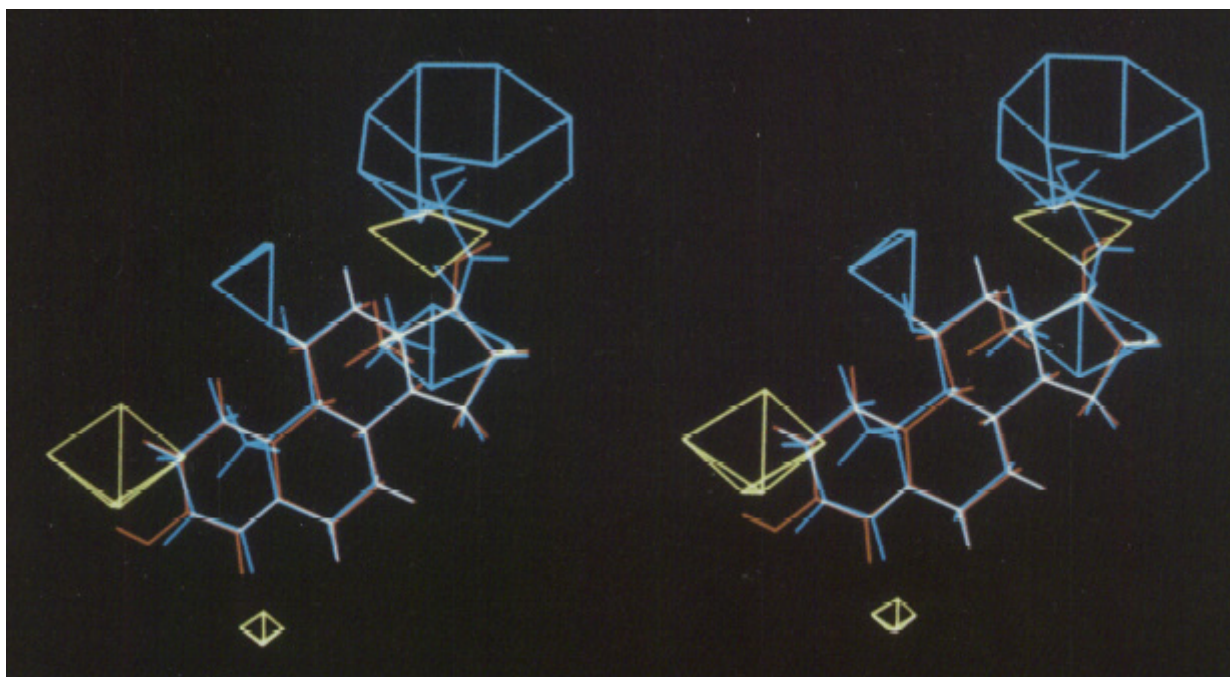


Application of CoMFA:
Affinity of steroids to the
testosterone binding globulin

Lit: R.D. Cramer et al.
J.Am.Chem.Soc.
110 (1988) 5959.

Comparative Molecular Field Analysis (IV)

Analog to QSAR descriptors, the CoMFA variables can be interpreted. Here (color coded) contour maps are helpful

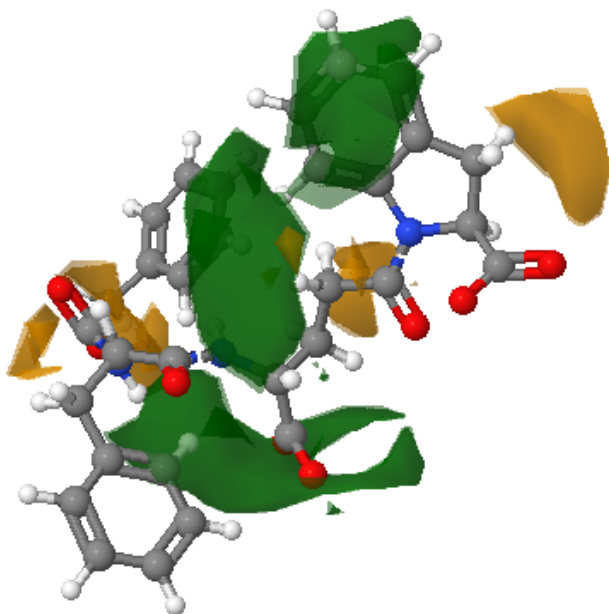


yellow: regions of unfavorable steric interaction

blue: regions of favorable steric interaction

Lit: R.D. Cramer et al. *J.Am.Chem.Soc.* **110** (1988) 5959

CoMFA (V) 3-D Database online:



„A 3-D QSAR Models
Database for Virtual Screening“

Compounds can be screened
against a large set of
precalculated models

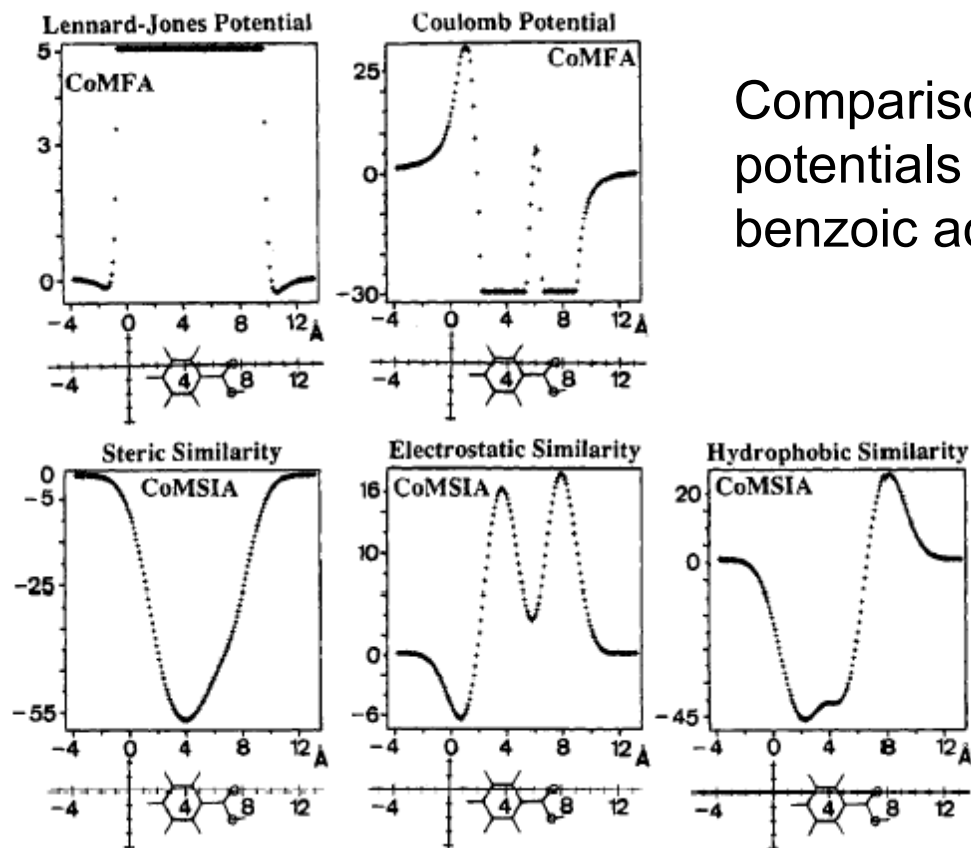
Jmol

Maps Table											
%	0	10	20	30	40	50	60	70	80	90	100
PLS_Coeff	☒	☐	☐	☐	☐	☐	☐	☐	☐	☐	☐
CoMFA_Maps	☐	☐	☐	☐	☐	☒	☐	☐	☐	☐	☐

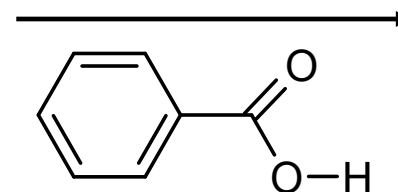
Rino Ragno et al. Università di Roma (Italy)

Comparative Molecular Similarity Indices Analysis (CoMSIA)

CoMFA based on similarity indices at the grid points



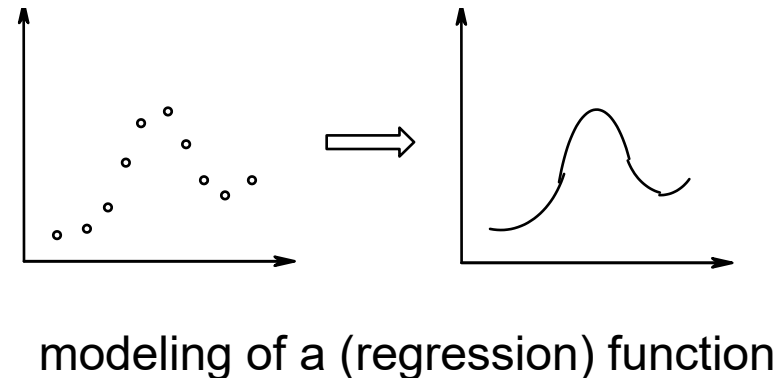
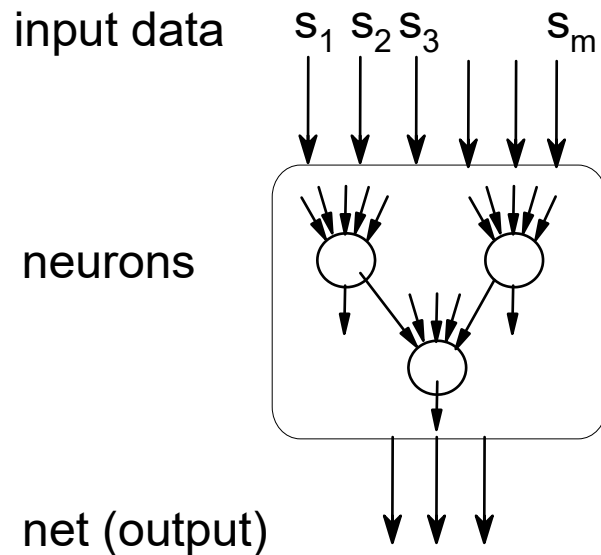
Comparison of CoMFA and CoMSIA potentials shown along one axis of benzoic acid



Lit: G.Klebe et al. *J.Med.Chem.* **37** (1994) 4130.

Neural Networks (I)

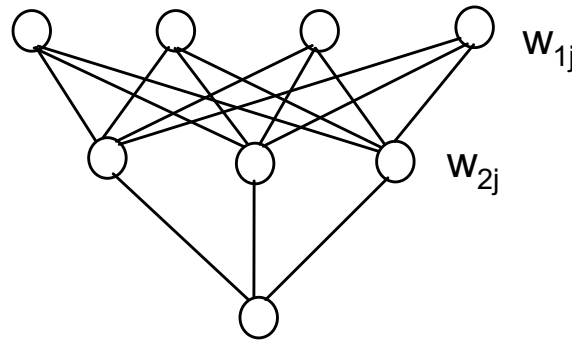
Neural networks can be regarded as a common implementation of artificial intelligence. The name is derived from the network-like connection between the switches (neurons) within the system. Thus they can also handle inter-correlated descriptors.



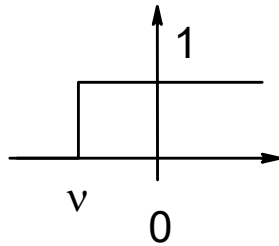
From the many types of neural networks, backpropagation and unsupervised maps are the most frequently used.

Neural Networks (II)

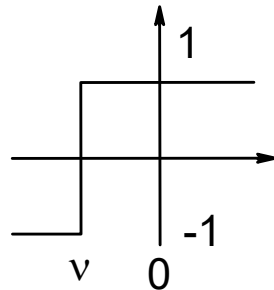
A typical backpropagation net consists of neurons organized as the *input layer*, one or more *hidden layers*, and the *output layer*



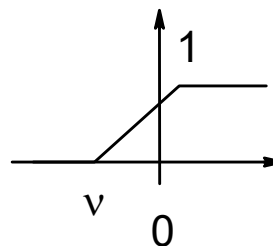
Furthermore, the actual kind of signal transduction between the neurons can be different:



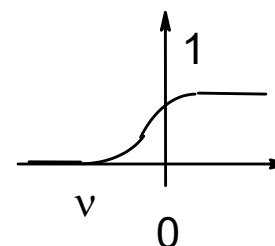
hard limiter
if $\text{inp} > v$



bipolar
hard limiter



threshold
logic



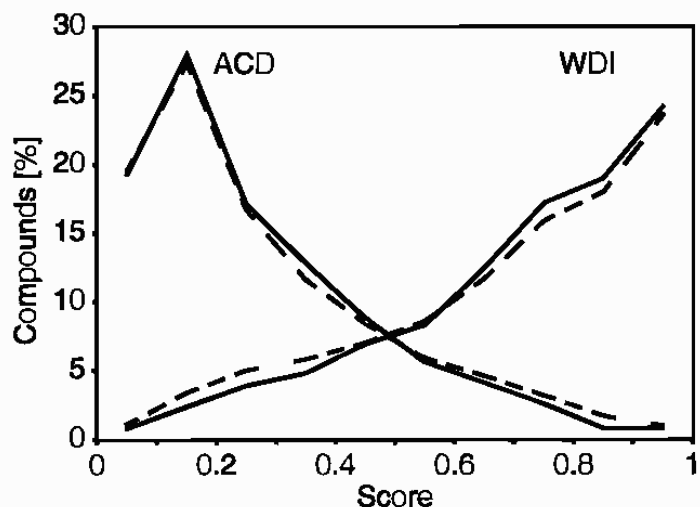
sigmoidal
transfer
logic

Recursive Partitioning

Instead of quantitative values often there is only qualitative information available, e.g. substrates versus non-substrates

Thus we need classification methods such as

- decision trees, naïve Bayes classification
- support vector machines
- boosting
- (neural networks): partition at what score value ?



Picture: J. Sadowski & H. Kubinyi *J.Med.Chem.* **41** (1998) 3325.

Decision Trees

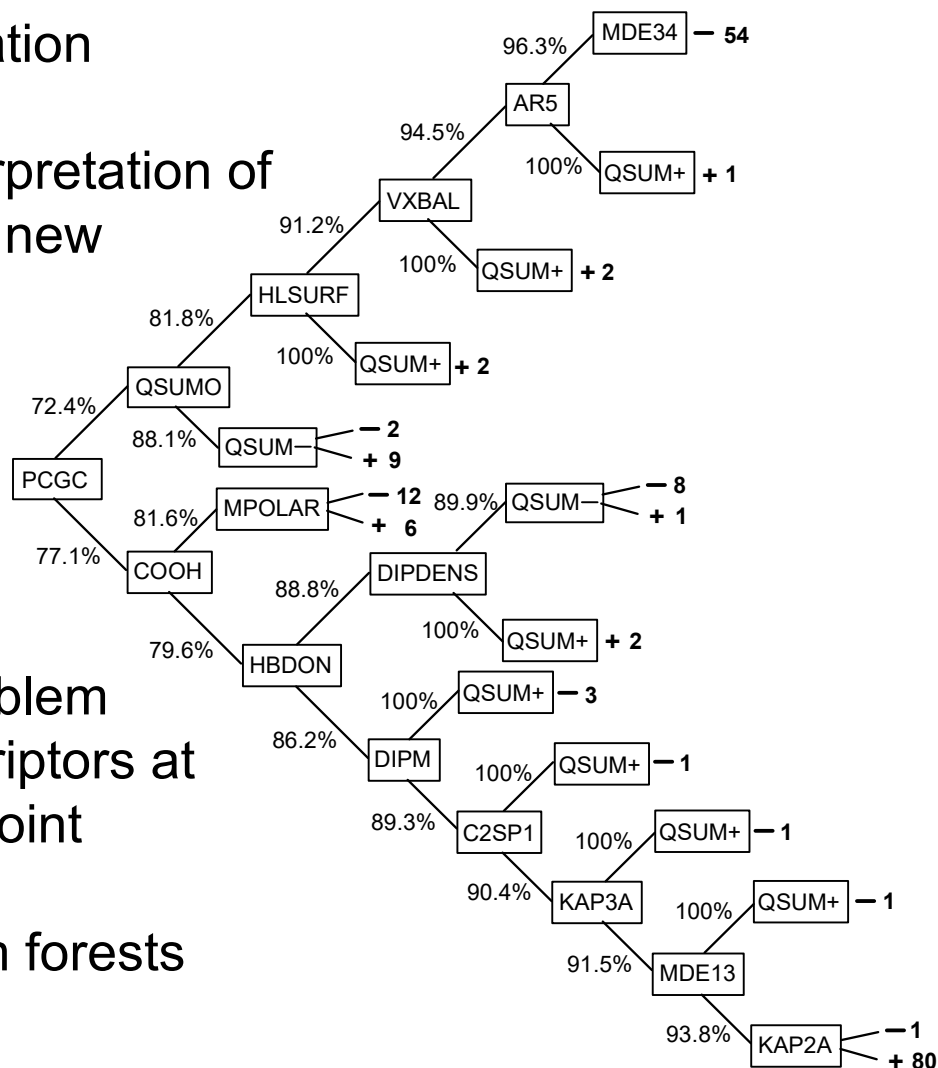
Iterative classification

Advantages: Interpretation of results, design of new compounds with desired properties

Disadvantage:
Local minima problem
choosing the descriptors at each branching point

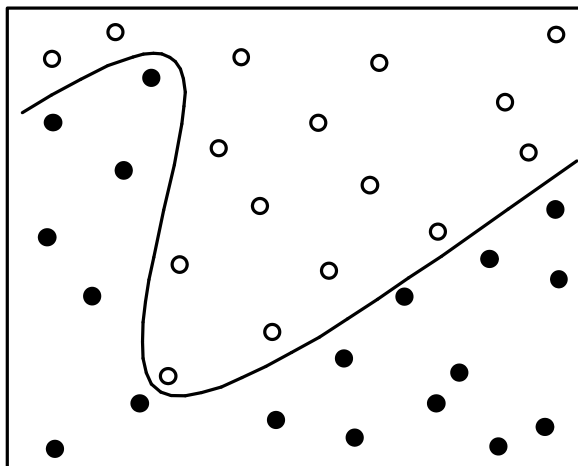
Solution: Random forests

Lit: J.R. Quinlan *Machine Learning* 1 (1986) 81.



Support Vector Machines

Support vector machines generate a hyperplane in the multi-dimensional space of the descriptors that separates the data points.



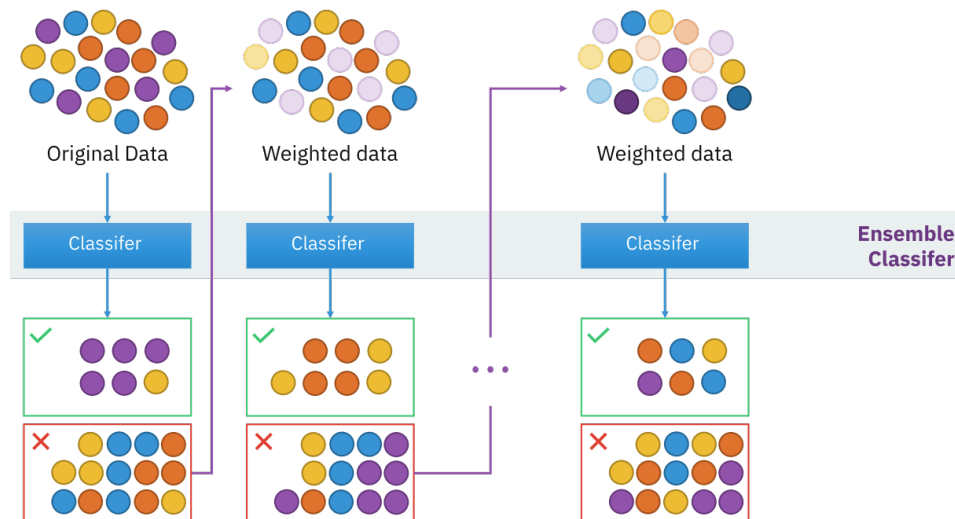
Advantages: accuracy, a minimum of descriptors (= support vectors) used

Disadvantage: Interpretation of results, design of new compounds with desired properties, which descriptors for input

Boosting

Like decision trees, the idea is to find classifiers in a sequential way, but using several of them at the same time (weak classifiers). In each step determine those descriptors that classify most of the remaining wrongly assigned data points correctly. → AdaBoost

Further variations: Gradient Boosting Methods



source:

[https://en.wikipedia.org/wiki/Boosting_\(machine_learning\)#/media/File:Ensemble_Boosting.svg](https://en.wikipedia.org/wiki/Boosting_(machine_learning)#/media/File:Ensemble_Boosting.svg)

Property prediction: So what?

Classical QSAR equations: small data sets, few descriptors that are (hopefully) easy to understand

CoMFA: small data sets, lots of descriptors } easy visual interpretation of resulting interaction regions

Partial least square: small data sets, many descriptors

black box methods

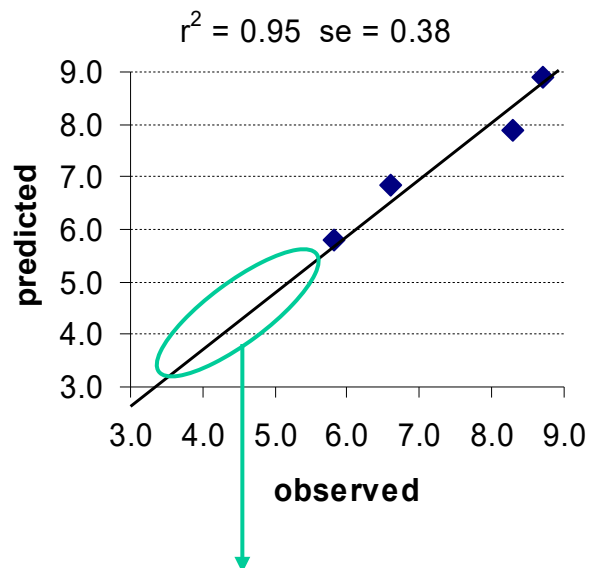
Neural nets: large data sets, some, preselected descriptors

Support vector machines: large data sets, many descriptors

interpretation of results often difficult

Interpretation of QSAR equations (1)

Caution is required when extrapolating beyond the underlying data range. Outside this range no reliable predictions can be made



Beyond the
black stump ...



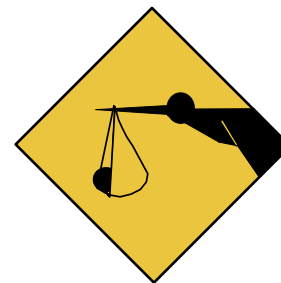
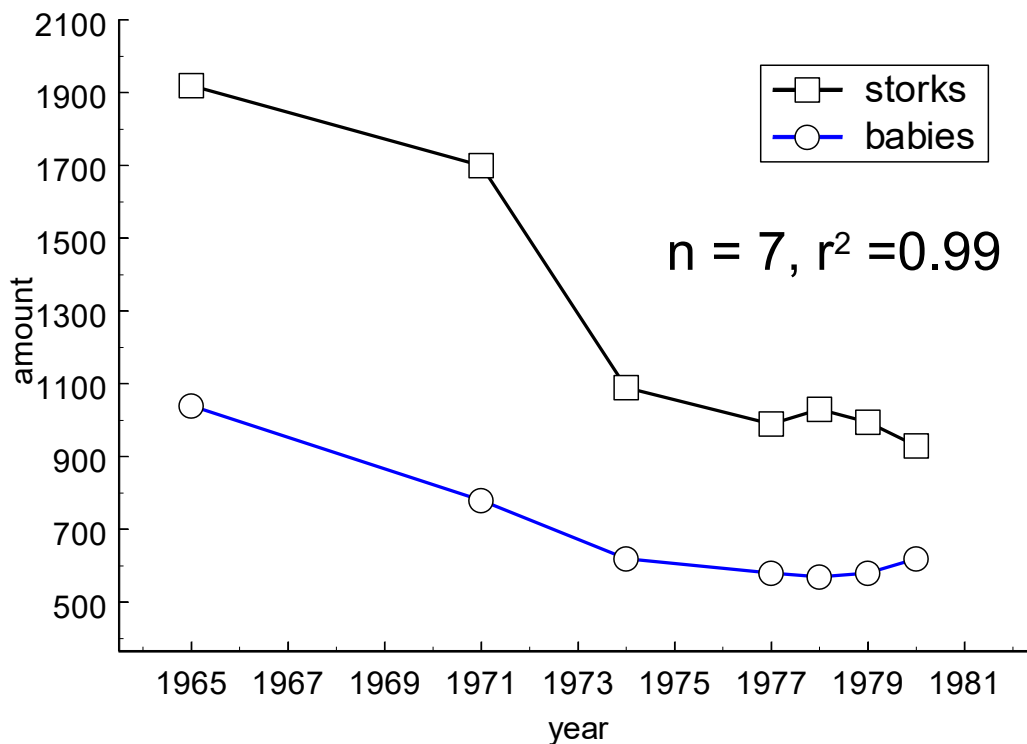
Kimberley, Western Australia

Interpretation of QSAR equations (2)

There should be a reasonable connection between the used descriptors and the predicted quantity.

Example: H. Sies *Nature* **332** (1988) 495.

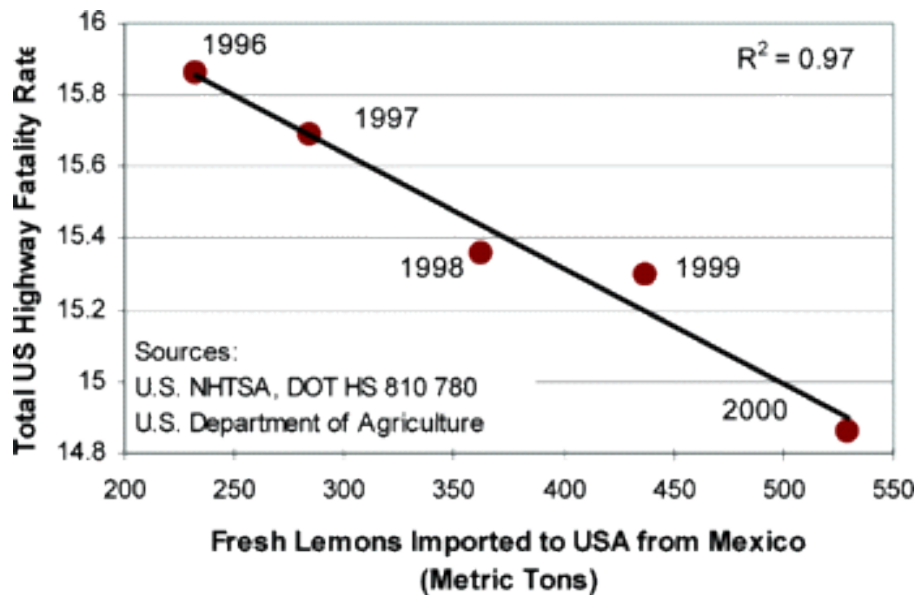
Scientific proof that babies are delivered by storks



Interpretation of QSAR equations (3)

Another striking correlation

„QSAR has evolved into a perfectly practiced art of logical fallacy“



$n = 5, r^2 = 0.97$

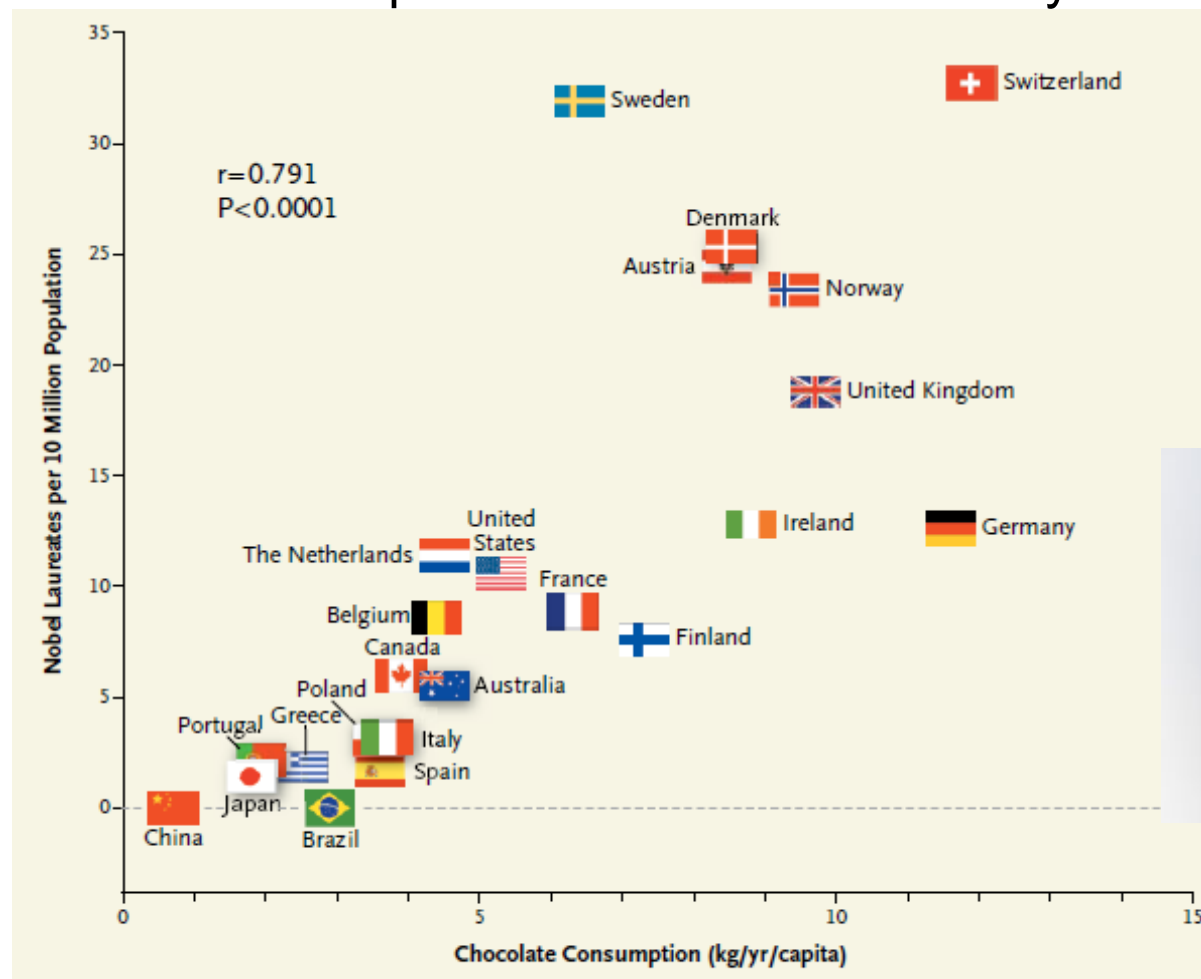
very small
data set

S.R. Johnson *J.Chem.Inf.Model.* **48** (2008) 25.

→ the more descriptors are available, the higher is the chance of finding some that show a chance correlation

Interpretation of QSAR equations (4)

The scientific proof that chocolate makes you smarter....



$n = 22, r^2 = 0.63$

small data set



Figure 1. Correlation between Countries' Annual Per Capita Chocolate Consumption and the Number of Nobel Laureates per 10 Million Population.

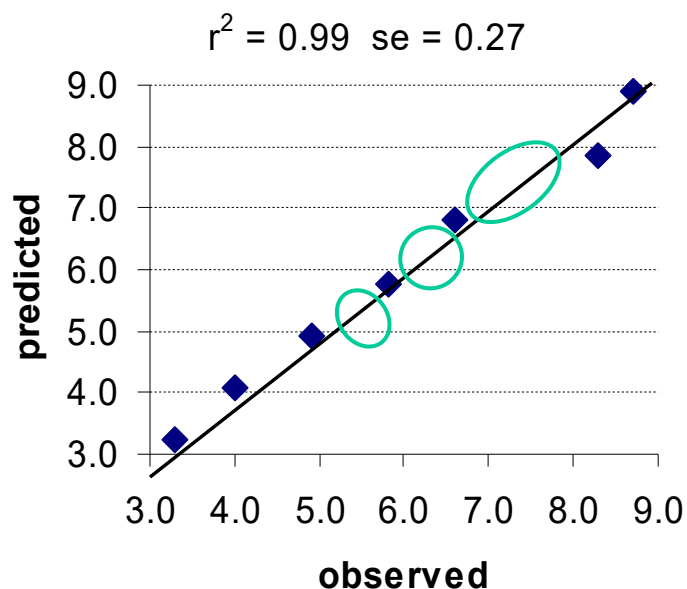
F.H. Messerli *New England J. Med.* Oct.10, 2012 DOI:10.1056/NEJMon1211064

Interpretation of QSAR equations (6)

Predictivity of QSAR equations in between data points.

The hypersurface is not smooth: activity islands vs. activity cliffs:
Even small changes in structure can change the activity strongly.

In other words, what is in between the present molecules?



Bryce Canyon National Park, Utah

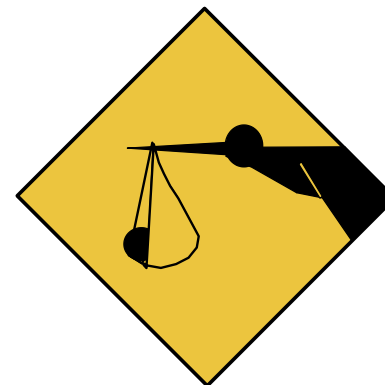
Lit: G.M. Maggiora *J.Chem.Inf.Model.* **46** (2006) 1535.

S.R. Johnson *J.Chem.Inf.Model.* **48** (2008) 25.

Interpretation of QSAR equations (6)

Which QSAR performance is realistic and where does overfitting start?

- standard deviation (se) of 0.2–0.3 log units corresponds to a typical 2-fold error in experiments („soft data“). This gives rise to an upper limit of
- r^2 between 0.77–0.88 (for biological systems)
→ obtained correlations above 0.90 are highly likely to be accidental or due to overfitting (except for physico-chemical properties that show small errors, e.g. boiling points, logP, NMR ^{13}C shifts)

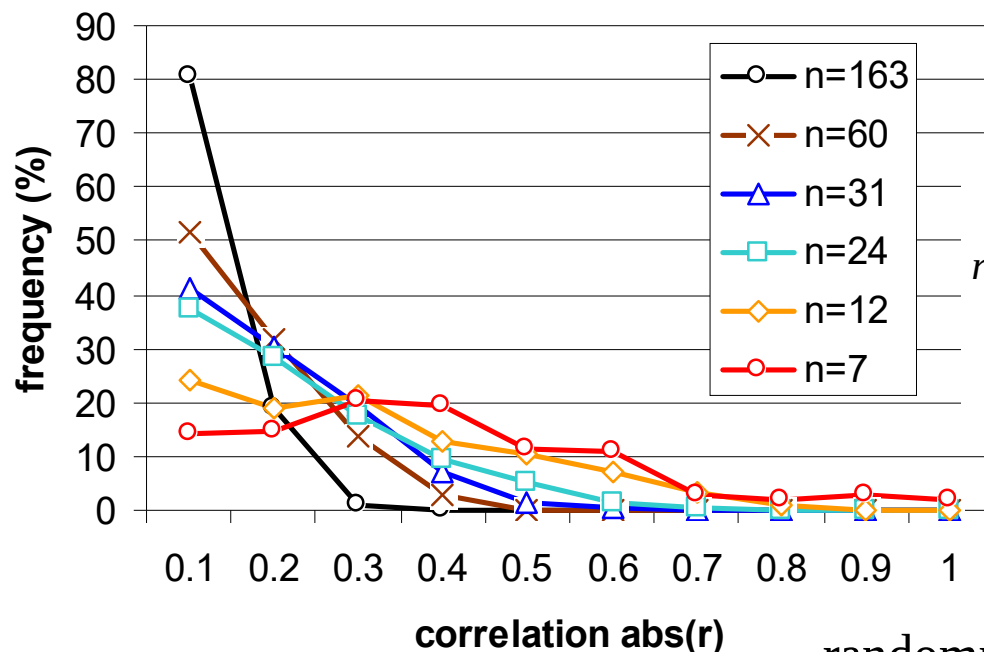


But: even random correlations can sometimes be as high as 0.84

Lit: A.M.Doweyko *J.Comput.-Aided Mol.Des.* **22** (2008) 81-89.

Interpretation of QSAR equations (7)

Accidental correlation of a single descriptor (1000 random descriptors)



n = number of data points

$$r = \frac{\sum_{i=1}^n (x_i - \bar{x})(y_i - \bar{y})}{\sqrt{\left(\sum_{i=1}^n (x_i - \bar{x})^2\right) \left(\sum_{i=1}^n (y_i - \bar{y})^2\right)}} \in [-1 \dots 1]$$

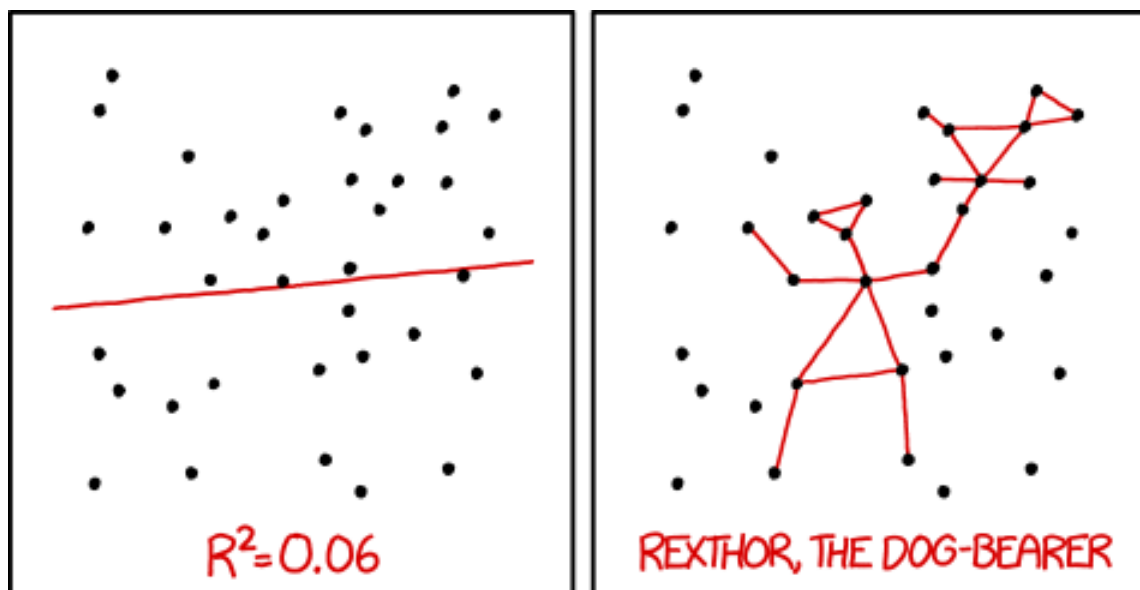
$$\text{randomness (\%)} = \frac{10\sqrt{2n}}{\sqrt{3}} \exp\left(\frac{-n \cdot r^2}{3}\right)$$

→ Dismiss unsuitable variables from the pool of descriptors.

Lit: M.C.Hutter *J.Chem.Inf.Model.* (2011) DOI: 10.1021/ci200403j

Interpretation of QSAR equations (8)

Low correlations...



I DON'T TRUST LINEAR REGRESSIONS WHEN IT'S HARDER
TO GUESS THE DIRECTION OF THE CORRELATION FROM THE
SCATTER PLOT THAN TO FIND NEW CONSTELLATIONS ON IT.

Source: <https://xkcd.com>

Interpretation of QSAR equations (9)

According to statistics more people die after being hit by a donkey than from the consequences of an airplane crash.



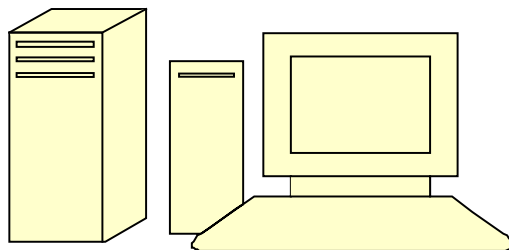
„An unsophisticated forecaster uses statistics as a drunken man uses lamp-posts – for support rather than for illumination“

Andrew Lang (1844 – 1912)

further literature: R.Guha *J.Comput.-Aided Mol.Des.* **22** (2008) 857-871.

Similarity Searching

2D-fingerprints allow to comb even through large substance databases: Fingerprints have to be computed only once, and can be stored separately.



Practical issues:

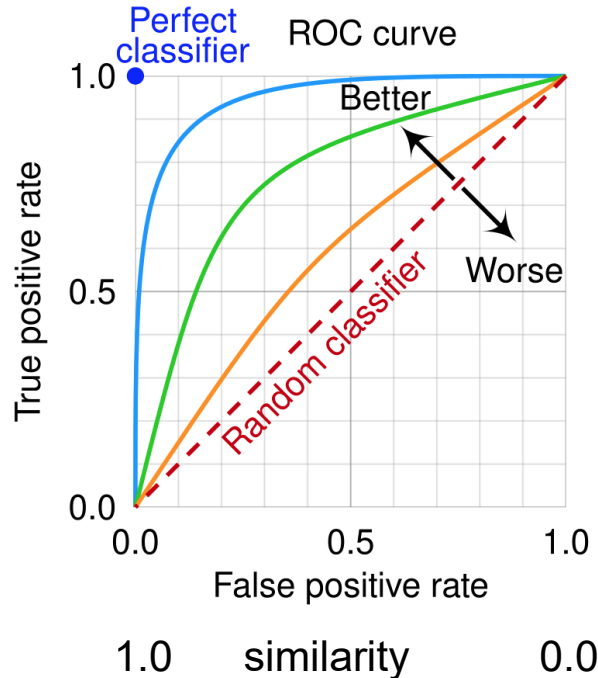
Choice of fingerprint method (multiple, combine results)

Is there a cut-off value that separates active molecules from inactive ones?

Which query molecule(s) to use?

Performance Measures in Similarity Searching (I)

Receiver Operator Characteristic



AUC: Area Under the Curve ≤ 1

What we need are true positives that are detected early
(= with high similarity values)

Picture source:

https://en.wikipedia.org/wiki/Receiver_operating_characteristic

Performance Measures in Similarity Searching (II)

Major drawback of the AUC:

Depends on the distribution of actives and inactives among the dataset

EF: Enrichment Factor

Number of retrieved actives compared to random results at a given threshold.

BEDROC: Boltzmann-Enhanced Discrimination of ROC

Obtained values are bounded between 0 and 1 (as the AUC)

Uses only one parameter α (typically $\alpha=20$) that determines how much emphasis is put on early recovered compounds.

Literature: JF. Truchon & C.I. Bayly *J.Chem.Inf.Model.* **47** (2007) 488.

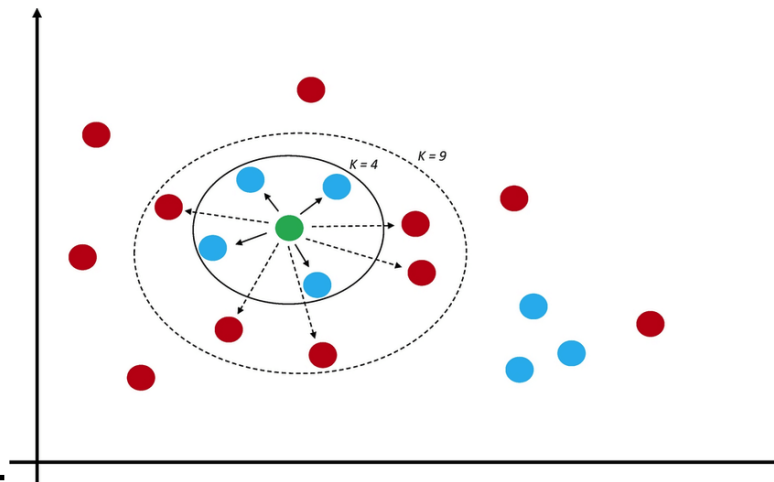
Choice of Query(s) for Searching

Choice of query molecule(s):

The most active substance?

The most „average“ substance (most similar to all others)?

One or more randomly chosen substances?



Choosing multiple query molecules:

1. The pair-wise similarity of all (active) compounds in the dataset is computed and summed up for each compound.
2. The n -top ranked compounds are used as query molecules ($n = 5, 10, \dots$) „sum of ranks“, „data fusion“
→ 5NN or 10NN approach (Nearest Neighbor)