QSAR, QSPR, statistics, correlation, similarity & descriptors

The tools of trade for the computer based rational drug design, particularly if there is no structural information about the target (protein) available.

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

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

The presence of experimentally measured data for a number of known compounds is required, e.g. from high throughput screening.
Introduction to QSAR (I)

Suppose we have experimentally determined the binding constants for the following compounds

\[ K_i \left[10^{-9} \text{ mol l}^{-1}\right] \]

\[ \begin{array}{cccc}
1550 & 250 & 5.0 & 2.0 \\
\end{array} \]

Which feature/property is responsible for binding?
Introduction to QSAR (II)

Using the number of fluorine atoms as descriptor we obtain following regression equation:

\[ \log(1/K_i) = a \cdot n_{\text{fluorine}} + b \]

\[ \log(1/K_i) = 1.037 \cdot n_{\text{fluorine}} + 5.797 \]
Introduction to QSAR (III)

Now we add some other compounds

Which features/properties are now responsible for binding?
Introduction to QSAR (IV)

We assume that following descriptors play a major role:
- number of fluorine atoms
- number of OH groups

\[
\log(1/K_i) = a_1 \cdot n_{\text{fluorine}} + a_2 \cdot n_{\text{OH}} + b
\]

\[
\log(1/K_i) = 1.049 \cdot n_{\text{fluorine}} - 0.843 \cdot n_{\text{OH}} + 5.768
\]
Introduction to QSAR (V)

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

$$r^2 = 0.99 \quad se = 0.27$$

Is our prediction sound or just pure coincidence?

→ We will need statistical proof (e.g. using a test set, $$\chi^2$$-test, p-values, cross-validation, boots trapping, ...)

$$K_i [10^{-9} \text{ mol l}^{-1}]$$

500000 100000 12500 1550 250 5.0 2.0
Correlation (I)

The most frequently used value is Pearson's correlation coefficient:

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

- High degree of correlation: \( r > 0.84 \)
- Low degree of correlation: \( 0 < r < 0.84 \)
- Anti-correlated: \( r < 0.5 \)

→ A plot tells more than pure numbers!
Definition of terms

QSAR: quantitative structure-activity relationship
QSPR: quantitative structure-property relationship

activity and property can be for example:

\[
\log(1/K_i) \quad \text{constant of binding}
\]

\[
\log(1/IC_{50}) \quad \text{concentration that produces 50\% effect}
\]

physical quantities, such as boiling point, solubility, …

aim: prediction of molecular properties from their structure
without the need to perform the experiment.

→ in silico instead of in vitro or in vivo

advantages: saves time and resources
Development of QSAR methods over time (I)

1868  A.C.Brown, T.Fraser:
Physiological activity is a function of the chemical
constitution (composition)
but: An absolute direct relationship is not possible,
only by using differences in activity.

Remember:
1865  Suggestion for the structure of benzene by
A. Kekulé. The chemical structure of most organic
compounds at that time was still unknown!
1893  H.H.Meyer, C.E.Overton
The toxicity of organic compounds is related to their
partition between aqueous and lipophilic biological
phase.
Development of QSAR method over time (II)

1868  E.Fischer
Key and lock principle for enzymes. Again no structural information about enzymes was available!

1930-40 Hammet equation: reactivity of compounds physical, organic, theoretic chemistry

1964  C.Hansch, J.W.Wilson, S.M.Free, F.Fujita
birth of modern QSAR-methods
**Hansch analysis** and **Free-Wilson analysis**

\[
\log(1/C) = k_1 \cdot P_1 + k_2 \cdot P_2 + \ldots + k_n \cdot P_n
\]

**coefficients (constant)**  **descriptors or variables**

linear free energy-related approach
Descriptors

Approaches that form a mathematical relationship between numerical quantities (descriptors $P_i$) and the physico-chemical properties of a compound (e.g. biological activity $\log(1/C)$), are called QSAR or QSPR, respectively.

\[
\log(1/C) = k_1 \cdot P_1 + k_2 \cdot P_2 + \ldots + k_n \cdot P_n
\]

Furthermore, descriptors are used to quantify molecules in the context of diversity analysis and in combinatorial libraries.

In principle any molecular or numerical property can be used as descriptors

More about descriptors see
http://www.codessa-pro.com/descriptors/index.htm
Flow of information in a **drug discovery pipeline**
Compound selection

X-Ray with drug
X-Ray of protein
series of functional compounds
few hits from HTS
knowledge of enzymatic functionality (e.g. kinase, GPCR, ion channel)

eADME filter

HTS

docking

active site

QSAR, generate pharmacophore

combi chem

Setting up a virtual library

5th lecture
Modern Methods in Drug Discovery WS12/13
Descriptors based on molecular properties used to predict ADME properties

\( \text{logP} \) water/octanol partitioning coefficient
Lipinski’s rule of five
topological indices
polar surface area
similarity / dissimilarity
...

QSAR quantitative structure activity relationship
QSPR quantitative structure property rel.
"1D" descriptors (I)

For some descriptors we need only the information that can be obtained from sum formula of the compound. Examples: 
molecular weight, total charge, number of halogen atoms, ...

Further 1-dimensional descriptors are obtained by the summation of atomic contributions. Examples:
sum of the atomic polarizabilities
refractivity (molar refractivity, $M_R$)

$$M_R = (n^2 - 1) \frac{MW}{(n^2 + 2) \ d}$$
with refractive index $n$, density $d$, molecular weight $MW$
Depends on the polarizability and moreover contains information about the molecular volume ($MW / d$)
**logP (I)**

The $n$-octanol / water partition coefficient, respectively its logarithmic value is called logP.

Frequently used to estimate the membrane permeability and the bioavailability of compounds, since an orally administered drug must be enough lipophilic to cross the lipid bilayer of the membranes, and on the other hand, must be sufficiently water soluble to be transported in the blood and the lymph.

hydrophilic $-4.0 < \text{logP} < +8.0$ lipophilic

citric acid $-1.72$ iodobenzene $+3.25$
„typical“ drugs $< 5.0$
logP (II)

An increasing number of methods to predict logP have been developed:

Based on molecular fragments (atoms, groups, and larger fragments)

problem: non-parameterized fragments
(up to 25% of all compounds in substance libraries)

based on atom types (similar to force field atom types)


**AlogP, MlogP, XlogP**...

Parameters for each method were obtained using a mathematical fitting procedure (linear regression, neural net, ...)

Review: R.Mannhold & H.van de Waaterbeemd,
Recent logP prediction methods more and more apply whole molecule properties, such as

- molecular surface (polar/non-polar area, or their electrostatic properties = electrostatic potential)
- dipole moment and molecular polarizability
- ratio of volume / surface (globularity)

Example: Neural net trained with quantum chemical data

\[ \text{logP} \quad T. \text{ Clark et al. } J.\text{Mol.\Model.} \ 3 \ (1997) \ 142. \]
“1D“ descriptors (II)

Further atomic descriptors use information based on empirical atom types like in force fields. Examples:

- Number of halogen atoms
- Number of sp\(^3\) hybridized carbon atoms
- Number of H-bond acceptors (N, O, S)
- Number of H-bond donors (OH, NH, SH)
- Number of aromatic rings
- Number of COOH groups
- Number of ionizable groups (NH\(_2\), COOH)
- Number of freely rotatable bonds
Fingerprints

Figure 2. Schematic illustration of primary methods used in molecular fingerprint creation: (a) Create 2-D and 3-D model of molecule; (b) deconstruct the molecule into pharmacophoric elements; (c) generate conformational models; (d) deconstruct the molecule into topological/substructural elements; (e) determine distance between pharmacophoric groups using bond counts; (f) determine 2-, 3-, or 4-center distance combinations of pharmacophoric groups for each conformation; and (g) determine the presence or absence of each descriptor element and combine to create a binary fingerprint.

binary *fingerprint* of a molecule
Lipinski’s Rule of 5

Combination of descriptors to estimate intestinal absorption. Insufficient uptake of compounds, if

Molecular weight > 500
logP > 5.0
> 5 H-bond donors (OH and NH)
>10 H-bond acceptors (N and O atoms)

slow diffusion
too lipophilic
to many H-bond with the head groups of the membrane

2D descriptors (I)

Descriptors derived from the configuration of the molecules (covalent bonding pattern) are denoted 2D descriptors. Since no coordinates of atoms are used, they are in general conformationally independent, despite containing topological information about the molecule. C.f. representation by SMILES

adjacency matrix $M$

```
C1 0 1 1 1 1 0 0
H2 1 0 0 0 0 0 0
H3 1 0 0 0 0 0 0
H4 1 0 0 0 0 0 0
C5 1 0 0 0 0 1 1
H6 0 0 0 0 1 0 0
O7 0 0 0 0 1 0 0
```

distance matrix $D$

```
0 1 1 1 1 2 2
1 0 2 2 2 3 3
1 2 0 2 2 3 3
1 2 2 0 2 3 3
1 2 2 2 0 1 1
2 3 3 3 1 0 2
2 3 3 3 1 2 0
```
2D descriptors (II)

The essential topological properties of a molecule are the degree of branching and the molecular shape.

An sp³ hybridized carbon has got 4 valences, an sp² carbon only 3.

Thus the ratio of the actual branching degree to the theoretically possible branching degree can be used as descriptor as it is related to the saturation.
2D descriptors (III)

Common definitions:

$Z_i$ ordinary number (H=1, C=6, N=7, LP=0)

$h_i$ number of H atoms bonded to atom $i$

$d_i$ number of non-hydrogen atoms bonded to atom $i$

Descriptors accounting for the degree of branching and the flexibility of a molecule:

Kier & Hall Connectivity Indices

$p_i$ sum of $s$ and $p$ valence electrons of atom $i$

$v_i = \frac{(p_i - h_i)}{(Z_i - p_i - 1)}$ for all non-hydrogen (heavy) atoms
Kier and Hall Connectivity Indices

$Z_i$ ordinary number (H=1, C=6, LP=0)
$d_i$ number of heavy atoms bonded to atom $i$
$p_i$ number of $s$ and $p$ valence electrons of atom $i$
$v_i = (p_i - h_i) / (Z_i - p_i - 1)$ for all heavy atoms

Chi0 0th order
\[ \chi_0 = \sum_i \frac{1}{\sqrt{d_i}} \quad \text{for all heavy atom with } d_i > 0 \]

Chi1 1st order
\[ \chi_1 = \sum_i \sum_{j>i} \frac{1}{\sqrt{d_i d_j}} \quad \text{for all heavy atoms if } \]
\[ i \text{ is bonded to } j \]

Chi0v Valence index
\[ \chi_{0v} = \sum_i \frac{1}{\sqrt{v_i}} \quad \text{for all heavy atoms with } v_i > 0 \]
Kier and Hall Shape Indices (I)

$n$ number of heavy atoms (non-hydrogen atoms)

$m$ total number of bonds between all heavy atoms

$p_2$ number of paths of length 2

$p_3$ number of paths of length 3 from the distance matrix $D$

**Kappa1**

\[
\kappa_1 = \frac{n(n-1)^2}{m^2}
\]

**Kappa2**

\[
\kappa_2 = \frac{(n-1)(n-2)^2}{p_2^2}
\]

**Kappa3**

\[
\kappa_3 = \frac{(n-1)(n-3)^2}{p_3^2} \text{ for even } n
\]

\[
\kappa_3 = \frac{(n-3)(n-2)^2}{p_3^2} \text{ for odd } n
\]
Kier and Hall Shape Indices (II)

Relating the atoms to sp\(^3\)-hybridized carbon atoms yields the Kappa alpha indices

\[
\alpha = \sum_{i}^{n} \frac{r_i}{r_c - 1} \quad r_i \text{ covalence radius of atom } i
\]

\[
r_c \text{ covalence radius of an sp}^3 \text{ carbon atom}
\]

\[
\kappa_{\alpha 1} = \frac{s(s-1)^2}{(m+\alpha)^2} \text{ with } s = n + \alpha
\]

<table>
<thead>
<tr>
<th>element</th>
<th>hybridization</th>
<th>(\alpha)</th>
</tr>
</thead>
<tbody>
<tr>
<td>C</td>
<td>sp(^3)</td>
<td>0</td>
</tr>
<tr>
<td>C</td>
<td>sp(^2)</td>
<td>-0.13</td>
</tr>
<tr>
<td>C</td>
<td>sp</td>
<td>-0.22</td>
</tr>
<tr>
<td>N</td>
<td>sp(^3)</td>
<td>-0.04</td>
</tr>
<tr>
<td>N</td>
<td>sp(^2)</td>
<td>-0.20</td>
</tr>
<tr>
<td>N</td>
<td>sp</td>
<td>-0.29</td>
</tr>
<tr>
<td>O</td>
<td>sp(^3)</td>
<td>-0.04</td>
</tr>
<tr>
<td>P</td>
<td>sp(^3)</td>
<td>+0.43</td>
</tr>
<tr>
<td>S</td>
<td>sp(^3)</td>
<td>+0.35</td>
</tr>
<tr>
<td>Cl</td>
<td></td>
<td>+0.29</td>
</tr>
</tbody>
</table>
Balaban, Wiener, and Zagreb Indices

- \( n \) number of heavy atoms (non-hydrogen atoms)
- \( m \) total number of bonds between all heavy atoms
- \( d_i \) number of heavy atoms bonded to atom \( i \)

\[
w_i = \sum_{i \neq j} D_{ij}
\]

Sum of the off-diagonal matrix elements of atom \( i \) in the distance matrix \( D \)

\[
\text{BalabanJ} = \frac{m}{m - n + 1} \sum_{i} \frac{1}{\sqrt{w_i w_j}}
\]

\[
\text{WienerJ (pfad number)} = \frac{1}{2} \sum_{i} w_i
\]

Correlates with the boiling points of alkanes

\[
\text{Wiener polarity} = \frac{1}{2} \sum_{i} w_i \text{ if } D_{ij} \geq 3
\]

\[
\text{Zagreb index} = \sum_{i} d_i^2 \text{ for all heavy atoms } i
\]
What message do topological indices contain?

topological indices are associated with the
• degree of branching in the molecule
• size and spatial extension of the molecule
• structural flexibility

Usually it is not possible to correlate a chemical property with only one index directly.

Although topological indices encode the same properties as fingerprints do, they are harder to interpret, but can be generated numerically more easily.
3D descriptors

Descriptors using the atomic coordinates \((x,y,z)\) of a molecule are therefore called **3D descriptors**.
As a consequence they usually depend on the conformation.

Examples:
van der Waals volume, molecular surface, polar surface, electrostatic potential (ESP), dipole moment
Chirality Descriptors

Most biological interactions are stereospecific e.g. ligand binding

Ideas for including chirality:
• Using differences of the van der Waals volume or the electrostatic potential after superposition (rotation)
• Adding +1/-1 to chiral centers in the adjacency matrix while computing topological descriptors
• Modifying the sign of 1D-descriptors (electronegativity, size, polarizability,...) with respect to the enantiomer

Quantum mechanical descriptors (selection)

Atomic charges \((partial\ atomic\ charges)\) No observables!
Mulliken population analysis
electrostatic potential (ESP) derived charges

dipole moment

polarizability

HOMO / LUMO
energies of the frontier orbitals
given in eV

covalent hydrogen bond acidity/basicity
difference of the HOMO/LUMO energies compared to those of water

(e)DRAGON

a computer program that generates >1400 descriptors

Roberto Todeschini
http://www.vcclab.org/lab/edragon/
Requires 3D-structure of molecules as input
Further information about descriptors

Roberto Todeschini, Viviana Consonni

1257 pages

CODEESSA    Alan R. Katritzky, Mati Karelson et al.
http://www.codessa-pro.com

MOLGEN    C. Rücker et al.
http://www.mathe2.uni-bayreuth.de/molgenqspr/index.html
PaDEL-Descriptor

Chun Wei Yap

http://padel.nus.edu.sg/software/padeldescriptor

Chosing the right compounds (I)

To derive meaningful QSAR predictions we need

- A sufficient number of compounds
- Structurally diverse compounds

statistically sound
tradeoff between count and similarity

How similar are compounds to each other?

→ Clustering using distance criteria that are based on the descriptors

<table>
<thead>
<tr>
<th>Chemical Structure</th>
<th>$K_i \times 10^{-9}$ (mol l$^{-1}$)</th>
</tr>
</thead>
<tbody>
<tr>
<td><img src="image1.png" alt="Chemical Structure 1" /></td>
<td>500000</td>
</tr>
<tr>
<td><img src="image2.png" alt="Chemical Structure 2" /></td>
<td>100000</td>
</tr>
<tr>
<td><img src="image3.png" alt="Chemical Structure 3" /></td>
<td>12500</td>
</tr>
<tr>
<td><img src="image4.png" alt="Chemical Structure 4" /></td>
<td>1550</td>
</tr>
<tr>
<td><img src="image5.png" alt="Chemical Structure 5" /></td>
<td>250</td>
</tr>
<tr>
<td><img src="image6.png" alt="Chemical Structure 6" /></td>
<td>5.0</td>
</tr>
<tr>
<td><img src="image7.png" alt="Chemical Structure 7" /></td>
<td>2.0</td>
</tr>
</tbody>
</table>
Distance criteria and similarity indices (I)

\( \chi_A \) fullfilled property of molecule \( A \)

|\( \chi_A \cap \chi_B \)| intersection of common properties of \( A \) and \( B \)

|\( \chi_A \cup \chi_B \)| unification of common properties of \( A \) and \( B \)

**Euklidian distance**

\[
D_{A,B} = \sqrt{\sum_{i=1}^{N} (x_{iA} - x_{iB})^2}
\]

**Manhattan distance**

\[
D_{A,B} = \sum_{i=1}^{N} |x_{iA} - x_{iB}|
\]

**formula**

**definition**

**range**

**other names**

\( \infty \) to 0

\( \infty \) to 0

City-Block, Hamming
Distance criteria and similarity indices (II)

**Soergel distance**

\[ D_{A,B} = \frac{\sum_{i=1}^{N} |x_{iA} - x_{iB}|}{\sum_{i=1}^{N} \max(x_{iA}, x_{iB})} \]

**Tanimoto index**

\[ S_{A,B} = \frac{\sum_{i=1}^{N} x_{iA} x_{iB}}{\left( \sum_{i=1}^{N} (x_{iA})^2 + \sum_{i=1}^{N} (x_{iB})^2 - \sum_{i=1}^{N} x_{iA} x_{iB} \right)} \]

For binary (dichotomous) values the Soergel distance is complementary to the Tanimoto index.

- 1 to 0
- $-0.333$ to $+1$ (continuous values)
- 0 to $+1$ (binary on/off values)

Jaccard coefficient

For binary (dichotomous) values the Soergel distance is complementary to the Tanimoto index.
Distance criteria and similarity indices (III)

**Dice coefficient**

\[
S_{A,B} = \frac{2 \sum_{i=1}^{N} x_{iA} x_{iB}}{\left( \sum_{i=1}^{N} (x_{iA})^2 + \sum_{i=1}^{N} (x_{iB})^2 \right)}
\]

-1 to +1

**Cosinus coefficient**

\[
S_{A,B} = \frac{\sum_{i=1}^{N} x_{iA} x_{iB}}{\sqrt{\sum_{i=1}^{N} (x_{iA})^2 + \sum_{i=1}^{N} (x_{iB})^2}}
\]

0 to +1 (continuous values)

\[
S_{A,B} = \frac{|x_A \cap x_B|}{|x_A| + |x_B|}
\]

0 to +1 (binary on/off values)

-0 to +1

- Hodgkin index
- Czekanowski coefficient
- Sørensen coefficient

- monotonic with the Tanimoto index

- Carbo index
- Ochiai coefficient

Highly correlated to the Tanimoto index
Correlation between descriptors (I)

Descriptors can also be inter-correlated (colinear) to each other → redundant information should be excluded

Usually we will have a wealth of descriptors (much more than the available molecules) to chose from. To obtain a reasonable combination in our QSAR equation, multivariate methods of statistic must be applied
Correlation between descriptors (II)

How many descriptors can be used in a QSAR equation?

Rule of thumb:
per descriptor used, at least 5 molecules (data points) should be present
otherwise the possibility of finding a coincidental correlation is too high.

(Ockham's razor: fit anything to anything)
Therefore:
Principle of parsimony
Deriving QSAR equations (I)

After removing the inter-correlated descriptors, we have to determine the coefficients $k_i$ for those descriptors that appear in the QSAR equation.

Such multiple linear regression analysis (*least square fit* of the according coefficients) is performed by statistics programs.

There are several ways to proceed:

1. Using the descriptor that shows the best correlation to the predicted property first and adding stepwise descriptors that yield the best improvement (*forward regression*)

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

$K_i$ [10$^{-9}$ mol l$^{-1}$]

500000
100000
12500
1550
250
5.0
2.0
Deriving QSAR equations (II)

2. Using all available descriptors first, and removing stepwise those descriptors that worsen the correlation fewest (backward regression/elimination)

3. Determining the best combination of the available descriptors for given number of descriptors appearing in the QSAR equation (2,3,4,...) (best combination regression)
   This is usually not possible due to the exponential runtime

   Problem of forward and backward regression:
   Risk of local minima

   Problem: Which descriptors are relevant or significant?
   Determination of such descriptors, see lecture 6