



“Computational approaches in drug discovery: expectations and reality.”

Stefano Moro

Molecular Modeling Section (MMS)

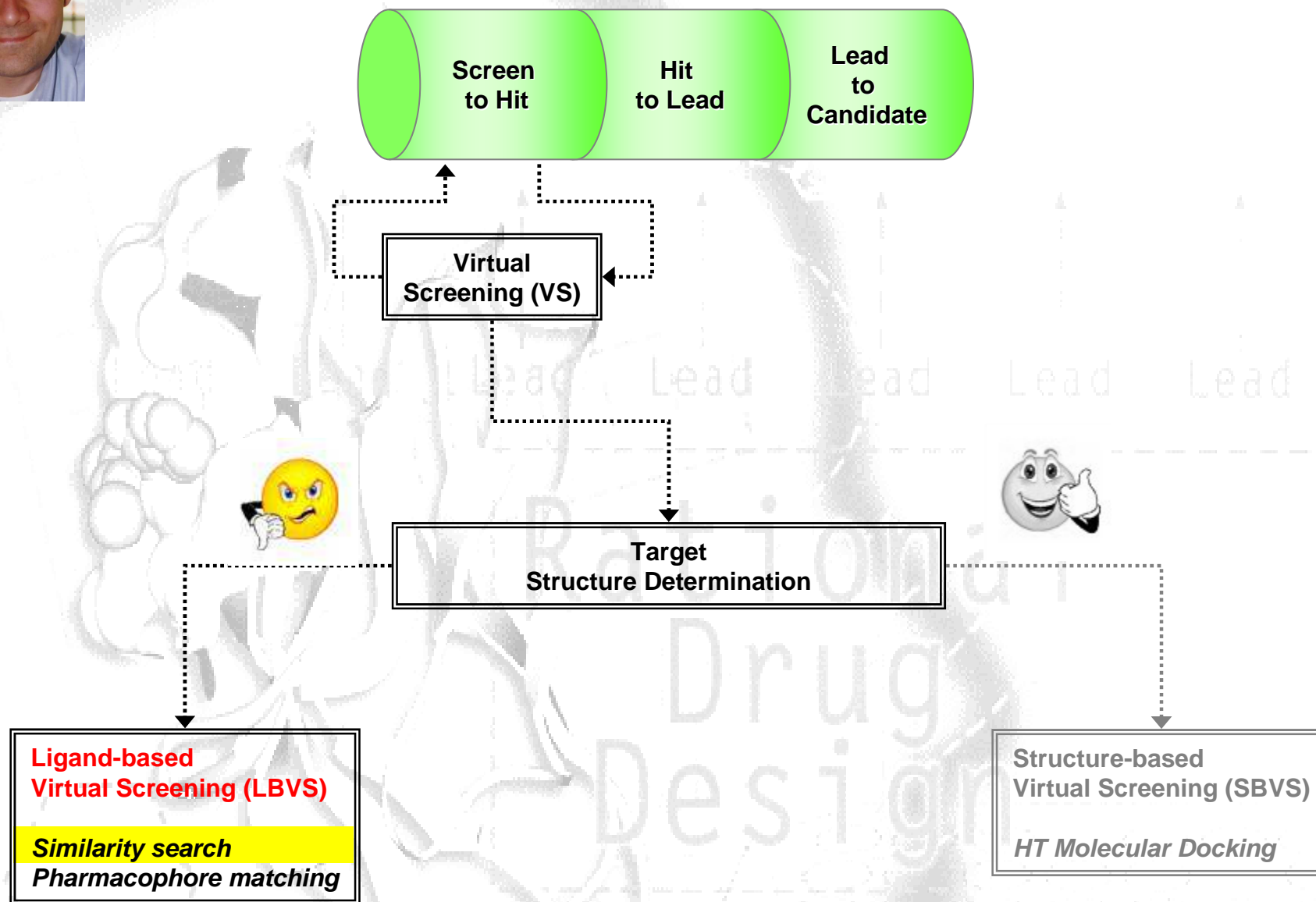
Department of Pharmaceutical and Pharmacological Sciences

University of Padova

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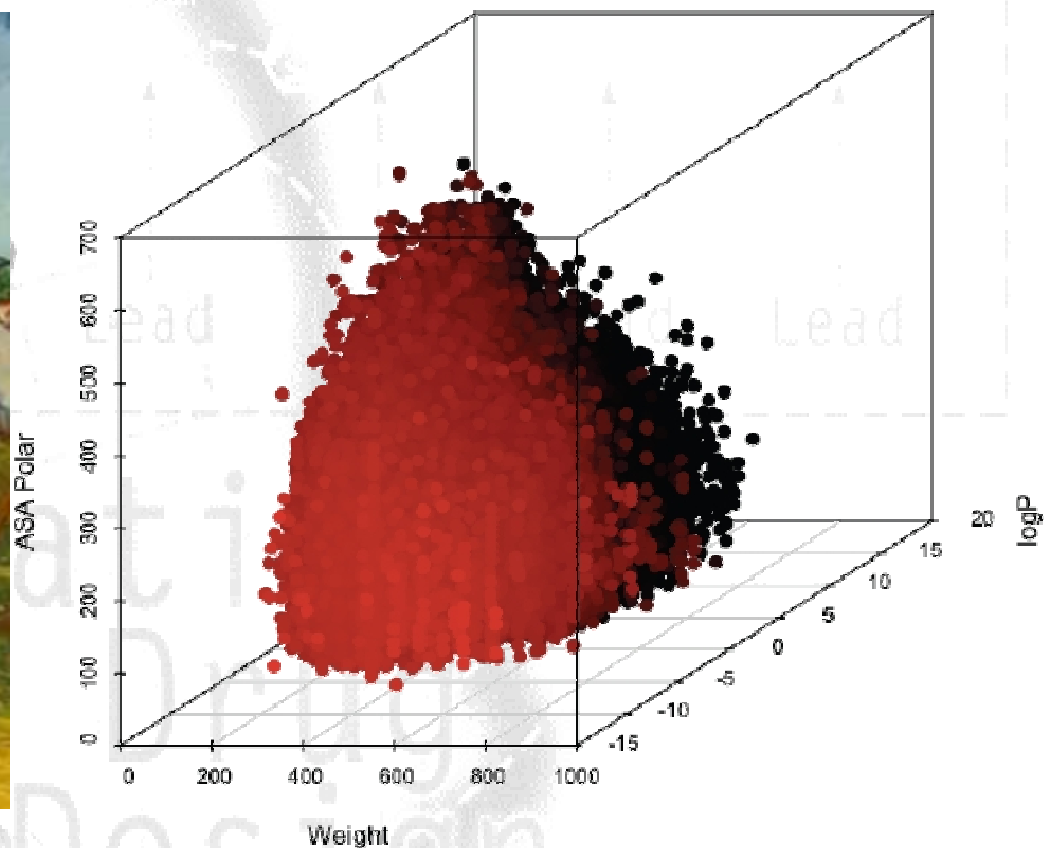
Here we are:





Back to the ratio xxx.000:1

Discovery a new drug is like to...





... molecular haystacks:



Chemical Abstract Service

(www.cas.org)

Date 06/06/2012 12:24:40 EST

Count

67,756,577 commercially available chemicals



... molecular haystacks:

PubChem <http://pubchem.ncbi.nlm.nih.gov/>

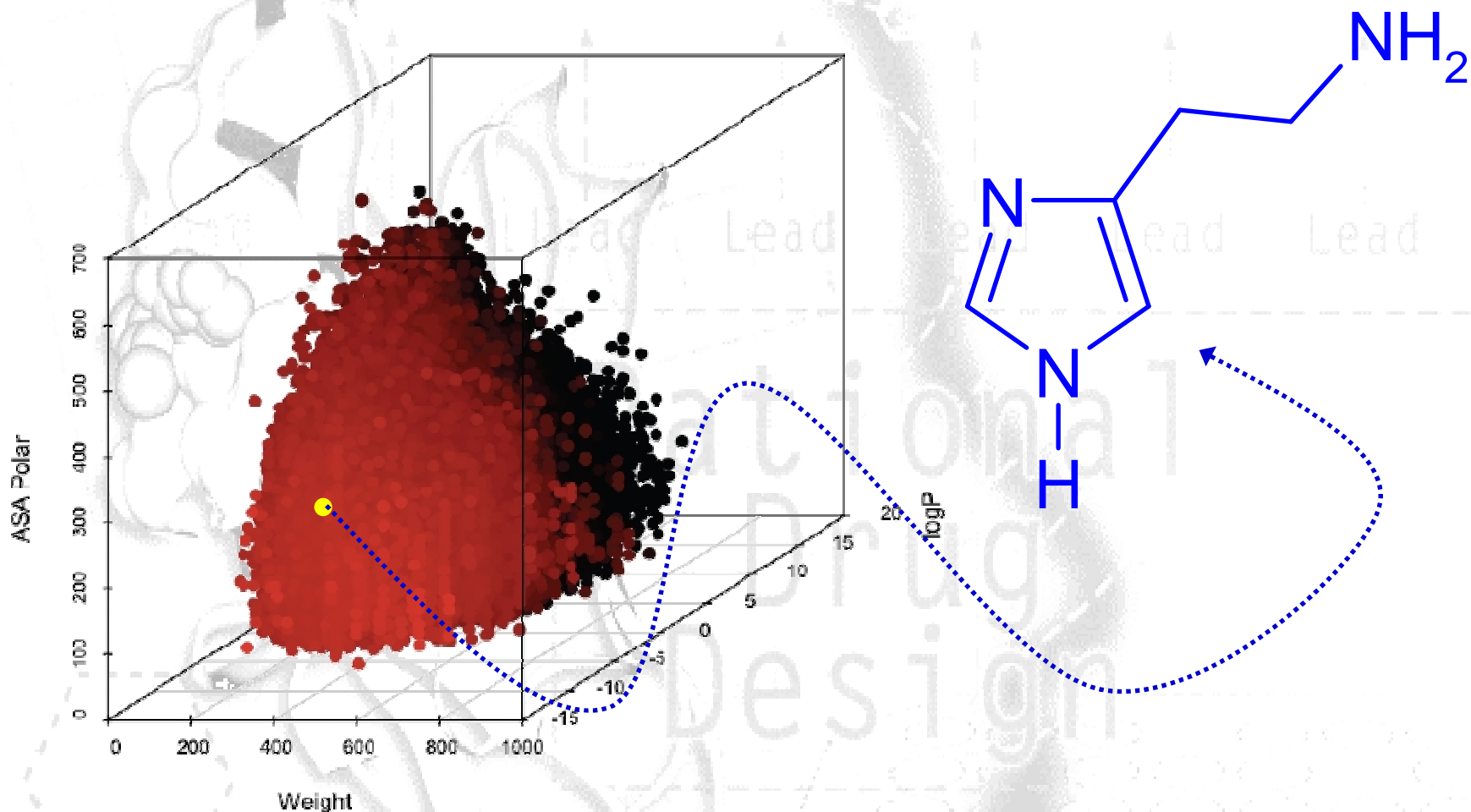
eMolecules <http://www.emolecules.com/>

 **ChemSpider** <http://www.chemspider.com/>
Building community for chemists

MMsINC <http://mms.dsfarm.unipd.it/MMsINC.html>

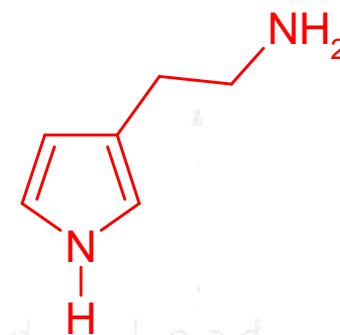
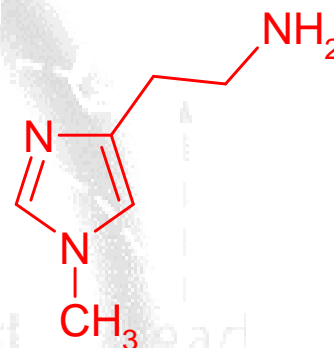
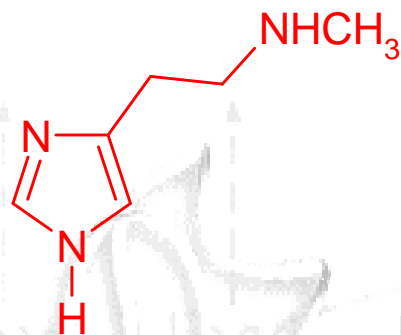
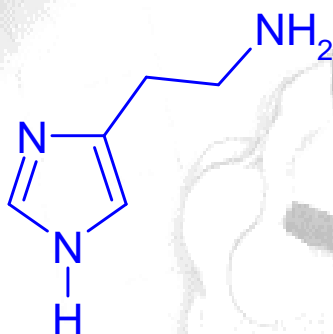


If you have only ONE active compound, could you suggest a possible strategy to fish out novel active analogs?

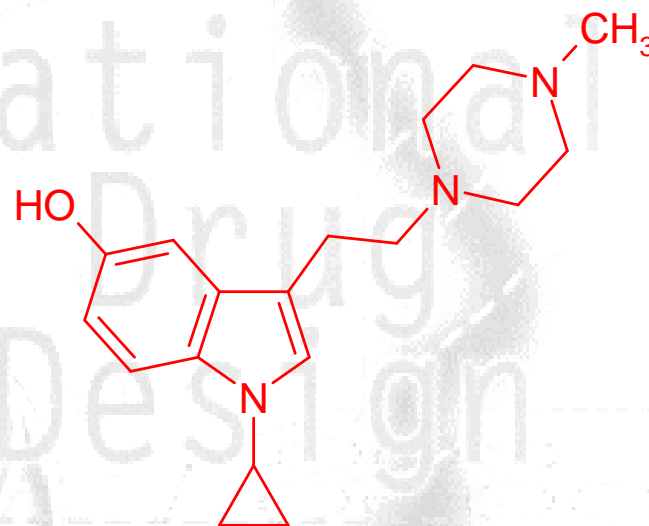




Probably using your chemical nose...

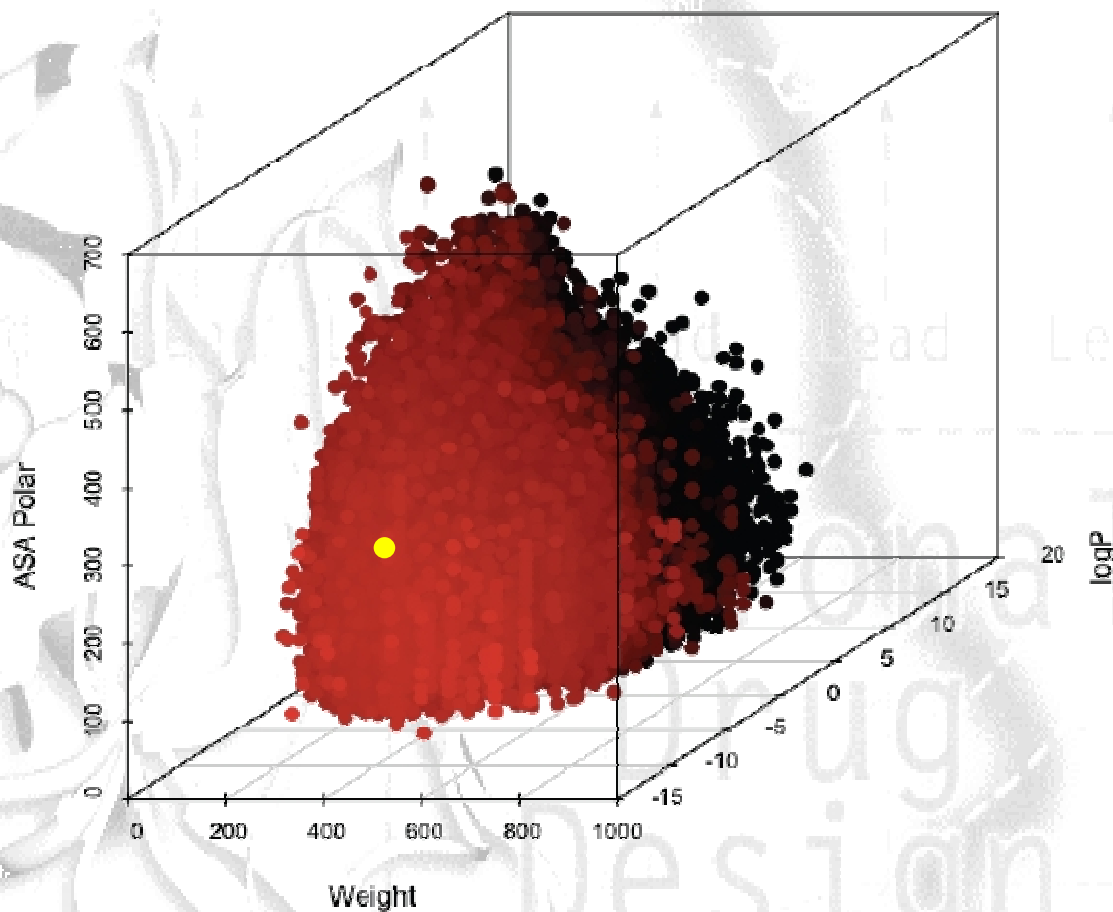


... reaching also more complex hypothesis:



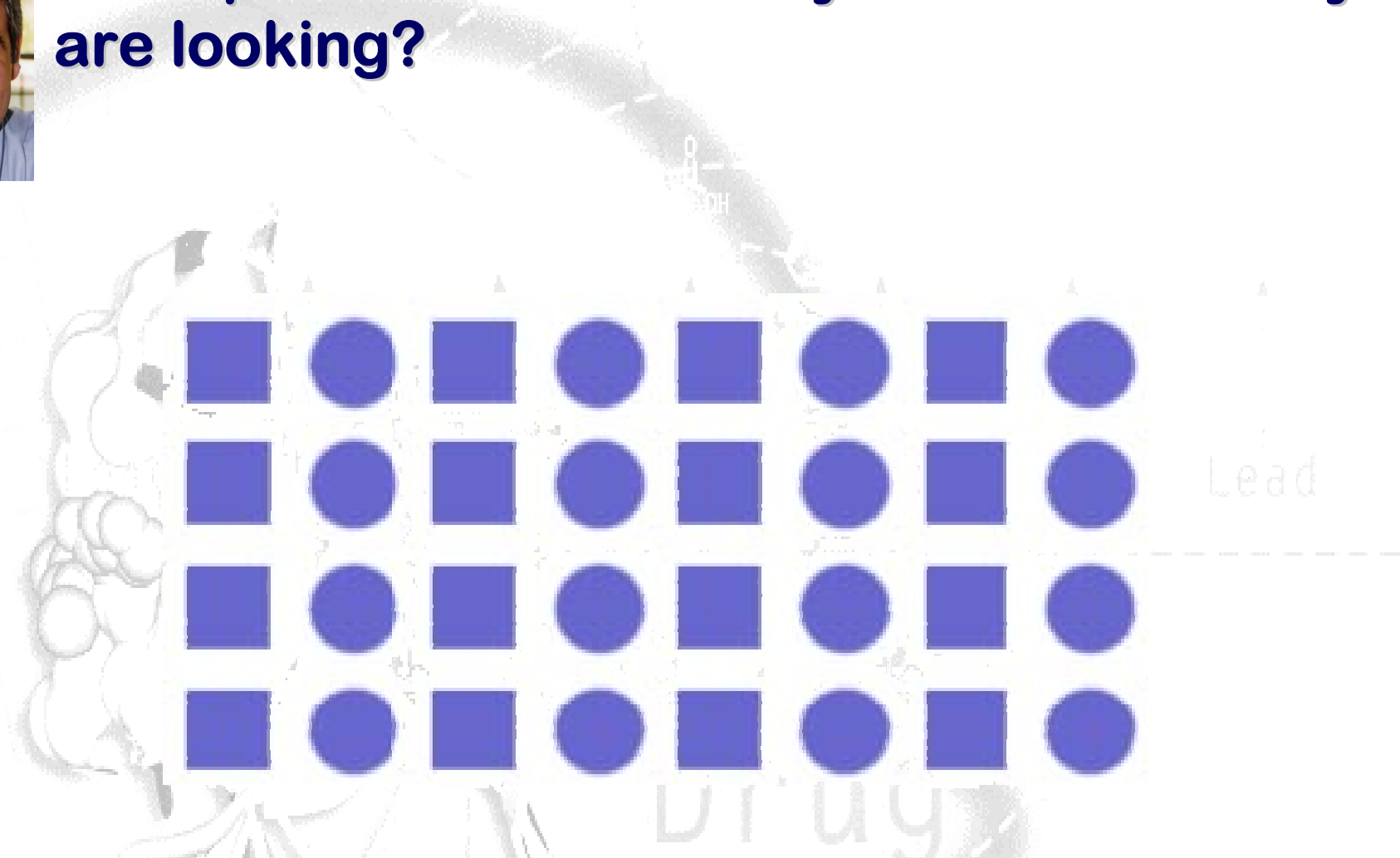


or more smartly?





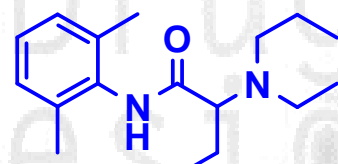
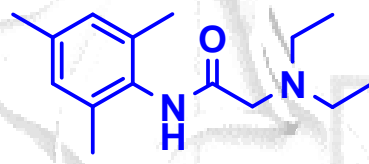
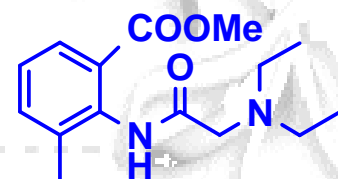
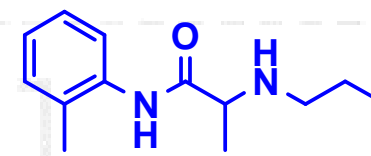
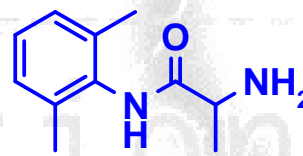
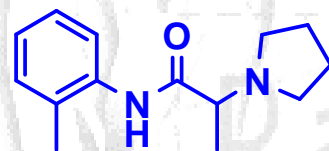
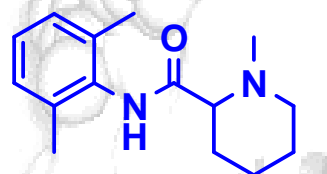
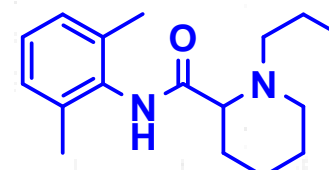
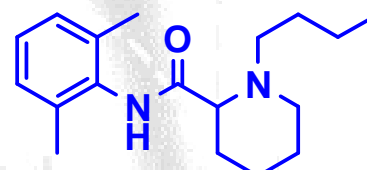
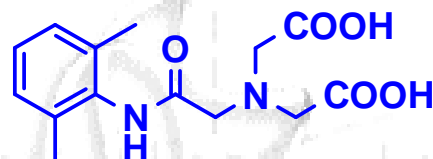
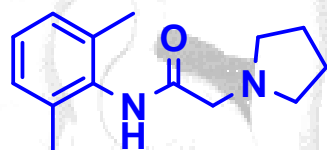
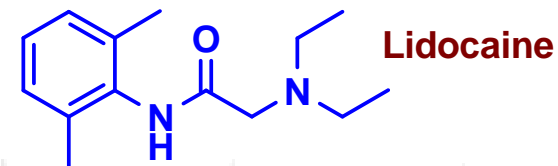
A simple exercise: could you tell me what you are looking?



Similarity law: similar objects are typically group together.

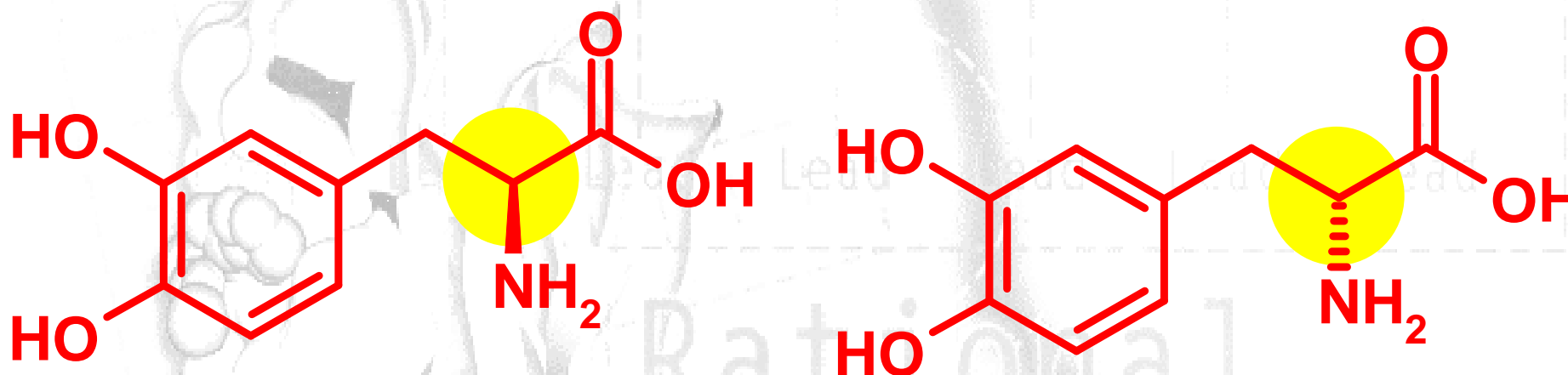


an, sometimes, this is true also in medchem:





Even if we **MUST** remember the “similarity
paradox”:



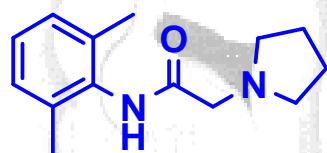
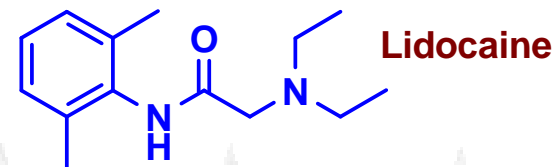
L-DOPA

D-DOPA

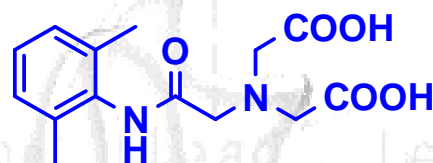


If we want to virtualize *chemical similarity* searching, we have to describe exactly what similarity is!

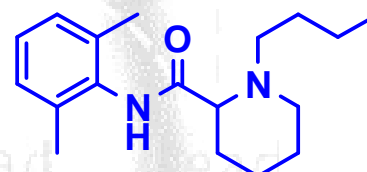
Are you able to scale *chemical similarity* of these analogs respect lidocaine?



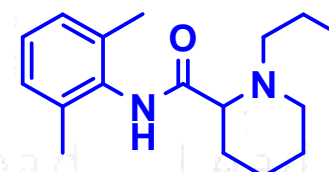
Pyrrocaine



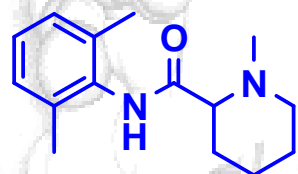
Lidofenin



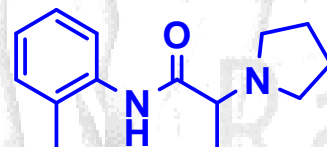
Bupivacaine



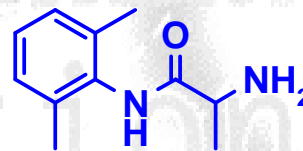
Ropivacaine



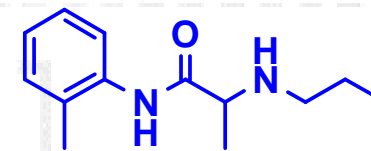
Mepivacaine



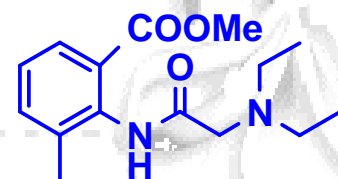
Aptocaine



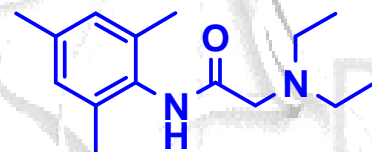
Tocainide



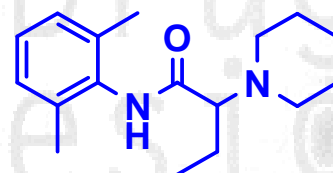
Prilocaine



Tolycaine



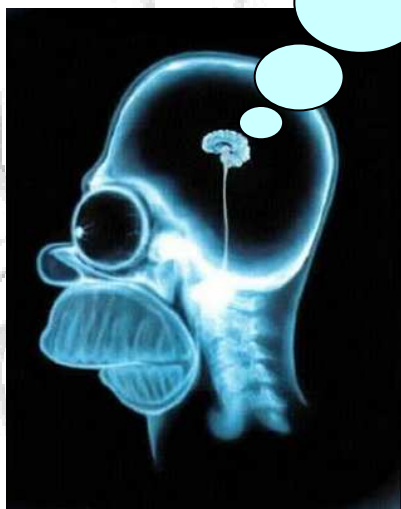
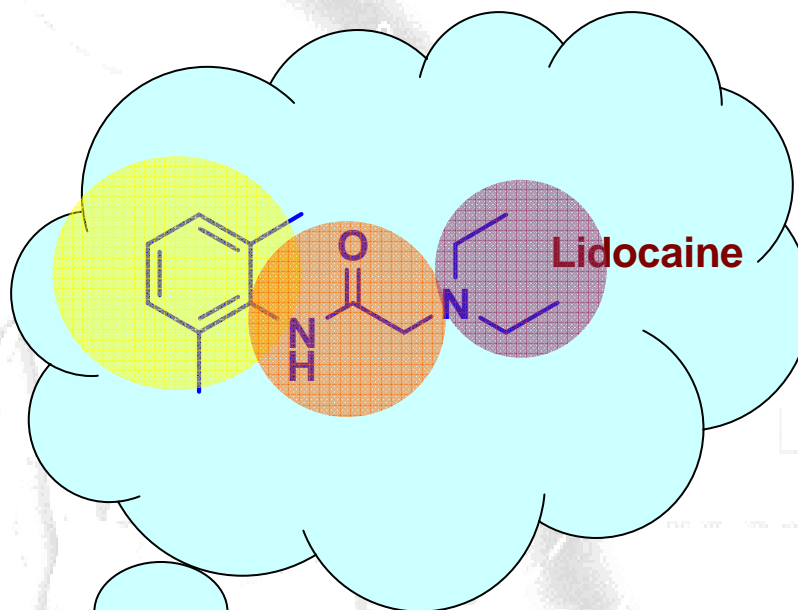
Trimecaine



Etidocaine

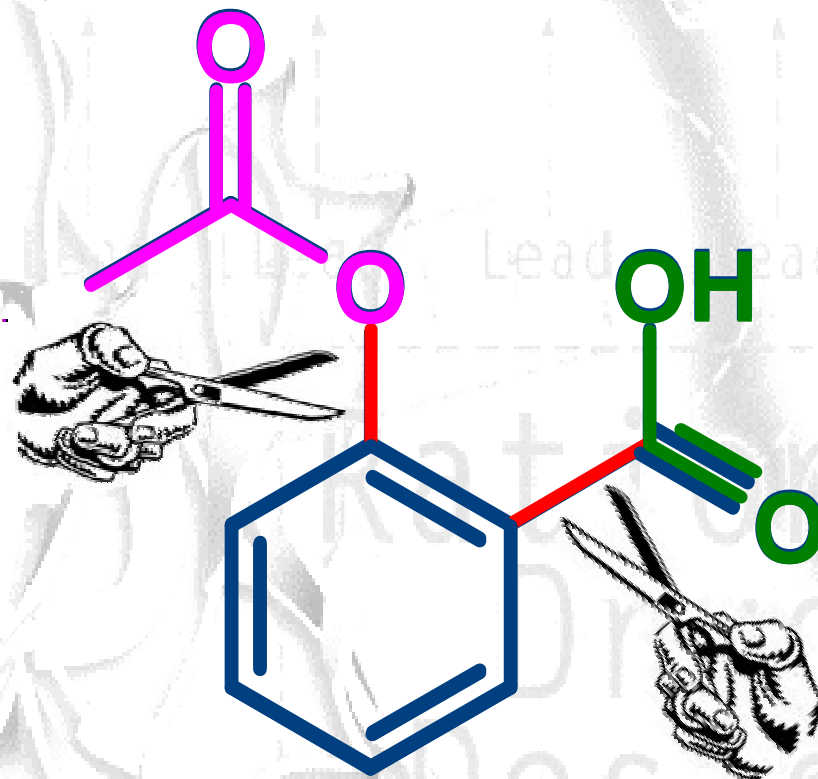


Tell me what you are thinking:



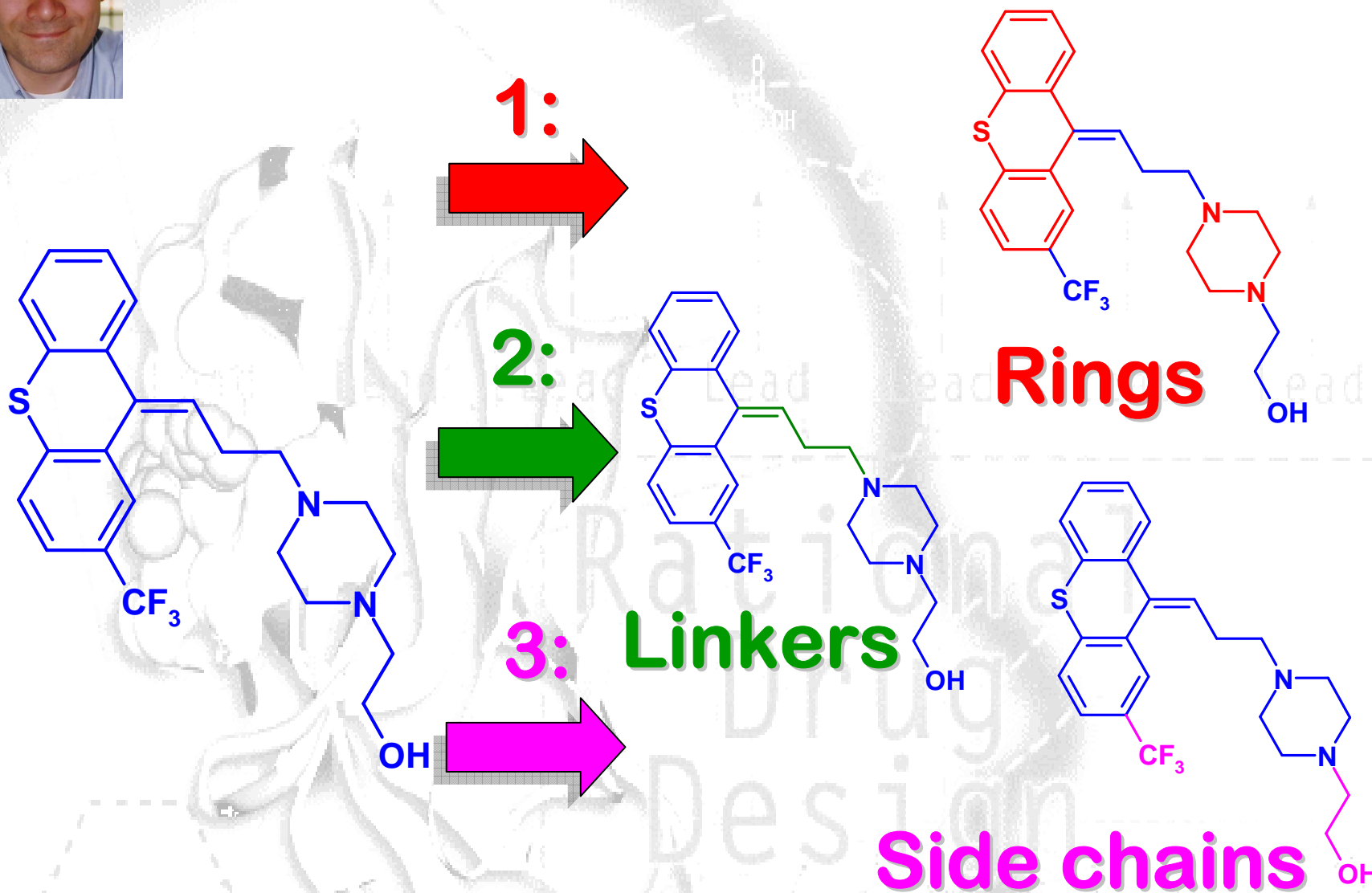


Exactly “*molecular fragmentation*”
could be a possible solution!





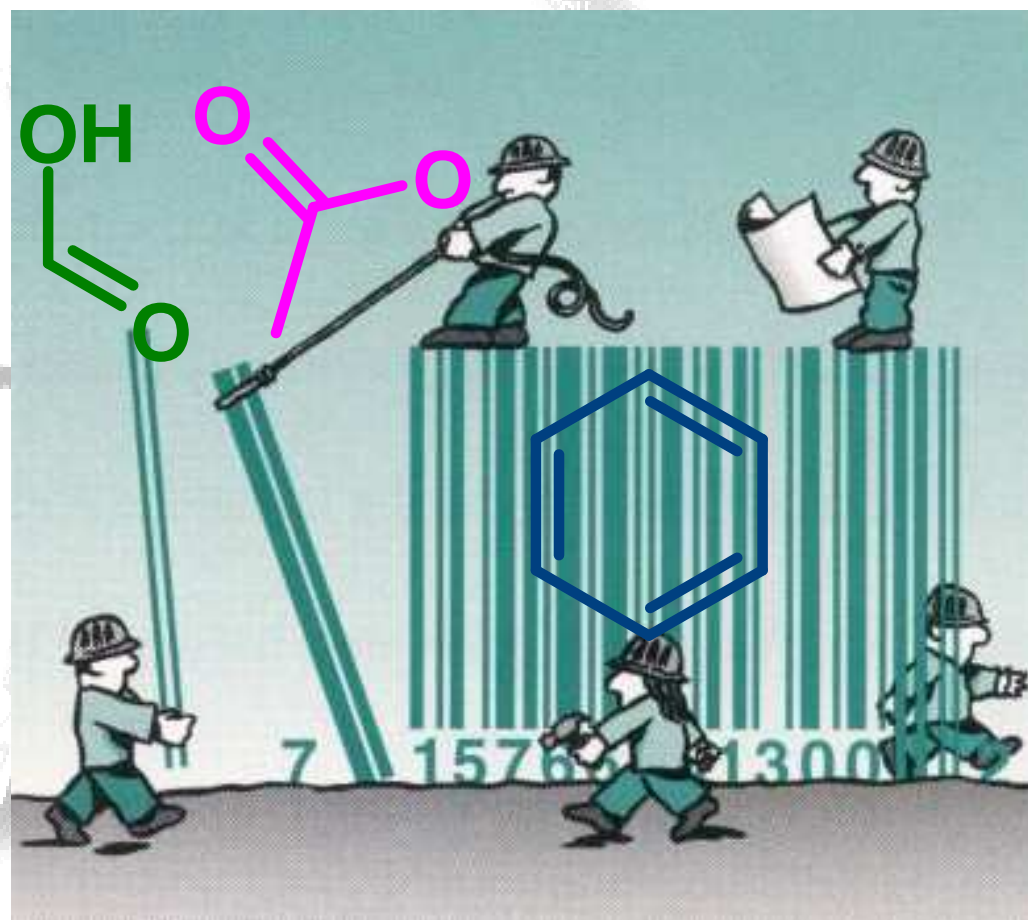
We need some rules:



G.W. Bemis, M. A. Murcko, J. Med. Chem. 1996, 39, 2887–2893.



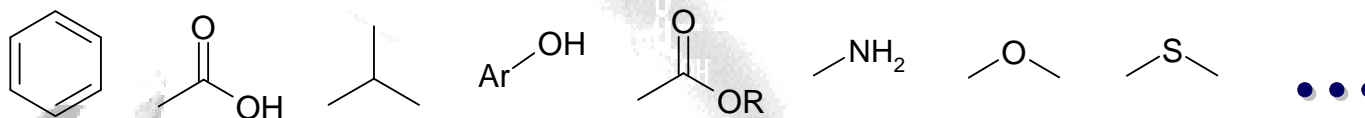
The sequence of fragments is like a molecular bar code...



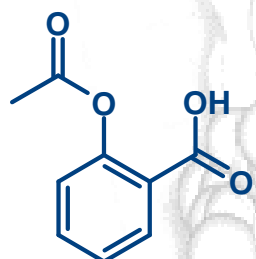
How we can build it up...

A useful concept: *structural keys*

1. Define all possible chemical fragments (*structural keys*):

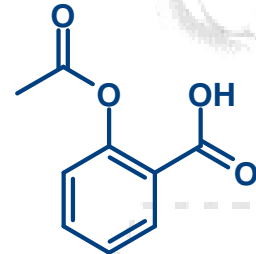


2. Assigne un *bit* for the each corrispondence in our molecule:

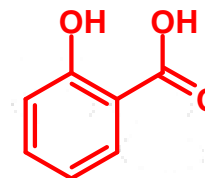


<chem>c1ccccc1</chem>	<chem>CC(=O)O</chem>	<chem>CC(C)C</chem>	<chem>Ar-OH</chem>	<chem>CC(=O)OR</chem>	<chem>CCN</chem>	<chem>CO</chem>	<chem>CS</chem>
1	1	0	0	1	0	0	0

3. Reiterate this procedure for each molecule of the database :



<chem>c1ccccc1</chem>	<chem>CC(=O)O</chem>	<chem>CC(C)C</chem>	<chem>Ar-OH</chem>	<chem>CC(=O)OR</chem>	<chem>CCN</chem>	<chem>CO</chem>	<chem>CS</chem>
1	1	0	0	1	0	0	0
1	1	0	1	0	0	0	0





Any standard?

MACCS (Molecular ACcess System) a collection of 166 functional groups representing the most accessible medchem chemical space.

MACCS keys, MDL Information Systems Inc., San Leandro, CA.





... so, now it is very easy to transform my molecular database in a collection of “*structural keys*”!



```
0000000100001101000000101010000000000110000010000100001000001000
0100010110010010010110011010011100111101000000110000000110001000
0100010100011101010000110000101000010011000010100000000100100000
0001101110011101111110100000100010000110110110000000100110100000
010001010011010001000000001000000001001000000100100001000101000
0100011100011101000100001011101100110110010010001101001100001000
0101110100110101010111111000010000011111100010000100001000101000
0100010100111101010000100010000000010010000010100100001000101000
00010001000101000101001000000000000001010000010000100000100000000
010001010001001100000000000000000001010000001000000000000000000
010001010001010000000000000001010000100100000000001000000000000
0101010101111100111110100000000000011010100011100100001100101000
0100010100011000010000011000000000010001000000110000000001100000
00000001000000000100001000000000000001010100000000100000100100000
010001010001010000000010000000000001000000000000000100001000011000
0001000100001100010010100000010100101011100010000100001000101000
0100011100010100010000100001001110010010000010001100000000101000
0101010100010100010100100000000000010010000010010100100100010000
```



... well, but why this transformation could help us in measuring chemical similarity?

000000100001101000001010100000000011000010000100001000001000
01000101100100100101100110100111001111010000011000000110001000
01000101000110101000011000010100001001100001010000000100100000
00011011100110111111010000010001000011011011000000100110100000
01000101001101000100000000100000001001000000100100001000101000
0100011100011101010100000101100110110010010001101001100001000
01011101001101010101111111000010000011111100010000100001000101000
0100010100111101010000100000000010010000100010000100001000101000
0001000100010100010100000000000001010000100010000100000100000000
01000101000100110000000000000000010100001000010000000000000000
01000101000101000000000000010100001001000000000100000000000000
01010101011111001111101000000000000101010001100100001100101000
01000101000110000100000110000000000100100000110000000001100000
00000001000000000100001000000000000101010000000100000100100000
010001010001010000000010000000000010000000000000100001000011000
0001000100001100010010100000010100101011100010000100001000101000
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0101010100010100010100100000000000010010000010010100100100010000

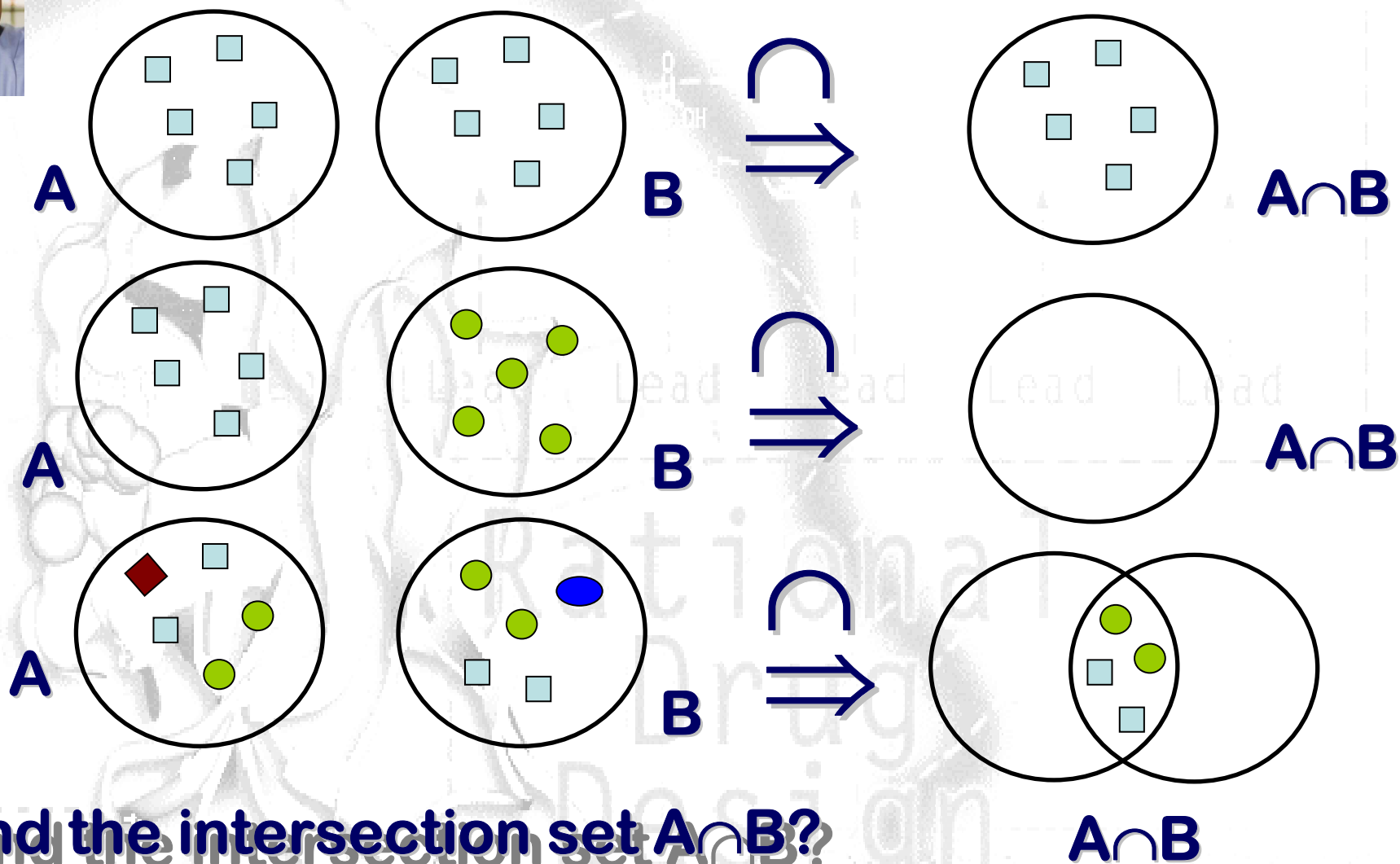


Lead

Design



Do you remember the Eulero-Venn diagrams?

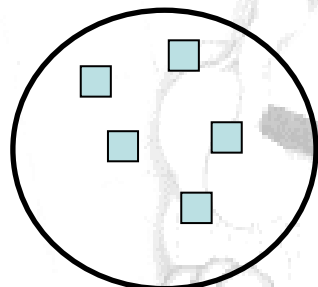




Now, I can introduce you the Jaccard e Tanimoto index!

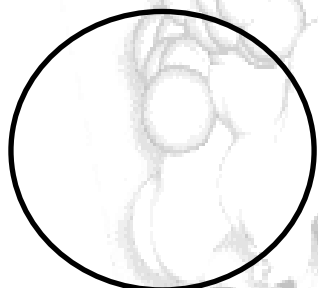
$$\text{Jaccard o Tanimoto Index} = \frac{A \cap B}{A_{\text{solo}} + B_{\text{solo}} + A \cap B}$$

Tanimoto, T.T. (1957) IBM Internal Report 17th Nov see also Jaccard, P. (1901) Bulletin del la Società Vaudoises des Sciences Naturelles 37, 241-272.



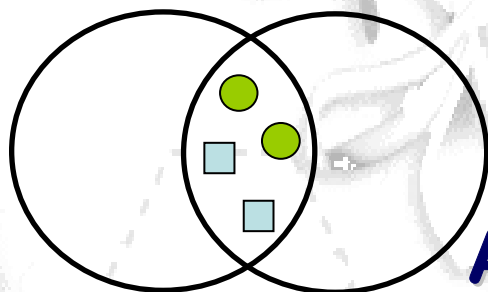
$A \cap B$

$= 1$



$A \cap B$

$= 0$

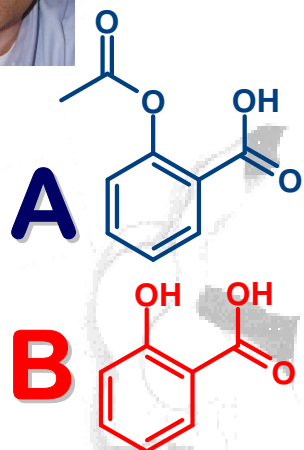


$A \cap B$

$$= \frac{4}{1 + 1 + 4} = 0.66$$



Eureka... now it's really easy!



1	1	0	0	1	0	0	0
1	1	0	1	0	0	0	0

Fragments only in A = 1

Fragments only in B = 1

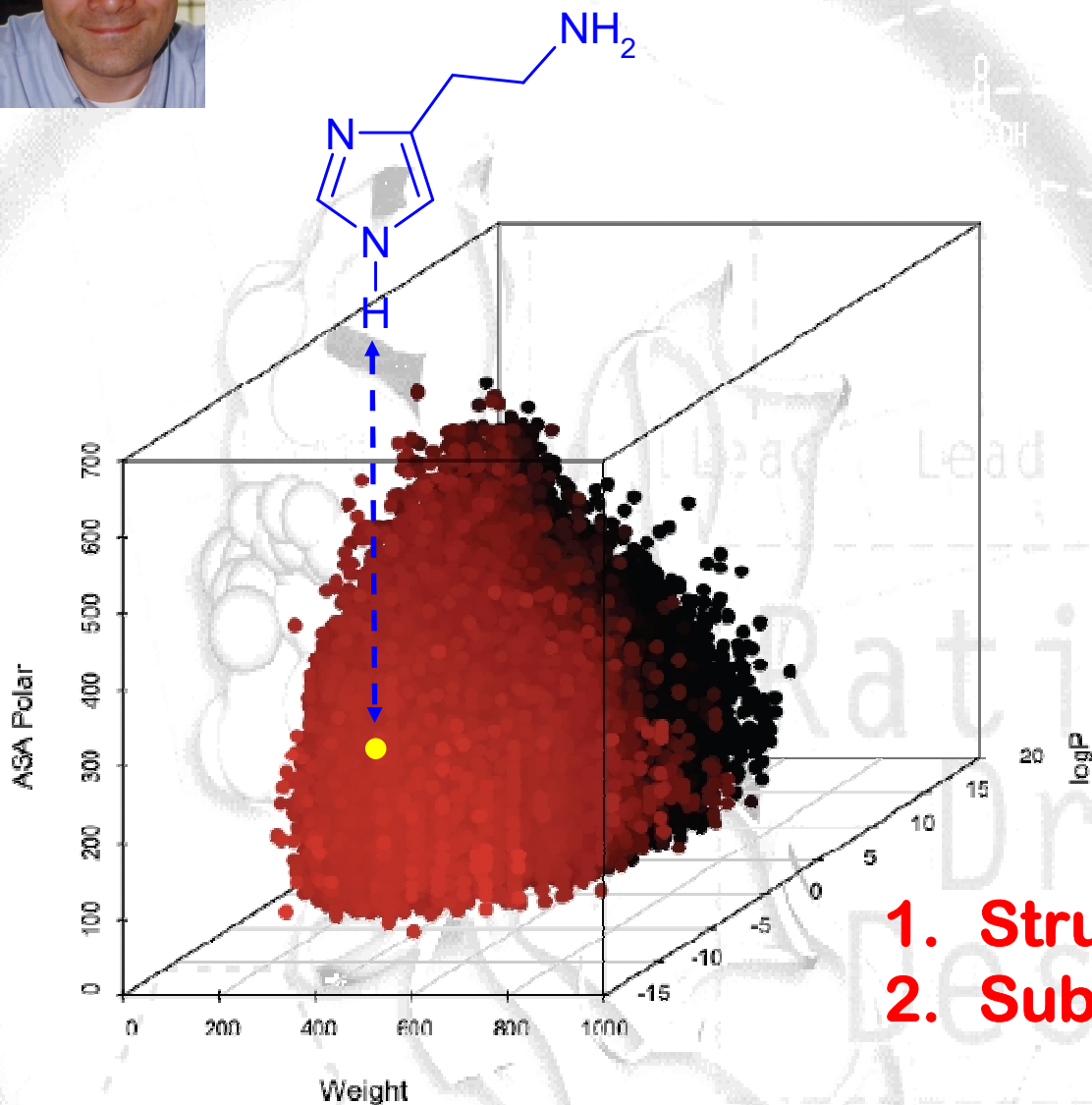
Fragments in $A \cap B$ = 2

Tanimoto similarity index

$$= \frac{2}{1 + 1 + 2} = 0.5$$



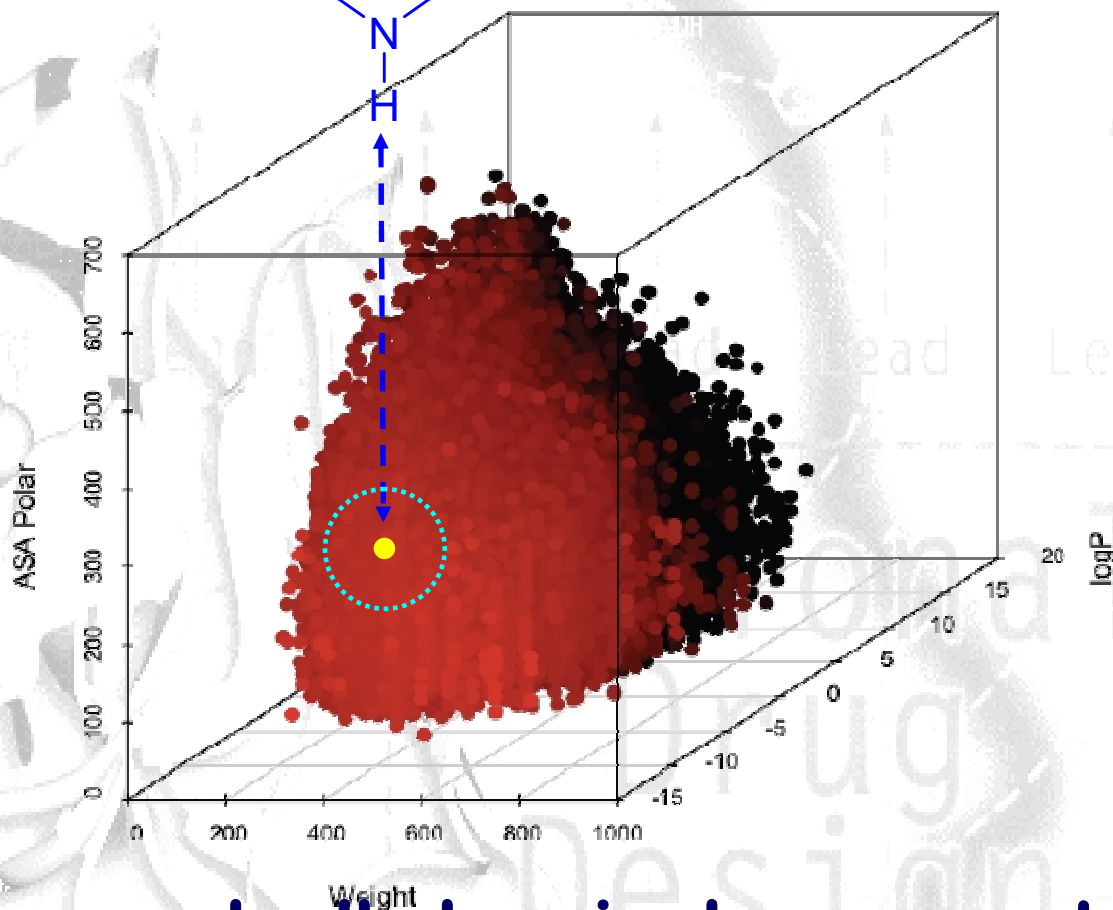
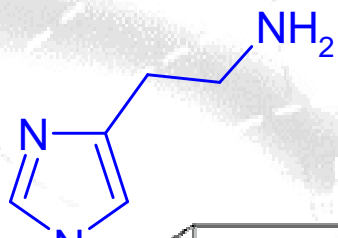
Now we can smartly explore our molecular haystack!



1. Structure similarity search;
2. Sub-structure search.



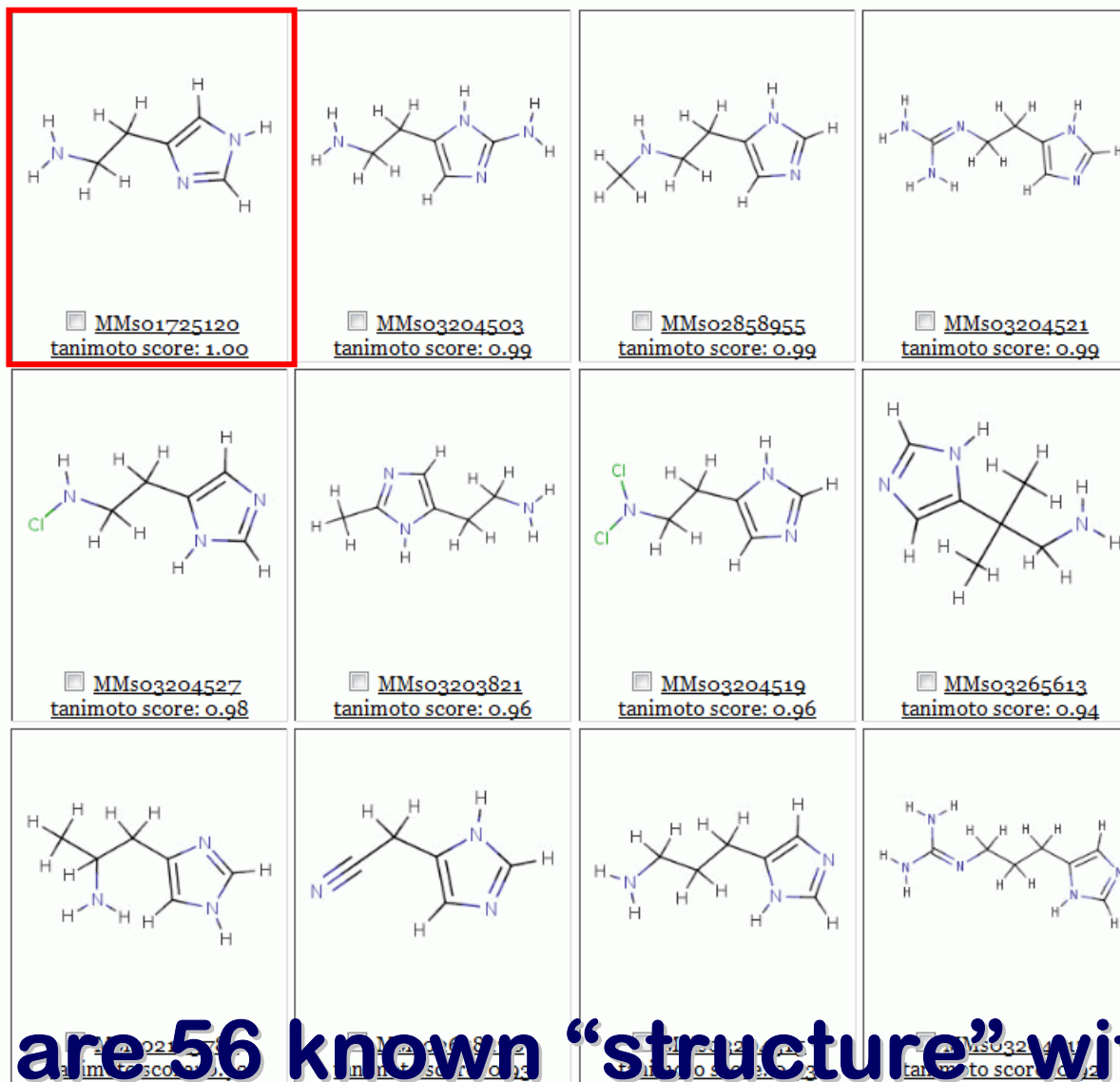
Here the first example:



Please, search all chemical representations with
Tanimoto index > 0.85?



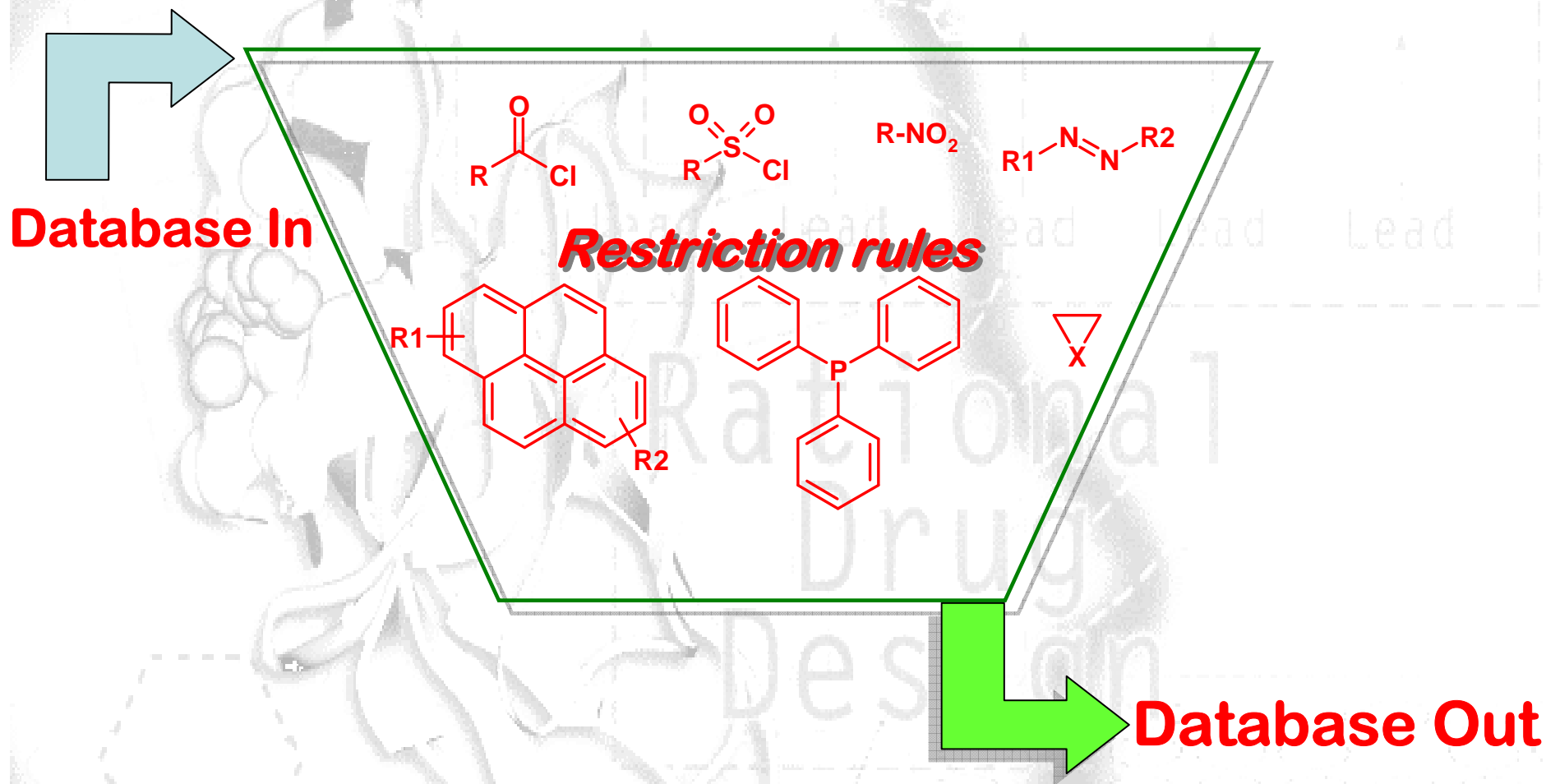
and look a possible result:



There are 56 known “structure” with a Tanimoto similarity index > 0.85!

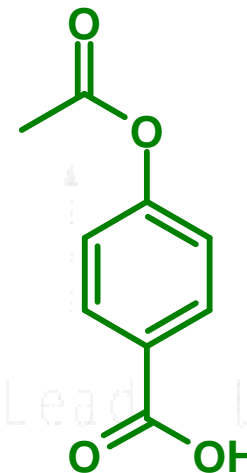
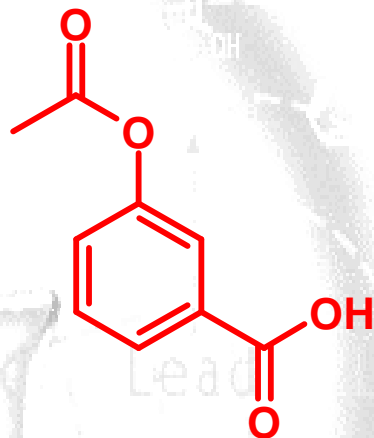
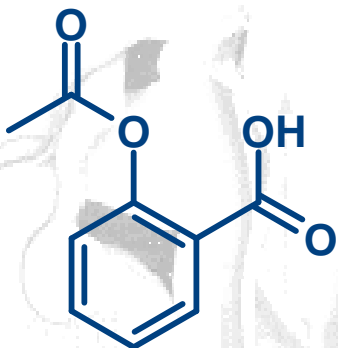


... or we can easily remove compound with undesirable fragments (chemical or biological reactivity, toxicity etc.)!





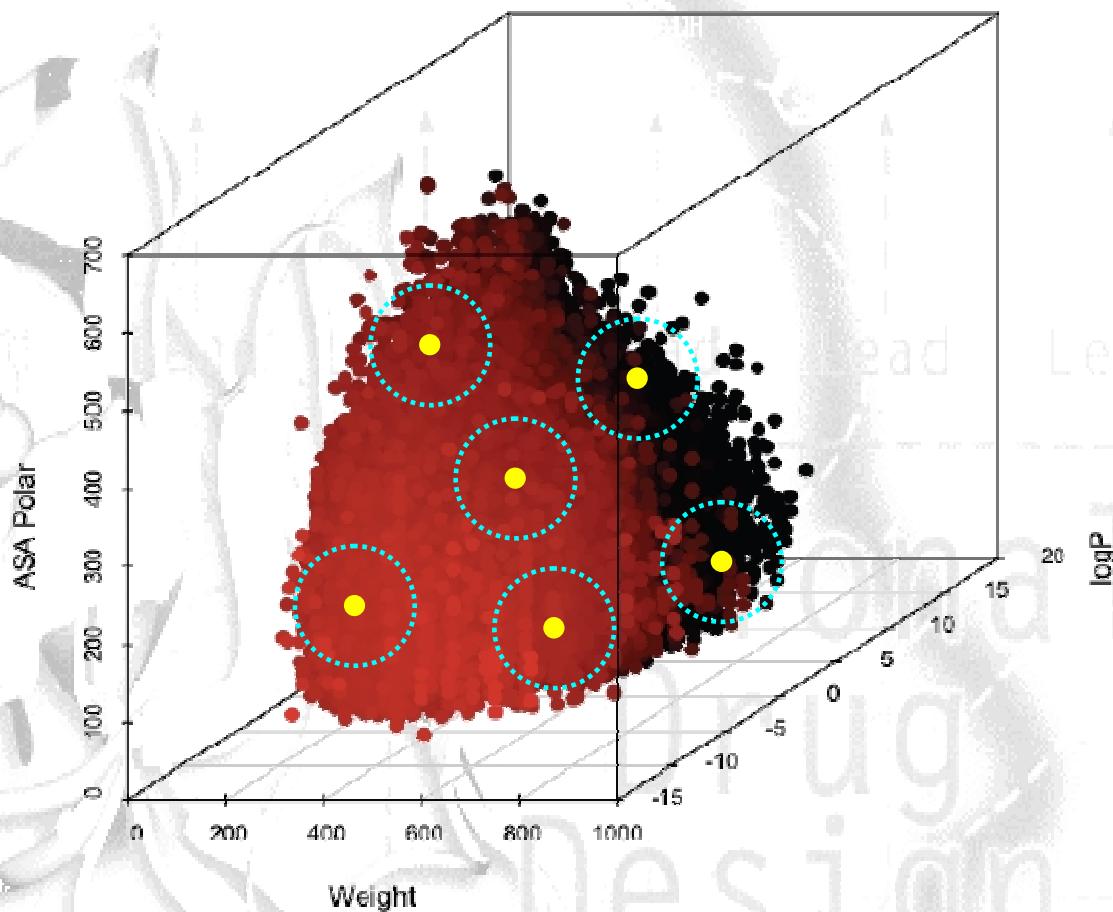
... as for any tool, there is a limitation!



			Ar-OH		-NH_2		
1	1	0	0	1	0	0	0
1	1	0	0	1	0	0	0
1	1	0	0	1	0	0	0



And don't forget:

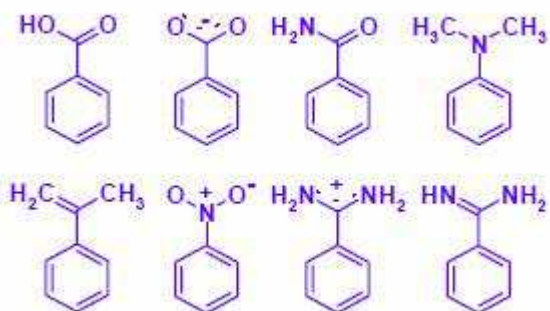


1- similarity = diversity

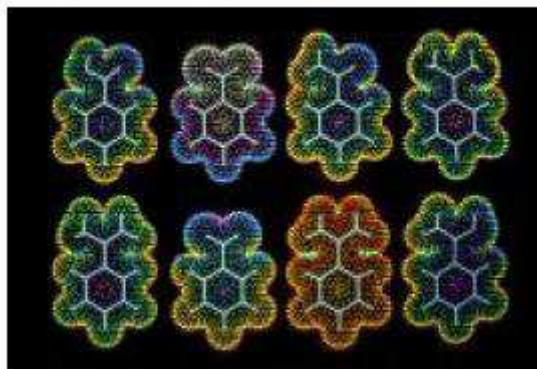


Structurally similar compounds can have very different 3D chemical properties!

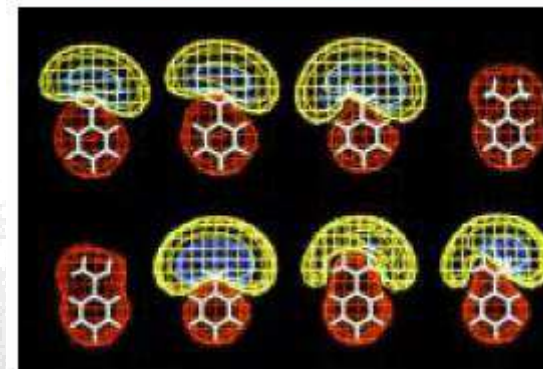
Similarity and Diversity



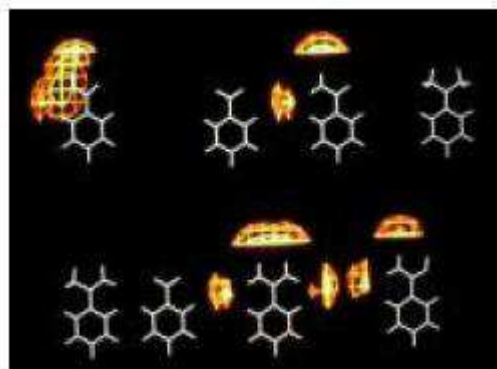
Volumes and Surface Potentials



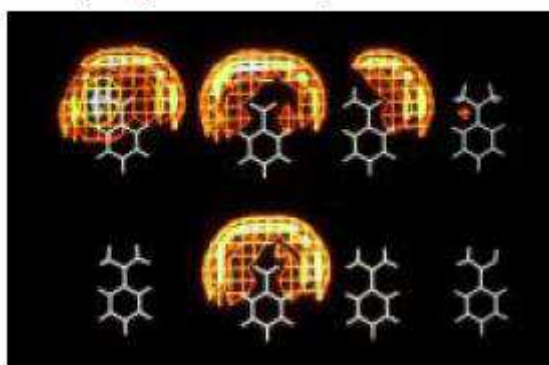
Hydrophobic and Polar Regions



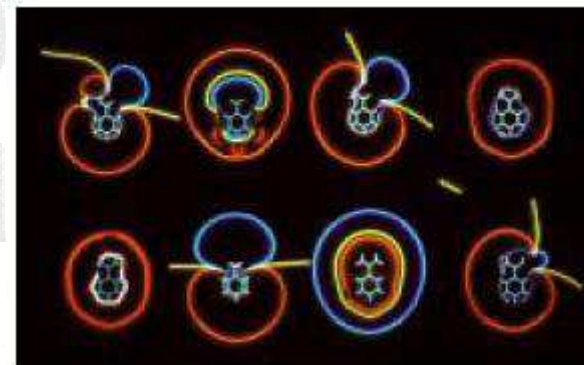
Hydrogen Bond Donor Potentials



Hydrogen Bond Acceptor Potentials



Molecular Electrostatic Potentials (MEP)



Kubinyi, H., Chemical Similarity and Biological activity



Pharmacophore definition:

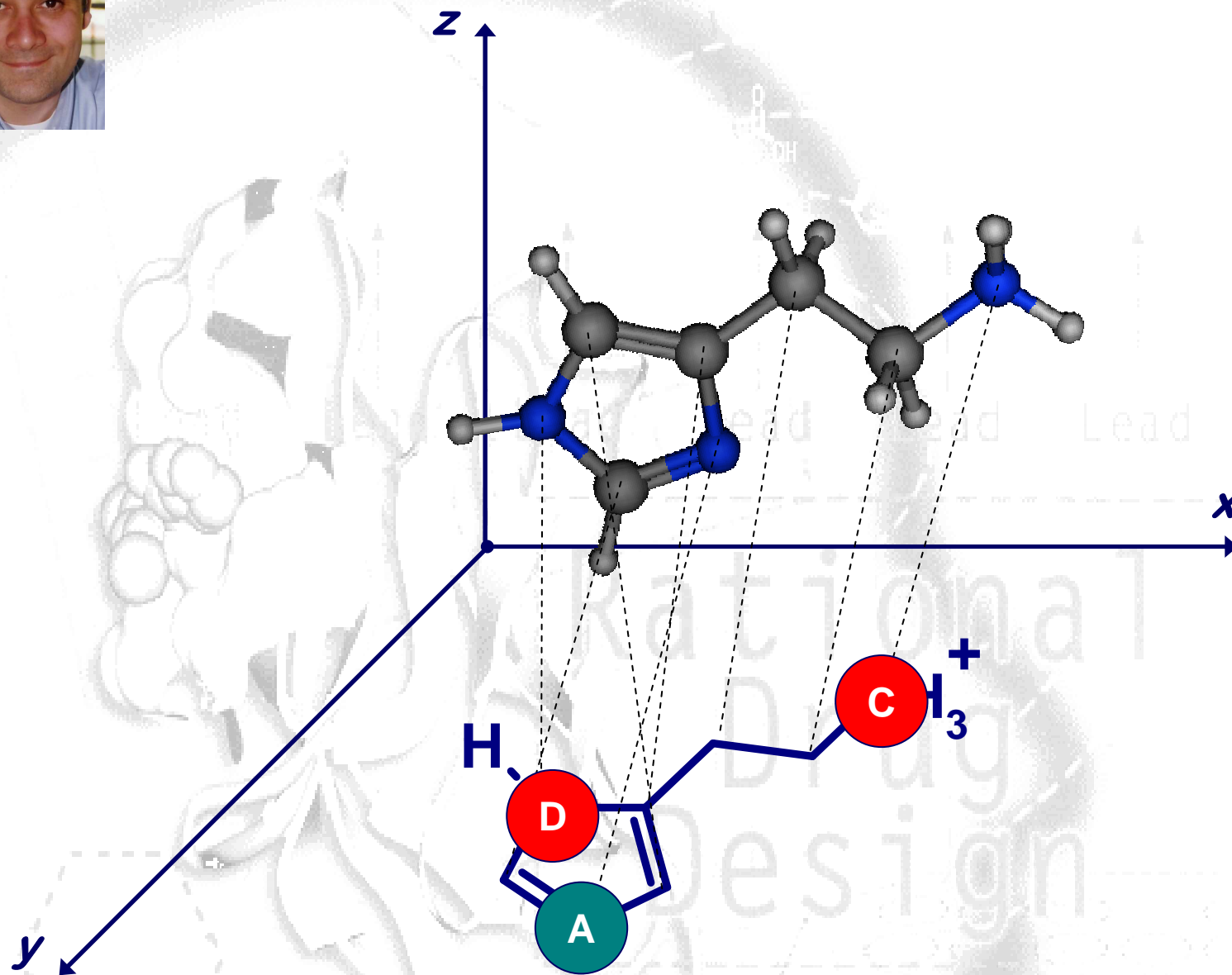
A "***pharmacophore***" is a three-dimensional substructure of a molecule that carries ("**phoros**") the essential features responsible for a drug's ("**pharmacon**") biological activity. Alternatively described as an ensemble of interactive functional groups with a defined geometry. Basically, one tries to talk the protein language by finding the "structural and chemical complementaries" (pharmacophore hypothesis) to target receptors.

**... a quick refresh: what is
the goal of every SAR study?**

**The generation of
pharmacophoric hypothesis
(models)!!!!**



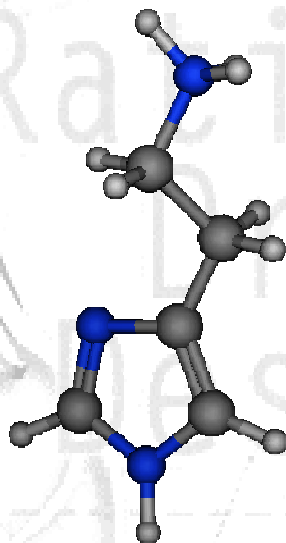
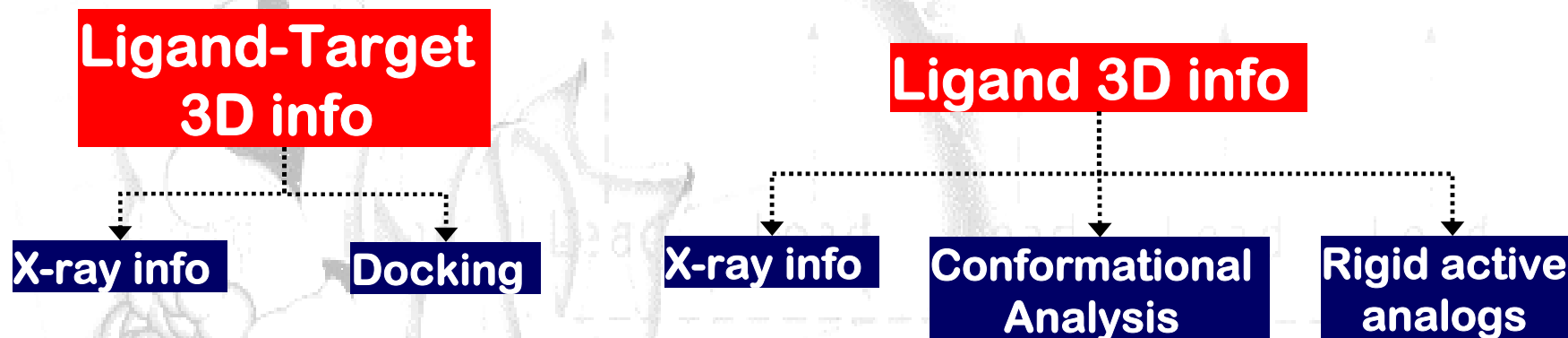
the shadow of the reality:





Pharmacophore definition:

1. *conformational selection*





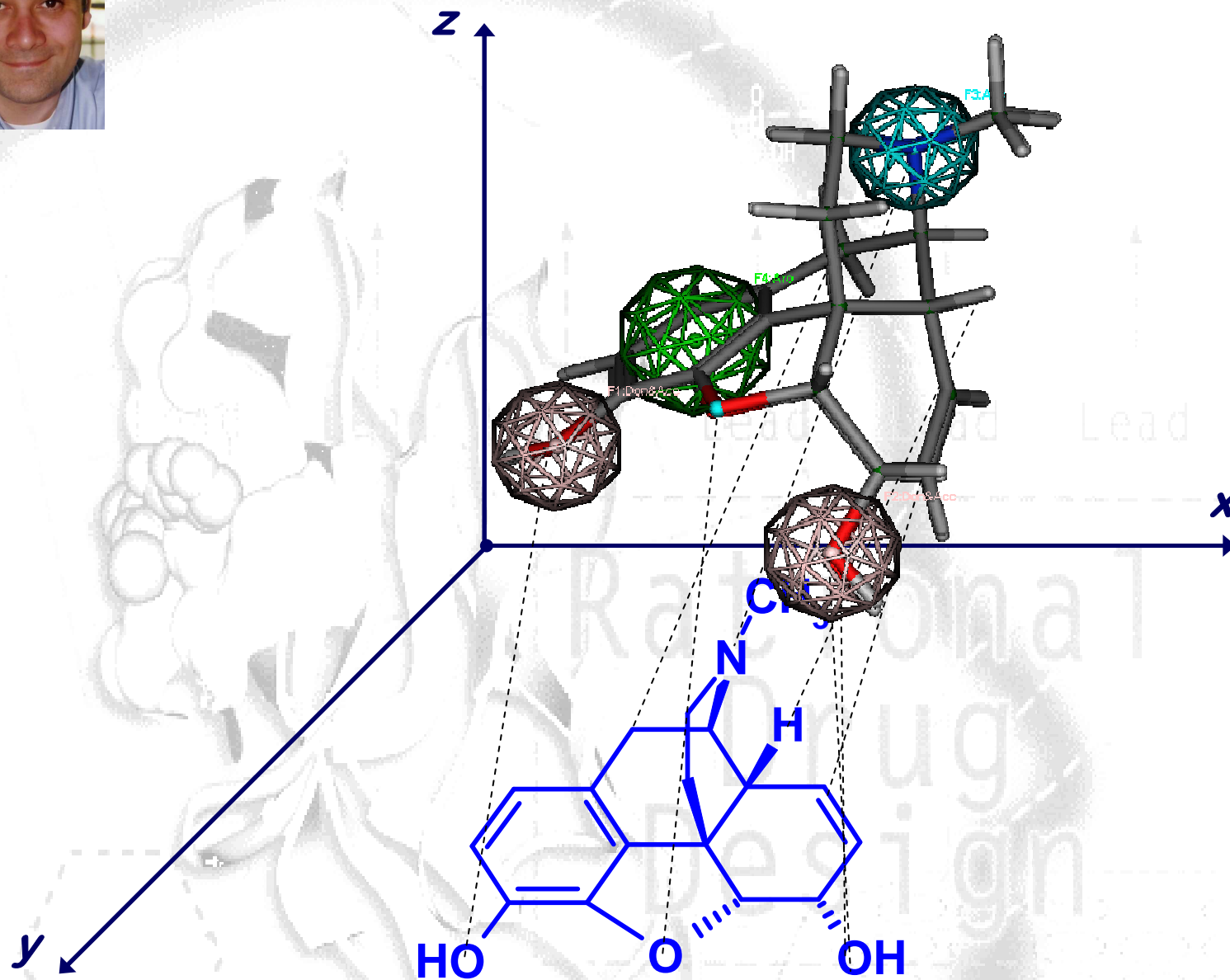
Two very interesting concepts:

Stability as a measure of the geometrical deformability of an object;

Rigidity as a measure of the reduction degree of the geometrical deformability of an object.



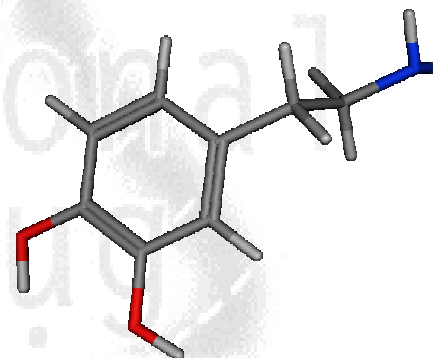
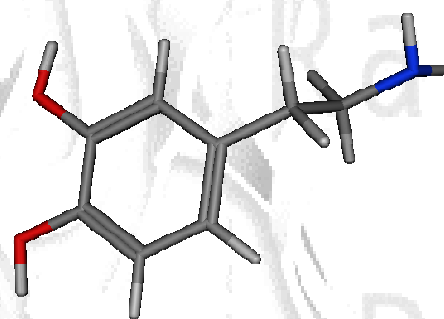
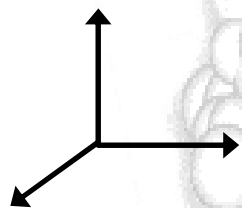
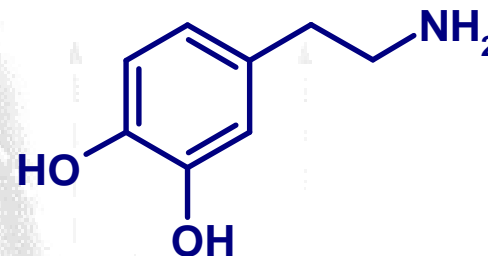
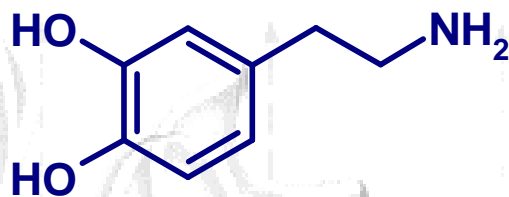
The magic behavior of cyclization:





A little memo: “Rigid Active analogs”

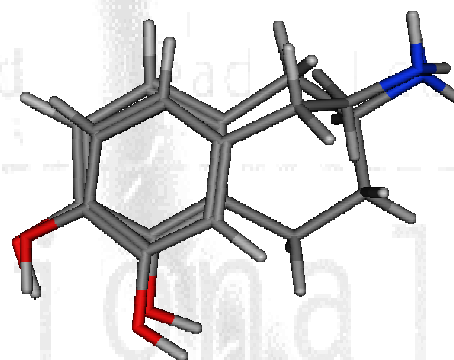
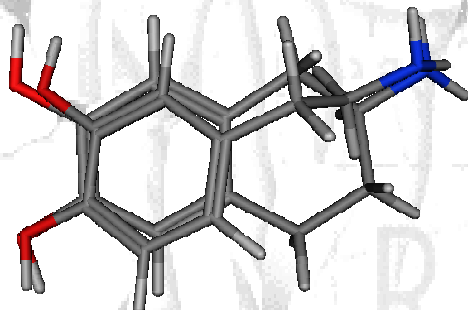
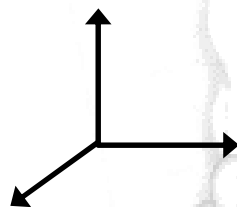
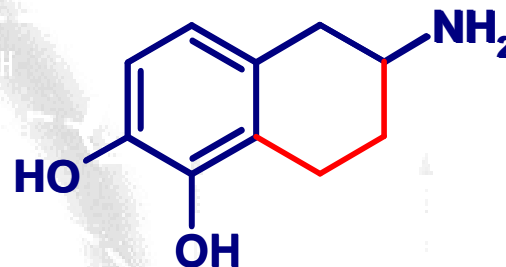
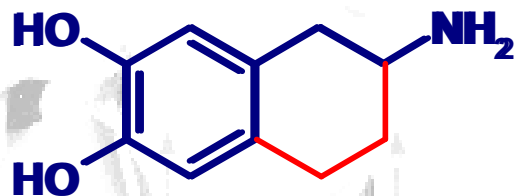
Dopamine and its rigid analogs



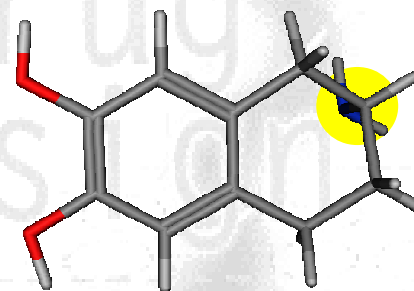
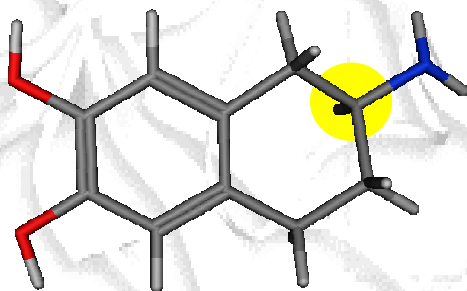


A little memo: "Rigid Active analogs"

Dopamine and its rigid analogs



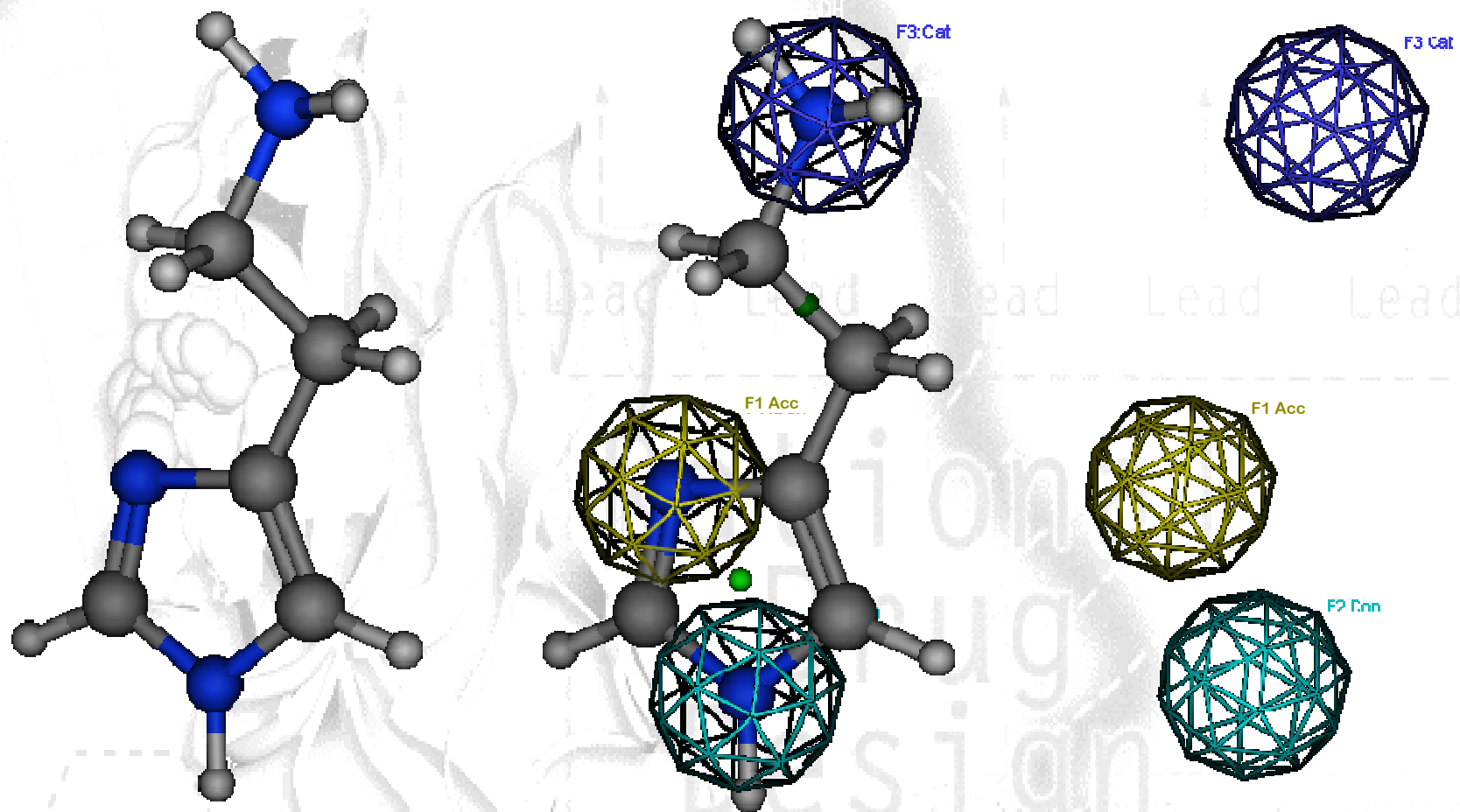
With a little 3D chemical trouble:





Pharmacophore definition:

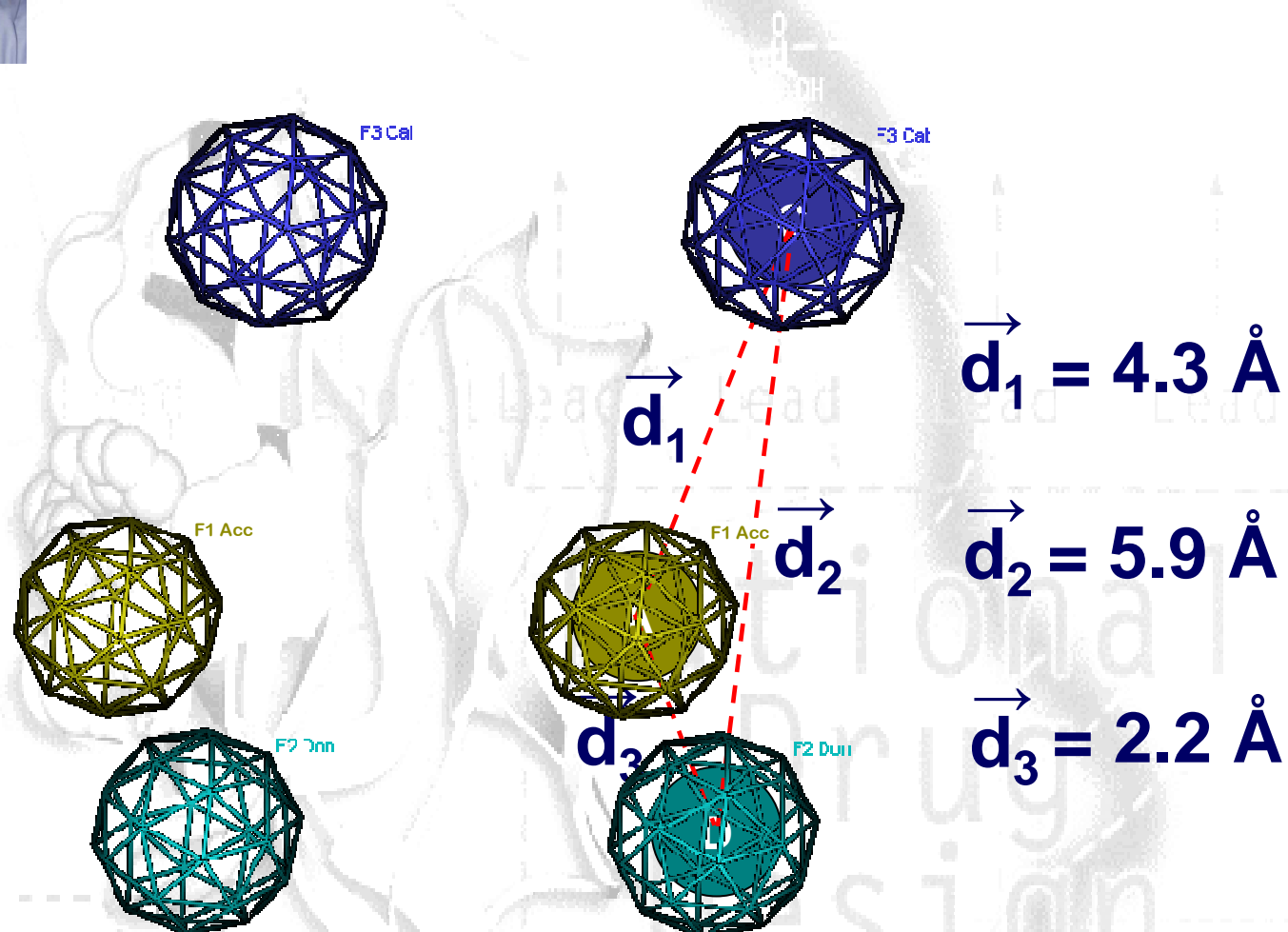
2. *Pharmacophoric keys selections*





Pharmacophore definition:

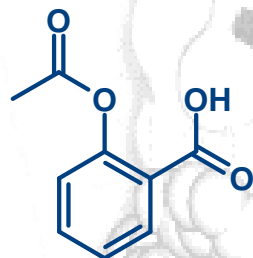
3. Interaction triangle





Pharmacophore definition:

4. From structural key to pharmacophoric key



1	1	0	0	1	0	0	0
Ar	Ac	H	D	A	A	A	H

Ar = aromatic

Ac = acid

H = hydrophobic

D = H-bonding donor

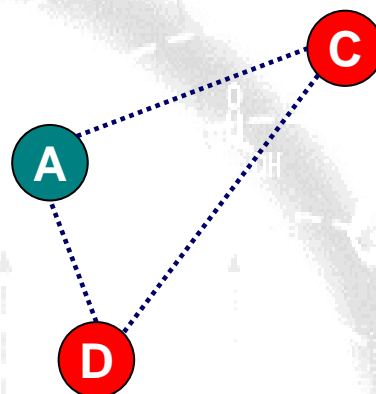
A = H-bonding acceptor

C = cation

An = anion



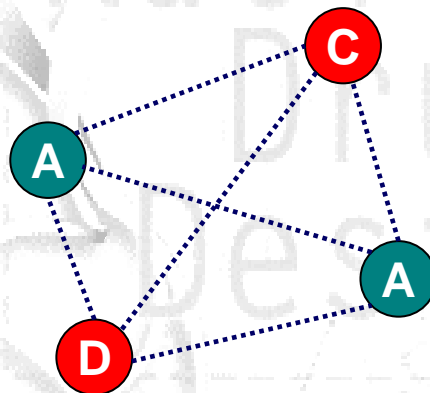
The triangle saga :



Any pharmacophoric triangle can be described as a three characters string: **ACD**

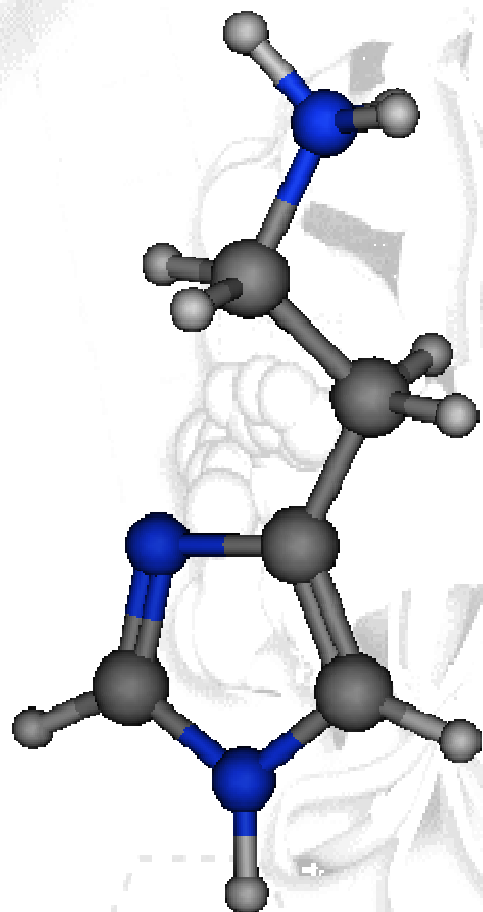
For any triangle we can calculate numerical descriptors: **perimeter, sides length.**

Any polygons can be subdivided into a sum of triangles:

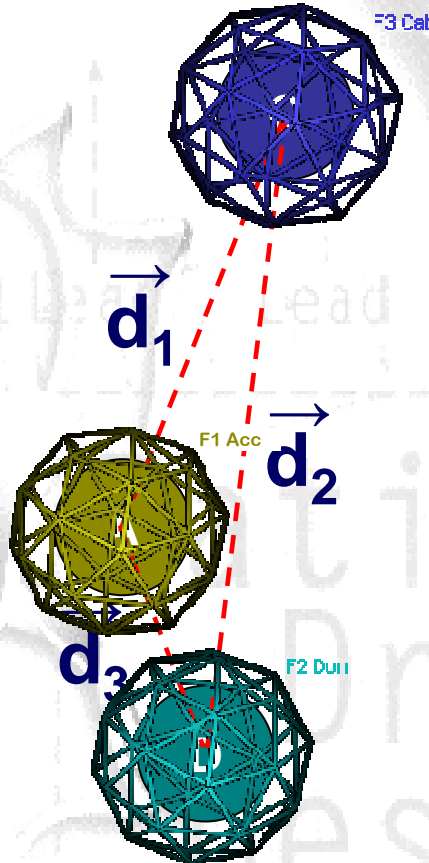




Here is another interesting 3D→1D chemical representation transformation!



3D



2D

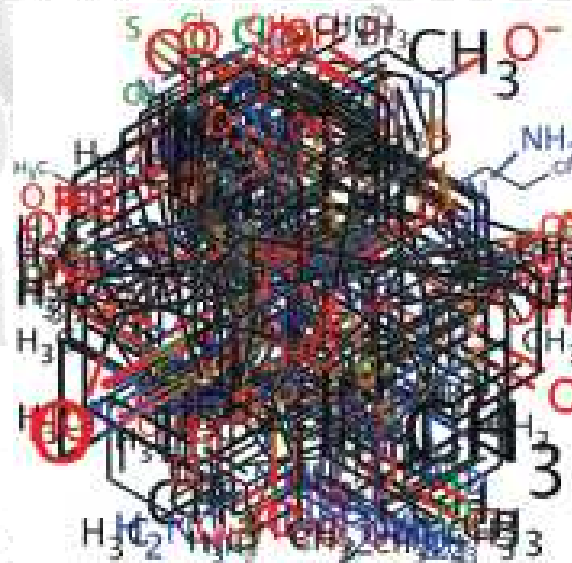
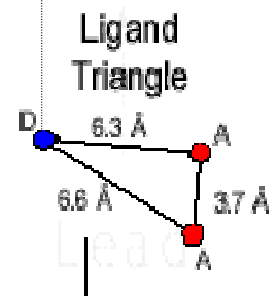
ACD 462 12

1D



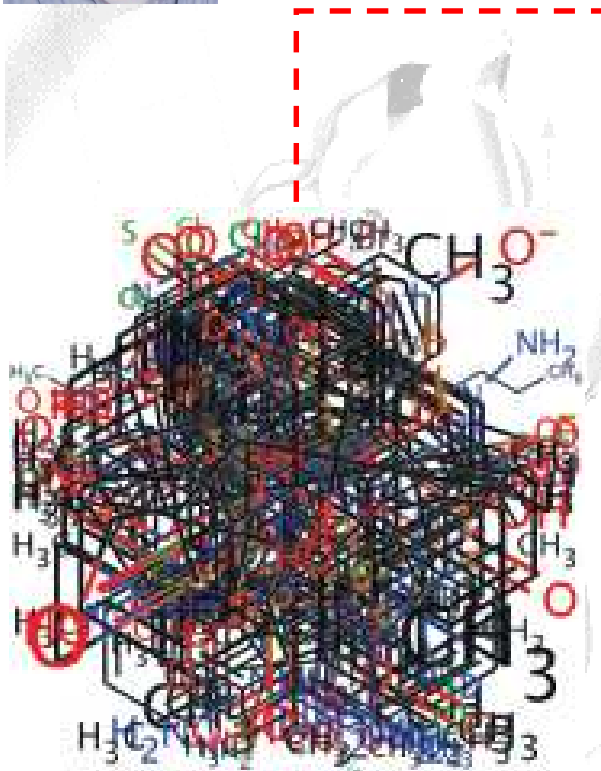
Pharmacophore definition:

5. *Geometric hashing scheme*





What we need for a good fishing?



① generation of a collection of good conformers for each chemicals;

② generation of all plausible pharmacophoric hypothesis;

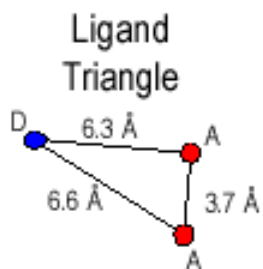
③ generation of all possible pharmacophoric triangles;

④ generation of all possible pharmacophoric strings.



Pharmacophore definition:

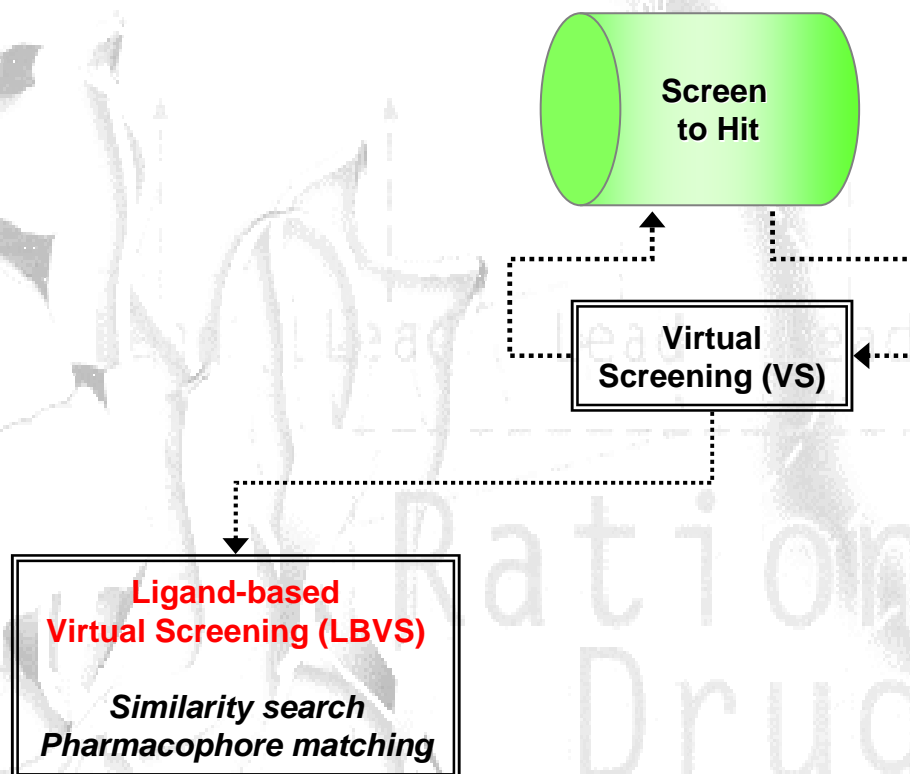
5. *Geometric hashing scheme*



D = HBond Donor
A = HBond Acceptor
H = Hydrophobic Point

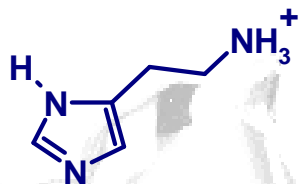


Here is a possible work-flow:

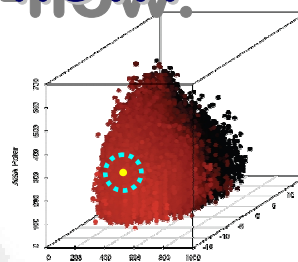




Here is a possible work-flow:

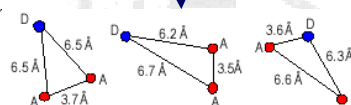
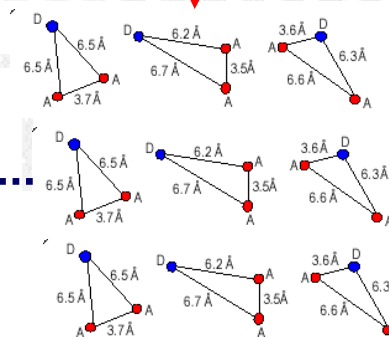
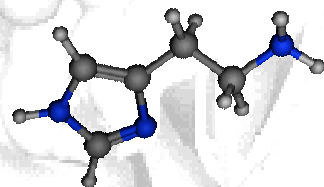


000011111001010101010



$$\frac{A \cap B}{A_{solo} + B_{solo} + A \cap B}$$

 MM00000000 training score: 0.99	 MM00000001 training score: 0.99	 MM00000010 training score: 0.99	 MM00000011 training score: 0.99
 MM00000010 training score: 0.98	 MM00000011 training score: 0.98	 MM00000010 training score: 0.96	 MM00000011 training score: 0.94
 MM00000010 training score: 0.93	 MM00000011 training score: 0.93	 MM00000010 training score: 0.93	 MM00000011 training score: 0.93



 MM00000000 training score: 1.00	 MM00000001 training score: 0.99	 MM00000010 training score: 0.99	 MM00000011 training score: 0.99
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