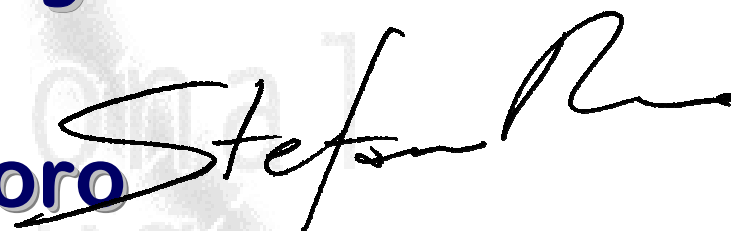


“Computational approaches in drug discovery: expectations and reality.”

Stefano Moro



Molecular Modeling Section (MMS)

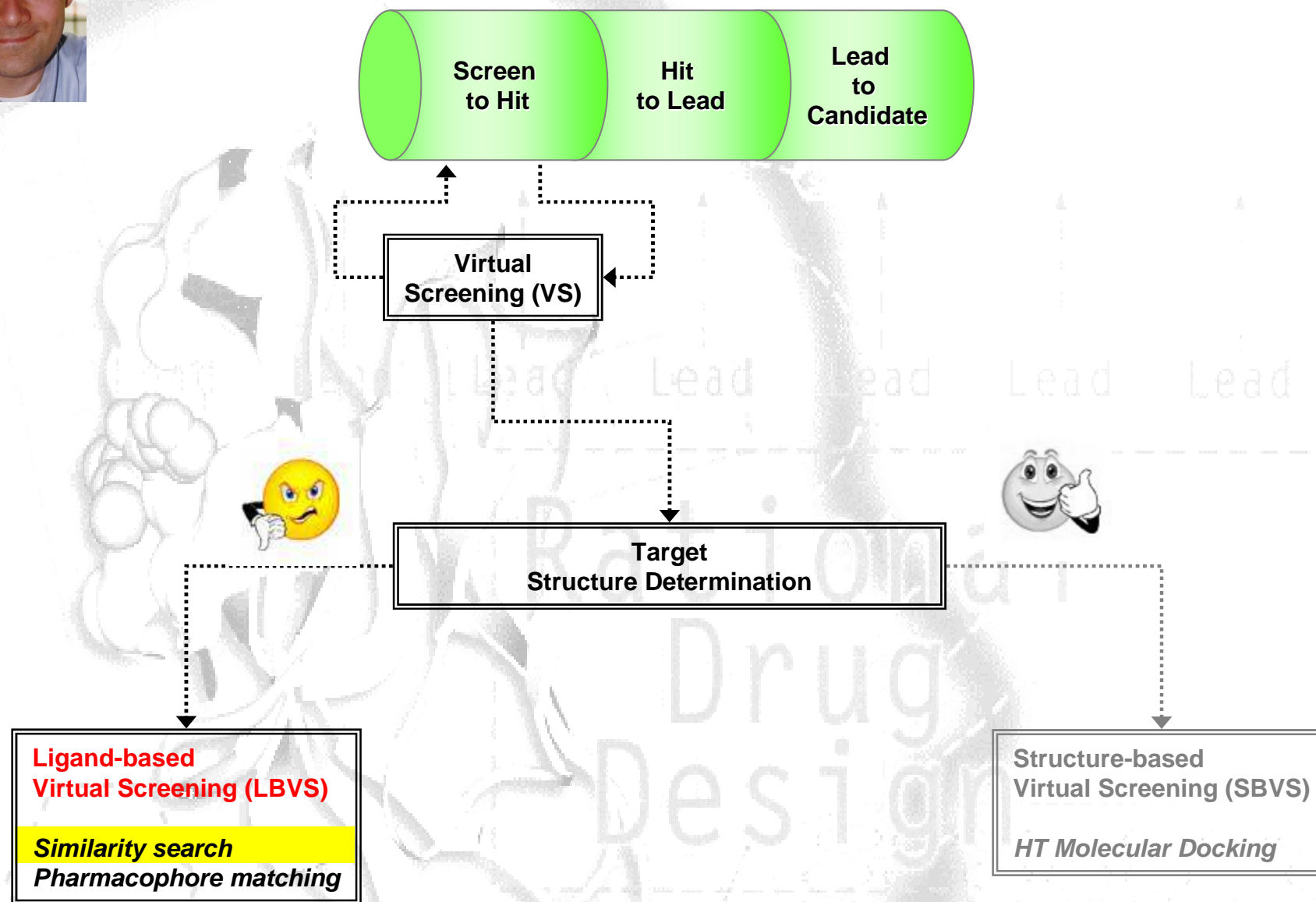
Department of Pharmaceutical and Pharmacological Sciences

University of Padova

©2012

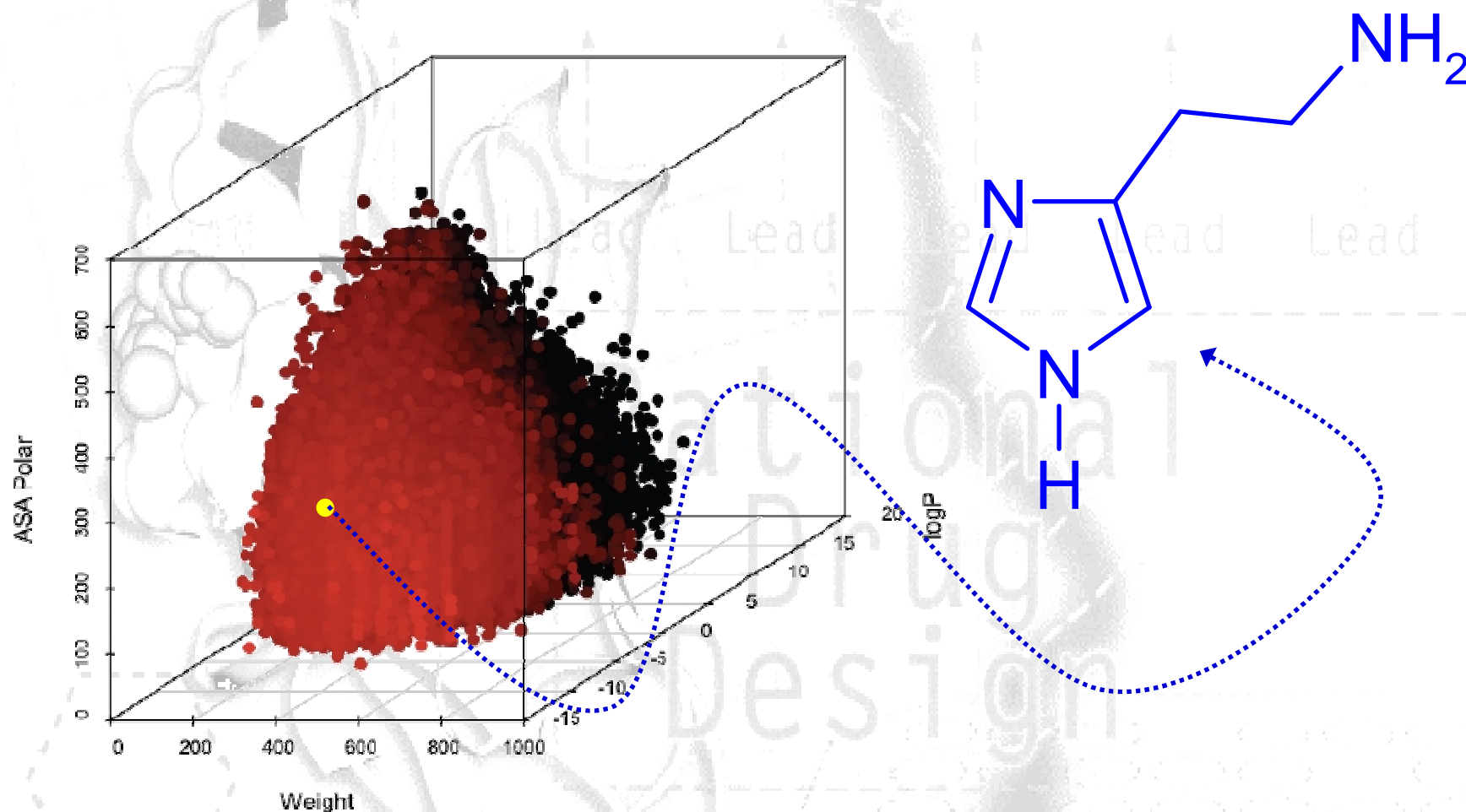


Here we are:



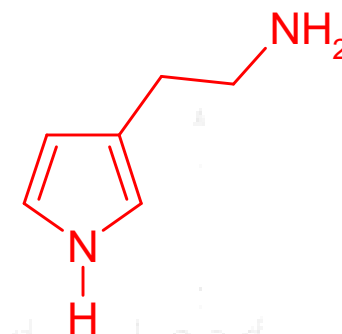
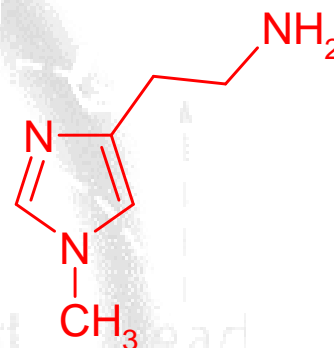
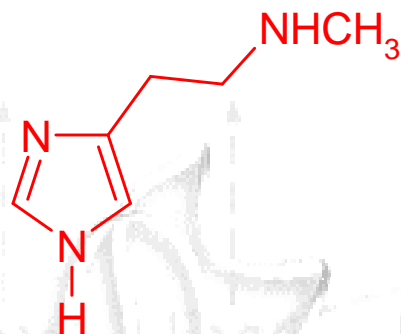
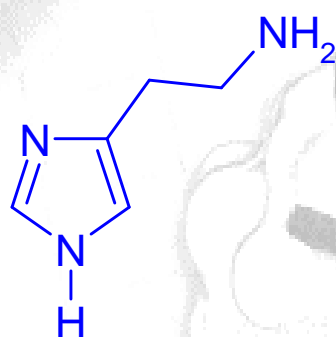


If you have only **ONE** active compound, could you suggest a possible strategy to fish out novel active analogs?

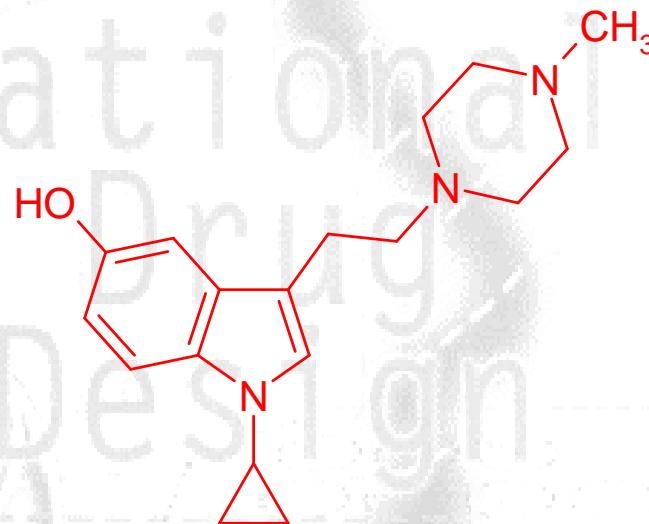




Probably using your chemical nose...

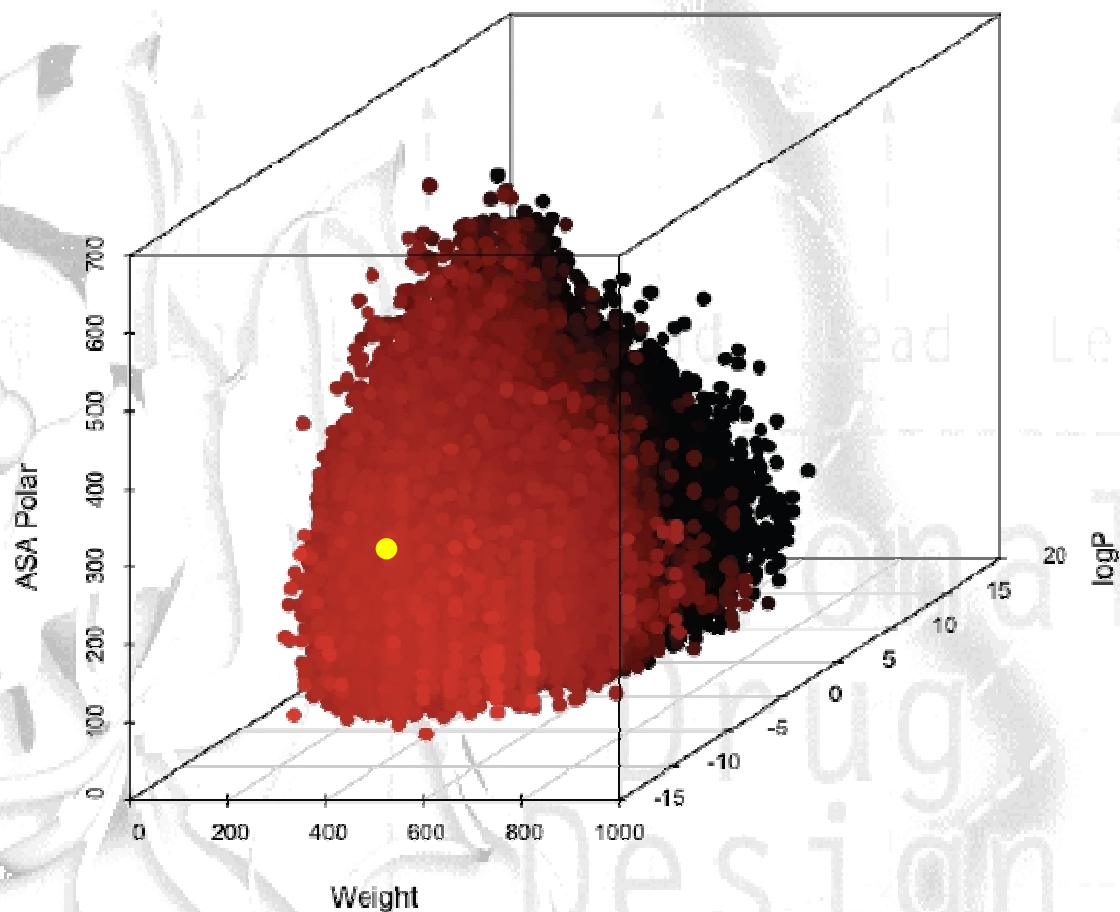


... reaching also more complex hypothesis:



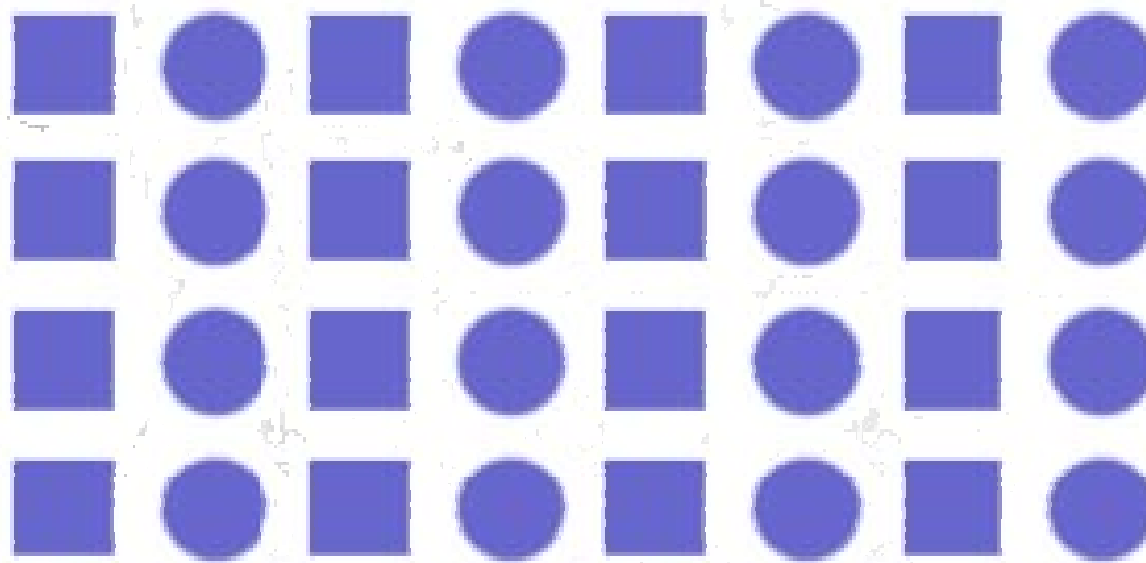


or more smartly?





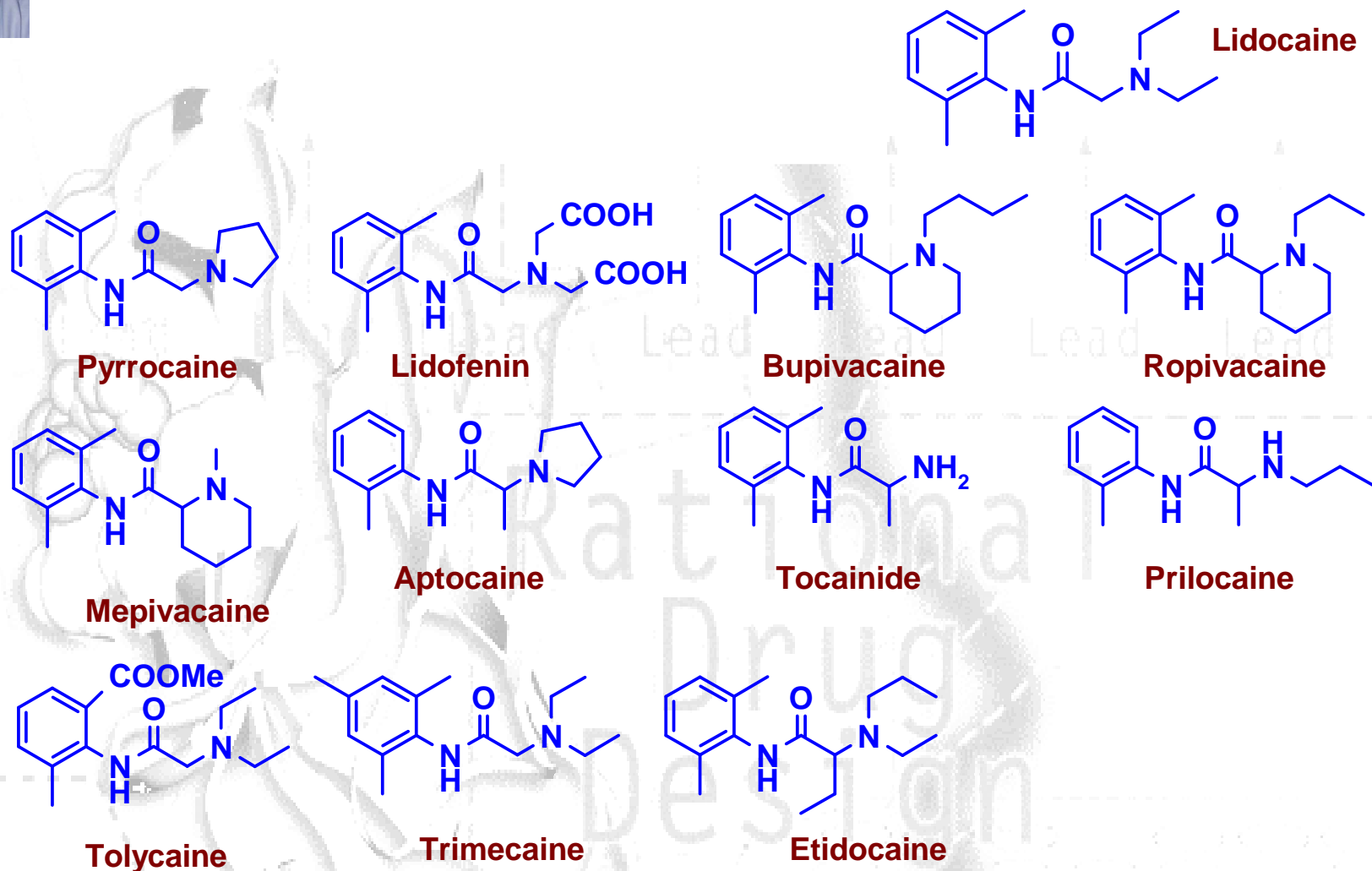
A simple exercise: could you tell me what you are looking?



Similarity law: similar objects are typically group together.

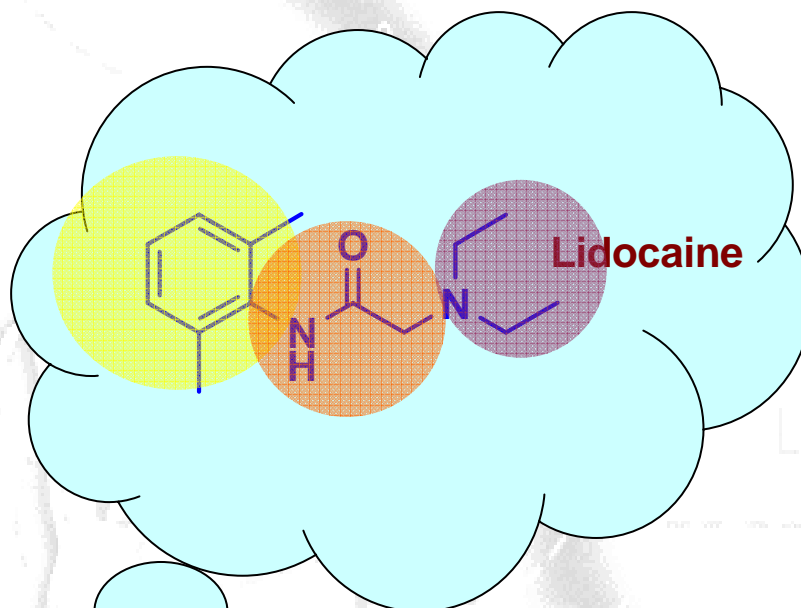


an, sometimes, this is true also in medchem:



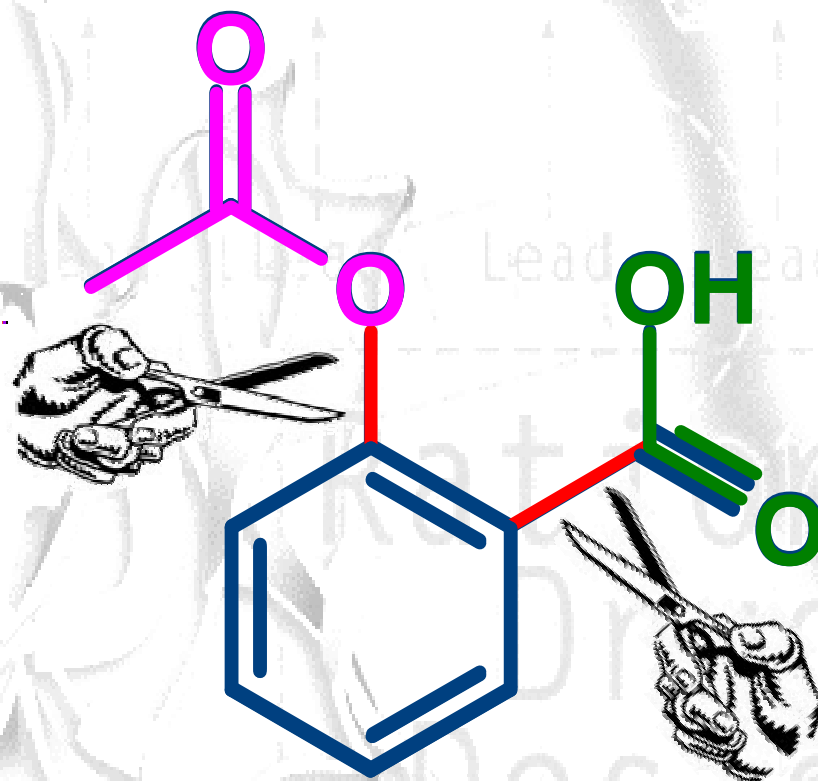


Tell me what you are thinking:



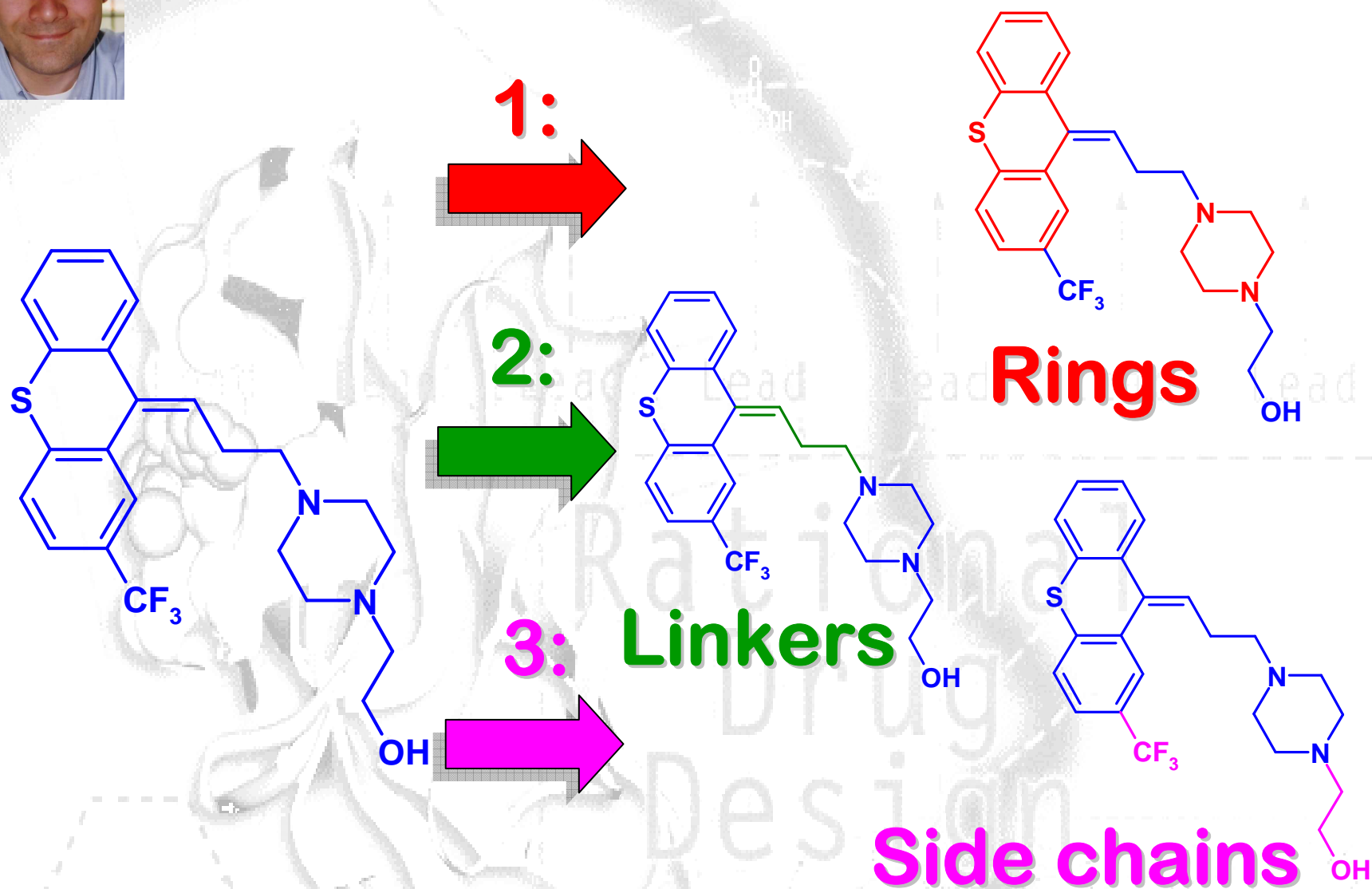


Exactly “*molecular fragmentation*”
could be a possible solution!





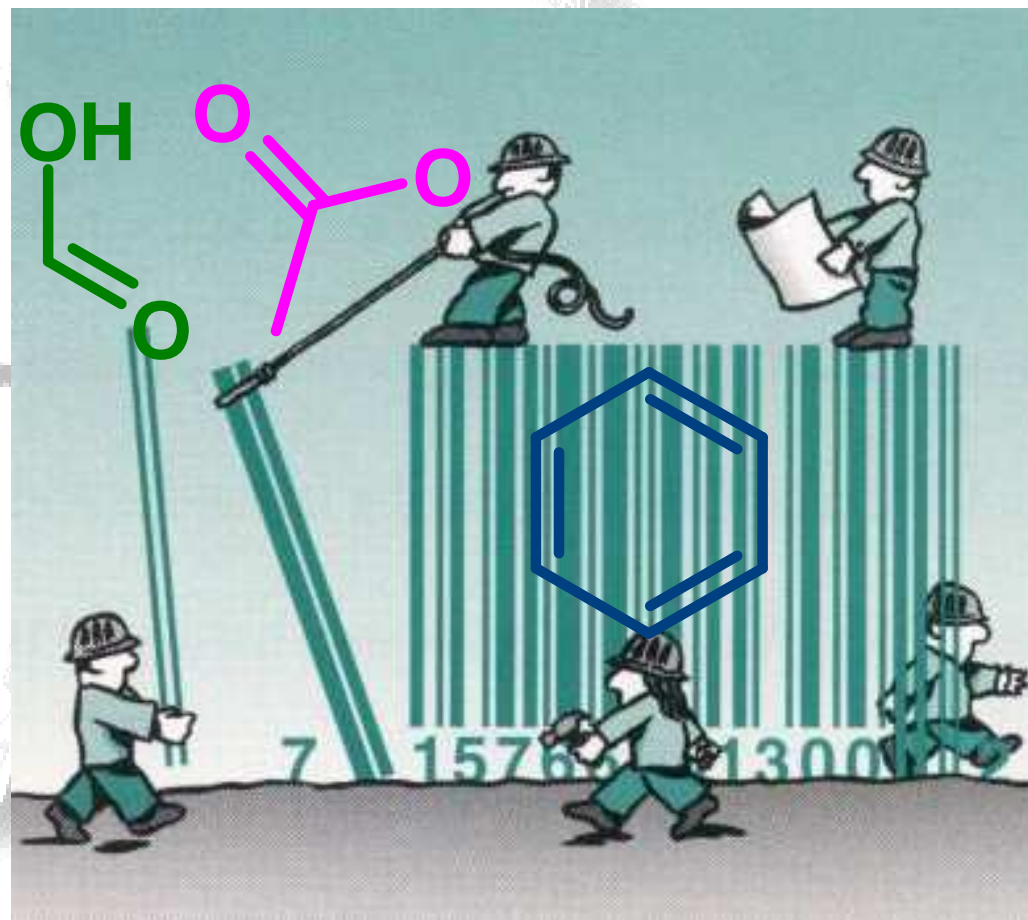
We need some rules:



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



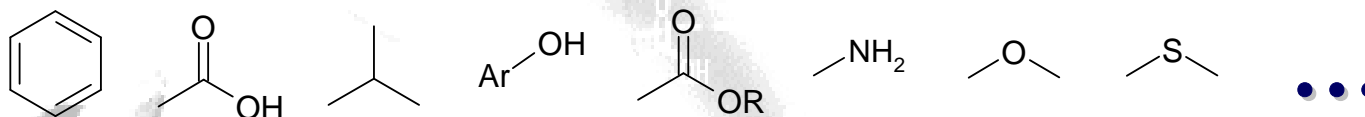
The sequence of fragments is like a molecular bar code...



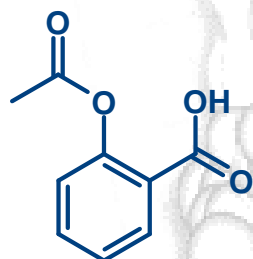
How we can build it up...

A useful concept: *structural keys*

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

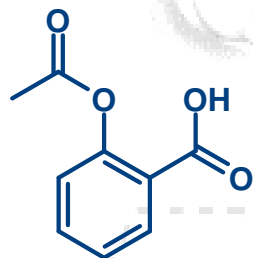


2. Assigne un *bit* for the each corrispondence in our molecule:

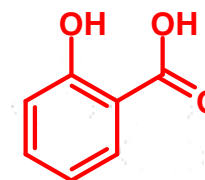


| <chem>c1ccccc1</chem> | <chem>CC(=O)O</chem> | <chem>CC(C)C</chem> | <chem>Ar-OH</chem> | <chem>CC(=O)OR</chem> | <chem>CCN</chem> | <chem>CCOC</chem> | <chem>CCSC</chem> |
|-----------------------|----------------------|---------------------|--------------------|-----------------------|------------------|-------------------|-------------------|
| 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>CCOC</chem> | <chem>CCSC</chem> |
|-----------------------|----------------------|---------------------|--------------------|-----------------------|------------------|-------------------|-------------------|
| 1 | 1 | 0 | 0 | 1 | 0 | 0 | 0 |
| 1 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |





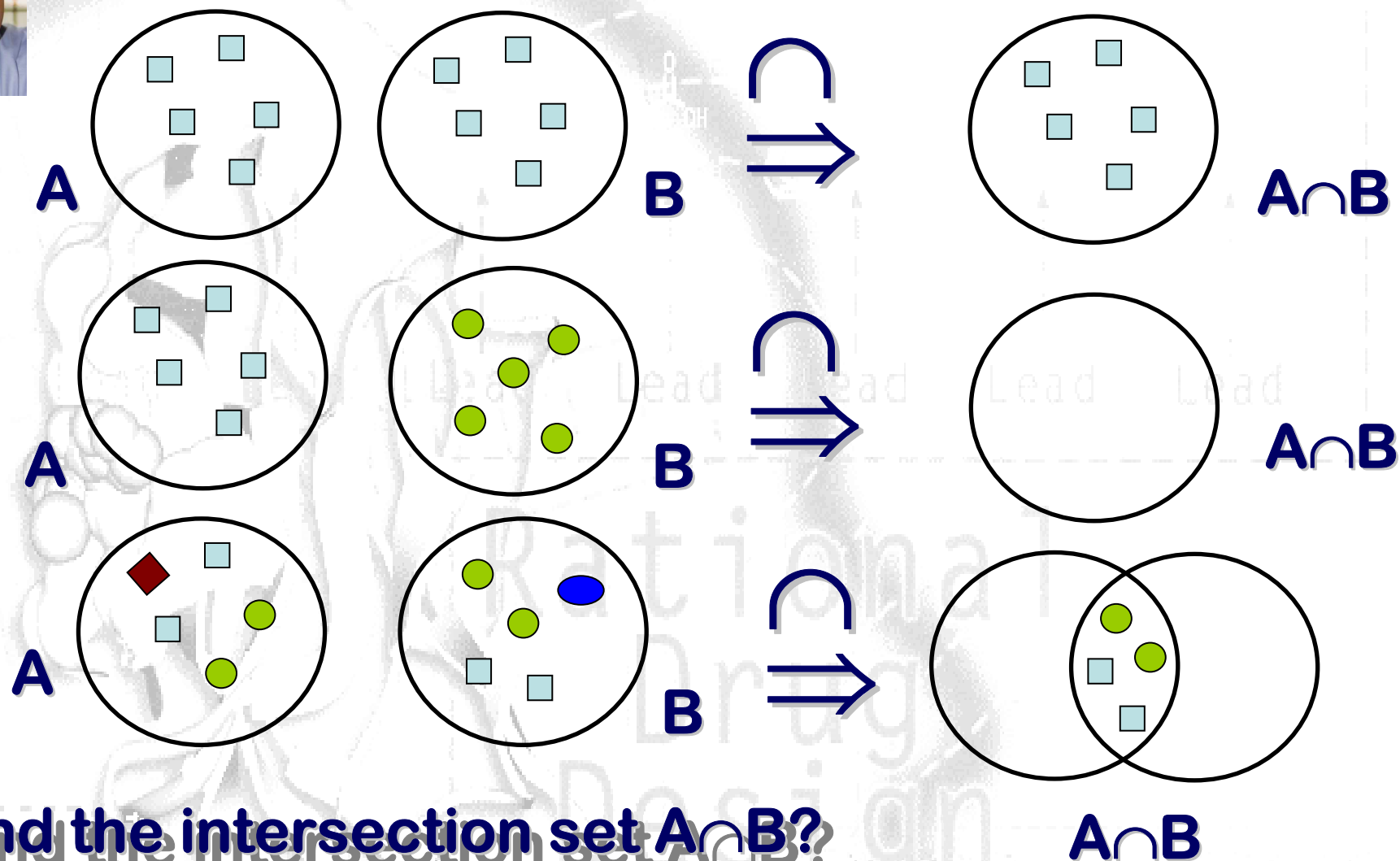
Any standard?

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.



Do you remember the Eulero-Venn diagrams?



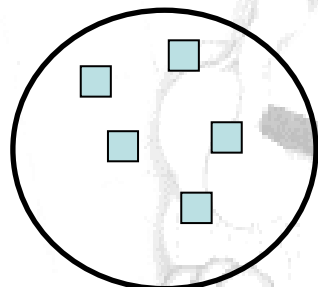
... and the intersection set $A \cap B$?



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

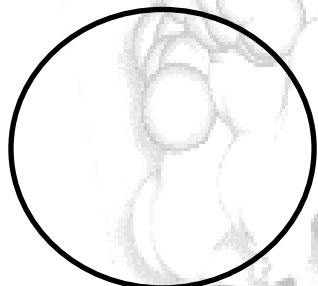
$$\text{Jaccard o Tanimoto Index} = \frac{A \cap B}{A_{\text{solo}} + B_{\text{solo}} + A \cap B}$$

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



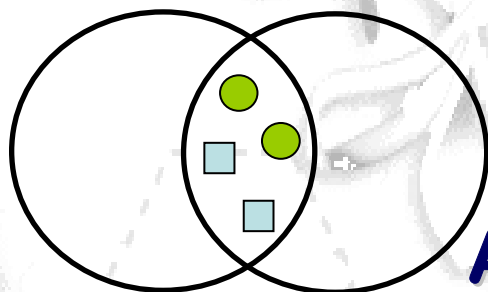
$A \cap B$

= 1



$A \cap B$

= 0

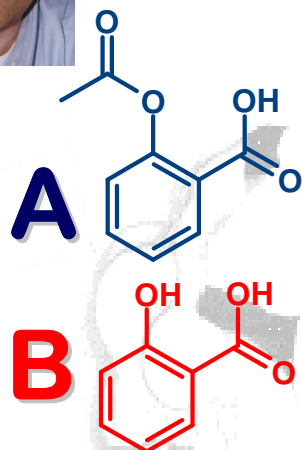


$A \cap B$

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



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

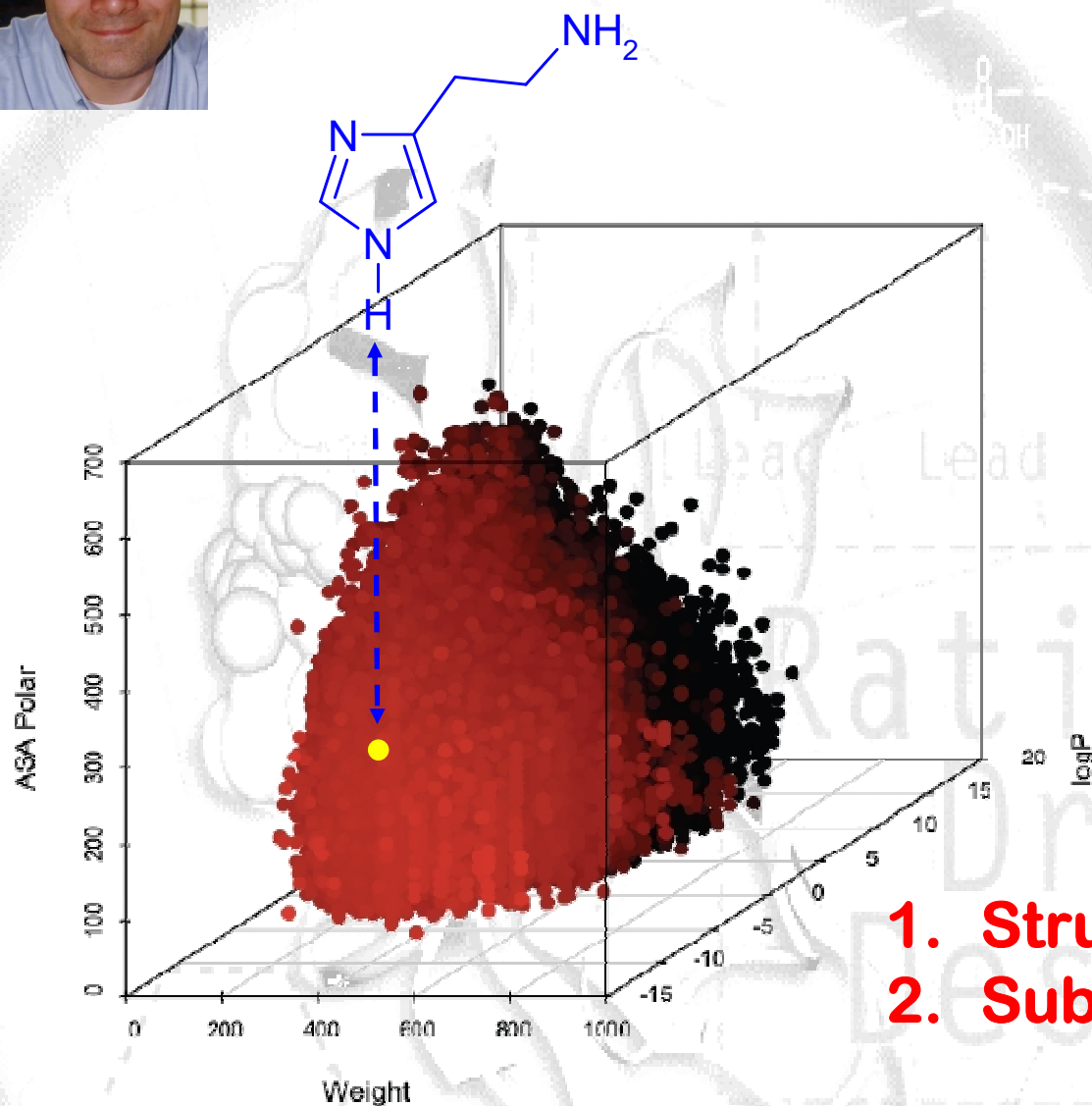
Fragments in $A \cap B$ = 2

Tanimoto similarity index

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



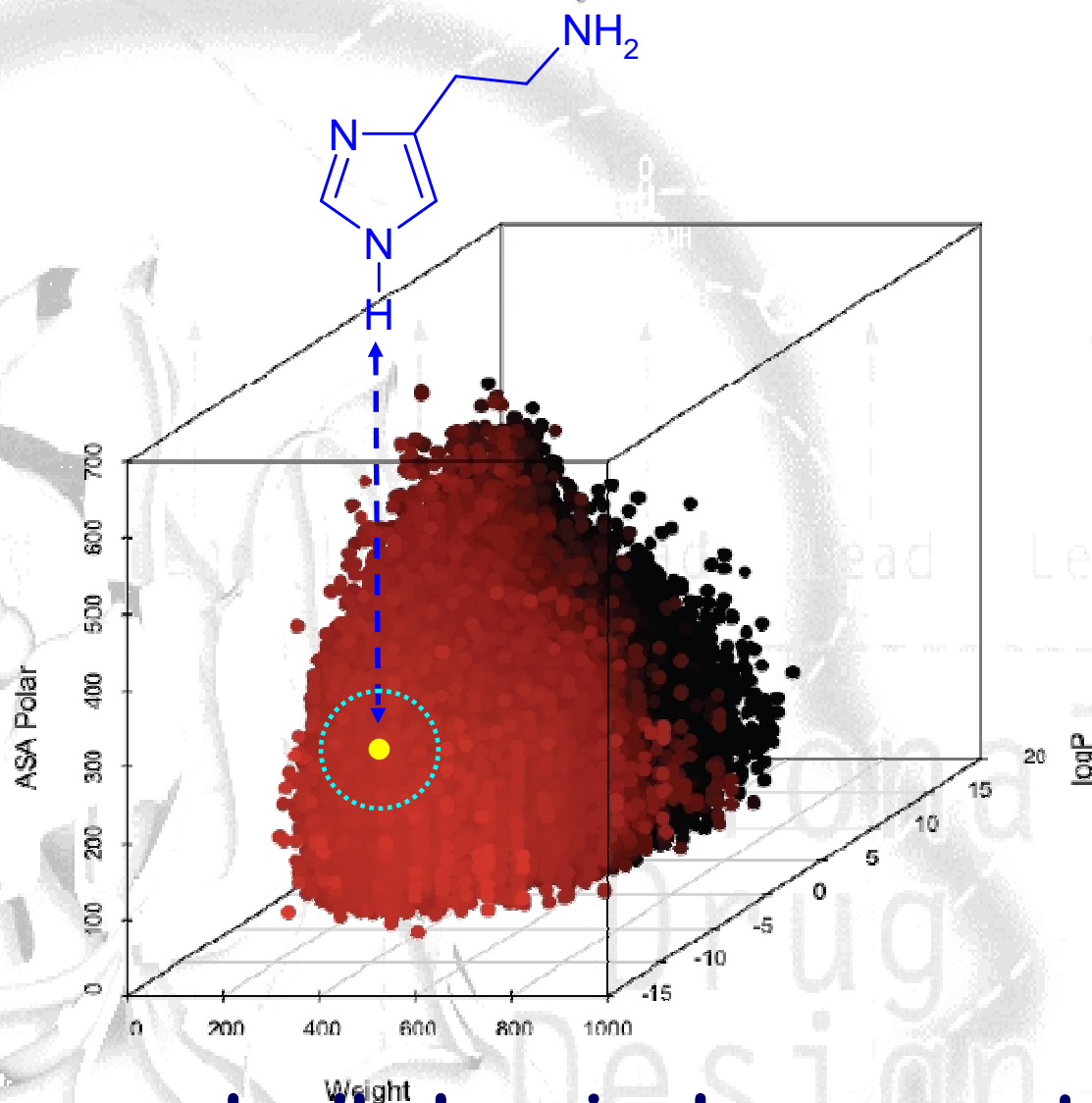
Now we can smartly explore our molecular haystack!



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



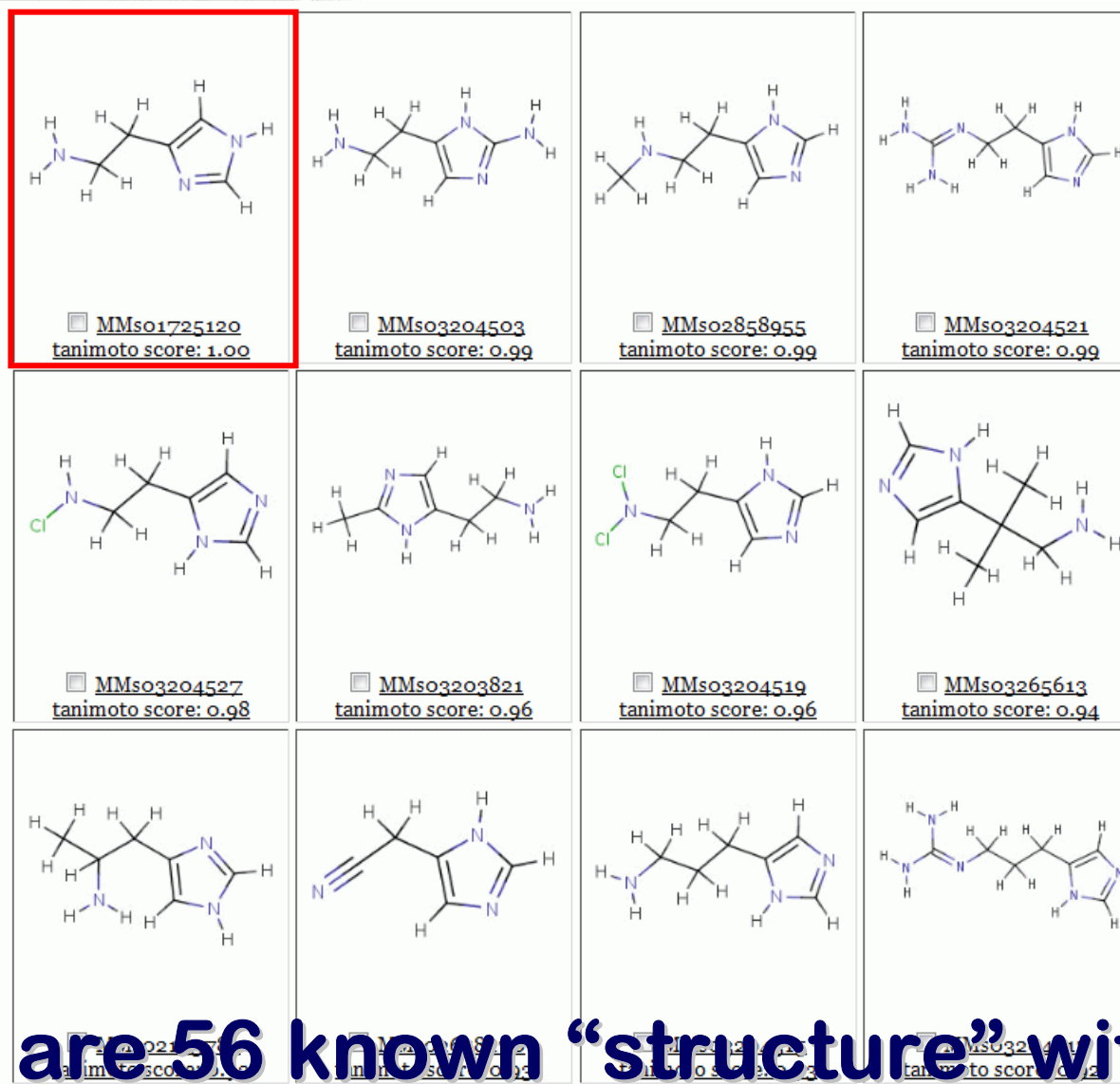
Here the first example:



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



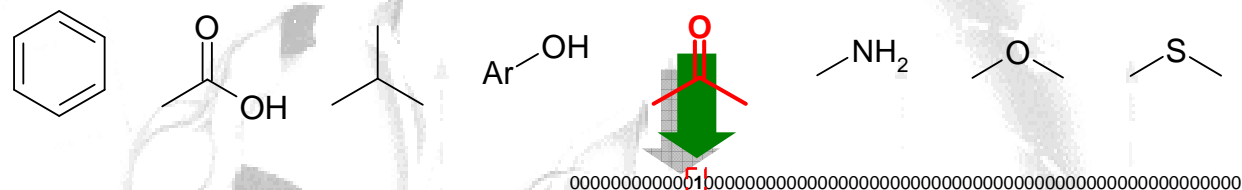
and look a possible result:



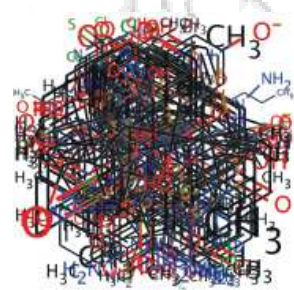
There are 56 known “structure” with a
Tanimoto similarity index > 0.85!



... but we can also run a sub-structure search!

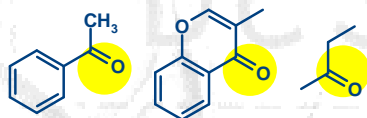


Query



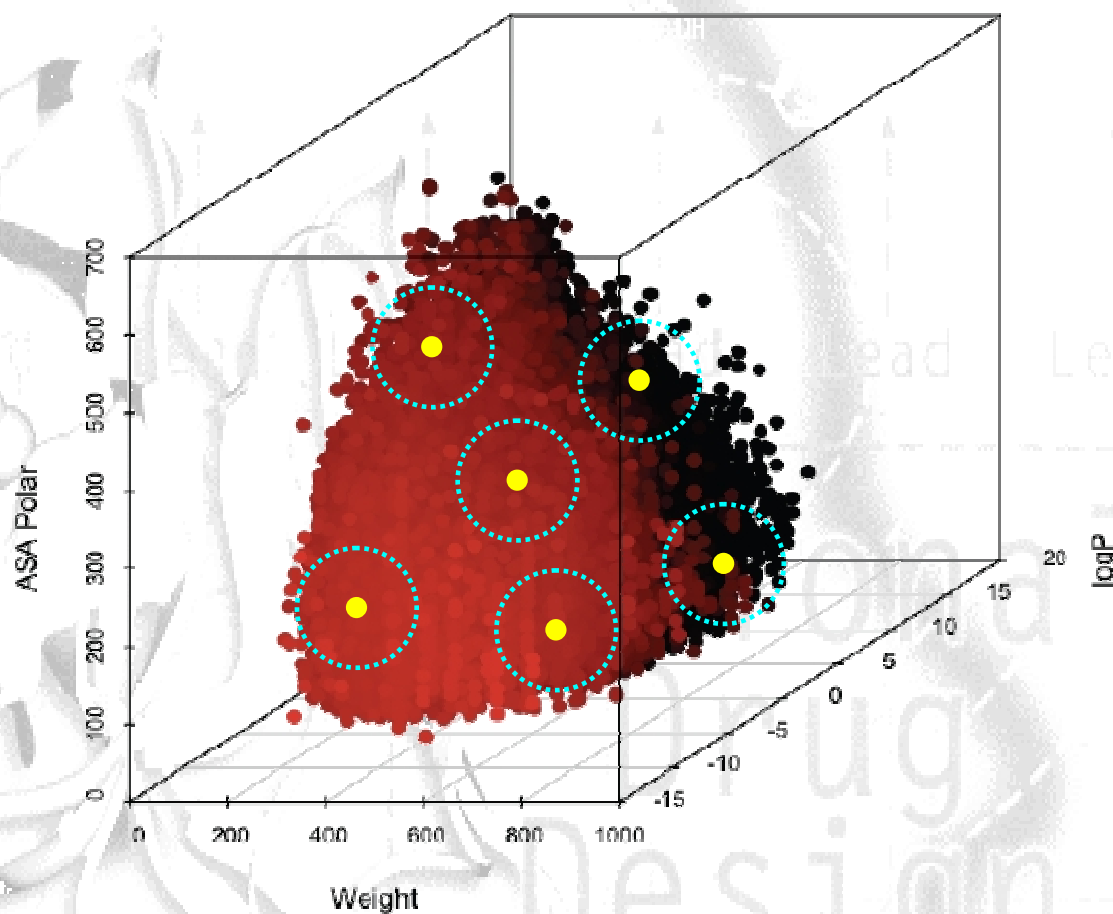
00000001000011010000001010100000000011000010000100001000
010001011001001001011001110011110100000110000000110001000
010001010001110101000011000010100001001100001010000000100100000
000110111001110111110100000100010000110110110000000100110100000
010001010011010001000000001000000001001000000100100001000101000
0100011100011101000100001011101100110110010010001101001100001000
01011101001101010101111100001000001111100010000100001000101000
0100010100111101010000100010000000010010000010100100001000101000
000100010001010001010010000000000001010000010000100000100000000
01000101000100110000000000000000000101000001000000000000000000
0100010100010100000000000000000000010100001001000000000100000000
0100010100010100000000000000000000010100001100100001100101000
01000101000101000000000000000000000100000000000000000000000000
00000001000000000000000000000000000101010000000100000100100000
01000101000101000000000000000000000100000000000000000000000000
00010001000011000010010100000010100101011000100001000010000101000
0100011100010100010000100001001110010010000010001100000000101000
0101010100010100010100100000000000010010000010010100100100010000

Database





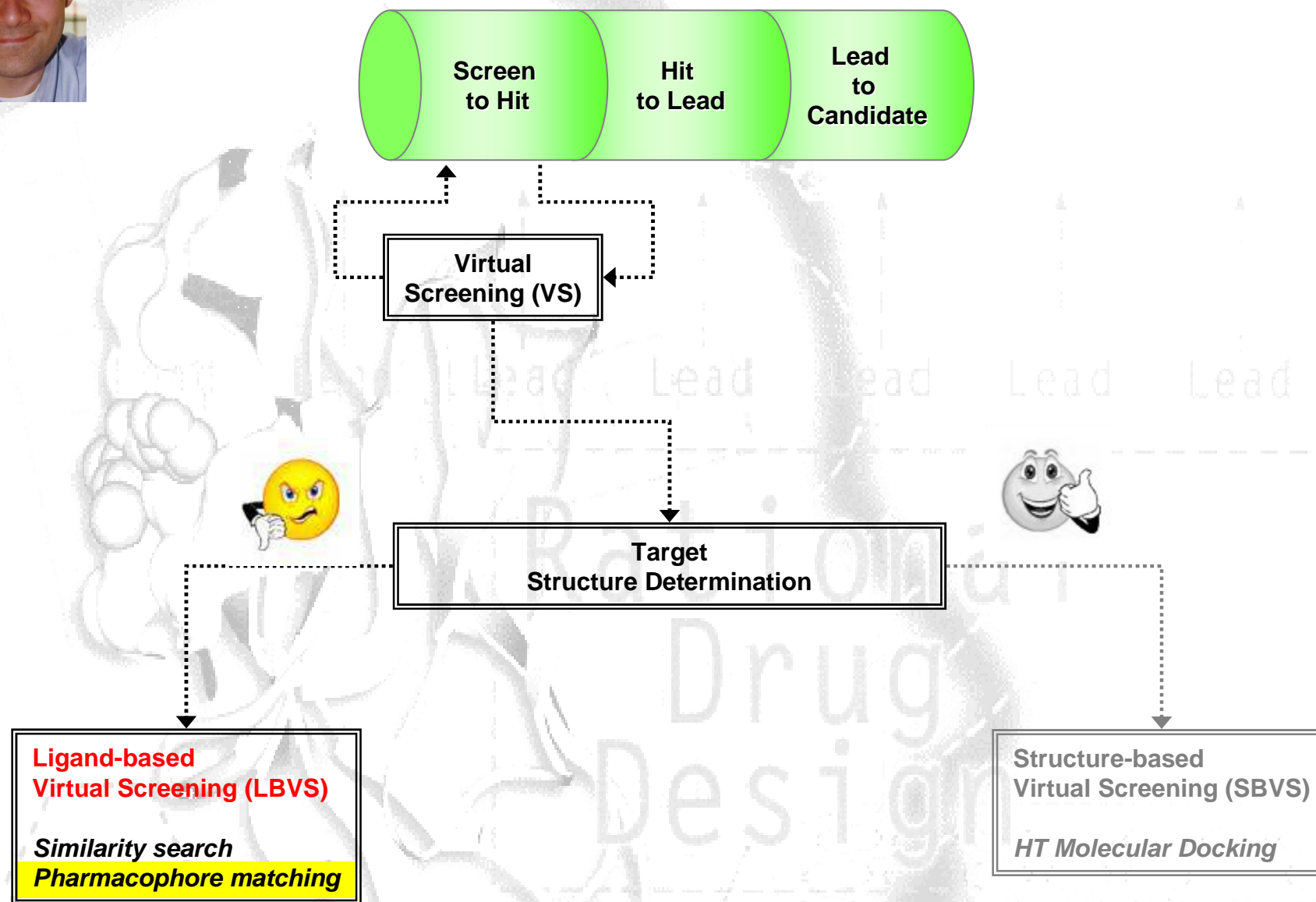
And don't forget:



1- similarity = diversity



Here we are again:





Pharmacophore definition:

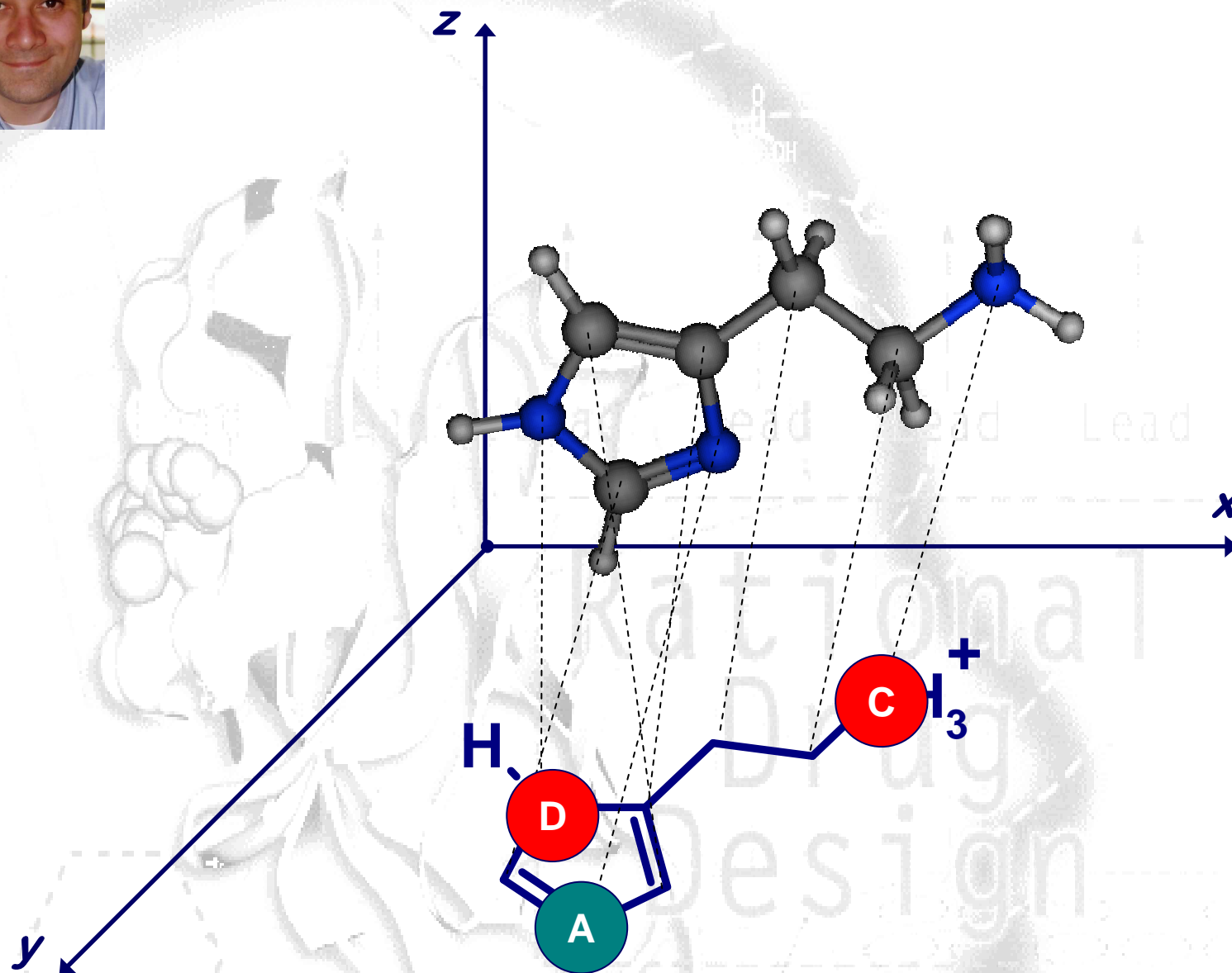
A "*pharmacophore*" is a three-dimensional substructure of a molecule that carries ("*phoros*") the essential features responsible for a drug's ("*pharmacon*") biological activity. Alternatively described as an ensemble of interactive functional groups with a defined geometry. Basically, one tries to 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)!!!!**



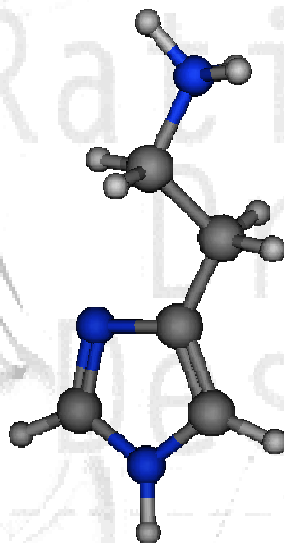
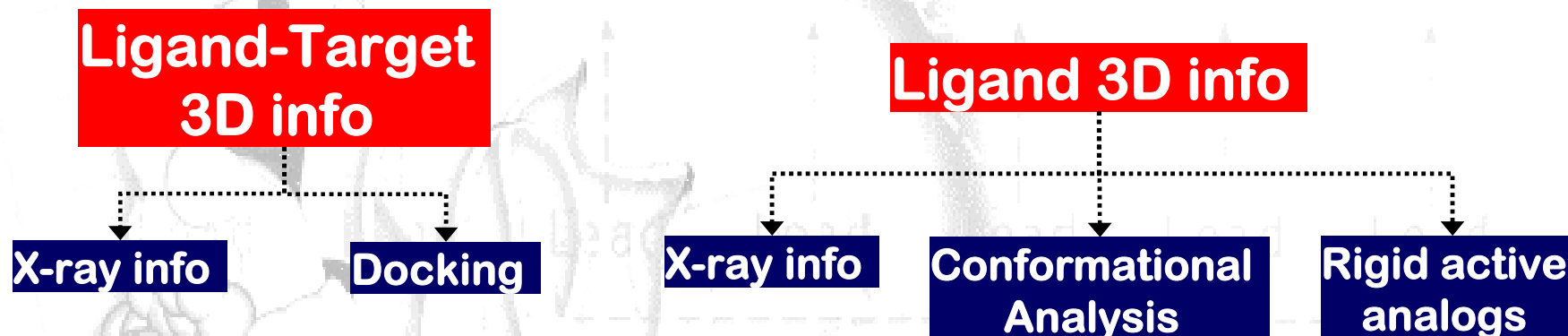
the shadow of the reality:





Pharmacophore definition:

1. *conformational selection*





Two very interesting concepts:

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

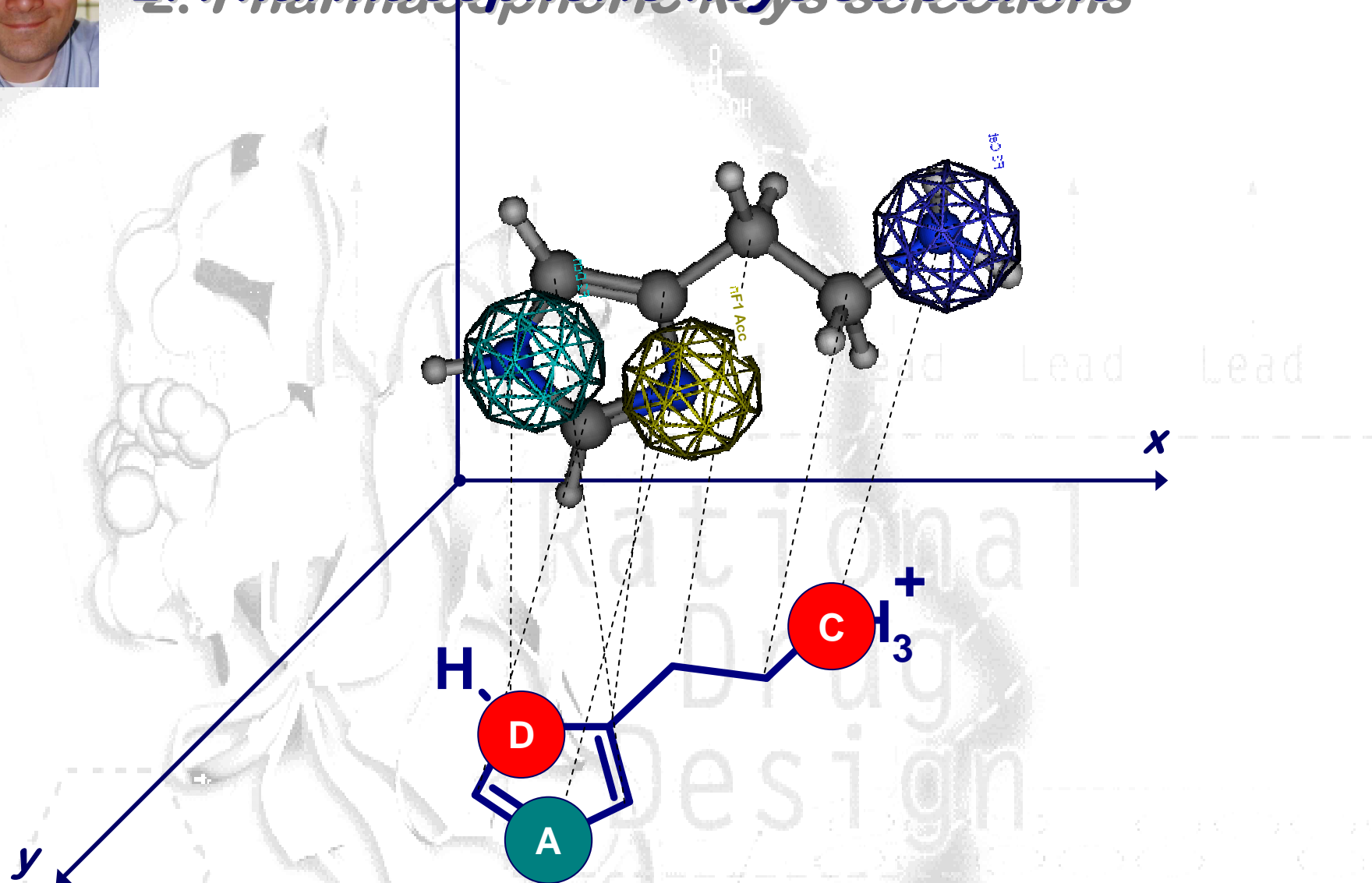
Rigidity as a measure of the reduction degree of the geometrical deformability of an object.





Pharmacophore definition:

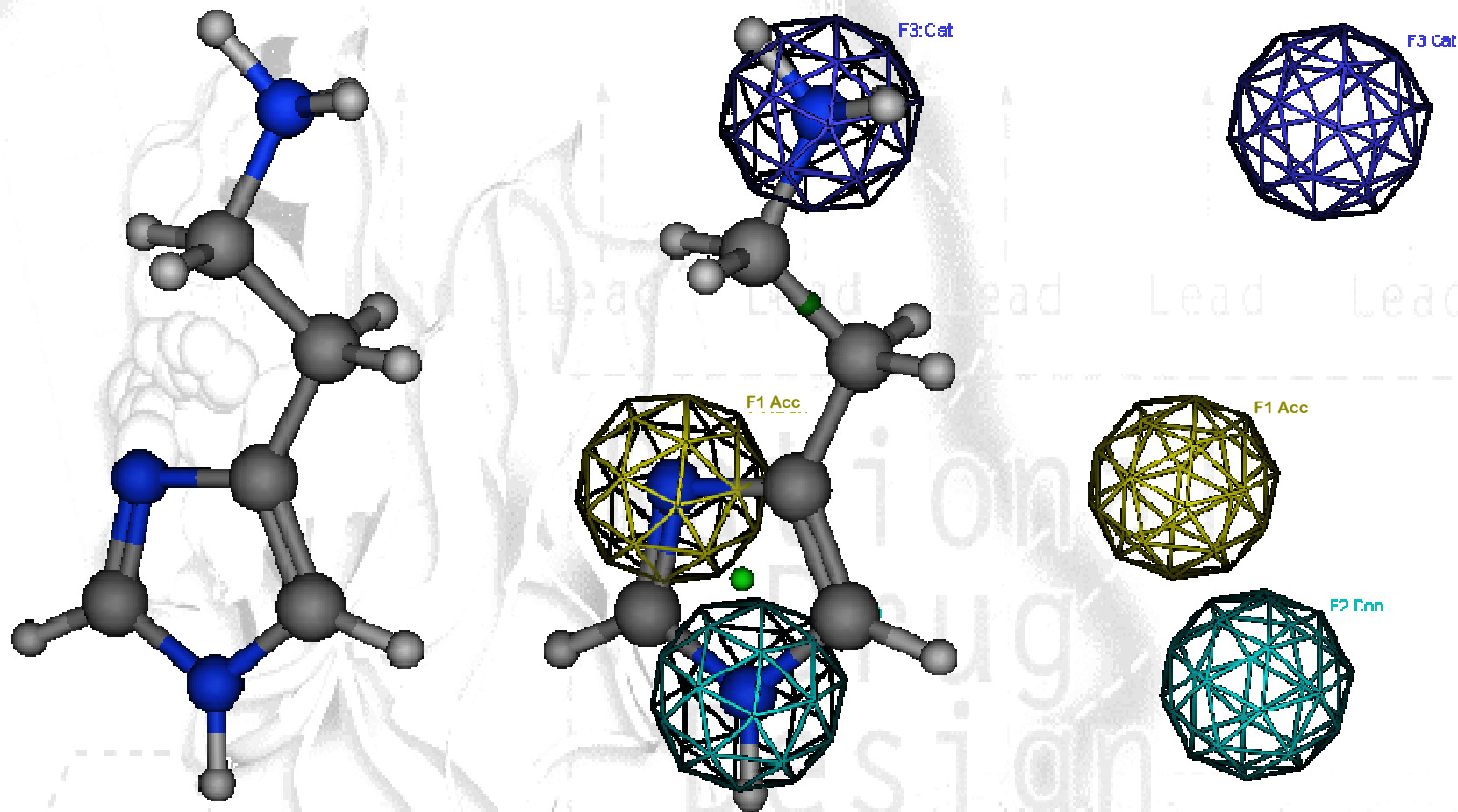
2. *Pharmacophoric keys selections*





Pharmacophore definition:

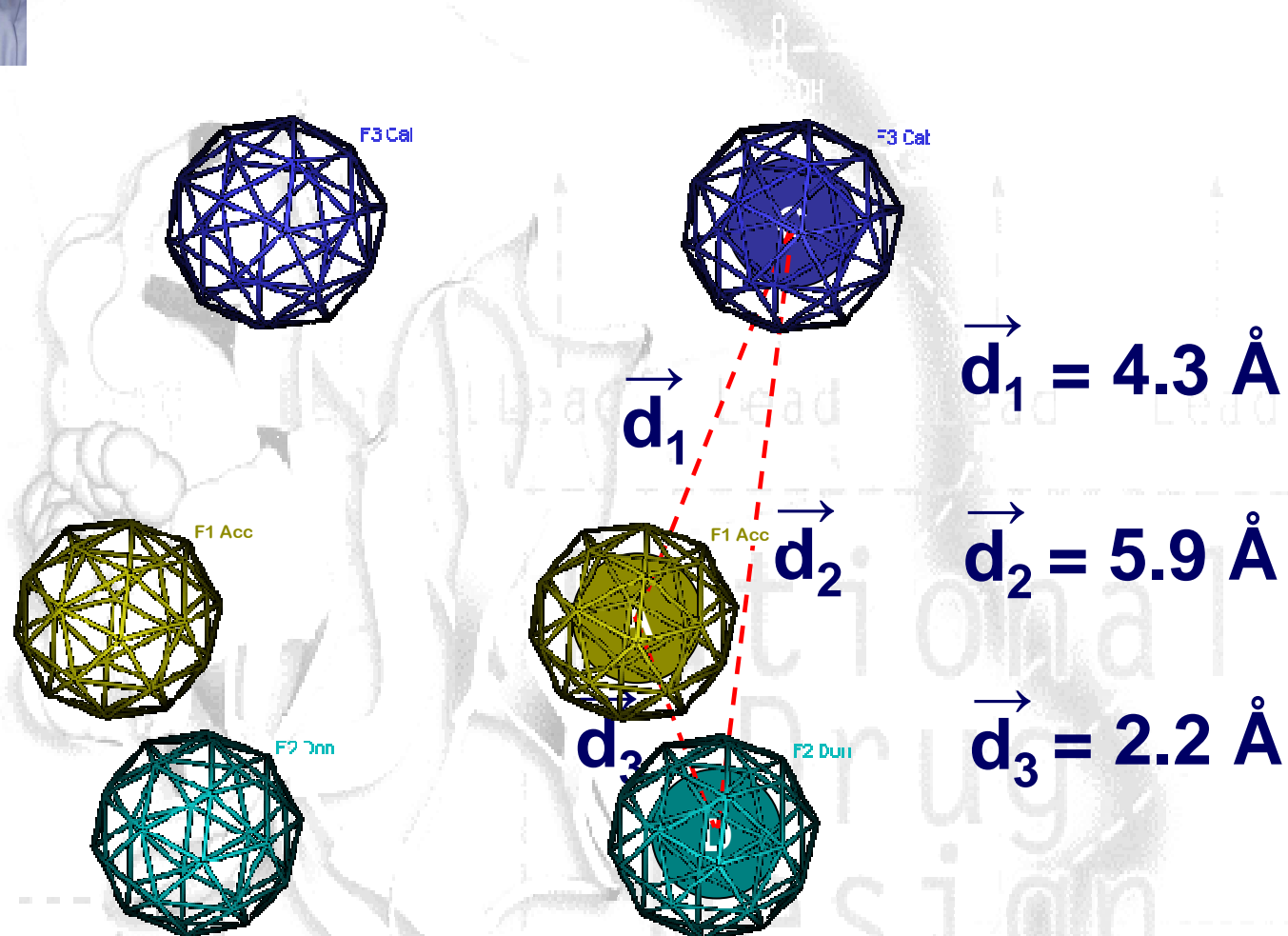
2. *Pharmacophoric keys selections*





Pharmacophore definition:

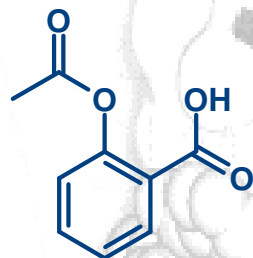
3. *Interaction triangle*





Pharmacophore definition:

4. From structural key to pharmacophoric key



| | | | | | | | |
|----|----|---|-------|---|---|---|---|
| | | | Ar-OH | | | | |
| 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

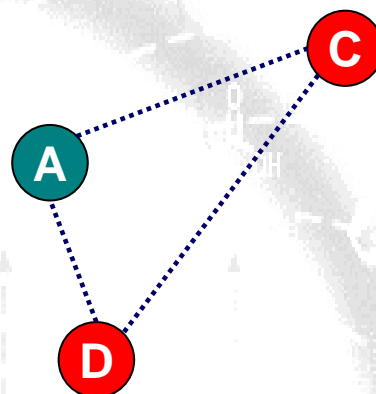
A = H-bonding acceptor

C = cation

An = anion



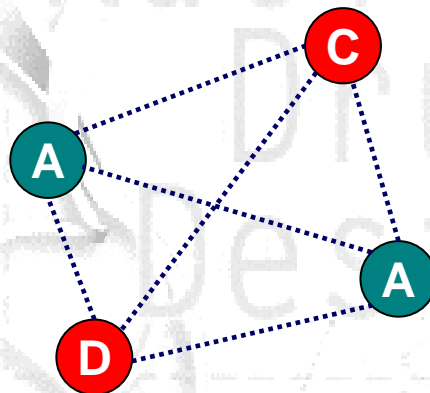
The triangle saga :



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

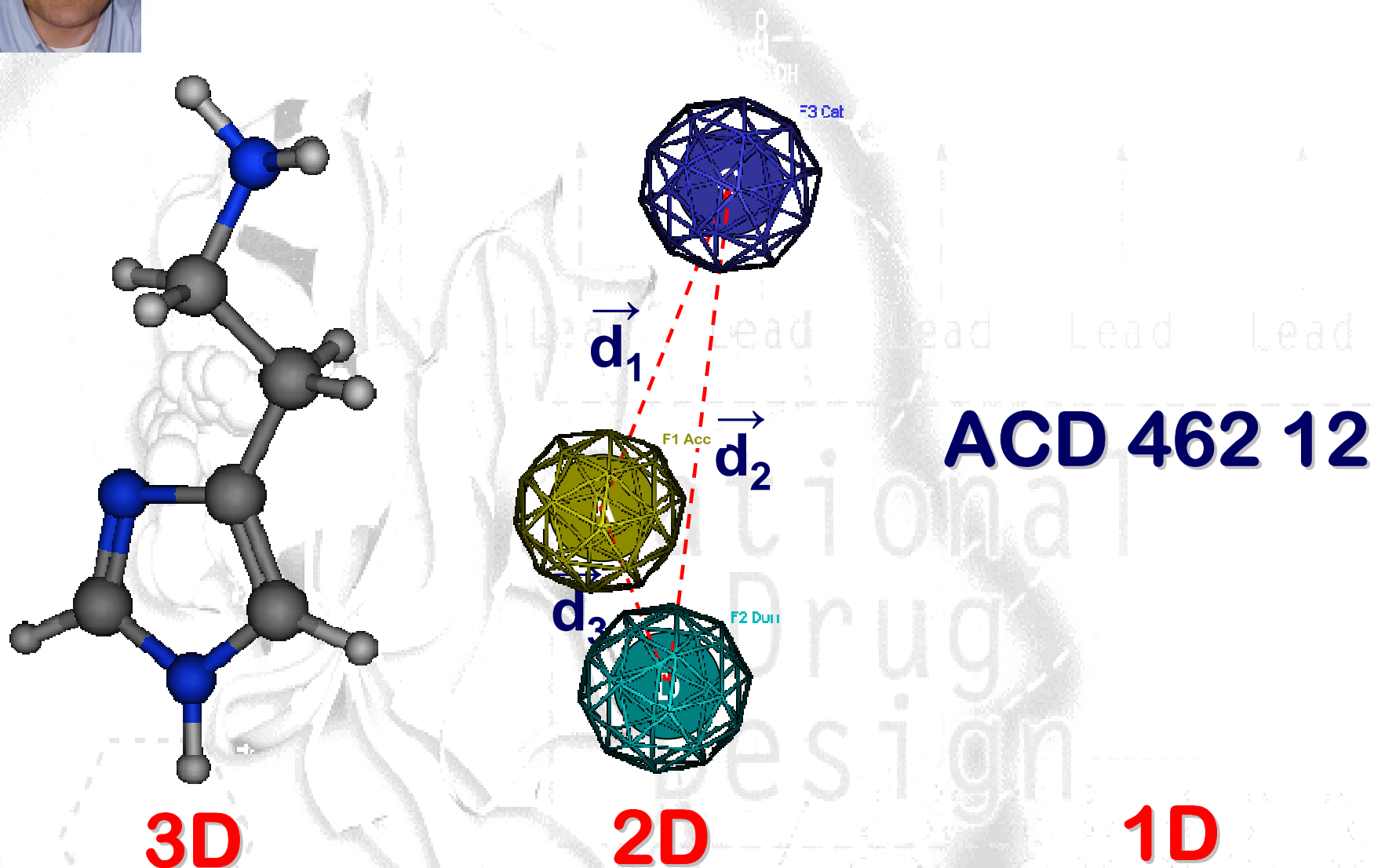
For any triangle we can calculate numerical descriptors: **perimeter, sides length.**

Any polygons can be subdivided into a sum of triangles:





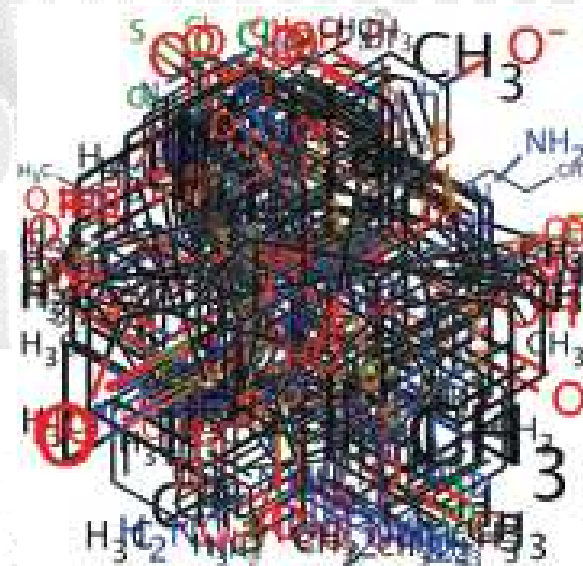
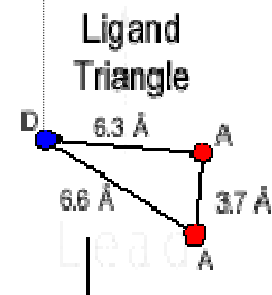
Here is another interesting 3D→1D chemical representation transformation!





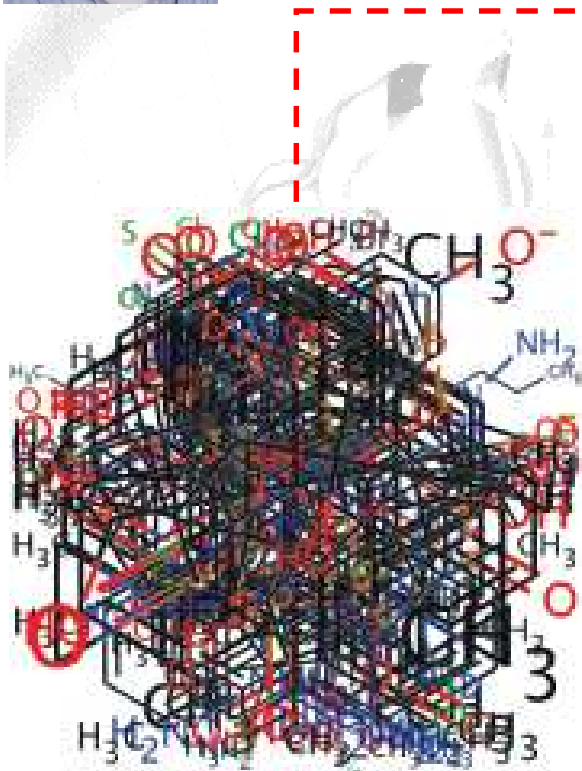
Pharmacophore definition:

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;

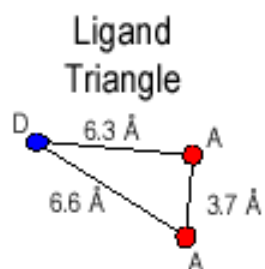
③ generation of all possible pharmacophoric triangles;

④ generation of all possible pharmacophoric strings.



Pharmacophore definition:

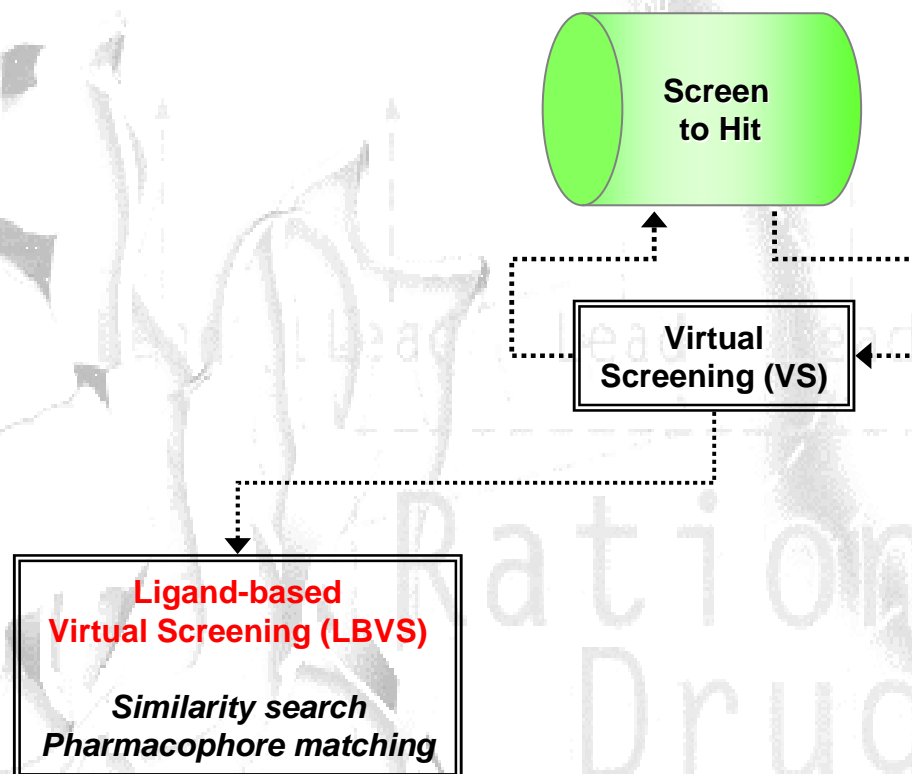
5. *Geometric hashing scheme*



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

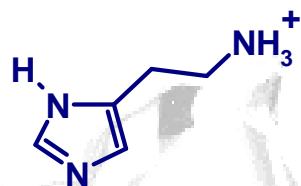


Here is a possible work-flow:

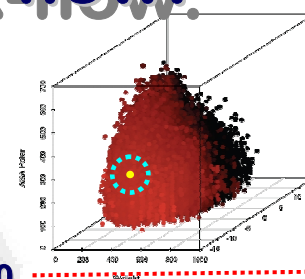




Here is a possible work-flow:

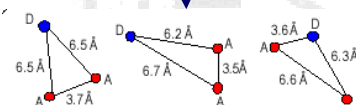
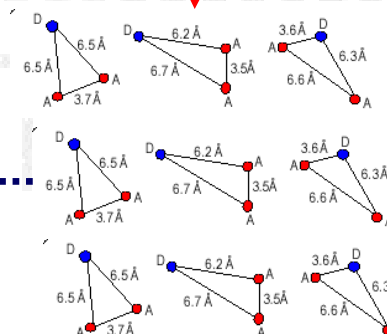
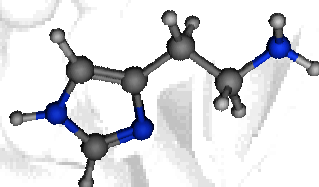


000011111001010101010



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

| | | | |
|---|---|---|---|
| MMscore00000 testimoto score: 0.99 | MMscore00000 testimoto score: 0.99 | MMscore00000 testimoto score: 0.99 | MMscore00000 testimoto score: 0.99 |
| MMscore00000 testimoto score: 0.98 | MMscore00000 testimoto score: 0.99 | MMscore00000 testimoto score: 0.99 | MMscore00000 testimoto score: 0.99 |
| MMscore00000 testimoto score: 0.99 | MMscore00000 testimoto score: 0.99 | MMscore00000 testimoto score: 0.99 | MMscore00000 testimoto score: 0.99 |



| | | | |
|---|---|---|---|
| MMscore00000 testimoto score: 0.99 | MMscore00000 testimoto score: 0.99 | MMscore00000 testimoto score: 0.99 | MMscore00000 testimoto score: 0.99 |
|---|---|---|---|