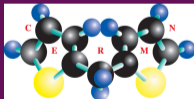


# Computation of pharmacophores and subsequent analyse\*s

Academic research carried out in Caen

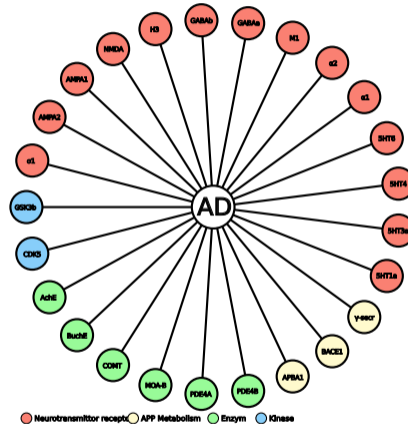
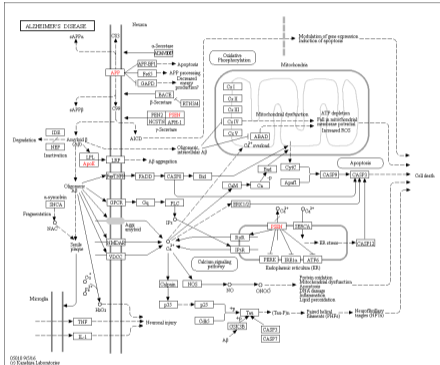
Normandie Univ, UNICAEN, ENSICAEN, CNRS, GREYC, CERMN,Caen, FRANCE

<https://www.greyc.fr/equipes/codag/>, <https://cermn.unicaen.fr/>



# Rational drug design

## Alzheimer disease



► KEGG PATHWAY Database, <http://www.genome.jp/kegg/pathway.html>



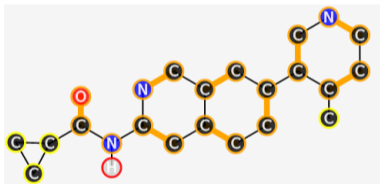
# The input: molecules (ligands) whose 2D structures are graphs

## SDF file format: the atoms/the vertices

```

24 27 0 0 0 0          999 V2000
2.1456   0.2461   0.0000 C   0  0
2.1446  -0.4139   0.0000 C   0  0
2.8584  -0.8275   0.0000 C   0  0
2.8570  -1.6525   0.0000 C   0  0
2.1419  -2.0639   0.0000 N   0  0
1.4281  -1.6503   0.0000 C   0  0
1.4293  -0.8252   0.0000 C   0  0
0.7145  -0.4125   0.0000 C   0  0
0.7145   0.4125   0.0000 C   0  0
0.0000   0.8250   0.0000 C   0  0
-0.7145  0.4125   0.0000 C   0  0
-1.4290  0.8250   0.0000 C   0  0
-2.1435  0.4125   0.0000 C   0  0
-2.8592  0.8238   0.0000 N   0  0
-3.5735  0.4100   0.0000 C   0  0
-3.5723 -0.2500   0.0000 O   0  0
-4.2892  0.8213   0.0000 C   0  0
-5.0707  0.7961   0.0000 C   0  0
-4.6582  1.5106   0.0000 C   0  0
-2.1435 -0.4125   0.0000 N   0  0
-1.4290 -0.8250   0.0000 C   0  0
-0.7145 -0.4125   0.0000 C   0  0
0.0000  -0.8250   0.0000 C   0  0
-2.8602  1.3738   0.0000 H   0  0

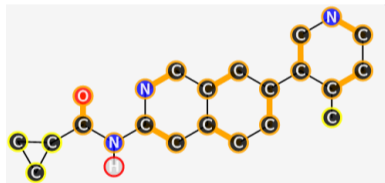
```



# The input: molecules (ligands) whose 2D structures are graphs

SDF file format: the bonds/edges

1	2	1	0
2	3	2	0
3	4	1	0
4	5	2	0
5	6	1	0
6	7	2	0
7	2	1	0
7	8	1	0
8	9	2	0
9	10	1	0
10	11	2	0
11	12	1	0
12	13	2	0
13	14	1	0



13	20	1	0
14	15	1	0
14	24	1	0
15	16	2	0
15	17	1	0
17	18	1	0
18	19	1	0
19	17	1	0
20	21	2	0
21	22	1	0
22	11	1	0
22	23	2	0
23	8	1	0

# The input: molecules (ligands) whose 2D structures are graphs

## SDF file format: the properties

```
> <CMPD_CHEMBLID>  
CHEMBL3685020
```

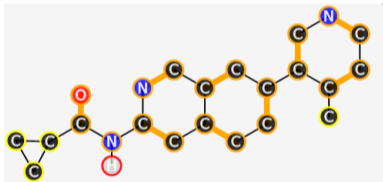
```
> <STANDARD_TYPE>  
Ki
```

```
> <RELATION>  
=
```

```
> <STANDARD_VALUE>  
0.03
```

```
> <STANDARD_UNITS>  
nM
```

```
> <Molecular_Weight>  
303.35778
```



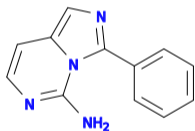
# The pharmacophoric graph

## An abstracted representation of a molecule

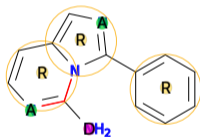
### Pharmacophoric features

- ▶ Hydrogen Bond **A**ceptor, Hydrogen Bond **D**onor, aromatic **R**ing, **H**ydrophobic area, **P**ositively ionizable group, **N**egatively ionizable group<sup>a</sup>
- ▶ an adjustable part of the input.

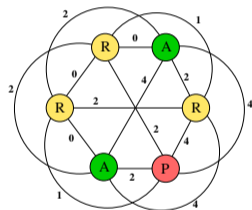
<sup>a</sup>OdenBabel. N. J. Cheminformatics 2011, 3, 33.



Skeletal formula



Feature occurrences

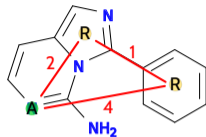
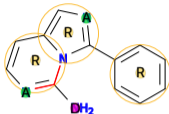
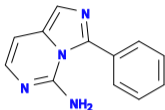


Pharmacophoric graph

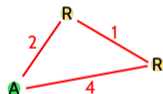
### The Pharmacophoric graph (of a molecule)

- ▶ A vertex: an occurrence of a feature
- ▶ An edge: the distance between two features

# A pharmacophore



- ▶ An **occurrence** of a pharmacophore in a molecule  
 $\iff$  an embedding that fits:
  - ▶ the labels of the features,
  - ▶ the distance constraints.



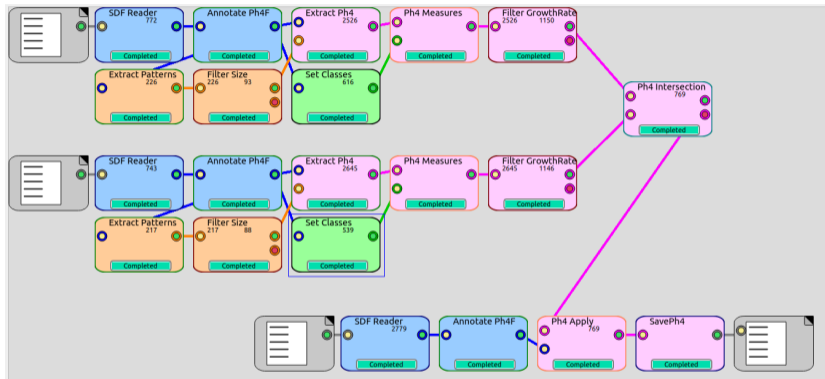
## A pharmacophore:

Given a dataset of molecules,

- ▶ A graph of pharmacophoric features whose extent is:
  - ▶ sufficiently large,
  - ▶ discriminative enough.



## A visual programming environment to implement a pharmacophore mining process




*The Pharmacophore Network: A Computational Method for Exploring Structure-Activity Relationships from*  
Jean-Philippe Métivier, Bertrand Cuissart, Ronan Bureau, Alban Lepailleur  
J. Med. Chem, 2018, Volume61, Issue8, Page 3551-3564

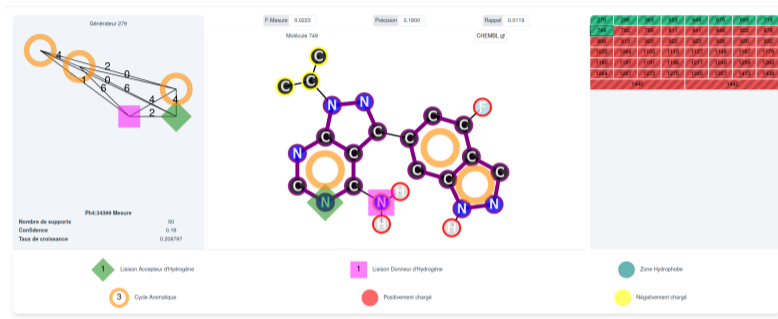
DOI10.1021/acs.jmedchem.7b01890


## A visual programming environment to implement a pharmacophore mining process



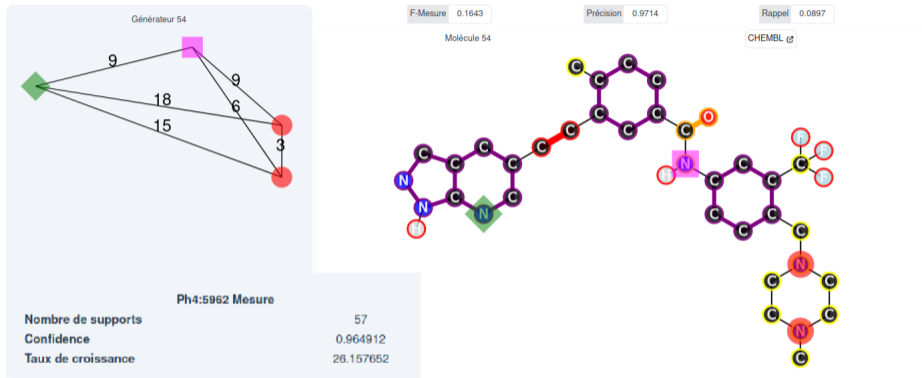
 *The Pharmacophore Network: A Computational Method for Exploring Structure-Activity Relationships from*  
 Jean-Philippe Métivier, Bertrand Cuissart, Ronan Bureau, Alban Lepailleur  
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DOI10.1021/acs.jmedchem.7b01890

- ▶ implementation of complex processes by connecting boxes,
- ▶ 60 configurable boxes that include:
  - ▶ reading/writing of molecules from/into files,
  - ▶ molecular representations,
  - ▶ pharmacophoric features mining,
  - ▶ pharmacophore selection,
  - ▶ **classifiers**

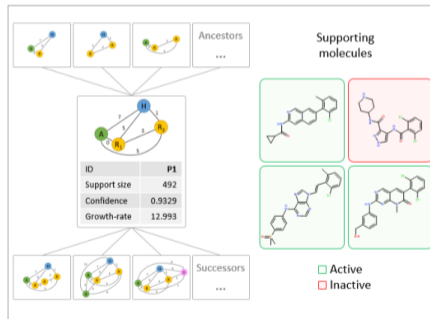
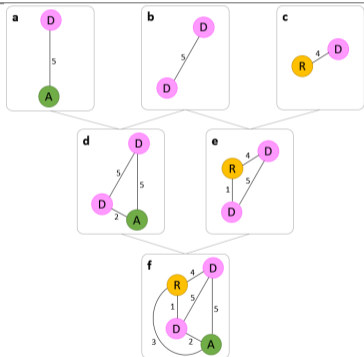
# Towards a pharmacophore network

## Exploration of Structure-Activity Relationships from a Large Chemical Data Set [?]

Relationship: the graph inclusion (being a subgraph of)

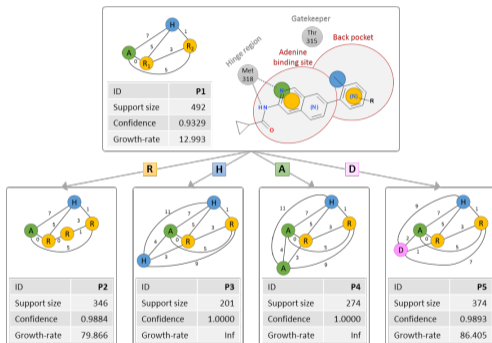
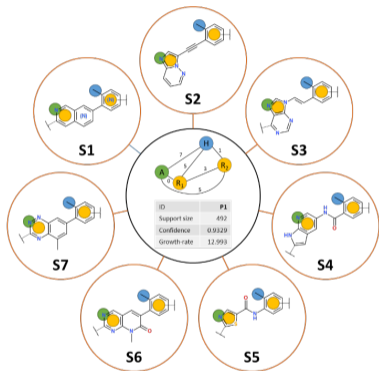
Hasse diagram

Navigation



# A principal pharmacophore

## Bcr-Abl



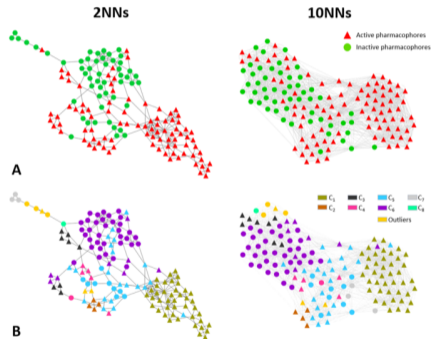
The addition of features on P1 improves its discriminative power.

# The pharmacophores and the SAR principle [?] <sup>1</sup>

## SAR principle

- ▶ Two “similar” chemical structures should be associated to a similar behaviour

- ▶ **Relationship**: a graph edit distance
- ▶ **separation** between the pharmacophores associated with active compounds and those associated with inactive ones,
- ▶ **clustering** → pharmacophores that occurs in molecules with similar structures and biological activities



<sup>1</sup>*Deciphering a Pharmacophore Network: A Case Study Using BCR-ABL Data*, Damien Geslin et al, J. Chem. Inf. Model., 2022

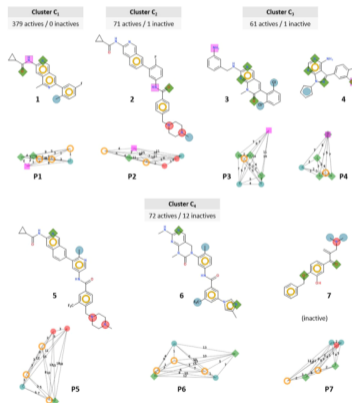


# The pharmacophores and the SAR principle [?] <sup>1</sup>

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# Perspectives related to GNNs

- ▶ screening of a molecular bank to compute a large activity profile
- ▶ location/identification of the parts of the graph that are the most important
- ▶ (re)definition of the pharmacophoric features