

# Task 5: Molecules



AIDS Antiviral Screen Database of Active Compounds

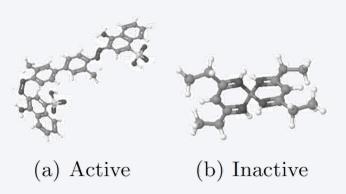


Two classes active 'a' and inactive 'i'

Annotated in train.txt and valid.txt

### Task

Classify the molecules of the validation set using KNN Distance: approximate Graph Edit Distance (GED)





# Input: Graph xml (gxl files)



#### XMLs with a lot of information

→ we only need nodes labeled with their chemical symbol and the unlabeled, undirected edges:

```
<node id=" 1"><attr name="symbol"><string>C</string></attr>
```

<edge from="\_1" to="\_2">

## Further info about the database (AIDS):

See riesen08graphdb.pdf  $\rightarrow$  section 2.8 (there are also images of molecules)

Hint: there are python libraries to parse XML files



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Compute approximate GED between pairs of molecules with

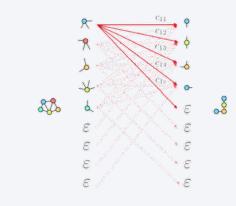
bipartite graph matching

(lecture 10, slide 21)

Build cost matrix (*Dirac*)

Hungarian Algorithm
To find optimal assignment

 $\mathbf{C} = \begin{bmatrix} c_{11} & c_{12} & \cdots & c_{1m} & c_{1\varepsilon} & \infty & \cdots & \infty \\ c_{21} & c_{22} & \cdots & c_{2m} & \infty & c_{2\varepsilon} & \ddots & \vdots \\ \vdots & \vdots & \ddots & \vdots & \vdots & \ddots & \ddots & \infty \\ c_{n1} & c_{n2} & \cdots & c_{nm} & \infty & \cdots & \infty & c_{n\varepsilon} \\ c_{\varepsilon 1} & \infty & \cdots & \infty & 0 & 0 & \cdots & 0 \\ \infty & c_{\varepsilon 2} & \ddots & \vdots & 0 & 0 & \ddots & \vdots \\ \vdots & \ddots & \ddots & \infty & \vdots & \ddots & \ddots & 0 \\ \infty & \cdots & \infty & c_{\varepsilon m} & 0 & \cdots & 0 & 0 \end{bmatrix}$ 



Derive Edit Path costs from the result (distance for classification)

KNN for classification (optimize for K)



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#### Recommendation

Use *Dirac* cost function for GED (optimize Cn and Ce) (lecture 9, slide 36)

Node substitution: 2\*Cn if symbols ≠, 0 otherwise

Node deletion/insertion: Cn

Edge deletion/insertion: Ce

Use an existing framework for the Hungarian algorithm