

Implementazione di algoritmi in linguaggio “Python” per lo sviluppo di modelli 3-D QSAR tramite l’interfacciamento tra UCSF Chimera e il portale www.3d-qsar.com

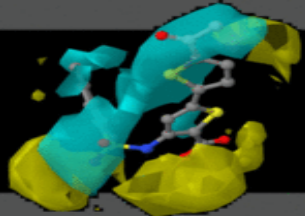


SAPIENZA
UNIVERSITÀ DI ROMA

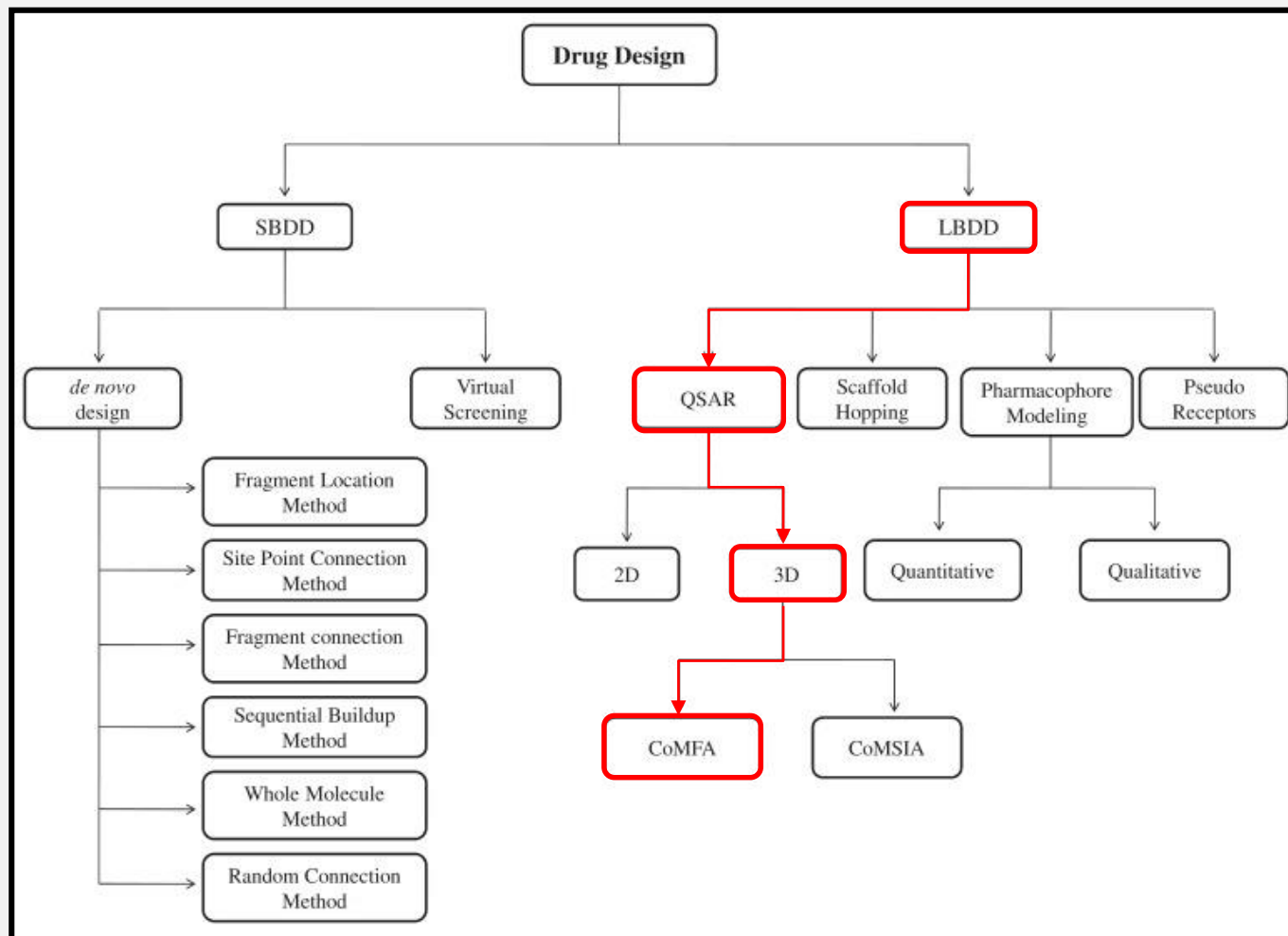
Facoltà di Farmacia e Medicina
Corso di laurea magistrale in Biotecnologie Farmaceutiche
Tesi di laurea sperimentale in Chimica Farmaceutica

Relatore:
Prof. Rino Ragno

Candidato:
Nikola Dino Capocchiano
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Introduzione

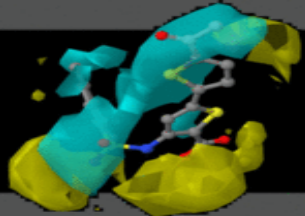


Ligand-**B**ased **D**rug **D**esign

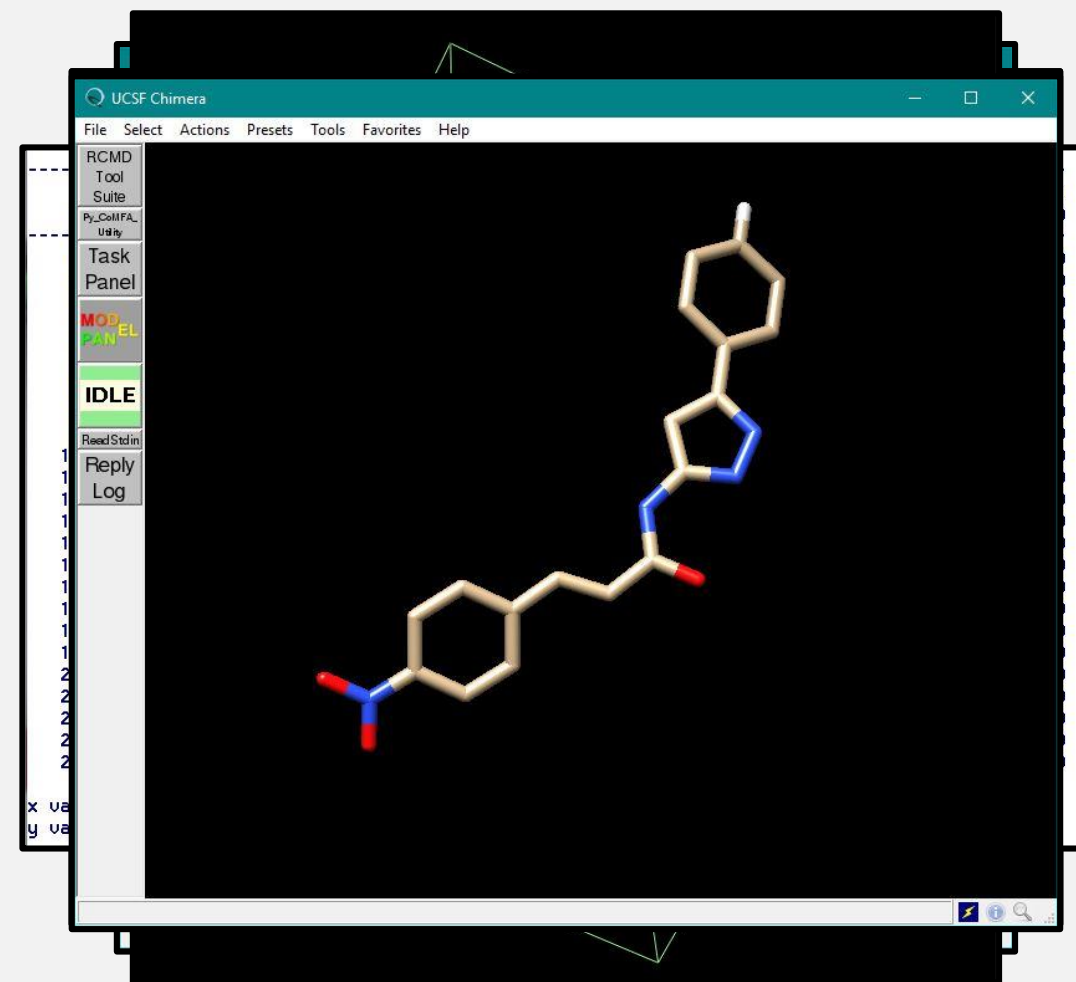
Quantitative **S**tructure-**A**ctivity **R**elationships

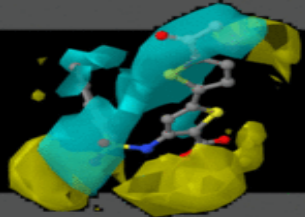
3-**D**imensional

Comparative **M**olecular **F**ield **A**nalysis



3-D QSAR





Punti Critici

1

Interfaccia Utente
Unificata

2

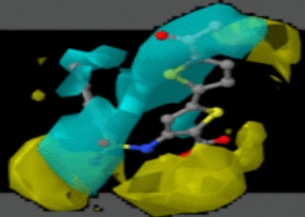
Prestazioni

3

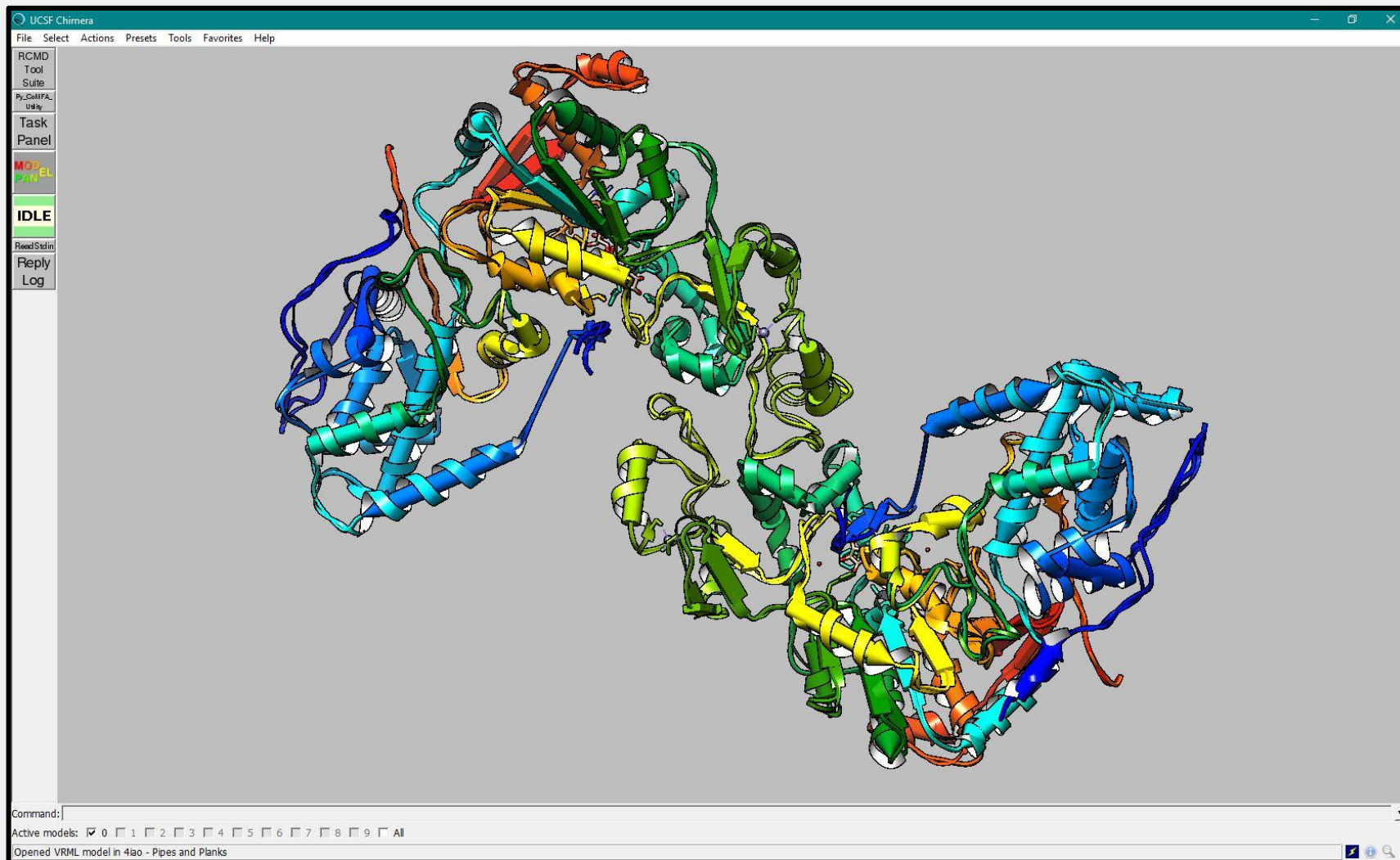
Esecuzione Remota

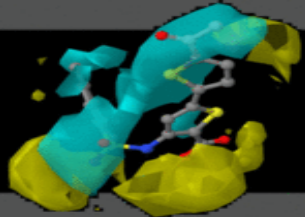
4

Facilità Di Utilizzo



UCSF Chimera

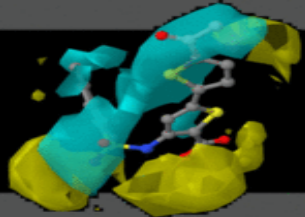




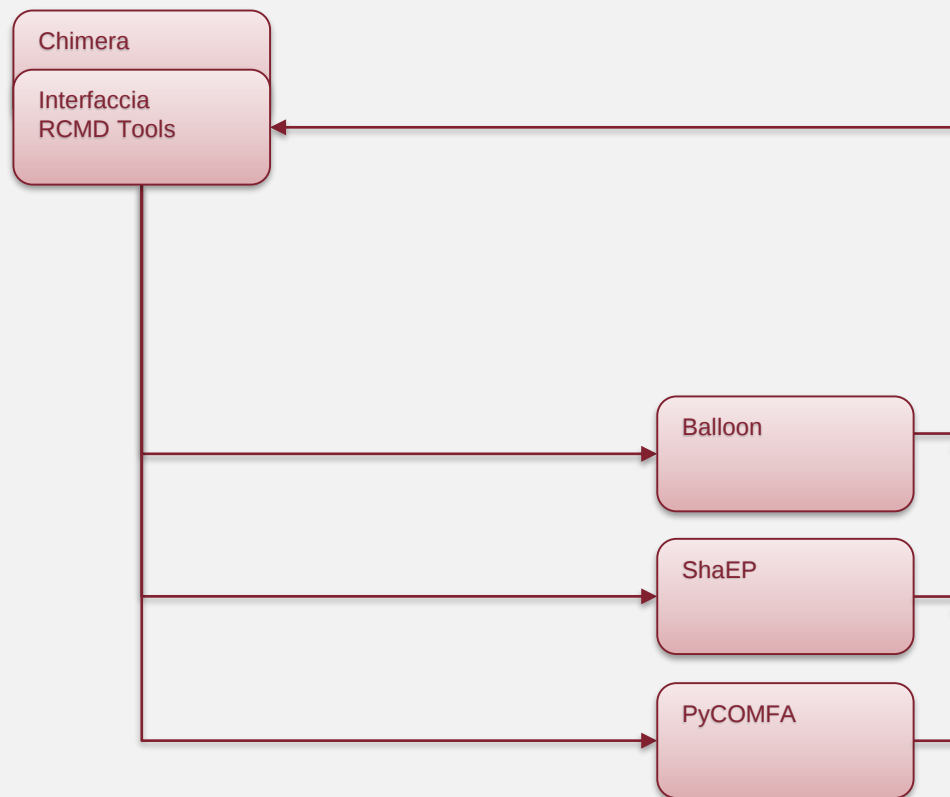
Python

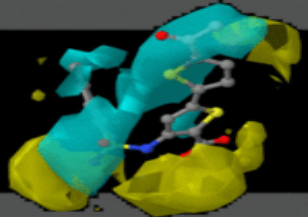


- **Python is:**
 - **A high-level programming language**
 - **Interpreted**
 - **Interactive**
 - **Object-Oriented**

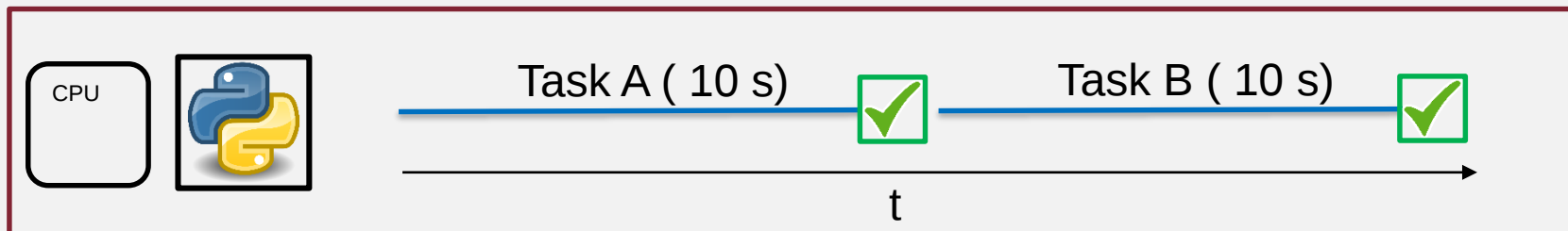


Organizzazione Plug-in

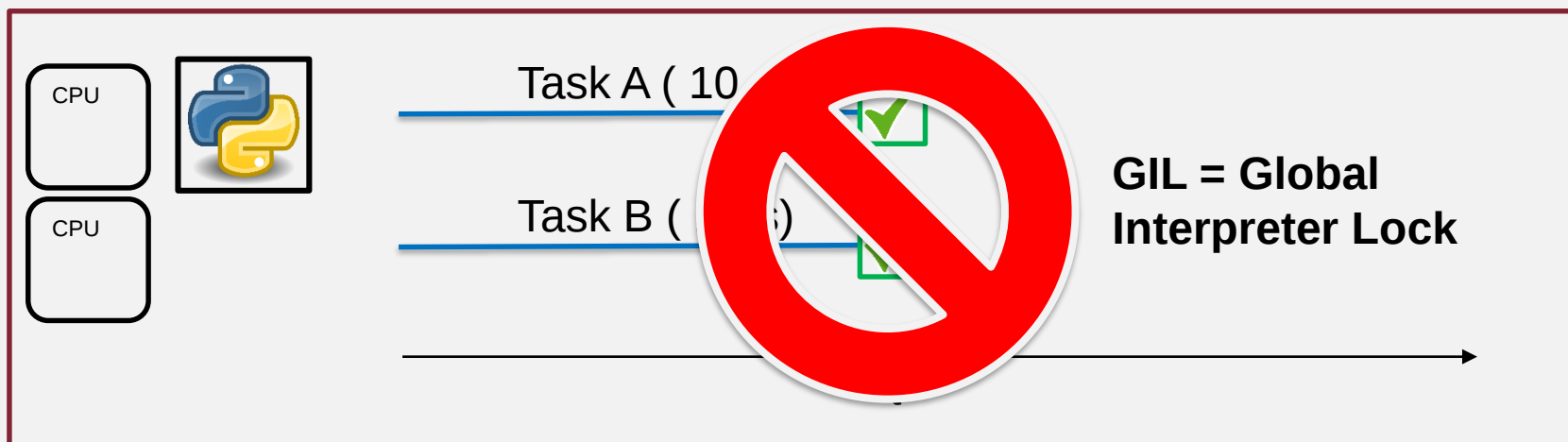




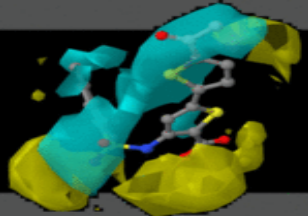
Prestazioni



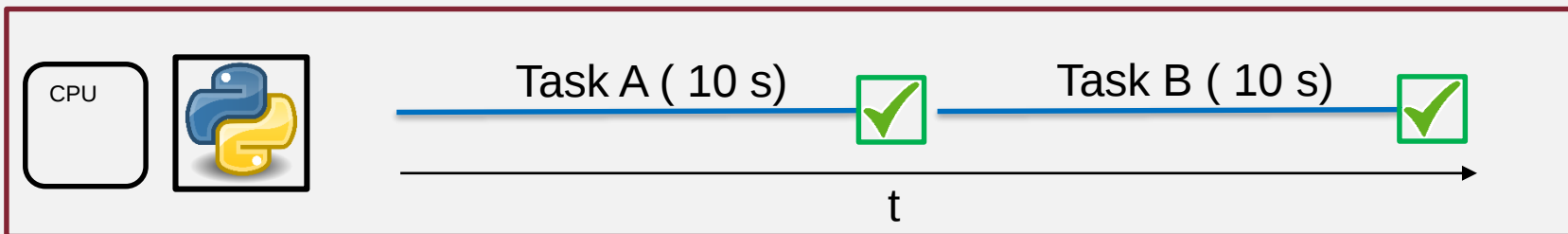
$$t_{\text{Finale}} = A + B = 20 \text{ secondi}$$



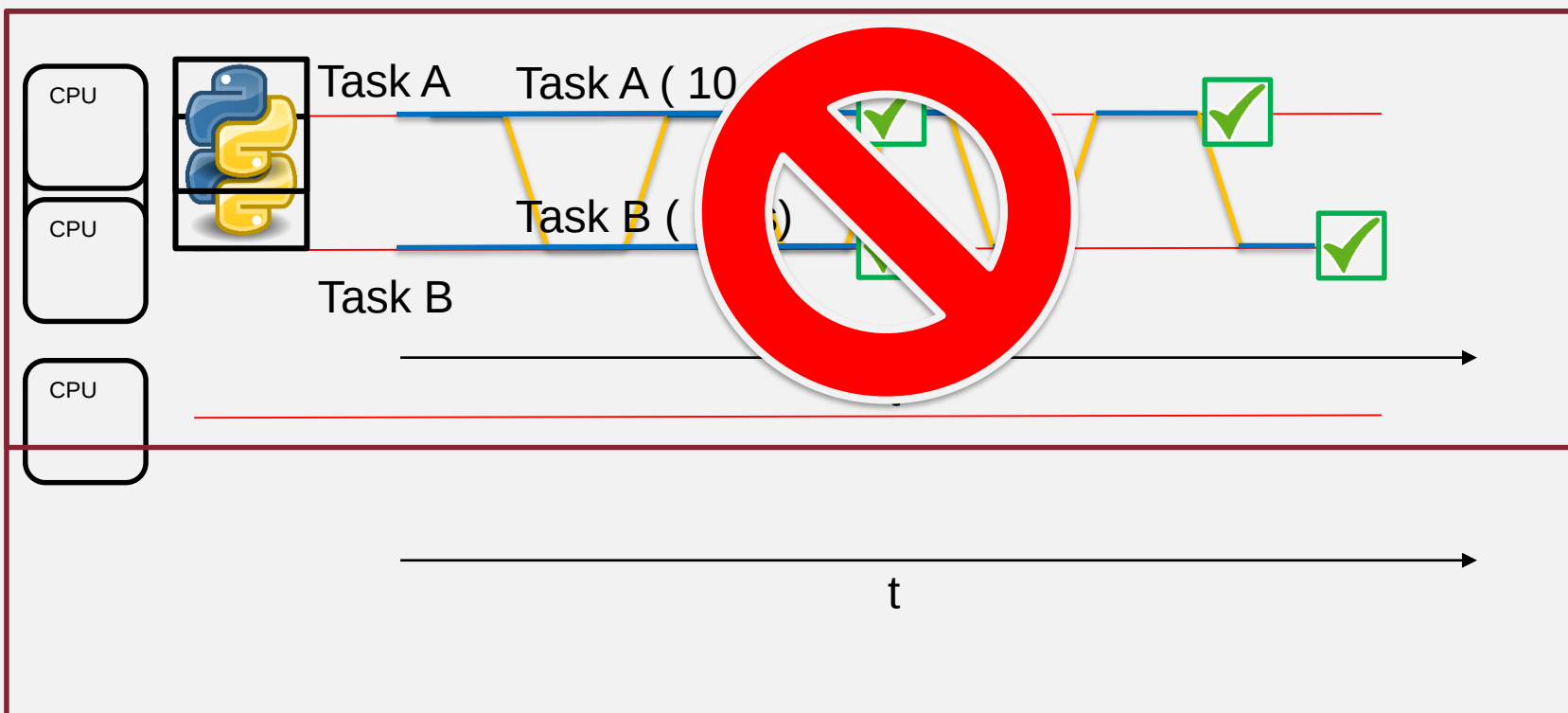
$$t_{\text{Finale}} = A = B = 10 \text{ secondi}$$



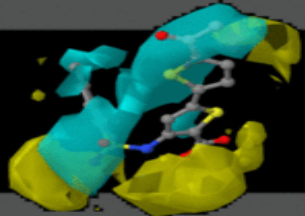
Prestazioni



$$t_{\text{Finale}} = A + B = 20 \text{ secondi}$$



$$t_{\text{Finale}} = ?$$



Prestazioni

```
def count(n):
    while n > 0:
        n -= 1

numero = 90000000

a = datetime.datetime.now().replace(microsecond=0)

count(numero)
count(numero)

b = datetime.datetime.now().replace(microsecond=0)

tempo_finale= b - a
print(«Done in: » + str(tempo_finale))
```

Funzione: Conta da valore X a 0

X = 90 000 000

Tempo Finale = 7 secondi chiamalo A

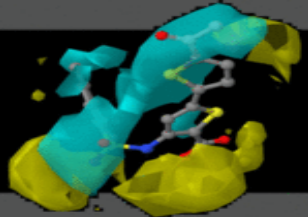
(3.5 secondi a ciclo)

sequenzialmente

Prendi il tempo in secondi, chiamalo B

Tempo finale = B - A

Stampa tempo finale



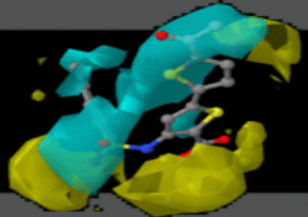
Prestazioni

```
def count(n):  
    while n > 0:  
        n -= 1  
  
numero = 90000000  
  
a = datetime.datetime.now().replace(microsecond=0)  
  
t1 = threading.Thread(target=count, args=(numero,))  
t1.start()  
t2 = threading.Thread(target=count, args=(numero,))  
t2.start()  
t1.join(); t2.join()  
  
b = datetime.datetime.now().replace(microsecond=0)  
  
tempo_finale= b - a  
print("Finito in:" + str(tempo_finale))
```

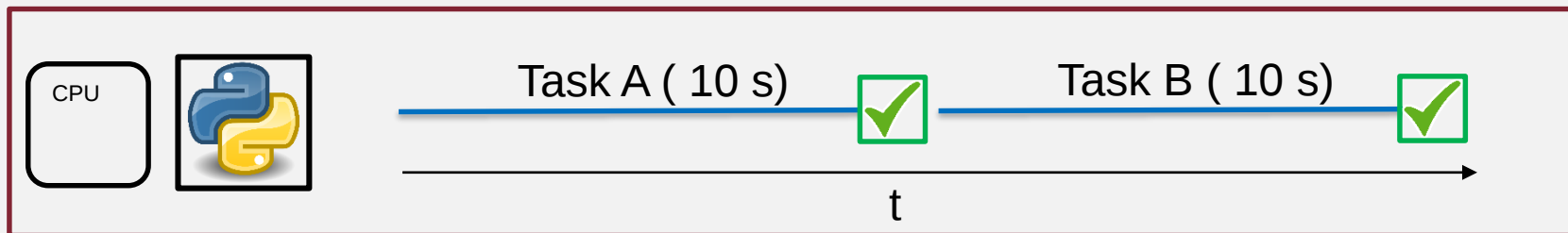
Tempo Finale = 14 secondi

Overhead di 7 secondi!

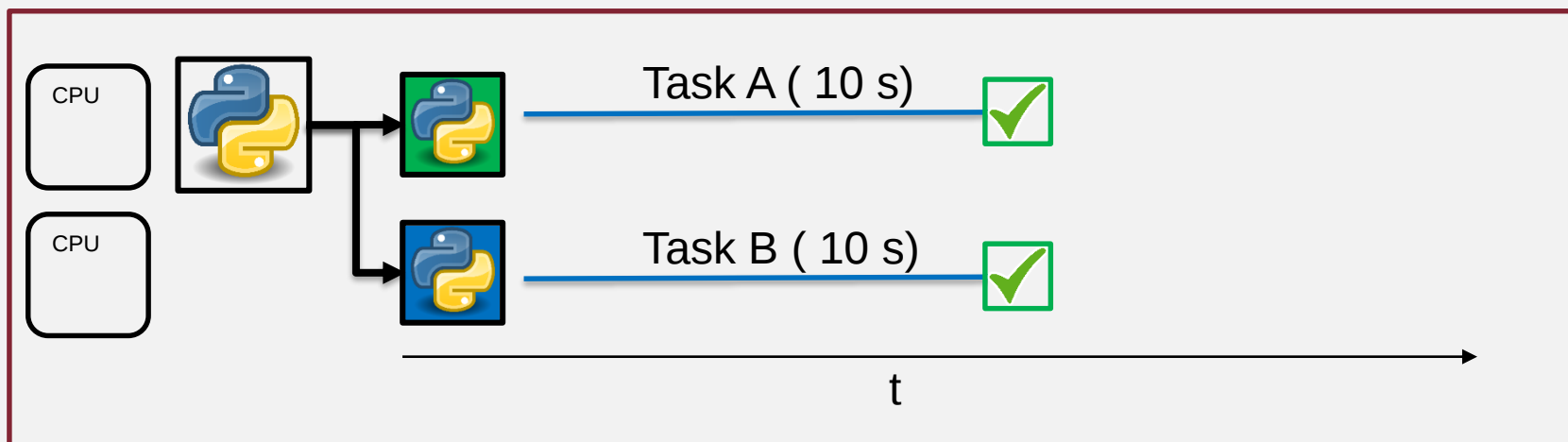
eseguono 1



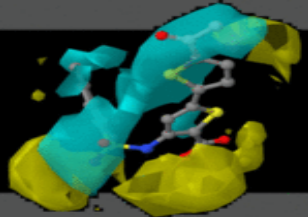
Prestazioni



$$t_{\text{Finale}} = A + B = 20 \text{ secondi}$$



$$t_{\text{Finale}} = A = B = 10 \text{ secondi}$$

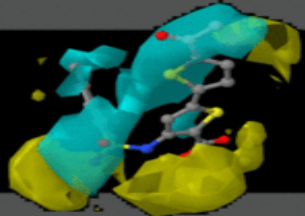


Prestazioni

```
def count(n):  
    while n > 0:  
        n -= 1  
    print "done"  
  
if __name__ == '__main__':  
    numero = 90000000  
    a = datetime.datetime.now().replace(microsecond=0)  
  
    p = multiprocessing.Process(target=count, args=(numero,))  
    n = multiprocessing.Process(target=count, args=(numero,))  
  
    p.start(); n.start()  
  
    p.join(); n.join()  
  
    b = datetime.datetime.now().replace(microsecond=0)  
    tempo_finale = b - a  
  
    print("Finito in:" + str(tempo_finale))
```

Tempo Finale = 4 secondi

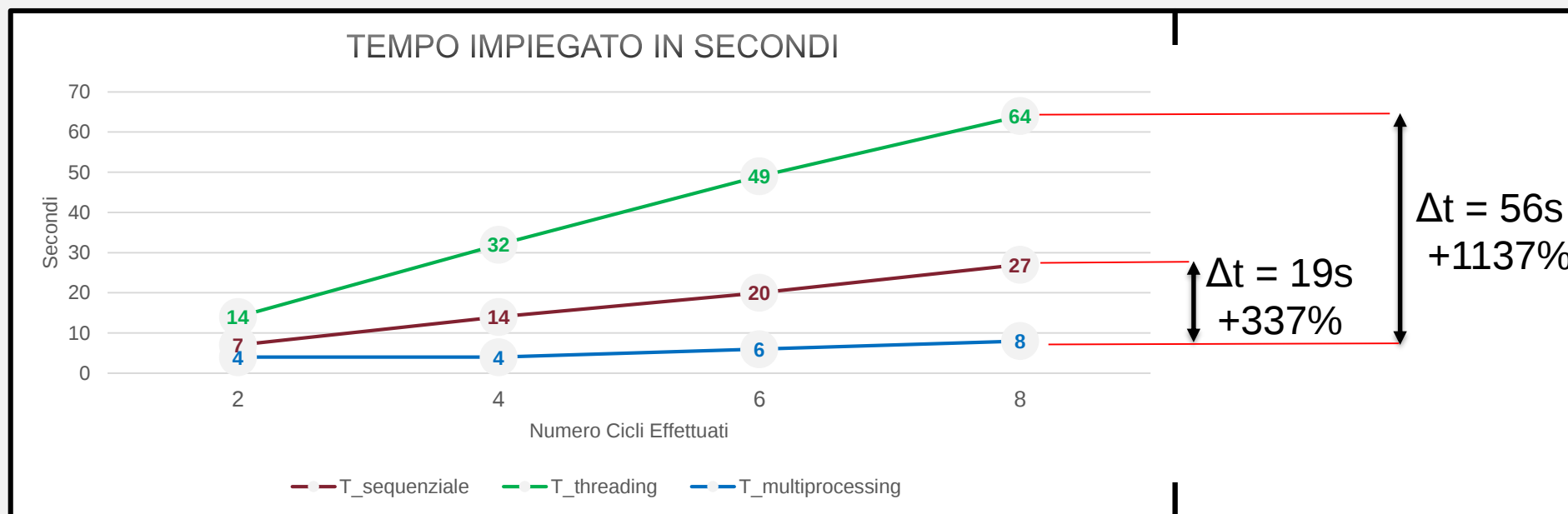
Crea 2 **processi** differenti che eseguono 1 ciclo della funzione ciascuno

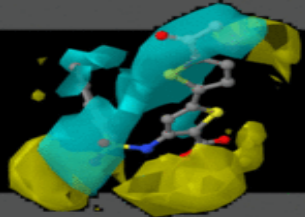


Prestazioni – Dati Conclusivi

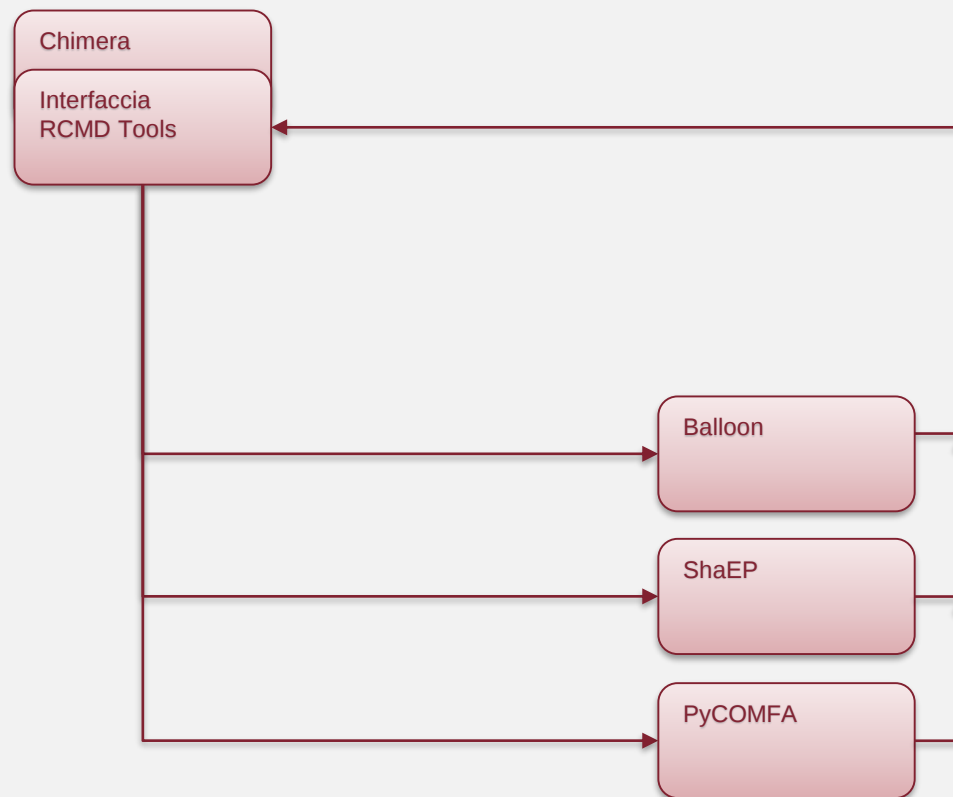
CPU
a 4 Core

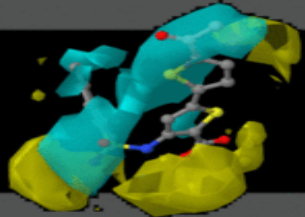
Numero di Cicli	T_sequenziale	T_threading	T_multiprocessing
2	7 secondi	14 secondi	4 secondi
4	14 secondi	32 secondi	4 secondi
6	20 secondi	49 secondi	6 secondi
8	27 secondi	64 secondi	8 secondi



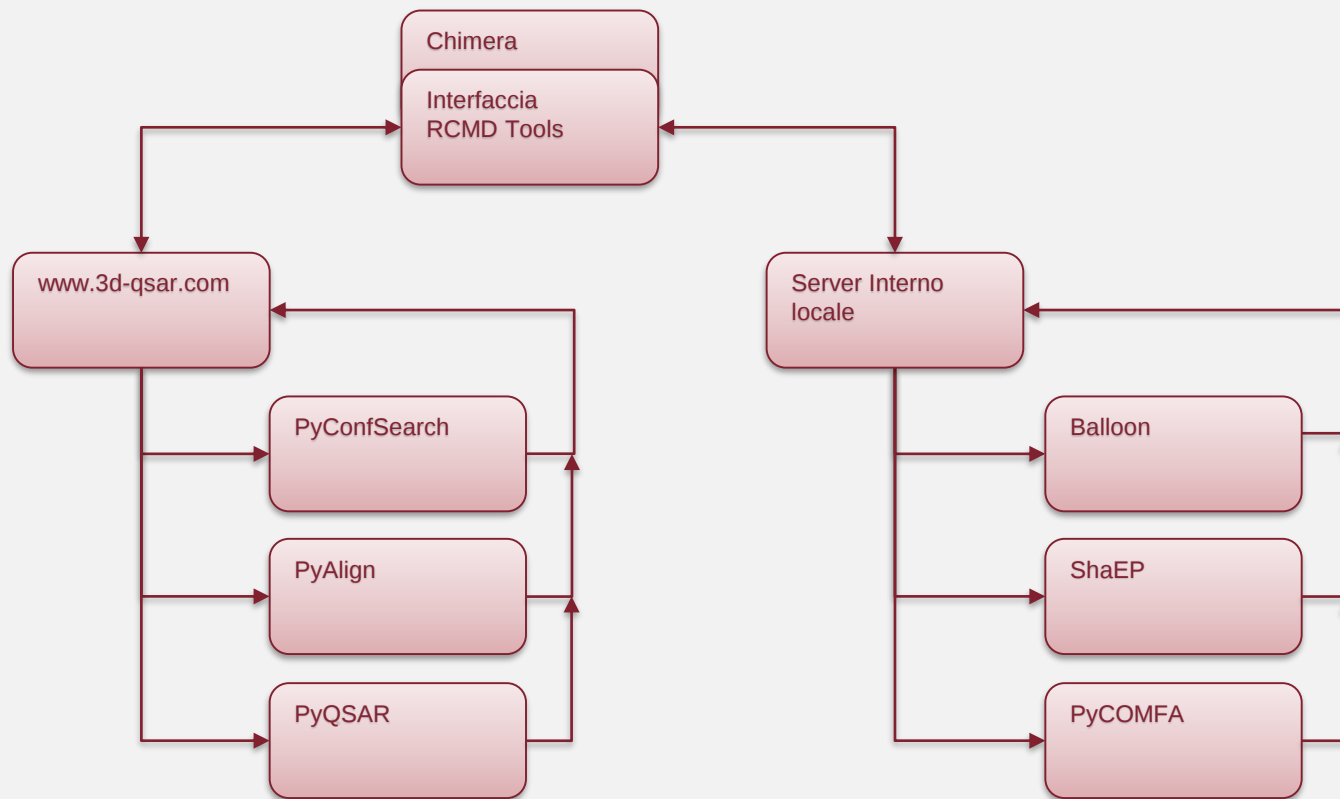


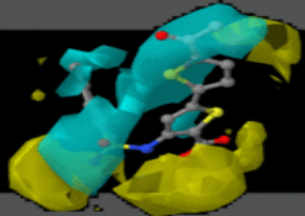
Organizzazione Plug-in





Organizzazione Plug-in





Interfaccia Principale

1

RCMD Tool Suite

[RCMD Tool Suite]

Open Molecule List:
Please select the desired molecules: [Default: None selected]

Reload All None

- 1) compound5g
- 2) compound5g
- 3) compound5g
- 4) compound5g
- 5) compound5g
- 6) compound5g
- 7) compound5g
- 8) compound5g
- 9) compound5g
- 10) compound5g

Rename Close Model Panel

3

Task Status Box:
-- No Pending Tasks Found --

Network Open Results Clear Log

2

Supported Programs:
Please select the desired programs to run:

1) Conformational Analysis:
☒ Balloon
☐ PyConfSearch

2) Alignment:
☐ ShaEP
☐ PyAlign

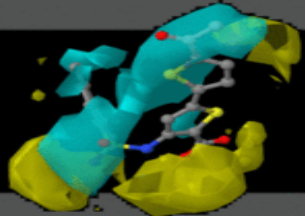
3) www.3D-QSAR.com - Login credentials
Username: dino
Password: *****

4

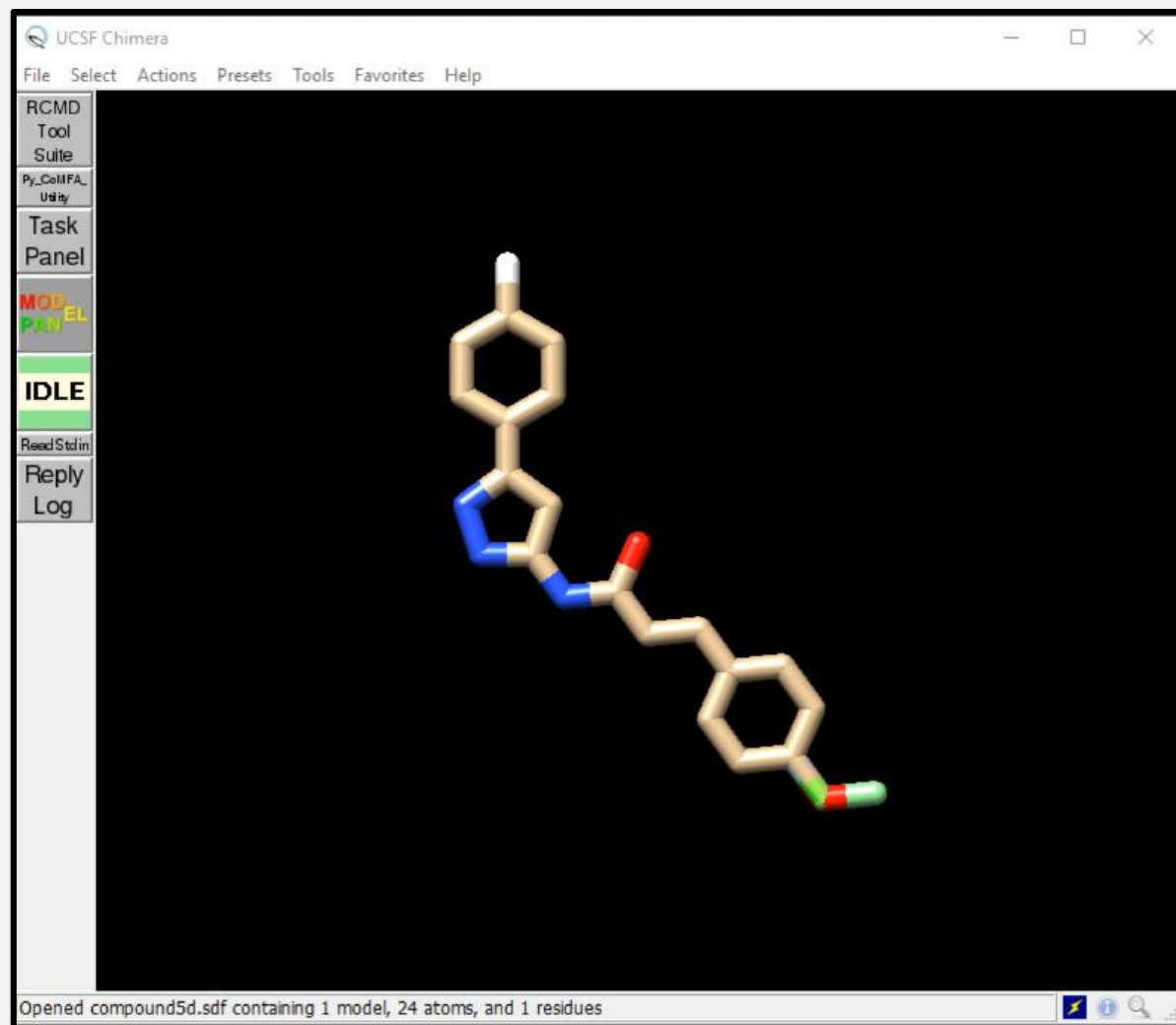
Experimental Options: [UNSTABLE]
General Network

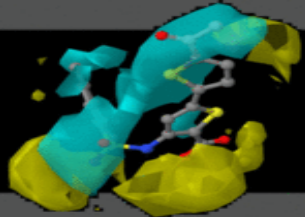
Host Address: localhost
Port: 4545
Timeout (s): 60
Force number of CPUs: 2

Start Close Help



Esempio di utilizzo





Punti Critici



Interfaccia Utente
Unificata

2

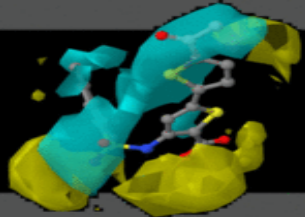
Prestazioni

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Esecuzione remota



Facilità di utilizzo



Punti Critici



Interfaccia Utente
Unificata



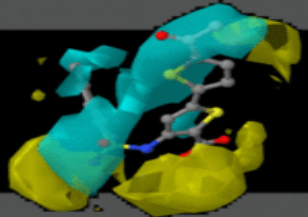
Prestazioni



Esecuzione remota



Facilità di utilizzo



Conclusioni

Risoluzione dei 4 punti critici presi in considerazione

Possibilità di espansione a Chromebook e Cellulari

Altamente modulare e di facile mantenimento

Nuovo strumento didattico