Drugs

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RDKit package is used for processing chemical structure. Tutorial
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Installation: follow this link.

conda install -c rdkit rdkit

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[1]: # import libraries
import os
import pandas as pd
from rdkit import Chem

# read in the csv file and display the head
file = 'Drugs.csv'
drugs = pd.read_csv(file)
drugs.head()
```

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[1]: Drug Name SMILES

0 Aspirin 0=C(C1=C(OC(C)=0)C=CC=C1)0

1 Morphine 0C1=C20[C@@H]3[C@]45C2=C(C=C1)C[C@@H](N(CC5)C)...

2 Apixaban C0C1=CC=C(N2N=C(C3=C2C(N(C4=CC=C(N5CCCCC5=0)C=...

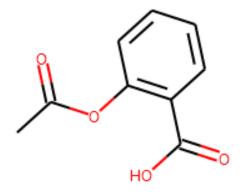
3 Lenalidomide NC1=CC=CC2=C1CN(C2=0)C3CCC(NC3=0)=0

4 Rivaroxaban C1C1=CC=C(C(NC[C@H]2CN(C3=CC=C(N4CCOCC4=0)C=C3...
```

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[2]: # Use Chem module from rdkit to read the SMILES string and display the structure
aspirin = Chem.MolFromSmiles('O=C(C1=C(OC(C)=0)C=CC=C1)O')
print('Aspirin structure:')
aspirin
```

Aspirin structure:

[2]:



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[3]: # set up directories for image, SMILES and mol files
smi_dir = './smi'
mol_dir = './mol'
sdf_dir = './sdf'
img_dir = './img'

# make the directories if not exist
for d in [smi_dir, mol_dir, sdf_dir, img_dir]:
    if not os.path.exists(d):
        os.makedirs(d)
[4]: # initiate an empty list to accept all drug structure
structure_lst = []
```

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[4]: # initiate an empty list to accept all drug structure
    # iterate through the whole csv file
    for i in range(drugs.shape[0]):
       # get the drug name
       drug = drugs.loc[i, 'Drug Name']
       print(f'\n\033[1m{drug}\033[0m:')
       # get the SMILES string
       smiles = drugs.loc[i, 'SMILES']
       # convert SMILES string to structure
       structure = Chem.MolFromSmiles(smiles)
       # append the structure to the list
       structure_lst.append(structure)
       # configure the filename and path for .smi files
       smi_file = drug + '.smi'
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smi_path = os.path.join(smi_dir, smi_file)
   # configure the filename and path for .mol files
   mol_file = drug + '.mol'
   mol_path = os.path.join(mol_dir, mol_file)
   # configure the filename and path for .sdf files
   sdf file = drug + '.sdf'
   sdf_path = os.path.join(sdf_dir, sdf_file)
   # configure the filename and path for .png files
   img_file = drug + '.png'
   img_path = os.path.join(img_dir, img_file)
   # iterate through .smi, .mol and .sdf files
   for item in [smi_path, mol_path, sdf_path]:
      try:
         w = Chem.SDWriter(item)
         w.write(structure)
         w.close()
         print(f"\t.{item.rsplit('.',1)[1]} file saved")
      except:
         print(f"\t{item.rsplit('.',1)[1]} file failed")
         pass
   # export individual png file
   try:
      Chem. Draw. MolToFile(structure, img_path, size = (200,200), legend = ___
→drug)
      print('\t.png file saved')
   except:
      print('\tImage failed')
      pass
# configure the filename and path for drug_all.sdf file
sdf_all_file = 'Drugs.sdf'
sdf_all_path = os.path.join(sdf_dir, sdf_all_file)
try:
  w = Chem.SDWriter(sdf_all_path)
```

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for structure in structure_lst:
        w.write(structure)
    w.close()
    print('\nA big sdf file saved for all drugs as "drug_all.sdf".')
except:
    print('\tBig sdf for all drugs failed')
img_all_path = os.path.join(img_dir, 'drug_all.png')
# export a big png file for all drugs
try:
    img_all = Chem.Draw.MolsToGridImage(structure_lst, molsPerRow=4,_

¬subImgSize=(200,200),legends = drugs['Drug Name'].tolist())

    img_all.save(img_all_path)
    print('\nA big image saved for all drugs as "drug_all.png".')
except:
    print('\tBig image for all drugs failed')
    pass
print('\n\x1b[6;30;42m' + 'All DONE!' + '\x1b[0m')
Aspirin:
       .smi file saved
       .mol file saved
       .sdf file saved
       .png file saved
Morphine:
       .smi file saved
       .mol file saved
       .sdf file saved
       .png file saved
Apixaban:
       .smi file saved
       .mol file saved
       .sdf file saved
       .png file saved
Lenalidomide:
       .smi file saved
       .mol file saved
```

.sdf file saved .png file saved

Rivaroxaban:

.smi file saved
.mol file saved
.sdf file saved
.png file saved

Ibuprofen:

.smi file saved
.mol file saved
.sdf file saved
.png file saved

Propranolol:

.smi file saved
.mol file saved
.sdf file saved
.png file saved

Nicotine:

.smi file saved
.mol file saved
.sdf file saved
.png file saved

A big sdf file saved for all drugs as "drug_all.sdf".

A big image saved for all drugs as "drug_all.png".

All DONE!