```
! wget https://repo.anaconda.com/miniconda/Miniconda3-py37 4.8.2-Linux-x86 64.sh
! chmod +x Miniconda3-py37 4.8.2-Linux-x86 64.sh
! bash ./Miniconda3-py37_4.8.2-Linux-x86_64.sh -b -f -p /usr/local
! conda install -c rdkit rdkit -y
import sys
sys.path.append('/usr/local/lib/python3.7/site-packages/')
       setuptoois
                          pkgs/main/linux-b4::Setuptoois-45.2.0-py3/ v
₽
       six
                          pkgs/main/linux-64::six-1.14.0-py37 0
       sqlite
                          pkgs/main/linux-64::sqlite-3.31.1-h7b6447c 0
                          pkgs/main/linux-64::tk-8.6.8-hbc83047 0
       tk
                          pkgs/main/noarch::tqdm-4.42.1-py_0
       tqdm
                          pkgs/main/linux-64::urllib3-1.25.8-py37 0
       urllib3
       wheel
                          pkgs/main/linux-64::wheel-0.34.2-py37 0
                          pkgs/main/linux-64::xz-5.2.4-h14c3975 4
       ΧZ
       yaml
                          pkgs/main/linux-64::yaml-0.1.7-had09818_2
                          pkgs/main/linux-64::zlib-1.2.11-h7b6447c_3
       zlib
     Preparing transaction: done
     Executing transaction: done
     installation finished.
     WARNING:
         You currently have a PYTHONPATH environment variable set. This may cause
        unexpected behavior when running the Python interpreter in Miniconda3.
        For best results, please verify that your PYTHONPATH only points to
        directories of packages that are compatible with the Python interpreter
        in Miniconda3: /usr/local
     Collecting package metadata (current_repodata.json): done
     Solving environment: done
     ## Package Plan ##
       environment location: /usr/local
       added / updated specs:
        - rdkit
```

The following packages will be downloaded:

package	build	
blas-1.0	mkl	6 KB
bzip2-1.0.8	h7b6447c_0	78 KB
ca-certificates-2020.12.8	h06a4308 <u></u> 0	121 KB
cairo-1.14.12	h8948797_3	906 KB
certifi-2020.12.5	py37h06a4308 <u></u> 0	141 KB
conda-4.9.2	py37h06a4308 <u></u> 0	2.9 MB
fontconfig-2.13.0	h9420a91_0	227 KB
freetype-2.10.4	h5ab3b9f_0	596 KB
glib-2.66.1	h92f7085_0	2.9 MB
icu-58.2	he6710b0_3	10.5 MB
intel-openmp-2020.2	254	786 KB
jpeg-9b	h024ee3a_2	214 KB
lcms2-2.11	h396b838 <b>_</b> 0	307 KB
libboost-1.73.0	hf484d3e_11	13.9 MB
libffi-3.3	he6710b0_2	50 KB
libpng-1.6.37	hbc83047 <b>_</b> 0	278 KB
libtiff-4.1.0	h2733197 <b>_</b> 1	449 KB
libuuid-1.0.3	h1bed415_2	15 KB
libxcb-1.14	h7b6447c <b>_</b> 0	505 KB
libxml2-2.9.10	hb55368b_3	1.2 MB
lz4-c-1.9.2	heb0550a_3	175 KB
mk1 2020 2	256	120 2 MD

```
52 KB
         mkl-service-2.3.0
                                        py37he8ac12f_0
         mkl_fft-1.2.0
                                       py37h23d657b_0
                                                               148 KB
import os
import pandas as pd
import numpy as np
from rdkit import Chem
from rdkit.Chem import Draw, Descriptors
from matplotlib import pyplot as plt
%matplotlib inline
cd /content/drive/MyDrive/ML_2/project/
     /content/drive/MyDrive/ML_2/project
df = pd.read_csv('250k_smiles.csv')
from sklearn.model_selection import train_test_split
smiles_train, smiles_test = train_test_split(df["smiles"], random_state=42)
print(smiles_train.shape)
print(smiles_test.shape)
     (187091,)
     (62364,)
charset = set("".join(list(df.smiles))+"!E")
char_to_int = dict((c,i) for i,c in enumerate(charset))
int_to_char = dict((i,c) for i,c in enumerate(charset))
embed = max([len(smile) for smile in df.smiles]) + 5
print (str(charset))
print(len(charset), embed)
     {'N', '2', '1', '4', '\n', '5', 'r', 'n', ')', '6', 'o', 'S', '\\', 'P', 'H', ']', 'c', '(', 's', '7', 'C', '#', '0', '+', '8', '@', 'I', '1', '-', 'B', '/', 'F', 'E', '[', '3', '!', '='}
     37 115
def vectorize(smiles):
        one_hot = np.zeros((smiles.shape[0], embed , len(charset)),dtype=np.int8)
        for i,smile in enumerate(smiles):
            #encode the startchar
            one_hot[i,0,char_to_int["!"]] = 1
            #encode the rest of the chars
            for j,c in enumerate(smile):
                one_hot[i,j+1,char_to_int[c]] = 1
            #Encode endchar
            one_hot[i,len(smile)+1:,char_to_int["E"]] = 1
        #Return two, one for input and the other for output
        return one_hot[:,0:-1,:], one_hot[:,1:,:]
X_train, Y_train = vectorize(smiles_train.values)
X_test,Y_test = vectorize(smiles_test.values)
print (smiles_train.iloc[0])
plt.matshow(X_train[0].T)
#print X_train.shape
```

130.3 MD

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```
Cc1cc(F)cc([C@H](N)C2([NH+](C)C)CCC2)c1
     <matplotlib.image.AxesImage at 0x7f3457233a20>
       0
                                     40
                                                   60
                                                                  80
                                                                                 100
                      20
      5 -
     10 -
     15 -
     20 -
     25 -
print (X_train.shape)
     (187091, 114, 37)
"".join([int_to_char[idx] for idx in np.argmax(X_train[0,:,:], axis=1)])
     from keras.models import Model
from keras.layers import Input
from keras.layers import LSTM
from keras.layers import Dense
from keras.layers import Concatenate
from keras import regularizers
input_shape = X_train.shape[1:]
output_dim = Y_train.shape[-1]
latent_dim = 64
lstm_dim = 64
unroll = False
encoder_inputs = Input(shape=input_shape)
encoder = LSTM(lstm_dim, return_state=True,
              unroll=unroll)
encoder_outputs, state_h, state_c = encoder(encoder_inputs)
states = Concatenate(axis=-1)([state_h, state_c])
neck = Dense(latent_dim, activation="relu")
neck_outputs = neck(states)
decode_h = Dense(lstm_dim, activation="relu")
decode_c = Dense(lstm_dim, activation="relu")
state h decoded = decode h(neck outputs)
state_c_decoded = decode_c(neck_outputs)
encoder_states = [state_h_decoded, state_c_decoded]
decoder inputs = Input(shape=input shape)
decoder_lstm = LSTM(lstm_dim,
                  return_sequences=True,
                  unroll=unroll
decoder_outputs = decoder_lstm(decoder_inputs, initial_state=encoder_states)
decoder_dense = Dense(output_dim, activation='softmax')
decoder_outputs = decoder_dense(decoder_outputs)
#Define the model, that inputs the training vector for two places, and predicts one character ahead of the input
model = Model([encoder_inputs, decoder_inputs], decoder_outputs)
```

print (model.summary())

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```
Model: "model"
   Layer (type)
                          Output Shape
                                         Param #
                                                 Connected to
   ______
   input_2 (InputLayer)
                          [(None, 114, 37)]
                                         0
   lstm_1 (LSTM)
                          [(None, 64), (None,
                                         26112
                                                 input_2[0][0]
   concatenate_1 (Concatenate)
                                                 lstm_1[0][1]
                          (None, 128)
                                         0
                                                 lstm_1[0][2]
   dense_1 (Dense)
                          (None, 64)
                                         8256
                                                 concatenate_1[0][0]
   input_3 (InputLayer)
                          [(None, 114, 37)]
                                         0
   dense_2 (Dense)
                          (None, 64)
                                         4160
                                                 dense_1[0][0]
   dense_3 (Dense)
                          (None, 64)
                                         4160
                                                 dense_1[0][0]
   lstm_2 (LSTM)
                                         26112
                                                 input_3[0][0]
                          (None, 114, 64)
                                                 dense_2[0][0]
                                                 dense_3[0][0]
   dense_4 (Dense)
                          (None, 114, 37)
                                         2405
                                                 lstm_2[0][0]
   _______
   Total params: 71,205
   Trainable params: 71,205
   Non-trainable params: 0
   None
from keras.callbacks import History, ReduceLROnPlateau
h = History()
rlr = ReduceLROnPlateau(monitor='val_loss', factor=0.5,patience=10, min_lr=0.000001, verbose=1, epsilon=1e-5)
   WARNING:tensorflow:`epsilon` argument is deprecated and will be removed, use `min_delta` instead.
from keras.optimizers import RMSprop, Adam
opt=Adam(lr=0.005) #Default 0.001
model.compile(optimizer=opt, loss='categorical_crossentropy')
model.fit([X_train,X_train],Y_train,
              epochs=200,
              batch_size=256,
              shuffle=True,
              callbacks=[h, rlr],
              validation_data=[X_test,Y_test])
   Epoch 81/200
   Epoch 00081: ReduceLROnPlateau reducing learning rate to 1.9531249563442543e-05.
   Epoch 82/200
   Epoch 83/200
   Epoch 84/200
   Epoch 85/200
```

1 1/s 20ms/ston loss, 0 107/ val loss, 0 00000,00

```
/ 31 / / 31 | ----
Epoch 86/200
Epoch 87/200
Epoch 88/200
Epoch 89/200
Epoch 90/200
Epoch 91/200
Epoch 00091: ReduceLROnPlateau reducing learning rate to 9.765624781721272e-06.
Epoch 92/200
Epoch 93/200
Epoch 94/200
Epoch 95/200
Epoch 96/200
Epoch 97/200
Epoch 98/200
Epoch 99/200
Epoch 100/200
Epoch 00101: ReduceLROnPlateau reducing learning rate to 4.882812390860636e-06.
Epoch 102/200
Epoch 103/200
Epoch 104/200
Epoch 105/200
Epoch 106/200
Epoch 107/200
model.save('Lstm.h5')
```

nlt nlot(h history["los

plt.plot(h.history["loss"], label="Loss")
plt.plot(h.history["val\_loss"], label="Val\_Loss")
plt.yscale("log")
plt.legend()

```
<matplotlib.legend.Legend at 0x7f333e683a20>
      3 \times 10^{-1}
Encoder:
smiles_to_latent_model = Model(encoder_inputs, neck_outputs)
smiles_to_latent_model.save("smi2lat.h5")
Decoder:
latent_input = Input(shape=(latent_dim,))
state_h_decoded_2 = decode_h(latent_input)
state_c_decoded_2 = decode_c(latent_input)
latent_to_states_model = Model(latent_input, [state_h_decoded_2, state_c_decoded_2])
latent_to_states_model.save("lat2state.h5")
LSTM layer:
inf_decoder_inputs = Input(batch_shape=(1, 1, input_shape[1]))
inf_decoder_lstm = LSTM(lstm_dim,
                    return_sequences=True,
                    unroll=unroll,
                    stateful=True
inf_decoder_outputs = inf_decoder_lstm(inf_decoder_inputs)
inf_decoder_dense = Dense(output_dim, activation='softmax')
inf_decoder_outputs = inf_decoder_dense(inf_decoder_outputs)
sample_model = Model(inf_decoder_inputs, inf_decoder_outputs)
```

for i in range(1,3):
 sample\_model.layers[i].set\_weights(model.layers[i+6].get\_weights())
sample\_model.save("Mol\_model.h5")
sample\_model.summary()

Model: "model 3"

Layer (type)	Output Shape	Param #
input_5 (InputLayer)	[(1, 1, 37)]	0
lstm_3 (LSTM)	(1, 1, 64)	26112
dense_5 (Dense)	(1, 1, 37)	2405
Total params: 28,517		

Trainable params: 28,517

```
Non-trainable params: 0
```

Latest space

```
x_latent = smiles_to_latent_model.predict(X_test)
```

## Creating molecules from latent space

```
molno = 5
latent_mol = smiles_to_latent_model.predict(X_test[molno:molno+1])
sorti = np.argsort(np.sum(np.abs(x_latent - latent_mol), axis=1))
print(sorti[0:10])
print(smiles_test.iloc[sorti[0:8]])
Draw.MolsToImage(smiles_test.iloc[sorti[0:8]].apply(Chem.MolFromSmiles))
     5 55207 59917 28317 33822 50798 20098 59383 48052 15992
     19753
                CCC(CC)([C@0H](0)c1ccc(OC)cc1OC)[NH+](C)C\n
     2103
                CCC1CCC(0)([C@@]2(C[NH3+])CCOc3ccccc32)CC1\n
     10929
               CCCO[C@0H]1CCCN(c2ccc(S(N)(=0)=0)c(N)c2)C1\n
     73320
               CCC(=0)N1CCC(Cc2cc(NC3CCCC3)nc(C)[nH+]2)CC1\n
               CCC[NH2+][C@H](c1ccc(F)cc1)C(C)(C)N1CCOCC1\n
     67465
     193133
                CCC[C@H](0)CNC(=0)NCc1cccc([N+]2=CCCC2)c1\n
     67732
                  CCC(CC)[C@@H]([NH2+]C)[C@@H]1CN(CC)CCO1\n
     60031
                CCC[NH+]1CCC(N2CCN(c3cccc(C)[nH+]3)CC2)CC1\n
     Name: smiles, dtype: object
```

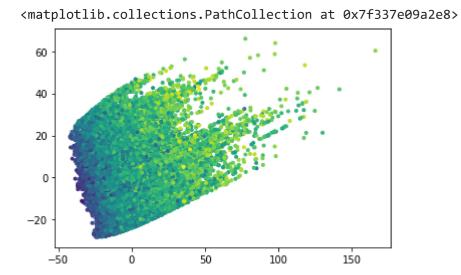
Draw.MolsToImage(smiles\_test.iloc[sorti[-8:]].apply(Chem.MolFromSmiles))



## ▼ Plotting molecules in latent space :

```
logp = smiles_test.apply(Chem.MolFromSmiles).apply(Descriptors.MolLogP)
from sklearn.decomposition import PCA
```

```
molwt = smiles_test.apply(Chem.MolFromSmiles).apply(Descriptors.MolMR)
plt.figure()
plt.scatter(red[:,0], red[:,1],marker='.', c= molwt)
```



## ▼ Interpolating between molecules

```
def latent_to_smiles(latent):
    #decode states and set Reset the LSTM cells with them
    states = latent_to_states_model.predict(latent)
    sample_model.layers[1].reset_states(states=[states[0],states[1]])
    #Prepare the input char
    startidx = char_to_int["!"]
    samplevec = np.zeros((1,1,37))
    samplevec[0,0,1] = 1
    smiles = ""
    #Loop and predict next char
    for i in range(37):
        o = sample_model.predict(samplevec)
        sampleidx = np.argmax(0)
```

```
samplechar = int_to_char[sampleidx]
        if samplechar != "E":
            smiles = smiles + int_to_char[sampleidx]
            samplevec = np.zeros((1,1,37))
            samplevec[0,0,sampleidx] = 1
        else:
            break
    return smiles
smiles = latent_to_smiles(x_latent[0:1])
print(smiles)
print(smiles_test.iloc[0])
     C[NH+]1CCC[C@H]1C(=0)NCC(=0)Nc1ccc(C
     C[NH+]1CCC(NC(=0)[C@H]2CCN(c3ccc(C1)c(C1)c3)C2=0)CC1
i = 0
j=2
latent1 = x_latent[j:j+1]
latent0 = x_latent[i:i+1]
mols1 = []
ratios = np.linspace(0,1,25)
for r in ratios:
    rlatent = (1.0-r)*latent0 + r*latent1
    smiles = latent_to_smiles(rlatent)
    mol = Chem.MolFromSmiles(smiles)
    if mol:
        mols1.append(mol)
    else:
        print(smiles)
     C[NH+]1CCC[C@H]1C(=0)NCC(=0)Nc1ccc(C
     COCCn1c(C)cc(NC(=0)N[C@@H](C)c2ccc(C(
     COC(=0)c1ccc(NC(=0)C(=0)N2CCC[C@@H](C
     COc1ccc(N2CCN(C(=0)C(=0)Nc3ccc(C(C)C)
     O=C(NC1CCCC1)[C@0H]1CCCN(C(=0)c2ccc(C
     O=C(NC1CCCC1)[C@@H]1CCCN(C(=0)c2ccc(C
     O=C(NCC1(c2cccc2)CCC1)N1CCN(C(=0)c2
     O=C(CCC1CCC1)N1CCC[C@@H](C(=O)N2CCC[
     O=C(Cc1cccc1)N1CCC[C@@H](C(=0)N2CCC[
     O=c1[nH]c(C(=0)N2CCC[C@@H]2c2cccc2)c
     N\#C[C@H](NC(=0)c2cccc2C1)C1(C1)C(=0
     N\#C[C@H](c2cccc2)N1C(=0)C[NH+]1CCC[
     NC(=0)c1ccc(CNC(=0)N2CCC[C@@H]2c2ccc(
     NC(=0)COc1ccc(C(=0)N2CCC[C@@H]2c2ccc(
     Cc1noc(CNC(=0)[C@@H]2CCCN(C(=0)c3ccc(
     Cc1n[nH]c1CCC(=0)N1CCC[C@0H](C(=0)Nc2
     Cc1n[nH]c1CCC(=0)N1CCC[C@0H](C(=0)Nc2
     Cc1nc(CCC(=0)NC[C@@H](C)C(=0)Nc2ccc(C
     Cc1c(C(=0)NCCc3ccccc3)ccc2[C@H](C)N(C
     Cc1cc(C)c(C(=0)NCCC[NH+](C)Cc3ccccc3)
     Cc1cc(C(=0)Nc3ccc(C(=0)NCc4cccc4)cc3
     Cc1cc(C(=0)Nc3ccc(C(=0)NCc4cccc4)cc3
     Cc1cc([C@H](C(=0)Nc4ccc(C1)cc4)CC3)c(
     Cc1ccc(C(=0)C(C)(C)C(=0)N2CCN(C)Cc2cc
     Cc1ccc(C(=0)C(C)(C)C(=0)N2CCN(C)C(=0)
```

```
len(smiles)
```

37

Sample around latent space to find molecules that can be plotted

```
latent = x_latent[0:1]
scale = 0.40
mols = []
for i in range(20):
    latent_r = latent + scale*(np.random.randn(latent.shape[1])) #TODO, try with
    smiles = latent to smiles(latent_r)
    mol = Chem.MolFromSmiles(smiles)
    if mol:
        mols.append(mol)
    else:
        print(smiles)
     C[NH+](CCC(=0)N1CCCC1)C(=0)N1CCC[C@@H
     C[C@H](NC(=O)N[C@@H]1CCC[C@@H]1C(=O)[
     C[NH+](C)CCNC(=0)N1CCC[C@@H](C(=0)Nc2
     C[NH+]1CCC[C@H]1C(=0)NCC(=0)Nc1ccc(C
     C[C@H](NC(=O)N[C@@H]1CCC[C@@H]1C(=O)N
     C[C@H](NC(=0)NC[C@@H]1CCCO1)c1ccc(C(=
     C[NH+](C)CCNC(=0)N1CCC[C@@H](C(=0)Nc2
     C[C@H](NC(=0)N[C@@H]1CCC[C@@H]1C(=0)[
     C[NH+](CCC(=0)N1CCCC1)C(=0)N1CCC[C@H
     C[NH+](CCC(=0)N1CCCC1)C(=0)N1CCC[C@@H
     C[NH+](CCC(=0)N1CCCC1)C(=0)N1CCC[C@@H
     C[NH+](C)CCNC(=0)N1CCC[C@H](C(=0)Nc2
     C[C@H](NC(=0)N1CCC[C@H](C(=0)Nc2cccc
     C[C@H](NC(=O)N[C@@H]1CCC[C@@H]1C(=O)[
     C[C@H](C(=0)N1CCCCC1)N1CCN(C(=0)c2ccc
     C[C@H](NC(=0)NC[C@@H]1CCCO1)[C@@H]1CC
     C[C@H](CC(=0)N1CCCCC1)[C@@H](C)[NH+]1
     C[NH+](C)CCNC(=0)N1CCC[C@@H](C(=0)Nc2
mols
     [<rdkit.Chem.rdchem.Mol at 0x7f3022c72710>,
      <rdkit.Chem.rdchem.Mol at 0x7f3022c72cb0>]
Draw.MolsToGridImage(mols, molsPerRow=5)
```

