final

December 12, 2024

0.1 Abstract

GPU in use:

0.2 Package import

```
[41]: import os
      os.environ["KERAS_BACKEND"] = "tensorflow"
      import ast
      import numpy as np
      from tensorflow import keras
[42]: #from tensorflow.keras import ops
      from tensorflow.keras import layers
      import pandas as pd
      from sklearn.model_selection import train_test_split
      import matplotlib.pyplot as plt
      from rdkit import Chem, RDLogger
      from rdkit.Chem import BondType
      from rdkit.Chem.Draw import MolsToGridImage
      from rdkit.Chem import Draw
      from rdkit import Chem
      from rdkit. Chem import rdmolops, AllChem
      from tensorflow.keras.regularizers import 11_12
      RDLogger.DisableLog("rdApp.*")
[43]: import tensorflow as tf
      print("TensorFlow version:", tf.__version__)
      print("GPU available:", tf.config.list_physical_devices('GPU'))
      print("GPU in use:", tf.test.gpu device name())
     TensorFlow version: 2.16.2
     GPU available: []
```

0.3 Database pharsing

```
[44]: '''
      read the entire dataset
      df = pd.read_csv('dataset1.csv')
      df.drop([0,1,2,3,4], inplace=True)
      df=df.rename(columns = {'PUBCHEM_EXT_DATASOURCE_SMILES':
       →'SMILES', 'PUBCHEM_ACTIVITY_OUTCOME': 'Activity', 'PUBCHEM_ACTIVITY_SCORE':

¬'Score'})
      columns_to_drop = [col for col in df.columns if col not in ['SMILES',_
       ⇔'Activity', 'Score', 'Potency', 'Efficacy']]
      df = df.drop(columns = columns_to_drop)
      #df=df.drop(['Unnamed: 3', 'Unnamed: 4', 'Unnamed: 5'], axis=1)
      df = df.dropna(subset=['SMILES'])
      df=df.fillna(0)
      print(df.head())
      print(df.info())
                                                    SMILES
                                                            Activity
                                                                      Score
     5
                  CNCC1=NC2=C(C=C(C=C2)C1)C(=N1)C3=CC=CN3
                                                           Inactive
                                                                        0.0
     6
                        CCSC(=NC1=CC=C(C=C1)C(F)(F)F)N.C1
                                                            Inactive
                                                                        0.0
     7 CCN(CC1=CC(=CC=C1)S(=0)(=0)[0-])C2=CC=C(C=C2)C... Inactive
                                                                      0.0
     8 CC1=CC=C(C=C1)S(=0)(=0)N2CCN(CC2)C3=NC(=NC4=CC... Inactive
                                                                      0.0
     9 CC1=CC=C(C=C1)S(=0)(=0)N2CCN(CC2)C3=NC(=NC4=CC... Inactive
                                                                      0.0
        Potency Efficacy
     5
            0.0
                      0.0
            0.0
                      0.0
     6
     7
            0.0
                      0.0
     8
            0.0
                      0.0
            0.0
                      0.0
     <class 'pandas.core.frame.DataFrame'>
     Index: 342051 entries, 5 to 342072
     Data columns (total 5 columns):
      #
          Column
                    Non-Null Count
                                     Dtype
          ____
                    -----
      0
          SMILES
                    342051 non-null object
      1
          Activity 342051 non-null object
      2
                    342051 non-null float64
          Score
                    342051 non-null float64
          Potency
          Efficacy 342051 non-null float64
     dtypes: float64(3), object(2)
     memory usage: 15.7+ MB
     None
```

```
[45]: valid_indices = []
      # Loop through each SMILES string in the DataFrame
      for i in range(len(df)):
          smiles = df.iloc[i]['SMILES'] # Use iloc for positional indexing
          # Convert SMILES to molecule
          mol = Chem.MolFromSmiles(smiles)
          # Check if the molecule is valid and has <= 50 atoms
          if mol is not None and mol.GetNumAtoms() <= 50:</pre>
              valid indices.append(i)
      # Filter the DataFrame to include only valid molecules
      df_50 = df.iloc[valid_indices]
[46]: df_50
[46]:
                                                         SMILES Activity
                                                                           Score \
     5
                        CNCC1=NC2=C(C=C(C=C2)C1)C(=N1)C3=CC=CN3
                                                                 Inactive
                                                                              0.0
      6
                              CCSC(=NC1=CC=C(C=C1)C(F)(F)F)N.Cl Inactive
                                                                              0.0
      8
              CC1=CC=C(C=C1)S(=0)(=0)N2CCN(CC2)C3=NC(=NC4=CC... Inactive
                                                                            0.0
              CC1=CC=C(C=C1)S(=0)(=0)N2CCN(CC2)C3=NC(=NC4=CC... Inactive
                                                                            0.0
              C1CN(CCN1C2=NC(=NC3=CC=CC=C32)C4=CC=CS4)S(=0)(... Inactive
      10
                                                                            0.0
      342068 CC(=0)NC1=CC=C(C=C1)OCC2=C(C=CC(=C2)CN(CC3=CC=... Inactive
                                                                            0.0
      342069 CC(=0)NC1=CC=C(C=C1)OCC2=C(C=C2)CN(CC3=CC=... Inactive
                                                                            0.0
      342070 CC(=0)NC1=CC=C(C=C1)OCC2=C(C=C2)CN(CC3=CC=... Inactive
                                                                            0.0
      342071 CC(=0)NC1=CC=C(C=C1)C(=0)N(CC2=CC=CC2)CC3=CC... Inactive
                                                                            0.0
      342072 CC(=0)NC1=CC=C(C=C1)OCC2=C(C=C2)CN(CC3=CC=... Inactive
                                                                            0.0
              Potency Efficacy
      5
                  0.0
                            0.0
                  0.0
      6
                            0.0
                  0.0
                            0.0
      8
                  0.0
                            0.0
      9
      10
                  0.0
                            0.0
      342068
                  0.0
                            0.0
      342069
                  0.0
                            0.0
      342070
                  0.0
                            0.0
                  0.0
                            0.0
      342071
      342072
                  0.0
                            0.0
      [341260 rows x 5 columns]
[47]: def is_charged(smiles):
          mol = Chem.MolFromSmiles(smiles)
          if not mol:
```

```
return False # Invalid SMILES
return any(atom.GetFormalCharge() != 0 for atom in mol.GetAtoms())
# Test the function
print(is_charged("CC1=C(SC(=C1C#N)NC(=0)C2=CC(C=C2)OC)[N+](=0)"))
```

True

```
[48]: df_50['Charged'] = df_50['SMILES'].apply(is_charged)
uncharged = df_50[df_50['Charged'] == False]
uncharged
```

/var/folders/jn/kkchdcr94t50xrmycsvkq2x80000gn/T/ipykernel_85584/162626946.py:1: SettingWithCopyWarning:

A value is trying to be set on a copy of a slice from a DataFrame. Try using .loc[row_indexer,col_indexer] = value instead

See the caveats in the documentation: https://pandas.pydata.org/pandas-docs/stable/user_guide/indexing.html#returning-a-view-versus-a-copy df_50['Charged'] = df_50['SMILES'].apply(is_charged)

[48]:		SMILES	S Activity	Score	\
	5	CNCC1=NC2=C(C=C(C=C2)C1)C(=N1)C3=CC=CN3	3 Inactive	0.0	
	6	CCSC(=NC1=CC=C(C=C1)C(F)(F)F)N.CC	l Inactive	0.0	
	8	CC1=CC=C(C=C1)S(=0)(=0)N2CCN(CC2)C3=NC(=NC4=CC	Inactive	0.0	
	9	CC1=CC=C(C=C1)S(=0)(=0)N2CCN(CC2)C3=NC(=NC4=CC	Inactive	0.0	
	10	C1CN(CCN1C2=NC(=NC3=CC=CC=C32)C4=CC=CS4)S(=0)(Inactive	0.0	
	•••	•••			
	342068	CC(=O) NC1 = CC = C(C = C1) OCC2 = C(C = CC(=C2) CN (CC3 = CC =)	Inactive	0.0	
	342069	CC(=O) NC1 = CC = C(C = C1) OCC2 = C(C = CC(=C2) CN (CC3 = CC =)	Inactive	0.0	
	342070	CC(=O) NC1 = CC = C(C = C1) OCC2 = C(C = CC(=C2) CN (CC3 = CC =)	Inactive	0.0	
	342071	CC(=O) NC1 = CC = C(C = C1) C(=O) N(CC2 = CC = CC = C2) CC3 = CC	Inactive	0.0	
	342072	CC(=O) NC1 = CC = C(C = C1) OCC2 = C(C = CC(=C2) CN (CC3 = CC =)	Inactive	0.0	
		D			

	Potency	Efficacy	Charged
5	0.0	0.0	False
6	0.0	0.0	False
8	0.0	0.0	False
9	0.0	0.0	False
10	0.0	0.0	False
	•••		
342068	0.0	0.0	False
342069	0.0	0.0	False
342070	0.0	0.0	False
342071	0.0	0.0	False
342072	0.0	0.0	False

[322199 rows x 6 columns]

```
[49]: # Picking all "Active" molecules from the dataset
     active_df = uncharged[uncharged['Activity'] == 'Active']
     active_df.info()
     # Picking all "Inactive" molecules from the dataset
     inactive_df = uncharged[uncharged['Activity'] == 'Inactive']
     inactive_df.info()
     # Randomly sample from inactive_df to match the size of active_df
     inactive_sampled = inactive_df.sample(n=len(active_df), random_state=42)
     # Combine the active and sampled inactive molecules
     balanced_df = pd.concat([active_df, inactive_sampled])
     # Shuffle the combined dataset
     balanced_df = balanced_df.sample(frac=1, random_state=42).reset_index(drop=True)
     balanced df.info()
     <class 'pandas.core.frame.DataFrame'>
     Index: 6273 entries, 13 to 341825
     Data columns (total 6 columns):
         Column
                 Non-Null Count Dtype
     --- -----
                  -----
         SMILES 6273 non-null object
      0
         Activity 6273 non-null object
      1
      2
         Score 6273 non-null float64
         Potency 6273 non-null
                                  float64
         Efficacy 6273 non-null float64
         Charged 6273 non-null
                                 bool
     dtypes: bool(1), float64(3), object(2)
     memory usage: 300.2+ KB
     <class 'pandas.core.frame.DataFrame'>
     Index: 304069 entries, 5 to 342072
     Data columns (total 6 columns):
                 Non-Null Count Dtype
         Column
         _____
                   _____
      0
         SMILES 304069 non-null object
         Activity 304069 non-null object
      1
                   304069 non-null float64
      2
         Score
                   304069 non-null float64
      3
         Potency
         Efficacy 304069 non-null float64
         Charged 304069 non-null bool
     dtypes: bool(1), float64(3), object(2)
     memory usage: 14.2+ MB
     <class 'pandas.core.frame.DataFrame'>
```

RangeIndex: 12546 entries, 0 to 12545 Data columns (total 6 columns): Column Non-Null Count Dtype 0 SMILES 12546 non-null object Activity 12546 non-null object 1 2 Score 12546 non-null float64 Potency 12546 non-null float64 Efficacy 12546 non-null float64 5 Charged 12546 non-null bool dtypes: bool(1), float64(3), object(2) memory usage: 502.5+ KB [50]: filtered_df = balanced_df filtered_df [50]: Activity Score \ SMILES 0 CC1=C(C=CC=C1Br)NC(=0)C2=C(C=CS2)N3C=CC=C3 Active 82.0 1 CCCCCC(C(C)CC(=0)NC1CCCCC1)C(=0)OActive 43.0 2 CC1=CC=C(C=C1)S(=0)(=0)NC2=NN3C(C=C(NC3=N2)C)C... Active 41.0 3 CC1=CC(=0) 0C2=C1C=C(C=C2) 0CC(=0) NC3=CC=CC(=C3)... Inactive 0.0 4 CC1=CC(=C(N1C)C)C(=0)COC(=0)C23CC4CC(C2)CC(C4)...Inactive 0.0 C1CN(CCN1C(=0)C2=CC=CC=C2CC3=CC=CC=C3)S(=0)(=0... 0.0 12541 Inactive 12542 C1=CC=C(C=C1)OC2=NC=NC(=C2)N3C=NC=N3 Active 64.0 12543 CC1=C(C(=CC=C1)N2CCN(CC2)C3=NC4=CC=CC=C4C(=0)N... Active 42.0 12544 CCC(C)NC(=0)CSC1=NC2=CC=CC=C2C3=NC(C(=0)N31)C4...Active 42.0 12545 CC(C)C1=CC=C(C=C1)S(=0)(=0)NC2CCCC2Inactive 0.0 Potency Efficacy Charged 0 8.9125 140.7280 False 1 12.5893 136.6590 False 2 22.3872 166.6580 False 3 0.0000 0.0000 False 4 0.0000 0.0000 False 12541 0.0000 0.0000 False False 12542 2.8184 74.9734 12543 17.7828 126.5240 False 12544 15.8489 139.3040 False 12545 0.0000 0.0000 False

[12546 rows x 6 columns]

0.4 Parameter setting

```
[51]: '''
      scan through all the molecules to obtain unique atom types
      smiles = filtered_df['SMILES'].tolist()
      search_elements=[]
      for smile in smiles:
          mol = Chem.MolFromSmiles(smile)
          atoms = list(set([atom.GetSymbol() for atom in mol.GetAtoms()]))
          search elements += atoms
          search_elements = list(set(search_elements))
      search elements.append("H")
      print(search_elements)
     ['C', 'F', 'N', 'I', 'O', 'P', 'Br', 'B', 'S', 'Cl', 'As', 'H']
[52]: '''
      Setting up the atom mapping and bond mapping.
      Code adopted from https://keras.io/examples/generative/molecule generation/
      SMILE_CHARSET = str(search_elements)
      bond mapping = {"SINGLE": 0, "DOUBLE": 1, "TRIPLE": 2, "AROMATIC": 3}
      bond_mapping.update(
          {0: BondType.SINGLE, 1: BondType.DOUBLE, 2: BondType.TRIPLE, 3: BondType.
       →AROMATIC}
      SMILE_CHARSET = ast.literal_eval(SMILE_CHARSET)
      MAX_MOLSIZE = max(filtered_df['SMILES'].str.len())
      SMILE_to_index = dict((c, i) for i, c in enumerate(SMILE_CHARSET))
      index_to_SMILE = dict((i, c) for i, c in enumerate(SMILE_CHARSET))
      atom_mapping = dict(SMILE_to_index)
      atom_mapping.update(index_to_SMILE)
      print(atom_mapping)
      print("Max molecule size: {}".format(MAX_MOLSIZE))
      print("Character set Length: {}".format(len(SMILE CHARSET)))
     {'C': 0, 'F': 1, 'N': 2, 'I': 3, 'O': 4, 'P': 5, 'Br': 6, 'B': 7, 'S': 8, 'Cl':
     9, 'As': 10, 'H': 11, 0: 'C', 1: 'F', 2: 'N', 3: 'I', 4: 'O', 5: 'P', 6: 'Br',
     7: 'B', 8: 'S', 9: 'Cl', 10: 'As', 11: 'H'}
     Max molecule size: 117
     Character set Length: 12
```

0.5 Hyperparameters

```
[53]:

Defining the Hyperparameters of the model

NUM_ATOMS = 50 #Max number of atoms

ATOM_DIM = len(SMILE_CHARSET) # Number of atom types

BOND_DIM = 5 # Number of bond types
```

0.6 Molecule featurization

```
[54]: '''
      Defining functions to convert smiles string into node graph and recover
       \hookrightarrow molecule structure from it.
      Code referenced from: https://keras.io/examples/generative/molecule_generation/
      def smiles_to_graph(smiles):
          Reference: https://keras.io/examples/generative/wgan-graphs/
          # Converts SMILES to molecule object
          molecule = Chem.MolFromSmiles(smiles)
          #molecule = Chem.AddHs(molecule)
          # Initialize adjacency and feature tensor
          adjacency = np.zeros((BOND_DIM, NUM_ATOMS, NUM_ATOMS), "float32")
          features = np.zeros((NUM_ATOMS, ATOM_DIM), "float32")
          # loop over each atom in molecule
          for atom in molecule.GetAtoms():
              i = atom.GetIdx()
              atom_type = atom_mapping[atom.GetSymbol()]
              features[i] = np.eye(ATOM_DIM)[atom_type]
              # loop over one-hop neighbors
              for neighbor in atom.GetNeighbors():
                  j = neighbor.GetIdx()
                  bond = molecule.GetBondBetweenAtoms(i, j)
                  bond_type_idx = bond_mapping[bond.GetBondType().name]
                  adjacency[bond_type_idx, [i, j], [j, i]] = 1
          # Where no bond, add 1 to last channel (indicating "non-bond")
          # Notice: channels-first
          adjacency[-1, np.sum(adjacency, axis=0) == 0] = 1
          # Where no atom, add 1 to last column (indicating "non-atom")
```

```
features[np.where(np.sum(features, axis=1) == 0)[0], -1] = 1
   return adjacency, features
def graph_to_molecule(adjacency, features):
    # RWMol is a molecule object intended to be edited
   molecule = Chem.RWMol()
    # Remove "no atoms" & atoms with no bonds
   keep_idx = np.where(
        (np.argmax(features, axis=1) != ATOM_DIM - 1)
        & (np.sum(adjacency[:-1], axis=(0, 1)) > 0))[0]
   features = features[keep idx]
   adjacency = adjacency[:, keep_idx][:, :, keep_idx]
    # Add atoms to molecule
   for atom_type_idx in np.argmax(features, axis=1):
        atom = Chem.Atom(atom_mapping[atom_type_idx])
        _ = molecule.AddAtom(atom)
   added_bonds = set()
    (bonds_ij, atoms_i, atoms_j) = np.where(np.triu(adjacency) == 1)
   for (bond_ij, atom_i, atom_j) in zip(bonds_ij, atoms_i, atoms_j):
        if atom_i == atom_j or bond_ij == BOND_DIM - 1:
            continue
       bond_type = bond_mapping.get(bond_ij, None)
        if (atom_i, atom_j) in added_bonds or (atom_j, atom_i) in added_bonds:
            continue
       molecule.AddBond(int(atom_i), int(atom_j), bond_type)
        added_bonds.add((atom_i, atom_j))
     # Sanitize without Kekulization
   try:
        Chem.SanitizeMol(molecule, sanitizeOps=Chem.SanitizeFlags.SANITIZE_ALL_
 → Chem.SanitizeFlags.SANITIZE_KEKULIZE)
    except Exception as e:
       print(f"Sanitization failed: {e}")
       return None
   # Add explicit hydrogens
   molecule_with_h = Chem.AddHs(molecule)
   # Fix aromaticity in aromatic rings
   for atom in molecule_with_h.GetAtoms():
        if atom.GetIsAromatic():
```

```
atom.SetIsAromatic(False) # Clear aromaticity if needed

# Force Kekulization to alternate bond orders in aromatic rings

try:
    Chem.Kekulize(molecule_with_h, clearAromaticFlags=True)

except Chem.KekulizeException as e:
    print(f"Kekulization failed: {e}")
    return molecule_with_h # Return molecule without Kekulé bonds

return molecule_with_h
```

0.7 Building model

```
[55]: '''
          Defining GCN
          Reference: https://keras.io/examples/generative/wgan-graphs/
          The Encoder takes as input a molecule's graph adjacency matrix and feature \Box
       \hookrightarrow matrix.
      111
      class RelationalGraphConvLayer(keras.layers.Layer):
          def __init__(
              self,
              units=128,
              activation="relu",
              use_bias=False,
              kernel_initializer="glorot_uniform",
              bias initializer="zeros",
              kernel_regularizer=None,
              bias_regularizer=None,
              **kwargs
          ):
              super().__init__(**kwargs)
              self.units = units
              self.activation = keras.activations.get(activation)
              self.use_bias = use_bias
              self.kernel_initializer = keras.initializers.get(kernel_initializer)
              self.bias_initializer = keras.initializers.get(bias_initializer)
              self.kernel_regularizer = keras.regularizers.get(kernel_regularizer)
              self.bias_regularizer = keras.regularizers.get(bias_regularizer)
          def build(self, input_shape):
              bond_dim = input_shape[0][1]
              atom_dim = input_shape[1][2]
              self.kernel = self.add_weight(
                  shape=(bond_dim, atom_dim, self.units),
```

```
initializer=self.kernel_initializer,
        regularizer=self.kernel_regularizer,
        trainable=True,
        name="W",
        dtype=tf.float32,
    )
    if self.use_bias:
        self.bias = self.add weight(
            shape=(bond_dim, 1, self.units),
            initializer=self.bias initializer,
            regularizer=self.bias_regularizer,
            trainable=True,
            name="b",
            dtype=tf.float32,
        )
    self.built = True
def call(self, inputs, training=False):
    adjacency, features = inputs
    # Aggregate information from neighbors
    x = tf.matmul(adjacency, features[:, None, :, :])
    # Apply linear transformation
    x = tf.matmul(x, self.kernel)
    if self.use bias:
        x += self.bias
    # Reduce bond types dim
    x_reduced = tf.reduce_sum(x, axis=1)
    # Apply non-linear transformation
    return self.activation(x_reduced)
```

0.8 Build the Encoder and Decoder

```
# Graph convolution layers
    features_transformed = features
    for units in gconv_units:
        features_transformed = RelationalGraphConvLayer(units)(
            [adjacency, features_transformed]
        )
    # Reduce 2D representation to 1D
    x = keras.layers.GlobalAveragePooling1D()(features_transformed)
    # Concatenate the score (condition) to the reduced graph representation
    x = keras.layers.Concatenate()([x, scores])
    # Fully connected layers
    for units in dense_units:
        x = layers.Dense(units, activation="relu", u
 →kernel_regularizer=regularizer)(x)
        x = layers.Dropout(dropout_rate)(x)
    # Latent space
    z_mean = layers.Dense(latent_dim, name="z_mean")(x)
    z_log_var = layers.Dense(latent_dim, name="z_log_var")(x)
    # Create encoder model
    encoder = keras.Model(inputs=[adjacency, features, scores],__
 →outputs=[z_mean, z_log_var], name="encoder")
    encoder.summarv()
    return encoder
class SymmetrizeLayer(layers.Layer):
    def call(self, x):
        return (x + tf.transpose(x, (0, 1, 3, 2))) / 2
def get_decoder(dense_units, latent_dim, adjacency_shape, feature_shape, u
 →dropout_rate, regularizer=None):
    latent_input = keras.Input(shape=(latent_dim,), name="latent_input")
    scores = keras.Input(shape=(1,), name="score_input") # Conditional input_
 \hookrightarrow (scalar)
    # Concatenate latent input with the conditional score
    x = keras.layers.Concatenate()([latent_input, scores])
    # Dense layers
    for units in dense_units:
```

```
x = keras.layers.Dense(units, activation="tanh", __
→kernel_regularizer=regularizer)(x)
      x = keras.layers.Dropout(dropout_rate)(x)
  # Adjacency reconstruction
  adj output = keras.layers.Dense(tf.math.reduce prod(adjacency shape).
→numpy().astype(int))(x)
  adj_output = keras.layers.Reshape(adjacency_shape)(adj_output)
  adj_output = SymmetrizeLayer()(adj_output)
  adj_output = keras.layers.Softmax(axis=1)(adj_output)
  # Feature reconstruction
  feat_output = keras.layers.Dense(tf.math.reduce_prod(feature_shape).numpy().
→astype(int))(x)
  feat_output = keras.layers.Reshape(feature_shape)(feat_output)
  feat_output = keras.layers.Softmax(axis=2)(feat_output)
  # Create decoder model
  decoder = keras.Model(inputs=[latent_input, scores], outputs=[adj_output,_u

¬feat_output], name="decoder")
  decoder.summary()
  return decoder
```

0.9 Build the VAE

```
[57]: ['''
      defining the VAE
      Code adopted and modified from https://keras.io/examples/generative/
       →molecule generation/
      ,,,
      class VAE(keras.Model):
          def __init__(self, encoder, decoder, beta=1.0, **kwargs):
              super(VAE, self).__init__(**kwargs)
              self.encoder = encoder
              self.decoder = decoder
              self.beta = beta
          def call(self, inputs):
              adjacency, features, scores = inputs
              z_mean, z_log_var = self.encoder([adjacency, features, scores])
              z = self.reparameterize(z_mean, z_log_var)
              return self.decoder([z, scores])
          def sampling(self, args):
              n n n
              Reparameterization trick: Sample from a Gaussian distribution using
```

```
z = z_mean + epsilon * exp(z_log_var / 2), where epsilon is sampled_\( \)
from N(0, 1).

"""

z_mean, z_log_var = args
batch = tf.shape(z_mean)[0]
dim = tf.shape(z_mean)[1]
epsilon = tf.keras.backend.random_normal(shape=(batch, dim)) #\( \)
$\infty Standard normal noise
return z_mean + tf.exp(0.5 * z_log_var) * epsilon
```

0.10 Model training

```
[58]: '''
      splitting the dataset into training and testing
      train, test = train_test_split(filtered_df,test_size=0.2,random_state=42)
      train_df, val_df = train_test_split(train, test_size=0.2, random_state=42)
      train_df.reset_index(drop=True, inplace=True)
      val df.reset index(drop=True, inplace=True)
      test.reset_index(drop=True, inplace=True)
      adj_train, fea_train, score_train = [], [], []
      adj_val, fea_val, score_val = [], [], []
      for idx in range(len(train_df)):
          adjacency, features = smiles_to_graph(train_df.loc[idx]["SMILES"])
          score = train_df.loc[idx]["Score"]
          adj_train.append(adjacency)
          fea_train.append(features)
          score_train.append(score)
      for idx in range(len(val df)):
          adjacency, features = smiles_to_graph(val_df.loc[idx]["SMILES"])
          score = val df.loc[idx]["Score"]
          adj val.append(adjacency)
          fea_val.append(features)
          score val.append(score)
      adj_train = np.array(adj_train)
      fea_train = np.array(fea_train)
      score_train_ = np.array(score_train).reshape(-1,1)
      adj_val = np.array(adj_val)
      fea_val = np.array(fea_val)
      score_val_ = np.array(score_val).reshape(-1,1)
```

```
[59]: from sklearn.preprocessing import MinMaxScaler
      scaler = MinMaxScaler()
      score_train_n = scaler.fit_transform(score_train_)
      score_val_n = scaler.transform(score_val_)
[60]: print(adj_train.shape)
      print(fea_train.shape)
      print(score_train_.shape)
      print(adj_val.shape)
      print(fea_val.shape)
      print(score_val_.shape)
     (8028, 5, 50, 50)
     (8028, 50, 12)
     (8028, 1)
     (2008, 5, 50, 50)
     (2008, 50, 12)
     (2008, 1)
[61]: print(np.max(score_train_n))
     0.999999999999999
[62]: #Hyperparameters
      BATCH SIZE = 64
      EPOCHS = 25
      VAE_LR = 3e-4 \# changed to 1e-3
      LATENT_DIM = 256 # Size of the latent space
[63]: '''
      compiling the VAE
      I I I
      encoder = get_encoder(
          gconv_units=[16],
          adjacency_shape=(BOND_DIM, NUM_ATOMS, NUM_ATOMS),
          feature_shape=(NUM_ATOMS, ATOM_DIM),
          latent_dim=LATENT_DIM,
          dense_units=[256, 512],
          dropout_rate=0,
          regularizer=11_12(11=1e-6, 12=1e-3)
      decoder = get_decoder(
          dense_units=[128, 256, 512],
          dropout_rate=0.3,
          latent_dim=LATENT_DIM,
```

```
adjacency_shape=(BOND_DIM, NUM_ATOMS, NUM_ATOMS),
  feature_shape=(NUM_ATOMS, ATOM_DIM),
  regularizer=11_12(l1=1e-4, l2=1e-2)
)
vae = VAE(encoder, decoder)
vae.compile(optimizer=keras.optimizers.Adam(learning_rate=VAE_LR))
```

Model: "encoder"

Layer (type)	Output Shape	Param #	Connected to
adjacency_input (InputLayer)	(None, 5, 50, 50)	0	-
<pre>feature_input (InputLayer)</pre>	(None, 50, 12)	0	-
relational_graph_c (RelationalGraphCo	(None, 50, 16)	960	<pre>adjacency_input[feature_input[0]</pre>
global_average_poo (GlobalAveragePool	(None, 16)	0	relational_graph
<pre>score_input (InputLayer)</pre>	(None, 1)	0	-
<pre>concatenate_2 (Concatenate)</pre>	(None, 17)	0	<pre>global_average_p score_input[0][0]</pre>
dense_7 (Dense)	(None, 256)	4,608	concatenate_2[0]
dropout_5 (Dropout)	(None, 256)	0	dense_7[0][0]
dense_8 (Dense)	(None, 512)	131,584	dropout_5[0][0]
<pre>dropout_6 (Dropout)</pre>	(None, 512)	0	dense_8[0][0]
z_mean (Dense)	(None, 256)	131,328	dropout_6[0][0]
z_log_var (Dense)	(None, 256)	131,328	dropout_6[0][0]

Total params: 399,808 (1.53 MB)

Trainable params: 399,808 (1.53 MB)

Non-trainable params: 0 (0.00 B)

Model: "decoder"

Layer (type)	Output	Shape	Param #	Connected to
<pre>latent_input (InputLayer)</pre>	(None,	256)	0	-
<pre>score_input (InputLayer)</pre>	(None,	1)	0	-
<pre>concatenate_3 (Concatenate)</pre>	(None,	257)	0	<pre>latent_input[0][score_input[0][0]</pre>
dense_9 (Dense)	(None,	128)	33,024	concatenate_3[0]
<pre>dropout_7 (Dropout)</pre>	(None,	128)	0	dense_9[0][0]
dense_10 (Dense)	(None,	256)	33,024	dropout_7[0][0]
dropout_8 (Dropout)	(None,	256)	0	dense_10[0][0]
dense_11 (Dense)	(None,	512)	131,584	dropout_8[0][0]
dropout_9 (Dropout)	(None,	512)	0	dense_11[0][0]
dense_12 (Dense)	(None,	12500)	6,412,500	dropout_9[0][0]
reshape_2 (Reshape)	(None,	5, 50, 50)	0	dense_12[0][0]
dense_13 (Dense)	(None,	600)	307,800	dropout_9[0][0]
<pre>symmetrize_layer_1 (SymmetrizeLayer)</pre>	(None,	5, 50, 50)	0	reshape_2[0][0]
reshape_3 (Reshape)	(None,	50, 12)	0	dense_13[0][0]
softmax_2 (Softmax)	(None,	5, 50, 50)	0	symmetrize_layer
softmax_3 (Softmax)	(None,	50, 12)	0	reshape_3[0][0]

```
Total params: 6,917,932 (26.39 MB)
      Trainable params: 6,917,932 (26.39 MB)
      Non-trainable params: 0 (0.00 B)
[64]: val loss list = []
      train_loss_list = []
      kl_{theshold} = 1.0
[65]: train_dataset = tf.data.Dataset.from_tensor_slices((adj_train, fea_train,
      ⇒score_train_)).batch(BATCH_SIZE)
      val_dataset = tf.data.Dataset.from_tensor_slices((adj_val, fea_val,_
       ⇒score_val_)).batch(BATCH_SIZE)
[66]: for epoch in range(EPOCHS):
          print(f"Epoch {epoch + 1}/{EPOCHS}")
          if epoch < 10:</pre>
              beta = 0.05
          else:
              beta = epoch*0.01
          # Training Loop
          train_loss = 0
          for (adjacency, features, scores) in train_dataset:
              with tf.GradientTape() as tape:
                  # Forward pass
                  z_mean, z_log_var = vae.encoder([adjacency, features, scores])
                  z = vae.sampling([z_mean, z_log_var])
                  adj_reconstruction, feature_reconstruction = vae.decoder([z,_
       ⇔scores])
                  # Compute losses
                  adj_loss = tf.reduce_mean(
                      tf.reduce_sum(keras.losses.binary_crossentropy(adjacency,_
       →adj_reconstruction), axis=(1, 2))
                  feat_loss = tf.reduce_mean(
                      tf.reduce_sum(keras.losses.categorical_crossentropy(features,_
       →feature_reconstruction), axis=1)
                  reconstruction_loss = adj_loss + feat_loss
                  kl_loss = -0.5 * tf.reduce_mean(
                      tf.reduce_sum(1 + z_log_var - tf.square(z_mean) - tf.
       →exp(z_log_var), axis=1)
```

```
total_loss = reconstruction_loss + beta * kl_loss
      # Backpropagation
      grads = tape.gradient(total_loss, vae.trainable_weights)
      vae.optimizer.apply_gradients(zip(grads, vae.trainable_weights))
      train_loss += total_loss
  train_loss /= len(train_dataset)
  train loss list.append(train loss)
  print(f"Train Loss: {train_loss.numpy()}, KL Loss: {kl_loss.numpy()},
→ Reconstruction Loss: {reconstruction_loss.numpy()}")
  # Validation Loop
  val loss = 0
  for (val_adjacency, val_features, val_scores) in val_dataset:
      # Forward pass
      z_mean, z_log_var = vae.encoder([val_adjacency, val_features,_
→val scores])
      z = vae.sampling([z_mean, z_log_var])
      val_adj_reconstruction, val_feat_reconstruction = vae.decoder([z,_
⇔val_scores])
      # Compute losses
      val_adj_loss = tf.reduce_mean(
          tf.reduce_sum(keras.losses.binary_crossentropy(val_adjacency,_
→val_adj_reconstruction), axis=(1, 2))
      val_feat_loss = tf.reduce_mean(
          tf.reduce_sum(keras.losses.categorical_crossentropy(val_features,_
→val feat reconstruction), axis=1)
      val_reconstruction_loss = val_adj_loss + val_feat_loss
      val_kl_loss = -0.5 * tf.reduce_mean(
          tf.reduce_sum(1 + z_log_var - tf.square(z_mean) - tf.
→exp(z_log_var), axis=1)
      val_total_loss = val_reconstruction_loss + beta * val_kl_loss
      val_loss += val_total_loss
  val_loss /= len(val_dataset)
  val_loss_list.append(val_loss)
```

```
# Adjust beta if KL loss is very low
    if kl loss < kl theshold:</pre>
        beta = 0.05
    print(f"Validation Loss: {val_loss.numpy()}, KL Loss: {val_kl_loss.
  numpy()}, Reconstruction Loss: {val_reconstruction_loss.numpy()}")
    print('BETA is: ', beta)
Epoch 1/25
2024-12-12 17:21:02.544078: W tensorflow/core/framework/local_rendezvous.cc:404]
Local rendezvous is aborting with status: OUT_OF_RANGE: End of sequence
Train Loss: 68.91028594970703, KL Loss: 7.779871940612793, Reconstruction Loss:
36.89194869995117
2024-12-12 17:21:03.088554: W tensorflow/core/framework/local_rendezvous.cc:404]
Local rendezvous is aborting with status: OUT_OF_RANGE: End of sequence
Validation Loss: 38.474632263183594, KL Loss: 8.145179748535156, Reconstruction
Loss: 35.19890213012695
BETA is: 0.05
Epoch 2/25
2024-12-12 17:21:11.252029: W tensorflow/core/framework/local_rendezvous.cc:404]
Local rendezvous is aborting with status: OUT OF RANGE: End of sequence
Train Loss: 38.19132614135742, KL Loss: 6.249152183532715, Reconstruction Loss:
36.3538703918457
2024-12-12 17:21:11.743643: W tensorflow/core/framework/local_rendezvous.cc:404]
Local rendezvous is aborting with status: OUT_OF_RANGE: End of sequence
Validation Loss: 37.70018768310547, KL Loss: 6.261404514312744, Reconstruction
Loss: 34.54112243652344
BETA is: 0.05
Epoch 3/25
2024-12-12 17:21:20.409496: W tensorflow/core/framework/local rendezvous.cc:404]
Local rendezvous is aborting with status: OUT_OF_RANGE: End of sequence
Train Loss: 34.51367950439453, KL Loss: 13.664953231811523, Reconstruction Loss:
31.250965118408203
2024-12-12 17:21:20.986430: W tensorflow/core/framework/local_rendezvous.cc:404]
Local rendezvous is aborting with status: OUT OF RANGE: End of sequence
Validation Loss: 32.2878532409668, KL Loss: 15.250144004821777, Reconstruction
Loss: 29.549442291259766
BETA is: 0.05
Epoch 4/25
2024-12-12 17:21:29.239712: W tensorflow/core/framework/local_rendezvous.cc:404]
```

Local rendezvous is aborting with status: OUT_OF_RANGE: End of sequence

Train Loss: 31.502199172973633, KL Loss: 15.679722785949707, Reconstruction Loss: 29.572856903076172

2024-12-12 17:21:29.762721: W tensorflow/core/framework/local_rendezvous.cc:404] Local rendezvous is aborting with status: OUT_OF_RANGE: End of sequence

Validation Loss: 30.959915161132812, KL Loss: 16.123620986938477, Reconstruction Loss: 27.809680938720703

BETA is: 0.05 Epoch 5/25

2024-12-12 17:21:38.111342: W tensorflow/core/framework/local_rendezvous.cc:404] Local rendezvous is aborting with status: OUT_OF_RANGE: End of sequence

Train Loss: 30.889602661132812, KL Loss: 22.45930290222168, Reconstruction Loss: 29.952455520629883

2024-12-12 17:21:38.646042: W tensorflow/core/framework/local_rendezvous.cc:404] Local rendezvous is aborting with status: OUT_OF_RANGE: End of sequence

Validation Loss: 31.159833908081055, KL Loss: 23.79697608947754, Reconstruction Loss: 27.594343185424805

BETA is: 0.05 Epoch 6/25

2024-12-12 17:21:46.881732: W tensorflow/core/framework/local_rendezvous.cc:404] Local rendezvous is aborting with status: OUT_OF_RANGE: End of sequence

Train Loss: 30.447965621948242, KL Loss: 15.691713333129883, Reconstruction Loss: 29.284475326538086

2024-12-12 17:21:47.390822: W tensorflow/core/framework/local_rendezvous.cc:404] Local rendezvous is aborting with status: OUT_OF_RANGE: End of sequence

Validation Loss: 30.32613754272461, KL Loss: 16.700641632080078, Reconstruction Loss: 27.07956886291504

BETA is: 0.05 Epoch 7/25

2024-12-12 17:21:55.525929: W tensorflow/core/framework/local_rendezvous.cc:404] Local rendezvous is aborting with status: OUT_OF_RANGE: End of sequence

Train Loss: 30.181785583496094, KL Loss: 16.22941017150879, Reconstruction Loss: 28.883907318115234

2024-12-12 17:21:56.042309: W tensorflow/core/framework/local_rendezvous.cc:404] Local rendezvous is aborting with status: OUT_OF_RANGE: End of sequence

Validation Loss: 30.266613006591797, KL Loss: 18.08345603942871, Reconstruction Loss: 27.33583641052246

BETA is: 0.05 Epoch 8/25

2024-12-12 17:22:04.189308: W tensorflow/core/framework/local_rendezvous.cc:404] Local rendezvous is aborting with status: OUT_OF_RANGE: End of sequence

Train Loss: 30.127744674682617, KL Loss: 20.35752296447754, Reconstruction Loss: 28.729433059692383

2024-12-12 17:22:04.692006: W tensorflow/core/framework/local_rendezvous.cc:404] Local rendezvous is aborting with status: OUT_OF_RANGE: End of sequence

Validation Loss: 30.800703048706055, KL Loss: 25.1715145111084, Reconstruction

Loss: 26.672801971435547

BETA is: 0.05 Epoch 9/25

2024-12-12 17:22:12.987030: W tensorflow/core/framework/local_rendezvous.cc:404] Local rendezvous is aborting with status: OUT_OF_RANGE: End of sequence

Train Loss: 30.214324951171875, KL Loss: 18.05396842956543, Reconstruction Loss: 28.242427825927734

2024-12-12 17:22:13.494476: W tensorflow/core/framework/local_rendezvous.cc:404] Local rendezvous is aborting with status: OUT_OF_RANGE: End of sequence

Validation Loss: 30.074146270751953, KL Loss: 21.178232192993164, Reconstruction

Loss: 26.774690628051758

BETA is: 0.05 Epoch 10/25

2024-12-12 17:22:21.702547: W tensorflow/core/framework/local_rendezvous.cc:404] Local rendezvous is aborting with status: OUT_OF_RANGE: End of sequence

Train Loss: 29.747447967529297, KL Loss: 17.097835540771484, Reconstruction Loss: 28.723173141479492

2024-12-12 17:22:22.195476: W tensorflow/core/framework/local_rendezvous.cc:404] Local rendezvous is aborting with status: OUT_OF_RANGE: End of sequence

Validation Loss: 29.811180114746094, KL Loss: 18.44583511352539, Reconstruction Loss: 26.424243927001953

BETA is: 0.05 Epoch 11/25

2024-12-12 17:22:30.591361: W tensorflow/core/framework/local_rendezvous.cc:404] Local rendezvous is aborting with status: OUT_OF_RANGE: End of sequence

Train Loss: 31.037004470825195, KL Loss: 12.73255443572998, Reconstruction Loss: 29.01826286315918

2024-12-12 17:22:31.091786: W tensorflow/core/framework/local_rendezvous.cc:404] Local rendezvous is aborting with status: OUT_OF_RANGE: End of sequence

Validation Loss: 30.877723693847656, KL Loss: 14.323649406433105, Reconstruction Loss: 27.287395477294922

BETA is: 0.1 Epoch 12/25

2024-12-12 17:22:39.209865: W tensorflow/core/framework/local_rendezvous.cc:404] Local rendezvous is aborting with status: OUT_OF_RANGE: End of sequence

Train Loss: 30.499980926513672, KL Loss: 10.85240364074707, Reconstruction Loss: 28.324087142944336

2024-12-12 17:22:39.745998: W tensorflow/core/framework/local_rendezvous.cc:404] Local rendezvous is aborting with status: OUT_OF_RANGE: End of sequence

Validation Loss: 30.541812896728516, KL Loss: 11.892852783203125, Reconstruction Loss: 26.887807846069336

BETA is: 0.11 Epoch 13/25

2024-12-12 17:22:48.002980: W tensorflow/core/framework/local_rendezvous.cc:404] Local rendezvous is aborting with status: OUT_OF_RANGE: End of sequence

Train Loss: 30.403913497924805, KL Loss: 10.170090675354004, Reconstruction Loss: 28.70667266845703

2024-12-12 17:22:48.517025: W tensorflow/core/framework/local_rendezvous.cc:404] Local rendezvous is aborting with status: OUT_OF_RANGE: End of sequence

Validation Loss: 30.583871841430664, KL Loss: 11.136874198913574, Reconstruction Loss: 27.300884246826172

BETA is: 0.12 Epoch 14/25

2024-12-12 17:22:56.771999: W tensorflow/core/framework/local_rendezvous.cc:404] Local rendezvous is aborting with status: OUT_OF_RANGE: End of sequence

Train Loss: 30.579753875732422, KL Loss: 13.000872611999512, Reconstruction Loss: 28.078094482421875

2024-12-12 17:22:57.325739: W tensorflow/core/framework/local_rendezvous.cc:404] Local rendezvous is aborting with status: OUT_OF_RANGE: End of sequence

Validation Loss: 30.881484985351562, KL Loss: 15.099629402160645, Reconstruction Loss: 26.69998550415039

BETA is: 0.13 Epoch 15/25

2024-12-12 17:23:05.608689: W tensorflow/core/framework/local_rendezvous.cc:404] Local rendezvous is aborting with status: OUT_OF_RANGE: End of sequence

Train Loss: 30.937511444091797, KL Loss: 8.691962242126465, Reconstruction Loss: 28.908405303955078

2024-12-12 17:23:06.118145: W tensorflow/core/framework/local_rendezvous.cc:404] Local rendezvous is aborting with status: OUT_OF_RANGE: End of sequence

Validation Loss: 30.21919059753418, KL Loss: 8.964917182922363, Reconstruction Loss: 26.512496948242188

BETA is: 0.14 Epoch 16/25

2024-12-12 17:23:14.447687: W tensorflow/core/framework/local_rendezvous.cc:404] Local rendezvous is aborting with status: OUT_OF_RANGE: End of sequence

Train Loss: 30.1827335357666, KL Loss: 7.548756122589111, Reconstruction Loss: 28.51205062866211

2024-12-12 17:23:14.970779: W tensorflow/core/framework/local_rendezvous.cc:404] Local rendezvous is aborting with status: OUT_OF_RANGE: End of sequence

Validation Loss: 30.00826072692871, KL Loss: 8.155345916748047, Reconstruction Loss: 26.154333114624023

BETA is: 0.15 Epoch 17/25

2024-12-12 17:23:23.180159: W tensorflow/core/framework/local_rendezvous.cc:404] Local rendezvous is aborting with status: OUT_OF_RANGE: End of sequence

Train Loss: 30.075735092163086, KL Loss: 8.922811508178711, Reconstruction Loss: 28.410953521728516

2024-12-12 17:23:23.701358: W tensorflow/core/framework/local_rendezvous.cc:404] Local rendezvous is aborting with status: OUT_OF_RANGE: End of sequence

Validation Loss: 30.165538787841797, KL Loss: 9.908827781677246, Reconstruction Loss: 26.140899658203125

BETA is: 0.16 Epoch 18/25

2024-12-12 17:23:31.976399: W tensorflow/core/framework/local_rendezvous.cc:404] Local rendezvous is aborting with status: OUT_OF_RANGE: End of sequence

Train Loss: 31.197227478027344, KL Loss: 8.02535343170166, Reconstruction Loss: 28.406192779541016

2024-12-12 17:23:32.509688: W tensorflow/core/framework/local_rendezvous.cc:404] Local rendezvous is aborting with status: OUT_OF_RANGE: End of sequence

Validation Loss: 30.137964248657227, KL Loss: 8.88626480102539, Reconstruction Loss: 26.36162567138672

BETA is: 0.17 Epoch 19/25

2024-12-12 17:23:40.842922: W tensorflow/core/framework/local_rendezvous.cc:404] Local rendezvous is aborting with status: OUT_OF_RANGE: End of sequence

Train Loss: 30.23228645324707, KL Loss: 6.64791202545166, Reconstruction Loss: 27.832008361816406

2024-12-12 17:23:41.364096: W tensorflow/core/framework/local_rendezvous.cc:404] Local rendezvous is aborting with status: OUT_OF_RANGE: End of sequence

Validation Loss: 30.204572677612305, KL Loss: 6.791245937347412, Reconstruction Loss: 26.046464920043945

BETA is: 0.18 Epoch 20/25

2024-12-12 17:23:49.589155: W tensorflow/core/framework/local_rendezvous.cc:404] Local rendezvous is aborting with status: OUT_OF_RANGE: End of sequence

Train Loss: 29.780221939086914, KL Loss: 5.496977806091309, Reconstruction Loss: 28.1712703704834

2024-12-12 17:23:50.107682: W tensorflow/core/framework/local_rendezvous.cc:404] Local rendezvous is aborting with status: OUT_OF_RANGE: End of sequence

Validation Loss: 30.085216522216797, KL Loss: 6.130113124847412, Reconstruction Loss: 26.218666076660156

BETA is: 0.19 Epoch 21/25

2024-12-12 17:23:58.334305: W tensorflow/core/framework/local_rendezvous.cc:404] Local rendezvous is aborting with status: OUT_OF_RANGE: End of sequence

Train Loss: 30.237884521484375, KL Loss: 5.381424427032471, Reconstruction Loss: 27.847518920898438

2024-12-12 17:23:58.846479: W tensorflow/core/framework/local_rendezvous.cc:404] Local rendezvous is aborting with status: OUT_OF_RANGE: End of sequence

Validation Loss: 29.62075424194336, KL Loss: 5.987636089324951, Reconstruction Loss: 26.267263412475586

BETA is: 0.2 Epoch 22/25

2024-12-12 17:24:07.609413: W tensorflow/core/framework/local_rendezvous.cc:404] Local rendezvous is aborting with status: OUT_OF_RANGE: End of sequence

Train Loss: 29.630918502807617, KL Loss: 5.401956081390381, Reconstruction Loss: 27.718236923217773

2024-12-12 17:24:08.119300: W tensorflow/core/framework/local_rendezvous.cc:404] Local rendezvous is aborting with status: OUT_OF_RANGE: End of sequence

Validation Loss: 29.647912979125977, KL Loss: 5.8228912353515625, Reconstruction Loss: 26.322053909301758

BETA is: 0.21 Epoch 23/25

2024-12-12 17:24:16.412561: W tensorflow/core/framework/local_rendezvous.cc:404] Local rendezvous is aborting with status: OUT_OF_RANGE: End of sequence

Train Loss: 30.10558319091797, KL Loss: 6.751118183135986, Reconstruction Loss: 27.911895751953125

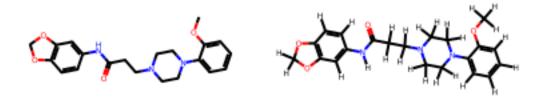
2024-12-12 17:24:16.938123: W tensorflow/core/framework/local_rendezvous.cc:404] Local rendezvous is aborting with status: OUT_OF_RANGE: End of sequence

Validation Loss: 30.011207580566406, KL Loss: 8.217364311218262, Reconstruction Loss: 25.707765579223633

BETA is: 0.22 Epoch 24/25

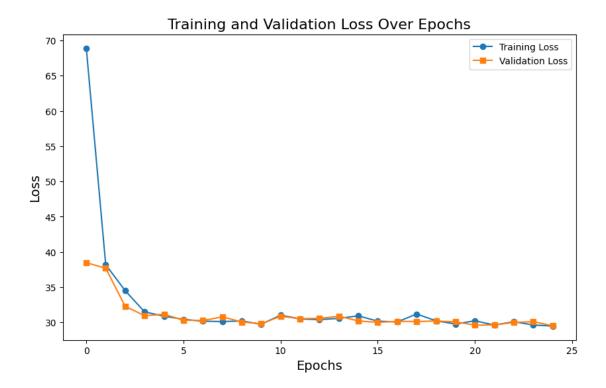
2024-12-12 17:24:25.177309: W tensorflow/core/framework/local_rendezvous.cc:404] Local rendezvous is aborting with status: OUT_OF_RANGE: End of sequence

```
Train Loss: 29.646812438964844, KL Loss: 6.321861743927002, Reconstruction Loss:
     27.694355010986328
     2024-12-12 17:24:25.684668: W tensorflow/core/framework/local_rendezvous.cc:404]
     Local rendezvous is aborting with status: OUT OF RANGE: End of sequence
     Validation Loss: 30.11176872253418, KL Loss: 7.073030948638916, Reconstruction
     Loss: 25.828048706054688
     BETA is: 0.23
     Epoch 25/25
     2024-12-12 17:24:34.059265: W tensorflow/core/framework/local rendezvous.cc:404]
     Local rendezvous is aborting with status: OUT OF RANGE: End of sequence
     Train Loss: 29.490495681762695, KL Loss: 4.3524909019470215, Reconstruction
     Loss: 27.740766525268555
     Validation Loss: 29.537527084350586, KL Loss: 4.7590861320495605, Reconstruction
     Loss: 26.03545570373535
     BETA is: 0.24
     2024-12-12 17:24:34.576585: W tensorflow/core/framework/local rendezvous.cc:404]
     Local rendezvous is aborting with status: OUT_OF_RANGE: End of sequence
[67]: '''
      Checking the model's ability to reconstruct a molecule from the training dataset
      i = 10
      adjacency_check, features_check = smiles_to_graph(train_df.loc[i]["SMILES"])
      score_check = [train_df.loc[i]["Score"]]
      molobj = Chem.MolFromSmiles(train df.loc[i]["SMILES"])
      adj0 = np.expand_dims(adjacency_check,axis=0)
      feature0 = np.expand_dims(features_check,axis=0)
      score0 = np.expand_dims(score_check,axis=0)
      print(adj0.shape)
      print(feature0.shape)
      print(score0.shape)
     (1, 5, 50, 50)
     (1, 50, 12)
     (1, 1)
[68]: mole_pred = graph_to_molecule(adj0[0], feature0[0])
      Draw.MolsToGridImage([molobj,mole_pred], molsPerRow=2,)
[68]:
```



```
[69]: plt.figure(figsize=(10, 6))
    plt.plot(range(EPOCHS), train_loss_list, label='Training Loss', marker='o')
    plt.plot(range(EPOCHS), val_loss_list, label='Validation Loss', marker='s')

# Add title and labels
    plt.title('Training and Validation Loss Over Epochs', fontsize=16)
    plt.xlabel('Epochs', fontsize=14)
    plt.ylabel('Loss', fontsize=14)
    plt.legend()
    plt.show()
```



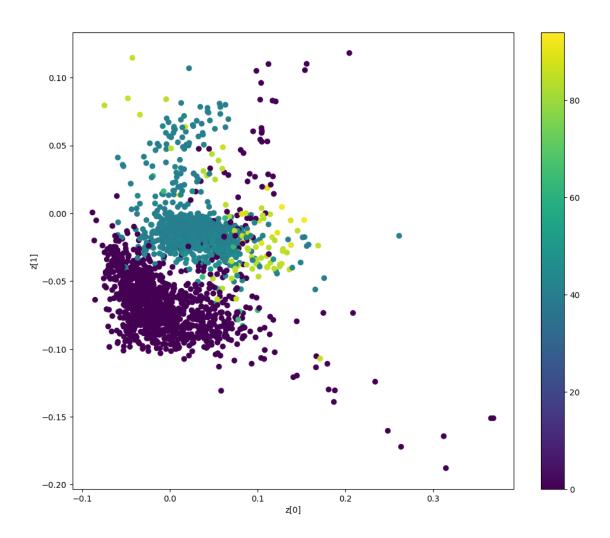
0.11 Visualize latent space

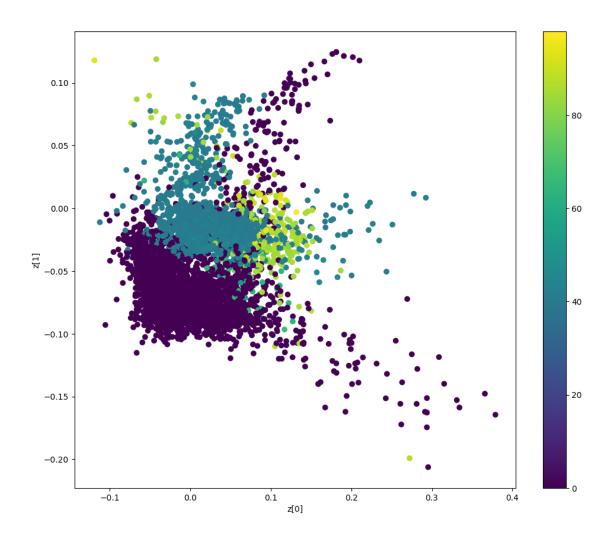
```
[70]: adj_test, fea_test, score_test = [], [], []
      for idx in range(len(test)):
          adjacency, features = smiles_to_graph(test.loc[idx]["SMILES"])
          score = test.loc[idx]["Score"]
          adj_test.append(adjacency)
          fea_test.append(features)
          score_test.append(score)
      adj_test = np.array(adj_test)
      fea_test = np.array(fea_test)
      score_test_ = np.array(score_test).reshape(-1,1)
      score_test_n = scaler.transform(score_test_)
[71]: ls_train = vae.encoder.predict([adj_train, fea_train, score_train_])
      ls_test = vae.encoder.predict([adj_test, fea_test, score_test_])
     251/251
                         Os 1ms/step
     79/79
                       Os 1ms/step
```

```
[72]: ls_train_ = np.array(ls_train)
      ls_test_ = np.array(ls_test)
[73]: z_mean, _ = vae.encoder.predict([adj_test, fea_test, score_test_])
     79/79
                       0s 848us/step
[74]: latent_noise = np.random.normal(scale=0.1, size=z_mean.shape) # Adjust scale_u
       ⇔as needed
      adj_pred, feature_pred = vae.decoder.predict([z_mean, score_test_])
      print("Shape of adj_pred:", adj_pred.shape)
      print("Shape of feature_pred:", feature_pred.shape)
      # Reconstruct molecules
      gen molecules = [
          graph to molecule(adj pred[i], feature pred[i])
          for i in range(adj_pred.shape[0])
     ]
     79/79
                       Os 4ms/step
     Shape of adj_pred: (2510, 5, 50, 50)
     Shape of feature_pred: (2510, 50, 12)
[75]: from scipy.stats import pearsonr
      # Correlate latent dimensions with molecular scores
      correlations = [pearsonr(z_mean[:, i], score_test_.flatten())[0] for i in_
       →range(z_mean.shape[1])]
      print("Correlations between latent dimensions and scores:", correlations)
     Correlations between latent dimensions and scores: [0.43693076863524927,
     0.6458182163928556, 0.5315790713378814, -0.041525544983638946,
     -0.5453206234128087, 0.27651514797541354, -0.2025655396442772,
     0.9075695019942163, 0.8320360810000553, 0.8989103496578915, -0.6432961649580947,
     0.7306387961762596, -0.6180187404340671, -0.4886460623848657,
     0.9240378844815753, -0.8611331757415476, 0.8382176854159732,
     -0.9400239344371479, 0.2778360892107996, 0.8678939592866706, 0.9053311618017323,
     -0.5292029900265793, 0.5341352412189297, -0.7170257516197571, 0.724299010486355,
     0.6104088284937204, 0.7626398025691812, -0.23543282208908284,
     0.8263745011386103, 0.7882786743779907, -0.9248352120038561, 0.5131734637761092,
     -0.5923120852073069, 0.9281137651821356, -0.7270253492269785,
     -0.8115047826774604, 0.8966585457319981, 0.7754990730081102,
     0.05203248343829952, -0.801432094460618, -0.841706317665667, 0.5824081634941394,
     -0.5631339729512872, -0.4567626925162528, 0.6673706299782768,
     -0.6391112272081758, 0.6017029545359756, -0.3589247852523813,
     -0.7769279774032881, -0.7778355982029415, 0.7731216968016852,
     -0.5565482601040326, -0.5971709660433001, 0.6279345112770491,
     0.18204615128450485, -0.8903125690972353, -0.5153799743279579,
     -0.8404132605720162, 0.6257658022677505, -0.44375887906770617,
```

```
-0.8201011547974539, 0.7668748110379051, 0.34513410442651227,
0.3512017948973034, -0.8970692737574888, 0.48971532021328995,
-0.6703689507171706, -0.3200898441108734, -0.8089706423083505,
-0.09425211774637757, 0.9234053376369638, -0.03932443932429845,
0.19419645822029255, -0.6712865076747813, 0.297871903979944,
-0.8719070556696706, 0.6834532333937009, -0.5548354570672189,
0.4378141119970578, 0.827797895689106, -0.580488339194429, 0.6095240555631715,
-0.37537597890104324, 0.676186207189819, 0.6286921396494096,
-0.7621541185358156, -0.23408406537676432, 0.33821310820200645,
-0.34448938067626467, -0.8170898716359402, -0.03824877812255295,
0.38168973655569566, 0.3908850066126446, -0.8049908094060851,
0.5569112555758211, -0.8995223103172105, -0.09515742879935934,
-0.04281520658449054, 0.0006577860547918746, -0.1353361609716848,
0.03147870688847587, 0.41645086774227447, -0.9317143884679505,
0.11384852356943198, 0.06466981829877852, 0.44645502410171933,
-0.14887889526812498, 0.5560570648233627, -0.7135170917340019,
-0.46780204836926775, 0.7309778183625266, -0.033626947225412554,
-0.811633578183703, -0.5731403778395354, 0.6393540914719886, 0.890581534008148,
-0.7582324983221603, -0.6144058169778475, -0.020479379466469074,
0.7948437841161935, 0.23231148709417937, 0.8656580871044224,
0.44071265464958376, 0.59629377698668, -0.1931243064805609, -0.3300846815667597,
0.7478632133129859, -0.48627657227804677, 0.7751503532831596,
0.44962573486438273, 0.6406877677293241, -0.7094739806347756,
0.09303550280308892, -0.8840676342068382, -0.8306318087939335,
0.8675279351597966, 0.8259178372174545, -0.46124665064916615,
0.5960537239457002, 0.03585240569688615, -0.160713789169105, 0.7476964159666163,
0.46478570109350026, 0.030603157349616994, 0.8736984053912613,
-0.19405149802861943, 0.12930338970727084, -0.3235522240052505,
-0.9075570492259131, 0.7249772215256738, -0.7266750925991974,
0.6948620549344214, 0.8825842266588264, 0.48927638941365703, 0.7885316302409083,
0.1856054053865332, -0.05052425423703526, -0.4116923266866568,
0.9088438587518193, -0.6563605649272276, 0.8828110000492244, 0.7801212983239934,
0.9218310761910156, 0.7855056988000226, 0.9143422359421899,
-0.14803153678701486, -0.9287874427870663, -0.22722272107348868,
0.2709198293619329, -0.6592139194603186, -0.8847690956607112,
-0.1394970765122106, 0.8614096821723354, -0.28314541543776606,
-0.8262167487670504, -0.8944727865892675, 0.8229272616441996,
-0.042766310861424135, -0.28845019154589596, -0.6254742225326949,
-0.8676122821882234, 0.8726348359151328, -0.8275876981338667, 0.825533210758939,
-0.3223876769305887, -0.008551691735595345, 0.8384475981682669,
-0.6561141015510922, -0.12081726579184388, 0.9259706903652266,
-0.7210063840695797, 0.8958922980403142, -0.8110303070092791,
-0.8931674752410304, 0.7369990611467508, -0.9269416230569404,
-0.9252114623459915, 0.5713558909475865, 0.0412837530797445,
-0.5003196677603783, 0.8560252249851077, -0.6301211730371439,
0.9137487849777629, -0.8724627114940815, 0.9009506503902698,
0.27502535939720874, 0.39021583440532803, -0.7435920749906377,
0.8993128618444177, 0.8835019419037545, -0.8278547525482134,
```

```
0.28852806384884705, -0.5591899753824054, 0.9106140948720491,
     -0.7749289804115912, 0.316678610813845, -0.7019898168875951, 0.9037186062262093,
     0.835329387634747, -0.22639877303764291, 0.9173529244179112,
     -0.05284659258836827, 0.26775381805756704, 0.45406283070331477,
     -0.678758792252544, -0.8722253434706944, -0.3223518293485731,
     0.7346527638494009, 0.023691550681189985, 0.606806976695201, 0.5296379387828218,
     0.8475955414919019, 0.26799271569295396, -0.5818634753481793,
     -0.5883488729769852, -0.8387821153765493, 0.10040388694805213,
     0.6484891054098649, 0.2817484259341585, 0.7142913582479601, 0.08876064050648189,
     -0.8323202602304973, -0.2762461492278687, 0.6615788866015145,
     -0.06561262210582236, 0.7282508734803184, 0.8390871058174897,
     -0.4093936395877963, 0.9064527343803632, -0.016334784709051812,
     0.6421914854072382, -0.6249345472769086, -0.2664077543381597,
     0.17607913843430992, 0.4487125386128529, 0.882377626965308]
[76]: plt.figure(figsize=(12, 10))
      plt.scatter(z_mean[:, 0], z_mean[:, 1], c=score_test_)
      plt.colorbar()
      plt.xlabel("z[0]")
      plt.ylabel("z[1]")
      plt.show()
```





[]:

0.12 Model Inferencing

We would be inferring our model to predict over random latent space and try to generate 100 new valid molecules.

0.12.1 Generate unique Molecules with the model

```
[79]: def inference(model=vae, batch_size=1000, dim = LATENT_DIM, activity=10):
    z = np.random.normal(size=(batch_size, dim))
    activityarray = (np.zeros(batch_size) + activity).reshape(-1,1)

    reconstruction_adjacency, reconstruction_features = model.decoder.
    predict([z,activityarray])
    # obtain one-hot encoded adjacency tensor
    adjacency = tf.argmax(reconstruction_adjacency, axis=1)
```

```
adjacency = tf.one_hot(adjacency, depth=BOND_DIM, axis=1)
    # Remove potential self-loops from adjacency
   adjacency = tf.linalg.set_diag(adjacency, tf.zeros(tf.shape(adjacency)[:
 →-1]))
    # obtain one-hot encoded feature tensor
   features = tf.argmax(reconstruction features, axis=2)
   features = tf.one_hot(features, depth=ATOM_DIM, axis=2)
   return [
        graph_to_molecule(adjacency[i] numpy(), features[i] numpy())
        for i in range(batch_size)
   ]
MolsToGridImage([m for m in gen mols if m is not None][:1000], molsPerRow=5, u
```

```
[80]: gen_mols = inference(batch_size=1000,activity=10)
       ⇒subImgSize=(260, 160))
```

32/32 Os 3ms/step Sanitization failed: Explicit valence for atom # 23 C, 7, is greater than permitted Sanitization failed: Explicit valence for atom # 6 Cl, 3, is greater than permitted Sanitization failed: Explicit valence for atom # 0 I, 84, is greater than permitted Sanitization failed: Explicit valence for atom # 0 P, 45, is greater than permitted Sanitization failed: Explicit valence for atom # 4 Cl, 5, is greater than permitted Sanitization failed: Explicit valence for atom # 21 C, 7, is greater than permitted Sanitization failed: Explicit valence for atom # 13 N, 6, is greater than permitted Sanitization failed: Explicit valence for atom # 1 0, 5, is greater than permitted Sanitization failed: Explicit valence for atom # 0 As, 102, is greater than permitted Sanitization failed: Explicit valence for atom # 25 C, 6, is greater than permitted

Sanitization failed: Explicit valence for atom # 0 C, 7, is greater than permitted

Sanitization failed: Explicit valence for atom # 0 I, 42, is greater than permitted

Sanitization failed: Explicit valence for atom # 0 I, 91, is greater than permitted

/Users/thinh/Library/Python/3.12/lib/python/sitepackages/rdkit/Chem/Draw/IPythonConsole.py:261: UserWarning: Truncating the list of molecules to be displayed to 50. Change the maxMols value to display more.

warnings.warn(

[80]:

***************	**************************************	******	44444444444444444444444444444444444444	************
444444k	*******	**************************************	444444444	********
**************************************	********	4444444 <u>4</u>	44444444444444444444444444444444444444	<i>\</i> \\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\
* *********	444444k	**************************************	*******	4444444 <u>4</u>
*********	*******	**************************************	***********	44444444444444444444444444444444444444
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******	*XHHHHHH	***************************************	**************************************	*XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
**************************************	****	**	**********	~

[]:[