

## Machine Learning for Molecular Engineering

### Problem Set 3

**Date:** March 5, 2022

**Due:** March 17, 2022 at 10 PM ET

**Instructions** Please submit your solution on Canvas as an IPython (Jupyter) Notebook file, `*.ipynb`. We highly suggest using Google Colab for this course and using this [template](#) for this problem set. Your submission should contain *all* of the code that is needed to fully answer the questions in this problem set when executed from top to bottom and should run without errors (unless intentional). Please ensure that your plots are visible in the output file and that you are printing any additional comments or variables as needed.

To get started, open your Google Colab or Jupyter notebook starting from the problem set template file `pset3.ipynb` ([direct Colab link](#)). You will need to use the data files [here](#).

## Background

In part 1, you will build a sequence-based deep learning model to classify [DNA binding sites](#) based on a DNA sequence. DNA binding sites are fragments in DNA sequence where other molecules/proteins may bind for biological functions. Binding activities in DNA are also associated with important biological process like transcription, a process to turn your DNA into mRNA which is later used to synthesize proteins in your cells. The dataset you will work with is from [ChIP sequencing](#) which is an experimental method to probe protein interactions with DNA.

In part 2, you will explore some unsupervised learning techniques to decode the hidden message your data is trying to tell you without any labels.

## Part 1: Predicting DNA Binding Sites

In this part, you will write a pipeline that builds and trains a model to predict if a section of DNA sequence is a binding site for a protein. You will be provided a dataset of DNA sequences and a binary label 0/1 that indicates if the sequence binds to a protein or not. The sample data format is presented in Table 1.

DNA sequence	binder or not
'ATCGGGAA...'	1
'TGCAGTAT...'	0
...	...

Table 1: Dataframe snapshot from DNA binding data

This part will require you to implement a deep neural network in PyTorch, just as you did in Problem Set 2. If you need to, please review Part 3 from Problem Set 2 before beginning this problem. If you did not do this previously, also go through the PyTorch tutorial [here](#) and the quickstart guide [here](#).

As in Problem Set 2, you'll want a GPU for this part. Request one now.

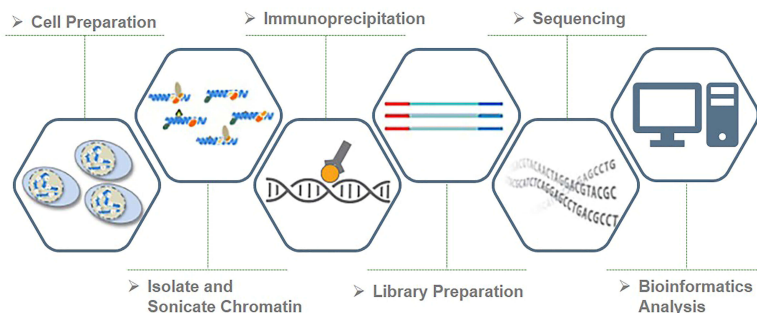


Figure 1: A typical ChIP workflow ([source](#))

### Part 1.1 (15 points) Build Datasets and DataLoaders in PyTorch

Now you will construct your data processing pipeline. First load the DNA sequence data with the code provided. Because the data is loaded as strings like “ATGTCA...”, you will need to one-hot encode the DNA sequences into bit vectors of size 4 (corresponding to the 4 possible DNA bases A, T, G, and C) and split the data set into 80% train and 20% test. Further retrieve 10% of your training data as the validation set which will be used to check for training convergence. Because training a deep neural network takes time, so we won’t perform cross validation or hyperparameter optimization as you did in previous psets. However, you might still want to do it in your final project if you decide to use a neural network based model.

Next, you need to construct your dataset and loader, with `torch.utils.data.Dataset` and `torch.utils.data.DataLoader`. Mimic our code from Problem Set 2 and the Quickstart guide to write a `dataset` class. Essentially, you need to implement the `__getitem__()` method that return a sequence `x` and its corresponding label `y` given an `index`. Construct train, validation and test data loader with `batch_size=256`, using your train, validation and test datasets.

The concept of batching data might still be new to you, so take a moment to think about what it’s doing and why (and optionally, do some brief research on your own about batching in deep learning). What is the benefit of batching your data into mini-batches versus using the entire dataset to optimize the model all at once?

### Part 1.2 (20 points) Write an LSTM-based classifier

In this section, you will build a DNA sequence classifier with recurrent neural networks. In contrast to a standard feed forward neural network (i.e. a multi-layer perceptron), an RNN is a specialized network architecture that operates on sequential data such as text, DNA sequences, and stock market prices. When RNNs operate on an input at a current time point, it considers not just the value of the current input, but also what it has learned from the inputs it received previously through a hidden context vector. It is through this persistent context vector that the model architectures captures the sequential structure of our data.

Now, let us try to understand the math behind a RNN. First, recall that a single transformation of a neural network requires the following computation:

$$\sigma(Wx + b) \tag{1}$$

where  $x$  is the data,  $W$  is a learned matrix,  $\sigma$  is a element-wise nonlinear transformation, and  $b$  is a learned bias. If we applied this calculation to our sequential data as one vector, we will have

ignored the sequential (e.g., time-varying) nature of our data. RNNs are designed to operate on sequences one element at a time. Suppose our data has the form  $\{x_0, x_1, x_2, \dots, x_t, \dots, x_T\}$ ; an RNN will sequentially construct a hidden embedding  $h_t$  for each  $x_t$ :

$$h_t = \sigma(W_{ih}x_t + b_{ih} + W_{hh}h_{t-1} + b_{hh}) \quad (2)$$

In this equation  $t$  is the index for the element in your sequence.  $x_t$  is your sequence data, and the embedding  $h_t$  is the representation learned up to time  $t$ . At step  $t$ ,  $W_{ih}x_t + b_{ih}$  transforms the data  $x_t$  to a hidden state and  $W_{hh}h_{(t-1)} + b_{hh}$  linearly transforms the hidden embedding of the *previous* state  $h_{t-1}$  to produce the next hidden state  $h_t$ . The two contributions (from  $h_{t-1}$  and  $x_t$ ) are added together and passed through a nonlinear activation function,  $\sigma$ . This procedure is applied to the sequence from  $x_0$  all the way to  $x_T$  with the same set of parameters  $W_{ih}, W_{hh}, b_{ih}, b_{hh}$  for  $T + 1$  times.

For this pset, we will use a long short-term memory (LSTM) model, which is a variant of the vanilla RNN described above. LSTMs have been very successful in deep learning applications for natural language processing. In 2017, Facebook switched to using LSTMs to perform billions of language translations on user comments. In contrast to regular RNNs described above, LSTMs contain a gated ‘memory cell’ to store long-range correlation along the sequence. You are not required to understand the inner-workings of an LSTM for this assignment (although you are encouraged to read about it on your own [here](#)).

Now, let us talk about how to construct a classifier using LSTMs in PyTorch. You will first apply an LSTM on the one-hot encoded sequential data you prepared in the previous part using the `torch.nn.LSTM` class to construct a learned representation. Then, you will extract the parameterized hidden state after the final input,  $h_T$ , as an input to an MLP. The input dimension of the MLP should have the same dimension as the  $h_t$  and should output a scalar for each sample. Finally, a sigmoid activation function on the scalar output will provide a probability between 0 and 1 corresponding to the probability that this sequence is a DNA binding site. To summarize, there are three elements you need to construct:

- **lstm**: a LSTM module (`torch.nn.LSTM()`)
- **mlp**: a neural net (`torch.nn.Sequential()`, as in Problem Set 2). Use 2 hidden layers, each with tanh activation, and a final output layer with 1 output dimension.
- **sigmoid**: an element-wise sigmoid transformation (`torch.nn.Sigmoid()`)

In terms of mathematical equations:

$$\begin{aligned} \{h_t\}, h_T, c_T &= \text{lstm}(\{x_t\}) \\ \text{prob} &= \text{sigmoid}(\text{mlp}(h_T)) \end{aligned} \quad (3)$$

In this equation,  $x_t$  is the one-hot encoded DNA sequence,  $h_t$  are the hidden embeddings of the sequence,  $h_T$  is the embedding of the last element of the sequence.  $c_T$  is the cell state of the last element in the sequence.  $h_T$  is parameterized to encode the information of the entire sequence, and is the representation you need to use to feed into an MLP regressor.

For `torch.nn.LSTM`, please set `batch_first=True`, `num_layers=1`, `bidirectional=True`, and specify `hidden_size=hidden_dim` (the input to the `LSTMSeq` class). Since we’re using a bidirectional LSTM, you’ll have two hidden states produced (one for each direction); use the one corresponding

to the backwards direction as input for the MLP, which will be  $h_T[1]$  or  $h_T[-1]$ . For the `mlp`, use hidden dimensionality of `hidden_dim` in both layers. We have provided an example computation of LSTM-based classifier in the template file to help guide you, as well as some skeleton code.

### Part 1.3 (25 points) Implement functions for training and testing

As in Problem Set 2, set up the Adam optimizer to train your model, with a learning rate `lr` of `1e-2`. In this problem, we will also be using a learning rate scheduler, specifically the scheduler `torch.optim.lr_scheduler.ReduceLROnPlateau`. This is a common strategy to prevent overfitting or overshooting a loss minimum by gradually reducing the learning rate during training. We have provided the scheduler for you in the skeleton code.

Next, write your training loop, following the Quickstart guide or the example we provided in Problem Set 2. Unlike before, this is a classification problem, so you will want to compute the binary cross entropy loss (`nn.functional.binary_cross_entropy()`) which requires you to input classification probabilities and the ground truth labels from your data. This should be implemented in the provided `train()` function, which already loops over minibatches for you. Record the loss of each batch and compute the average loss for all batches. Your `train()` function should return the average training loss.

Similarly, complete the `validate()` function to iterate over validation data and return the mean validation loss; remember to ensure that the validation function does not call the optimizer because the validation dataset is not used for training. You can make sure this is the case by calling `model.eval()` and turn on the `torch.no_grad()` context manager at the beginning of your validation function (we have implemented that for you). You will need to call `model.train()` to turn the gradients and optimizer updates back on in the `train()` function.

Finally, complete the `evaluate()` function. This function takes in data and produces the model's predictions, along with the true values for that dataset. You'll use it to evaluate your model's predictions on the test data and measure model performance.

Looping over the entire training data set once is called an *epoch*. The `train()` and `test()` function you will implement is only for one epoch, and should return a train loss and validation loss computed as averages over all the batches. Train and validate your model for 500 epochs; we have provided you with the code for this. This will take a few minutes.

Record the average train and validation loss for each epoch and plot these on a single graph, using our provided code. Finally report your test AUC score of your trained model on the test data. You would need to transform your prediction from `torch.Tensor` to `np.array` to compute ROC/AUC scores. As usual, you should use `sklearn.metrics.roc_auc_score`.

## Part 2: Dimensionality Reduction for Molecular Representations

In this part, you will be performing dimensionality reduction analysis on a set of candidate molecules tested against the [Mitogen-Activated Protein Kinase](#), also called MAPK1 or ERK2. The data is from the [DUD-E database](#).

Converting the complex structure and topology of a molecule into a vector representation is not straightforward. The cheminformatics community has developed a variety of algorithms to numerically encode the structural information of molecules. [Morgan fingerprints](#), also known as circular fingerprints, represent the molecular graph as a unique bit string that encodes the molecular topology. You can understand it as a bit-vector categorical encoding with 1 for substructures present

in the molecule and 0 for those not present. Some implementations of fingerprints use counts of how many times a substructure is present, instead of just 0s and 1s for absence/presence. Morgan fingerprints are typically high dimensional to maximize their descriptive power and sizes of 512, 1024 or 2048 are common (you can choose the number of bits when generating these fingerprints with the Morgan Algorithm). Morgan fingerprints provide a vector representation of molecules that is nearly unique for each molecule (although fingerprint collisions for non-identical molecules are possible), on which we can apply machine learning algorithms.

In this question, you will apply dimensionality reduction algorithms on a high-dimensional molecular fingerprint data we provided.

### Part 2.1 (10 points) Principal Component Analysis on Molecular Fingerprints

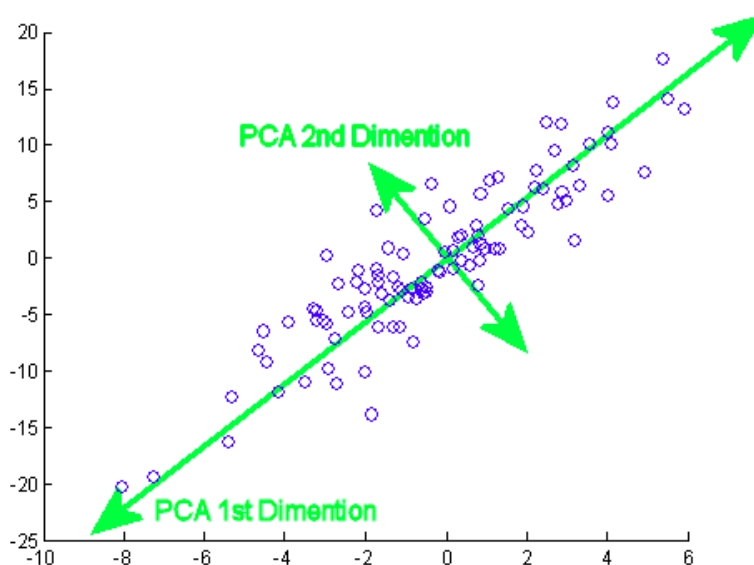


Figure 2: An example PCA analysis on a 2D dataset. The principal components are marked in green arrows. ([source](#))

First load the fingerprint data arrays of 512 bit size and the molecule dataframe with the code we provided to you (The row in the fingerprint array is mapped one-to-one to the row of the molecule dataframe). The fingerprint is computed with the Morgan algorithm implemented in the [RDkit](#) package. In the dataframe, we also provided a binary label to indicate if the molecule tested active against the target protein.

Each molecular fingerprint spans a 512-dimensional space, so it is hard to make sense of it. We encourage you to think about the size of the space that can be encoded in such representation.

Principal Component Analysis (PCA) is a dimensionality-reduction method that is often used to tackle high-dimensional, large data sets. In PCA, a large set of variables is transformed into a smaller one that contains as much of the information in the larger set as possible. PCA performs a linear transformation on your data by re-projecting in onto a new orthogonal basis. These new basis is chosen such that the fewest basis vectors best explain the variance of your data. Because of ease of visualization, it is common to just interrogate the first two dimensions (also called eigenvectors or components) of the PCA, but its possible to select additional dimensions.

You should perform PCA on the fingerprint data with `sklearn.decomposition.PCA()`. Use

100 components by setting `n_components=100`. This will reduce your original 512 dimensional space onto just a space of just 100 dimensions. Visualize the first two components of your data in a 2D scatter plot and color the active and inactive molecules differently. What is the total explained variance ratio of the first 100 principal components? (This is an estimate of how much information is preserved after this dimensionality reduction procedure) You can retrieve the ratios of explained variances by checking the `.explained_variance_ratio_` attribute of a `PCA()` object.

Inspect the scatter plot. Do you observe any patterns in the distribution of active drugs in this 2D plot?

## Part 2.2 (10 points) t-SNE analysis on Molecular Fingerprints

PCA applies linear transformations on your data, but may struggle to tease out subtle underlying patterns in your data. Non-linear transformations can distort or compress the dimensions much more effectively and can uncover much more complex structure in the dataset. There are two popular choices for non-linear dimension reduction: UMAP and t-SNE. t-Distributed Stochastic Neighbor Embedding (t-SNE) performs a stochastic non-linear transformation on your data and it is implemented in `sklearn` (`(sklearn.manifold.TSNE())`). In general, t-SNE is a random algorithm so you will have different looking embeddings every time; it is also sensitive to *perplexities* which balance attention between local and global aspects of your data during the optimization. Read the documentation for `TSNE()` to understand these options.

Apply t-SNE on your the 100-dimensional embedding you obtained from previous part with `n_components=2` with a perplexity value of 2, 30 and 500 separately and produce three labeled t-SNE plots with active and inactive drugs in different colors. The t-SNE computation might take a few minutes. Do you notice any differences in the clustering? Focus on the plots obtained with `perplexity=30`. In your 2D scatter plot, do you observe any patterns for the active drugs?

## Part 2.3 (15 points) Are the low dimensional embeddings meaningful?

In this question, you will be asked to make sense of the extracted low dimensional embeddings and how they may relate to prediction performance in a supervised learning task. You will need to train a Random Forest classifier of active vs. inactive compounds and then relate the performance of this supervised to the embeddings you learned in the previous part.

Split your data into 10 folds using `sklearn.model_selection.KFold()` and train a random forest classifier with 100 trees (`n_estimators=100`). Use the full fingerprint (not the low-dimensional embedding) as your featurization for the random forest. Just as you did in PSet 1, use `sklearn.ensemble.RandomForestClassifier`. Test each fold with models trained on the other 9 folds, and record your prediction in a dataframe or an array. Classify your predictions in 4 categories: True Positives (TP), True Negatives (TN), False Positives (FP) and False Negatives (FN). Make a scatter plot with the t-SNE embeddings, and color each of the four categories above with different colors. Inspect your plot; do you observe any patterns in the prediction categories (TP, TN, FP, FN) on your t-SNE plots?

## Part 3: Feedback Survey

### Part 3.1 (5 points) Please finish the feedback survey on our Canvas site