# Gas Chromatography - Mass Spectrometry (GC-MS) Prediction Models

Two deep learning tensorflow models:

1. spectra2formula: predict molecular formula from GC-MS spectra
2. spectra2smiles: predict SMILES (simplified molecular-input line-entry system notation) from GC-MS spectra

# Data

This supervised training relies on the NIST data set (https://www.nist.gov/srd) which contains 242466 spectrum-label pairs. This training data contains a total of 71 different elements/isotopes and to initially reduce the complexity of the problem, only covalently bound compounds containing (C, O, H, N) were selected reducing the number of samples to 116354. Out of these 116354 samples, 6354 were saved for a final testing set and 10000 were used as a validation set to assist in hyper-parameter picking and to prevent overfitting. This resulted in 100000 final training samples.

1. Spectrum Input: The spectral input is represented as a two-dimensional numerical matrix with the rows equal to the number of samples and the number of columns equal to the highest mass integer in the spectra. The intensities for each spectral peak in the NIST data range from 0.0 to 999.0 and are subsequently normalized to a range of 0.0 to 1.0.
2. Formula Labels: The formula label is represented as a two-dimensional matrix with the rows equal to number of samples and the number of columns equal to the number of chemical elements. For predicting the formulas from only the organic compounds, the number of elements equals 4 (Carbon, Hydrogen, Nitrogen, Oxygen). The value of the matrix is an integer representing the number of atoms of the respective element contained in the compound and thus, predicting the formula is a multilabel regression problem.
3. SMILES Labels: The canonical SMILES maintain all the structural information of the molecule within a string (http://www.daylight.com/dayhtml/doc/theory/theory.smiles.html) The SMILES label is represented as a three-dimensional matrix in the form (number of samples x length of SMILES x vocabulary size of SMILES). A value of 1.0 is added if the character is present in that location in the SMILES string and a 0.0 elsewise. For the NIST data, the length of the longest SMILES is 185 and there are 17 possible choices for the vocabulary. Note that covalent Hydrogen is not needed as an explicit character since the location of hydrogen in a compound is easily determined from the canonical SMILES and elementary bonding rules. The 17 characters used are: C, O, N, =, #, (, ), 1, 2, 3, 4, 5, 6, 7, 8, 9, End of String

# Model

(see spectra2formula\_model.pdf and spectra2smiles\_model.pdf for visualization)

1. spectra2formula: The spectra input is fed into a variable level convolution subnetwork that follows the following repeating structure: Convolution-> Pooling-> Batch Norm-> Dropout-> Elu Activation. The resulting state is fed into a fully connected variable level dense subnetwork that follows the following repeating structure: State-> Batch Norm -> Dropout -> Elu Activation. A final set of weights transforms the last state to the regression results for the four elements.
2. spectra2smiles: The spectra input is fed into a variable level convolution subnetwork that follows the following repeating structure: Convolution-> Pooling-> Batch Norm-> Dropout-> Elu Activation. The state from each convolution layer is fed into a fully connected variable level "translation" subnetwork. The translated convolution states are then fed into their corresponding LSTM layer. In addition to the translated convolution states, the LSTM subnetwork is input with a zero matrix the size of the SMILES labels. A final set of weights transforms the output of the LSTM subnetwork to the SMILES prediction.

# Regularization

Several techniques were tried to improve generalization performance. These include the standard L2-regularization and node dropout methods as well as adding Gaussian noise to the gradients during back propagation. (Arvind Neelakantan, Luke Vilnis, Quoc V. Le, Ilya Sutskever, Lukasz Kaiser, Karol Kurach, James Martens, "Adding Gradient Noise Improves Learning for Very Deep Networks", arXiv:1511.06807)

# Results

# For the spectra2smiles model, the accuracy results for the validation set were very low reaching around 1% which was not unexpected (see discussion below). Due to the difficulty in predicting the entire SMILES, I instead chose to investigate what was the average percentage of each SMILES that could be predicted. As can be seen in the following plot which displays this partial accuracy for some of the best models, the partial accuracy only reaches around 53%.

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# Discussion

The objective of this project was to predict either the chemical formula or the SMILES string from the GC-MS experimental spectra. Two models were created to solves these problems and are called spectra2formula and spectra2smiles respectively.

There are several challenges that presented themselves which are unique to mass spectrometry prediction and that are the stumbling blocks to good accuracy scores. Firstly, while 71 different elements are represented in the NIST dataset, many of these are found in only 1-4 samples rendering them non-ideal for serious feature extraction. By focusing on only the organic compounds, the number of samples for training was effectively cut in half from 200 thousand to 100 thousand. Secondly, the GC-MS experimental data from the is low resolution with each mass/charge peak taking whole integer values. This means that separate peaks representing unique atoms are combined obscuring good features. Thirdly, there is a large disparity in the ratio of different elements with the decreasing order of hydrogen, carbon, oxygen, nitrogen. For the specra2formula model, this is not a factor since for each of the four elements, there is a distinct regression output. However, for the spectra2smiles model, the choice of which character to predict at EACH location of the SMILES string is dominated by choosing carbon (covalent hydrogen is not an option for SMILES string as they can be implicitly determined). It was noted that for the spectra2smiles model, the average percentage of each SMILES that was predicted correctly jumped to around 46% and then slowly increased to a maximum of around 53%. The 46% was easily obtained by the network assigning all characters to be chosen as carbon and it was only very slowly that this degeneracy was disrupted. Fourthly, the size of the samples is not uniformly distributed with some SMILES strings as small as three characters and as large as 185 characters while the bulk of the samples fall in the middle around 70 characters. The difficulty in getting high accuracy is not surprising given that as many as 185 sequential characters ALL must be predicted correctly for the SMILES string to be considered correct.