

# **SMILES and CNN**

Seongok Ryu
Department of Chemistry, KAIST



#### **Contents**

- End-to-end learning
- SMILES molecular representation by a string
- Prediction of logP using SMILES and CNN
- Assignment #4



# How can we improve the models? (at the last lecture)

#### **Possibilities**

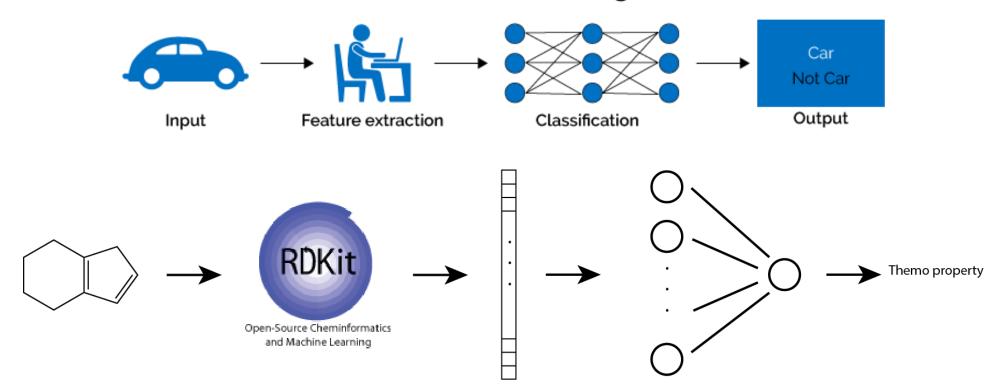
- Learning rate is too small or big.
- Missing regularizations (prior regularization, dropout)
- Input, the molecular fingerprint, is not good.
- Need better model, instead of MLP
  - → Using raw input, e.g.) SMILES, molecular graph rather than featurized inputs, e.g.) molecular fingerprint
  - → Using better model, e.g.) CNN, RNN, Graph NN.



### **End-to-end learning**

- We used molecular fingerprints for inputs of the models.
- The molecular fingerprint is a "featurized(pre-processed) input.
- It means that an expert(prior)-knowledge can be unintentional biases.

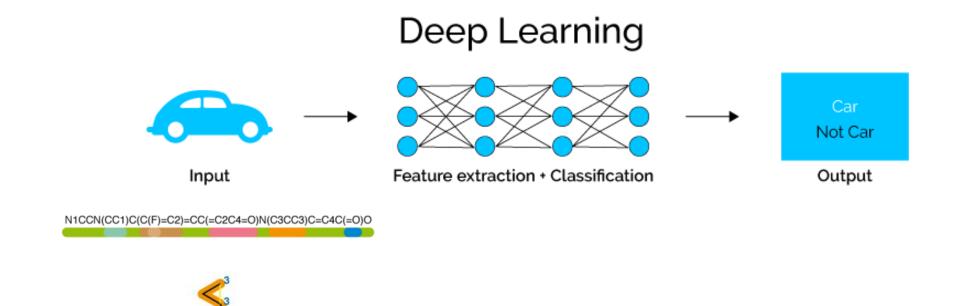
#### Machine Learning





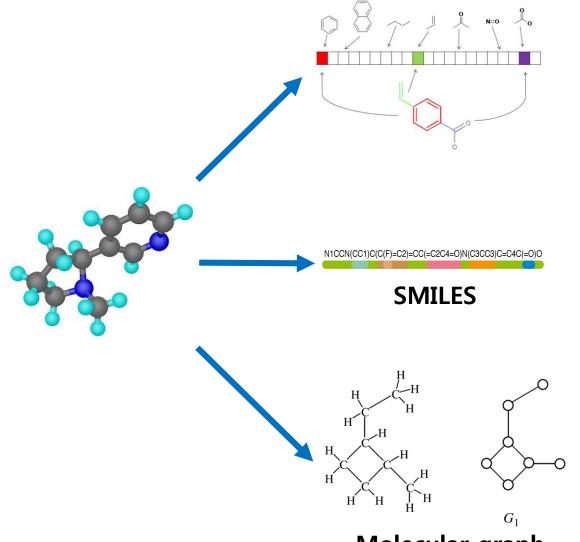
### **End-to-end learning**

- How about use raw inputs rather than featurized inputs?
- SMILES and molecular graph can describe the molecular structure.
- Let machines to learn both featurization and prediction by itself. It is the heart of deep learning!





#### SMILES – molecular representation by a string





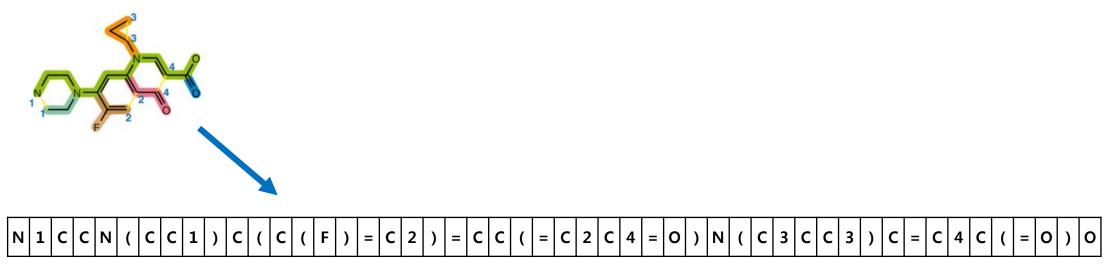
#### SMILES – molecular representation by a string



"The **simplified molecular-input line-entry system** (**SMILES**) is a specification in form of a <u>line notation</u> for describing the structure of <u>chemical species</u> using short <u>ASCII strings</u>. SMILES strings can be imported by most <u>molecule editors</u> for conversion back into <u>two-dimensional</u> drawings or <u>three-dimensional</u> models of the molecules."

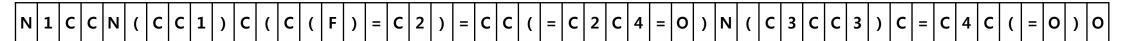
https://en.wikipedia.org/wiki/Simplified\_molecular-input\_line-entry\_system



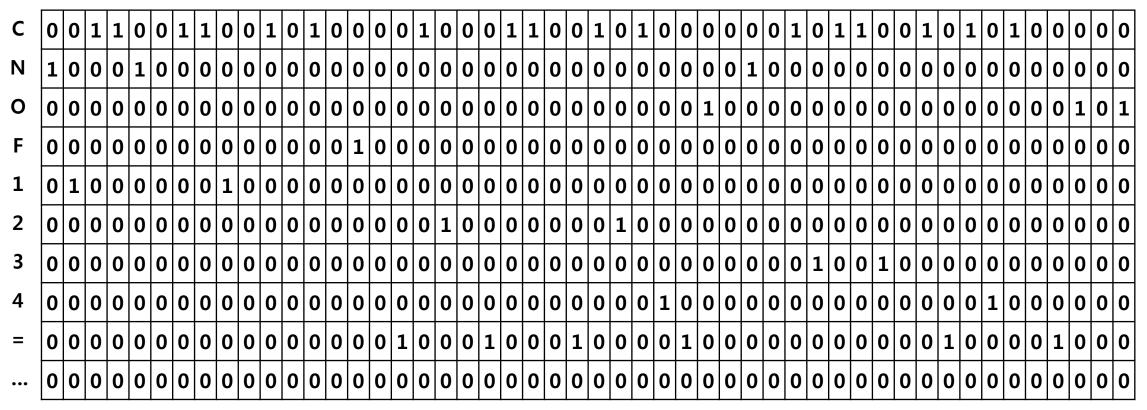


shape = [#batch, #characters]

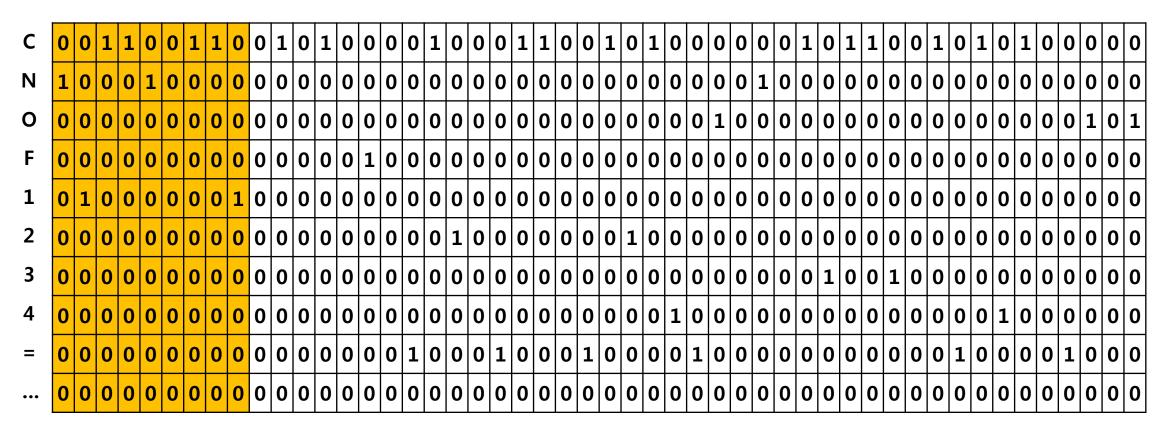




#### **One-hot encoding**

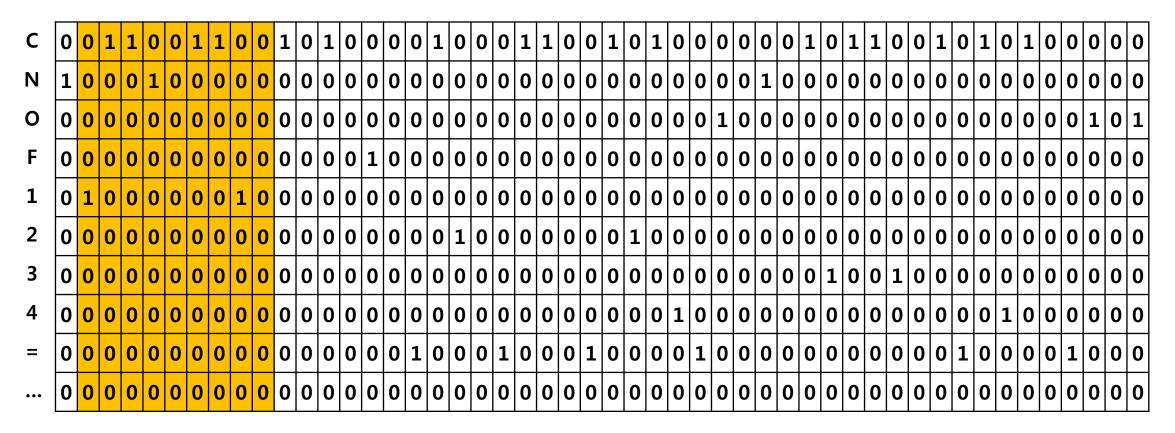






1d convolution

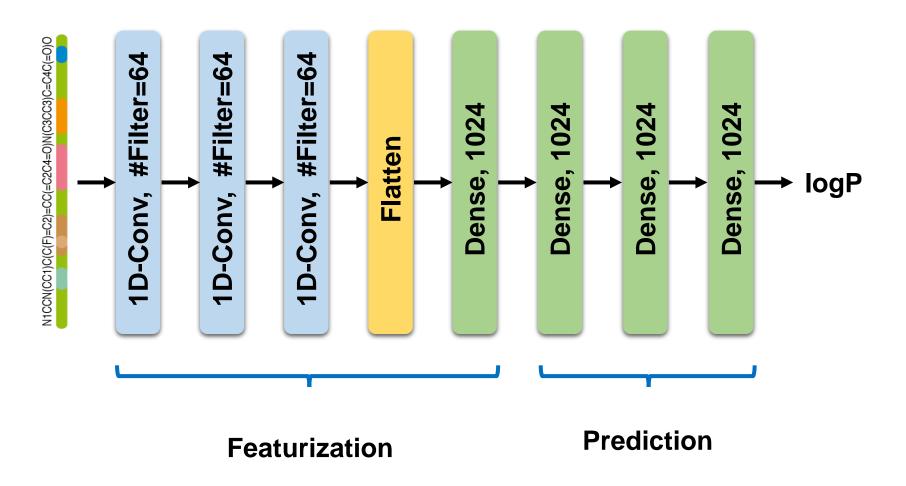




1d convolution, stride=1, padding='same'

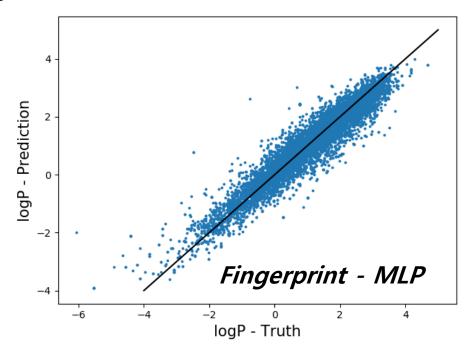


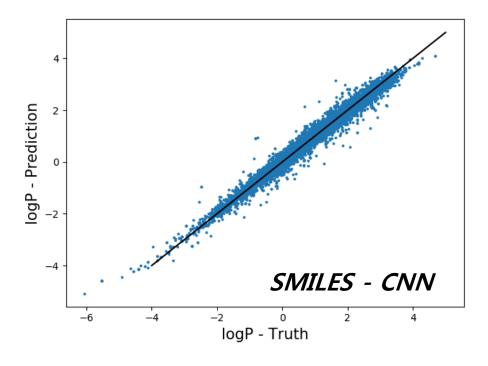
Overall architecture of the CNN model





#### **Results**





- ✓ Hidden dim = 1024
- ✓ Regularization lambda = 0.01
- ✓ No dropout
- √ 30000/1000/1000 train/val/test

	Fingerprint - MLP	SMILES - CNN	Graph - later
MAE	0.31	0.42	?
Std. dev	0.15	0.20	?



## **Assignment #4**

#### Improve the vanilla CNN model

- In this class, TA showed vanilla the CNN model which is consisted of three convolutional layers and predictor composed of three dense layers.
- We learned wider and deeper model InceptionNet and ResNet in today's lecture.
- Therefore, try to develop better model than the vanilla CNN.
   Using the inception modules or deeper model with the skip-connections can improve the vanilla CNN.
- Report your results MAE, std. dev, and truth-prediction plot.

