

```
In [1]: n_repeats = 5
n_splits = 10
n_epochs = 1000
```

```
In [2]: import warnings
warnings.filterwarnings('ignore')
```

```
In [3]: # 回歸問題不能用stratifiedKFold
from sklearn.model_selection import RepeatedKFold
import sklearn.metrics
import numpy as np
```

```
In [4]: import tensorflow as tf
from tensorflow import keras
from tensorflow.keras import layers
from tensorflow.keras import regularizers
import matplotlib.pyplot as plt
```

```
In [5]: from sklearn.datasets import load_diabetes
(X, y) = load_diabetes(return_X_y=True, as_frame=True)
X.head()
# data是被normalize過的
```

Out[5]:

	age	sex	bmi	bp	s1	s2	s3	s4	s5
0	0.038076	0.050680	0.061696	0.021872	-0.044223	-0.034821	-0.043401	-0.002592	0.019908
1	-0.001882	-0.044642	-0.051474	-0.026328	-0.008449	-0.019163	0.074412	-0.039493	-0.068330
2	0.085299	0.050680	0.044451	-0.005671	-0.045599	-0.034194	-0.032356	-0.002592	0.002864
3	-0.089063	-0.044642	-0.011595	-0.036656	0.012191	0.024991	-0.036038	0.034309	0.022692
4	0.005383	-0.044642	-0.036385	0.021872	0.003935	0.015596	0.008142	-0.002592	-0.031991

```
In [6]: from sklearn.preprocessing import OneHotEncoder
enc = OneHotEncoder(handle_unknown='ignore')
def one_hot(x):
    return enc.fit_transform(x.reshape(-1, 1)).toarray()
```

```
In [7]: X_nbp = np.array(X.drop(['bp'], axis=1))
sex = np.array(one_hot(np.array(X['sex'])))
s = np.array(X.iloc[:, 4:])
ab = np.array(X[['age', 'bmi']])
abb = np.array(X[['age', 'bmi', 'bp']])
y = np.array(y)
X = np.array(X)

# 不考慮血壓 · 找一個最好的model
# sequential, autokeras: X_nbp
# funtional: ("ab" + s + sex)

# 考慮血壓 · 找一個最好的model
# sequential, autokeras: X
# funtional: ("abb" + s + sex)
```

```
In [8]: sex[0]
```

```
Out[8]: array([0., 1.])
```

model_0(sequential)跟model_1(functional)吃沒有血壓的feature · 挑一個比較好的model

```
In [9]: model_0 = tf.keras.Sequential(name="sequentialNbp")
model_0.add(layers.Dense(1,
                        input_shape=(X_nbp.shape[1], )))
```

```
In [10]: ab_in_m1 = keras.Input(shape=(ab.shape[1],), name='ab_in_m1')
ab_h1_m1 = layers.Dense(3, activation='relu',\
                        kernel_regularizer=\
                        keras.regularizers.l1_l2(l1=0.1, l2=0.01))(ab_in_m1)
o_1_m1 = layers.Dense(2)(ab_h1_m1)
s_in_m1 = keras.Input(shape=(s.shape[1],), name='s_in_m1')
s_h1_m1 = layers.Dense(4, activation='relu',\
                        kernel_regularizer=\
                        keras.regularizers.l1_l2(l1=0.1, l2=0.01))(s_in_m1)
o_2_m1 = layers.Dense(4)(s_h1_m1)
sex_m1 = keras.Input(shape=(sex.shape[1],), name='sex_m1')
o_3_m1 = layers.Dense(1)(sex_m1)
concat_m1 = layers.Concatenate()([o_1_m1, o_2_m1, o_3_m1])
h1_m1 = layers.Dense(4, name='h1_m1')(concat_m1)
outputs_m1 = layers.Dense(1, activation='linear', name='y')(h1_m1)
model_1 = keras.Model(inputs=[ab_in_m1, s_in_m1, sex_m1], \
                      outputs=outputs_m1, name='functionalNbp')
print("model_1(tf functional API)", model_1.summary())
```

Model: "functionalNbp"

Layer (type)	Output Shape	Param #	Connected to
ab_in_m1 (InputLayer)	[(None, 2)]	0	
s_in_m1 (InputLayer)	[(None, 6)]	0	
dense_1 (Dense)	(None, 3)	9	ab_in_m1[0][0]
dense_3 (Dense)	(None, 4)	28	s_in_m1[0][0]
sex_m1 (InputLayer)	[(None, 2)]	0	
dense_2 (Dense)	(None, 2)	8	dense_1[0][0]
dense_4 (Dense)	(None, 4)	20	dense_3[0][0]
dense_5 (Dense)	(None, 1)	3	sex_m1[0][0]
concatenate (Concatenate)	(None, 7)	0	dense_2[0][0] dense_4[0][0] dense_5[0][0]
h1_m1 (Dense)	(None, 4)	32	concatenate[0][0]

y (Dense)	(None, 1)	5	h1_m1[0][0]
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Total params: 105
Trainable params: 105
Non-trainable params: 0

model_1(tf functional API) None

```
In [11]: model_2 = tf.keras.Sequential(name="sequentialWbp")
model_2.add(layers.Dense(1,
                          input_shape=(X.shape[1], )))
```

model_2 3 是仿照0 1 的架構 但是feature有含血壓的 也挑一個比較好的model

```
In [12]: abb_in_m3 = keras.Input(shape=(abb.shape[1],), name='abb_in_m3')
abb_h1_m3 = layers.Dense(3, activation='relu',\
                        kernel_regularizer=\
                        keras.regularizers.l1_l2(l1=0.1, l2=0.01))(abb_in_m3)
o_1_m3 = layers.Dense(3)(abb_h1_m3)
s_in_m3 = keras.Input(shape=(s.shape[1],), name='s_in_m3')
s_h1_m3 = layers.Dense(4, activation='relu',\
                        kernel_regularizer=\
                        keras.regularizers.l1_l2(l1=0.1, l2=0.01))(s_in_m3)
o_2_m3 = layers.Dense(4)(s_h1_m3)
sex_m3 = keras.Input(shape=(sex.shape[1],), name='sex_m3')
o_3_m3 = layers.Dense(1)(sex_m3)
concat_m3 = layers.Concatenate()([o_1_m3, o_2_m3, o_3_m3])
h1_m3 = layers.Dense(3, name='h1_m3')(concat_m3)
outputs_m3 = layers.Dense(1, activation='linear', name='y')(h1_m3)
model_3 = keras.Model(inputs=[abb_in_m3, s_in_m3, sex_m3], \
                      outputs=outputs_m3, name='functionalWbp')
print("model_3(tf functional API)", model_3.summary())
```

Model: "functionalWbp"

Layer (type)	Output Shape	Param #	Connected to
abb_in_m3 (InputLayer)	[(None, 3)]	0	
s_in_m3 (InputLayer)	[(None, 6)]	0	
dense_7 (Dense) [0]	(None, 3)	12	abb_in_m3[0]
dense_9 (Dense)	(None, 4)	28	s_in_m3[0][0]
sex_m3 (InputLayer)	[(None, 2)]	0	
dense_8 (Dense)	(None, 3)	12	dense_7[0][0]
dense_10 (Dense)	(None, 4)	20	dense_9[0][0]
dense_11 (Dense)	(None, 1)	3	sex_m3[0][0]
concatenate_1 (Concatenate)	(None, 8)	0	dense_8[0][0] dense_10[0][0] dense_11[0][0]

h1_m3 (Dense) [0][0]	(None, 3)	27	concatenate_1
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y (Dense)	(None, 1)	4	h1_m3[0][0]
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Total params: 106
Trainable params: 106
Non-trainable params: 0
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```
model_3(tf functional API) None
```

```

In [13]: # 回歸問題用MSE
n_models = 4
for i in range(n_models):
    locals()['model_{}'.format(i)].compile(
        optimizer='adam',
        loss=tf.keras.losses.MeanSquaredError())
    locals()['loss_model_{}'.format(i)] = []
    locals()['val_MSE_{}'.format(i)] = []

```

```

In [14]: %%time
early_stop = tf.keras.callbacks.EarlyStopping\
(monitor='loss', patience=1, min_delta=1e-4)
rskf = RepeatedKFold(n_repeats=n_repeats, n_splits=n_splits)
for train_index, test_index in rskf.split(X, y):

    # 切training testing data

    # 考慮血壓·找一個最好的model
    # sequential(model_0), autokeras(model_4): X_nbp
    # funtional(model_1): ("ab" + s + sex)

    # 不考慮血壓·找一個最好的model
    # sequential(model_2), autokeras(model_5): X
    # funtional(model_3): ("abb" + s + sex)
    X_tr, X_te = X[train_index], X[test_index]
    y_tr, y_te = y[train_index], y[test_index]
    ab_tr, s_tr, sex_tr = ab[train_index], s[train_index], sex[train_index]
    ab_te, s_te, sex_te = ab[test_index], s[test_index], sex[test_index]
    abb_tr, abb_te = abb[train_index], abb[test_index]
    X_nbp_tr, X_nbp_te = X_nbp[train_index], X_nbp[test_index]

    ###fit models###
    # 0 1 是不吃血壓的model 2 3是吃血壓的model
    history_0 = model_0.fit(X_nbp_tr, y_tr, epochs=n_epochs, \
                           verbose=0, callbacks=[early_stop])
    history_1 = model_1.fit(\
        {'ab_in_m1': ab_tr, 's_in_m1': s_tr, 'sex_in_m1': sex_tr},
        {'y': y_tr}, epochs=n_epochs, \
        verbose=0, callbacks=[early_stop])

    history_2 = model_2.fit(X_tr, y_tr, epochs=n_epochs, \
                           verbose=0, callbacks=[early_stop])
    history_3 = model_3.fit(\
        {'abb_in_m3': abb_tr, 's_in_m3': s_tr, 'sex_in_m3': sex_tr},
        {'y': y_tr}, epochs=n_epochs, \
        verbose=0, callbacks=[early_stop])

    ###拿到各model的prediction來算MSE
    pred_0 = model_0.predict(X_nbp_te)
    pred_1 = model_1.predict(
        {'ab_in_m1': ab_te, 's_in_m1': s_te, 'sex_in_m1': sex_te})
    pred_2 = model_2.predict(X_te)
    pred_3 = model_3.predict(
        {'abb_in_m3': abb_te, 's_in_m3': s_te, 'sex_in_m3': sex_te})

    for i in range(n_models):

        ###把Loss存起來###
        locals()['loss_model_{}'.format(i)].extend\
        (locals()['history_{}'.format(i)].history['loss'])

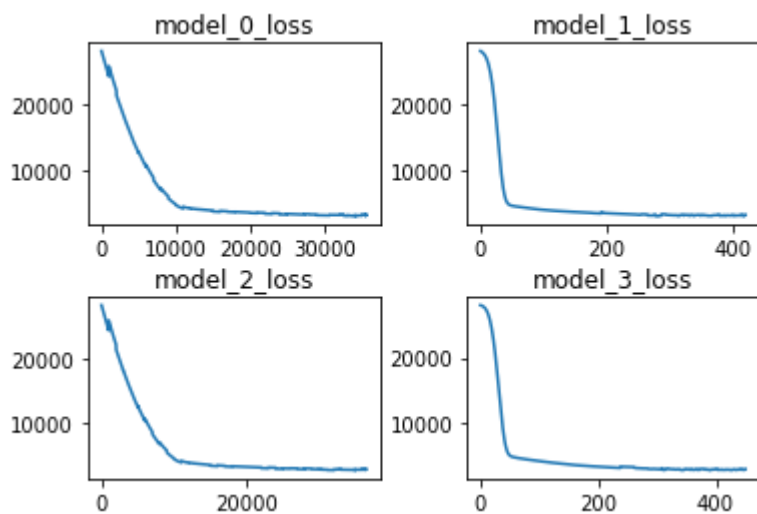
        ###validation data用來evaluate model好壞by MSE###
        locals()['val_MSE_{}'.format(i)].append\
        (sklearn.metrics.mean_squared_error\

```

```
(y_te, locals()['pred_{}'.format(i)])
```

Wall time: 8min 17s

```
In [15]: plt.subplots_adjust(hspace=0.4, wspace=0.3)
for i in range(n_models):
    plt.subplot(2, 2, i+1)
    plt.title('model_{}_loss'.format(i))
    plt.plot(locals()['loss_model_{}'.format(i)])
```



```
In [16]: # 把每次cv完的結果取平均
for i in range(n_models):
    locals()['mean_val_MSE_{}'.format(i)] = \
    np.mean(locals()['val_MSE_{}'.format(i)])
    # mean of (n_splits * n_repeats) values
```



```
In [18]: k = locals()
no_bp_model_MSE = [(k['mean_val_MSE_{}'.format(i)]) for i in range(2)]
no_bp_model_best_idx = np.argmin(no_bp_model_MSE)
no_bp_model_best_MSE = np.min(no_bp_model_MSE)
with_bp_model_MSE = [(k['mean_val_MSE_{}'.format(i)]) for i in range(2, 4)]
with_bp_model_best_idx = np.argmin(with_bp_model_MSE) + 2
with_bp_model_best_MSE = np.min(with_bp_model_MSE)

print('不考慮血壓model裡面，預測能力最好的是model_{}'.format(no_bp_model_best_idx), '平均MSE={}'.format(no_bp_model_best_MSE))
print('考慮血壓model裡面，預測能力最好的是model_{}'.format(with_bp_model_best_idx), '平均MSE={}'.format(with_bp_model_best_MSE))

if no_bp_model_best_MSE < with_bp_model_best_MSE:
    print('考慮血壓的模型有較高的MSE，可知血壓對於糖尿病病程的影響不大，若考慮血壓會降')
else:
    print('考慮血壓的模型有較低的MSE，可知血壓這個feature對於預測糖尿病病程有一定的貢獻')
```

不考慮血壓model裡面，預測能力最好的是model_1，平均MSE=3133.710642613691。

考慮血壓model裡面，預測能力最好的是model_3，平均MSE=2971.6992045433326。

考慮血壓的模型有較低的MSE，可知血壓這個feature對於預測糖尿病病程有一定的貢獻