Raman spectroscopy of Diabetes

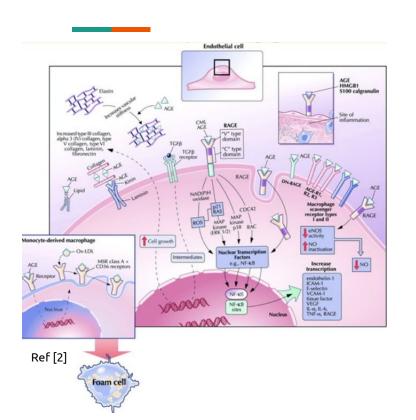
Present to:

Dr. Chaklam Silpasuwanchai

Present by:

Ati Tesakulsiri st123009 Sorn Rambo st12348 Duc Nguyen Hong st122934 Pyae Sone Kyaw Min Set Aung st122825 Nguyen Thai Anh st122910

Introduction



Traditionally, we can test the diabete on blood. While at our **skin** we also have **marker** to test them.

Including

- 3-deoxyglucosone
- glyoxal
- glyoxal-lysine dimer GOLD
- methylglyoxal
- methylglyoxal-derived hydroimidazolone
- pentosidine

Luckily, the raman spectroscopy technique can detect these marker.

Meanwhile, It quite hard to detect because our skin surface also have other that can also detected.



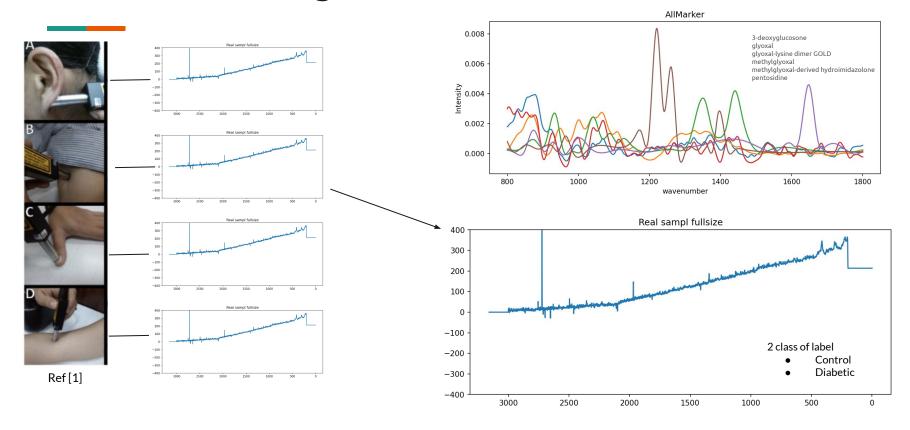
Objective

- To apply our data scientist skill in other kind of dataset.
- To classify the diabetic person using the raman spectrum with ML and DL method.
- Compare and find ML, DL models that will bring high efficiency.

Inspiration

• Come up with the better deep learning model compare the owner with more **testing set** (4 compare to 2)

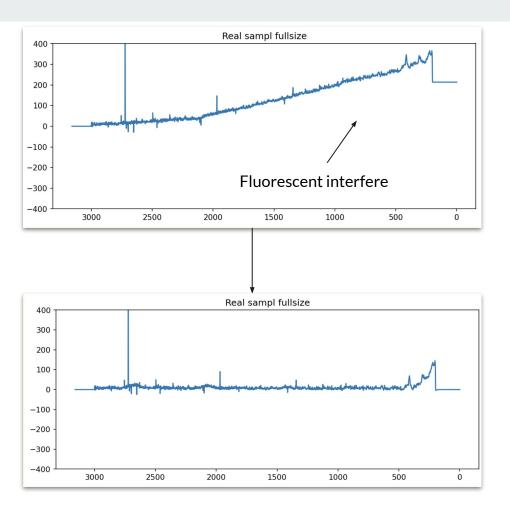
Data understanding



Preprocessing of spectrum

Baseline Removal (Fluorescence Removal)

Vancouver raman algorithm

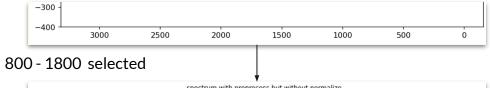


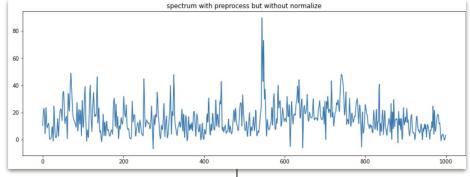
(Input) slicing

Preprocessing

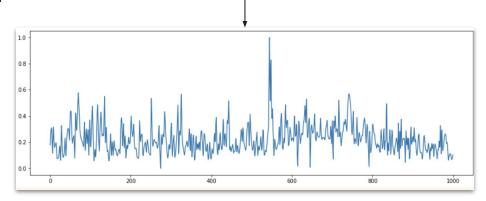
of spectrum

WaveNumber





Normalization with Min max scaler



Train test split

• 20% (4 samples) of each location was used as testing data and kept secret.

• Remaining 80% (16 samples of each location) will be split for training and validating with 3:1 ratio.

Modeling and Training

SVM

SVM (Support Vector Machine)

- SVM is a supervised learning
- SVM has four different kernels(Linear, Polynomial, RBF and sigmoid)
- In this project we use Linear, Polynomial and RBF kernels to calculate the cross validation(cv=5) to know which kernels has better score
- After comparing the cross validation score we choose linear kernel to build our prediction model
- use sklearn library

Estimated Average Cross Validation score from Linear Kernel(CV=5)

	EarLobe	Inner Arm	Thumb Nails	Veins
Linear kernel	57%	57%	62%	57%
Polynomial Kernel	63%	52%	58%	50%
RBF (radial basis function) Kernel	25%	37%	52%	41%

F1 Precision and Recall score

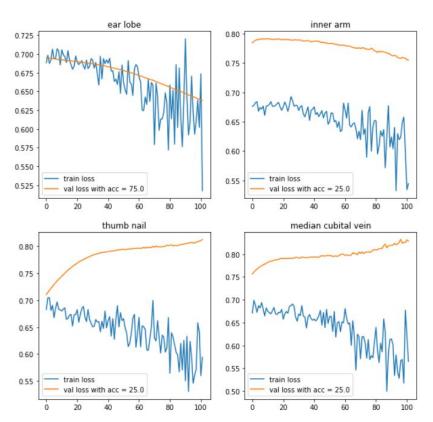
	Earlobe	Inner arm	Thumb nail	Vein
F1	42.86	73.3	42.86	73.33
Precision	37.5	75	37.50	75.00
Recall	50	83.3	50.00	83.33

Deep learning

Fixed parameter

- Loss function Cross Entropy Loss
- Optimizer Adam
- Learning rate 0.0001
- epochs = 5000
- Cross validation 5 time
 - Seed [25811243, 34806794, 2022, 1910, 222]

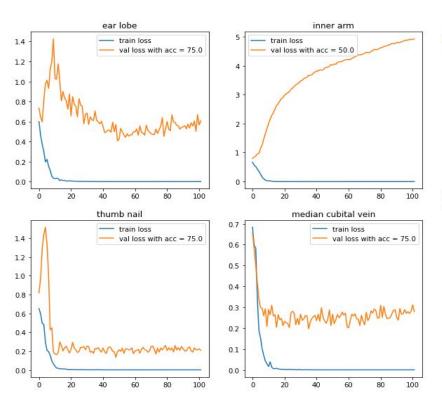
Modeling: Artificial Neural Network (ANN)



```
IntANN(
   (fc1): Linear(in_features=1000, out_features=28, bias=True)
   (snm): Softmax(dim=1)
   (do1): Dropout(p=0.5, inplace=False)
   (fc2): Linear(in_features=28, out_features=14, bias=True)
   (fc3): Linear(in_features=14, out_features=2, bias=True)
)
```

Convolutional Neural Network-1D

loss plot for CNN 22



```
RamConv1d_mx(
   (conv1): Conv1d(1, 10, kernel_size=(3,), stride=(1,))
   (relu1): ReLU()
   (conv2): Conv1d(10, 50, kernel_size=(3,), stride=(1,))
   (maxpool1): MaxPool1d(kernel_size=2, stride=2, padding=0, dilation=1, ceil_mode=False)
   (maxpool2): MaxPool1d(kernel_size=2, stride=2, padding=0, dilation=1, ceil_mode=False)
   (relu2): ReLU()
   (drop): Dropout(p=0.5, inplace=False)
   (fc1): Linear(in_features=12400, out_features=1000, bias=True)
   (fc2): Linear(in_features=1000, out_features=14, bias=True)
   (fc3): Linear(in_features=14, out_features=2, bias=True)
)
```

Convolutional Neural Network-1D

```
Epoch [5000/5000], Step [1/1.0], Loss: 0.0000 ++++++Validation+++++ Loss: 0.61 - Acc: 75.00

END OF MODEL for ear lobe with val acc = 75.0

Epoch [5000/5000], Step [1/1.0], Loss: 0.0000 ++++++Validation+++++ Loss: 4.92 - Acc: 50.00

END OF MODEL for inner arm with val acc = 50.0

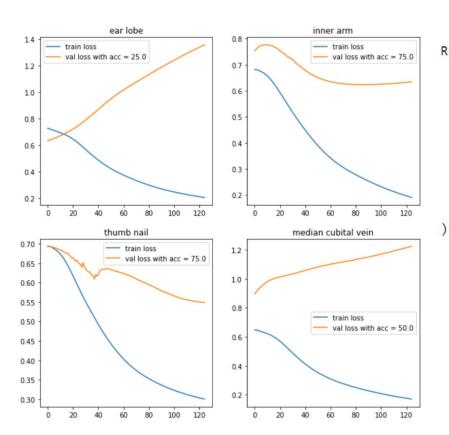
Epoch [5000/5000], Step [1/1.0], Loss: 0.0000 ++++++Validation+++++ Loss: 0.21 - Acc: 75.00

END OF MODEL for thumb nail with val acc = 75.0

Epoch [5000/5000], Step [1/1.0], Loss: 0.0000 ++++++Validation+++++ Loss: 0.28 - Acc: 75.00 ++++++Validation++++++ Loss: 0.27 - Acc: 75.00

END OF MODEL for median cubital vein with val acc = 75.0
```

Modeling - RNN



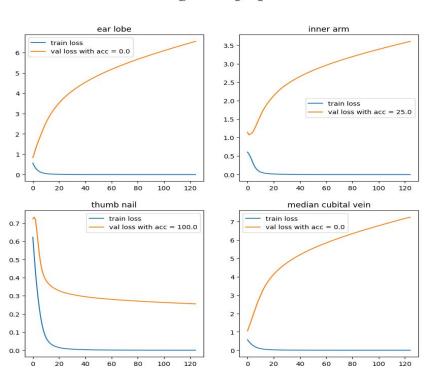
```
RamanLSTM(
  (lstm): LSTM(1000, 224, batch_first=True, dropout=0.5)
  (linear): Linear(in_features=224, out_features=112, bias=True)
  (linear2): Linear(in_features=112, out_features=56, bias=True)
  (linear3): Linear(in_features=56, out_features=28, bias=True)
  (linear4): Linear(in_features=28, out_features=14, bias=True)
  (linear5): Linear(in_features=14, out_features=2, bias=True)
  (do): Dropout(p=0.4, inplace=False)
  (relu): ReLU()
  (softmax): Softmax(dim=1)
)
```

Modeling - RNN

```
Epoch [5000/5000], Step [1/1.0], Loss: 0.1779 ++++++Validation+++++ Loss: 1.45 - Acc: 25.00 ++++++Validation+++++ Loss: 1.45 - Acc: 25.00 END OF MODEL for ear lobe with val acc = 25.0 Epoch [5000/5000], Step [1/1.0], Loss: 0.1877 ++++++Validation+++++ Loss: 0.64 - Acc: 75.00 END OF MODEL for inner arm with val acc = 75.0 Epoch [5000/5000], Step [1/1.0], Loss: 0.1868 ++++++Validation+++++ Loss: 0.58 - Acc: 75.00 ++++++Validation+++++ Loss: 0.57 - Acc: 75.00 END OF MODEL for thumb nail with val acc = 75.0 Epoch [5000/5000], Step [1/1.0], Loss: 0.3349 ++++++Validation+++++ Loss: 1.38 - Acc: 25.00 ++++++Validation+++++ Loss: 1.09 - Acc: 0.00 ++++++Validation+++++ Loss: 1.33 - Acc: 25.00 END OF MODEL for median cubital vein with val acc = 25.0
```

RNN with GRU

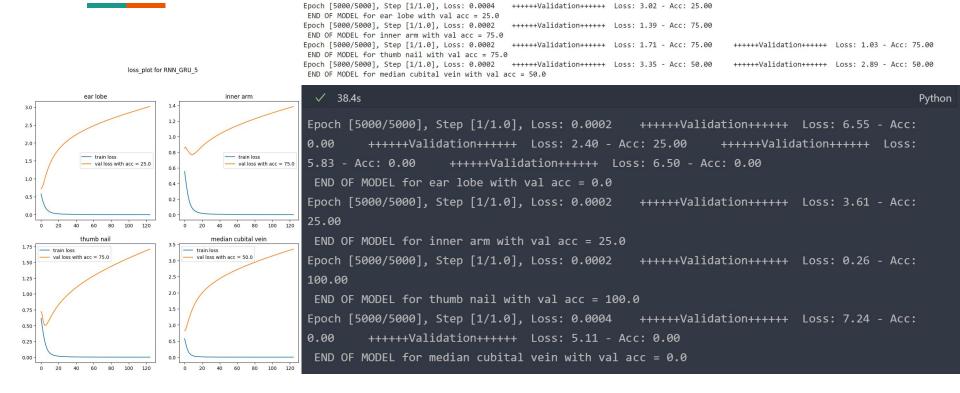
loss plot for RNN GRU 4



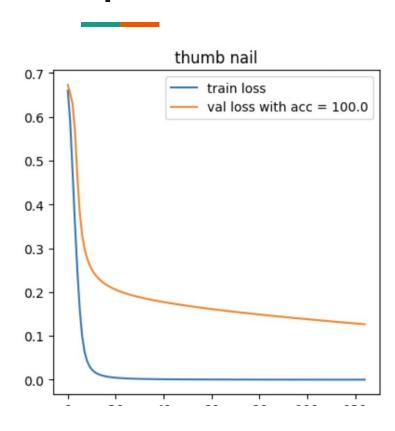
```
class RamGRU(nn.Module):
        def init (self, input size = 1000, hidden size=50, out size=2):
           super(). init ()
           self.gru = nn.GRU(input_size, hidden_size, batch_first=True, dropout=0.2)
           self.linear = nn.Linear(hidden_size, out_size)
       def forward(self, seg):
           out, _ = self.gru(seq)
           out = self.linear(out)
           return out
   model = RamGRU().to(device)
   criterion = nn.CrossEntropyLoss()
   optimizer = torch.optim.Adam(model.parameters(), Lr=0.0001)
   model
RamGRU(
  (gru): GRU(1000, 50, batch_first=True, dropout=0.2)
  (linear): Linear(in features=50, out features=2, bias=True)
```

So why GRU?

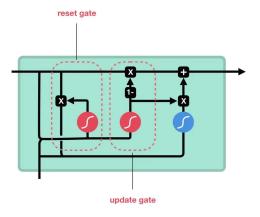
"Computationally efficient" to get fair and balanced accuracy!



"Simple and Effective!"

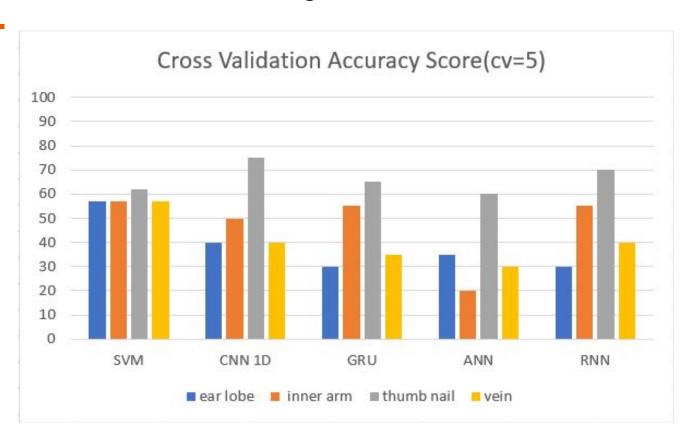




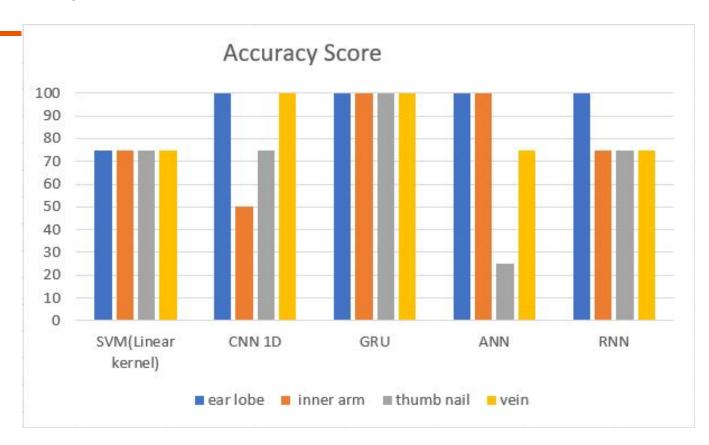


Conclusion

Cross Validation Accuracy score of different models



Accuracy Score of models with test dataset



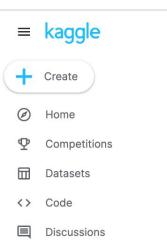
Reference

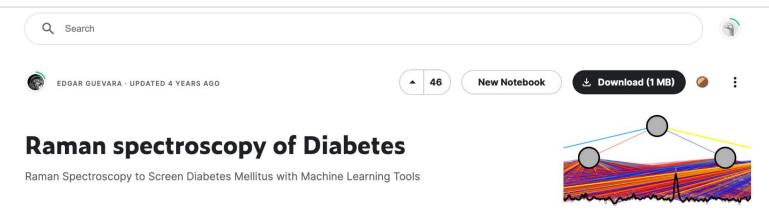
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Thank you

Data source







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Contributors 6















• MAIN Raman spectroscopy of Diabetes

this respiratory created for implement few ML model.

- Plant Village
- EEG Motor Movement/Imagery

MLproject_group2work

RAMAN FOR Depth profiling of ADIPOSETISSUE

Contributor

- st123009 Ati Tesakulsiri
- st123418 Sorn Rambo link
- st122934 Duc Nguyen link
- st123225 Pyae Sone Kyaw link
- st122825 Min Set Aung link
- st122910 Nguyen Thai Anh Link











Fluorescence Removal

