SN_DREAMS Risk Factor Clustering using Autoencoders

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Recap

- 13 Risk Factors for Diabetic Retinopathy (DR)
- 4 Categorical and 9 Continuous Columns
- Expert-Labelled Primary and Secondary Risk Factors
- Data points (Patients) with DR = 1 are sparse => Imbalanced Data
- 3 Approaches used before:
 - 1. K-means, Agglomerative Clustering
 - 2. KNN Classifier and ROC_AUC Score
 - 3. VAE and Weight Score

Modifications to previous code (1)

- Continuous Columns:
 - 4 risk factors
 - Range: >=0
 - Standard Scaler applied
- Categorical Columns:
 - 9 risk factors
 - Range: [0, 1]
 - No Standardization Applied
- Evaluation of Primary/Secondary prediction using a Confusion Matrix

Evaluation using Confusion Matrix

- Compare 'Actual' and 'Predicted' labels
- 'Actual' labels (Experts)
- Create Confusion Matrix
- Count TP, TN, FP, FN

 	+ Actual Primary +	++ Actual Secondary				
Predicted Primary Predicted Secondary	4 2	2				
Features in Correct clusters = 9 Features in Wrong clusters = 4						

+	+	++	+
Risk Factor	Actual	Predicted	Correctness
+	+	++	+
gen_cat	2	2	Correct
Hypertension_cat	1	2	Wrong
IHD_cat	2	2	Correct
insulin_treatment_cat	1	2	Wrong
fam_his_diab_cat	2	2	Correct
bp_sys	1	1	Correct
Physical_AS_cat	2	2	Correct
ann_family_in	2	2	Correct
HbA1c_grade_cat	1	1	Correct
agegrp_cat	2	1	Wrong
BMIcat	2	1	Wrong
DurYrs	1	1	Correct
FBS_Grp_cat	1	1	Correct
+	+	++	+

KNN Results

- KNN
 - SMOTE-ENN
 - 70:30 Train Test Split
 - K = 5
 - Metrics: ROC-AUC Score and Classification Accuracy
- 8 Incorrectly Classified Features
 - 4 False Positives
 - 4 False Negatives

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Wrongly Classified Features:

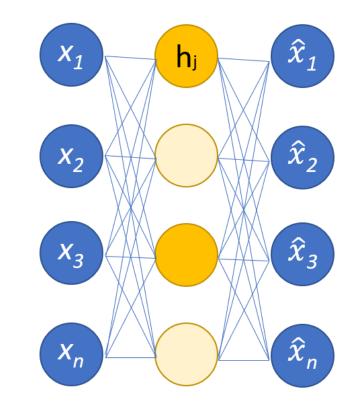
gen_cat
IHD_cat
insulin_treatment_cat
bp_sys
HbA1c_grade_cat
agegrp_cat
BMIcat
FBS_Grp_cat
```

Intro to Autoencoders

 Motivation: Using a Dense representation via Deep Learning may better be suited for Feature Selection (Primary/Secondary)

Autoencoder

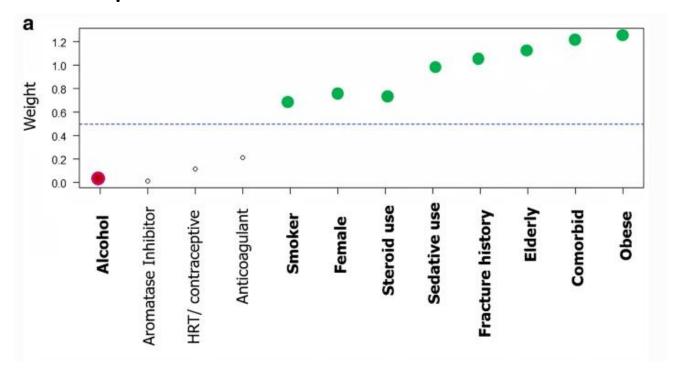
- Artificial Neural Network
- Learns representation (Encoding) from data
- Validates, Refines the encoding
- Used as generative models
- Encoder: Maps [Input -> Code]
- Decoder: Maps [Code -> Reconstructed Input]



Reference Paper

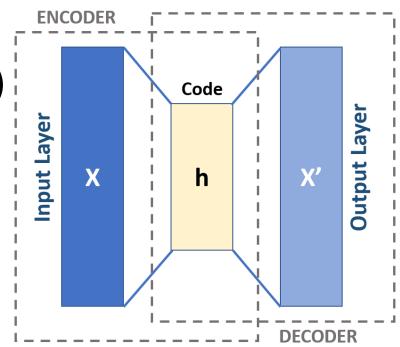
- Autoencoder Weights to select Features
- 8 risk factors Selected
- Same as those identified by clinical experts

Machine Learning for Feature Selection and Cluster Analysis in Drug Utilisation Research [Khalid et al. 2019]



Autoencoder (Attempt 3)

- 70:30 Train Test Split
- Standard Scaler (Only to continuous Columns)
- 2-layer Autoencoder
 - Densely Connected *Code Layer* (7 neurons)
 - Dense Output Layer (13 neurons)
 - 202 Parameters
- Training
 - Mean Absolute Error, Adam Optimizer, 15 epochs
- Metric: Weights Learnt by Code Layer to score features
- Threshold = Median (?)



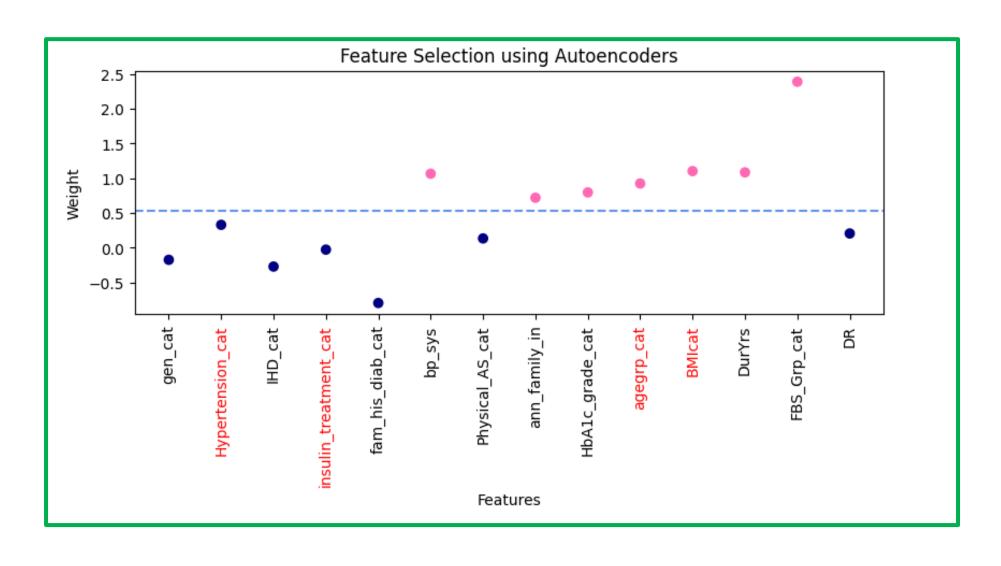
Nature of Results

- Good Results most of the time (<=4 errors)
- However, lot of variation
- Threshold Selection
 - A. Threshold
 - B. Median
- Save Weights on a good result (<=2 results)
- Reload Weights (To eliminate training time)

Autoencoder Results (1)

+	+	·	++
Risk Factor	Actual	Predicted	Correctness
+			++
gen_cat	2	2	Correct
Hypertension_cat	1	2	Wrong
IHD_cat	2	2	Correct
insulin_treatment_cat	1	2	Wrong
fam_his_diab_cat	2	2	Correct
bp_sys	1	1	Correct
Physical_AS_cat	2	2	Correct
ann_family_in	2	2	Correct
HbA1c_grade_cat	1	1	Correct
agegrp_cat	2	1	Wrong
BMIcat	2	1	Wrong
DurYrs	1	1	Correct
FBS_Grp_cat	1	1	Correct
+	+	+	++

Autoencoder Results (2)



References

- https://www.tensorflow.org/tutorials/generative/autoencoder
- https://scikit-learn.org/stable/modules/classes.html#module-sklearn.cluster
- https://towardsdatascience.com/dimensionality-reduction-pca-versus-autoencoders-338fcaf3297d
- Khalid, S., Prieto-Alhambra, D. Machine Learning for Feature Selection and Cluster Analysis in Drug Utilisation Research. *Curr Epidemiol Rep* **6**, 364–372 (2019).