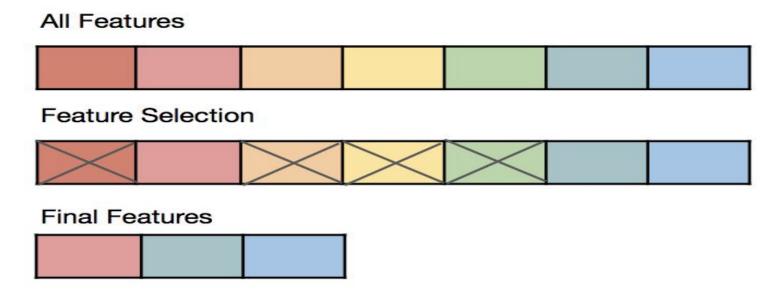
Agnostic Feature Selection

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1. Feature Selection

- Feature Selection is the process of selecting a subset of relevant features for use in model construction.
- Reasons for feature selection:
 - simplification of models to make them easier to interpret
 - shorter training times
 - avoid the curse of dimensionality
 - enhanced generalization by reducing overfitting
- The central premise when using a feature selection technique is that the data contains some features that are either redundant or irrelevant, and can thus be removed without incurring much loss of information.
- In difference to feature extraction, which creates new features from functions of the original features, feature selection returns a subset of the features.
- Possible applications:
 - Reduce text data
 - DNA microarray



Source: 1)

3. AgnoS

- Problems with Vanilla Autoencoder (AE) for feature selection:
 - O How to extract the feature importance from the model?
 - How to estimate the hidden layer size?
 - How to prevent the model from focusing on redundant features?
- Solutions for the above problems (introducing AgnoS):
 - Use a score function that extracts the feature importance from the trained AE
 - Use the Poisson model to estimate the intrinsic dimension (ID) of the feature space
 - Use one of three regularizers to enforce sparsity in the model

Algorithm AgnoS

: Feature set $F = \{f_1, ..., f_D\}$ Input

Parameter : λ

: Ranking of features in F Output

Normalize each feature with zero and unit variance.

Estimate intrinsic dimension ID of F.

Initialize neural network with d = ID neurons in the hidden layer.

R epeat

Backpropagate L(F)

until convergence

Rank features by decreasing scores with Score (f_i)

$$AgnosW: L(F) = \sum_{i=1}^{D} \|\hat{f}_{i} - f_{i}\|_{2}^{2} + \lambda \sum_{i=1}^{D} \|W_{i,.}\|_{2}$$

$$Score_W(f_i) = ||W_{i,.}||_{\infty}$$

$$AgnosG: L(F) = \sum_{i}^{D} \|\hat{f}_i - f_i\|_2^2 + \lambda \sum_{i=1}^{D} \sqrt{\sum_{k=1}^{n} \sum_{j=1}^{d} (\frac{\partial \phi_j}{\partial f_i}(x_k))^2}$$

$$Score_G(f_i) = \max_{j \in [1, \dots, d]} \sum_{k=1}^{n} (\frac{\partial \phi_j}{\partial f_i}(x_k))^2$$

$$Score_G(f_i) = \max_{j \in [1, ..., d]} \sum_{k=1}^{n} \left(\frac{\partial \phi_j}{\partial f_i}(x_k)\right)^2$$

$$AgnosS: L(F) = \sum_{i}^{D} ||\hat{f}_{i} - f_{i}||_{2}^{2} + \lambda \sum_{i=1}^{D} |a_{i}|$$

 $Score_S(f_i) = |a_i|$

Site notes:

- W: Matrix of encoder weights
- f_i : Feature at position i
- : Reconstructed feature i
- λ: Regularization coefficient
- D: Dimensionality of the feature space
- ID: Estimated intrinsic dimensionality
- W_i : Weight vector for feature i
- Φ : Output vector of the encoder function with dimensionality d
- x_k : Sample in row k of the dataset
- a: Slack variable vector with dimensionality D

2. Experimental Setting

- Hyperparameters
 - Hidden layer size: Chosen by ID estimator; Adam Optimizer; Mean squared error loss; Learning rate: 0.01; Epochs: 150; Regularization factor: 1
- Metrics
- K-means clustering accuracy (ACC) and coefficient determination (R² score)

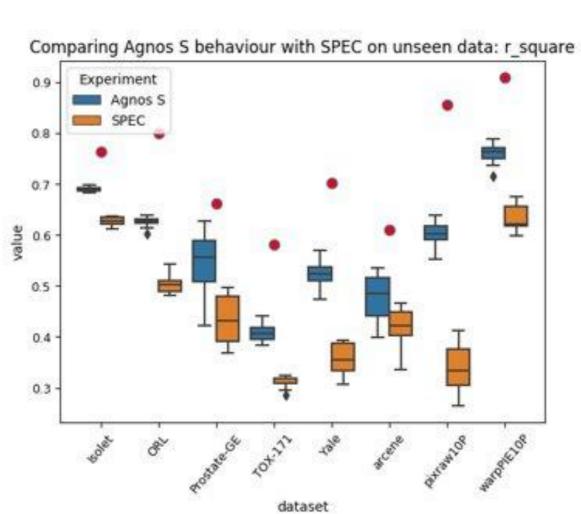
Dataset	# Samples	# Features	# Classes	ID	Data Type
arcene	200	10000	2	40	Medical
Isolet	1560	617	26	9	Sound processing
ORL	400	1024	40	6	Face image
pixraw10P	100	10000	10	4	Face image
ProstateGE	102	5966	2	23	Medical
TOX171	171	5748	4	15	Medical
warpPie10P	130	2400	10	3	Face image
Yale	165	1024	15	10	Face image
BASEHOCK	1993	4862	2	PCA	Text
COIL20	1440	1024	50	PCA	Object Images
GLI-85	85	22283	2	PCA	Microarray, biological

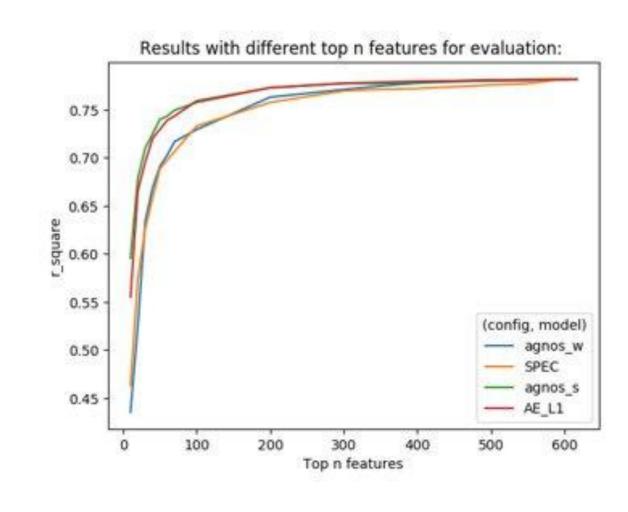
4. Results

- We managed to achieve comparable results to the paper using AgnoS-S and AgnoS-W
- The introduced R² score is less susceptible to variations
- Experiment 1 comparing AgnoS-S to SPEC
 - AgnoS-S performs slightly better but has more variance
 - But AgnoS-S takes a lot longer to train than its counterpart
- Experiment 2 comparing AgnoS-S to SPEC with unseen data
 - Complex algorithms are worse at generalizing Accuracy is now more in favor of SPEC
- R² is still better when using AgnoS-S
- Random feature selection was very close in terms of accuracy and R²

• Experiment 3 - comparing AgnoS-S to random feature selection

- score and in some cases it was even better than the AgnoS-S values
- Experiment 4 comparing different scores on top n features
 - In the paper only the top 100 features are selected for evaluation
- So we tried using a different amount of top selected features
- Drawback of AgnoS is the long runtime
 - Added early stopping reduce it
- A L1 regularized autoencoder performs worse than AgnoS-S
- A plain autoencoder performs pretty similar to AgnoS-S and better than AgnoS-W





Experiment 2

Experiment 4

- Two plots for each experiment one for accuracy and one for R² score
- The red circle in the boxplot shows the results in the paper

5. Conclusion

- Random feature selection is not as bad as it seemed to be
- It is hard to replicate paper results just using the paper as guidance
- The R² scores are pretty similar for every method on one dataset, this raises doubts for its information value
- It makes sense to question everything explained by the authors, as one can learn a lot more and have different points of view

Sources:

Leibniz Universität Hannover

1) https://en.wikipedia.org/wiki/Feature selection 2) https://ecmlpkdd2019.org/downloads/paper/744.pdf

https://nielsmitie.github.io/DM Lab/

https://github.com/Nielsmitie/DM Lab

Agnostic Feature Selection repository:

Check out our website