

# Efficient Feature Selection in the Presence of Multiple Feature Classes

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# Outline

- 1 Features come in Classes
- 2 Our Approach
  - Feature Selection using Information Theory
  - Three Part Coding (TPC) scheme
- 3 Experimental Results
- 4 Conclusion



# Feature Classes are Everywhere...

- Genes may be divided into different **Gene Families** or **Pathways**.
- In **WSD tasks**, one can have feature classes like adjacent words (  $word-1$ ,  $word+1$ ), the part of speech of the word ( $pos$ ), the topic of the document the word is in ( $tp$ ) etc.

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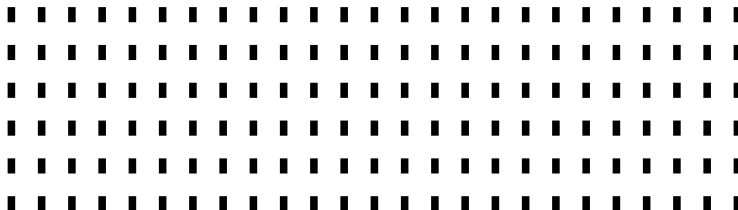
Or...

- You can use your favorite NIPS / UCI datasets and get new feature classes by doing **PCA**, **NNMF**, **Square**, **Square Root** or any other algebraic manipulation of the original features!



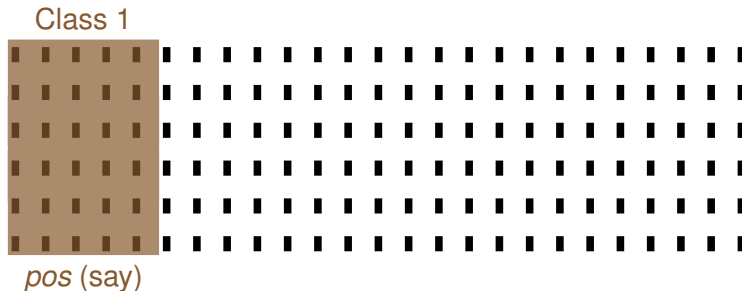
# Feature Classes in Data

## X Matrix with Feature Classes (Standard Setting)



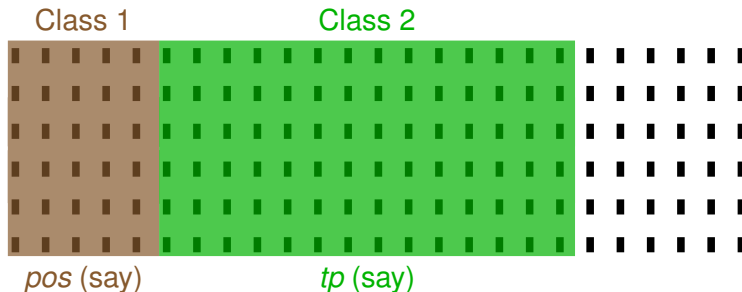
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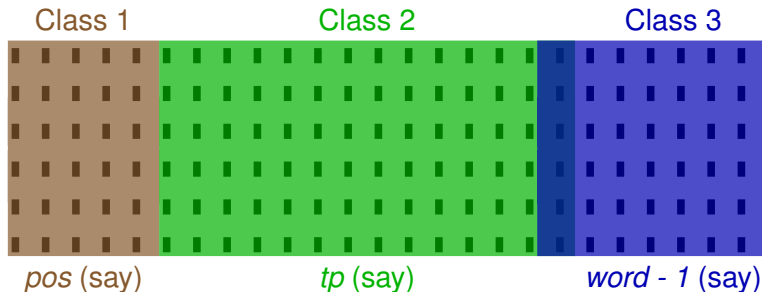
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# Feature Classes contd . . .

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- For e.g. when disambiguating various senses of word Paris (i.e. either Paris (France) or Paris Hilton), a feature class like **topic of the document** would contain more beneficial features than a feature class like **# words in the document**.



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- For e.g. when disambiguating various senses of word Paris (i.e. either Paris (France) or Paris Hilton), a feature class like **topic of the document** would contain more beneficial features than a feature class like **# words in the document**.
- Standard  $L_0$  and  $L_1$  penalty based feature selection methods are oblivious to this structure in data.



# The Big Picture of our Model

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**Once you have found good feature classes, preferentially draw features from them.**
- We provide an information theoretic approach called **Three Part Coding** to exploit the structure in data.
- TPC is a penalized likelihood method based on the MDL principle.
- TPC assumes a setting in which  $n \ll p$  i.e. lots of features and few observations.



# Formulation of TPC scheme

- The Total Description Length (TDL) can be written as:

$$S = S_E + S_M$$

$S_E \mapsto$  # Bits for encoding the residual errors given the model.

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- Reduction in TDL by adding feature 'i' to the model:

$$\Delta S^i = \Delta S_E^i - \Delta S_M^i$$

- The goal is to maximize  $\Delta S$  i.e. paying less for adding a new feature, while at the same time getting more accurate model due to increased likelihood.



# Formulation of TPC scheme contd . . .

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- We assume a Gaussian model for linear regression:

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- $\Delta S_M = I_c + I_i + I_\theta$  (Three Part Coding)

$I_c \mapsto$  # Bits to code the index of the feature class of the feature.

$I_i \mapsto$  # Bits to code the index of the feature within its feature class.

$I_\theta \mapsto$  # Bits to code the coefficient of the feature.



# Formulation of TPC scheme contd ...

- If there are 'K' feature classes and 'Q' of them are currently in the model, then

$$I_C = \begin{cases} \log(K) & \text{if the feature class is not in the model} \\ \log(Q) & \text{if the feature class is already in the model} \end{cases}$$



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- $I_\theta = 2$  (AIC like penalty)



# Analysis of TPC Scheme

- Baseline= RIC Penalty for feature indices + AIC Penalty for coefficients
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- Baseline= RIC Penalty for feature indices + AIC Penalty for coefficients
- RIC  $\mapsto$  Optimal penalty for the case  $n \ll p$  [Foster and George '94]
- **TPC wins when all or most of the features lie in a small number of Feature Classes i.e. multiple 'good' features per Feature Class.**
- $[TPC - Baseline]_{bits} = (q - Q)\log(\frac{K}{Q})$   
q  $\mapsto$  # Features Selected  
Q  $\mapsto$  # Feature Classes Selected  
K  $\mapsto$  Total # Feature Classes



# Experimental Setup and Datasets Used

- WSD Datasets containing 6 verbs  $\sim$  7000 features each [Chen and Palmer '05].
- Feature Classes  $\mapsto$  *'tp', 'word-1', 'word+1', 'pos' etc.* [# 75]





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- Feature Classes  $\mapsto$  '*tp*', '*word-1*', '*word+1*', '*pos*' etc. [# 75]
- GSEA Datasets containing 5 different phenotypes and  $\sim$  10000 features each [Mootha et. al '03].
- Feature Classes  $\mapsto$  *Gene Classes* [# 318]



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- WSD Datasets containing 6 verbs  $\sim$  7000 features each [Chen and Palmer '05].
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- Feature Classes  $\mapsto$  *Gene Classes* [# 318]
- We compare TPC to its standard counterparts i.e. Standard Stepwise and Streamwise Regressions and also to Lasso [Tibshirani '96] [ $L_1$  penalty] and Elastic Nets [Zou and Hastie '05] [ $L_1 + L_2$  penalty].



# WSD Experimental Results

- 10 Fold CV Errors (RMS Value) for WSD Datasets

Dataset	TPC	RIC	Lasso	EN
ADD	0.39	0.42	0.42	0.40
BEGIN	0.27	0.31	0.32	0.32
CALL	0.15	0.16	0.24	0.30
CARRY	0.26	0.29	0.37	0.30
DEVELOP	0.41	0.42	0.52	0.48
DRAW	0.20	0.23	0.24	0.25



# Genomic Experimental Results

- 10 Fold CV Errors (RMS Value) for GSEA Datasets

Dataset	TPC	RIC	Lasso	EN
Leukemia	0.41	0.43	0.71	0.71
Gender 1	0.21	0.24	0.73	0.73
Diabetes	0.51	0.53	0.59	0.66
Gender 2	0.21	0.26	0.90	0.84
P53	0.52	0.53	0.75	0.72

- TPC is always (significantly) better.
- Only  $\sim 14\%$  Feature Classes and  $< 1\%$  features get selected on average. So, TPC induces sparsity at the level of Feature Classes as well at the level of features.



# Conclusion

- TPC is a penalized likelihood method
  - based on the MDL principle.
  - exploits the presence of feature classes
    - unlike standard  $L_0$  and  $L_1$  methods
  - works best when good features are concentrated in a small number of features classes
  - outperforms competitors on WSD and GSEA datasets



# Thanks

