

# Multi-Task Feature Selection using the Multiple Inclusion Criterion (MIC)

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# Multiple Inclusion Criterion (MIC)

- Addresses Joint feature selection for related tasks
  - A set of related tasks, with shared feature space
  - Large number of available features, only a handful are finally relevant.
  - Goal is better predictive accuracy and interpretability of selected features
  - Example tasks: predict size of the tumor and prognosis, using gene expression values.



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  - Example tasks: predict size of the tumor and prognosis, using gene expression values.
- MIC imposes sparsity at two levels (  $\ell_0 - \ell_0$  )
  - Small number of features selected for each task (first  $\ell_0$ )
  - Small number of tasks associated with each feature (second  $\ell_0$ )



# Previous Work

- BBLasso [*Obozinski, Taskar and Jordan '09*]
  - $l_1/l_2$  penalty to enforce “Block sparsity”, feature added to all or none of the tasks.
  - Convex problem.
  - **Exact solution to approximate problem**



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- Proposed method: MIC
  - uses  $\ell_0 - \ell_0$  penalty
  - non-convex problem, but greedy algorithm yields good approximation in practice.
  - **Approximate solution to exact problem**



# General Methodology

- MIC uses MDL based coding scheme to specify a penalized likelihood method.
- 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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$S_E \mapsto$  # Bits for encoding the residual errors given the model.

$S_M \mapsto$  # Bits for encoding the model

- Maximize reduction in Description Length when adding a feature 'j' to the model:

$$\max \quad \Delta S_j = \Delta S_{jE} - \Delta S_{jM}$$





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- Assume a simple linear regression model:  $Y = WX + \epsilon$
- In this case:  $S_E = -\log\left(\exp\left(-\frac{\sum_{i=1}^n (y_i - wx_i)^2}{2\sigma^2}\right)\right)$
- $S_M = \log(m) + 2$  i.e. bits to code the feature (RIC Penalty) and its coefficient (AIC Penalty).



# Coding Schemes for MIC

- The goal is to maximize  $\Delta S_j^k = \Delta S_{jE}^k - \Delta S_{jM}^k$  i.e. the reduction in TDL by adding a feature 'j' to a subset  $k$  of  $h$  tasks.



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- The cost to code  $S_{jE}^k$  i.e. the decrease in error by adding the feature to the model of  $k$  tasks is:
- $S_E = -\log(P(Y|X, w))$

$$P(Y|X, w) = \frac{1}{((2\pi)^h |\Sigma|)^{\frac{n}{2}}} \exp \left( -\frac{1}{2} \sum_{i=1}^n [(y_i - wx_i)^T \Sigma^{-1} (y_i - wx_i)] \right)$$

where  $\Sigma$  is the  $h \times h$  covariance matrix.



# Coding Schemes for MIC contd ...

- The cost to code the model is  $S_{jM}^k$  is  $I_l + I_H + I_\theta$
- Cost to code:
  - The feature being included:  $I_l = \log(m)$ .
  - How many and which of the  $h$  tasks have that feature  $I_H = \log(h) + \log\binom{h}{k}$
  - The coefficient of the feature being included:  $I_\theta = 2 \times k$ .



# Variations of MIC

- **Full MIC**

- A feature is added to all or none of the tasks
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- **Independent MIC**

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## ● Independent MIC

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## ● Partial MIC

- A feature can be added to all, none or a subset of the tasks.





# Experimental Setup

| Name          | # Tasks<br>$h$ | # Obs.<br>$n$ | # Features<br>$m$ | Source                   |
|---------------|----------------|---------------|-------------------|--------------------------|
| Yeast Dataset | 20             | 104           | 6715              | [Litvin et. al. '09]     |
| Breast Cancer | 5              | 100           | 5000              | [van't Veer et. al. '02] |

- We compared the three versions of MIC (Partial, Full and Independent) against BBLasso [Obozinski et. al. '09] and AndoZhang [Ando et. al. '05]
- For BBLasso and AndoZhang we used their standard implementations from Berkeley Transfer Learning Toolkit.



# Experiments contd...

**Table:** 5 fold CV accuracies. *Note:* AndoZhang's NA values are due to the fact that it does not explicitly select features.

| Method        | Test Error                        | # Features Selected | # Active Coefs. |
|---------------|-----------------------------------|---------------------|-----------------|
| Yeast Dataset |                                   |                     |                 |
| Partial MIC   | <b><math>0.38 \pm 0.04</math></b> | $4 \pm 0$           | $22 \pm 4$      |
| Full MIC      | $0.39 \pm 0.04$                   | $3 \pm 0$           | $64 \pm 4$      |
| Independent   | $0.41 \pm 0.05$                   | $9 \pm 1$           | $9 \pm 1$       |
| AndoZhang     | $0.39 \pm 0.03$                   | NA                  | NA              |
| BBLasso       | $0.43 \pm 0.03$                   | $63 \pm 14$         | $1268 \pm 279$  |



# Experiments contd...

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| Method                | Test Error                        | # Features Selected. | # Active Coefs. |
|-----------------------|-----------------------------------|----------------------|-----------------|
| Breast Cancer Dataset |                                   |                      |                 |
| Partial MIC           | <b><math>0.33 \pm 0.08</math></b> | $2 \pm 0$            | $3 \pm 0$       |
| Full MIC              | $0.37 \pm 0.08$                   | $2 \pm 0$            | $11 \pm 1$      |
| Independent           | $0.36 \pm 0.08$                   | $2 \pm 0$            | $2 \pm 0$       |
| AndoZhang             | $0.44 \pm 0.03$                   | NA                   | NA              |
| BBLasso               | <b><math>0.33 \pm 0.08</math></b> | $12 \pm 4$           | $61 \pm 19$     |



# Conclusion

- MIC gives flexible coding schemes for doing “joint feature selection” in related tasks.
- Coding schemes can easily be customized to fit the problem at hand
- They capture the spirit of Bayesian priors
- Significantly (5% level, paired t-test) better than AndoZhang, on Yeast and Breast Cancer datasets.
- Comparable in accuracy to BBLasso, but provides simpler and sparser models.



# Thanks

