### Multitask Multiple Kernel Learning

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#### Multitask learning

- Common bottleneck: insufficient training data
- Combine information from several related tasks
- In order to know mutual relevance, task similarity is needed
- We seek task structure

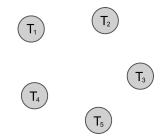


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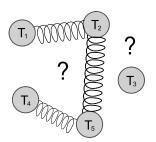


Figure: Task structure in MTL

#### MTL Framework



▶ We start from a well established MT-SVM formulation by Evgeniou and Pontil [2004]

$$\min_{\mathbf{w}_{1}, \dots, \mathbf{w}_{T}} \frac{1}{2} \sum_{t=1}^{T} \left|\left|\mathbf{w}_{t}\right|\right|^{2} + \sum_{t=1}^{T} \left|\left|\mathbf{w}_{t} - \mathbf{w}_{0}\right|\right|^{2} + C \sum_{t=1}^{T} \sum_{(\mathbf{x}, \mathbf{y}) \in \mathcal{D}_{t}} \ell\left(\left\langle \mathbf{x}, \mathbf{w}_{t} \right\rangle, \mathbf{y}\right),$$

where  $\ell$  is the hinge loss,  $\ell(z, y) = \max\{1 - yz, 0\}$ ,  $\mathbf{w}_0$  is the avrg.

▶ This corresponds to the dual (leaving out some constants)

$$\tilde{K}(\mathbf{x}_i, \mathbf{x}_j) = \beta_1 K_B(\mathbf{x}_i, \mathbf{x}_j) + \beta_2 \delta_{t(i), t(j)} K_B(\mathbf{x}_i, \mathbf{x}_j),$$

where is t(i) a task indicator function and  $eta_1,eta_2\geq 0$ 

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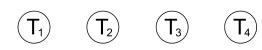


Figure: Generalization to meta-tasks.

- ▶ We use concept of meta-tasks to describe task-relationships
- ▶ Meta-task *S* captures shared property between sub-set of tasks
- ightharpoonup The collection of meta-tasks  $\mathcal I$  captures task structure



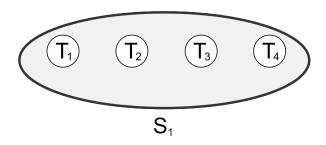


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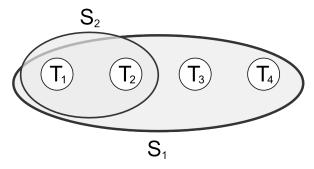


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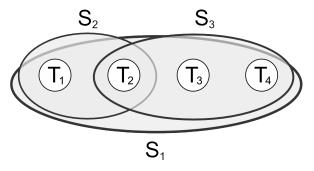


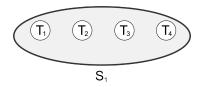
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### Decomposition of kernel matrix

$$K_S(x,y) = \left\{ egin{array}{ll} K_B(x,y), & ext{if } \mathsf{task}(x) \in S \land \mathsf{task}(y) \in S \\ 0, & ext{else} \end{array} \right.$$

Thus,  $K_S$  defines kernel w.r.t. meta-task S



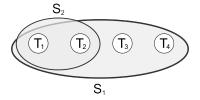
Example for collection of meta-tasks:

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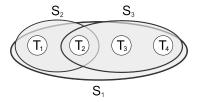
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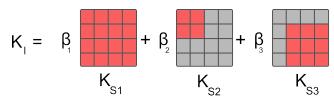
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Example for collection of meta-tasks:



### Optimization strategy: q-norm MKL

We use the MKL formulation by Kloft et al. [2009]:

$$\min_{\boldsymbol{\beta}} \max_{\boldsymbol{\alpha}} \quad \mathbf{1}^{T} \boldsymbol{\alpha} - \frac{1}{2} \sum_{i,j} \alpha_{i} \alpha_{j} y_{i} y_{j} \sum_{t=1}^{|\mathcal{L}|} \beta_{t} K_{S_{t}}(x_{i}, x_{j})$$
s.t. 
$$||\boldsymbol{\beta}||_{q}^{q} \leq 1, \boldsymbol{\beta} \geq 0$$

$$\mathbf{Y}^{T} \boldsymbol{\alpha} = 0, 0 \leq \boldsymbol{\alpha} \leq C$$

- We learn the weights  $\sum_{t=1}^{|\mathcal{I}|} \beta_t K_{S_t}$
- q lets us choose the appropriate norm (sparse/non-sparse)

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## Power-set based approach



If no prior information available:

$$\mathcal{I}_{\mathcal{P}} = \{ S | S \in \mathcal{P}(\mathcal{T}) \land S \neq \emptyset \}$$

- ▶ Consider Powerset  $\mathcal{P}(\mathcal{T})$
- Most meta-tasks in power-set will be meaningless  $\rightarrow$  learn sparse weights: q=1
- ▶ Approach can be used to identify task structure ab-initio
- $ightharpoonup 2^M$  meta-tasks ightharpoonup computationally expensive

## Hierarchical decomposition



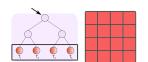










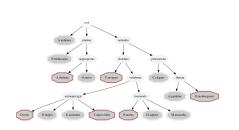
Figure: Example of taxonomy-based decomposition.

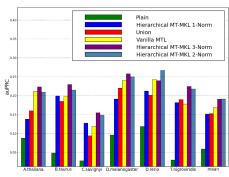
$$\mathcal{I}_{\mathcal{G}} = \{ \textit{leaves}(\textit{node}) | \textit{node} \in \mathcal{G} \}$$

- lacktriangle Meta-tasks are defined by taxonomy  ${\cal G}$
- ightharpoonup Taxonomy  $\mathcal G$  gives us reasonable groups
  - Idea is to refine structure
  - Non-sparse combination (q>1) for groupings







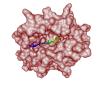


- ightharpoonup Taxonomy is used to define collection of meta-tasks  ${\mathcal I}$
- ▶ Baselines: Plain, Union, Vanilla
- ▶ Best performance for norm q = 2

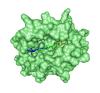
## Experiments (b): MHC-I binding prediction











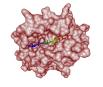
Method	Plain	Union	Vanilla MTL	Powerset MT-MKL
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- No task structure (used): Powerset MT-MKL
- Question: Can we identify meaningful structure?













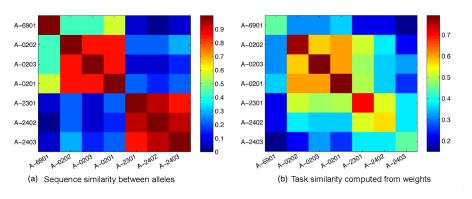
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Learned weights can also be used for interpretation purposes:

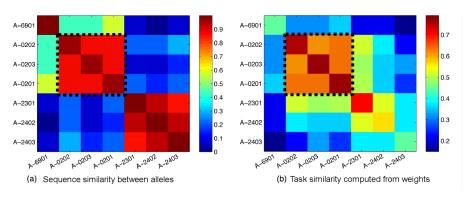


- Similarity computed from meta-task weights
- Comparison to similarity between peptide sequences
- Successfully identifies biological meaningful structure

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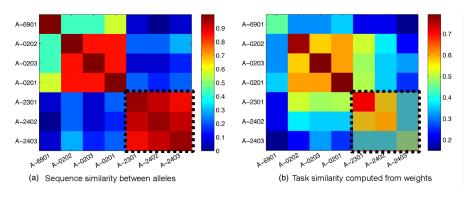


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- ► Successfully identifies biological meaningful structure

#### Conclusion



- Summary
  - ► Idea: Learning/Refining meta-tasks with MKL
  - Hierarchical Decomposition
  - Power-set approach
  - Two applications from Computational Biology
- Future work
  - Efficient optimization strategy for Powerset
  - Use other variants of MKL?

## Acknowledgments



- Nora C. Toussaint <sup>4</sup>
- Yasemin Altun<sup>2</sup>
- ▶ Jose Leiva <sup>1,2</sup>
- ► Sören Sonnenburg<sup>3</sup>
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Thank you for your attention.

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#### References I

Theodoros Evgeniou and Massimiliano Pontil. Regularized multi–task learning. In Won Kim, Ron Kohavi, Johannes Gehrke, and William DuMouchel, editors, Proceedings of the Tenth ACM SIGKDD International Conference on Knowledge Discovery and Data Mining, Seattle, Washington, USA, August 22-25, 2004, pages 109–117. ACM, 2004. ISBN 1-58113-888-1.

Marius Kloft, Ulf Brefeld, Sören Sonnenburg, Pavel Laskov, Klaus-Robert Müller, and Alexander Zien. Efficient and accurate lp-norm multiple kernel learning. In Y. Bengio, D. Schuurmans, J. Lafferty, C. K. I. Williams, and A. Culotta, editors, *Advances in Neural Information Processing Systems 22*, pages 997–1005. MIT Press, 2009.

### Proof of positive semi-definiteness I

$$\hat{K}(x,z) = M(x,z) \cdot K_{\mathsf{base}}(x,z)$$

$$\mathbf{a}^T M \mathbf{a} > 0 \quad \forall \mathbf{a} \in \mathbb{R}^n$$

$$a^{T}M\mathbf{a} = \mathbf{a}^{T} \cdot \begin{bmatrix} a_{1} & \dots & a_{1} \\ & \ddots & \\ & a_{k} & \dots & a_{k} \end{bmatrix} & 0 \\ & a_{k} & \dots & a_{k} \end{bmatrix} = \sum_{i=1}^{k} (\mathbf{a}_{i} \cdot (\sum_{j=1}^{k} \mathbf{a}_{j}))$$
$$= (\sum_{i=1}^{k} \mathbf{a}_{i}) \cdot (\sum_{j=1}^{k} \mathbf{a}_{j}) = (\sum_{j=1}^{k} \mathbf{a}_{j})^{2} \geq 0. \quad \square$$

#### Prediction function I

$$f_t(y) = \sum_{i=0}^{N} \alpha_i y_i \sum_{S_j \in \mathcal{I}; t \in S_j} \beta_j K_{S_j}(x_i, y),$$

where N is the total number of training examples of all tasks combined.

### Computing task similarity from weights I

We define the collection of task sets containing task  $t_k$  as  $\mathcal{T}_{t_k} = \{S | t_k \in S \land S \in \mathcal{T}\}$ . Using this definition, we can define the similarity  $\gamma_{k,l}$  between two tasks by summing up the weights of the shared task sets  $S_i$ 

$$\gamma_{k,l} = \sum_{S_i \in \mathcal{T}_{t_k} \cap \mathcal{T}_{t_l}} \beta_i. \tag{1}$$