NIPS*07 buzzwords

- Stochastic Gradient Descent
 - In practice for large scale problems we don't care about asymptotic convergence!
 - Do not optimize to death!
 - It is not the objective value we are interested in but the test error!
- Deep Learning
 - Template matchers (aka SVMs) are not the right approach!
 - Convolutionary neural networks with enough hidden layers are faster and more accurate!
 - Don't be afraid of non convexity, local minima!
- Invariances
 - Deep Learning will not help us with variable objects (think of cat detection)!
 - What we really need is to encode or learn invariances!

Multiple Kernel Learning

(via Semi-Infinite Linear Programming)

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Institut Rechnerarchitektur und Softwaretechnik

- Introduction and Motivation
 - When is Multiple Kernel Learning useful?
- Multiple Kernel Learning
 - Deriving the Semi-Infinite Linear Program
 - MKL SILP Algorithm
- 3 Applications, Extensions, Outlook
 - Extensions
 - Applications
 - Speed
 - Outlook



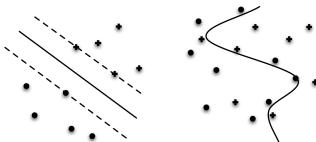
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Classification

Given training examples $(\mathbf{x}_i, y_i)_{i=1}^N \in (\mathcal{X}, \{-1, +1\})^N$



- Linear Classifier $f(\mathbf{x}) = \operatorname{sign}(\mathbf{w} \cdot \mathbf{x} + b)$
- Kernel Machine (e.g. Support Vector Machine), learn weighting $\alpha \in \mathbb{R}^N$ on training examples in kernel feature space $\Phi(\mathbf{x})$ $f(\mathbf{x}) = \operatorname{sign}\left(\sum_{i=1}^N y_i \alpha_i \mathbf{k}(\mathbf{x}, \mathbf{x}_i) + b\right),$

where Kernel $k(\mathbf{x}, \mathbf{x}') = \Phi(\mathbf{x}) \cdot \Phi(\mathbf{x}')$



Classification using Kernel Machines I

Single Kernel

- Kernel Machine (e.g. Support Vector Machine)
 - learn weighting $\alpha \in \mathbb{R}^N$ on training examples $(\mathbf{x}_i, y_i)_{i=1}^N$ in kernel feature space $\Phi(\mathbf{x})$

$$f(\mathbf{x}) = \operatorname{sign}\left(\sum_{i=1}^{N} y_i \alpha_i \mathbf{k}(\mathbf{x}, \mathbf{x}_i) + b\right)$$

- where Kernel $k(\mathbf{x}, \mathbf{x}') = \Phi(\mathbf{x}) \cdot \Phi(\mathbf{x}')$
- still linear classifier $f(\mathbf{x}) = \operatorname{sign}(\mathbf{w} \cdot \mathbf{x} + b)$ in kernel feature space, with weighting $\mathbf{w} = \sum_{i=1}^{N} y_i \alpha_i \Phi(\mathbf{x}_i)$ and examples $\mathbf{x} \mapsto \Phi(\mathbf{x})$

via kernel: non-linear discrimination in input space



Classification using Kernel Machines II

Multiple Kernels

• Linear combination of kernels $k(\mathbf{x}, \mathbf{x}') = \sum_{j=1}^{M} \beta_j \, k_j(\mathbf{x}, \mathbf{x}')$, $\beta_j \geq 0$. Learn α and β . Resulting classifier:

$$f(\mathbf{x}) = \operatorname{sign}\left(\sum_{j=1}^{M} \beta_j \sum_{i=1}^{N} y_i \alpha_i \mathsf{k}_j(\mathbf{x}, \mathbf{x}_i) + b\right)$$

Learn weighting over training examples lpha and kernels eta

Combining Heterogeneous Data

 Consider data from different domains: e.g Bioinformatics features: DNA-strings, binding energies, conservation, structure,...

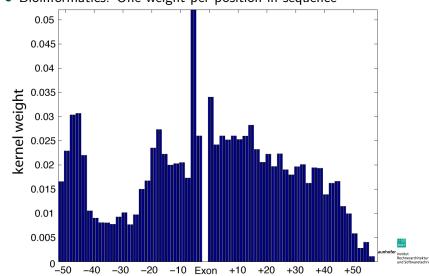
$$k(\mathbf{x}, \mathbf{x}') = \beta_1 k_{dna}(\mathbf{x}_{dna}, \mathbf{x}'_{dna}) + \beta_2 k_{nrg}(\mathbf{x}_{nrg}, \mathbf{x}'_{nrg}) + \beta_3 k_{3d}(\mathbf{x}_{3d}, \mathbf{x}'_{3d}) + \cdots$$



Interpretability

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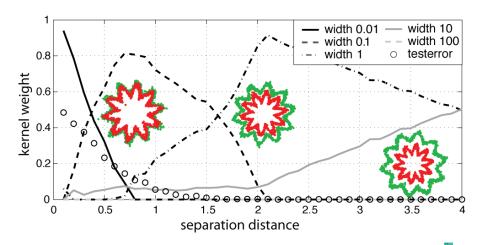
• Bioinformatics: One weight per position in sequence



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When is Multiple Kernel Learning useful?

Automated Model Selection



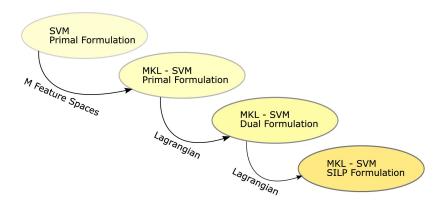


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Derivation



For details see Sonnenburg, Rätsch, Schäfer, Schölkopf 2006



SVM Primal Formulation

$$\begin{aligned} & \min & & \frac{1}{2} \|\mathbf{w}\|_2^2 + C \sum_{i=1}^N \xi_n \\ & \text{w.r.t.} & & \mathbf{w} \in \mathbb{R}^D, \boldsymbol{\xi} \in \mathbb{R}_+^N, b \in \mathbb{R} \\ & \text{s.t.} & & y_i \left(\mathbf{w}^\mathsf{T} \Phi(\mathbf{x}_i) + b \right) \geq 1 - \xi_i, \forall i = 1, \dots, N \end{aligned}$$

MKL Primal Formulation

$$\begin{aligned} & \min & & \frac{1}{2} \left(\sum_{j=1}^{M} \beta_{j} \| \mathbf{w}_{j} \|_{2} \right)^{2} + C \sum_{i=1}^{N} \xi_{n} \\ & \text{w.r.t.} & & \mathbf{w} = (\mathbf{w}_{1}, \dots, \mathbf{w}_{M}), \, \mathbf{w}_{j} \in \mathbb{R}^{D_{j}}, \quad \forall j = 1 \dots M \\ & & \beta \in \mathbb{R}_{+}^{M}, \, \boldsymbol{\xi} \in \mathbb{R}_{+}^{N}, \, \, b \in \mathbb{R} \end{aligned}$$

$$& \text{s.t.} & y_{i} \left(\sum_{j=1}^{M} \beta_{j} \mathbf{w}_{j}^{\mathsf{T}} \Phi_{j}(\mathbf{x}_{i}) + b \right) \geq 1 - \xi_{i}, \, \forall i = 1, \dots, N$$

$$& \sum_{i=1}^{M} \beta_{j} = 1$$

Properties: equivalent to SVM for M = 1; solution sparse in "blocks"; each block j corresponds to one kernel



MKL Dual Formulation

Bach, Lanckriet, Jordan 2004:

$$\begin{aligned} & \min \qquad \gamma - \sum_{i=1}^{N} \alpha_i \\ & \text{w.r.t.} \qquad \gamma \in \mathbb{R}, \boldsymbol{\alpha} \in \mathbb{R}^N \\ & \text{s.t.} \qquad 0 \leq \boldsymbol{\alpha} \leq C, \sum_{i=1}^{N} \alpha_i y_i = 0 \\ & \qquad \frac{1}{2} \sum_{r=1}^{N} \sum_{s=1}^{N} \alpha_r \alpha_s y_r y_s \mathcal{K}_j(\mathbf{x}_r, \mathbf{x}_s) - \gamma \leq 0, \ \forall j = 1, \dots, M \end{aligned}$$

Properties: equivalent to SVM for M = 1



The Semi-Infinite Linear Program I

$$\max \quad \theta$$
w.r.t.
$$\theta \in \mathbb{R}, \beta \in \mathbb{R}_{+}^{M} \text{ with } \sum_{j=1}^{M} \beta_{j} = 1$$
s.t.
$$\sum_{j=1}^{M} \beta_{j} \left(\frac{1}{2} \sum_{r=1}^{N} \sum_{s=1}^{N} \alpha_{r} \alpha_{s} y_{r} y_{s} K_{j}(\mathbf{x}_{r}, \mathbf{x}_{s}) - \sum_{i=1}^{N} \alpha_{i} \right) \geq \theta$$

$$=: S_{j}(\alpha)$$
for all α with $0 \leq \alpha \leq C$ and $\sum_{i=1}^{N} y_{i} \alpha_{i} = 0$

Properties:

- ullet linear, optimize over a convex combination of eta
- infinitely many constraints, one for each $0 \le \alpha \le C$
- can use standard SVM to identify most violated constraints

The Semi-Infinite Linear Program II

$$\begin{array}{ll} \max & \theta \\ \text{w.r.t.} & \theta \in \mathbb{R}, \beta \in \mathbb{R}_+^M \text{ with } \sum_{j=1}^M \beta_j = 1 \\ \\ \text{s.t.} & \sum_{j=1}^M \beta_j \left(\frac{1}{2} S_j(\alpha) - \sum_{i=1}^N \alpha_i \right) \geq \theta \\ \\ \text{for all } \alpha \text{ with } 0 \leq \alpha \leq C \text{ and } \sum_{i=1}^N y_i \alpha_i = 0 \end{array}$$

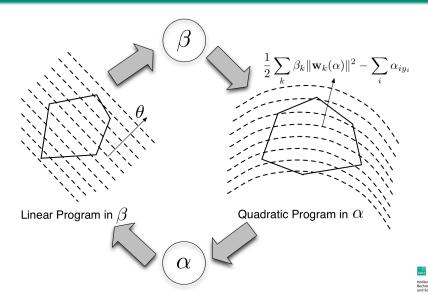
Solving the SILP:

- Column Generation
 - fast, but no known convergence rate
- Use Boosting like techniques: Arc-GV or AdaBoost*
 - known convergence rate $\mathcal{O}(\log(M)/\varepsilon^2)$
- Chunking like algorithm
 - consider suboptimal SVM solutions: empirically 3-5 times faster



Deriving the Semi-Infinite Linear Program

Solving the SILP: Column Generation I



Solving the SILP: Column Generation II

$$\label{eq:definition} \begin{split} \max &\quad \theta \\ \text{w.r.t.} &\quad \theta \in \mathbb{R}, \boldsymbol{\beta} \in \mathbb{R}_+^M \text{ with } \sum_{j=1}^M \beta_j = 1 \\ \text{s.t.} &\quad \sum_{j=1}^M \beta_j \left(\frac{1}{2} S_j(\boldsymbol{\alpha}) - \sum_{i=1}^N \alpha_i \right) \geq \theta \\ &\quad \text{for all } \boldsymbol{\alpha} \text{ with } 0 \leq \boldsymbol{\alpha} \leq C \text{ and } \sum_{i=1}^N y_i \alpha_i = 0 \end{split}$$

 iteratively find most violated constraints, solve linear program with current constraints, ..., till convergence to the global optimum

$$\sum_{i=1}^{M} \beta_{j} \left(\frac{1}{2} S_{j}(\boldsymbol{\alpha}) - \sum_{i=1}^{N} \alpha_{i} \right) = \frac{1}{2} \sum_{r=1}^{N} \sum_{s=1}^{N} \alpha_{r} \alpha_{s} y_{r} y_{s} \sum_{i=1}^{M} \beta_{j} k_{j}(\mathbf{x}_{r}, \mathbf{x}_{s}) - \sum_{i=1}^{N} \alpha_{i},$$

- solved by taking set of most violated constraints into account
- ullet most violated constraints given by SVM solution for fixed $oldsymbol{eta}$



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Regression

Primal Formulation:

min
$$\frac{1}{2} \left(\sum_{j=1}^{M} \beta_{j} \| \mathbf{w}_{j} \| \right)^{2} + C \sum_{i=1}^{N} (\xi_{i} + \xi_{i}^{*})$$
w.r.t.
$$\mathbf{w} = (\mathbf{w}_{1}, \dots, \mathbf{w}_{M}), \mathbf{w}_{j} \in \mathbb{R}^{D_{j}}, \quad \forall j = 1 \dots M$$

$$\beta \in \mathbb{R}_{+}^{M}, \ \boldsymbol{\xi} \in \mathbb{R}^{N}, \ \boldsymbol{\xi}^{*} \in \mathbb{R}_{+}^{N}, \ b \in \mathbb{R}$$
s.t.
$$\sum_{j=1}^{M} \beta_{j} \mathbf{w}_{j}^{\mathsf{T}} \Phi_{j}(\mathbf{x}_{i}) + b \leq y_{i} + \varepsilon + \xi_{i}, \ \forall i = 1 \dots N$$

$$\sum_{j=1}^{M} \beta_{j} \mathbf{w}_{j}^{\mathsf{T}} \Phi_{j}(\mathbf{x}_{i}) + b \geq y_{i} - \varepsilon - \xi_{i}^{*}, \ \forall i = 1 \dots N$$

$$M$$

One Class

Primal Formulation:

$$\begin{aligned} & \min & \quad \frac{1}{2} \left(\sum_{j=1}^{M} \beta_{j} \left\| \mathbf{w}_{j} \right\|_{2} \right)^{2} + C \sum_{i=1}^{N} \xi_{i} - \rho \\ & \text{w.r.t.} & \quad \mathbf{w} = \left(\mathbf{w}_{1}, \dots, \mathbf{w}_{M} \right), \, \mathbf{w}_{j} \in \mathbb{R}^{D_{j}}, \quad \forall j = 1 \dots M \\ & \quad \boldsymbol{\beta} \in \mathbb{R}_{+}^{M}, \, \boldsymbol{\xi} \in \mathbb{R}_{+}^{N} \\ & \text{s.t.} & \quad y_{i} \left(\sum_{j=1}^{M} \beta_{j} \mathbf{w}_{j}^{\mathsf{T}} \Phi_{j}(\mathbf{x}_{i}) \right) \geq \rho - \xi_{i}, \forall i = 1, \dots, N \\ & \quad \sum_{j=1}^{M} \beta_{j} = 1 \end{aligned}$$

Generalized for arbitrary strictly convex differentiable loss functions (Sonnenburg, Rätsch, Schäfer, Schölkopf 2006)



Multiclass

Primal Formulation (Zien, Ong 2007):

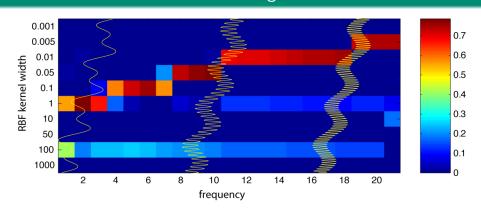
min
$$\frac{1}{2} \left(\sum_{j=1}^{M} \beta_{j} \|\mathbf{w}_{j}\|_{2} \right)^{2} + C \sum_{i=1}^{N} \xi_{n}$$
w.r.t.
$$\mathbf{w} = (\mathbf{w}_{1}, \dots, \mathbf{w}_{M}), \mathbf{w}_{j} \in \mathbb{R}^{k_{j}}, \quad \forall j = 1 \dots M$$

$$\boldsymbol{\beta} \in \mathbb{R}_{+}^{M}, \mathbf{s} \in \mathbb{R}^{N \times c}, \boldsymbol{\xi} \in \mathbb{R}_{+}^{N}, \ b \in \mathbb{R}$$
s.t.
$$\xi_{i} = \max_{u \neq y_{i}} s_{iu}, \ s_{iu} \geq 0,$$

$$\sum_{j=1}^{M} \beta_{j} \mathbf{w}_{j}^{\mathsf{T}} (\Phi_{j}(\mathbf{x}_{i}, y_{i}) - \Phi_{j}(\mathbf{x}_{i}, u)) + b_{y_{i}} - b_{u} \geq 1 - s_{iu},$$

$$\forall i = 1 \dots N, \ \forall u = 1 \dots c$$

Automated Model Selection - Regression

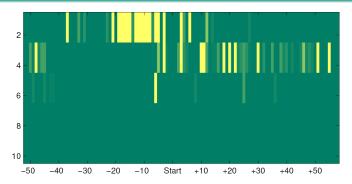


- $f(x) = \sin(ax) + \sin(bx) + cx$ for varying a
- Support Vector Regression with 10 RBF-Kernels of different width





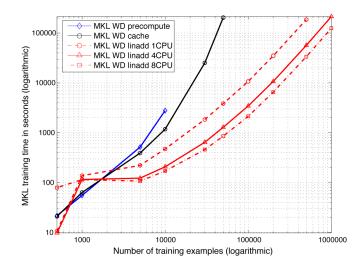
Feature Extraction



- Support Vector Classification on Bioinformatics problem, distinguish "splice sites" form "fake sites" (aligned DNA sequences)
- One weight β_j per position and per sub-sequence length
- Displayed: Learned weights of 500 kernels



A word about speed.





Summary and Outlook

MKL learns convex combination of kernels

- ⇒ allows (to some extend) for automated model selection
- ⇒ allows for interpreting SVM result
- ⇒ matches prior knowledge on real-world bioinformatics problem
 - Simple: iterative wrapper algorithm around single kernel SVM
 - General: same technique applicable to a wide range of problems (1-class, 2-class, Multiclass, Regression, ...)
 - Fast: suitable for large scale problems (> 100,000 examples)

Download free source http://www.shogun-toolbox.org.

