

Support vector machine prediction of signal peptide cleavage site using a new class of kernels for strings

Jean-Philippe Vert

Bioinformatics Center, Kyoto University,
Japan

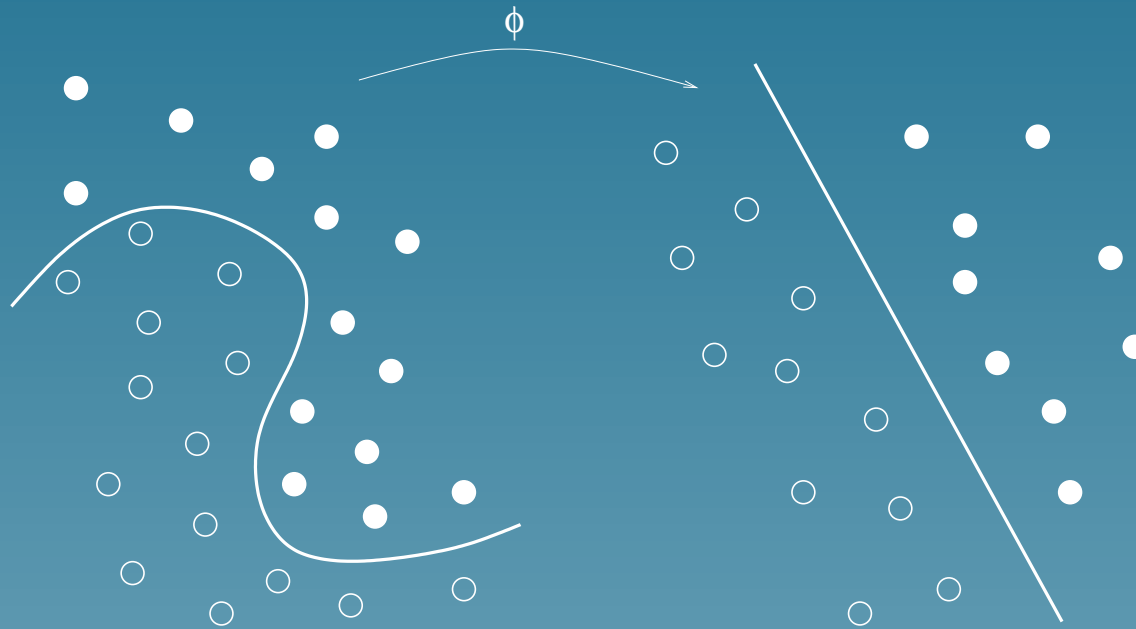
Outline

1. SVM and kernel methods
2. New kernels for bioinformatics
3. Example: signal peptide cleavage site prediction

Part 1

SVM and kernel methods

Support vector machines



- Objects to classified x mapped to a feature space
- Largest margin separating hyperplan in the feature space

The kernel trick

- Implicit definition of $x \rightarrow \Phi(x)$ through the kernel:

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- Simple kernels can represent complex Φ
- For a given kernel, not only SVM but also clustering, PCA, ICA... possible in the feature space = **kernel methods**

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 - ★ Spectrum kernel (Leslie et al., PSB 2002)

Kernel engineering

Use prior knowledge to build the geometry of the feature space through $K(\cdot, \cdot)$

Part 2

New kernels for bioinformatics

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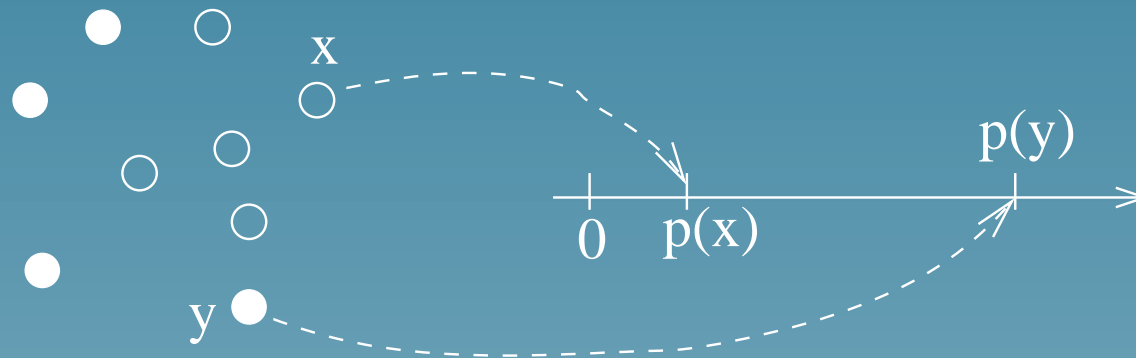
- \mathcal{X} a set of (structured) objects
- $p(x)$ a probability distribution on \mathcal{X}
- How to build $K(x, y)$ from $p(x)$?

Product kernel

$$K_{prod}(x, y) = p(x)p(y)$$

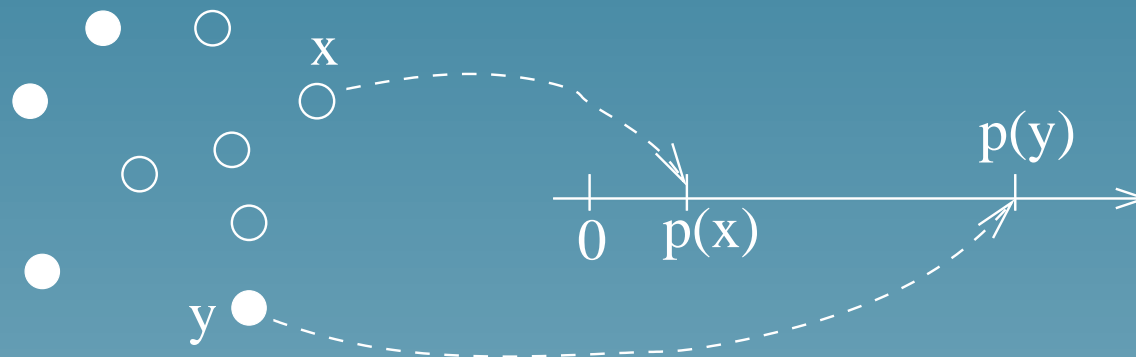
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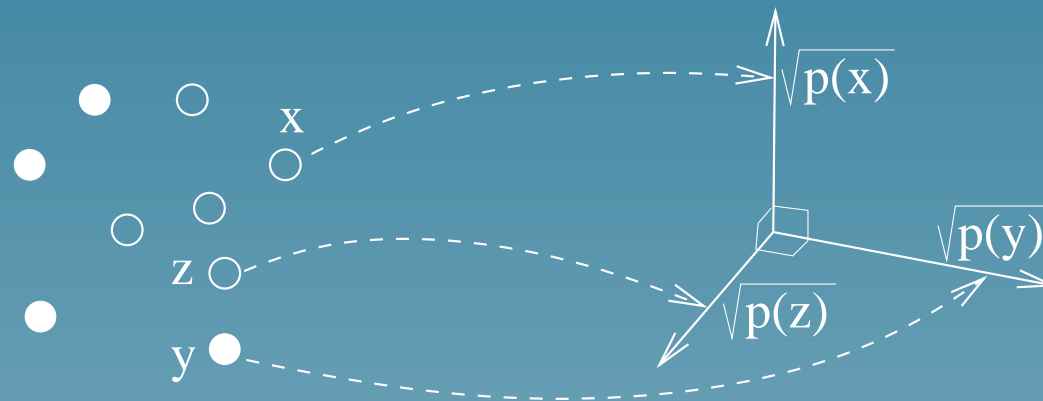
SVM = Bayesian classifier

Diagonal kernel

$$K_{diag}(x, y) = p(x)\delta(x, y)$$

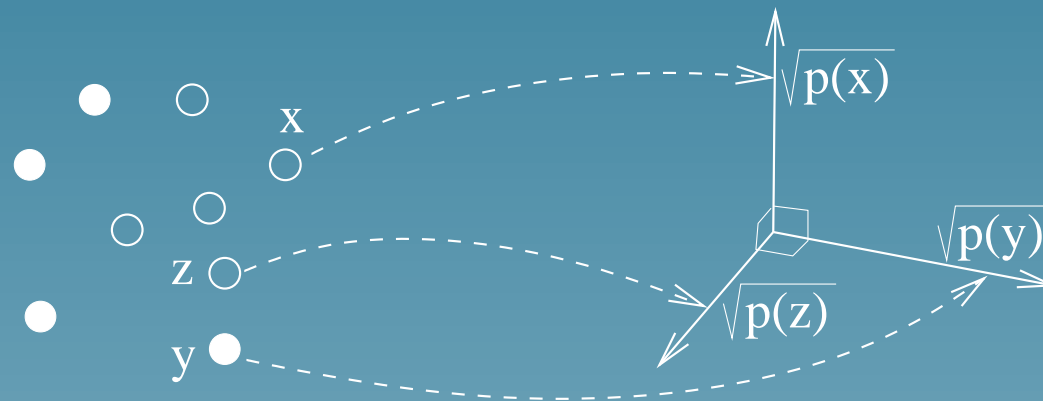
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No learning

Interpolated kernel

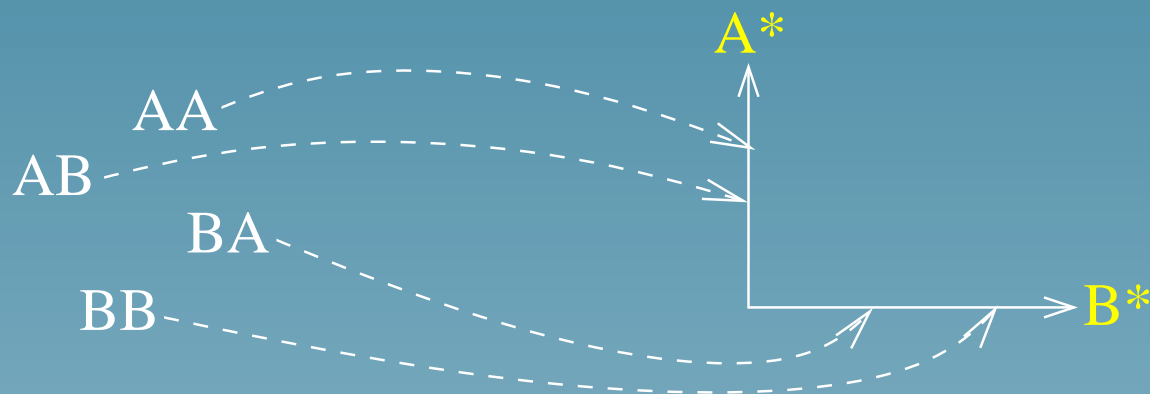
If objects are composite: $x = (x_1, x_2)$:

$$K(x, y) = K_{diag}(x_1, y_1)K_{prod}(x_2, y_2)$$

Interpolated kernel

If objects are composite: $x = (x_1, x_2)$:

$$\begin{aligned} K(x, y) &= K_{diag}(x_1, y_1)K_{prod}(x_2, y_2) \\ &= p(x_1)\delta(x_1, y_1) \times p(x_2|x_1)p(y_2|y_1) \end{aligned}$$



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- Interpolated kernel:

$$K_{\mathcal{V}}(x, y) = \frac{1}{|\mathcal{V}|} \sum_{I \in \mathcal{V}} K_{diag}(x_I, y_I) K_{prod}(x_{I^c}, y_{I^c})$$

Rare common subparts

For a given $p(x)$ and $p(y)$, we have:

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x and y get closer in the feature space when they share rare common subparts

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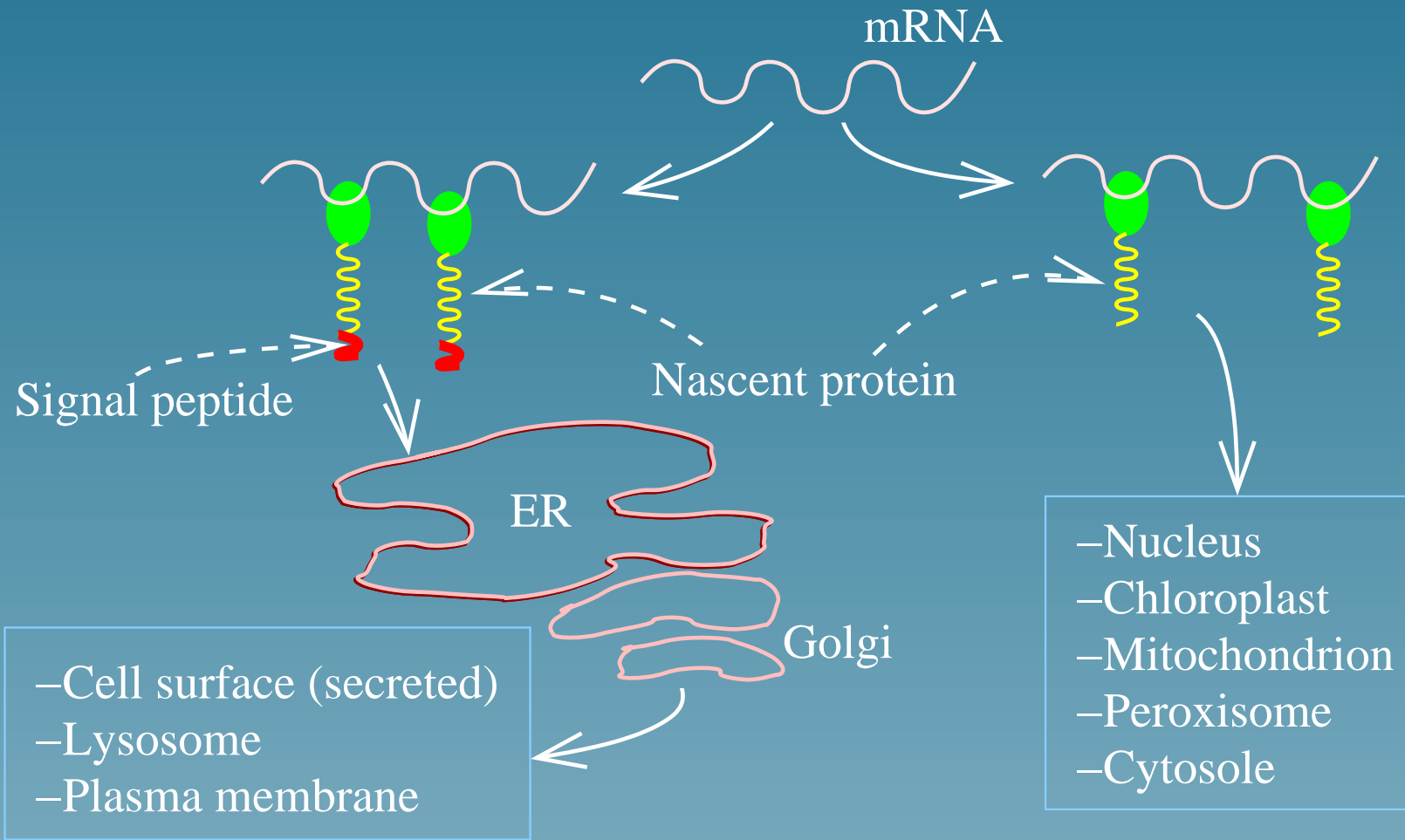
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 - ★ implementation in $O(n)$

Part 3

Application:
SVM prediction of signal peptide
cleavage site

Secretory pathway



Signal peptides

Protein	-1	+1
(1)	MKANAKTIIAGMIALAISHTAMA	EE...
(2)	MKQSTIALALLPLLFTPVTKA	RT...
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- 6-12 hydrophobic residues (in yellow)
- (-3,-1) : small uncharged residues

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- Challenge : classification of aminoacids windows, positive if cleavage occurs between -1 and +1:

$$[x_{-8}, x_{-7}, \dots, x_{-1}, x_1, x_2]$$

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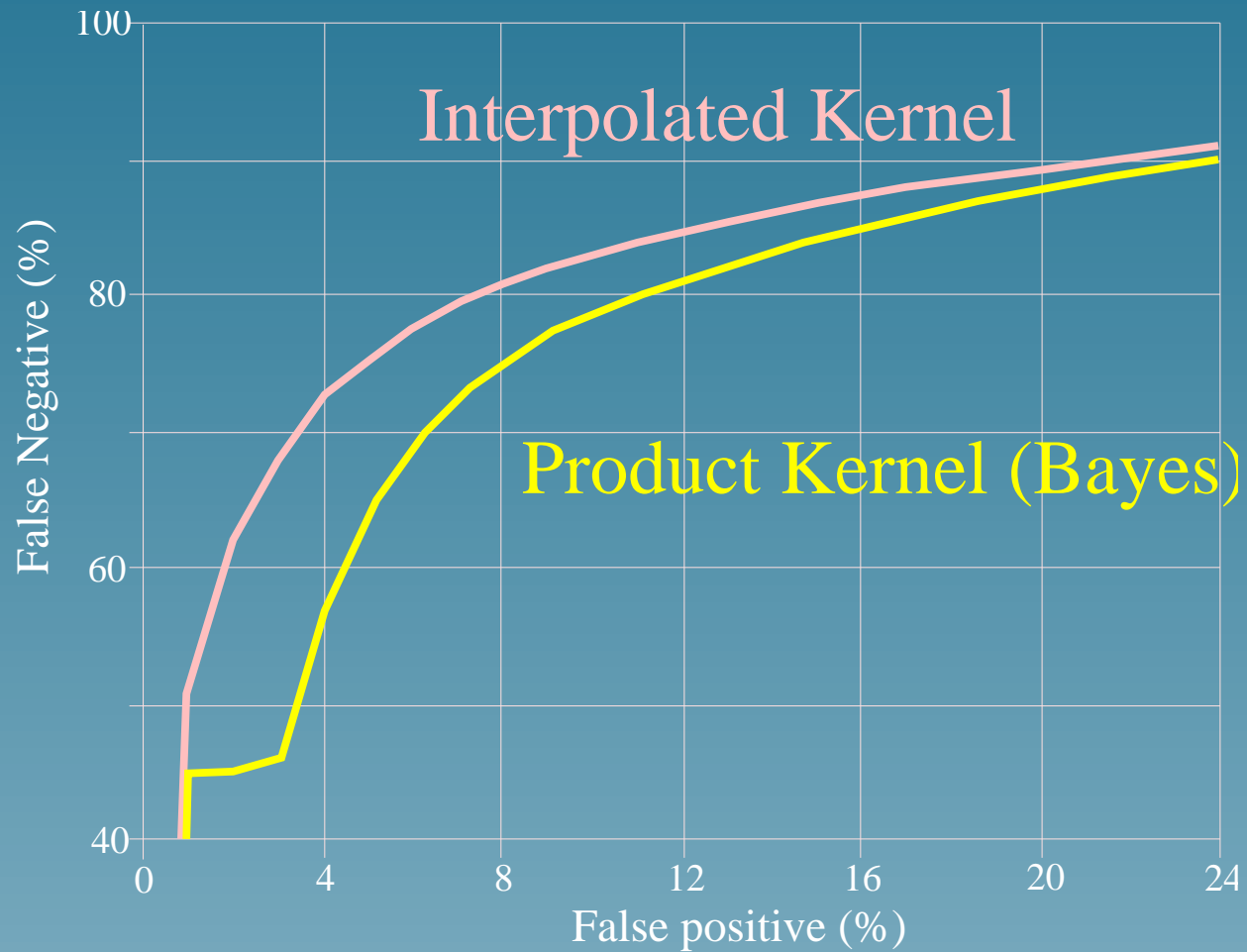
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- Computation of a weight matrix:
 $SVM + K_{prod}$ (naive Bayes) vs $SVM + K_{interpolated}$

Result: ROC curves



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- Encouraging results on real-world application' "how to improve a weight matrix based classifier"
- Future work: more application-specific kernels

Acknowledgement

- Minoru Kanehisa
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