

Recent SVM applications to bioinformatics: a very partial bibliography

1. Chenghai Xue, Fei Li, Tao He, Guo-Ping Liu, Yanda Li, Xuegong Zhang. [Classification of real and pseudo microRNA precursors using features and support vector machine](#). *BMC Bioinformatics*, **6**:310, 2005
2. Hongbo Zhu, Francisco S Domingues, Ingolf Sommer, Thomas Lengauer. [NOXclass: prediction of protein-protein local structure-sequence interaction types](#). *BMC Bioinformatics*, **7**:27, 2006
3. J. R. Bradford, David R. Westhead. [Improved prediction of protein-protein binding sites using a support vector machines approach](#). *BIOINFORMATICS*, **21**, 8, 1487–1494, 2005
4. Yu Chen, Dong Xu. [Understanding protein dispensability through machine-learning analysis of high-throughput data](#). *BIOINFORMATICS*, **21**, 5, 575–581, 2005
5. Gideon Dror, Rotem Sorek, Ron Shamir. [Accurate identification of alternatively spliced exons using support vector machine](#). *BIOINFORMATICS*, **21**, 7, 897–901, 2005
6. Caroline C. Friedel, Katharina H. V. Jahn, Selina Sommer, Stephen Rudd, Hans W. Mewes, Igor V. Tetko. [Support vector machines for separation of mixed plant-pathogen EST collections based on codon usage](#). *BIOINFORMATICS*, **21**, 8, 383–1388, 2005
7. Volkan Atalay, Rengul Cetin-Atalay. [Implicit motif distribution based hybrid computational kernel for sequence classification](#). *BIOINFORMATICS*, **21**, 8, 1429–1436, 2005
8. Rajeev Gangal, Pankaj Sharma. [Human pol II promoter prediction: time series descriptors and machine learning](#). *Nucleic Acids Research*, **33**, 4, 1332–1336, 2005
9. Torsten Haferlach, Alexander Kohlmann, Susanne Schnittger, Martin Dugas, Wolfgang Hiddemann, Wolfgang Kern, Claudia Schoch. [A global approach to the diagnosis of leukemia using gene expression profiling](#). *Blood* First Edition Paper, prepublished online May 5, 2005
10. Oliver Hofmann, Dietmar Schomburg. [Concept-based annotation of enzyme classes](#). *BIOINFORMATICS*, **21**, 9, 2059–2066, 2005
11. Lei Bao, Yan Cui. [Prediction of the phenotypic effects of non-synonymous single nucleotide polymorphisms using structural and evolutionary information](#). *BIOINFORMATICS*, **21**, 10, 2185–2190, 2005
12. R. A. O’Flanagan, G. Paillard, R. Lavery, A. M. Sengupta. [Non-additivity in protein-DNA binding](#). *BIOINFORMATICS*, **21**, 10, 2254–2263, 2005
13. Qidong Zhang, Sukjoon Yoon, William J. Welsh. [Improved method for predicting \$\beta\$ -turn using support vector machine](#). *BIOINFORMATICS*, **21**, 10, 2370–2374, 2005
14. I. Reš, I. Mihalek, O. Lichtarge. [An evolution based classifier for prediction of protein interfaces without using protein structures](#). *BIOINFORMATICS*, **21**, 10, 2496–2501, 2005
15. Dariusz Plewczynski, Adrian Tkacz, Lucjan Stanisław Wyrwicz, Leszek Rychlewski. [AutoMotif server: prediction of single residue post-translational modifications in proteins](#). *BIOINFORMATICS*, **21**, 10, 2525–2527, 2005
16. Richard W. Tothill, Adam Kowalczyk, Danny Rischin, Alex Bousioutas, Izhak Haviv, Ryan K. van Laar, Paul M. Waring, John Zalcberg, Robyn Ward, Andrew V. Biankin, Robert L. Sutherland, Susan M. Henshall, Kwun Fong, Jonathan R. Pollack, David D.L. Bowtell, Andrew J. Holloway. [An Expression-Based Site of Origin Diagnostic Method Designed for Clinical Application to Cancer of Unknown Origin](#). *Cancer Res*, **65**, 10, 2005

17. Daehee Hwang, Jennifer J. Smith, Deena M. Leslie, Andrea D. Weston, Alistair G. Rust, Stephen Ramsey, Pedro de Atauri, Andrew F. Siegel, Hamid Bolouri, John D. Aitchison, Leroy Hood. [A data integration methodology for systems biology: Experimental verification](#). *PNAS*, **102**, 48, 17302–17307, 2005
18. Jian Qiu, Martial Hue, Asa Ben-Hur, Jean-Philippe Ver, William Stafford Noble. [Classifying protein structures using support vector machines](#), proceedings of AFP 2006 (Automated Function Prediction), August 30 - September 01, 2006, San Diego, CA, USA

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