## References

- [1] Shumeet Baluja and R. Caruana. Removing the genetics from the standard genetic algorithm. In *The Proceedings of the 12th Annual Conference on Machine Learning*, pages 38 46. Morgan Kaufmann Publishers, 1995.
- [2] Shummet Baluja. Population-based incremental learning: A method for integrating genetic search based function optimization and competitive learning. Technical report, Carnegie Mellon University Pittsburgh, PA, USA, Pittsburgh, PA, USA, 1994.
- [3] Endika Bengoetxea, Pedro Larrañaga, Isabelle Bloch, and Aymeric Perchant. Estimation of distribution algorithms: A new evolutionary computation approach for graph matching problems. In *Energy Minimization Methods in Computer Vision and Pattern Recognition*, volume 2134 of *Lecture Notes in Computer Science*, pages 454–469. Springer Berlin / Heidelberg, 2001.
- [4] Olivier Chapelle, Vladimir Vapnik, Olivier Bousquet, and Sayan Mukherjee. Choosing multiple parameters for support vector machines. *Machine Learning*, 46:131–159, 2002. 10.1023/A:1012450327387.
- [5] Corinna Cortes and Vladimir Vapnik. Support-vector networks. Machine Learning, 20:273–297, 1995. 10.1007/BF00994018.
- [6] Nello Cristianini and John Shawe-Taylor. An introduction to support vector machines: and other kernel-based learning methods. Cambridge University Press, 1 edition, March 2000.
- [7] Yoav Freund and Robert E. Schapire. Large margin classification using the perceptron algorithm. *Machine Learning*, 37:277–296, December 1999.
- [8] David E. Goldberg. Genetic Algorithms in Search, Optimization and Machine Learning. Addison-Wesley Longman Publishing Co., Inc., Boston, MA, USA, 1st edition, 1989.
- [9] Isabelle Guyon and André Elisseeff. An introduction to variable and feature selection. Machine Learning, 3:1157–1182, March 2003.
- [10] Georges Harik, Fernando G. Lobo, and David E. Goldberg. The compact genetic algorithm. In *IEEE Transactions on Evolutionary Computation*, pages 523–528, 1998.
- [11] David Heckerman. A tutorial on learning with Bayesian networks, pages 301–354. MIT Press, Cambridge, MA, USA, 1999.
- [12] Mary S. Lipton and Ljiljana Pasa-Tolic. Mass Spectrometry of Proteins and Peptides: Methods and Protocols. Humman Press, 2008.

 $\sim$ 

- [13] H. Muhlenbein and G. Paag. From recombination of genes to the estimation of distributions: I. binary parameters. In Hans-Michael Voigt, Werner Ebeling, Ingo Rechenberg, and Hans-Paul Schwefel, editors, *Parallel Problem Solving from Nature PPSN IV*, volume 1141 of *Lecture Notes in Computer Science*, pages 178–187. Springer Berlin / Heidelberg, 1996.
- [14] Heinz Muhlenbein, Thilo Mahnig, and Alberto Ochoa Rodriguez. Schemata, distributions and graphical models in evolutionary optimization. *Journal of Heuristics*, 5:215–247, July 1999.
- [15] Pedro Larra naga, Ramon Etxeberria, Jose A. Lozano, and Jose M. Pe na. Combinatorial optimization by learning and simulation of bayesian networks. In *Proceedings of the Sixteenth Conference on Uncertainty in Artificial Intelligence*, pages 343–352. Morgan Kaufmann, 2000.
- [16] Iñaki Inza, Marisa Merino, Pedro Larra naga, Jorge Quiroga, Basilio Sierra, and Marcos Girala. Feature subset selection by genetic algorithms and estimation of distribution algorithms. a case study in the survival of cirrhotic patients treated with tips. *BioData Mining*, 2000.
- [17] Iñaki Inza, Pedro Larra naga, Ramon Etxeberria, and Basilio Sierra. Feature subset selection by bayesian network-based optimization. Artificial Intelligence, pages 157–184, 2000.
- [18] Rubn Arma nanzas, Iñaki Inza, Roberto Santana, Yvan Saeys, Jose Luis Flores, Jose Antonio Lozano, Yves Van De Peer, Rosa Blanco, Vctor Robles, Concha Bielza, and Pedro Larra naga. A review of estimation of distribution algorithms in bioinformatics. *BioData Mining*, 2008.
- [19] Martin Pelikan, David E. Goldberg, and Erick Cantu-Paz. Boa: The bayesian optimization algorithm. In *Genetic and Evolutionary Computation Conference (GECCO-1999)*, pages 525–532. Morgan Kaufmann, 1999.
- [20] Sergio Rojas and Delmiro Fernandez-Reyes. Adapting multiple kernel parameters for support vector machines using genetic algorithms. In 2005 IEEE Congress on Evolutionary Computation (CEC-2005), 2005.
- [21] Sergio Rojas, Emily Hsieh, Dan Agranoff, Sanjeev Krishna, and Delmiro Fernandez-Reyes. Estimation of relevant variables on high-dimensional biological patterns using iterated weighted kernel functions. *PLoS ONE*, 3:e1806, 03 2008.
- [22] Frank Rosenblatt. The perceptron: a probabilistic model for information storage and organization in the brain, pages 386–408.

  American Psychological Association, 1956.

- [23] Yvan Saeys, Sven Degroeve, Dirk Aeyels, and Yves Van De Peer. Fast feature selection using a simple estimation of distribution algorithm: A case study on splice site prediction. *Bioinformatics*, 19, 2003.
- [24] Yvan Saeys, Iñaki Inza, and Pedro Larrañaga. A review of feature selection techniques in bioinformatics. *Bioinformatics*, 23:2507–2517, September 2007.
- [25] Kumara Sastry, David E. Goldberg, and Xavier Llora. Towards billion bit optimization via parallel estimation of distribution algorithm. In *Genetic and Evolutionary Computation Conference (GECCO-2007)*, pages 577–584, 2007.
- [26] John Shawe-Taylor and Nello Cristianini. Kernel Methods for Pattern Analysis. Cambridge University Press, New York, NY, USA, 2004.