

Kernel Methods In Computational Biology

Kernel Methods in Computational Biology

Kernel Methods in Bioengineering, Signal and Image Processing

Handbook of Statistical Bioinformatics

Learning with Kernels

Kernel Methods in Chemo- and Bioinformatics

Learning Theory and Kernel Machines

Introduction to Data Mining for the Life Sciences

Methods in Computational Biology

Machine Learning in Bioinformatics

Elements of Computational Systems Biology

Artificial Intelligence and Heuristic Methods in Bioinformatics

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Semi-Supervised Learning

Kernel-based Data Fusion for Machine Learning

Kernel Methods for Pattern Analysis

Algorithms on Strings, Trees and Sequences

Computational Systems Biology of Cancer

Introduction to Machine Learning and Bioinformatics

Analysis of Biological Data

6th International Conference on Practical Applications of Computational Biology & Bioinformatics

Intelligent Computing Technology

Computational Methods in Systems Biology

Medical Informatics: Concepts, Methodologies, Tools, and Applications

Computational Methods in Systems Biology

Computational Methods in Systems Biology

Computational Methods for Understanding Complexity: The Use of Formal Methods in Biology

Handbook of Research on Systems Biology Applications in Medicine

Handbook of Statistical Bioinformatics

Computational Methods in Molecular Biology

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2007-01-01 Gustavo Camps-Valls "This book presents an extensive introduction to the field of kernel methods and real world applications. The book is organized in four parts: the first is an introductory chapter providing a framework of kernel methods; the others address Bioengineering, Signal Processing and Communications and Image Processing"-- Provided by publisher.

2011-05-17 Henry Horng-Shing Lu Numerous fascinating breakthroughs in biotechnology have generated large volumes and diverse types of high throughput data that demand the development of efficient and appropriate tools in computational statistics integrated with biological knowledge and computational algorithms. This volume collects contributed chapters from leading researchers to survey the many active research topics and promote the visibility of this research area. This volume is intended to provide an introductory and reference book for students and researchers who are interested in the recent developments of computational statistics in computational biology.

1998-06-19 S.L. Salzberg Computational biology is a rapidly expanding field, and the number and variety of computational methods used for DNA and protein sequence analysis is growing every day. These algorithms are extremely valuable to biotechnology companies

and to researchers and teachers in universities. This book explains the latest computer technology for analyzing DNA, RNA, and protein sequences. Clear and easy to follow, designed specifically for the non-computer scientist, it will help biologists make better choices on which algorithm to use. New techniques and demonstrations are elucidated, as are state-of-the-art problems, and more advanced material on the latest algorithms. The primary audience for this volume are molecular biologists working either in biotechnology companies or academic research environments, individual researchers and the institutions they work for, and students. Any biologist who relies on computers should want this book. A secondary audience will be computer scientists developing techniques with applications in biology. An excellent reference for leading techniques, it will also help introduce computer scientists to the biology problems. This is an outstanding work which will be ideal for the increasing number of scientists moving into computational biology.

2011-03-29 Shi Yu Data fusion problems arise frequently in many different fields. This book provides a specific introduction to data fusion problems using support vector machines. In the first part, this book begins with a brief survey of additive models and Rayleigh quotient objectives in machine learning, and then introduces kernel fusion as the additive expansion of support vector machines in the

dual problem. The second part presents several novel kernel fusion algorithms and some real applications in supervised and unsupervised learning. The last part of the book substantiates the value of the proposed theories and algorithms in MerKator, an open software to identify disease relevant genes based on the integration of heterogeneous genomic data sources in multiple species. The topics presented in this book are meant for researchers or students who use support vector machines. Several topics addressed in the book may also be interesting to computational biologists who want to tackle data fusion challenges in real applications. The background required of the reader is a good knowledge of data mining, machine learning and linear algebra.

2010-03-25 Huma M. Lodhi Groundbreaking, long-ranging research in this emergent field that enables solutions to complex biological problems Computational systems biology is an emerging discipline that is evolving quickly due to recent advances in biology such as genome sequencing, high-throughput technologies, and the recent development of sophisticated computational methodologies. Elements of Computational Systems Biology is a comprehensive reference covering the computational frameworks and techniques needed to help research scientists and professionals in computer science, biology, chemistry, pharmaceutical science, and physics

solve complex biological problems. Written by leading experts in the field, this practical resource gives detailed descriptions of core subjects, including biological network modeling, analysis, and inference; presents a measured introduction to foundational topics like genomics; and describes state-of-the-art software tools for systems biology. Offers a coordinated integrated systems view of defining and applying computational and mathematical tools and methods to solving problems in systems biology Chapters provide a multidisciplinary approach and range from analysis, modeling, prediction, reasoning, inference, and exploration of biological systems to the implications of computational systems biology on drug design and medicine Helps reduce the gap between mathematics and biology by presenting chapters on mathematical models of biological systems Establishes solutions in computer science, biology, chemistry, and physics by presenting an in-depth description of computational methodologies for systems biology Elements of Computational Systems Biology is intended for academic/industry researchers and scientists in computer science, biology, mathematics, chemistry, physics, biotechnology, and pharmaceutical science. It is also accessible to undergraduate and graduate students in machine learning, data mining, bioinformatics, computational biology, and systems biology courses.

2007-09-04 Muffy Calder This book constitutes the refereed proceedings of the International Conference on Computational Methods in Systems Biology, CMSB 2007, held in Edinburgh, Scotland, September 2007. The 16 revised full papers presented present a variety of techniques from computer science, such as language design, concurrency theory, software engineering, and formal methods, for biologists, physicists, and mathematicians interested in the systems-level understanding of cellular processes.

2011-05-19 Henry Horng Lu

2008-06-05 Sushmita Mitra Lucidly Integrates Current Activities Focusing on both fundamentals and recent advances, Introduction to Machine Learning and Bioinformatics presents an informative and accessible account of the ways in which these two increasingly intertwined areas relate to each other. Examines Connections between Machine Learning & Bioinformatics The book begins with a brief historical overview of the technological developments in biology. It then describes the main problems in bioinformatics and the fundamental concepts and algorithms of machine learning. After forming this foundation, the authors explore how machine learning techniques apply to bioinformatics problems, such as electron density map interpretation, biclustering, DNA sequence analysis, and tumor classification. They also

include exercises at the end of some chapters and offer supplementary materials on their website. Explores How Machine Learning Techniques Can Help Solve Bioinformatics Problems Shedding light on aspects of both machine learning and bioinformatics, this text shows how the innovative tools and techniques of machine learning help extract knowledge from the deluge of information produced by today's biological experiments.

2008-11-30 Daskalaki, Andriani "This book highlights the use of systems approaches including genomic, cellular, proteomic, metabolomic, bioinformatics, molecular, and biochemical, to address fundamental questions in complex diseases like cancer diabetes but also in ageing"--Provided by publisher.

2010-01-22 Olivier Chapelle A comprehensive review of an area of machine learning that deals with the use of unlabeled data in classification problems: state-of-the-art algorithms, a taxonomy of the field, applications, benchmark experiments, and directions for future research. In the field of machine learning, semi-supervised learning (SSL) occupies the middle ground, between supervised learning (in which all training examples are labeled) and unsupervised learning (in which no label data are given). Interest in SSL has increased in recent years, particularly because of application domains in which unlabeled data are plentiful, such as

images, text, and bioinformatics. This first comprehensive overview of SSL presents state-of-the-art algorithms, a taxonomy of the field, selected applications, benchmark experiments, and perspectives on ongoing and future research. Semi-Supervised Learning first presents the key assumptions and ideas underlying the field: smoothness, cluster or low-density separation, manifold structure, and transduction. The core of the book is the presentation of SSL methods, organized according to algorithmic strategies. After an examination of generative models, the book describes algorithms that implement the low-density separation assumption, graph-based methods, and algorithms that perform two-step learning. The book then discusses SSL applications and offers guidelines for SSL practitioners by analyzing the results of extensive benchmark experiments. Finally, the book looks at interesting directions for SSL research. The book closes with a discussion of the relationship between semi-supervised learning and transduction.

2003 Paolo Frasconi The 14 papers consider how various methods in artificial intelligence are applied to problems in bioinformatics. Among the topics are statistical learning and kernel methods in bioinformatics, new machine learning methods for predicting protein topologies, multiple sequence alignments information in structure and function prediction, pattern discovery and the

algorithms of surprise, the computational identification of regulatory sites in DNA sequences, computer system gene discovery for promoter structure analysis, and data acquisition and analysis in near-genome-wide expressions screening of tumor suppressor pathways using model cell lines with inducible transcription factors. There is no subject index. Annotation : 2004 Book News, Inc., Portland, OR (booknews.com).

2009-02-23 Yanqing Zhang An introduction to machine learning methods and their applications to problems in bioinformatics Machine learning techniques are increasingly being used to address problems in computational biology and bioinformatics. Novel computational techniques to analyze high throughput data in the form of sequences, gene and protein expressions, pathways, and images are becoming vital for understanding diseases and future drug discovery. Machine learning techniques such as Markov models, support vector machines, neural networks, and graphical models have been successful in analyzing life science data because of their capabilities in handling randomness and uncertainty of data noise and in generalization. From an internationally recognized panel of prominent researchers in the field, Machine Learning in Bioinformatics compiles recent approaches in machine learning methods and their applications in addressing contemporary problems in bioinformatics. Coverage includes:

feature selection for genomic and proteomic data mining; comparing variable selection methods in gene selection and classification of microarray data; fuzzy gene mining; sequence-based prediction of residue-level properties in proteins; probabilistic methods for long-range features in biosequences; and much more. Machine Learning in Bioinformatics is an indispensable resource for computer scientists, engineers, biologists, mathematicians, researchers, clinicians, physicians, and medical informaticists. It is also a valuable reference text for computer science, engineering, and biology courses at the upper undergraduate and graduate levels.

2012-08-25 Emmanuel Barillot The future of cancer research and the development of new therapeutic strategies rely on our ability to convert biological and clinical questions into mathematical models—integrating our knowledge of tumour progression mechanisms with the tsunami of information brought by high-throughput technologies such as microarrays and next-generation sequencing. Offering promising insights on how to defeat cancer, the emerging field of systems biology captures the complexity of biological phenomena using mathematical and computational tools. Novel Approaches to Fighting Cancer Drawn from the authors' decade-long work in the cancer computational systems biology laboratory at Institut Curie (Paris, France), Computational Systems Biology

of Cancer explains how to apply computational systems biology approaches to cancer research. The authors provide proven techniques and tools for cancer bioinformatics and systems biology research. Effectively Use Algorithmic Methods and Bioinformatics Tools in Real Biological Applications Suitable for readers in both the computational and life sciences, this self-contained guide assumes very limited background in biology, mathematics, and computer science. It explores how computational systems biology can help fight cancer in three essential aspects: Categorising tumours Finding new targets Designing improved and tailored therapeutic strategies Each chapter introduces a problem, presents applicable concepts and state-of-the-art methods, describes existing tools, illustrates applications using real cases, lists publically available data and software, and includes references to further reading. Some chapters also contain exercises. Figures from the text and scripts/data for reproducing a breast cancer data analysis are available at www.cancer-systems-biology.net.

2007 Sanghamitra Bandyopadhyay Bioinformatics, a field devoted to the interpretation and analysis of biological data using computational techniques, has evolved tremendously in recent years due to the explosive growth of biological information generated by the scientific community. Soft computing is a consortium of methodologies

that work synergistically and provides, in one form or another, flexible information processing capabilities for handling real-life ambiguous situations. Several research articles dealing with the application of soft computing tools to bioinformatics have been published in the recent past; however, they are scattered in different journals, conference proceedings and technical reports, thus causing inconvenience to readers, students and researchers. This book, unique in its nature, is aimed at providing a treatise in a unified framework, with both theoretical and experimental results, describing the basic principles of soft computing and demonstrating the various ways in which they can be used for analyzing biological data in an efficient manner. Interesting research articles from eminent scientists around the world are brought together in a systematic way such that the reader will be able to understand the issues and challenges in this domain, the existing ways of tackling them, recent trends, and future directions. This book is the first of its kind to bring together two important research areas, soft computing and bioinformatics, in order to demonstrate how the tools and techniques in the former can be used for efficiently solving several problems in the latter. Sample Chapter(s). Chapter 1: Bioinformatics: Mining the Massive Data from High Throughput Genomics Experiments (160 KB). Contents: Overview: Bioinformatics: Mining the Massive Data from High Throughput Genomics Experiments (H Tang & S Kim); An

Introduction to Soft Computing (A Konar & S Das); Biological Sequence and Structure Analysis: Reconstructing Phylogenies with Memetic Algorithms and Branch-and-Bound (J E Gallardo et al.); Classification of RNA Sequences with Support Vector Machines (J T L Wang & X Wu); Beyond String Algorithms: Protein Sequence Analysis Using Wavelet Transforms (A Krishnan & K-B Li); Filtering Protein Surface Motifs Using Negative Instances of Active Sites Candidates (N L Shrestha & T Ohkawa); Distill: A Machine Learning Approach to Ab Initio Protein Structure Prediction (G Pollastri et al.); In Silico Design of Ligands Using Properties of Target Active Sites (S Bandyopadhyay et al.); Gene Expression and Microarray Data Analysis: Inferring Regulations in a Genomic Network from Gene Expression Profiles (N Noman & H Iba); A Reliable Classification of Gene Clusters for Cancer Samples Using a Hybrid Multi-Objective Evolutionary Procedure (K Deb et al.); Feature Selection for Cancer Classification Using Ant Colony Optimization and Support Vector Machines (A Gupta et al.); Sophisticated Methods for Cancer Classification Using Microarray Data (S-B Cho & H-S Park); Multiobjective Evolutionary Approach to Fuzzy Clustering of Microarray Data (A Mukhopadhyay et al.). Readership: Graduate students and researchers in computer science, bioinformatics, computational and molecular biology, artificial intelligence, data mining, machine learning, electrical engineering,

system science; researchers in pharmaceutical industries.

2004-06-28 John Shawe-Taylor Publisher
Description

1997-05-28 Dan Gusfield String algorithms are a traditional area of study in computer science. In recent years their importance has grown dramatically with the huge increase of electronically stored text and of molecular sequence data (DNA or protein sequences) produced by various genome projects. This 1997 book is a general text on computer algorithms for string processing. In addition to pure computer science, the book contains extensive discussions on biological problems that are cast as string problems, and on methods developed to solve them. It emphasises the fundamental ideas and techniques central to today's applications. New approaches to this complex material simplify methods that up to now have been for the specialist alone. With over 400 exercises to reinforce the material and develop additional topics, the book is suitable as a text for graduate or advanced undergraduate students in computer science, computational biology, or bio-informatics. Its discussion of current algorithms and techniques also makes it a reference for professionals.

2012-09-28 David Gilbert This book constitutes the thoroughly refereed conference

proceedings of the 10th International Conference on Computational Methods in Systems Biology, CMSB 2012, held in London, UK, during October 3-5, 2012. The 17 revised full papers and 8 flash posters presented together with the summaries of 3 invited papers were carefully reviewed and selected from 62 submissions. The papers cover the analysis of biological systems, networks, and data ranging from intercellular to multiscale. Topics included high-performance computing, and for the first time papers on synthetic biology.

2009-06-29 Luonan Chen Alternative techniques and tools for analyzing biomolecular networks With the recent rapid advances in molecular biology, high-throughput experimental methods have resulted in enormous amounts of data that can be used to study biomolecular networks in living organisms. With this development has come recognition of the fact that a complicated living organism cannot be fully understood by merely analyzing individual components. Rather, it is the interactions of components or biomolecular networks that are ultimately responsible for an organism's form and function. This book addresses the important need for a new set of computational tools to reveal essential biological mechanisms from a systems biology approach. Readers will get comprehensive coverage of analyzing biomolecular networks in cellular systems based on available experimental data with an emphasis on the

aspects of network, system, integration, and engineering. Each topic is treated in depth with specific biological problems and novel computational methods: GENE NETWORKS—Transcriptional regulation; reconstruction of gene regulatory networks; and inference of transcriptional regulatory networks PROTEIN INTERACTION NETWORKS—Prediction of protein-protein interactions; topological structure of biomolecular networks; alignment of biomolecular networks; and network-based prediction of protein function METABOLIC NETWORKS AND SIGNALING NETWORKS—Analysis, reconstruction, and applications of metabolic networks; modeling and inference of signaling networks; and other topics and new trends In addition to theoretical results and methods, many computational software tools are referenced and available from the authors' Web sites. Biomolecular Networks is an indispensable reference for researchers and graduate students in bioinformatics, computational biology, systems biology, computer science, and applied mathematics.

2012-01-07 Rob Sullivan Data mining provides a set of new techniques to integrate, synthesize, and analyze data, uncovering the hidden patterns that exist within. Traditionally, techniques such as kernel learning methods, pattern recognition, and data mining, have been the domain of researchers in areas such

as artificial intelligence, but leveraging these tools, techniques, and concepts against your data asset to identify problems early, understand interactions that exist and highlight previously unrealized relationships through the combination of these different disciplines can provide significant value for the investigator and her organization.

2006 Holger Fröhlich This thesis is devoted to the finding of possible solutions for some machine learning related problems in modern chemo- and bioinformatics by means of so-called kernel methods. They are a special family of learning algorithms that have attracted a growing interest during the last years due to their good theoretical foundation and many successful practical applications in various disciplines. At the core of all kernel methods is the usage of a kernel function, which can be thought of as a special similarity measure between arbitrary objects. At the beginning of this thesis fundamentals and principles of kernel machines are reviewed. Afterwards a novel algorithm for model selection for Support Vector Machines (SVMs) in classification and regression is proposed, which is based on ideas from global optimization theory. It does not make any assumptions about special properties of the kernel function, like differentiability, and is highly efficient. Experimental comparisons to existing algorithms yield good results. After this we turn our point of interest to applications of kernel methods in chemo- and bioinformatics:

For the ADME in silico prediction problem in modern drug discovery descriptor and graph-based representations of molecules are investigated. A descriptor selection algorithm is proposed, which can improve the statistical stability of an existing method. Furthermore, a novel class of specialized kernel functions is introduced that allows the comparison of a pair of molecules on a graph-based level. Various combinations of graph and descriptor-based representations are investigated, which on one hand allow the incorporation of expert domain knowledge and on the other hand the integration of different notions of molecular similarity in one SVM model. Furthermore, a reduced graph representation for molecular structures is proposed, in which certain structural elements are condensed in one node of the graph. Our experiments indicate that with our method improvements of the prediction performance compared to state-of-the-art modelling approaches can be achieved. At the same time our method is computationally rather cheap, unified and highly flexible. Another question, that is examined in the content of this thesis, is, which features of the membrane potential (MP) determine the generation of action potentials (APs) in cortical neurons in vivo. SVMs are trained to predict the occurrence of an AP before its onset based on several extracted features of the MP. A specialized feature selection algorithm is then used to select the most important features simultaneously in several in vivo recordings. In

conclusion we find that the occurrence of an AP not only depends on the value of the MP shortly before AP onset, but also on the MP rate of change, the increase of the membrane potential several ms before AP onset, and the long range mean MP. Our findings systematically extend investigations by other researchers and are partially also confirmed by their results. As a last application of kernel methods in this thesis, we deal with the problem of clustering genes with regard to their function based on their Gene Ontology (GO) annotation. For this purpose specialized kernel functions are developed, which measure the similarity between gene products with respect to the structure of the GO graph. Using several clustering algorithms, like kernel k-means, spectral clustering and average linkage, we can detect meaningful clusters with our method. Applications to other ontologies or taxonomies in principle are possible.

2008-09-30 Tan, Joseph Provides a collection of medical IT research in topics such as clinical knowledge management, medical informatics, mobile health and service delivery, and gene expression.

2006-10-11 Corrado Priami This book constitutes the refereed proceedings of the International Conference on Computational Methods in Systems Biology, CMSB 2006, held in Trento, Italy, in October 2006. The 22 fully revised papers presented together with 2

invited talks were carefully reviewed and selected from 68 submissions. The papers present a variety of techniques from computer sciences, such as language design, concurrency theory, software engineering, and formal methods.

2012-07-23 De-Shuang Huang This book constitutes the first of 3 volumes of refereed conference proceedings of the 8th International Conference on Intelligent Computing, ICIC 2012, held in Huangshan, China, in July 2012. The 242 revised full papers presented were carefully reviewed and selected from 753 submissions. The 84 papers included in this volume are organized in topical sections on evolutionary learning and genetic algorithms, fuzzy theory and models, swarm intelligence and optimization, kernel methods and supporting vector machines, nature inspired computing and optimization, systems biology and computational biology, knowledge discovery and data mining, graph theory and algorithms, machine learning theory and methods, biomedical informatics theory and methods, complex systems theory and methods, pervasive/ubiquitous computing theory and methods, intelligent computing in bioinformatics, intelligent computing in pattern recognition, intelligent computing in image processing, intelligent computing in robotics, intelligent computing in computer vision, intelligent computing in Petri nets/transportation systems, intelligent data

fusion and information security, intelligent sensor networks, knowledge representation/reasoning and expert systems, hybrid optimization, and bio-inspired computing and application.

2016-11-21 David A. Rosenblueth, The complexity of living organisms surpasses our unaided abilities of analysis. Hence, computational and mathematical methods are necessary for increasing our understanding of biological systems. At the same time, there has been a phenomenal recent progress allowing the application of novel formal methods to new domains. This progress has spurred a conspicuous optimism in computational biology. This optimism, in turn, has promoted a rapid increase in collaboration between specialists of biology with specialists of computer science. Through sheer complexity, however, many important biological problems are at present intractable, and it is not clear whether we will ever be able to solve such problems. We are in the process of learning what kind of model and what kind of analysis and synthesis techniques to use for a particular problem. Some existing formalisms have been readily used in biological problems, others have been adapted to biological needs, and still others have been especially developed for biological systems. This Research Topic has examples of cases (1) employing existing methods, (2) adapting methods to biology, and (3) developing new methods. We can also see discrete and Boolean

models, and the use of both simulators and model checkers. Synthesis is exemplified by manual and by machine-learning methods. We hope that the articles collected in this Research Topic will stimulate new research.

2004 Bernhard Schölkopf A detailed overview of current research in kernel methods and their application to computational biology.

2014-01-15 Bernhard Scholkopf

2019-07-03 Ross Carlson Modern biology is rapidly becoming a study of large sets of data. Understanding these data sets is a major challenge for most life sciences, including the medical, environmental, and bioprocess fields. Computational biology approaches are essential for leveraging this ongoing revolution in omics data. A primary goal of this Special Issue, entitled “Methods in Computational Biology”, is the communication of computational biology methods, which can extract biological design principles from complex data sets, described in enough detail to permit the reproduction of the results. This issue integrates interdisciplinary researchers such as biologists, computer scientists, engineers, and mathematicians to advance biological systems analysis. The Special Issue contains the following sections: • Reviews of Computational Methods • Computational Analysis of Biological Dynamics: From Molecular to Cellular to Tissue/Consortia Levels • The Interface of Biotic and Abiotic

Processes • Processing of Large Data Sets for Enhanced Analysis • Parameter Optimization and Measurement

2012-03-05 Miguel P. Rocha The growth in the Bioinformatics and Computational Biology fields over the last few years has been remarkable and the trend is to increase its pace. In fact, the need for computational techniques that can efficiently handle the huge amounts of data produced by the new experimental techniques in Biology is still increasing driven by new advances in Next Generation Sequencing, several types of the so called omics data and image acquisition, just to name a few. The analysis of the datasets that produces and its integration call for new algorithms and approaches from fields such as Databases, Statistics, Data Mining, Machine Learning, Optimization, Computer Science and Artificial Intelligence. Within this scenario of

increasing data availability, Systems Biology has also been emerging as an alternative to the reductionist view that dominated biological research in the last decades. Indeed, Biology is more and more a science of information requiring tools from the computational sciences. In the last few years, we have seen the surge of a new generation of interdisciplinary scientists that have a strong background in the biological and computational sciences. In this context, the interaction of researchers from different scientific fields is, more than ever, of foremost importance boosting the research efforts in the field and contributing to the education of a new generation of Bioinformatics scientists. PACBB'12 hopes to contribute to this effort promoting this fruitful interaction. PACBB'12 technical program included 32 papers from a submission pool of 61 papers spanning many

different sub-fields in Bioinformatics and Computational Biology. Therefore, the conference will certainly have promoted the interaction of scientists from diverse research groups and with a distinct background (computer scientists, mathematicians, biologists). The scientific content will certainly be challenging and will promote the improvement of the work that is being developed by each of the participants.

2007 Bernhard Schölkopf The annual Neural Information Processing Systems (NIPS) conference is the flagship meeting on neural computation and machine learning. This volume contains the papers presented at the December 2006 meeting, held in Vancouver.

2002 Bernhard Schölkopf A comprehensive introduction to Support Vector Machines and related kernel methods.