Hidden Markov Models Baum Welch Algorithm

Hidden Markov Models for Bioinformatics

A comprehensive introduction to machine learning that uses probabilistic models and inference as a unifying approach. Today's Web-enabled deluge of electronic data calls for automated methods of data analysis. Machine learning provides these, developing methods that can automatically detect patterns in data and then use the uncovered patterns to predict future data. This textbook offers a comprehensive and self-contained introduction to the field of machine learning, based on a unified, probabilistic approach. The coverage combines breadth and depth, offering necessary background material on such topics as probability, optimization, and linear algebra as well as discussion of recent developments in the field, including conditional random fields, L1 regularization, and deep learning. The book is written in an informal, accessible style, complete with pseudo-code for the most important algorithms. All topics are copiously illustrated with color images and worked examples drawn from such application domains as biology, text processing, computer vision, and robotics. Rather than providing a cookbook of different heuristic methods, the book stresses a principled model-based approach, often using the language of graphical models to specify models in a concise and intuitive way. Almost all the models described have been implemented in a MATLAB software package—PMTK (probabilistic modeling toolkit)—that is freely available online. The book is suitable for upper-level undergraduates with an introductory-level college math background and beginning graduate students.

This book reflects decades of important research on the mathematical foundations of speech recognition. It focuses on underlying statistical techniques such as hidden Markov models, decision trees, the expectation-maximization algorithm, information theoretic goodness criteria, maximum entropy probability estimation, parameter and data clustering, and smoothing of probability distributions. The author's goal is to present these principles clearly in the simplest setting, to show the advantages of self-organization from real data, and to enable the reader to apply the techniques.

Hidden Markov Models and Dynamical SystemsSIAM

This book focuses on the problem of moving in a cluttered environment with pedestrians and vehicles. A framework based on Hidden Markov models is developed to learn typical motion patterns which can be used to predict motion on the basis of sensor data.

This volume proceedings contains revised selected papers from the 4th International Conference on Artificial Intelligence and Computational Intelligence, AICI 2012, held in Chengdu, China, in October 2012. The total of 163 high-quality papers presented were carefully reviewed and selected from 724 submissions. The papers are organized into topical sections on applications of artificial intelligence, applications of computational intelligence, data mining and knowledge discovery, evolution strategy, expert and decision support systems, fuzzy computation, information security, intelligent control, intelligent image processing, intelligent information fusion, intelligent signal processing, machine learning, neural computation, neural networks, particle swarm optimization, and pattern recognition.

This Festschrift volume is published in honor of Günter Haring on the occasion of his emerital celebration and contains invited papers by key researchers in the field of performance evaluation presented at the workshop Performance Evaluation of Computer and Communication Systems - Milestones and Future Challenges, PERFORM 2010, held in Vienna, Austria, in October 2010. Günter Haring has dedicated most of his scientific professional life to performance evaluation and the design of distributed systems, contributing in particular to the field of workload characterization. In addition to his own contributions and leadership in international research projects, he is and has been an excellent mentor of young researchers demonstrated by their own brilliant scientific careers. The 20 thoroughly refereed papers range from visionary to in-depth research papers and are organized in the following topical sections: milestones and evolutions; trends: green ICT and virtual machines; modeling; mobility and mobile networks; communication and computer networks; and load balancing, analysis, and management.

Introduction to Machine Learning with Applications in Information Security provides a class-tested introduction to a wide variety of machine learning algorithms, reinforced through realistic applications. The book is accessible and doesn't prove theorems, or otherwise dwell on mathematical theory. The goal is to present topics at an intuitive level, with just enough detail to clarify the underlying concepts. The book covers core machine learning topics in-depth, including Hidden Markov Models, Principal Component Analysis, Support Vector Machines, and Clustering. It also includes coverage of Nearest Neighbors, Neural Networks, Boosting and AdaBoost, Random Forests, Linear Discriminant Analysis, Vector Quantization, Naive Bayes, Regression Analysis, Conditional Random Fields, and Data Analysis. Most of the examples in the book are drawn from the field of information security, with many of the machine learning applications specifically focused on malware. The applications presented are designed to demystify machine learning techniques by providing straightforward scenarios. Many of the exercises in this book require some programming, and basic computing concepts are assumed in a few of the application sections. However, anyone with a modest amount of programming experience should have no trouble with this aspect of the book. Instructor resources, including PowerPoint slides, lecture videos, and other relevant material are provided on an accompanying website: http://www.cs.sjsu.edu/~stamp/ML/. For the reader's benefit, the figures in the book are also available in electronic form, and in color. About the Author Mark Stamp has been a Professor of Computer Science at San Jose State University since 2002. Prior to that, he worked at the National Security Agency (NSA) for seven years, and a Silicon Valley startup company for two years. He received his Ph.D. from Texas Tech University in 1992. His love affair with machine learning began in the early 1990s, when he was working at the NSA, and continues today at SJSU, where he has supervised vast numbers of master's student projects, most of which involve a combination of information security and machine learning.

I present a Dempster-Shafer approach to estimating limits from Poisson counting data with nuisance parameters and two new methods, Conditional Baum-Welch and Dynamic Model Surgery, for achieving maximum-likelihood or maximum a-posteriori estimates of the parameters of Profile hidden Markov Models. Dempster-Shafer (DS) is a statistical framework that generalizes Bayesian statistics. DS calculus augments traditional probability by allowing mass to be distributed over power sets of the event space. This eliminates the Bayesian dependence on prior distributions while allowing the incorporation of prior information when it is available. I use the Poisson Dempster-Shafer model (DSM) to derive a posterior DSM for the "Banff upper limits challenge" three-Poisson model. Profile hidden Markov Models (Profile HMMs) are widely used for protein sequence family modeling. The algorithm commonly used to estimate the parameters of Profile HMMs, Baum-Welch (BW), is prone to prematurely converge to local optima. I provide a description and proof of the Conditional Baum-Welch (CBW) algorithm, and show that it is able to parameterize Profile HMMs better than BW under a range of conditions including both protein and DNA sequence family models. I also introduce the Dynamic Model Surgery (DMS) method, which can be applied to either BW or CBW to help them achieve higher maxima by dynamically altering the structure of the Profile HMM during BW or CBW training. I conclude by describing the results of an application of these methods to the transposon (interspersed repeat) modeling problem that originally inspired the research.

The past decade has seen powerful new computational tools for modeling which combine a Bayesian approach with recent Monte simulation techniques based on Markov chains. This book is the first to offer a systematic presentation of the Bayesian perspective of finite mixture modelling. The book is designed to show finite mixture and Markov switching models are formulated, what structures they imply on the data, their potential uses, and how they are estimated. Presenting its concepts informally without sacrificing mathematical correctness, it will serve a wide readership including statisticians as well as biologists, economists, engineers, financial and market researchers.

This book explores important aspects of Markov and hidden Markov processes and the applications of these ideas to various problems in computational biology. The book starts from first principles, so that no previous knowledge of probability is necessary. However, the work is rigorous and mathematical, making it useful to engineers and mathematicians, even those not interested in biological applications. A range of exercises is provided, including drills to familiarize the reader with concepts and more advanced problems that require deep thinking about the theory. Biological applications are taken from post-genomic biology, especially genomics and proteomics. The topics examined include standard material such as the Perron-Frobenius theorem, transient and recurrent states, hitting probabilities and hitting times, maximum likelihood estimation, the Viterbi algorithm, and the Baum-Welch algorithm. The book contains discussions of extremely useful topics not usually seen at the basic level, such as ergodicity of Markov processes, Markov Chain Monte Carlo (MCMC), information theory, and large deviation theory for both i.i.d and Markov processes. The book also presents state-of-the-art realization theory for hidden Markov models. Among biological applications, it offers an in-depth look at the BLAST (Basic Local Alignment Search Technique) algorithm, including a comprehensive explanation of the underlying theory. Other applications such as profile hidden Markov models are also explored.

Presents algorithms for using HMMs and explains the derivation of those algorithms for the dynamical systems community.

This text is based on a set of not es produced for courses given for gradu ate students in mathematics, computer science and biochemistry during the academic year 1998-1999 at the University of Turku in Turku and at the Royal Institute of Technology (KTH) in Stockholm. The course in Turku was organized by Professor Mats Gyllenberg's groupI and was also included 2 within the postgraduate program ComBi , a Graduate School in Compu tational Biology, Bioinformatics, and Biometry, directed by Professor Esko Ukkonen at the University of Helsinki. The purpose of the courses was to give a thorough and systematic intro duc ti on to probabilistic modelling in bioinformatics for advanced undergraduate and graduate students who had a fairly limited background in prob ability theory, but were otherwise well trained in mathematics and were already familiar with at least some of the techniques of algorithmic sequence analysis. Portions of the material have also been lectured at shorter graduate courses and seminars both in Finland and in Sweden. The initial set of notes circulated also for a time outside those two countries via the World Wide Web. The intermediate course in probability theory and techniques of discrete mathematics held by the author at the University College of Södertörn (Hud dinge, Sweden) during the academic year 1997-1998 has also influenced the presentation. The opportunity to give this course is hereby gratefully ac knowledged.

Please note that the content of this book primarily consists of articles available from Wikipedia or other free sources online. Pages: 90. Chapters: Absorbing Markov chain, Algorithmic composition, Baum-Welch algorithm, Bernoulli scheme, Burst error, Dependability state model, Detailed balance, Discrete phase-type distribution, Dynamics of Markovian particles, Dynamic Markov compression, Entropy rate, Examples of Markov chains, Forward algorithm, Forward-backward algorithm, Gene prediction, GLIMMER, Google matrix, Hidden Markov model, Iterative Viterbi decoding, Kalman filter, Language model, Markovian discrimination, Markov chain geostatistics, Markov chain Monte Carlo, Markov partition, Markov property, Markov switching multifractal, Mark V Shaney, Maximum-entropy Markov model, Models of DNA evolution, Multiple sequence alignment, PageRank, Part-of-speech tagging, Path dependence, Population process, Pop music automation, Quantum Markov chain, Queueing model, Queueing theory, Reinforcement learning, Snakes and Ladders, Soft output Viterbi algorithm, Stochastic matrix, Transiogram, Variable-order Bayesian network, Variable-order Markov model. Excerpt: The Kalman filter, also known as linear quadratic estimation (LQE), is an algorithm that uses a series of measurements observed over time, containing noise (random variations) and other inaccuracies, and produces estimates of unknown variables that tend to be more precise than those based on a single measurement alone. More formally, the Kalman filter operates recursively on streams of noisy input data to produce a statistically optimal estimate of the underlying system state. The filter is named for Rudolf (Rudy) E. Kalman, one of the primary developers of its theory. The Kalman filter has numerous applications in technology. A common application is for guidance, navigation and control of vehicles, particularly aircraft and spacecraft. Furthermore, the Kalman filter is a widely applied concept in time...

A practical introduction perfect for final-year undergraduate and graduate students without a solid background in linear algebra and calculus.

The overall goal of this project (Phases I & II) was to develop computerized procedures that detect Road Weather Information System (RWIS) sensor malfunctions. In the first phase of the research we applied three classification algorithms and six regression algorithms to data generated by RWIS sensors in order to predict malfunctions. In this phase we investigate the use of Hidden Markov models as predictors of sensor values. The Hidden Markov model (HMM) is a technique used to model a sequence of temporal events. For example, suppose we have the sequence of values produced by a given sensor over a fixed time period. An HMM can be used to produce this sequence and then to determine the probability of occurrence of another sequence of values, such as that produced by the given sensor for a subsequent time period. If the actual values produced by the sensor deviate from the predicted sequence then a malfunction may have occurred. This report provides an overview of the Hidden Markov model and three algorithms, namely, the Forward- Backward algorithms, the Baum-Welch algorithm, and the Viterbi algorithm, that were used in our development of Hidden Markov models to predict sensor

values. We performed a series of experiments to evaluate the use of HMMs as predictors of temperature and precipitation sensor values.

Probabilistic models are becoming increasingly important in analysing the huge amount of data being produced by large-scale DNA-sequencing efforts such as the Human Genome Project. For example, hidden Markov models are used for analysing biological sequences, linguistic-grammar-based probabilistic models for identifying RNA secondary structure, and probabilistic evolutionary models for inferring phylogenies of sequences from different organisms. This book gives a unified, up-to-date and self-contained account, with a Bayesian slant, of such methods, and more generally to probabilistic methods of sequence analysis. Written by an interdisciplinary team of authors, it aims to be accessible to molecular biologists, computer scientists, and mathematicians with no formal knowledge of the other fields, and at the same time present the state-of-the-art in this new and highly important field.

This volume presents advanced techniques to modeling markets, with a wide spectrum of topics, including advanced individual demand models, time series analysis, state space models, spatial models, structural models, mediation, models that specify competition and diffusion models. It is intended as a follow-on and companion to Modeling Markets (2015), in which the authors presented the basics of modeling markets along the classical steps of the model building process: specification, data collection, estimation, validation and implementation. This volume builds on the concepts presented in Modeling Markets with an emphasis on advanced methods that are used to specify, estimate and validate marketing models, including structural equation models, partial least squares, mixture models, and hidden Markov models, as well as generalized methods of moments, Bayesian analysis, non/semi-parametric estimation and endogeneity issues. Specific attention is given to big data. The market environment is changing rapidly and constantly. Models that provide information about the sensitivity of market behavior to marketing activities such as advertising, pricing, promotions and distribution are now routinely used by managers for the identification of changes in marketing programs that can improve brand performance. In today's environment of information overload, the challenge is to make sense of the data that is being provided globally, in real time, from thousands of sources. Although marketing models are now widely accepted, the quality of the marketing decisions is critically dependent upon the quality of the models on which those decisions are based. This volume provides an authoritative and comprehensive review, with each chapter including: · an introduction to the method/methodology · a numerical example/application in marketing · references to other marketing applications · suggestions about software. Featuring contributions from top authors in the field, this volume will explore current and future aspects of modeling markets, providing relevant and timely research and techniques to scientists, researchers, students, academics and practitioners in marketing, management and economics.

Earthquake occurrence modeling is a rapidly developing research area. This book deals with its critical issues, ranging from theoretical advances to practical applications. The introductory chapter outlines state-of-the-art earthquake modeling approaches based on stochastic models. Chapter 2 presents seismogenesis in association with the evolving stress field. Chapters 3 to 5 present earthquake occurrence modeling by means of hidden (semi-)Markov models and discuss associated characteristic measures and relative estimation aspects. Further comparisons, the most important results and our concluding remarks are provided in Chapters 6 and 7.

A novel two-channel algorithm is proposed in this paper for discriminative training of Hidden Markov Models (HMMs). It adjusts the symbol emission coefficients of an existing HMM to maximize the separable distance between a pair of confusable training samples. The method is applied to identify the visemes of visual speech. The results indicate that the two-channel training method provides better accuracy on separating similar visemes than the conventional Baum-Welch estimation.

Bioinformatics Algorithms: an Active Learning Approach is one of the first textbooks to emerge from the recent Massive Online Open Course (MOOC) revolution. A light-hearted and analogy-filled companion to the authors' acclaimed online course (http://coursera.org/course/bioinformatics), this book presents students with a dynamic approach to learning bioinformatics. It strikes a unique balance between practical challenges in modern biology and fundamental algorithmic ideas, thus capturing the interest of students of biology and computer science students alike. Each chapter begins with a central biological question, such as "Are There Fragile Regions in the Human Genome?" or "Which DNA Patterns Play the Role of Molecular Clocks?" and then steadily develops the algorithmic sophistication required to answer this question. Hundreds of exercises are incorporated directly into the text as soon as they are needed; readers can test their knowledge through automated coding challenges on Rosalind (http://rosalind.info), an online platform for learning bioinformatics.The textbook website (http://bioinformaticsalgorithms.org) directs readers toward additional educational materials, including video lectures and PowerPoint slides.

A general theory of continuous-state hidden Markov models is developed, with continuous-state analogs of the Baum, Viterbi, and Baum-Welch algorithms formulated for this class of models. The algorithms are specialized to models with linear Gaussian densities, thereby unifying the theory of hidden Markov models and Kalman filters. The Baum and Viterbi algorithms for Gaussian models are shown to be implemented by two different formulations of the fixed-interval Kalman smoother. Moreover, the measurement likelihoods obtained from the forward pass of the Baum algorithm and from the Kalman-filter Innovation sequence are found to be equivalent A direct link between the Baum-Welch algorithm and an existing expectation-maximization algorithm for linear Gaussian models is demonstrated. The general continuous-state and Gaussian models are extended to incorporate mixture densities for the prior probability of the initial state. For the Gaussian models, a new expression for the cross covariance between time adjacent states is derived from the off-diagonal block of the conditional joint covariance matrix and a parameter invariance structure is observed when the system matrices are time invariant.

Our ability to generate and collect data has been increasing rapidly. Not only are all of our business, scientific, and government transactions now computerized, but the

widespread use of digital cameras, publication tools, and bar codes also generate data. On the collection side, scanned text and image platforms, satellite remote sensing systems, and the World Wide Web have flooded us with a tremendous amount of data. This explosive growth has generated an even more urgent need for new techniques and automated tools that can help us transform this data into useful information and knowledge. Like the first edition, voted the most popular data mining book by KD Nuggets readers, this book explores concepts and techniques for the discovery of patterns hidden in large data sets, focusing on issues relating to their feasibility, usefulness, effectiveness, and scalability. However, since the publication of the first edition, great progress has been made in the development of new data mining methods, systems, and applications. This new edition substantially enhances the first edition, and new chapters have been added to address recent developments on mining complex types of data—including stream data, sequence data, graph structured data, social network data, and multi-relational data. A comprehensive, practical look at the concepts and techniques you need to know to get the most out of real business data Updates that incorporate input from readers, changes in the field, and more material on statistics and machine learning Dozens of algorithms and implementation examples, all in easily understood pseudo-code and suitable for use in real-world, large-scale data mining projects Complete classroom support for instructors at www.mkp.com/datamining2e companion site

Hidden Markov models (HMMs) originally emerged in the domain of speech recognition. In recent years, they have attracted growing interest in the area of computer vision as well. This book is a collection of articles on new developments in the theory of HMMs and their application in computer vision. It addresses topics such as handwriting recognition, shape recognition, face and gesture recognition, tracking, and image database retrieval. This book is also published as a special issue of the International Journal of Pattern Recognition and Artificial Intelligence (February 2001). Contents: Introduction: A Simple Complex in Artificial Intelligence and Machine Learning (B H Juang)An Introduction to Hidden Markov Models and Bayesian Networks (Z Chahramani)Multi-Lingual Machine Printed OCR (P Natarajan et al.)Using a Statistical Language Model to Improve the Performance of an HMM-Based Cursive Handwriting Recognition System (U-V Marti & H Bunke)A 2-D HMM Method for Offline Handwritten Character Recognition (H-S Park et al.)Data-Driven Design of HMM Topology for Online Handwriting Recognition (J J Lee et al.)Hidden Markov Models for Modeling and Recognizing Gesture Under Variation (A D Wilson & A F Bobick)Sentence Lipreading Using Hidden Markov Model with Integrated Grammar (K Yu et al.)Tracking and Surveillance in Wide-Area Spatial Environments Using the Abstract Hidden Markov Model (H H Bui et al.)Shape Tracking and Production Using Hidden Markov Models (T Caelli et al.)An Integrated Approach to Shape and Color-Based Image Retrieval of Rotated Objects Using Hidden Markov Models (S Müller et al.) Readership: Graduate students of computer science, electrical engineering and related fields, as well as researchers at academic and industrial institutions. Keywords:Hidden Markov Models;Gesture Recognitoin;Bayesian Networks;Optical Character Recognition;Handwriting Character Recognition;Cartography;Shape Extraction;Image Feature Extraction.

We address the problem of learning discrete hidden Markov models from very long sequences of observations. Incremental versions of the Baum-Welch algorithm that approximate the beta-values used in the backward procedure are commonly used for this problem since their memory complexity is independent of the sequence length. However, traditional approaches have two main disadvantages: the approximation of the beta-values deviates far from the real values, and the learning algorithm requires previous knowledge of the topology of the model. This dissertation describes a new incremental Baum-Welch algorithm with a novel backward procedure that improves the approximation of the â-values based on a one-step lookahead in the training sequence and investigates heuristics to prune unnecessary states from an initial complex model. Two new approaches for pruning, greedy and controlled, are introduced and a novel method for identification of ill-conditioned models is presented. Incremental learning of multiple independent observations is also investigated. We justify the new approaches analytically and report empirical results that show they converge faster than the traditional Baum-Welch algorithm using fewer computer resources. Furthermore, we demonstrate that the new learning algorithms converge faster than the previous incremental approaches and can be used to perform online learning of high-quality models useful for classification tasks. Finally, this dissertation explores the use of the new algorithms for anomaly detection in computer systems, that improve our previous research work on detectors based on hidden Markov models integrated into real-world monitoring systems of high-performance computers.

The seven-volume set LNCS 12137, 12138, 12139, 12140, 12141, 12142, and 12143 constitutes the proceedings of the 20th International Conference on Computational Science, ICCS 2020, held in Amsterdam, The Netherlands, in June 2020.* The total of 101 papers and 248 workshop papers presented in this book set were carefully reviewed and selected from 719 submissions (230 submissions to the main track and 489 submissions to the workshops). The papers were organized in topical sections named: Part I: ICCS Main Track Part II: ICCS Main Track Part III: Advances in High-Performance Computational Earth Sciences: Applications and Frameworks; Agent-Based Simulations, Adaptive Algorithms and Solvers; Applications of Computational Methods in Artificial Intelligence and Machine Learning; Biomedical and Bioinformatics Challenges for Computer Science Part IV: Classifier Learning from Difficult Data; Complex Social Systems through the Lens of Computational Science; Computational Health; Computational Methods for Emerging Problems in (Dis-)Information Analysis Part V: Computational Optimization, Modelling and Simulation; Computational Science in IoT and Smart Systems; Computer Graphics, Image Processing and Artificial Intelligence Part VI: Data Driven Computational Sciences; Machine Learning and Data Assimilation for Dynamical Systems; Meshfree Methods in Computational Sciences; Multiscale Modelling and Simulation; Quantum Computing Workshop Part VII: Simulations of Flow and Transport: Modeling, Algorithms and Computation; Smart Systems: Bringing Together Computer Vision, Sensor Networks and Machine Learning; Software Engineering for Computational Science; Solving Problems with Uncerntanties; Teaching Computational Science; UNcErtainty QUantIficatiOn for ComputationAl modeLs *The conference was canceled due to the COVID-19 pandemic.

Abstract: "We present a learning algorithm for hidden Markov models with continuous state and observation spaces. All necessary probability density functions are approximated using samples, along with density trees generated from such samples. A Monte Carlo version of Baum-Welch (EM) is employed to learn models from data, just as in regular HMM learning. Regularization during learning is obtained using an exponential shrinking technique. The shrinkage factor, which determines the effective capacity of the learning algorithm, is annealed down over multiple iterations of Baum-Welch, and early stopping is applied to select the right model. We prove that under mild assumptions, Monte Carlo Hidden Markov Models converge to a local maximum in likelihood space, just like conventional HMMs. In addition, we provide empirical results obtained in a gesture recognition domain, which illustrate the appropriateness of the approach in practice."

Hidden Markov Models (HMMs), although known for decades, have made a big career nowadays and are still in state of development. This book presents theoretical issues and a variety of HMMs applications in speech recognition and synthesis, medicine, neurosciences, computational biology, bioinformatics, seismology, environment protection and engineering. I hope that the reader will find this book useful and helpful for their own research.

Please note that the content of this book primarily consists of articles available from Wikipedia or other free sources online. Pages: 102. Chapters: Bayesian networks, Markov models, Markov chain, Queueing theory, Snakes and ladders, Hidden Markov model, Poisson process, Reinforcement learning, Burst error, Mark V Shaney, Kalman filter, PageRank, Multiple sequence alignment, Models of DNA evolution, Forward-backward algorithm, Path dependence, Belief propagation, Structural equation modeling, Viterbi algorithm, Algorithmic composition, Part-of-speech tagging, Gene prediction, Google matrix, Markov switching multifractal, Conditional random field, Influence diagram, Markov random field, Markov chain Monte Carlo, Bayesian inference in phylogeny, Graphical models for protein structure, Queueing model, Pop music automation, Dynamic Markov compression, Subshift of finite type, Stochastic matrix, Language model, Examples of Markov chains, Hierarchical Bayes model, Factor graph, Markov property, Path analysis, Detailed balance, Bernoulli scheme, Variational message passing, Latent variable, Layered hidden Markov model, Markov partition, Hierarchical hidden Markov model, Discrete phase-type distribution, GLIMMER, Kolmogorov backward equations, Baum-Welch algorithm, Dependability state model, Plate notation, Junction tree algorithm, Variable-order Bayesian network, Iterative Viterbi decoding, Markovian discrimination, Forward algorithm, Entropy rate, Hidden semi-Markov model, Maximum entropy Markov model, Population process, Markov blanket, Collider, Soft output Viterbi algorithm, Moral graph, M-separation, Dynamics of Markovian particles, Markov chain geostatistics, Quantum Markov chain, Transiogram, Ancestral graph, Causal Markov condition, Poisson hidden Markov model, Dynamic Bayesian network.

This book constitutes the refereed proceedings of the 10th Congress of the Italian Association for Artificial Intelligence, AI*IA 2007, held in Rome, Italy, in September 2007. The 42 revised full papers presented together with 14 revised poster papers and 3 invited talks were carefully reviewed and selected from 80 submissions. The papers are organized in topical sections on knowledge representation and reasoning, multiagent systems, distributed AIai, knowledge engineering, ontologies and the semantic Web, machine learning, natural language processing, information retrieval and extraction, planning and scheduling, AI and applications. Three special tracks depicting progresses in significant application fields that represent increasingly relevant topics contain 18 additional papers on AI and robotics, AI and expressive media, and intelligent access to multimedia information.

This book constitutes the refereed proceedings of the 15th International Conference on the Theory and Application of Cryptology and Information Security, ASIACRYPT 2009, held in Tokyo, Japan, in December 2009. The 41 revised full papers presented were carefully reviewed and selected from 298 submissions. The papers are organized in topical sections on block ciphers, quantum and post-quantum, hash functions I, encryption schemes, multi party computation, cryptographic protocols, hash funtions II, models and frameworks I, cryptoanalysis: square and quadratic, models and framework II, hash functions III, lattice-based, and side channels.

Based on a NATO Advanced Study Institute held in 1993, this book addresses recent advances in automatic speech recognition and speech coding. The book contains contributions by many of the most outstanding researchers from the best laboratories worldwide in the field. The contributions have been grouped into five parts: on acoustic modeling; language modeling; speech processing, analysis and synthesis; speech coding; and vector quantization and neural nets. For each of these topics, some of the best-known researchers were invited to give a lecture. In addition to these lectures, the topics were complemented with discussions and presentations of the work of those attending. Altogether, the reader is given a wide perspective on recent advances in the field and will be able to see the trends for future work.

Hidden Markov Models for Time Series: An Introduction Using R, Second Edition illustrates the great flexibility of hidden Markov models (HMMs) as general-purpose models for time series data. The book provides a broad understanding of the models and their uses. After presenting the basic model formulation, the book covers estimation, forecasting, decoding, prediction, model selection, and Bayesian inference for HMMs. Through examples and applications, the authors describe how to extend and generalize the basic model so that it can be applied in a rich variety of situations. The book demonstrates how HMMs can be applied to a wide range of types of time series: continuous-valued, circular, multivariate, binary, bounded and unbounded counts, and categorical observations. It also discusses how to employ the freely available computing environment R to carry out the computations. Features Presents an accessible overview of HMMs Explores a variety of applications in ecology, finance, epidemiology, climatology, and sociology Includes numerous theoretical and programming exercises Provides most of the analysed data sets online New to the second edition A total of five chapters on extensions, including HMMs for longitudinal data, hidden semi-Markov models and models with continuous-valued state process New case studies on animal movement, rainfall occurrence and capture-recapture data

This text provides an introduction to hidden Markov models (HMMs) for the dynamical systems community. It is a valuable text for third or fourth year undergraduates studying engineering, mathematics, or science that includes work in probability, linear algebra and differential equations. The book presents algorithms for using HMMs, and it explains the derivation of those algorithms. It presents Kalman filtering as the extension to a continuous state space of a basic HMM algorithm. The book concludes with an application to biomedical signals. This text is distinctive for providing essential introductory material as well as presenting enough of the theory behind the basic algorithms so that the reader can use it as a guide to developing their own variants.

This book presents cutting-edge research on innovative human systems integration and human–machine interaction, with an emphasis on artificial intelligence and automation, as well as computational modeling and simulation. It covers a wide range of applications in the area of design, construction and operation of products, systems and services, including lifecycle development and human–technology interaction. The book describes advanced methodologies and tools for evaluating and improving interface usability, new models, and case studies and best practices in virtual, augmented and mixed reality systems, with a special focus on dynamic environments. It also discusses various factors concerning the human user, hardware, and artificial intelligence software. Based on the proceedings of the 2nd International Conference on Intelligent Human Systems Integration (IHSI 2019), held on February 7–10, 2019, in San Diego, California, USA, the book also examines the forces that are currently shaping the nature of computing and cognitive systems, such as the need to reduce hardware costs; the importance of infusing intelligence and automation; the trend toward hardware miniaturization and power reduction; the need for a better assimilation of computation in the environment; and social concerns regarding access to computers and systems for people with special needs. It offers a timely survey and a practice-oriented reference guide for policy- and decision-makers,

human factors engineers, systems developers and users alike.

The Application of Hidden Markov Models in Speech Recognition presents the core architecture of a HMM-based LVCSR system and proceeds to describe the various refinements which are needed to achieve state-of-the-art performance.

This book presents, in an integrated form, both the analysis and synthesis of three different types of hidden Markov models. Unlike other books on the subject, it is generic and does not focus on a specific theme, e.g. speech processing. Moreover, it presents the translation of hidden Markov models' concepts from the domain of formal mathematics into computer codes using MATLAB®. The unique feature of this book is that the theoretical concepts are first presented using an intuition-based approach followed by the description of the fundamental algorithms behind hidden Markov models using MATLAB®. This approach, by means of analysis followed by synthesis, is suitable for those who want to study the subject using a more empirical approach. Key Selling Points: Presents a broad range of concepts related to Hidden Markov Models (HMM), from simple problems to advanced theory Covers the analysis of both continuous and discrete Markov chains Discusses the translation of HMM concepts from the realm of formal mathematics into computer code Offers many examples to supplement mathematical notation when explaining new concepts