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Presentation tools such as PowerPoint were initially created to simulate physical slides and have inherited a lot of their limitations. In this dissertation we identify the shortcomings and unmet user needs in presentation software by means of literature study, observations, a survey and the programmatic analysis of over 12000 PowerPoint documents. The results indicate that user needs are slowly evolving while existing software has hardly changed over the last 30 years. We motivate the need to rethink the concept of a presentation and we provide conceptual and technical foundations that can enable interoperable and well-integrated solutions for the identified shortcomings. The resulting MindXpres platform consists of a new conceptual framework, content model, information system and presentation engine. We present MindXpres as a presentation platform that enables researchers and developers to build innovative presentation solutions that cannot be implemented in the existing tools. We further demonstrate the flexibility of the MindXpres platform by discussing a wide range of proof-of-concept plug-in solutions for the identified shortcomings and unmet user needs. Innovating is for doers: you don't need to wait for an earth-shattering idea, but can build one with a hunch and scale it up to impact. Innovation is the subject of countless books and courses, but there's very little out there about how you actually innovate. Innovation and entrepreneurship are not one and the same, although aspiring innovators often think of them that way. They are told to get an idea and a team and to build a show-and-tell for potential investors. In Innovating, Luis Perez-Breva describes another approach—a doer's approach developed over a decade at MIT and internationally in workshops, classes, and companies. He shows that to start innovating it doesn't require an earth-shattering idea; all it takes is a hunch. Anyone can do it. By prototyping a problem and learning by being wrong, innovating can be scaled up to make an impact. As Perez-Breva demonstrates, "no thing is new" at the outset of what we only later celebrate as innovation. In Innovating, the process—illustrated by unique and dynamic artwork—is shown to be empirical, experimental, nonlinear, and incremental. You give your hunch the structure of a problem. Anything can be a part. Your innovating accrues other people's knowledge and skills. Perez-Breva describes how to create a kit for innovating, and outlines questions that will help you think in new ways. Finally, he shows how to systematize what you've learned: to advocate, communicate, scale up, manage innovating continuously, and document—"you need a notebook to converse with yourself," he advises. Everyone interested in innovating also needs to read this book.

Digital practices are shaped by graphical representations that appear on the computer screen, which is the principal surface for designing, visualizing, and interacting with digital information. Before any digital image or graphical interface is rendered on the screen there is a series of layers that affect its visual properties. To discover such processes it is necessary to investigate software applications, graphical user interfaces, programming languages and code, algorithms, data structures, and data types in their relationship with graphical outcomes and design possibilities. This book studies interfaces as images and images as interfaces. It offers a comprehensible framework to study graphical representations of visual information. It explores the relationship between visual information and its graphical supports, taking into account contributions from fields of visual computing. Graphical supports are considered as material but also as formal aspects underlying the representation of digital images on the digital screen. The two-volume set LNCS 11295 and 11296 constitutes the thoroughly refereed proceedings of the 25th International Conference on MultiMedia Modeling, MMM 2019, held in Thessaloniki, Greece, in January 2019. Of the 172 submitted full papers, 49 were selected for oral presentation and 47 for poster presentation; in addition, 6 demonstration papers, 5 industry papers, 6 workshop papers, and 6 papers for the Video Browser Showdown 2019 were accepted. All papers presented were carefully reviewed and selected from 204 submissions.

Bioinformatics is an integrative field of computer science, genetics, genomics, proteomics, and statistics, which has undoubtedly revolutionized the study of biology and medicine in past decades. It mainly assists in modeling, predicting and interpreting large multidimensional biological data by utilizing advanced computational methods. Despite its enormous potential, bioinformatics is not widely integrated into the academic curriculum as most life science students and researchers are still not equipped with the necessary knowledge to take advantage of this powerful tool. Hence, the primary purpose of our book is to supplement this unmet need by providing an easily accessible platform for students and researchers starting their career in life sciences. This book aims to avoid sophisticated computational algorithms and programming. Instead, it mostly focuses on simple DIY analysis and interpretation of biological data with personal computers. Our belief is that once the beginners acquire these basic skillsets, they will be able to handle most of the bioinformatics tools for their research work and to better understand their experimental outcomes. Unlike other bioinformatics books which are mostly theoretical, this book provides practical examples for the readers on state-of-the-art open source tools to solve biological problems. Flow charts of experiments, graphical illustrations, and mock data are included for quick reference. Volume I is therefore an ideal companion for students and early stage professionals wishing to master this blooming field. The first book to comprehensively cover the field of systems genetics, gathering contributions from leading scientists.

Health informatics plays a central role in the digital transformation of the healthcare sector. The integration and connection of health services, practitioners and consumers is critical to the realisation of the improvements promised by digital health, and the secondary use of health data has led to ground-breaking research discoveries. Increased reliance upon all types of digital media has also established health informatics as a viable specialisation in healthcare. This book presents the proceedings of the 26th national Health Informatics Conference (HIC 2018), Australia's premier health informatics event, held in Sydney, Australia, in July/August 2018. The conference provides an environment for clinicians, researchers, health IT professionals, industry and consumers to integrate, educate and share the knowledge which drives innovative thinking, and this year's theme, 'Today's best practice, innovation today and preparing for tomorrow', focuses on the important issues of connecting the system, being smart with data, and enhancing the practitioner and consumer experience in healthcare interactions. The papers presented here reflect this theme, highlighting cutting-edge research evidence, technology updates and innovations from the digital transformation of the healthcare sector. Covering a wide spectrum of work, and encompassing major theoretical concepts, examples of key applications of new technologies and important new developments in the field of health informatics, the book will be of interest to all those working in the healthcare sector. Create and publish your own interactive data visualization projects on the web—even if you have little or no experience with data visualization or web development. It's inspiring and fun with this friendly, accessible, and practical hands-on introduction. This fully updated and expanded second edition takes you through the fundamental concepts and methods of D3, the most powerful JavaScript library for expressing data visually in a web browser. Ideal for designers with no coding experience, reporters exploring data journalism, and anyone who wants to visualize and share data, this step-by-step guide will also help you expand your web programming skills by teaching you the basics of HTML, CSS, JavaScript, and SVG. Learn D3 4.x—the latest D3 version—with downloadable code and over 140 examples Create bar charts, scatter plots, pie charts, stacked bar charts, and force-directed graphs Use smooth, animated transitions to show changes in your data Introduce interactivity to help users explore your data Create custom geographic maps with panning, zooming, labels, and tooltips

Walk through the creation of a complete visualization project, from start to finish Explore inspiring case studies with nine accomplished designers talking about their D3-based projects

Wring more out of the data with a scientific approach to analysis Graph Analysis and Visualization brings graph theory out of the lab and into the real world. Using sophisticated methods and tools that span analysis functions, this guide shows you how to exploit graph and network analytic techniques to enable the discovery of new business insights and opportunities. Published in full color, the book describes the process of creating powerful visualizations using a rich and engaging set of examples from sports, finance, marketing, security, social media, and more. You will find practical guidance toward pattern identification and using various data sources, including Big Data, plus clear instruction on the use of software and programming. The companion website offers data sets, full code examples in Python, and links to all the tools covered in the book. Science has already reaped the benefit of network and graph theory, which has powered breakthroughs in physics, economics, genetics, and more. This book brings those proven techniques into the world of business, finance, strategy, and design, helping extract more information from data and better communicate the results to decision-makers. Study graphical examples of networks using clear and insightful visualizations Analyze specifically-curated, easy-to-use data sets from various industries Learn the software tools and programming languages that extract insights from data Code examples using the popular Python programming language There is a tremendous body of scientific work on network and graph theory, but very little of it directly applies to analyst functions outside of the core sciences – until now. Written for those seeking empirically based, systematic analysis methods and powerful tools that apply outside the lab, Graph Analysis and Visualization is a thorough, authoritative resource.

The five-volume set LNCS 11536, 11537, 11538, 11539, and 11540 constitutes the proceedings of the 19th International Conference on Computational Science, ICCS 2019, held in Faro, Portugal, in June 2019. The total of 65 full papers and 168 workshop papers presented in this book set were carefully reviewed and selected from 573 submissions (228 submissions to the main track and 345 submissions to the workshops). The papers were organized in topical sections named: Part I: ICCS Main Track Part II: ICCS Main Track; Track of Advances in High-Performance Computational Earth Sciences: Applications and Frameworks; Track of Agent-Based Simulations, Adaptive Algorithms and Solvers; Track of Applications of Matrix Methods in Artificial Intelligence and Machine Learning; Track of Architecture, Languages, Compilation and Hardware Support for Emerging and Heterogeneous Systems Part III: Track of Biomedical and Bioinformatics Challenges for Computer Science; Track of Classifier Learning from Difficult Data; Track of Computational Finance and Business Intelligence; Track of Computational Optimization, Modelling and Simulation; Track of Computational Science in IoT and Smart Systems Part IV: Track of Data-Driven Computational Sciences; Track of Machine Learning and Data Assimilation for Dynamical Systems; Track of Marine Computing in the Interconnected World for the Benefit of the Society; Track of Multiscale Modelling and Simulation; Track of Simulations of Flow and Transport: Modeling, Algorithms and Computation Part V: Track of Smart Systems: Computer Vision, Sensor Networks and Machine Learning; Track of Solving Problems

with Uncertainties; Track of Teaching Computational Science; Poster Track ICCS 2019 Chapter "Comparing Domain-decomposition Methods for the Parallelization of Distributed Land Surface Models" is available open access under a Creative Commons Attribution 4.0 International License via link.springer.com.

The open access two-volume set LNCS 12224 and 12225 constitutes the refereed proceedings of the 32st International Conference on Computer Aided Verification, CAV 2020, held in Los Angeles, CA, USA, in July 2020.* The 43 full papers presented together with 18 tool papers and 4 case studies, were carefully reviewed and selected from 240 submissions. The papers were organized in the following topical sections: Part I: AI verification; blockchain and Security; Concurrency; hardware verification and decision procedures; and hybrid and dynamic systems. Part II: model checking; software verification; stochastic systems; and synthesis. *The conference was held virtually due to the COVID-19 pandemic.

This book presents the first comprehensive compilation of genome research on the Hevea brasiliensis rubber tree. The genomes of Hevea tree clones (cultivars) are described by three major international groups. Chapters on omics-driven investigations address a broad range of topics including genome annotation and utilisation, transcriptome and gene family analysis, genetic mapping, metabolic pathways in latex and molecular breeding. Additionally, an overview of fundamental rubber biology, especially on laticifers, provides a historical background that is relevant to rubber genome analysis. The book concludes with several perspectives on the future needs of rubber investigations and prospects of rubber genomics. Given the scope of topics, this book will appeal to researchers and university students working in genomics and biotechnology of the rubber tree, and to rubber breeders with an interest in non-conventional approaches to trait analysis, selection and breeding.

Computational Intelligence Methods for Bioinformatics and Biostatistics16th International Meeting, CIBB 2019, Bergamo, Italy, September 4–6, 2019, Revised Selected PapersSpringer NatureSpace Operations: Inspiring Humankind's FutureSpringer

This book constitutes the thoroughly refereed proceedings of the 6th Joint International Semantic Technology Conference, JIST 2016, held in Singapore, Singapore, in November 2016. The main topics of JIST 2016 include among others ontology and reasoning; linked data; knowledge graph. The JIST 2016 conference consists of two keynotes, a main technical track, including (full and short papers) from the research and the in-use tracks, a Poster and Demo session, a workshop and two tutorials. The 16 full and 8 short papers presented were carefully reviewed and selected from 34 submissions. The papers cover the following topics: ontology and data management; linked data; information retrieval and knowledge discovery; RDF and query; knowledge graph; application of semantic technologies.

Soil salinity is a key abiotic-stress and poses serious threats to crop yields and quality of produce. Owing to the underlying complexity, conventional breeding programs have met with limited success. Even genetic engineering approaches, via transferring/overexpressing a single 'direct action gene' per event did not yield optimal results. Nevertheless, the biotechnological advents in last decade coupled with the availability of genomic sequences of major crops and model plants have opened new vistas for understanding salinity-responses and improving salinity tolerance in important

glycophytic crops. Our goal is to summarize these findings for those who wish to understand and target the molecular mechanisms for producing salt-tolerant and high-yielding crops. Through this 2-volume book series, we critically assess the potential venues for imparting salt stress tolerance to major crops in the post-genomic era. Accordingly, perspectives on improving crop salinity tolerance by targeting the sensory, ion-transport and signaling mechanisms were presented in Volume 1. Volume 2 now focuses on the potency of post-genomic era tools that include RNAi, genomic intervention, genome editing and systems biology approaches for producing salt tolerant crops.

Health and Biomedical Informatics is a rapidly evolving multidisciplinary field; one in which new developments may prove crucial in meeting the challenge of providing cost-effective, patient-centered healthcare worldwide. This book presents the proceedings of MEDINFO 2015, held in São Paulo, Brazil, in August 2015. The theme of this conference is 'eHealth-enabled Health', and the broad spectrum of topics covered ranges from emerging methodologies to successful implementations of innovative applications, integration and evaluation of eHealth systems and solutions. Included here are 178 full papers and 248 poster abstracts, selected after a rigorous review process from nearly 800 submissions by 2,500 authors from 59 countries. The conference brings together researchers, clinicians, technologists and managers from all over the world to share their experiences on the use of information methods, systems and technologies to promote patient-centered care, improving patient safety, enhancing care outcomes, facilitating translational research and enabling precision medicine, as well as advancing education and skills in Health and Biomedical Informatics. This comprehensive overview of Health and Biomedical Informatics will be of interest to all those involved in designing, commissioning and providing healthcare, wherever they may be.

Introduces biological concepts and biotechnologies producing the data, graph and network theory, cluster analysis and machine learning, using real-world biological and medical examples.

This book includes a selection of 30 reviewed and enhanced manuscripts published during the 15th SpaceOps Conference held in May 2018 in Marseille, France. The selection was driven by their quality and relevance to the space operations community. The papers represent a cross-section of three main subject areas: Mission Management – management tasks for designing, preparing and operating a particular mission Spacecraft Operations – preparation and implementation of all activities to operate a space vehicle (crewed and uncrewed) under all conditions Ground Operations – preparation, qualification, and operations of a mission dedicated ground segment and appropriate infrastructure including antennas, control centers, and communication means and interfaces This book promotes the SpaceOps Committee's mission to foster the technical interchange on all aspects of space mission operations and ground data systems while promoting and maintaining an international community of space operations experts.

Computational immunology offers in silico strategies for understanding of complex processes occurring in the natural immune system of a living organism that are difficult to explore by traditional in vivo or in vitro techniques. The monograph introduces conceptual languages and approaches for modelling biological processes. The Agent

Modelling Language is investigated for conceptualisation of immune processes. AML-based diagrams represent properties and processes occurring in a lymph node. Current interest in fractal dimensions of networks is the result of more than a century of previous research on dimensions. Fractal Dimensions of Networks ties the theory and methods for computing fractal dimensions of networks to the "classic" theory of dimensions of geometric objects. The goal of the book is to provide a unified treatment of fractal dimensions of sets and networks. Since almost all of the major concepts in fractal dimensions originated in the study of sets, the book achieves this goal by first clearly presenting, with an abundance of examples and illustrations, the theory and algorithms for sets, and then showing how the theory and algorithms have been applied to networks. Thus, the book presents the classical theory and algorithms for the box counting dimension for sets, and then presents the box counting dimension for networks. All the major fractal dimensions are studied, e.g., the correlation dimension, the information dimension, the Hausdorff dimension, the multifractal spectrum, as well as many lesser known dimensions. Algorithm descriptions are accompanied by worked examples, many applications of the methods are presented, and many exercises, ranging in difficulty from easy to research level, are included.

Covering a wide-ranging facet of a "gold-standard" targeted mass spectrometry (MS) method for the consistent detection and accurate quantification of preselected proteins in complex biological matrices, Selected Reaction Monitoring Mass Spectrometry (SRM-MS) in Proteomics: A Comprehensive View describes: The knowledge-based development of highly efficient SRM methodology including assay workflow, selection of proteins, peptides, transitions and its validation, and quality assessment Available bioinformatic tools – for both pre-acquisition method development and post-MS acquisition data analysis and data repositories Various relative and absolute quantification techniques SRM-MS' widespread applications in biomarker development and in clinical studies, as well as in the analysis of various posttranslational modifications (PTMs) Current challenges and contemporary trends to overcome those difficulties In addition, it features the historical development of modern-day mass spectrometry with its vivid applications and also covers basic MS instrumentation, ionization techniques, and various proteomics approaches. Comprehensive discussion, extensive references at the end of each chapter, and the list of review articles in the bibliography offer invaluable resources for advanced readings. Researchers from the undergraduate to postgraduate level and beyond in both academic or industry settings studying and working on mass spectrometry and/or proteomics will benefit from this book.

This book constitutes the refereed proceedings of the 19th International Conference on Computational Methods in Systems Biology, CMSB 2021, held in Bordeaux, France, September 22–24, 2021.*The 13 full papers and 5 tool papers were carefully reviewed and selected from 32 submissions. The topics of interest include biological process modelling; biological system model verification, validation, analysis, and simulation; high-performance computational systems biology; model inference from experimental data; multi-scale modeling and analysis methods; computational approaches for synthetic biology; machine learning and data-driven approaches; microbial ecology modelling and analysis; methods and protocols for populations and their variability; models, applications, and case studies in systems and synthetic biology. The chapters

"Microbial Community Decision Making Models in Batch", "Population design for synthetic gene circuits", "BioFVM-X: An MPI+OpenMP 3-D Simulator for Biological Systems" are published open access under a CC BY license (Creative Commons Attribution 4.0 International License). * The conference was held in a hybrid mode due to the COVID-19 pandemic.

This open access two-volume set LNCS 10980 and 10981 constitutes the refereed proceedings of the 30th International Conference on Computer Aided Verification, CAV 2018, held in Oxford, UK, in July 2018. The 52 full and 13 tool papers presented together with 3 invited papers and 2 tutorials were carefully reviewed and selected from 215 submissions. The papers cover a wide range of topics and techniques, from algorithmic and logical foundations of verification to practical applications in distributed, networked, cyber-physical, and autonomous systems. They are organized in topical sections on model checking, program analysis using polyhedra, synthesis, learning, runtime verification, hybrid and timed systems, tools, probabilistic systems, static analysis, theory and security, SAT, SMT and decisions procedures, concurrency, and CPS, hardware, industrial applications.

"Social networks fundamentally shape our lives. Networks channel the ways that information, emotions, and diseases flow through populations. Networks reflect differences in power and status in settings ranging from small peer groups to international relations across the globe. Network tools even provide insights into the ways that concepts, ideas and other socially generated contents shape culture and meaning. As such, the rich and diverse field of social network analysis has emerged as a central tool across the social sciences. This Handbook provides an overview of the theory, methods, and substantive contributions of this field. The thirty-three chapters move through the basics of social network analysis aimed at those seeking an introduction to advanced and novel approaches to modeling social networks statistically. The Handbook includes chapters on data collection and visualization, theoretical innovations, links between networks and computational social science, and how social network analysis has contributed substantively across numerous fields. As networks are everywhere in social life, the field is inherently interdisciplinary and this Handbook includes contributions from leading scholars in sociology, archaeology, economics, statistics, and information science among others"--

Providing a comprehensive overview of cutting-edge research on Omics applications in plant sciences field,"Plant Stress Tolerance" focuses on different approaches towards plant stress tolerance including both biotic stresses and abiotic stresses. This book outlines the challenges facing this area of research, with solid, up-to-date information for graduate students, academic scientists and researchers on using the recent advances of Omics technologies on plant stresses.

This book gathers the proceedings of MEDICON 2019 – the XV Mediterranean Conference on Medical and Biological Engineering and Computing – which was held in September 26-28, 2019, in Coimbra, Portugal. A special emphasis has been given to practical findings, techniques and methods, aimed at fostering an effective patient empowerment, i.e. to position the patient at the heart of the health system and encourages them to be actively involved in managing their own healthcare needs. The book reports on research and development in electrical engineering, computing, data science and instrumentation, and on many topics at the interface between those

disciplines. It provides academics and professionals with extensive knowledge on cutting-edge techniques and tools for detection, prevention, treatment and management of diseases. A special emphasis is given to effective advances, as well as new directions and challenges towards improving healthcare through holistic patient empowerment.

This edited volume summarizes the recent advancements made in plant science including molecular biology and genome editing , particularly in the development of novel pathways tolerant to climate change-induced stresses such as drought, extreme temperatures, cold, salinity, flooding, etc. These stresses are liable for decrease in yields in many crop plants at global level. Till date conventional plant breeding approaches have resulted in significant improvement of crop plants for producing higher yields during adverse climatic conditions. However, the pace of improvement through conventional plant breeding needs to be accelerated in keeping with the growing demand of food and increasing human populationl, particularly in developing world. This book serves as a comprehensive reference material for researchers, teachers, and students involved in climate change-related abiotic stress tolerance studies in plants. This book constitutes the refereed proceedings of the 7th International Conference on Rigorous State-Based Methods, ABZ 2020, which was due to be held in Ulm, Germany, in May 2020. The conference was cancelled due to the COVID-19 pandemic. The 12 full papers and 9 short papers were carefully reviewed and selected from 61 submissions. They are presented in this volume together with 2 invited papers, 6 PhD-Symposium-contributions, as well as the case study and 6 accepted papers outlining solutions to it. The papers are organized in the following sections: keynotes and invited papers; regular research articles; short articles; articles contributing to the case study; short articles of the PhD-symposium (work in progress).

This book constitutes the thoroughly refereed post-conference proceedings of the 15th International Meeting on Computational Intelligence Methods for Bioinformatics and Biostatistics., CIBB 2018, held in Caparica, Portugal, in September 2018. The 32 revised full papers were carefully reviewed and selected from 51 submissions. The papers present current trends at the edge of computer and life sciences, the application of computational intelligence to a system and synthetic biology and the consequent impact on innovative medicine were presented. Theoretical and experimental biologists also presented novel challenges and fostered multidisciplinary collaboration aiming to blend theory and practice, where the founding theories of the techniques used for modelling and analyzing biological systems are investigated and used for practical applications and the supporting technologies.

Biological Network Analysis: Trends, Approaches, Graph Theory, and Algorithms considers three major biological networks, including Gene Regulatory Networks (GRN), Protein-Protein Interaction Networks (PPIN), and Human Brain Connectomes. The book's authors discuss various graph theoretic and data analytics approaches used to analyze these networks with respect to available tools, technologies, standards, algorithms and databases for generating, representing and analyzing graphical data. As a wide variety of algorithms have been developed to analyze and compare networks, this book is a timely resource. Presents recent advances in biological network analysis, combining Graph Theory, Graph Analysis, and various network models Discusses three major biological networks, including Gene Regulatory Networks (GRN), Protein-Protein Interaction Networks (PPIN) and Human Brain Connectomes Includes a discussion of various graph theoretic and data analytics approaches

This groundbreaking, open access volume analyses and compares data practices across several fields through the analysis of specific cases of data journeys. It brings together leading

scholars in the philosophy, history and social studies of science to achieve two goals: tracking the travel of data across different spaces, times and domains of research practice; and documenting how such journeys affect the use of data as evidence and the knowledge being produced. The volume captures the opportunities, challenges and concerns involved in making data move from the sites in which they are originally produced to sites where they can be integrated with other data, analysed and re-used for a variety of purposes. The in-depth study of data journeys provides the necessary ground to examine disciplinary, geographical and historical differences and similarities in data management, processing and interpretation, thus identifying the key conditions of possibility for the widespread data sharing associated with Big and Open Data. The chapters are ordered in sections that broadly correspond to different stages of the journeys of data, from their generation to the legitimisation of their use for specific purposes. Additionally, the preface to the volume provides a variety of alternative "roadmaps" aimed to serve the different interests and entry points of readers; and the introduction provides a substantive overview of what data journeys can teach about the methods and epistemology of research.

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This book constitutes the refereed proceedings of the 15th International Conference on Computational Methods in Systems Biology, CMSB 2017, held in Darmstadt, Germany, in September 2017. The 15 full papers, 4 tool papers and 4 posters presented together with 1 invited talk were carefully reviewed and selected from 41 regular paper submissions. Topics of interest include formalisms for modeling biological processes; models and their biological applications; frameworks for model verication, validation, analysis, and simulation of biological systems; high-performance computational systems biology and parallel implementations; model inference from experimental data; model integration from biological databases; multi-scale modeling and analysis methods; and computational approaches for synthetic biology.
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