Life Sciences Computing Corporation

Cannataro, Mario

IBM Reference Architecture for High Performance Data and AI in Healthcare and Life Sciences Dino Quintero,Frank N. Lee,2019

IBM Reference Architecture for High Performance Data and AI in Healthcare and Life Sciences Dino Quintero,Frank N. Lee,IBM Redbooks,2019-09-08 This IBM® Redpaper publication provides an update to the original description of IBM Reference Architecture for Genomics. This paper expands the reference architecture to cover all of the major vertical areas of healthcare and life sciences industries, such as genomics, imaging, and clinical and translational research. The architecture was renamed IBM Reference Architecture for High Performance Data and AI in Healthcare and Life Sciences to reflect the fact that it incorporates key building blocks for high-performance computing (HPC) and software-defined storage, and that it supports an expanding infrastructure of leading industry partners, platforms, and frameworks. The reference architecture defines a highly flexible, scalable, and cost-effective platform for accessing, managing, storing, sharing, integrating, and analyzing big data, which can be deployed on-premises, in the cloud, or as a hybrid of the two. IT organizations can use the reference architecture as a high-level guide for overcoming data management challenges and processing bottlenecks that are frequently encountered in personalized healthcare initiatives, and in compute-intensive and data-intensive biomedical workloads. This reference architecture also provides a framework and context for modern healthcare and life sciences institutions to adopt cutting-edge technologies, such as cognitive life sciences solutions, machine learning and deep learning, Spark for analytics, and cloud computing. To illustrate these points, this paper includes case studies describing how clients and IBM Business Partners alike used the reference architecture in the deployments of demanding infrastructures for precision medicine. This publication targets technical professionals (consultants, technical support staff, IT Architects, and IT Specialists) who are responsible for providing life sciences solutions and support.

Python for the Life Sciences Alexander Lancaster,Gordon Webster,2019-09-27 Treat yourself to a lively, intuitive, and easy-to-follow introduction to computer programming in Python. The book was written specifically for biologists with little or no prior experience of writing code - with the goal of giving them not only a foundation in Python programming, but also the confidence and inspiration to start using Python in their own research. Virtually all of the examples in the book are drawn from across a wide spectrum of life science research, from simple biochemical calculations and sequence analysis, to modeling the dynamic interactions of genes and proteins in cells, or the drift of genes in an evolving population. Best of all, Python for the Life Sciences shows you how to implement all of these projects in Python, one of the most popular programming languages for scientific computing. If you are a life scientist interested in learning Python to jump-start your research, this is the book for you. What You'll Learn Write Python scripts to automate your lab calculations Search for important motifs in genome sequences Use object-oriented programming with Python Study mining interaction network data for patterns Review dynamic modeling of biochemical switches Who This Book Is For Life scientists with little or no programming experience, including undergraduate and graduate students, postdoctoral researchers in academia and industry, medical professionals, and teachers/lecturers. “A comprehensive introduction to using Python for computational biology... A lovely book with humor and perspective” -- John Novembre, Associate Professor of Human Genetics, University of Chicago and MacArthur Fellow “Fun, entertaining, witty and darn useful. A magical portal to the big data revolution” -- Sandro Santagata, Assistant Professor in Pathology, Harvard Medical School “Alex and Gordon’s enthusiasm for Python is contagious” -- Glenys Thomson Professor of Integrative Biology, University of California, Berkeley

Computers in Life Science Research William Siler,2013-11-11 45 certainty about Federal policy concern the University of Alabama cardiac in ing the support of training contribute tensive care monitoring system on ob to these difficulties. The problems are solete 1800 computers. Another re too broad and too complex to address sponded most efficaciously pointing out here. They are difficult for both aca that it is too bad that people lose sight of demia and government, and warrant the fact that a system on which a pro the active concern of the entire research gram is developed will always be able community. to do the job; change is not indicated Dr. Robert Macey introduced to the until the system ceases to be appropri ate. conference the exciting world of model development describing an application In another vein, the question opens to the area of membrane transport. The up a wide range of problems that can be discussion of his paper exposed the prob summarized as problems in the diffusion lern the modeler has of gaining ac of computer-based technology. At this ceptance of his particular approach, but juncture biomedical computing joins all mainly it provided a taste of the intellec the rest of biomedicine. The problems of tual excitement that modeling generates diffusion of advances in health research, among both doers and observers.

Computers in Life Science Research William Siler,2014-01-15

HealthGrid Applications and Technologies Meet Science Gateways for Life Sciences S. Gesing,2012-05-10 The integration of grid, cloud and other e-infrastructures into the fields of biology, bioinformatics, biomedicine, and healthcare are crucial if optimum use is to be made of the latest high-performance and distributed computer technology in these areas. Science gateways are concerned with offering intuitive graphical user interfaces to applications, data, and tools on distributed computing infrastructures. This book presents the joint proceedings of the Tenth HealthGrid Conference and the Fourth International Workshop on Science Gateways for Life Sciences (IWSG-Life), held in Amsterdam, Netherlands in May 2012. The HealthGrid conference promotes the exchange and debate of ideas, technologies and solutions likely to promote the integration of grids into biomedical research and health in the broadest sense. The IWSG-Life workshop series is a forum that brings together scientists from the field of life sciences, bioinformatics, and computer science to advance computational biology and chemistry in the context of science gateways. These events have been jointly organized to maximize the benefit from synergies and stimulate the forging of further links in joint research areas. The book is divided into three parts. Part I includes contributions accepted to the HealthGrid conference; Part II contains the papers about various aspects of the development and usage of science gateways for life sciences. The joint session is recorded in Part III, and addresses the topic of science gateways for biomedical research. The book will provide insights and new perspectives for all those involved in the research and use of infrastructures and technology for healthcare and life sciences.

Planning for Long-Term Use of Biomedical Data National Academies of Sciences, Engineering, and Medicine,Policy and Global Affairs,Board on Research Data and Information,Division on Earth and Life Studies,Board on Life Sciences,Division on Engineering and Physical Sciences,Computer Science and Telecommunications Board,Committee on Applied and Theoretical Statistics,Board on Mathematical Sciences and Analytics,2020-07-09 Biomedical research data sets are becoming larger and more complex, and computing capabilities are expanding to enable transformative scientific results. The National Institutes of Health's (NIH's) National Library of Medicine (NLM) has the unique role of ensuring that biomedical research data are findable, accessible, interoperable, and reusable in an ethical manner. Tools that forecast the costs of long-term data preservation could be useful as the cost to curate and manage these data in meaningful ways continues to increase, as could stewardship to assess and maintain data that have future value. The National Academies of Sciences, Engineering, and Medicine convened a workshop on July 11-12, 2019 to gather insight and information in order to develop and demonstrate a framework for forecasting long-term costs for preserving, archiving, and accessing biomedical data. Presenters and attendees discussed tools and practices that NLM could use to help researchers and funders better integrate risk management practices and considerations into data preservation, archiving, and accessing decisions; methods to encourage NIH-funded researchers to consider, update, and track lifetime data;

and burdens on the academic researchers and industry staff to implement these tools, methods, and practices. This publication summarizes the presentations and discussion of the workshop.

Biomedical Computing Joseph A. November,2012-06-01 Winner of the Computer History Museum Prize of the Special Interest Group: Computers, Information, and Society Imagine biology and medicine today without computers. What would laboratory work be like if electronic databases and statistical software did not exist? Would disciplines like genomics even be feasible if we lacked the means to manage and manipulate huge volumes of digital data? How would patients fare in a world absent CT scans, programmable pacemakers, and computerized medical records? Today, computers are a critical component of almost all research in biology and medicine. Yet, just fifty years ago, the study of life was by far the least digitized field of science, its living subject matter thought too complex and dynamic to be meaningfully analyzed by logic-driven computers. In this long-overdue study, historian Joseph November explores the early attempts, in the 1950s and 1960s, to computerize biomedical research in the United States. Computers and biomedical research are now so intimately connected that it is difficult to imagine when such critical work was offline. Biomedical Computing transports readers back to such a time and investigates how computers first appeared in the research lab and doctor's office. November examines the conditions that made possible the computerization of biology—including strong technological, institutional, and political support from the National Institutes of Health—and shows not only how digital technology transformed the life sciences but also how the intersection of the two led to important developments in computer architecture and software design. The history of this phenomenon has been only vaguely understood. November's thoroughly researched and lively study makes clear for readers the motives behind computerizing the study of life and how that technology profoundly affects biomedical research today.

Deep Learning for the Life Sciences Bharath Ramsundar,Peter Eastman,Patrick Walters,Vijay Pande,2019-04-10 Deep learning has already achieved remarkable results in many fields. Now it’s making waves throughout the sciences broadly and the life sciences in particular. This practical book teaches developers and scientists how to use deep learning for genomics, chemistry, biophysics, microscopy, medical analysis, and other fields. Ideal for practicing developers and scientists ready to apply their skills to scientific applications such as biology, genetics, and drug discovery, this book introduces several deep network primitives. You’ll follow a case study on the problem of designing new therapeutics that ties together physics, chemistry, biology, and medicine—an example that represents one of science’s greatest challenges. Learn the basics of performing machine learning on molecular data Understand why deep learning is a powerful tool for genetics and genomics Apply deep learning to understand biophysical systems Get a brief introduction to machine learning with DeepChem Use deep learning to analyze microscopic images Analyze medical scans using deep learning techniques Learn about variational autoencoders and generative adversarial networks Interpret what your model is doing and how it’s working

Grid Computing in Life Sciences Tin Wee Tan,Peter Arzberger,Akihiko Konagaya,2006 This is the second volume in the series of proceedings from the International Workshop on Life Science Grid. It represents the few, if not the only, dedicated proceedings volumes that gathers together the presentations of leaders in the emerging sub-discipline of grid computing for the life sciences. The volume covers the latest developments, trends and trajectories in life science grid computing from top names in bioinformatics and computational biology: A Konagaya; J C Wooley of the National Science Foundation (NSF) and DoE thought leader in supercomputing and life science computing, and one of the key people in the NSF CIBIO initiative; P Arzberger of PRAGMA fame; and R Sinnott of UK e-Science. Sample Chapter(s). Chapter 1: The Grid as a ba for Biomedical Knowledge Creation (155 KB). Contents: The Grid as a OC BaOCO for Biomedical Knowledge Creation (A Konagaya); Cyberinfrastructure for the Biological Sciences (CIBIO) (J C Wooley); Controlling the Chaos: Developing Post-Genomic Grid Infrastructures (R Sinnott & M Bayer); A Framework for Biological Analysis on the Grid (T Okumura et al.); An Architectural Design of Open Genome Services (R Umetsu et al.); Proteome Analysis Using iGAP in Gfarm (W W Li et al.); Large-Scale Simulation and Prediction of HLA-Epitope Complex Structures (A E H Png et al.); Process Integration for Bio-Manufacturing Grid (Z Q Shen et al.); and other papers. Readership: Practitioners of grid computing as applied to the life sciences, life scientists and biologists working on large computational solutions that require grid computing.

Handbook of Research on Computational Grid Technologies for Life Sciences, Biomedicine, and Healthcare Cannataro, Mario,2009-05-31 This book provides methodologies and developments of grid technologies applied in different fields of life sciences--Provided by publisher.

High Performance Computing Systems and Applications Robert D. Kent,Todd W. Sands,2012-12-06 High Performance Computing Systems and Applications contains fully refereed papers from the 15th Annual Symposium on High Performance Computing. These papers cover both fundamental and applied topics in HPC: parallel algorithms, distributed systems and architectures, distributed memory and performance, high level applications, tools and solvers, numerical methods and simulation, advanced computing systems, and the emerging area of computational grids. High Performance Computing Systems and Applications is suitable as a secondary text for graduate level courses, and as a reference for researchers and practitioners in industry.

A Bibliographic Guide to Resources in Scientific Computing, 1945-1975 Jeffrey R. Yost,2002-10-30 An essential contribution to the study of the history of computers, this work identifies the computer's impact on the physical, biological, cognitive, and medical sciences. References fundamental to the understudied area of the history of scientific computing also document the significant role of the sciences in helping to shape the development of computer technology. More broadly, the many resources on scientific computing help demonstrate how the computer was the most significant scientific instrument of the 20th century. The only guide of its kind covering the use and impact of computers on the the physical, biological, medical, and cognitive sciences, it contains more than 1,000 annotated citations to carefully selected secondary and primary resources. Historians of technology and science will find this a very useful resource. Computer scientists, physicians, biologists, chemists, and geologists will also benefit from this extensive bibliography on the history of computer applications and the sciences.

Introduction to Data Mining for the Life Sciences Rob Sullivan,2012-01-07 Data mining provides a set of new techniques to integrate, synthesize, and analyze tdata, 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.

Computers in Life Science Research William Siler,Donald A.B. Lindberg,1975

SEC Docket United States. Securities and Exchange Commission,1992

Open Source Software in Life Science Research Lee Harland,Mark Forster,2012-10-31 The free/open source approach has grown from a minor activity to become a significant producer of robust, task-orientated software for a wide variety of situations and applications. To life science informatics groups, these systems present an appealing proposition – high quality software at a very attractive price. Open source software in life science research considers how industry and applied research groups have embraced these resources, discussing practical implementations that address real-world business problems. The book is divided into four parts. Part one looks at laboratory data management and chemical informatics, covering software such as Bioclipse, OpenTox, ImageJ and KNIME. In part two, the focus turns to genomics

and bioinformatics tools, with chapters examining GenomicsTools and EBI Atlas software, as well as the practicalities of setting up an ‘omics’ platform and managing large volumes of data. Chapters in part three examine information and knowledge management, covering a range of topics including software for web-based collaboration, open source search and visualisation technologies for scientific business applications, and specific software such as DesignTracker and Utopia Documents. Part four looks at semantic technologies such as Semantic MediaWiki, TripleMap and Chem2Bio2RDF, before part five examines clinical analytics, and validation and regulatory compliance of free/open source software. Finally, the book concludes by looking at future perspectives and the economics and free/open source software in industry. Discusses a broad range of applications from a variety of sectors Provides a unique perspective on work normally performed behind closed doors Highlights the criteria used to compare and assess different approaches to solving problems

Catalyzing Inquiry at the Interface of Computing and Biology National Research Council,Division on Engineering and Physical Sciences,Computer Science and Telecommunications Board,Committee on Frontiers at the Interface of Computing and Biology,2005-12-01 Advances in computer science and technology and in biology over the last several years have opened up the possibility for computing to help answer fundamental questions in biology and for biology to help with new approaches to computing. Making the most of the research opportunities at the interface of computing and biology requires the active participation of people from both fields. While past attempts have been made in this direction, circumstances today appear to be much more favorable for progress. To help take advantage of these opportunities, this study was requested of the NRC by the National Science Foundation, the Department of Defense, the National Institutes of Health, and the Department of Energy. The report provides the basis for establishing cross-disciplinary collaboration between biology and computing including an analysis of potential impediments and strategies for overcoming them. The report also presents a wealth of examples that should encourage students in the biological sciences to look for ways to enable them to be more effective users of computing in their studies.

Official Gazette of the United States Patent and Trademark Office ,2004

IBM Reference Architecture for Genomics, Power Systems Edition Dino Quintero,Luis Bolinches,Marcelo Correia Lima,Katarzyna Pasierb,William dos Santos,IBM Redbooks,2016-04-05 This IBM® Redbooks® publication introduces the IBM Reference Architecture for Genomics, IBM Power SystemsTM edition on IBM POWER8®. It addresses topics such as why you would implement Life Sciences workloads on IBM POWER8, and shows how to use such solution to run Life Sciences workloads using IBM PlatformTM Computing software to help set up the workloads. It also provides technical content to introduce the IBM POWER8 clustered solution for Life Sciences workloads. This book customizes and tests Life Sciences workloads with a combination of an IBM Platform Computing software solution stack, Open Stack, and third party applications. All of these applications use IBM POWER8, and IBM Spectrum ScaleTM for a high performance file system. This book helps strengthen IBM Life Sciences solutions on IBM POWER8 with a well-defined and documented deployment model within an IBM Platform Computing and an IBM POWER8 clustered environment. This system provides clients in need of a modular, cost-effective, and robust solution with a planned foundation for future growth. This book highlights IBM POWER8 as a flexible infrastructure for clients looking to deploy life sciences workloads, and at the same time reduce capital expenditures, operational expenditures, and optimization of resources. This book helps answer clients' workload challenges in particular with Life Sciences applications, and provides expert-level documentation and how-to-skills to worldwide teams that provide Life Sciences solutions and support to give a broad understanding of a new architecture.

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