1. Record Nr. UNINA9910782719903321

| | |
|---|---|
| Autore | Berlekamp Elwyn R |
| Titolo | Winning ways for your mathematical plays . Vol. 3 [[electronic resource] /] / Elwyn R. Berlekamp, John H. Conway, Richard K. Guy |
| Pubbl/distr/stampa | Natick, Mass., : A.K. Peters, c2003 |
| ISBN | 0-429-94561-2<br>1-56881-596-4<br>1-56881-560-3 |
| Edizione | [2nd ed.] |
| Descrizione fisica | 1 online resource (363 p.) |
| Collana | Winning ways for your mathematical plays |
| Altri autori (Persone) | ConwayJohn Horton<br>GuyRichard K |
| Disciplina | 793.7/4 |
| Soggetti | Mathematical recreations |
| Lingua di pubblicazione | Inglese |
| Formato | Materiale a stampa |
| Livello bibliografico | Monografia |
| Note generali | Description based upon print version of record. |
| Nota di bibliografia | Includes bibliographical references and index. |
| Nota di contenuto | ""Contents""; ""Preface to the Second Edition""; ""Preface to the Original Edition""; ""Games in Clubs!""; ""-14- Turn and Turn About""; ""-15- Chips and Strips""; ""-16- Dots- and- Boxes""; ""-17- Spots and Sprouts""; ""-18- The Emperor and His Money""; ""-19- The King and the Consumer""; ""The Game of Kinggo""; ""-20- Fox and Geese""; ""-21- Hare and Hounds""; ""-22- Lines and Squares""; ""Index to Volumes 1a€?3"" |

2. Record Nr. UNINA9910556874303321

| | |
|---|---|
| Titolo | Safety, Health and Welfare in Agriculture and Agro-food Systems : Ragusa SHWA 2021 / / edited by Marcello Biocca, Eugenio Cavallo, Massimo Cecchini, Sabina Failla, Elio Romano |
| Pubbl/distr/stampa | Cham : , : Springer International Publishing : , : Imprint : Springer, , 2022 |
| ISBN | 3-030-98092-8 |
| Edizione | [1st ed. 2022.] |
| Descrizione fisica | 1 online resource (519 pages) |
| Collana | Lecture Notes in Civil Engineering, , 2366-2565 ; ; 252 |
| Disciplina | 338.10289 |
| Soggetti | Agricultural biotechnology<br>Environmental protection<br>Civil engineering<br>Food - Safety measures<br>Forests and forestry<br>Agricultural Biotechnology<br>Soil and Water Protection<br>Food Safety<br>Forestry |
| Lingua di pubblicazione | Inglese |
| Formato | Materiale a stampa |
| Livello bibliografico | Monografia |
| Nota di bibliografia | Includes bibliographical references and index. |
| Nota di contenuto | Intro -- Preface -- Organization -- Conference Scientific Committee -- Editorial Committee -- Convener -- Contents -- WMSDs Work Related Musculo-Skeletal Disorders -- Quantification of Trunk Postures Among Fruit and Vegetable Pickers in Sardinia -- Abstract -- 1 Introduction -- 2 Methods -- 3 Results -- 4 Discussion -- Acknowledgements -- References -- Image Analysis for Ergonomic Risk Assessment for Rope Arborists -- Abstract -- 1 Introduction -- 2 Materials and Methods -- 3 Results -- 4 Conclusions -- References -- Biomechanical Risk for the Hand-Arm System During Work Activities on Peach Fruit Tree -- Abstract -- 1 Introduction -- 2 Materials and Methods -- 2.1 Company Data, Total Exposed Workers and Identification of Repetitive Tasks -- 2.2 Net Working Time Calculation -- 2.3 Evaluation of Frequency and Technical Actions -- 2.4 Assessment of Incongruous Postures -- 2.5 |

Strength Risk Factors -- 2.6 Complementary Risk Factors -- 2.7 The Final Score of the OCRA Mini-Checklist -- 3 Results -- 4 Conclusions -- References -- Health and Safety Risks in Hop-Picking Activities: An Analysis of the State of the Art -- Abstract -- 1 Introduction -- 2 Methods -- 3 Results -- 3.1 Hop Harvesting Methods -- 3.2 Critical Issues in the Hop Harvest -- 3.3 Assessment and Prevention of Work-Related Health and Safety Risks -- 4 Conclusion -- References -- Machine Milking, Animal Welfare, Sustainable Livestock Farming -- Precision Livestock Farming for Mediterranean Water Buffalo: Some Applications and Opportunities from the Agridigit Project -- Abstract -- 1 Introduction -- 1.1 The Agridigit Project in Brief -- 2 Material and Methods -- 3 Results and Discussion -- 3.1 Ear Tag Sensors -- 3.2 Body Condition Score Evaluation -- 3.3 Laser Methane Pistols -- 4 Conclusion -- Aknowledgments -- References.
Pre-slaughtering Phases and Meat Quality of Highly Profitable Cattle (Piedmontese Fat Ox) -- Abstract -- 1 Introduction -- 1.1 Influence of Animal Welfare on the Quality of Beef -- 1.2 Effect of Prolonged Aging on Beef Quality -- 1.3 Aim of the Study -- 2 Materials and Methods -- 2.1 Experimental Plan -- 2.2 Cortisol Determination -- 2.3 Muscle pH Measurement -- 2.4 Aged Beef Quality Characteristics -- 3 Results and Discussion -- 3.1 Cortisol Determination -- 3.2 Evolution of Meat pH During the Prolonged Aging -- 3.3 Quality Characteristics of Long Aged Piedmontese Beef -- 4 Conclusions -- References -- Calculation of the Mixing Time as a Function of the Dairy Cow Diet Chemical Homogeneity Inside the Mixing Hopper -- Abstract -- 1 Introduction -- 2 Materials and Methods -- 2.1 Spectrometer -- 2.2 Integrated Measurement System -- 2.3 TMR Homogeneity Evaluation -- 2.4 Field Tests and Statistical Analysis -- 3 Results and Discussion -- 4 Conclusions -- References -- Using of NMR Milk Metabolomics to Evaluate Mammary Gland Health Status in Dairy Cows -- Abstract -- 1 Introduction -- 2 Materials and Methods -- 2.1 Animals and Milk Samples -- 2.2 NMR -- 2.2.1 Sample Preparation -- 2.2.2 NMR Analysis -- 2.3 Statistical Analysis -- 3 Results and Discussion -- 3.1 NMR Metabolites Assignment -- 3.2 Analysis of Metabolites -- 4 Conclusion -- Acknowledgement -- References -- Spatial Variability of Ammonia Concentrations in an Open-Sided Dairy Barn -- Abstract -- 1 Introduction -- 2 Materials and Methods -- 2.1 Barn Description and Management -- 2.2 Experimental Set-Up -- 2.3 Data Analysis -- 3 Results and Discussion -- 3.1 Spatial Distribution of NH3 Concentrations -- 3.2 Daily Variation of NH3 Concentrations -- 4 Conclusion -- Acknowledgements -- Funding -- References.
The Effect of Microclimatic Conditions on Ammonia Emissions from an Open-Sided Dairy Barn During Spring -- Abstract -- 1 Introduction -- 2 Materials and Methods -- 2.1 Barn Description and Management -- 2.2 Experimental Set-Up -- 2.3 Estimation of NH3 Emissions -- 2.4 Data Analysis -- 3 Results and Discussion -- 3.1 Microclimatic Conditions -- 3.2 Ammonia Emissions -- 4 Conclusion -- Funding -- References -- The COWBHAVE System: An Open-Source Accelerometer-Based System to Monitor Dairy Cows' Behavioural Activities -- Abstract -- 1 Introduction -- 2 The System Architecture -- 2.1 The COWBHAVE Firmware, the Acceleration-Based Variable, and the Threshold-Based Algorithm -- 2.2 The Database -- 2.3 The Graphical User Interface (GUI) and the Application Programming Interface (API) -- 3 The Experimental Tests in the Lab and in a Free-Stall Barn to Assess System Functioning -- 4 GUI Sections and API Functions of the Case Study -- 5 Conclusions -- Acknowledgements -- References -- On the Determination of Acceleration Thresholds for the Automatic Detection of Cow Behavioural Activities in Extensive Livestock Systems --

and Resonance -- 3 Results and Discussion -- 3.1 Data Obtained on the Bench -- 3.2 Data Obtained on the Seat -- 3.3 Transmissibility and Resonance -- 4 Conclusions -- Acknowledgement -- References -- Hand Arm Vibration: Comparison Between Laboratory and in Field Tests -- Abstract -- 1 Introduction -- 2 Material and Methods -- 2.1 The Harvester -- 2.2 The Test Bench -- 2.3 The Experimental Activity -- 3 Results and Discussion -- 4 Conclusions and Perspectives -- Acknowledgements -- References.
Fisherman's Exposure to the Noise Emitted by a Prototype of an On-Board Rotating Sorting Machine for Clams (Chamelea Gallina).

Sommario/riassunto

This book gathers the latest advances, innovations and applications in the field of agricultural biotechnology, agro-food systems and forestry, as presented by leading international researchers and engineers at the 5th International Conference on Safety, Health and Welfare in Agriculture and Agro-food Systems (SHWA), held in Ragusa, Italy, on September 15-18, 2021. The papers cover a range of topics such as agricultural assistive technologies, machine milking, animal welfare, sustainable livestock farming, work organization and logistic in agro-food supply chain, agricultural instrumentation and equipment, safety and health in building, agriculture 4.0, automation, occupational health, precision farming, effect of landscapes on human health, environmental safety, rural health, agricultural machinery, ROPS, augmented reality and IoT, cyber security. The contributions included in the book were selected by means of a rigorous peer-review process, and offer an extensive and multidisciplinary overview of interesting solutions in the field of sustainable agriculture.

3. Record Nr. UNINA9910747593303321

| | |
|---|---|
| Titolo | Bioinformatics Research and Applications : 19th International Symposium, ISBRA 2023, Wrocaw, Poland, October 9–12, 2023, Proceedings / / edited by Xuan Guo, Serghei Mangul, Murray Patterson, Alexander Zelikovsky |
| Pubbl/distr/stampa | Singapore : , : Springer Nature Singapore : , : Imprint : Springer, , 2023 |
| ISBN | 9789819970742<br>9819970741 |
| Edizione | [1st ed. 2023.] |
| Descrizione fisica | 1 online resource (xiii, 555 pages) : illustrations (chiefly color) |
| Collana | Lecture Notes in Bioinformatics, , 2366-6331 ; ; 14248 |
| Altri autori (Persone) | GuoXuan <1987-><br>MangulSerghei<br>PattersonM. G<br>ZelikovskyAlexander |
| Disciplina | 570.285 |
| Soggetti | Bioinformatics<br>Artificial intelligence<br>Computer networks<br>Computer engineering<br>Artificial Intelligence<br>Computer Communication Networks<br>Computer Engineering and Networks |
| Lingua di pubblicazione | Inglese |
| Formato | Materiale a stampa |
| Livello bibliografico | Monografia |
| Note generali | Includes author index. |
| Nota di contenuto | Unveiling the Robustness of Machine Learning Models in Classifying COVID-19 Spike Sequences -- Efficient Sequence Embedding For SARS-CoV-2 Variants Classification -- On Computing the Jaro Similarity Between Two Strings -- Identifying miRNA-disease Associations based on Simple Graph Convolution with DropMessage and Jumping Knowledge -- Reconciling Inconsistent Molecular Structures from Biochemical Databases -- Deep Learning Architectures For the Prediction of YY1-Mediated Chromatin Loops -- Neurogenesis-associated Protein, a Potential Prognostic Biomarker in anti-PD-1 based kidney renal clear cell carcinoma patients therapeutics -- MPFNet: ECG |

Arrhythmias Classication Based on Multi-Perspective Feature Fusion -- PCPI: Prediction of circRNA and protein interaction using machine learning method -- Radiology Report Generation via Visual Recalibration and Context Gating-aware -- Using Generating Functions to Prove Additivity of Gene-Neighborhood BasedPhylogenetics -- TCSA: A Text-guided Cross-view Medical Semantic Alignment Framework for Adaptive Multi-view Visual Representation Learning -- Multi-Class Cancer Classification of Whole Slide Images through Transformer and Multiple Instance Learning -- ricME: long-read based mobile element variant detection using sequence realignment and identity calculation -- scGASI: A graph autoencoder-based single-cell integration clustering method -- ABCAE: Artificial Bee Colony Algorithm with Adaptive Exploitation for Epistatic Interaction Detection -- USTAR: Improved Compression of k-mer Sets with Counters Using De Bruijn Graphs -- Graph-Based Motif Discovery in Mimotope Profiles of Serum Antibody Repertoire -- Sequence-Based Nanobody-Antigen Binding Prediction -- Approximating Rearrangement Distances with Replicas and Flexible Intergenic Regions -- The Ordered Covering Problem in Distance Geometry -- Phylogenetic Information as Soft Constraints in RNA Secondary Structure Prediction -- NeoMS: Identification of Novel MHC-I Peptides with Tandem Mass Spectrometry -- On Sorting by Flanked Transpositions -- Integrative analysis of gene expression and alternative polyadenylation from single-cell RNA-seq data -- SaID: Simulation-aware Image Denoising Pre-trained Model for Cryo-EM Micrographs -- Reducing the impact of domain rearrangement on sequence alignment and phylogeny reconstruction -- Identification and functional annotation of circRNAs in neuroblastoma based on bioinformatics -- SGMDD: Subgraph Neural Network-Based Model for Analyzing Functional Connectivity Signatures of Major Depressive Disorder -- PDB2Vec: Using 3D Structural Information For Improved Protein Analysi -- Hist2Vec: Kernel-Based Embeddings for Biological Sequence Classification -- DCNN: Dual-Level Collaborative Neural Network for Imbalanced Heart Anomaly Detection -- On the Realisability of Chemical Pathways -- A Brief Study ofGene Co-Expression Thresholding Algorithms -- Inferring Boolean Networks from Single-Cell Human Embryo Datasets -- Enhancing t-SNE Performance for Biological Sequencing Data through Kernel Selection -- Genetic Algorithm with Evolutionary Jumps -- HetBiSyn: Predicting Anticancer Synergistic Drug Combinations Featuring Bi-perspective Drug Embedding with Heterogeneous Data -- Clique-based topological characterization of chromatin interaction hubs -- Exploring Racial Disparities in Triple-Negative Breast Cancer: Insights from Feature Selection Algorithms -- Deep Learning Reveals Biological Basis of Racial Disparities in Quadruple-Negative Breast Cancer -- CSA-MEM: Enhancing Circular DNA Multiple Alignment through Text Indexing Algorithms -- A Convolutional Denoising Autoencoder for Protein Scaffold Filling -- Simulating tumor evolution from scDNA-seq as an accumulation of both SNVs and CNAs -- CHLPCA: Correntropy-Based Hypergraph Regularized Sparse PCA for Single-cell Type Identification.-
.

Sommario/riassunto

This book constitutes the refereed proceedings of the 19th International Symposium on Bioinformatics Research and Applications, ISBRA 2023, held in Wrocaw, Poland, during October 9–12, 2023. The 28 full papers and 16 short papers included in this book were carefully reviewed and selected from 89 submissions. They were organized in topical sections as follows: reconciling inconsistent molecular structures from biochemical databases; radiology report generation via visual recalibration and context gating-aware; sequence-based

nanobody-antigen binding prediction; and hist2Vec: kernel-based embeddings for biological sequence classification.