1. Record Nr.	UNINA9910585962603321
Autore	Anderson Michael
Titolo	Challenges to tackling antimicrobial resistance : economic and policy responses / / edited by Michael Anderson, Michele Cecchini, Elias Mossialos [[electronic resource]]
Pubbl/distr/stampa	Cambridge University Press, 2020 Cambridge : , : Cambridge University Press, , 2019
ISBN	1-108-87375-8 1-108-87482-7 1-108-86412-0
Descrizione fisica	1 online resource (xxi, 250 pages) : digital, PDF file(s)
Collana	European Observatory on Health Systems and Policies
Disciplina	616.9041
Soggetti	Drug resistance Drug development
Lingua di pubblicazione	Inglese
Formato	Materiale a stampa
Livello bibliografico	Monografia
Note generali	Title from publisher's bibliographic system (viewed on 06 Apr 2020).
Sommario/riassunto	Antimicrobial resistance (AMR) is a biological mechanism whereby a micro-organism evolves over time to develop the ability to become resistant to antimicrobial therapies such as antibiotics. The drivers of and potential solutions to AMR are complex, often spanning multiple sectors. The internationally recognised response to AMR advocates for a 'One Health' approach, which requires policies to be developed and implemented across human, animal, and environmental health. To date, misaligned economic incentives have slowed the development of novel antimicrobials and limited efforts to reduce antimicrobial usage. However, the research which underpins the variety of policy options to tackle AMR is rapidly evolving across multiple disciplines such as human medicine, veterinary medicine, agricultural sciences, epidemiology, economics, sociology and psychology. By bringing together in one place the latest evidence and analysing the different facets of the complex problem of tackling AMR, this book offers an accessible summary for policy-makers, academics and students on the big questions around AMR policy.

2. Record Nr.	UNINA9910337846603321
Titolo	Bioinformatics and Biomedical Engineering : 7th International Work-Conference, IWBBIO 2019, Granada, Spain, May 8-10, 2019, Proceedings, Part I / / edited by Ignacio Rojas, Olga Valenzuela, Fernando Rojas, Francisco Ortuño
Pubbl/distr/stampa	Cham : , : Springer International Publishing : , : Imprint : Springer, , 2019
ISBN	3-030-17938-9
Edizione	[1st ed. 2019.]
Descrizione fisica	1 online resource (XXX, 527 p. 208 illus., 153 illus. in color.)
Collana	Lecture Notes in Bioinformatics, , 2366-6331 ; ; 11465
Disciplina	570.285
Soggetti	Bioinformatics Machine learning Natural language processing (Computer science) Computer vision Computer networks Machine theory Computational and Systems Biology Machine Learning Natural Language Processing (NLP) Computer Vision Computer Communication Networks Formal Languages and Automata Theory
Lingua di pubblicazione	Inglese
Formato	Materiale a stampa
Livello bibliografico	Monografia
Nota di contenuto	High-throughput genomics: bioinformatic tools and medical applications -- A Coarse-Grained Representation for Discretizable Distance Geometry with Interval Data -- Fragment-based Drug Design to Discover Novel Inhibitor of Dipeptidyl Peptidase-4 as a Potential Drug for Type 2 Diabetes Therapy -- Discovery of Novel Alpha-Amylase Inhibitors For Type II Diabetes Mellitus Through The Fragment-Based Drug Design -- Compression of Nanopore FASTQ files -- De novo Transcriptome Global Assembly of Solea senegalensis v5.0

Using TransFlow -- Deciphering the role of PKC in calpain-CAST system through formal modeling approach -- The Application of Machine Learning Algorithms to Diagnose CKD Stages and Identify Critical Metabolites Features -- Expression change correlations between transposons and adjacent genes in lung cancer reveal a genomic location dependence and highlights cancer-significant genes -- Signal processing based CNV detection in bacterial genomes -- Omics data acquisition, processing, andanalysis -- Dependency Model for Visible Aquaphotomics -- Image based individual identification of Sumatra barb (Puntigrus tetrazona) -- Alignment of Sequences Allowing for Non-Overlapping Unbalanced Translocations of Adjacent Factors -- Probability in HPLC-MS metabolomics -- Pipeline for Electron Microscopy Images Processing -- A Greedy Algorithm for Detecting Mutually Exclusive Patterns in Cancer Mutation Data -- Qualitative Comparison of Selected Indel Detection Methods for RNA-Seq Data -- Structural and functional features of glutathione reductase transcripts from olive (Olea europaea L.) seeds -- Bioinformatics approaches for analyzing cancer sequencing data -- Prediction of thermophilic proteins using voting algorithm -- Classifying Breast Cancer Histopathological Images Using A Robust Artificial Neural Network Architecture -- Spatial Attention Lesion Detection on Automated Breast Ultrasound -- Essential Protein Detection from Protein-Protein Interaction Networks Using Immune Algorithm -- Integrating multiple datasets to discover stage-specific cancer related genes and stage-specific pathways -- Integrated detection of copy number variation based on assembly of NGS and 3GS data -- Protein Remote Homology Detection based on Profiles -- Next generation sequencing and sequence analysis -- Reads in NGS are distributed over a sequence very inhomogeneously -- Differential Expression Analysis of ZIKV Infected Human RNA Sequence Reveals Potential Genetic Biomarkers -- Identification of Immunoglobulin Gene Usage in Immune Repertoires Sequenced by Nanopore Technology -- Flexible and Efficient Algorithms for Abelian Matching in Genome Sequences -- Analysis of gene regulatory networks inferred from ChIP-seq data -- Structural Bioinformatics and Function -- Function vs. taxonomy: the case of fungi mitochondria ATP synthase genes -- Non-Coding Regions of Chloroplast Genomes Exhibit a Structuredness of Five Types -- Characteristics of Protein Fold Space Exhibits Close Dependence on Domain Usage -- Triplet Frequencies Implementation in Total Transcriptome Analysis -- A hierarchical and scalable strategy for protein structural classification -- Protein structural signatures revisited: geometric linearity of main chains are more relevant to classification performance than packing of residues -- Telemedicine for Smart Homes and Remote Monitoring -- Positioning Method for Arterial Blood Pressure Monitoring Wearable Sensor -- Study of the detection of falls using the SVM algorithm, different datasets of movements and ANOVA -- Influence of illuminance on sleep onset latency in IoT based lighting system environment -- Clustering and analysis of Biological Sequences with Optimization Algorithms -- Efficient online Laplacian eigenmap computation for dimensionality reduction in molecular phylogeny via optimisation on the sphere -- PROcket, an efficient algorithm to predict Protein Ligand Binding Site -- Gene Expression High-Dimensional Clustering towards a Novel, Robust, Clinically Relevant and HighlyCompact Cancer Signature -- Computational Approaches for Drug Repurposing and Personalized Medicine -- When Mathematics Outsmarts Cancer -- Influence of the stochasticity in the model on the certain drugs pharmacodynamics -- Graph Model for the Identification of Multi-Target Drug Information for Culinary Herbs --

On Identifying Candidates for Drug Repurposing for the Treatment of Ulcerative Colitis using Gene Expression. .

Sommario/riassunto

The two-volume set LNBI 11465 and LNBI 11466 constitutes the proceedings of the 7th International Work-Conference on Bioinformatics and Biomedical Engineering, IWBBIO 2019, held in Granada, Spain, in May 2019. The total of 97 papers presented in the proceedings, was carefully reviewed and selected from 301 submissions. The papers are organized in topical sections as follows: Part I: High-throughput genomics: bioinformatics tools and medical applications; omics data acquisition, processing, and analysis; bioinformatics approaches for analyzing cancer sequencing data; next generation sequencing and sequence analysis; structural bioinformatics and function; telemedicine for smart homes and remote monitoring; clustering and analysis of biological sequences with optimization algorithms; and computational approaches for drug repurposing and personalized medicine. Part II: Bioinformatics for healthcare and diseases; computational genomics/proteomics; computationalsystems for modelling biological processes; biomedical engineering; biomedical image analysis; and biomedicine and e-health. .