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| Nota di contenuto | Session introduction: Artificial intelligence for enhancing clinical medicine / Roxana Daneshjou ... [et al.] -- Predicting longitudinal outcomes of Alzheimer's disease via a tensor-based joint classification and regression model / Lodewijk Brand ... [et al.] -- Robustly extracting medical knowledge from EHRs: a case study of learning a health knowledge graph / Irene Y. Chen ... [et al.] -- Increasing clinical trial accrual via automated matching of biomarker criteria / Jessica W. Chen ... [et al.] -- Addressing the credit assignment problem in treatment outcome prediction using temporal difference learning / Sahar Harati ... [et al.] -- Multiclass disease classification from microbial whole-community metagenomes / Saad Khan and Libusha Kelly -- LitGen: genetic literature recommendation guided by human explanations / Allen Nie ... [et al.] -- From genome to phenome: predicting multiple cancer phenotypes based on somatic genomic alterations via the genomic impact transformer / Yifeng Tao ... [et al.] -- Automated phenotyping of patients wsith non-alcolholic fatty liver disease reveals clinically relevant disease subtypes / Maxence Vandromme [et al.] -- Monitoring ICU mortality risk with a long short-term memory recurrent neural network / Ke Yu ... [et al.] -- Multilevel self-attention model and its use on medical risk prediction / Xianlong Zeng ... [et al.] -- Identifying transitional high cost users from unstructured patient profiles written by primary care physicians / Haoran Zhang ... [et al.] -- |

Obtaining dual-energy computed tomography (CT) information from a single-energy CT image for quantitative imaging analysis of living subjects by using deep learning / Wei Zhao ... [et al.] -- On the importance of computational biology and bioinformatics to the origins and rapid progression of the intrinsically disordered proteins field / Lukasz Kurgan ... [et al.] -- Many-to-one binding by intrinsically disordered problem regions / Wei-Lun Alterovitz ... [et al.] -- Disordered function conjunction: on the in-silico function annotation of intrinsically disordered regions / Sina Ghadermarzi ... [et al.] -- De novo ensemble modeling suggests that AP2-binding to disordered regions can increase steric volume of Epsin but not Eps15 / N. Suhas Jagannathan ... [et al.] -- Modulation of p53 transactivation domain conformations by ligand binding and cancer-associated mutations / Xiaorong Liu and Jianhan Chen -- Exploring relationship between the density of charged tracts within disordered regions and phase separation / Ramiz Somjee, Diana M. Mitrea and Richard W. Kriwacki -- Session introduction: Mutational signatures: etiology, properties, and role in cancer / Mark D.M. Leiserson, Teresa M. Przytycka and Roded Sharan -- PhySigs: phylogenetic inference of mutational signature dynamics / Sarah Chistensen, Mark D.M. Leiserson and Mohammed El-Kebir -- TrackSigFreq: subclonal reconstructions based on mutation signatures and allele frequencies / Caitlin F. Harrigan ... [et al.] -- Impact of mutational signatures on microRNA and their response elements / Eirini Stamoulakatou ... [et al.] -- DNA repair footprint uncovers contribution of DNA repair mechanism to mutational signatures / Damian Wojtowicz ... [et al.] -- Genome gerrymandering: optimal division of the genome into regions with cancer type specific differences in mutation rates / Adamo Young ... [et al.] -- Ongoing challenges and innovative approaches for recognizing pattern across large-scale, integrative biomedical datasets / Shilpa Nadimpalli ... [et al.] -- Clinical concept embeddings learned from massive sources of multimodal medical data / Andrew L. Beam ... [et al.] -- Assessment of imputation methods for missing gene expression data in meta-analysis of distinct cohorts of tuberculosis patients / Carly A. Bobak ... [et al.] -- Towards identifying drug side effects from social media using active learning and crowd sourcing / Sophie Burkhardt ... [et al.] -- Microvascular dynamics from 4D microscopy using temporal segmentation / Shir Gur ... [et al.] -- Using transcriptional signatures to find cancer drivers with LURE / David Haan ... [et al.] -- and other papers.

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Sommario/riassunto

"The Pacific Symposium on Biocomputing (PSB) 2020 is an international, multidisciplinary conference for the presentation and discussion of current research in the theory and application of computational methods in problems of biological significance. Presentations are rigorously peer reviewed and are published in an archival proceedings volume. PSB 2020 will be held on January 3-7, 2020 in Kohala Coast, Hawaii. Tutorials and workshops will be offered prior to the start of the conference. PSB 2020 will bring together top researchers from the US, the Asian Pacific nations, and around the world to exchange research results and address open issues in all aspects of computational biology. It is a forum for the presentation of work in databases, algorithms, interfaces, visualization, modeling, and other computational methods, as applied to biological problems, with emphasis on applications in data-rich areas of molecular biology. The PSB has been designed to be responsive to the need for critical mass in sub-disciplines within biocomputing. For that reason, it is the only meeting whose sessions are defined dynamically each year in response to specific proposals. PSB sessions are organized by leaders of research in biocomputing's

'hot topics.' In this way, the meeting provides an early forum for serious examination of emerging methods and approaches in this rapidly changing field."--Publisher's website.