1.	Record Nr.	UNINA9910349464803321
	Autore	Altman Russ B
	Titolo	Biocomputing 2019 - Proceedings Of The Pacific Symposium
	Pubbl/distr/stampa	World Scientific Publishing Co, 2018 Singapore : , : World Scientific Publishing Company, , 2018 ©2019
	ISBN	981-327-982-6 981-327-981-8
	Descrizione fisica	1 online resource (471 pages)
	Altri autori (Persone)	DunkerA. Keith <1943-> (Alan Keith) HunterLawrence <1961-> RitchieMarylyn D MurrayTiffany A KleinTeri E
	Lingua di pubblicazione	Inglese
	Formato	Materiale a stampa
	Livello bibliografico	Monografia
	Nota di contenuto	Intro -- Preface -- PATTERN RECOGNITION IN BIOMEDICAL DATA: CHALLENGES IN PUTTING BIG DATA TO WORK -- Session introduction -- Introduction -- References -- Learning Contextual Hierarchical Structure of Medical Concepts with Poincairé Embeddings to Clarify Phenotypes -- 1. Introduction -- 2. Methods -- 2.1. Source Code -- 2.2. Data Source -- 2.3. Data Selection and Preprocessing -- 2.3.1. Reference ICD9 Example -- 2.3.2. Real Member Analyses -- 2.4. Poincaré Embeddings -- 2.5. Processing and Evaluating Embeddings -- 3. Results -- 3.1. ICD9 Hierarchy Evaluation -- 3.2. Poincaré Embeddings on 10 Million Members -- 3.3. Comparison with Euclidean Embeddings -- 3.4. Cohort Specific Embeddings -- 4. Discussion and Conclusion -- 5. Acknowledgments -- References -- The Effectiveness of Multitask Learning for Phenotyping with Electronic Health Records Data -- 1. Introduction -- 2. Background -- 2.1. Multitask nets -- 3. Methods -- 3.1. Dataset Construction and Design -- 3.2. Experimental Design -- 4. Experiments and Results -- 4.1. When Does Multitask Learning Improve Performance? -- 4.2. Relationship Between

real data -- 3.4. Software -- 4. Discussion -- References --
SNPs2ChIP: Latent Factors of ChIP-seq to infer functions of non-coding
SNPs -- 1. Introduction -- 2. Results -- 2.1. SNPs2ChIP analysis
framework overview -- 2.2. Batch normalization of heterogeneous
epigenetic features -- 2.3. Latent factor discovery and their biological
characterization -- 2.4. SNPs2ChIP identifies relevant functions of the
non-coding genome -- 2.4.1. Genome-wide SNPs coverage of the
reference datasets -- 2.4.2. Non-coding GWAS SNPs of systemic lupus
erythematosus -- 2.4.3. ChIP-seq peaks for vitamin D receptors.
2.5. Robustness Analysis in the latent factor identification.

Sommario/riassunto	The Pacific Symposium on Biocomputing (PSB) 2019 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 2019 will be held on January 3 – 7, 2019 in Kohala Coast, Hawaii. Tutorials and workshops will be offered prior to the start of the conference. PSB 2019 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.