1. Record Nr. UNINA9910346695703321

Autore	Altman Russ (Russell Biagio), <1961->
Titolo	Biocomputing 2013 - Proceedings of the Pacific Symposium
Pubbl/distr/stampa	Singapore, : World Scientific Publishing Company, 2012
ISBN	981-4447-97-8
Descrizione fisica	1 online resource (471 p.)
Disciplina	574.310724
Soggetti	Biology -- Computer simulation -- Congresses Biology -- Mathematical models -- Congresses Biology -- Mathematical models Biology Health & Biological Sciences Biology - General
Lingua di pubblicazione	Inglese
Formato	Materiale a stampa
Livello bibliografico	Monografia
Note generali	Description based upon print version of record.
Nota di contenuto	Modeling cell heterogeneity: from single-cell variations to mixed cells populations445; Computational Challenges of Mass Phenotyping454; The Future of Genome-Based Medicine456; 0session-intro-cdr.pdf; 1cheng; 1. Introduction; 2. Methods; 2.1. Data sources and data processing; 2.2. Pair-wise similarity scores; 2.3. Method nomenclature; 2.4. AUCs and p-values; 2.5. Expression signal strength; 3. Results; 4. Discussion; 5. Acknowledgments; 2felciano; 3phatak; 4shi; 5wang; 0intro-epigenomics.pdf; 1ahn; 2luo; 3sahu; 1gabr; 2gevaert; 3kim; 1. Introduction; 2. Methods 2.1. Introduction of the Module Cover Problem2.2. Integrated Module Cover; 2.3. Two-Step Module Cover; 3. Results; 3.1. Analysis of Glioblastoma Multiforme Data from GMDI; 3.1.1. Comparison of the Module Cover approaches. For an association to be specific in a given module, only a few regulatory associations should have highly significant p-values while the remaining loci are expected to have insignificant p-values. Thus, we defined the specificity of a module M as the area of a cumulative histogram of association significance values. Specifically, we partitioned the range from 0 to strength (M) into 10 bins of equal sizes and

defined cj to be the cumulative percentage of j-th bin. Then the specificity is defi...3.1.2. Analysis of GBM data; 3.1.3. Analysis of Ovarian Cancer Data; 4. Discussion

Uncovering modules that are associated with genomic alterations in a disease is a challenging task as well as an important step to understand complex diseases. To address this challenge we introduced a novel technique - module cover - that extends the concept of set cover to network modules. We provided a mathematical formalization of the problem and developed two heuristic solutions: the Integrated Module Cover approach, which greedily selects genes to cover disease cases while simultaneousl...

In general, the module cover approach is especially helpful in analyzing and classifying heterogeneous disease cases by exploring the way different combinations of dys-regulated of modules relate to a particular disease subcategory. Indeed, our analysis indicated that the gene set selected by module cover approach may be used for classification. Equally important, the selected module covers may help to interpret classifications that were obtained with other methods.5. Materials; 5.1 Data Treatment for Glioblastoma Multiforme Data from GMDI

Differentially Expressed Genes: Briefly, all samples were profiled using HG-U133 Plus 2.0 arrays that were normalized at the probe level with dChip (16, 19). Among probes representing each gene, we chose the probeset with the highest mean intensity in the tumor and control samples. We determined genes that are differentially expressed in each disease case compared to the non-tumor control cases with a Z-test. For a gene g and case c, we define cover(c, g) to be 1 if nominal p-value < 0.01 and...

Sommario/riassunto

The Pacific Symposium on Biocomputing (PSB) 2013 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 2013 will be held on January 3 - 7, 2013 in Kohala Coast, Hawaii. Tutorials and workshops will be offered prior to the start of the conference.PSB 2013 will bring together top researchers from the US, the Asian Pacific nations, and around the world t