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	Autore	Altman Russ
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		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...

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