VISUAL ANALYTICS PROCESSING OF ENRICHED BIOLOGICAL CONCEPTS ON OBESITY CAUSAL GENES

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Abstract: Obesity is the result of caloric imbalance (too few calories expended for the amount of calories consumed) and is mediated by genetic, behavioral, and environmental factors. Obesity is a risk factor for several chronic diseases including cancer, hypertension and diabetes. New analytical strategies such as visual analytics are needed to simultaneously address genetic and environmental aspects of complex traits. These efforts can translate to personalized medicine, nutrition or prevention. Bioinformatics databases, such as ConceptGen, contain data on enriched biological information for genes including noncoding RNAs, Gene Expression, and Gene Ontology. The objective of the reported investigation was to use visual analytics tools to integrate enriched biological information on genes investigated in the context of obesity. A total of 356 Human Genes were obtained from the 2005 Human Obesity Gene Map. ConceptGen analysis processed 348 genes associated with 8565 Concept Names and 15 Concept Types. 51 Genes were enriched with “Adipocyte” or “Adipose Tissue” Concept Names including the 3 known members of the UCP (Uncoupling Protein) Gene family: UCP1, UCP2 and UCP3. Members of the UCP Gene family are mitochondrial inner membrane ions carrier proteins that uncouple ATP synthesis by dissipating the proton gradient, a process that generates heat and decreases ATP production. They are linked to energy expenditure in adipose tissues and thus important in the pathogenesis and treatment of obesity. Visual Analytics processing helped in comparing enriched biological concepts stored in ConceptGen for the 3 genes. MicroRNAs unique or shared would potentially serve as intervention and diagnostic markers in obesity.

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