Feature selection from data integration through analysis of Copy Number Variation (CNV) for genotype-phenotype association of complex diseases

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Abstract

Complex diseases are usually consequences of intracellular and intercellular disorders in tissues and organs, being developed in a multifactorial way. Togetherwiththeproductionofafairlyhighvolumeofbiologicaldatagener performancesequencingtechniques, researchesinthisareanow involve integrative data analyses. In this context a computational framework was created to allow the integration of different types of biological data from the chromosomal location. This tool was used to study autism spectrum disorders (ASD), showing regions of Copy Number Variation - CNVs present only in samples of affected individuals, becoming a promising work to aid researches involving complex diseases.

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