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Poly-Omic Prediction of Complex Traits: OmicKriging

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High-confidence prediction of complex traits such as disease risk or drug response is an ultimate goal of personalized medicine. Although genome-wide association studies have discovered thousands of well-replicated polymorphisms associated with a broad spectrum of complex traits, the combined predictive power of these associations for any given trait is generally too low to be of clinical relevance. We propose a novel systems approach to complex trait prediction, which leverages similarity in genetic, transcriptomic or other omics-level data. We translate the omic similarity into phenotypic similarity using a method called Kriging, commonly used in geostatistics and machine learning. Our method called OmicKriging emphasizes the use of a wide variety of systems-level data, such as those increasingly made available by comprehensive surveys of the genome, transcriptome and epigenome, for complex trait prediction. The approach facilitates exploration of the etiology of disease risk or drug response by quantifying specific omic contributions to prediction. Our method is a fast, simple and flexible approach to polygenic, and more generally, poly-omic, prediction. Using seven diseases from the Wellcome Trust Case Control Consortium (WTCCC), we show that our method yields performance similar to more computationally intensive methods when restricted to genotypic data. Using a cellular growth phenotype, we show that integrating mRNA and microRNA data with genotypic data substantially increases performance. We provide guidelines on how to choose the similarity matrices and an R package to implement OmicKriging (this http URL).

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