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Mergeomics, A Multiomics Integration and Network Modeling Tool and Its Applications in Addiction Research

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Common complex diseases are the result of interactions between genetic and environmental risks factors and involve network perturbations across molecular entities, cell types, tissues, and organ systems. For addiction in particular, exposures to both genetic risk variants and substances affect the molecular networks of various brain regions and individual cell types to confer addiction vulnerability. Dissecting such complexity necessitates a multitissue multiomics approach that integrates bulk and single cell multiomics data (genome, epigenome, transcriptome, proteome, metabolome, etc) across relevant tissues and cell types. To this end, we developed Mergeomics, a computational tool for multiomics integration and causal network modeling to delineate the molecular, cellular, and tissue networks in individual complex diseases and enable network level comparisons across omics, studies, species, and diseases. Through collaborative studies, we showcase the application of Mergeomics in understanding addiction across mouse, rat, and human studies, revealing conserved mechanisms and key regulators for addiction.