

1155-92-141

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*Constructing regulatory modules using a sparse regression approach with application to interferon stimulated genes at homeostasis.*

Interferon stimulated genes (ISGs) are a collection of genes important in the early innate immune response. There are 100s of ISGs and their regulations is complex, involving dozens of regulatory factors and varying across cell types. The regulation of ISGs has been mostly studied in cells exposed to significant interferon stimulation, while less is known about ISG regulation in homeostatic regimes in which extracellular interferon levels are low. In order to better understand homeostatic ISG regulation, we collected expression datasets across multiple cell types from the NCBI GEO database. Using a novel approach based on sparse linear regression, we constructed regulatory modules which grouped subsets of ISGs with a small number of correlated regulation factors. Application of our approach to the GEO datasets reveals significant levels of ISG regulation at homeostatis. (Received January 08, 2020)