Exploring controllability in Developmental TENET gene regulatory networks across species

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Developmental process of a multicellular organism is primarily controlled by gene regulatory network (GRN). The concept of network controllability suggest that such biomolecular regulatory networks are difficult to control. In other words, driving a desired cellular state requires controlling most of the nodes or genes. While developmental biologists have explored the optimal combination of transcription factors for better controllability, the controllability of the entire developmental process, from the early embryo stage to final differentiation, has not been fully studied. To address this gap, we reconstructed GRNs for the trunks and branches of the developmental trajectory tree using single cell RNA sequencing data obtained from all developmental stages of zebrafish. Subsequently, we calculated the number of driver nodes for each GRN. Our comprehensive analysis revealed that the around 90 % of the nodes were driver nodes in most GRNs. Interestingly, we found that the ratio of driver nodes was significantly lower in the GRNs at the final developmental stage compared to earlier stages. This indicates that GRNs in the final stage is relatively easier to control than the GRNs in the early stage.