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Controllability of gene regulatory network in zebrafish embryogenesis

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The development in multicellular organisms is governed by gene regulatory networks (GRNs), which are often difficult to control. The concept of network controllability suggests that such biomolecular regulatory networks are difficult to control. While transcription factors (TFs) have been studied, the controllability of the entire developmental process, from early embryo to terminal differentiation, remains unclear. To address this, we reconstructed GRNs across developmental stages using single-cell RNA sequencing (scRNA-seq) data from zebrafish embryos. We inferred networks for both trunk and branch trajectories, and calculated the fraction of driver nodes for each. About 80% of nodes were driver nodes in most networks. Notably, the fraction of driver nodes was significantly lower at the final developmental phase than in earlier phases. This suggests that GRNs become more controllable as development progresses, with terminal-phase networks being relatively easier to control.