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Deciphering the Minimal Algorithm for Development and Information-genesis. ZHIYUAN LI, Princeton Center for Theoretical Science, Princeton University, CHAO TANG, Center for Quantitative Biology, Peking University, HAO LI, Dept. of Biochemistry and Biophysics and California Institute for Quantitative Biosciences, University of California, San Francisco — During development, cells with identical genomes acquires different fates in a highly organized manner. In order to decipher the principles underlining development, we used C. elegans as the model organism. Based on a large set of microscopy imaging, we first constructed a "standard worm" in silico: from the single zygotic cell to about 500 cell stage, the lineage, position, cell-cell contact and gene expression dynamics are quantified for each cell in order to investigate principles underlining these intensive data. Next, we reverse-engineered the possible gene-gene/cell-cell interaction rules that are capable of running a dynamic model recapitulating the early fate decisions during C.elegans development. we further formulized the C.elegans embryogenesis in the language of information genesis. Analysis towards data and model uncovered the global landscape of development in the cell fate space, suggested possible gene regulatory architectures and cell signaling processes, revealed diversity and robustness as the essential trade-offs in development, and demonstrated general strategies in building multicellular organisms.

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