Optimal decoding of cellular identities in a genetic network

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In developing organisms expression levels of multiple patterning genes determine spatially prescribed cell identities. It is unclear, however, what rules govern this specification, what is its precision, and how early in development it occurs. Using the gap gene network in the early fly embryo as an example, we show how expression levels of the four gap genes can be combined—or jointly decoded—into an optimal specification of position, which is precise to 1% of the embryo's length. As a test we apply this decoder to distorted patterns of gap gene expression in embryos lacking various primary maternal inputs. Output of the gap gene network are pair-rule genes producing each seven stripes along the embryo. We show that the decoder correctly predicts, with no free parameters and 1% accuracy, the patterns of these pair-rule stripes also in mutant backgrounds. Our results imply that individual cells use developmental enhancers to implement a mathematically optimal decoding strategy, in which developmental precision emerges from a simultaneous and absolute readout of all four gap gene levels. Precise cell identities are thus available at the earliest stages of development, in contrast to the prevailing view that positional information must be refined slowly across successive layers of the patterning network.