

URLs

SYSTEMS BIOLOGY

Linked-up loops: a reliable means of control

Depending on how you look at it, large gene-expression networks are dauntingly complicated or, if you're a mathematical modeller, elegantly simple and reducible to a discrete number of meaningful ON/OFF switches. A modelling study has begun to link these network 'building blocks' together by showing that an optimal output is obtained when two such switches are combined.

There are several well-characterized classes of switch-like elements, but this study concentrated on positive-feedback loops, in which *A* activates *B* and *B* activates *A*. Feedback loops operate in many signalling pathways, with some processes — such as oocyte maturation in frogs and the polarization of yeast cells — relying on more complicated switch arrangements, such as the coupling of two positive-feedback loops. This arrangement is initially rather puzzling: why combine two switches when a single one will carry out exactly the same function?

A computational modelling approach revealed a reason for the extra layer of complexity: slow loops are stable switches, but cannot transit between states quickly; by contrast, fast loops make for unstable (noisy) switches, but are quick at switching between states. Coupling two switches of the same kind together brings no overall benefit over having a single switch, but combining a fast and a slow switch yields an optimal output — that of a fast yet robust, reliable switch.

This type of dual positive-feedback loop is the one that is seen in the sub-circuits of many biological systems, and we now understand why this might be. This work also highlights the comforting thought that the details of a circuit are in fact dispensable, provided we have a good handle on the wiring.

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References and links

ORIGINAL RESEARCH PAPER

Brandman, O. *et al.* Interlinked fast and slow

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FURTHER READING Bornholdt, S. Less is more in modelling large genetic networks. *Science* **310**, 449–451 (2005) | Wall, M. E. *et al.* Design of gene circuits: lessons from bacteria. *Nature Rev. Genet.* **5**, 34–42 (2004)

