

# Cologne Evolution Colloquium

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## **The Evolutionary and Developmental Dynamics of the Gap Gene Network**

We have carried out a comprehensive integrative analysis of the patterning capacity and the evolutionary potential of an experimentally tractable developmental gene network, the gap gene system involved in patterning and segment determination during early embryogenesis in dipteran insects. Using a reverse-engineering approach we have created data-driven mathematical models of the gap gene network in three species of flies: *Drosophila melanogaster*, the scuttle fly *Megaselia abdita*, and the moth midge *Clogmia albipunctata*. Comparative analysis of these models reveals evolution by system drift, which allows the network to compensate for differing maternal inputs in different species. Our work provides precise causal-mechanistic mechanisms for this sort of compensatory evolution, and shows how random changes in regulatory interactions lead to non-random changes of gene expression dynamics. In addition, our models reveal a novel mechanism for the dynamic positioning of gap domains in different species. These shifting domains are driven by a damped oscillator which causes nuclei to express a stereotypical succession of gap genes. This mechanism shows surprising structural similarities to the short germband mode of segmentation, implying that long- and shortgerm band embryos are patterned by developmental processes that are much more similar to each other than previously thought

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University of Cologne, Institute for Genetics

Seminar Room 0.46

Hosted by Siegfried Roth and Matt Benton

Molecular Basis of  
Evolutionary Innovations

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