Characterizing gene networks capable of pattern formation.

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Development is the process by which the complex anatomy of multicellular organisms is built in each generation and it constitutes one of the very few natural processes capable of generating so much complexity in such a relatively short period of time. From a phenomenological point of view, development can be described as the sequence of transformations from one developmental pattern (i.e., a specific distribution of cell types along the embryo) to another that begins with the fertilized egg and finishes with the complete functional adult individual.

Although there are many intertwined mechanisms responsible for pattern transformation during development, in our work we focus only in what developmental biologists call inductive mechanisms, that is, we will only take into consideration those transformations that occur as a response to biochemical signals sent from one cell to another. In this sense, the main question we want to address is: "which gene networks regulating cell signaling (i.e, which network topologies of activatory and inhibitory interactions between gene products) can actually lead to proper pattern formation/transformation?".

Our theoretical analysis and numerical simulations, performed in the framework of reaction-diffusion equations, $\partial_t \boldsymbol{u}(t, \boldsymbol{x}) = f(\boldsymbol{u}) + D\nabla^2 \boldsymbol{u}(t, \boldsymbol{x})$, show that, regardless of the immense number of patterning networks that one can think of (specially when the number of gene products at hand is large), they can all be sorted out into just three fundamental types of gene networks capable of pattern formation/transformation. Gene networks within each of these three classes share the same topological properties, exhibit similar dynamics and lead to analogous patterns. In addition, patterns arising from each topological class exhibit very similar responses to noise and any other kind of external perturbation.