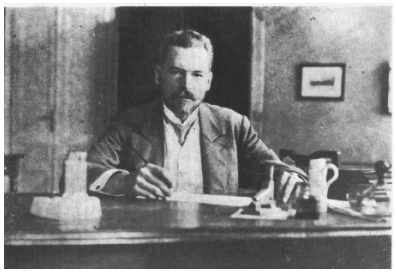

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Mapping the space of Turing patterns

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Patterns arise in nature at different scales. We can recognize animals based on their furry patterns alone, from the spots on a leopard to the stains on a cow. However, patterns are established also during embryonic development, through interactions of diffusing molecules that activate expression of target genes. As a result a striped pattern of gene expression emerges. These stripes will later on give raise to different body parts and organs. What is amazing is that this pattern is established with precision of a few cell diameters, being robust against perturbations from a noisy cellular environment. How this level of patterning reproducibility and robustness is achieved for each new organism is the central question of developmental biology.

We address this question by using concepts developed by Alan Turing. We focus on studying patterns emerging in systems with reaction-diffusion equations describing spreading and interactions of different chemical species (morphogens) inside the embryo. By analytically calculating conditions for parameters that need to be satisfied to observe diffusion driven instabilities that result in a spectrum of stable spatial patterns we define the Turing space. In this Turing space we investigate robustness of patterns against perturbation in parameters by identifying size and shape of regions resulting in the same number of stripes. We investigate systems with two and three interacting morphogens.

First, we show that for systems of infinite size their Turing space becomes a projective space. Thanks to scale invariance and other symmetries, we are able to find basis vectors whose linear combination parametrize the whole Turing space. This allowed us to derive explicit formulas for the robustness of patterns. Second, we use the properties of Turing space of infinite size systems to study the Turing space for finite size systems. We proved that Turing space is still connected, infinite and certain boundaries are also scale invariant. Similarly, we derived bounds and approximations for the robustness of patterns. Taken together, our results provide tools for both faster numerical exploration of Turing space, as well as for testing whether regions of Turing space indicating the highest robustness of patterns correspond to patterns observed in actual biological systems.

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