Quantitative Analysis of Gene Expression in Nematostella Vectensis

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Summary

The results of the four lines of research presented in the introduction are briefly summarized.

Geometry extraction:
The developmental geometries of Nematostella vectensis during early embryogenesis were extracted and interpolated. In the context of this extraction, it has been shown that the precise location of the endoderm-ectoderm boundary might be open for debate. In contrast to previous observations, present observations suggest that the pharynx might be mainly composed of ectodermal cells.

Data analysis:
It has been shown that quantified gene expression profiles from of early developmental stages of Nematostella vectensis can be classified and analyzed. The results suggest a hierarchical subdivision of the primary axis. More hypothetically, this could be taken to imply a generic domain-level regulatory cascade. With as much biological justification as possible, two gene-level instantiations of this domain-level cascade were derived.

Modeling framework:
A mathematical framework for modeling genetic regulatory networks was developed. The framework has less unknown constants than, for example, the much-used connectionist model, nevertheless remains closer to the underlying biochemistry, and has furthermore greater expressive power.

Parameter inference:
Finally, using the modeling framework and an automated parameter inference procedure, it could be shown that the two hypothetical instantiations of the domain-level regulatory cascade can, to a reasonable degree of accuracy, simulate the observed data.