

Learning local dominant force balances in active particle flows

Dominik Sturm^{1,2}, Suryanarayana Maddu^{3,4}, Ivo F. Sbalzarini^{5,6}

¹ Center for Advanced Systems Understanding, Görlitz, Germany

² Helmholtz-Zentrum Dresden-Rossendorf, Dresden, Germany

³ Center for Computational Biology, Flatiron Institute, New York, USA

⁴ Quantitative Biology Initiative, Harvard University, Boston, USA

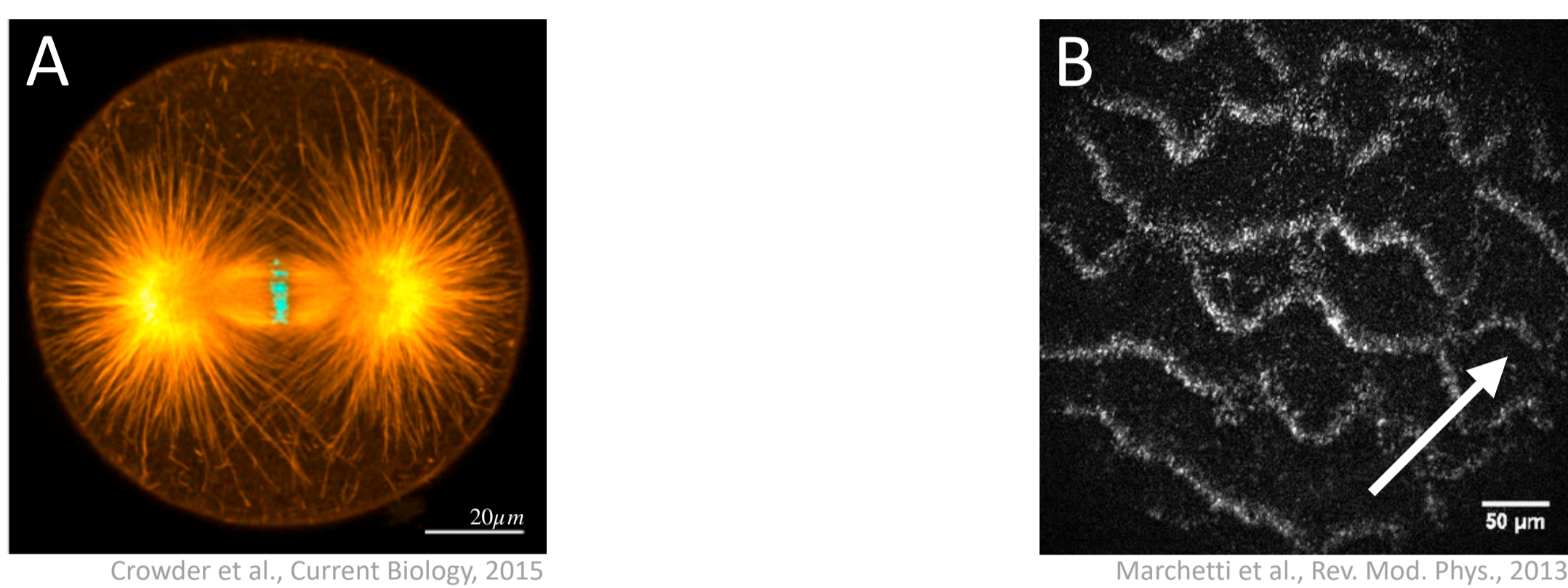
⁵ Faculty of Computer Science, Technische Universität, Dresden, Germany

⁶ Max Planck Institute of Molecular Cell Biology and Genetics, Dresden, Germany



Abstract

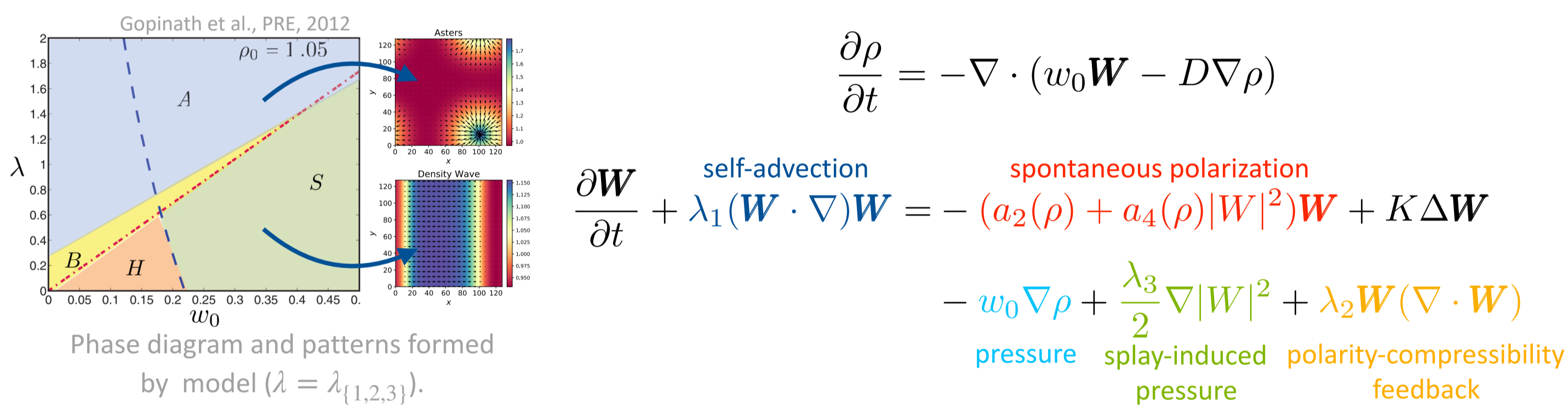
Systems of self-propelled particles exhibit self-organized collective behavior that leads to the formation of complex spatio-temporal patterns that can be observed all over nature (see i.e. Fig. below). Because of their abundance the question of *how* they form these rich macroscopic structures remains of central interest in cell biology. While there exist several hydrodynamic theories that are able to describe the observed dynamics, it is often hard to determine the local interactions that shape and regulate the structures. On the other hand, we also know that most systems can be locally well approximated by the balance of just a few dominant physical processes. The goal of this work is to extract such dominant balance models in a data-driven fashion and use them to understand which forces are locally driving the emergence of macroscopic patterns.



In vivo observations of patterns that can be reproduced by the hydrodynamic models considered here. A) Formation of asters during the assembly of the cellular mitotic spindle in the embryo of *C. marginatus*. B) Moving density waves in dense actin motility assays. Arrow denotes direction of movement.

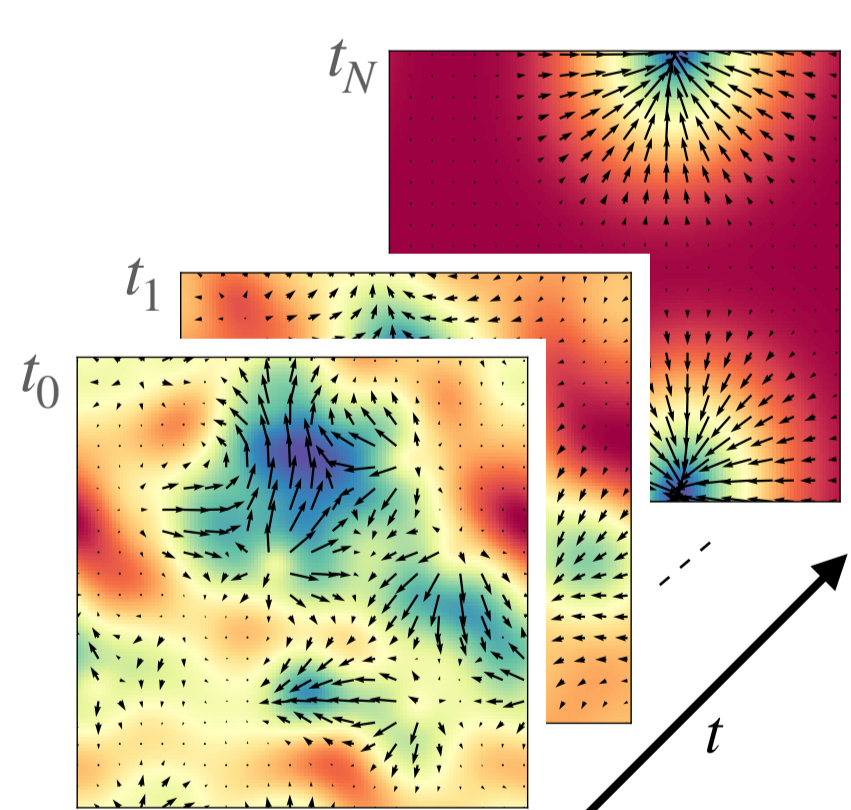
Macroscopic Model of Self-Propelled Particles

Hydrodynamic equations that describe the emergence of macroscopic motion from the microscopic interactions of self-propelled particles can be derived for various systems. Here we consider particles that move by a constant speed w_0 that can be modeled by the following coupled PDEs based on the density ρ and polarity \mathbf{W} of the particles.

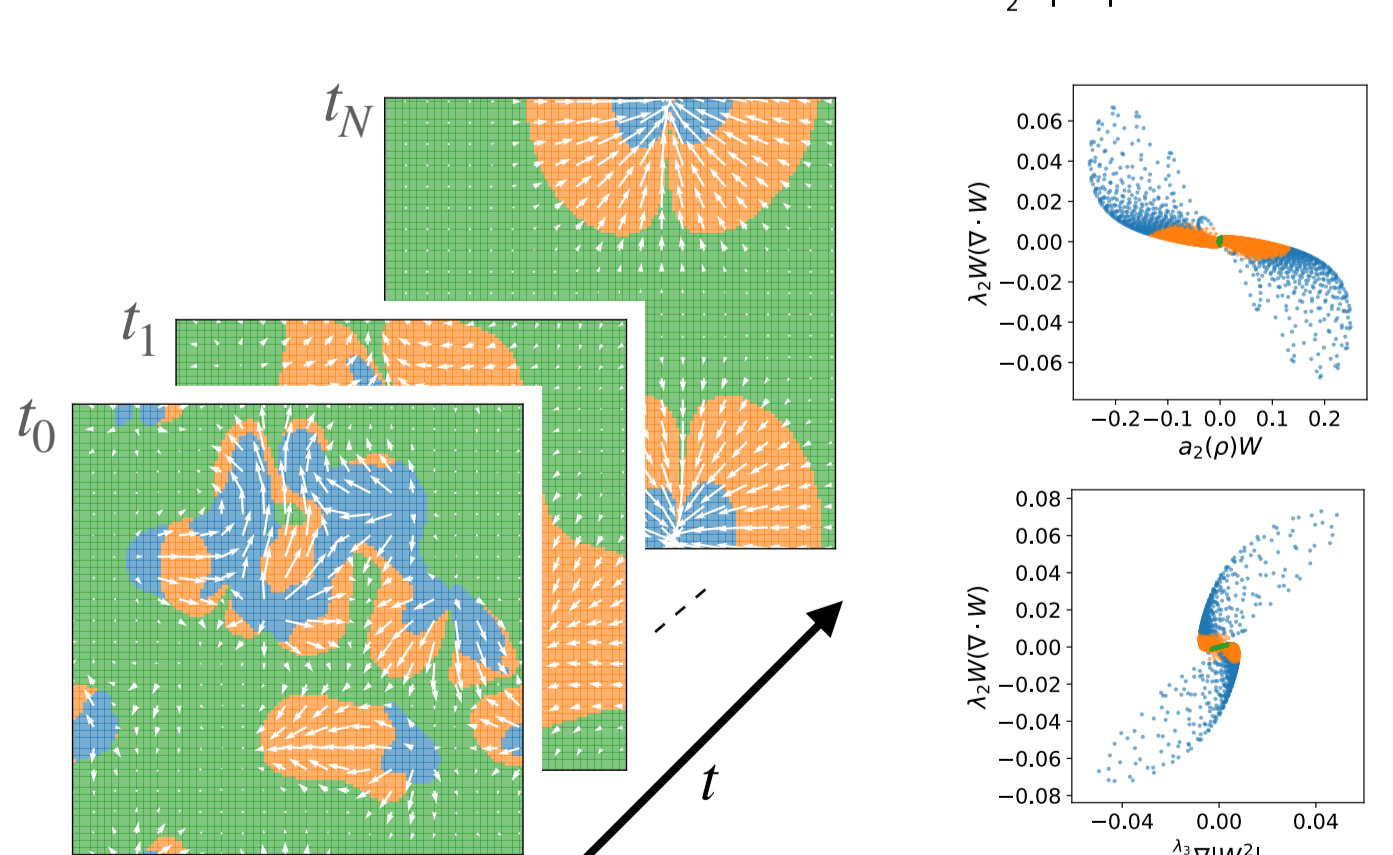
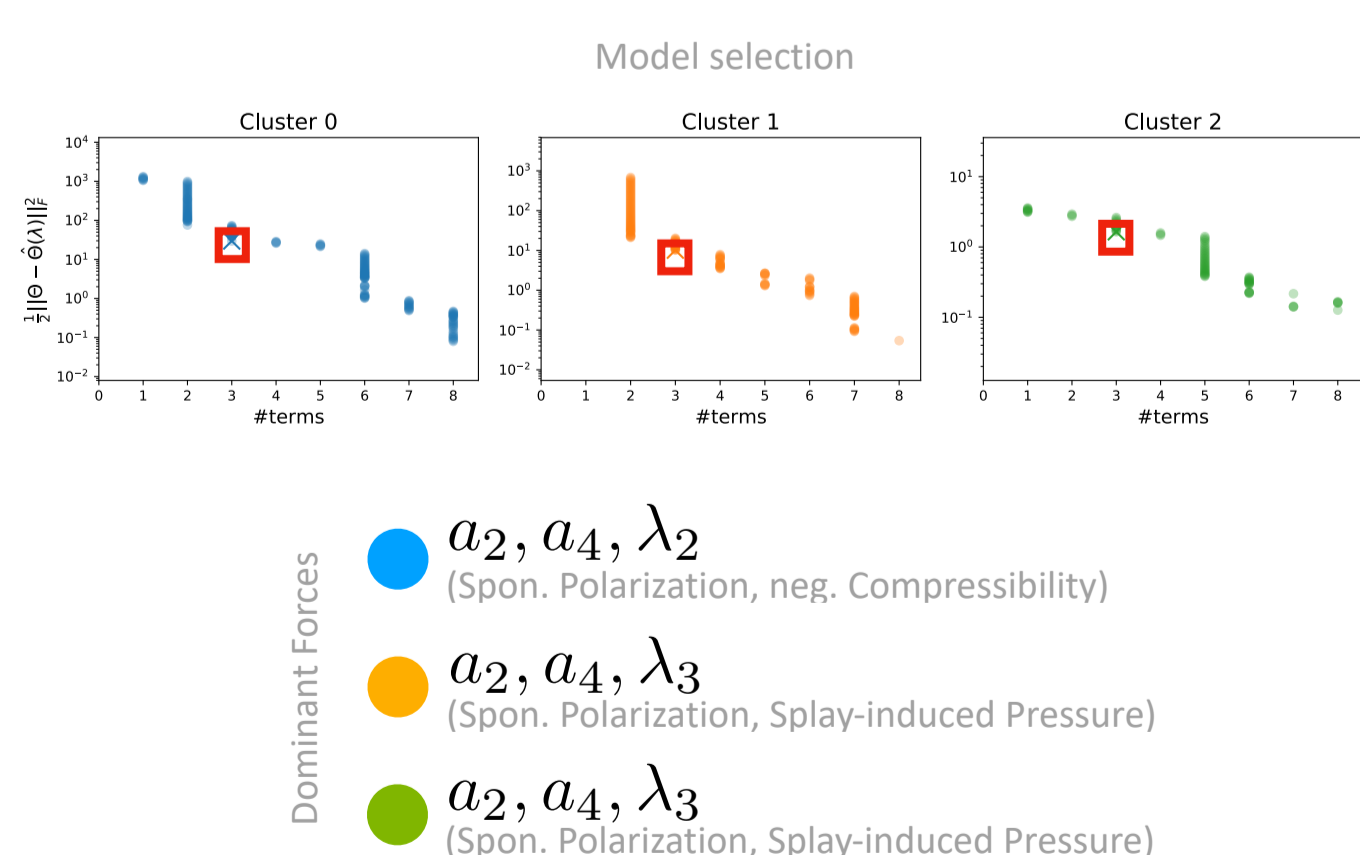
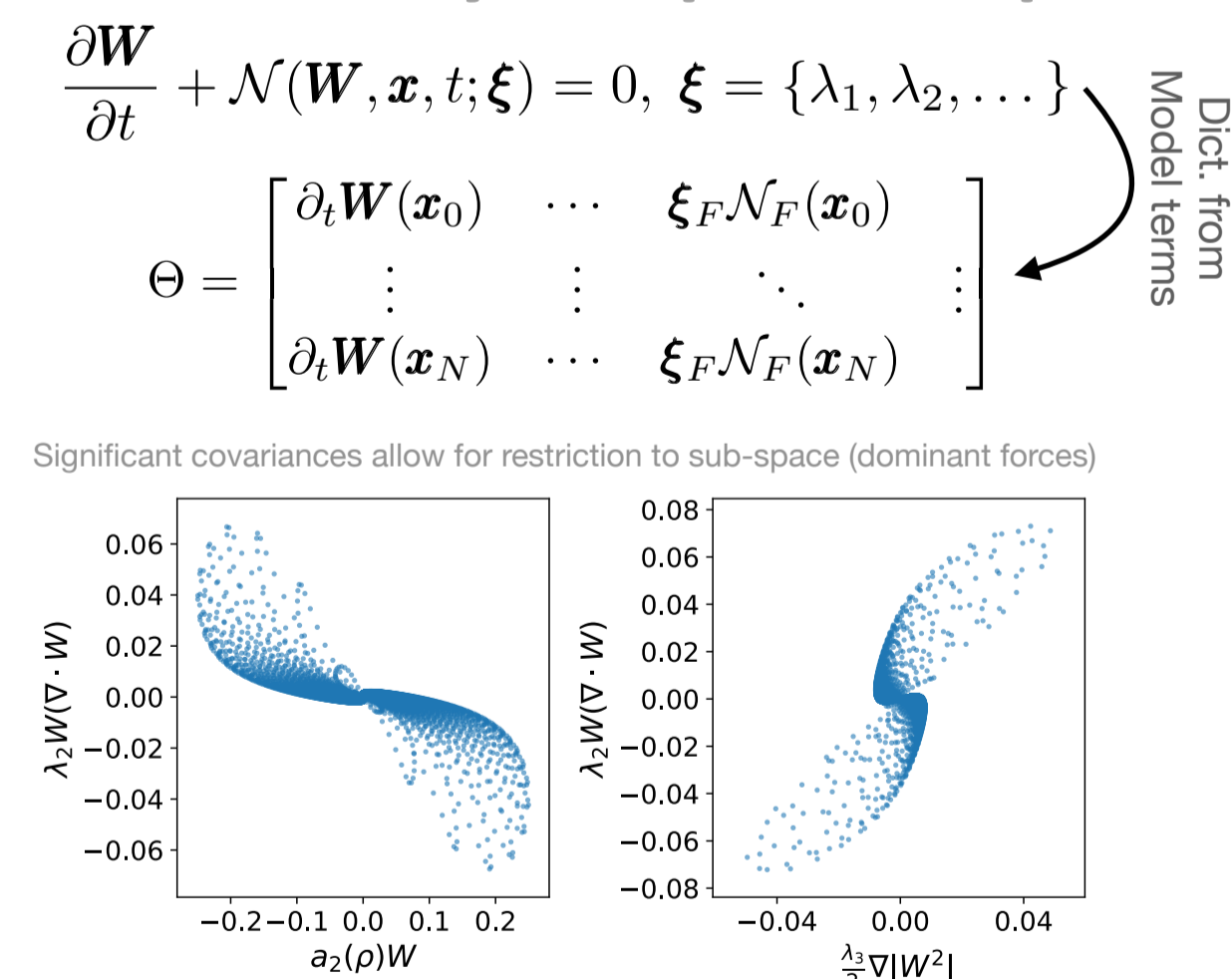


Method: Data-Driven Dominant Balance Models

1. Data Acquisition



2. Dictionary & Equation Space

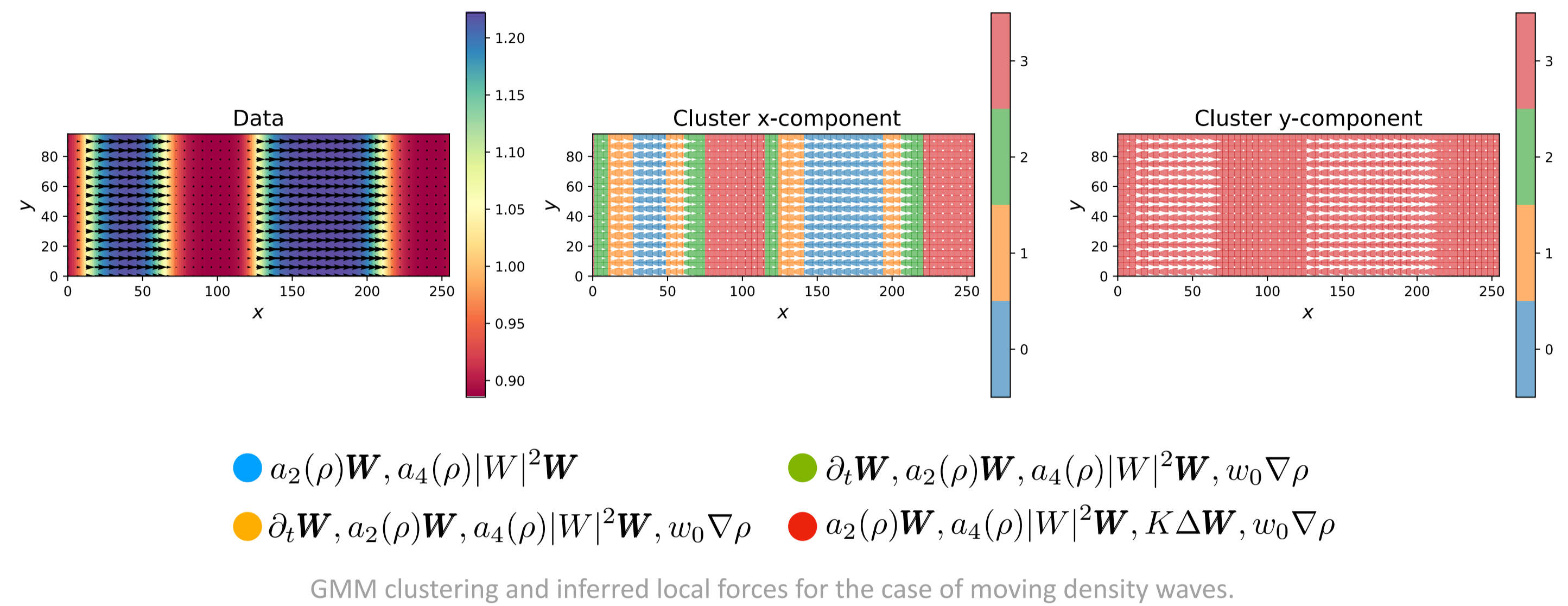


4. Sparse PCA & Model Selection

3. Gaussian Mixture Model Clustering

Results

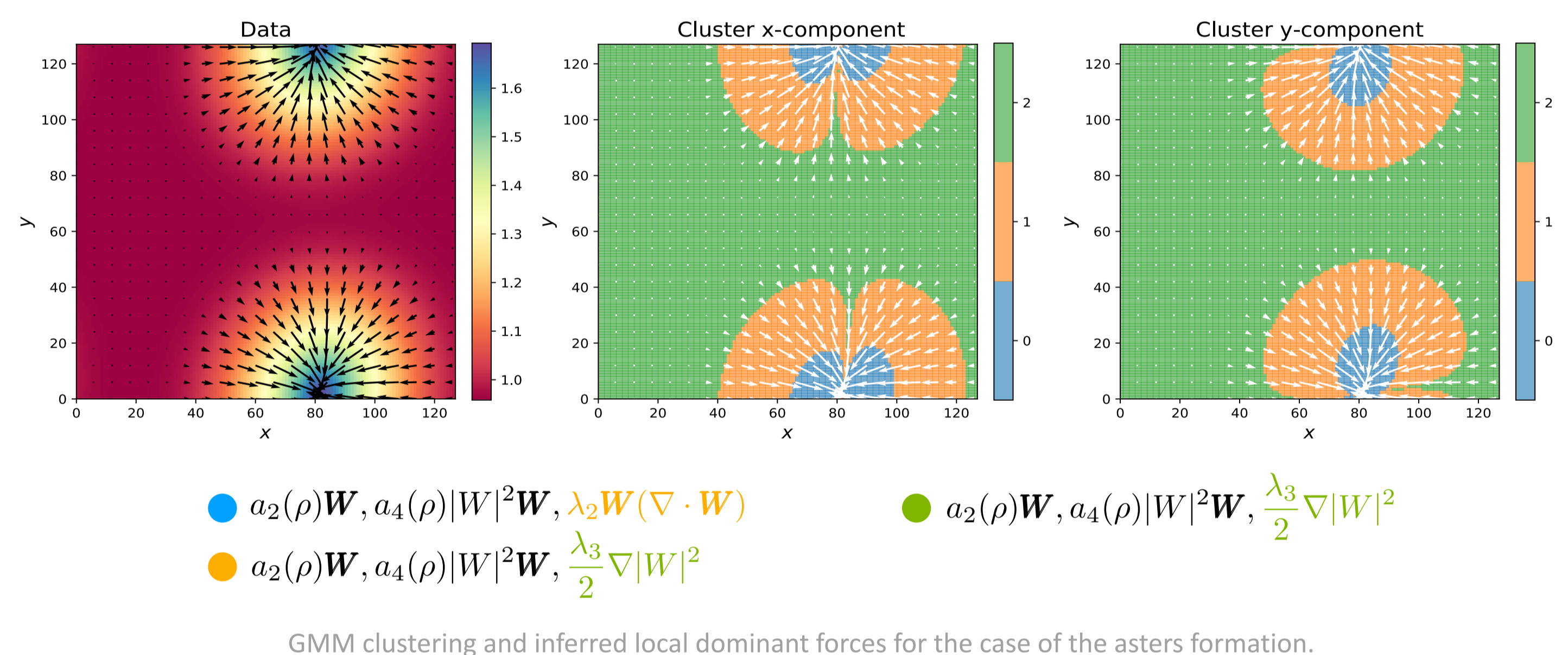
Formation of Moving Density Waves



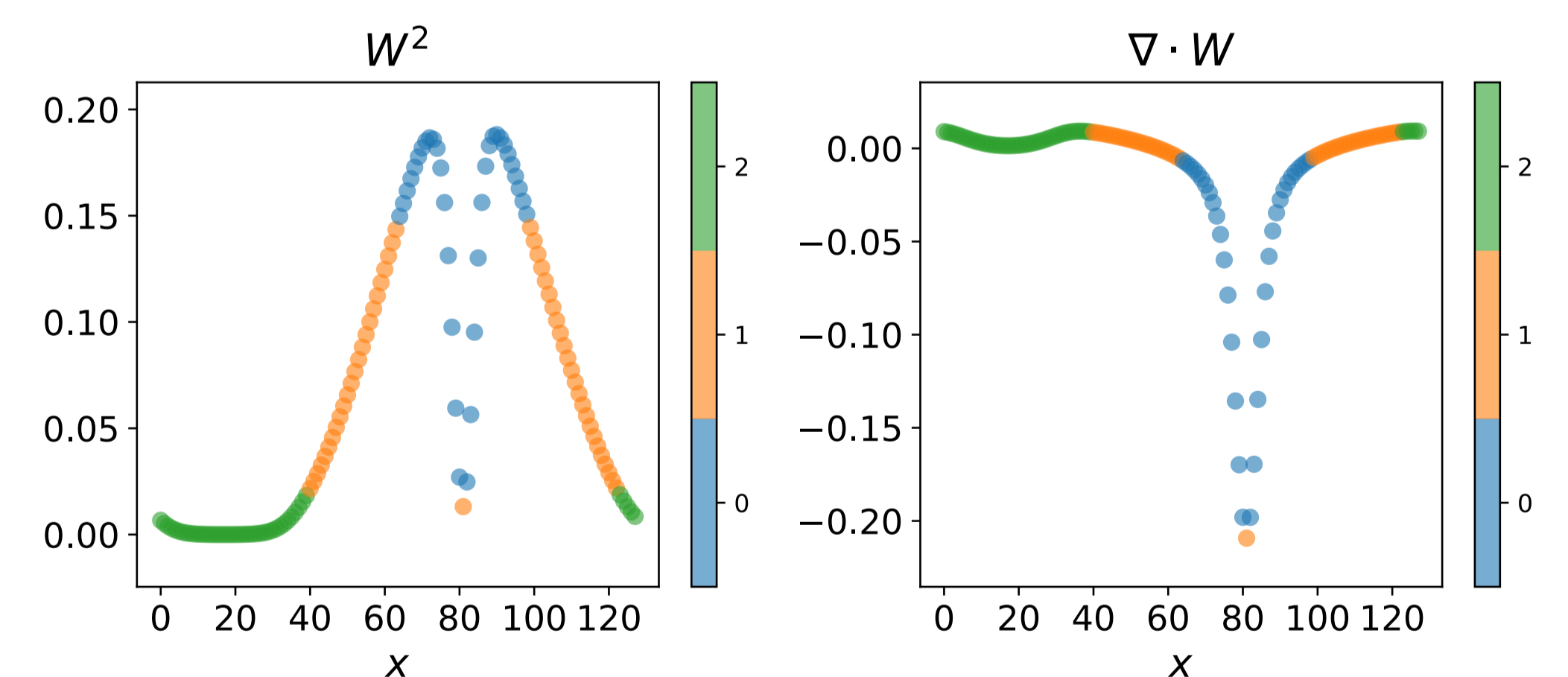
In the high density region we infer a steady state equation based on the spontaneous polarization terms. This means, in the vicinity of a characteristic density ρ_c the system will yield a stable polarized state with $\mathbf{W} = \sqrt{-a_2(\rho)/a_4(\rho)} \mathbf{e}_\theta$ due to local alignment interactions as predicted by the hydrodynamic theory. The emerging density gradient between the band and the background results in the stable convection of the high density region. Such mechanisms are in alignment with a separately derived description of moving density waves in (Gopinath et al., PRE, 2012) as

$$\frac{\partial \mathbf{W}}{\partial t} = - (a_2(\rho) + a_4(\rho) |\mathbf{W}|^2) \mathbf{W} - w_0 \frac{\partial \rho}{\partial x}$$

Splay-Induced Negative Compressibility and Asters



Similar to (Gopinath et al., PRE, 2012) we find that strong particle interactions leading to splay-induced pressure gradients and the negative compressibility near the center of the structures are the driving mechanism of asters formation.



Conclusions and Outlook

We have shown that data driven methods can be used to extract local dominant forces that lead to pattern formation in active matter systems. Moreover, in alignment to previous work we identified two distinct processes: 1) density waves are formed by alignment interactions and driven by density gradients; 2) asters are shaped through effects of negative compressibility due to strong particle interactions. We envision this framework to be used to gain more insight on dominant force balances in living systems, i.e. the assembly of cell structures like spindles or the organization of tissues.