## Turbulent patterns and the underlying invariant solutions in a continuum model of active fluids

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Collective motion in active fluids such as bacterial suspensions displays remarkable spatio-temporal patterns, including bacterial turbulence phases at zero Reynolds number. The effective coarse-grained dynamics of interacting active constituents can be described by hydrodynamic PDEs similar to the Navier-Stokes equations. Our aim is to understand emerging flow patterns far from onset and their parameter dependence to identify the mechanisms behind their origins. To this end, we transfer dynamical systems concepts from the study of Navier-Stokes turbulence to active fluids and specifically identify dynamically relevant fully nonlinear invariant solutions of the active Toner-Tu-Swift-Hohenberg model describing bacterial turbulence<sup>1</sup>

$$\left(\partial_t + \lambda_0 \boldsymbol{v} \cdot \nabla\right) \boldsymbol{v} = -\nabla p + \lambda_1 \nabla \boldsymbol{v}^2 - \left(\alpha + \beta |\boldsymbol{v}|^2\right) \boldsymbol{v} + \Gamma_0 \Delta \boldsymbol{v} - \Gamma_2 \Delta^2 \boldsymbol{v}$$

Using the amplitude equation formalism, we identify several solution branches in the weakly nonlinear regime close to onset. The branches are followed to the fully nonlinear regime using parametric continuation. To this end, a numerical interface between the Dedalus software (dedalus-project.org) for time integration and the Channelflow library (www.channelflow.ch) for dynamical systems analysis is created. We identify key invariant solutions that capture characteristic flow features including vortex lattices and transient jets, and show that these solutions are transiently visited by the turbulent dynamics. Bifurcation analysis reveals the origin of those nonlinear solutions and allows to rationalize the parameter dependence of observed flow patterns.

This fully nonlinear approach augments linear and weakly nonlinear methods to improve our understanding of self-organized flow patterns in bacterial turbulence.

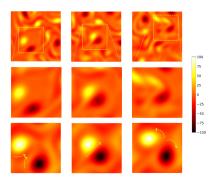


Figure 1: top - Vorticity field for the turbulent dynamics at different times, middle - zoomed in view that displays a jet of conter-rotating vortices, bottom - An invariant solution (*reletive periodic orbit*) that captures the formation and breakup of jet. Thus, the invariant solution shows key features of bacterial turbulence

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<sup>&</sup>lt;sup>1</sup>Wensink et al., *PNAS.* **109**, 14308 (2012).