

## Symmetry breaking in a bulk–surface reaction–diffusion model for signaling networks

**Andreas Rätz**

TU Dortmund, Germany  
[andreas.raetz@tu-dortmund.de](mailto:andreas.raetz@tu-dortmund.de)

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Small GTPases are key regulators of membrane trafficking. The cycling of these GTPases between active and passive states and between cytosolic and membrane-bound states is essential for their function. The mathematical modeling of this scenario leads us to a coupled system of reaction-diffusion equations inside and on the membrane. For our numerical investigations, the membrane is implicitly treated in a diffuse-interface approach to study the influence of Turing-type mechanisms for the localization of active/inactive GTPases. Furthermore, we use a phase field method in order to simulate a reaction-diffusion system which is coupled to the dynamics of the membrane.