

# BIG seminar

**Biology and integrative genetics**

**Monday,  
September 6  
17h**

**Auditorium Bâtiment Biophore  
Unil-Sorge at Dorigny**

**Sven Bergmann**  
Unil



**“Computational analysis of biological systems:  
From developmental patterning to genome-wide association  
association studies.”**

Quantitative modeling of biological systems can facilitate unraveling the mechanisms that evolved to ensure their robust functioning under fluctuating environmental conditions. As an illustration I will show how studying systems properties like precision and scale in developmental patterning can inform models of morphogen gradient formation in early *Drosophila* development. Yet, many biological systems are still poorly characterized, preventing such a quantitative approach. I will discuss the successes and limitations of recent genome-wide association studies for identifying new candidates for genes affecting a particular trait, as well as possible interactions.

BIG is an initiative of the Faculty of Biology and Medicine, University of Lausanne, and is organized by Uta Paszkowski, Laurent Keller, Henrik Kaessmann and Jan Roelof van der Meer.

Info: [www3.unil.ch/fbmens/reve/evenement\\_bigseminar\\_public.php](http://www3.unil.ch/fbmens/reve/evenement_bigseminar_public.php) contact: [uta.paszkowski@unil.ch](mailto:uta.paszkowski@unil.ch), [janroelof.vandermeer@unil.ch](mailto:janroelof.vandermeer@unil.ch)