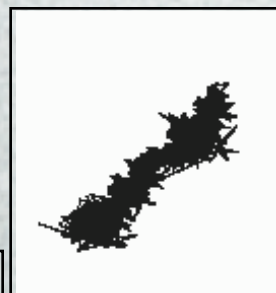


Computationally extracted virus trajectories from microscope videos and analysis.



# A Stochastic Model of Virus Motility

## Computational modeling and analysis of the motion of biological viruses

Computational modeling is rapidly becoming an important form of scientific investigation in virology. The modeling and analysis of virus trajectories before they penetrate the host cell can give significant insights into the entry pathways of viruses and the ways in which they may exploit the cell signaling network.

In this project, we will build a stochastic model of this virus motion on the cell membrane. We will be using this model to make predictions about the expected fre-

quency of certain events as they pertain to the viral entry pathways. The model is based on vast amounts of available tracking data from experiments (more than 50'000 tracks under different conditions) describing the motion of viruses on the membrane of their host cells. Previous projects already provided the tools needed to classify and decompose the data, such that all parameters of the stochastic model can be estimated.

The project is carried in an interdisciplinary environment providing insights to the methods of working and reasoning in life sciences and provides the opportunity to implement methods of statistical model-

ing and machine learning on large data sets. The project is in collaboration with the Institute of Biochemistry and the Institute of Zoology at the University ZH.

### PREREQUISITES

Knowledge in modeling/validation  
Matlab experience  
Stochastics or Machine Learn. classes  
Independent worker

### CONTACT

Ivo Sbalzarini  
Prof. Petros Koumoutsakos

e-mail : [petros@inf.ethz.ch](mailto:petros@inf.ethz.ch)