# PhD position (E13/65%) Machine learning driven analysis of super-resolution microscopy images

We offer a PhD position **in the data analysis of super-resolution fluorescence microscopy of protein complexes**. The project aims to develop machine learning methods to describe the motion statistics of single molecules across space and time which are obtained in the lab of Prof. Heilemann using quantitative single-molecule localization microscopy (qSMLM) in cells with near-molecular spatial resolution.

Overall, the aim of this PhD project is to develop mathematical and numerical tools to describe the collective motion of membrane receptors across space in living cells and to discover collective motion vectors embedded in the seemingly random motion of individual molecules. We invite applications from candidates with a strong interest in theoretical and/or experimental biophysics with a background in life sciences/physics who want to focus on modelling and machine learning. The ideal candidate should have an interest to work with theoretical data analysis approaches. We seek candidates with a background in physics, biophysics, math or computer science or related disciplines**.**

Candidates should hold a diploma or a master's degree and be enthusiastic about working in a competitive interdisciplinary research team. Good communication skills, a strong work ethic, ability to work remotely and excellent command of the English language are essential.

Our interdisciplinary team of chemists, biologists, and physicists consists of two scientific groups, the Tchumatchenko group and the Heilemann group, which will collaborate for this project. Our teams are excited about the interface between biology, super-resolution techniques and modeling and are eager to study cellular processes using both microscopes and mathematical models. We work at the interface between biology, (bio)chemistry and physical chemistry, using single-molecule and super-resolution techniques to study cellular processes with molecular resolution (further information at www.smb.uni-frankfurt.de and www.tchumatchenko.de).
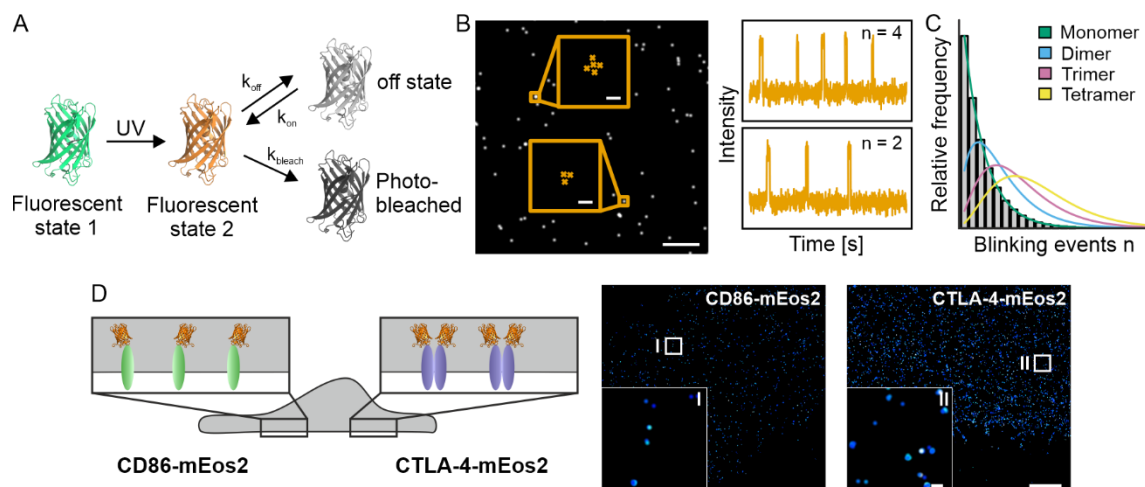
Experimental methods underlying the data analysis: Quantitative single-molecule super-resolution microscopy with photoactivated fluorescent proteins. (A) Photophysical transitions in a photoactivatable fluorescent protein

lead to multiple detection events for single fluorophores ("blinking") that (B, C) can be used for molecular quantification with molecular spatial resolution. (D) Quantitative super-resolution imaging revealed monomeric CD86 and dimeric CTLA4 in the plasma membrane of cells (Image taken from Dietz & Heilemann, Nanoscale 2019.)

Please send your application by email to

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