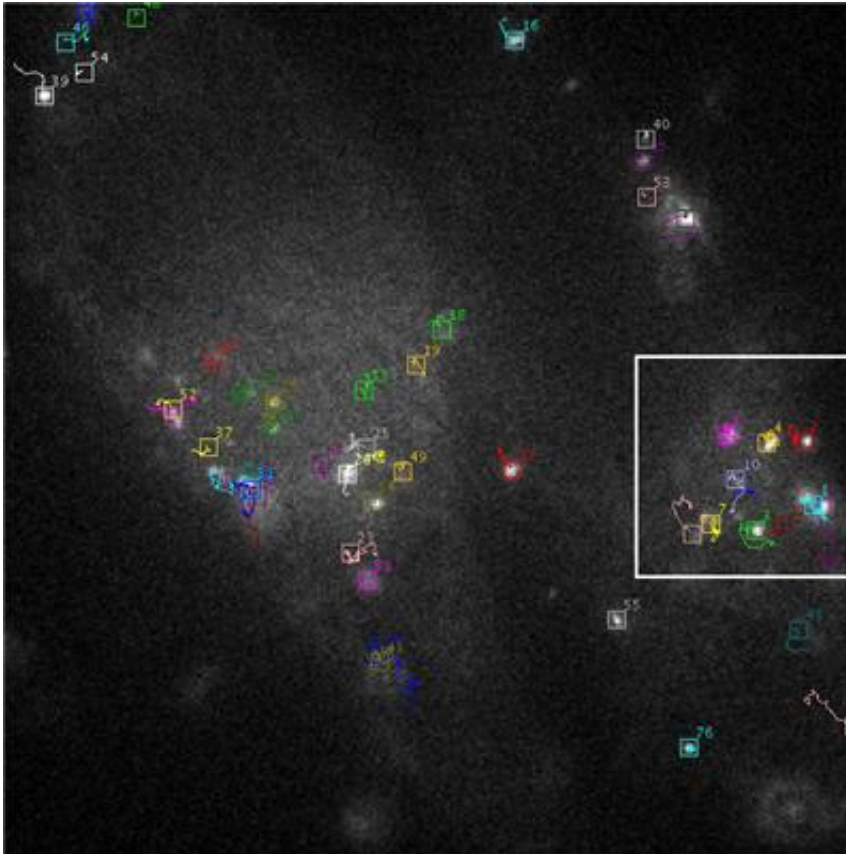


# Automatic tracking of biological particles in cell microscopy images

March 26 2014

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Tracking result for virus particles. Microscopy image of time-resolved data overlaid with automatically determined movement paths of HIV-1 particles, shown in different colours. The small boxes indicate the positions found at the current time point. Credit: W.J. Godinez, K. Rohr

In order to track the movements of biological particles in a cell,

scientists at Heidelberg University and the German Cancer Research Center have developed a powerful analysis method for live cell microscopy images. This so-called probabilistic particle tracking method is automatic, computer-based and can be used for time-resolved two- and three-dimensional microscopy image data. The Heidelberg method achieved the best overall result in an international competition that compared different methods for image analysis. The competition results were recently published in the journal *Nature Methods*.

The task of how to automatically track the movement of biological particles such as viruses, cell vesicles or cell receptors is of key importance in biomedical applications for the quantitative analysis of intracellular dynamic processes. Manually analysing time-resolved microscopy images with hundreds or thousands of moving objects is not feasible. In recent years, therefore, there has been increasing emphasis on the development of automatic [image analysis](#) methods for particle tracking. These methods are computer-based and determine the positions of particles over time. To objectively compare the performance of these methods, an international competition was organised in 2012 for the first time.

A total of 14 research teams participated in the "Particle Tracking Challenge," including Dr. William J. Godinez and Associate Professor Dr. Karl Rohr from Heidelberg University and the German Cancer Research Center (DKFZ). In the competition, the different image analysis methods were applied to a broad spectrum of two- and three-dimensional image data and their performance was quantified using different measures. The three best methods were determined for each category of data. With a total of 150 "Top 3 Rankings," the Heidelberg scientists achieved the best overall result.

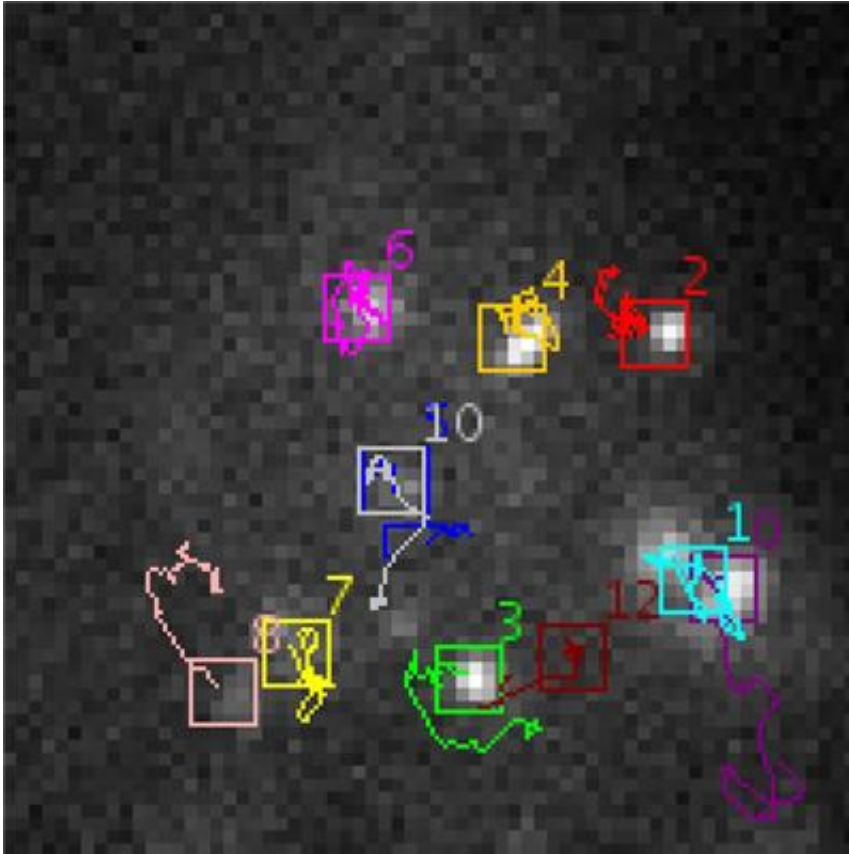


Image two shows an enlarged section of the area marked by the white rectangle in image one. Credit: Godinez, K. Rohr

The particle tracking method developed by Dr. Godinez and Dr. Rohr is based on a mathematically sound method from probability theory that takes into account uncertainties in the image data, e.g. due to noise, and exploits knowledge of the application domain. "Compared to deterministic methods, our probabilistic approach achieves high accuracy, especially for complicated image data with a large number of objects, high object density and a high level of noise," says Dr. Rohr. The method enables determining the movement paths of objects and quantifies relevant parameters such as speed, path length, motion type or object size. In addition, important dynamic events such as virus-cell fusions are detected automatically.

Karl Rohr heads the "Biomedical Computer Vision" (BMCV) research group that develops computer science methods to automatically analyse cell microscopy images as well as radiological images. This group is located at the BioQuant Center of Heidelberg University. It is part of the department "Bioinformatics and Functional Genomics" at Heidelberg University's Institute of Pharmacy and Molecular Biotechnology as well as the division "Theoretical Bioinformatics" of the DKFZ, both of which are headed by Prof. Dr. Roland Eils. William J. Godinez is pursuing postdoctoral work in the BMCV group on the development of computer-based particle tracking methods.

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