

COMP9517: Computer Vision

Motion Estimation and Tracking:
Applications in Biomedical Imaging

Professor Erik Meijering

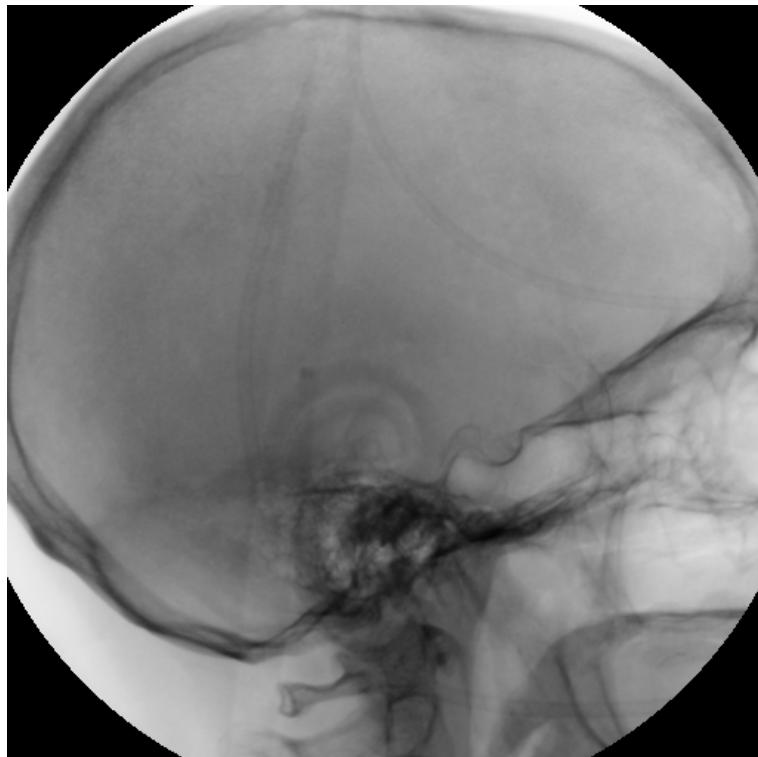
Topics

- Example of **change detection**
 - Patient motion correction in angiography
- Examples of **template matching**
 - Cell motion correction in microscopy
 - Monomodal brain image registration
 - Multimodal medical image registration
- Example of **optical flow**
 - Heart tissue motion estimation
- Examples of **object tracking**
 - Particle tracking in molecular biology
 - Bayesian multitarget tracking method
 - Heart motion tracking and analysis
 - Tracking for neuron reconstruction
 - Object tracking in cell biology

Example of Change Detection

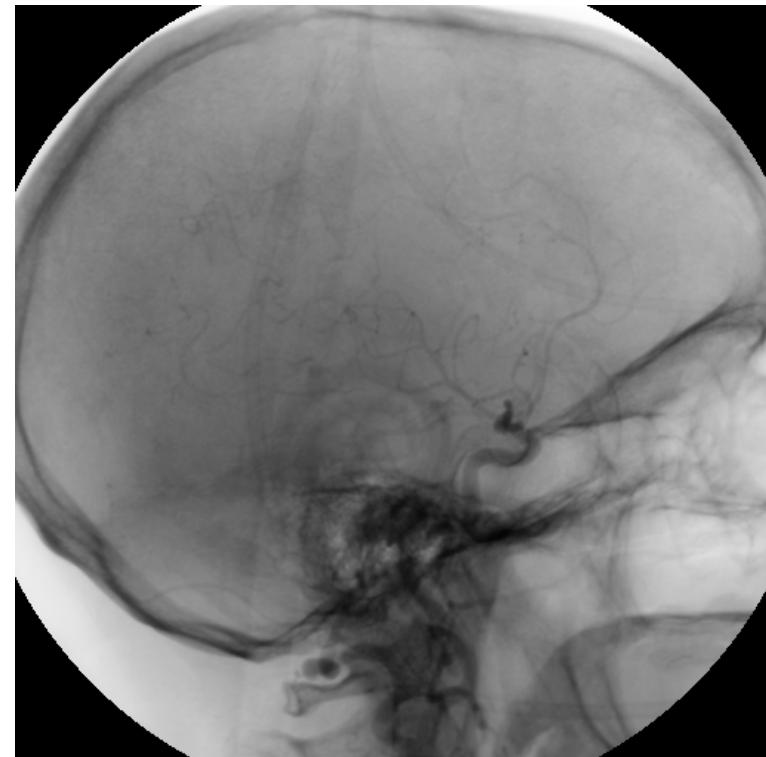
Digital Subtraction Angiography

X-ray at time t_0



Mask Image

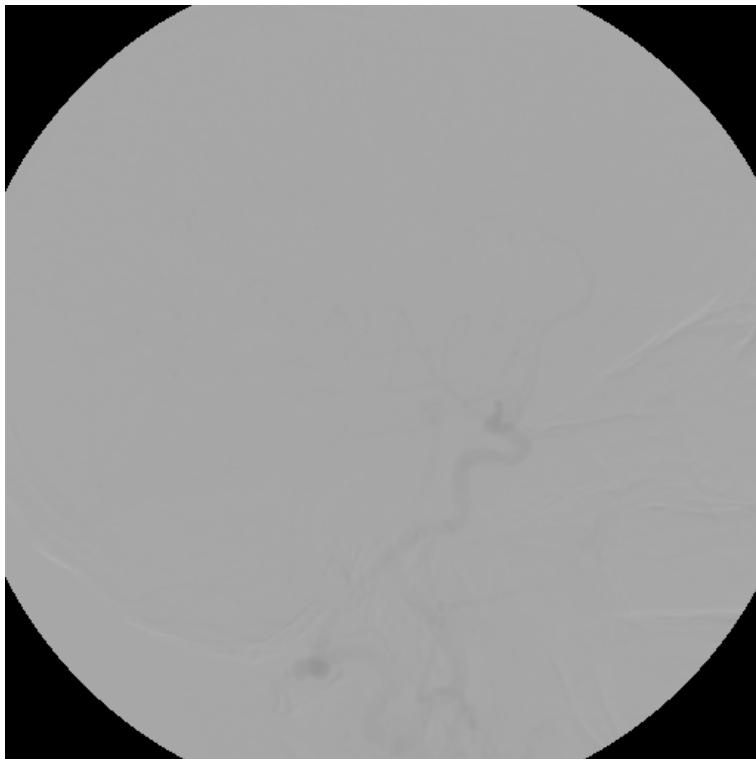
X-ray at time $t_0 + \Delta t$



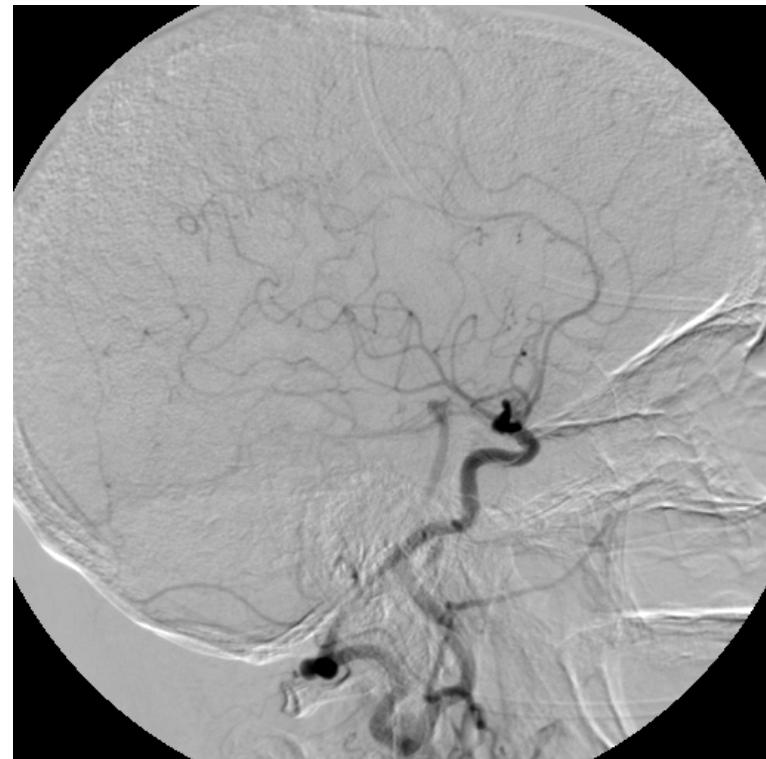
Live Image

Digital Subtraction Angiography

Live – Mask



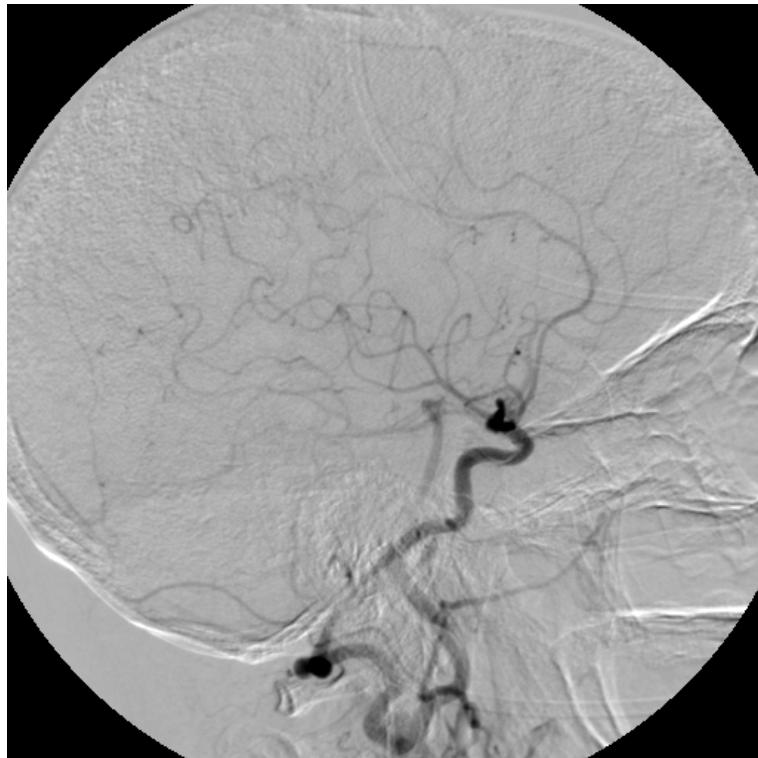
Contrast Stretched



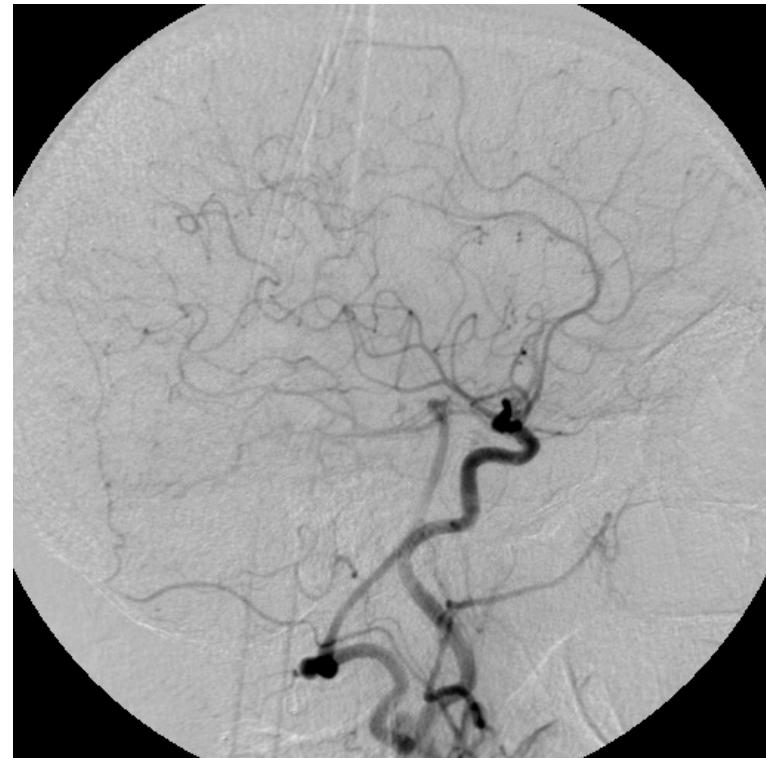
[Meijering et al., International Journal of Computer Vision, 1999](#)

Digital Subtraction Angiography

Contrast Stretched



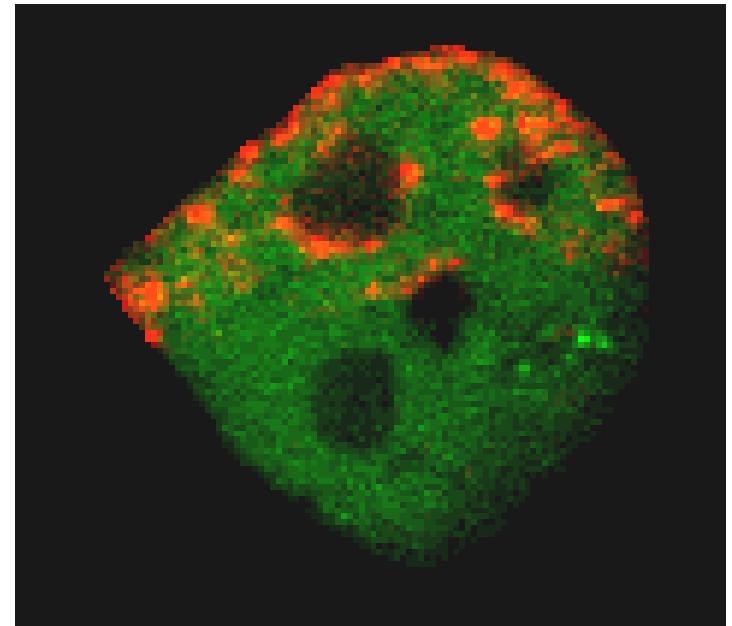
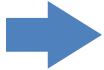
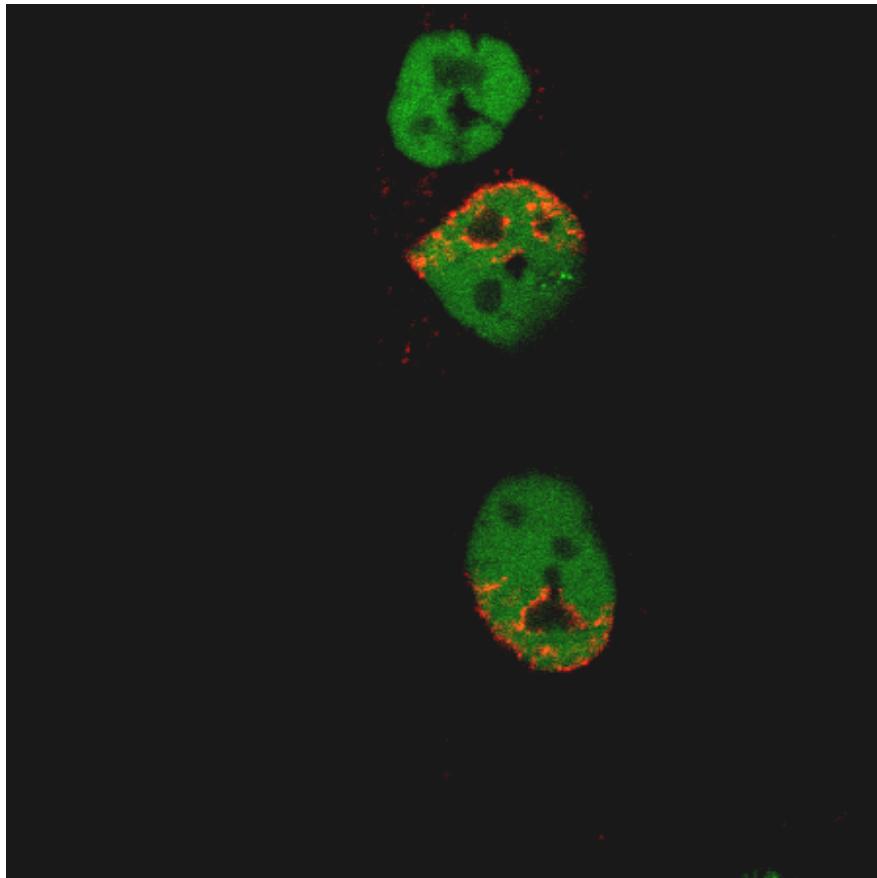
Motion Corrected



Automatic motion correction here is a form of template matching

Examples of Template Matching

Cell Motion Correction

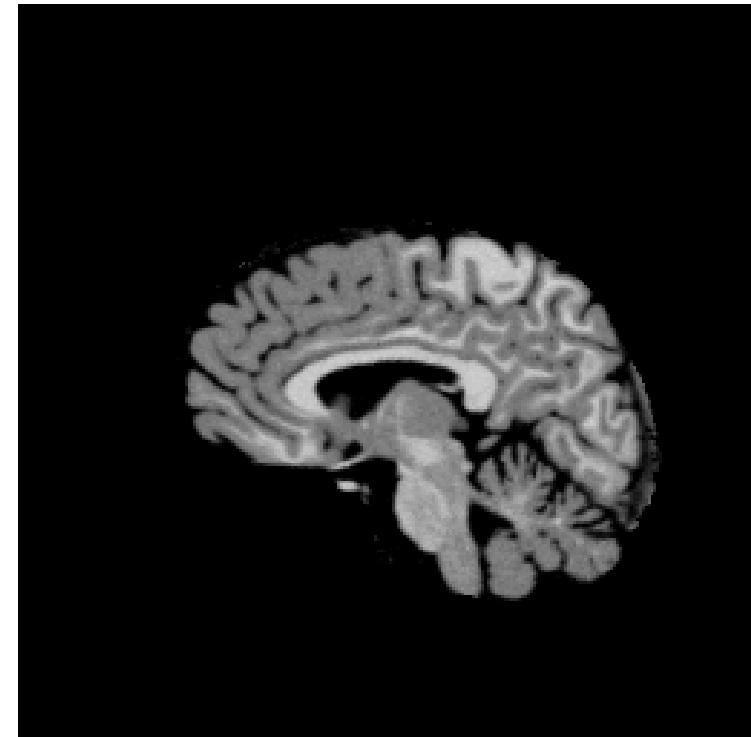
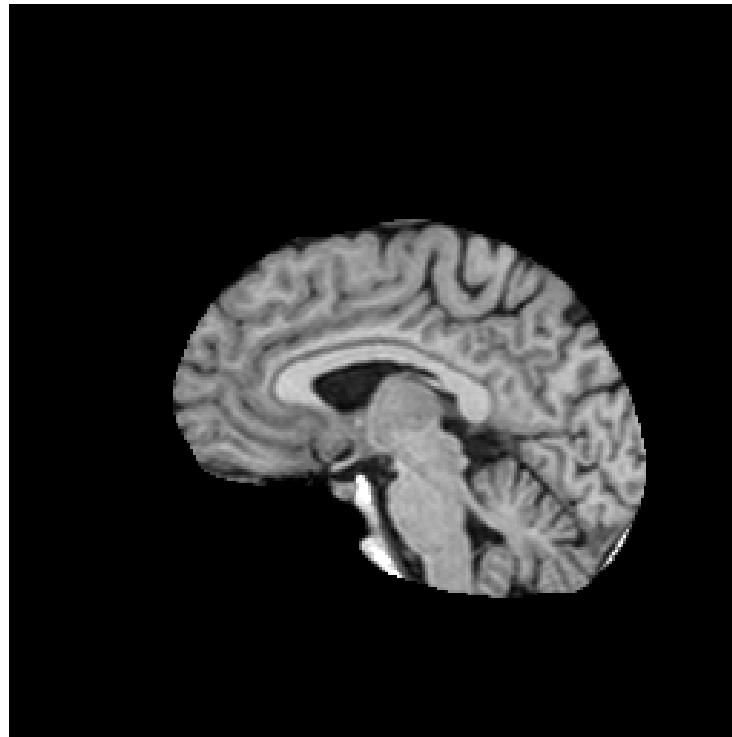


Cell fixation by image post-processing allows analysis of the internal changes over time

[Meijering et al., Bioinformatics, 2010](#)

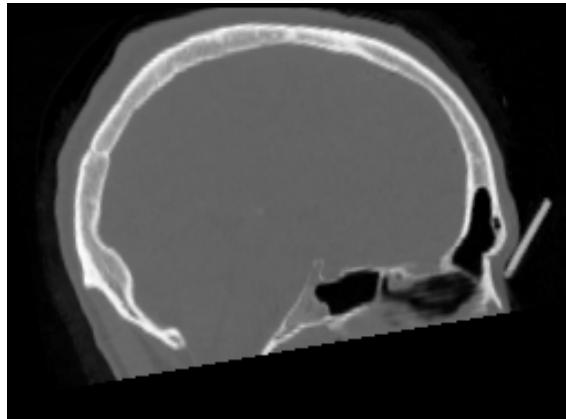
Brain Image Registration

To understand how the human brain develops from childhood to adulthood and to study developmental disorders we can use magnetic resonance imaging (MRI) at different ages and match the images to a template using automatic image registration techniques

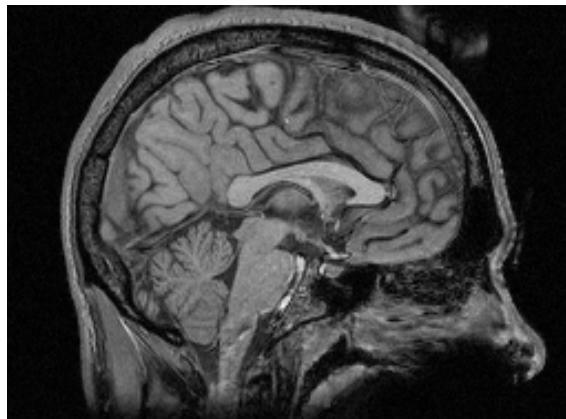
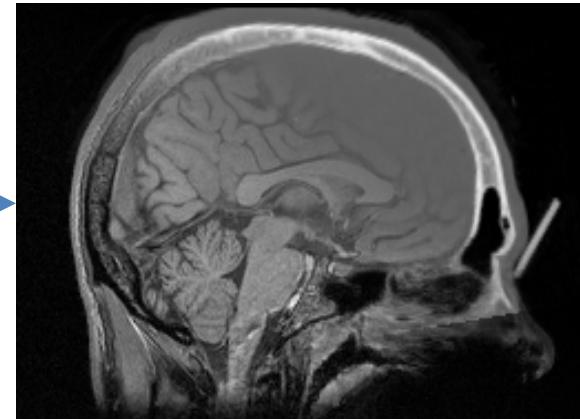


Multimodal Image Registration

Computed Tomography (CT)



Joint Visualization

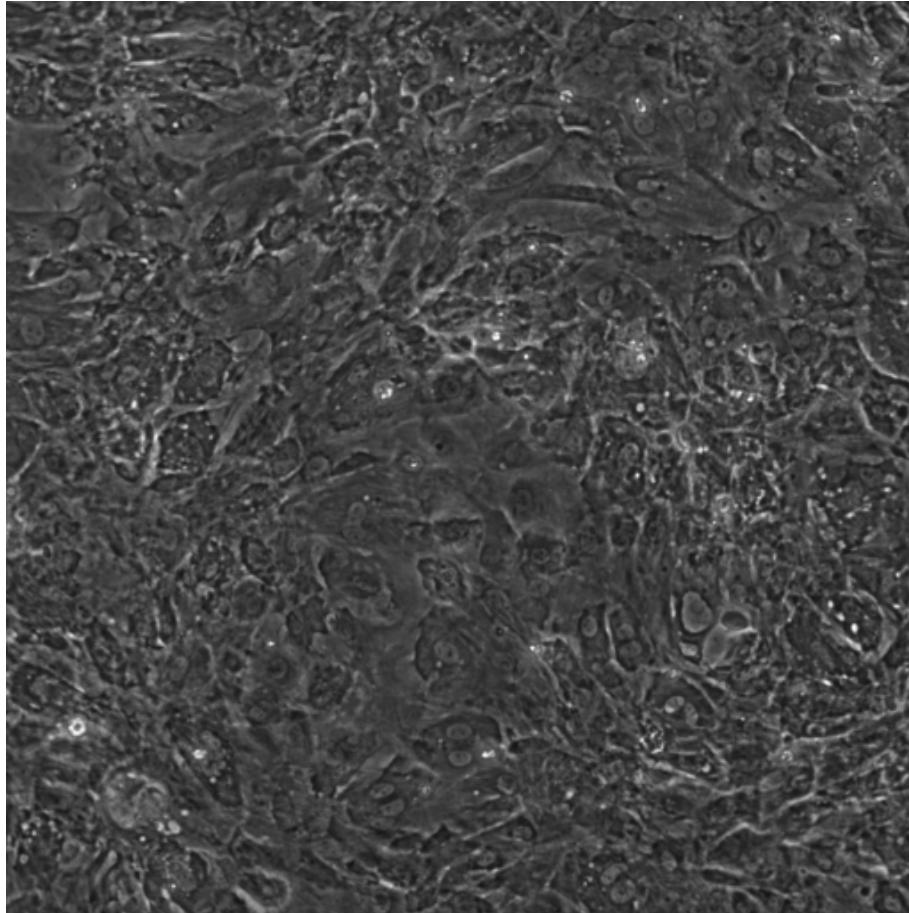


Magnetic Resonance (MR)

Registration (alignment) of images from multiple imaging modalities (devices) allows joint visualisation which may provide additional information to the physician

Example of Optical Flow

Heart Tissue Motion Estimation

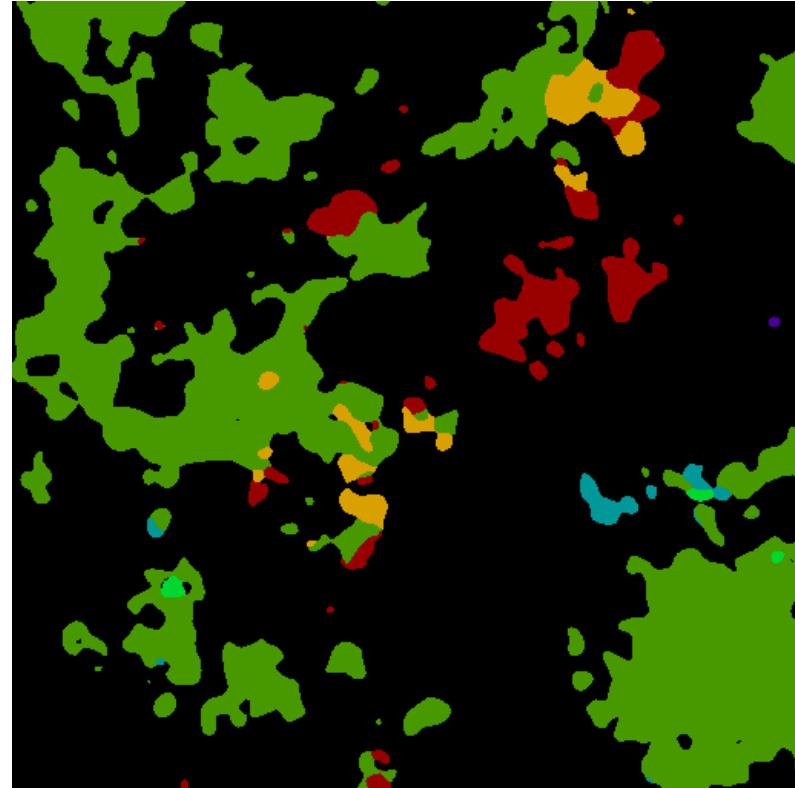
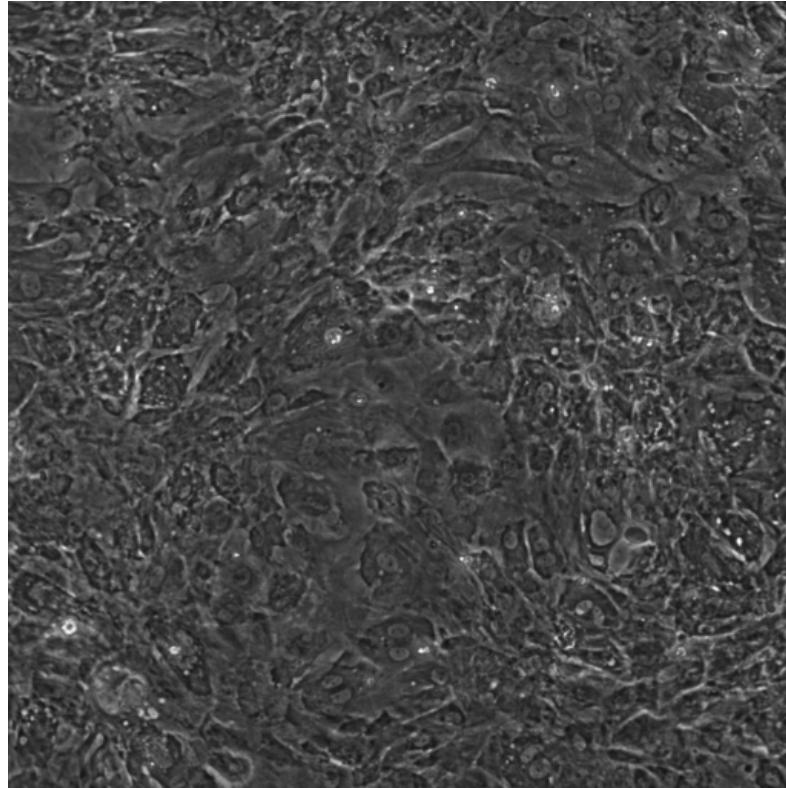
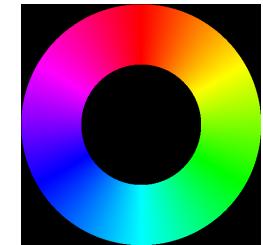


- Heart tissue cultured 6 days
- Mono-layer cardiomyocytes
- Phase-contrast microscopy
- Real-time imaging 24 fps

Since the images contain rich information it is easy to estimate local gradients with high accuracy so this is a perfect case for the optical flow method

$$\nabla f \cdot v = -f_t$$

Heart Tissue Motion

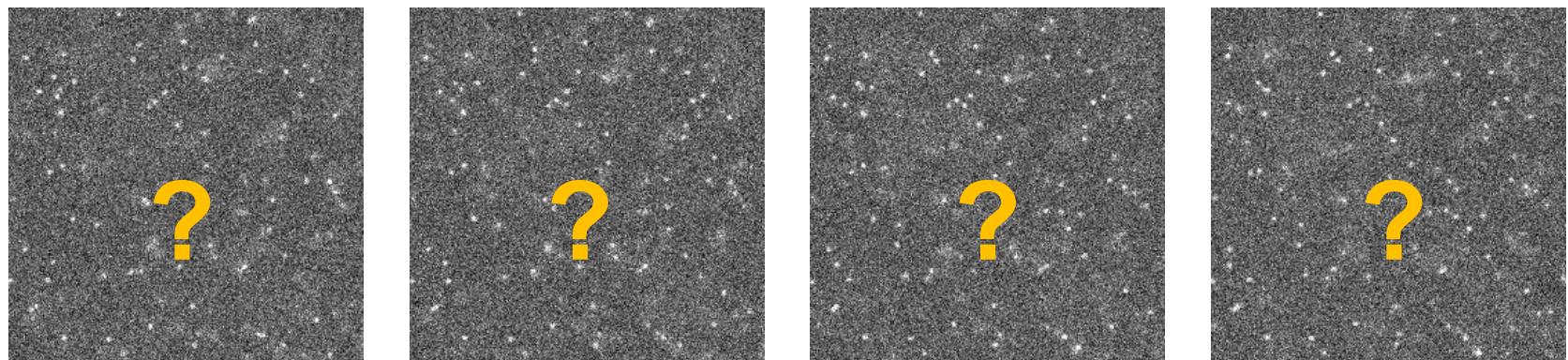
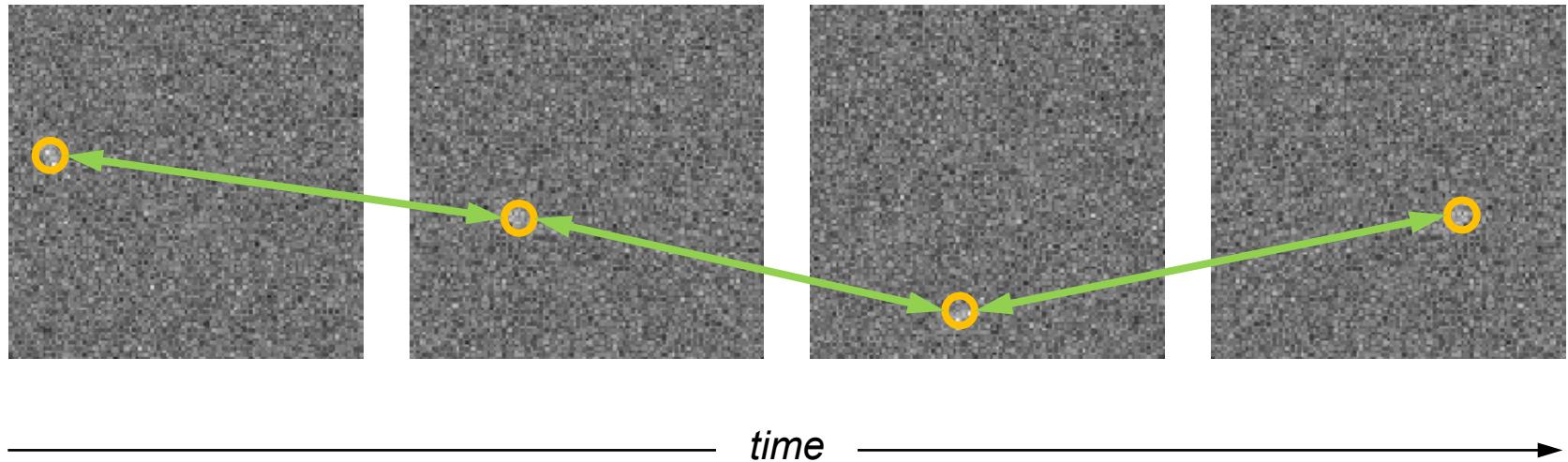


Motion vectors visualised by direction (colour) and magnitude (intensity)

[Essers et al., Biomaterials and Biosystems, 2022](#)

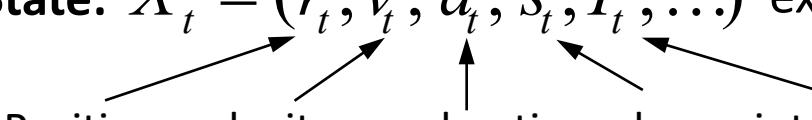
Examples of Object Tracking

Particle Tracking Problem

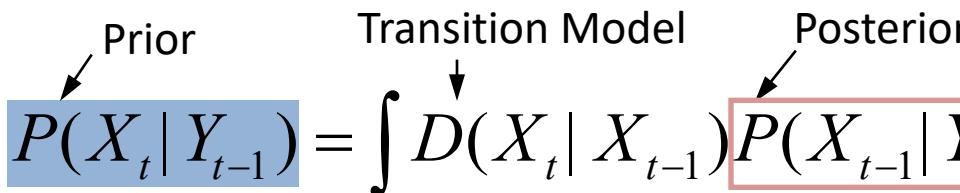


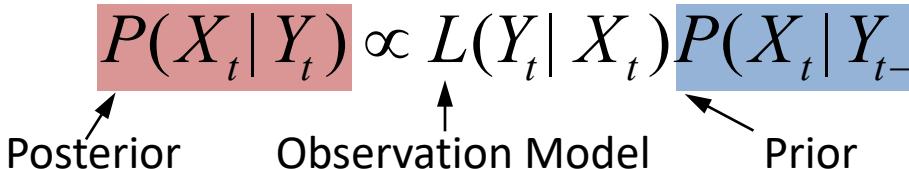
Bayesian Tracking

Computing the degree of belief in the object state by taking into account all available evidence up to the current time point

- **State:** $X_t = (r_t, v_t, a_t, s_t, I_t, \dots)$ expressed as probability density $P(X_t)$


- **Evidence:** a set of images or extracted features $Y_t = \{y_0, \dots, y_t\}$

- **Prediction:**
$$P(X_t | Y_{t-1}) = \int D(X_t | X_{t-1}) P(X_{t-1} | Y_{t-1}) dX_{t-1}$$


- **Correction:**
$$P(X_t | Y_t) \propto L(Y_t | X_t) P(X_t | Y_{t-1})$$


Bayesian Multitarget Tracking

- Extend the state space to include the states of all targets

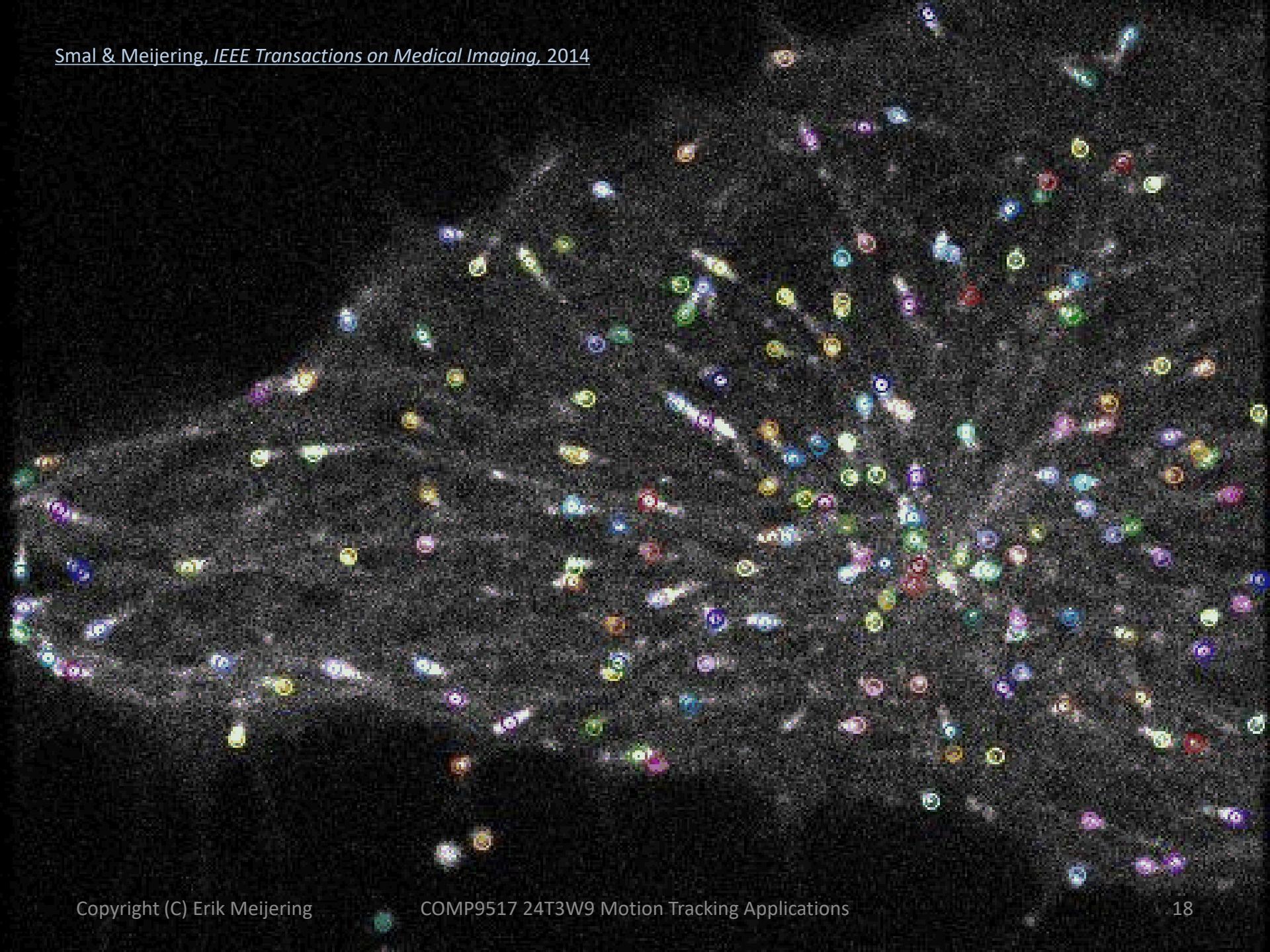
$$X_t = (X_{1;t}, X_{2;t}, \dots, X_{N;t})$$
$$X_{1;t} = (r_{1;t}, v_{1;t}, a_{1;t}, s_{1;t}, I_{1;t}, \dots)$$
$$X_{N;t} = (r_{N;t}, v_{N;t}, a_{N;t}, s_{N;t}, I_{N;t}, \dots)$$

Computational cost grows exponentially with the number of targets

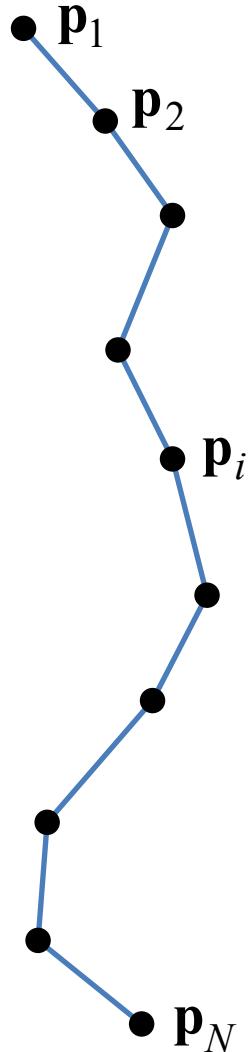
- Use a mixture model of single-target probability densities

$$P(X_t | Y_t) = \sum_{n=1}^N w_{n;t} P_n(X_t | Y_t)$$

Requires heuristics to keep track of number of targets and identities



Trajectory Analysis



Measure

Total distance traveled

Net distance traveled

Maximum distance traveled

Total trajectory time

Confinement ratio

Instantaneous angle

Directional change

Instantaneous speed

Mean curvilinear speed

Mean straight-line speed

Linearity of forward progression

Mean squared displacement

Definition

$$d_{\text{tot}} = \sum_{i=1}^{N-1} d(\mathbf{p}_i, \mathbf{p}_{i+1})$$

$$d_{\text{net}} = d(\mathbf{p}_1, \mathbf{p}_N)$$

$$d_{\text{max}} = \max_i d(\mathbf{p}_1, \mathbf{p}_i)$$

$$t_{\text{tot}} = (N - 1)\Delta t$$

$$r_{\text{con}} = d_{\text{net}} / d_{\text{tot}}$$

$$\alpha_i = \arctan((y_{i+1} - y_i) / (x_{i+1} - x_i))$$

$$\gamma_i = \alpha_i - \alpha_{i-1}$$

$$v_i = d(\mathbf{p}_i, \mathbf{p}_{i+1}) / \Delta t$$

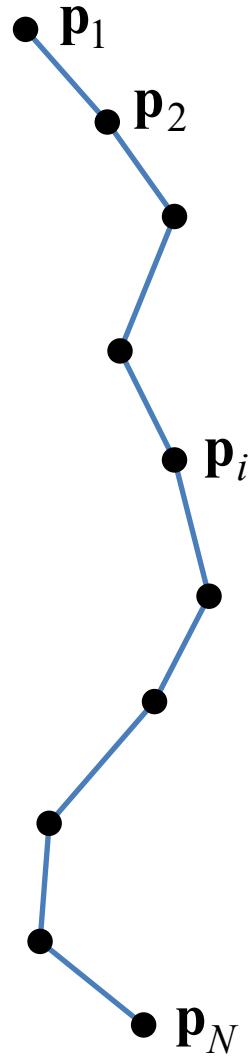
$$\bar{v} = \frac{1}{N-1} \sum_{i=1}^{N-1} v_i$$

$$v_{\text{lin}} = d_{\text{net}} / t_{\text{tot}}$$

$$r_{\text{lin}} = v_{\text{lin}} / \bar{v}$$

$$\text{MSD}(n) = \frac{1}{N-n} \sum_{i=1}^{N-n} d^2(\mathbf{p}_i, \mathbf{p}_{i+n})$$

[Meijering et al., Methods in Enzymology, 2012](#)

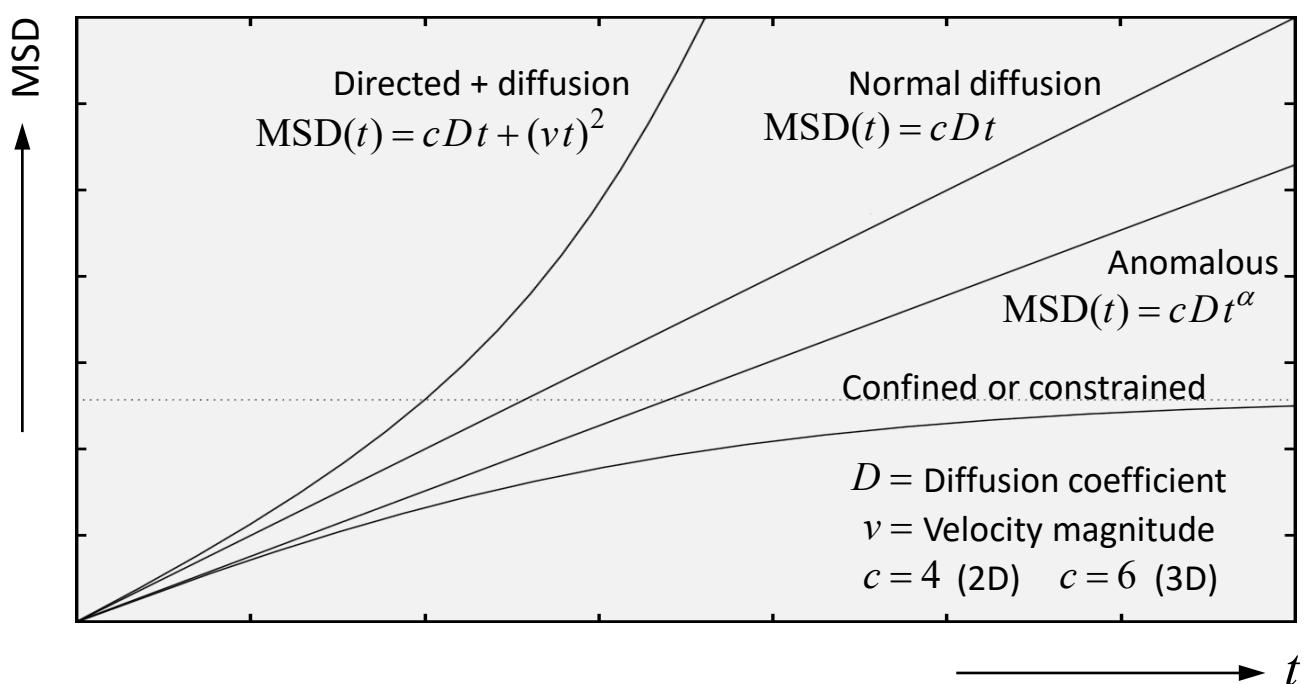


MSD Analysis

Mean
Squared
Displacement

Distance between track points: $d(\mathbf{p}_i, \mathbf{p}_j) = \|\mathbf{p}_j - \mathbf{p}_i\|_2$

MSD for a given time lag t : $\text{MSD}(t) = \frac{1}{N-t} \sum_{i=1}^{N-t} d^2(\mathbf{p}_i, \mathbf{p}_{i+t})$



[Meijering et al., Nature Methods, 2014](#)

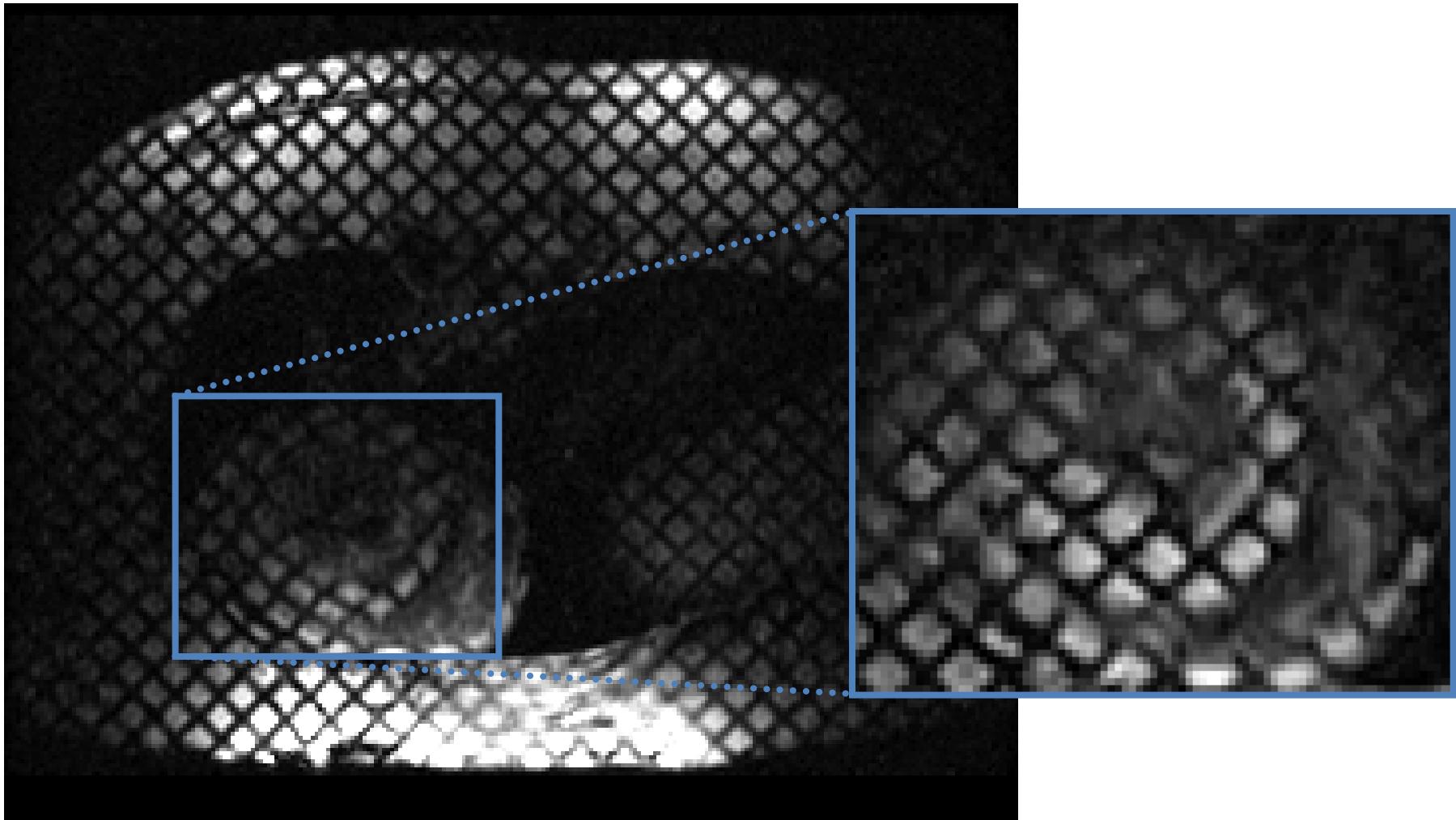
Objective comparison of particle tracking methods

Nicolas Chenouard^{1-3,25}, Ihor Smal^{4,5,25}, Fabrice de Chaumont^{1,25}, Martin Maška^{6,7,25}, Ivo F Sbalzarini⁸, Yuanhao Gong⁸, Janick Cardinale⁸, Craig Carthel⁹, Stefano Coraluppi⁹, Mark Winter¹⁰, Andrew R Cohen¹⁰, William J Godinez^{11,12}, Karl Rohr^{11,12}, Yannis Kalaidzidis^{13,14}, Liang Liang¹⁵, James Duncan¹⁵, Hongying Shen¹⁶, Yingke Xu¹⁷, Klas E G Magnusson¹⁸, Joakim Jaldén¹⁸, Helen M Blau¹⁹, Perrine Paul-Gilloteaux²⁰, Philippe Roudot²¹, Charles Kervrann²¹, François Waharte²⁰, Jean-Yves Tinevez²², Spencer L Shorte²², Joost Willemse²³, Katherine Celler²³, Gilles P van Wezel²³, Han-Wei Dan²⁴, Yuh-Show Tsai²⁴, Carlos Ortiz de Solórzano⁶, Jean-Christophe Olivo-Marin^{1,26} & Erik Meijering^{4,5,26}

Particle tracking is of key importance for quantitative analysis of intracellular dynamic processes from time-lapse microscopy image data. Because manually detecting and following large numbers of individual particles is not feasible, automated computational methods have been developed for these tasks by many groups. Aiming to perform an objective comparison of methods, we gathered the community and organized an open competition in which participating teams applied their own methods independently to a commonly defined data set

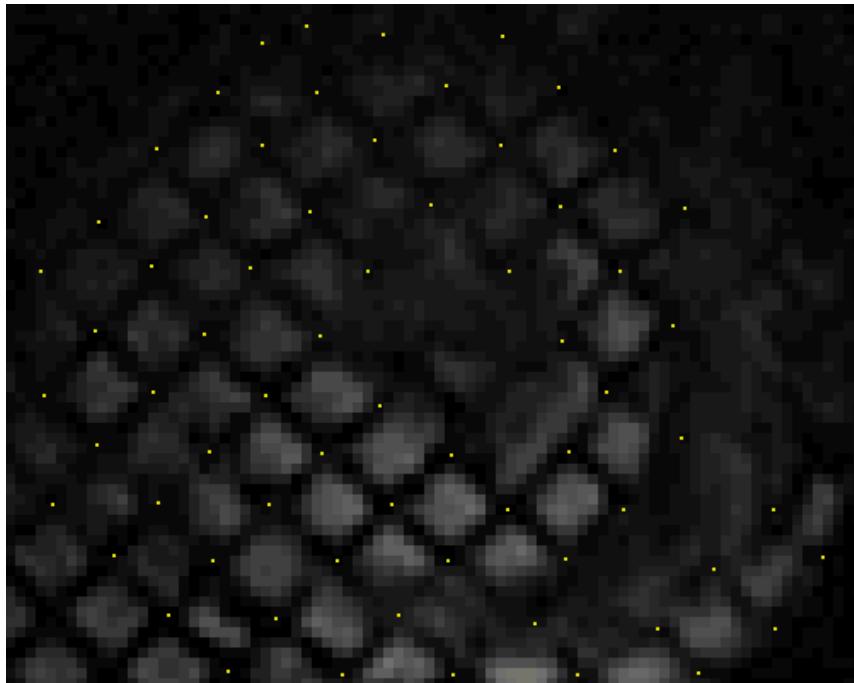
processes is particle tracking. Here, a ‘particle’ may be anything from a single molecule to a macromolecular complex, organelle, virus or microsphere¹², and the task of detecting and following individual particles in a time series of images is often (somewhat confusingly) referred to as ‘single-particle tracking’. As the number of particles may be very large (hundreds to thousands), requiring ‘multiple-particle tracking’¹³⁻¹⁵, manual annotation of the image data is not feasible, and computer algorithms are needed to perform the task.

Tracking Heart Motion in MRI

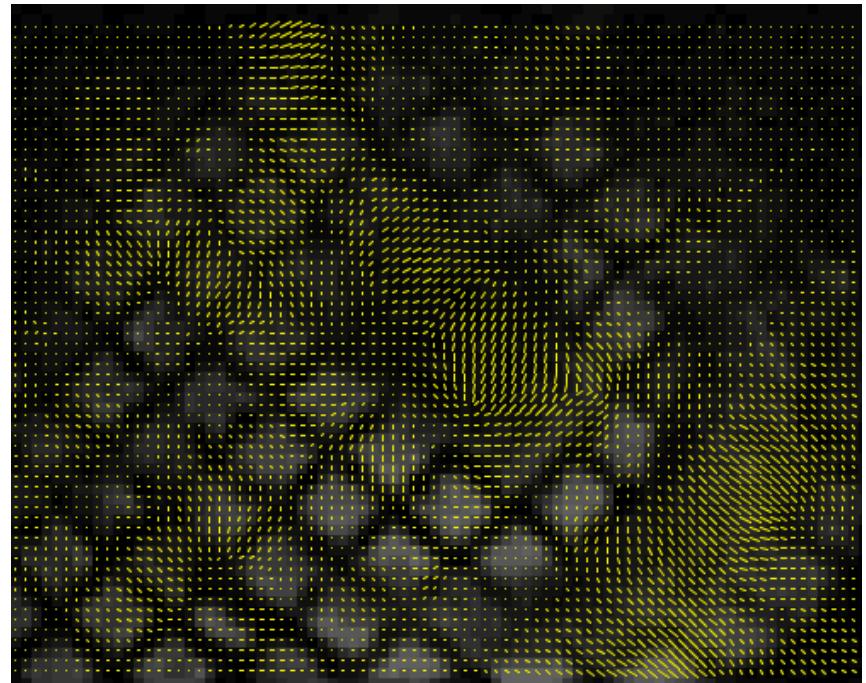


Tracking Heart Motion in MRI

Tracks

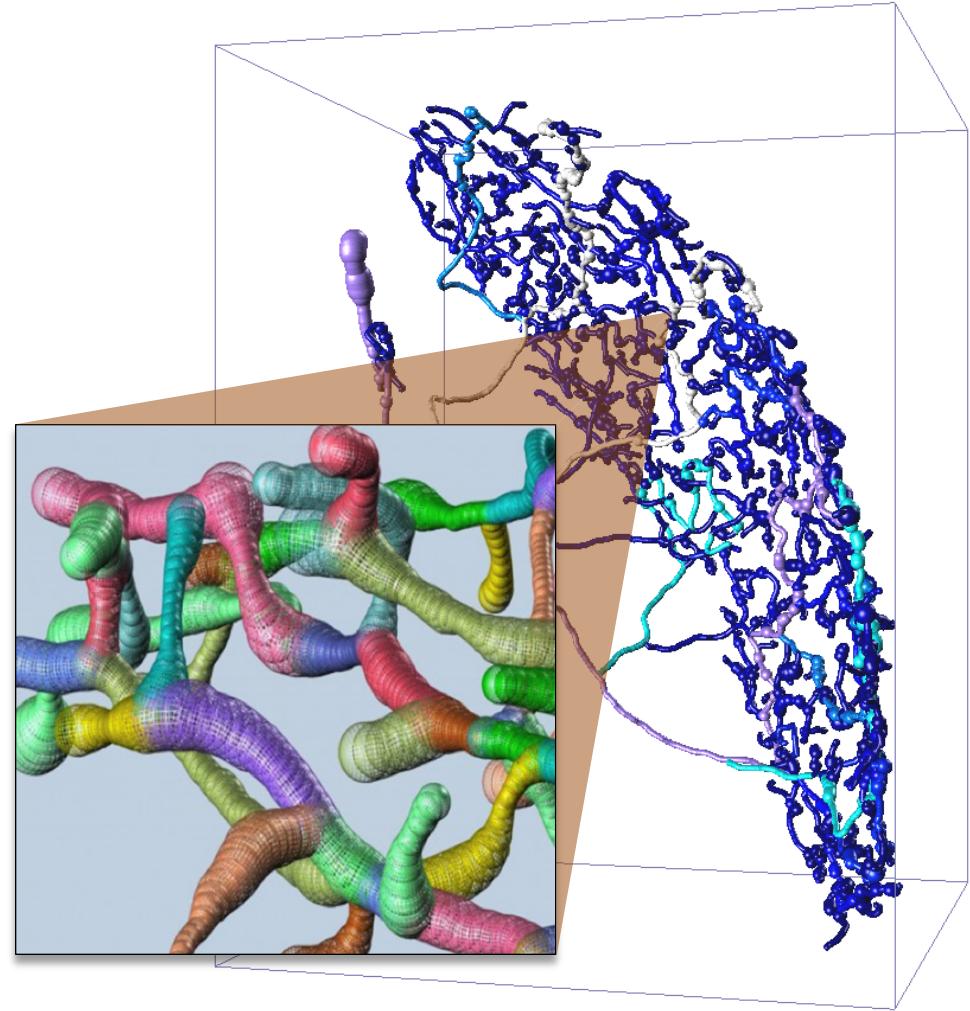
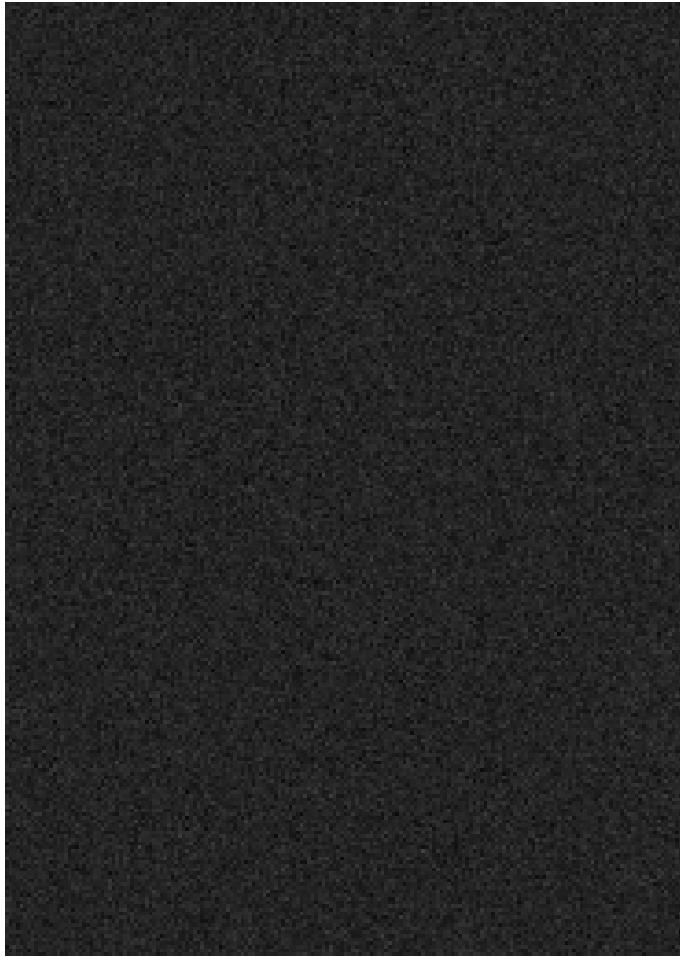


Strain

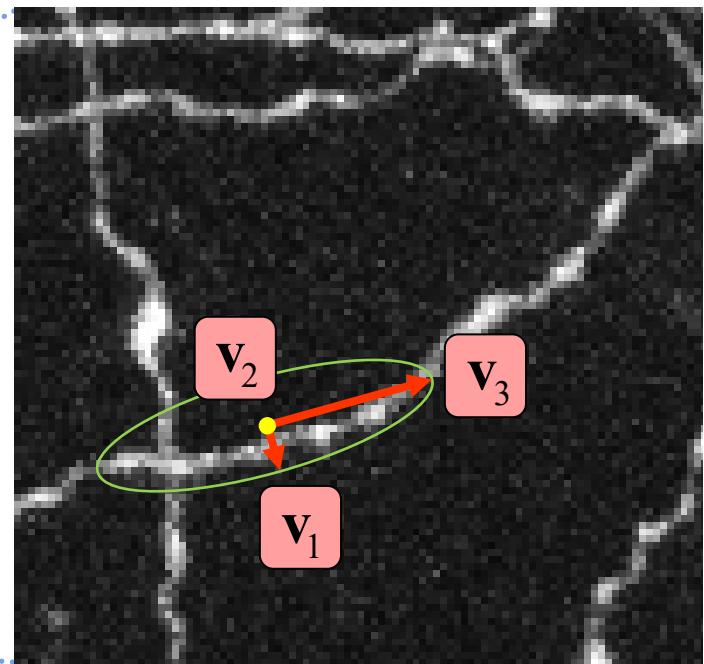
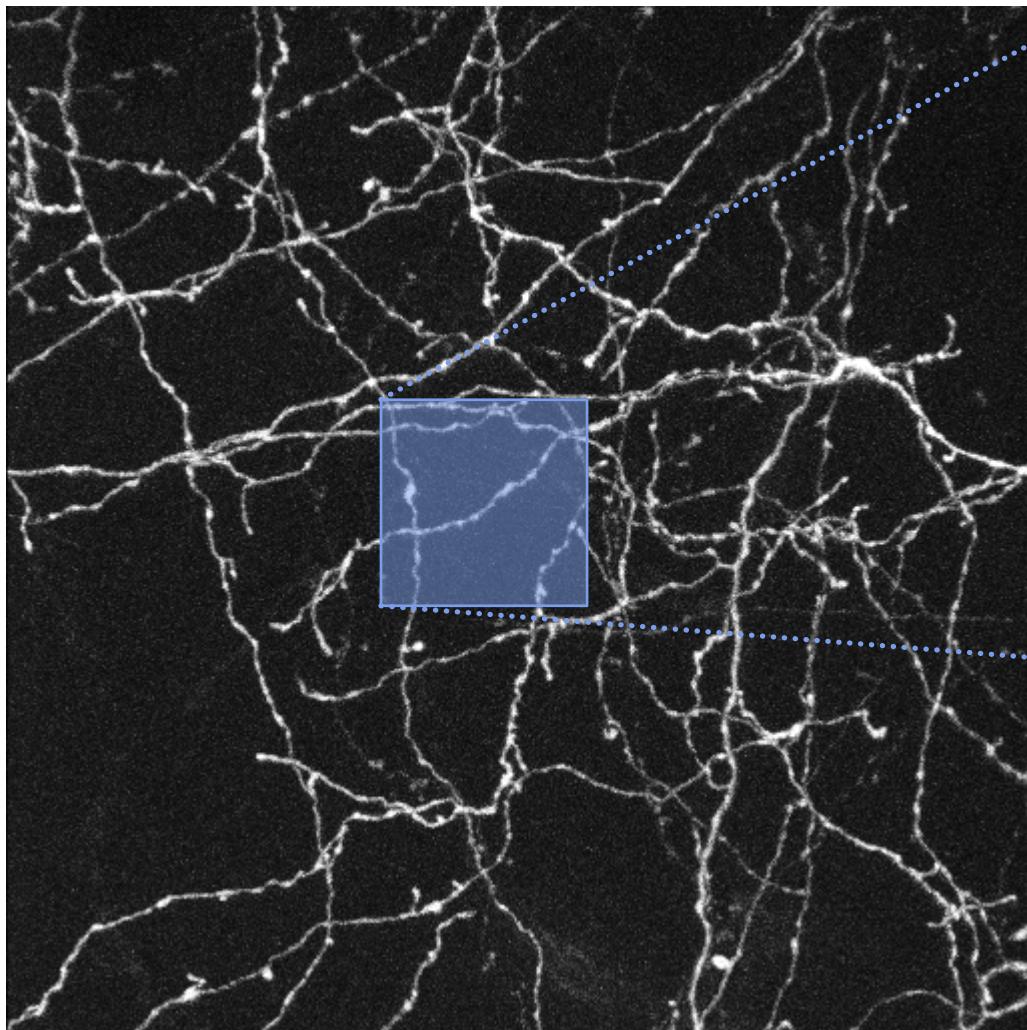


[Smal & Meijering, Medical Image Analysis, 2012](#)

Neuron Reconstruction



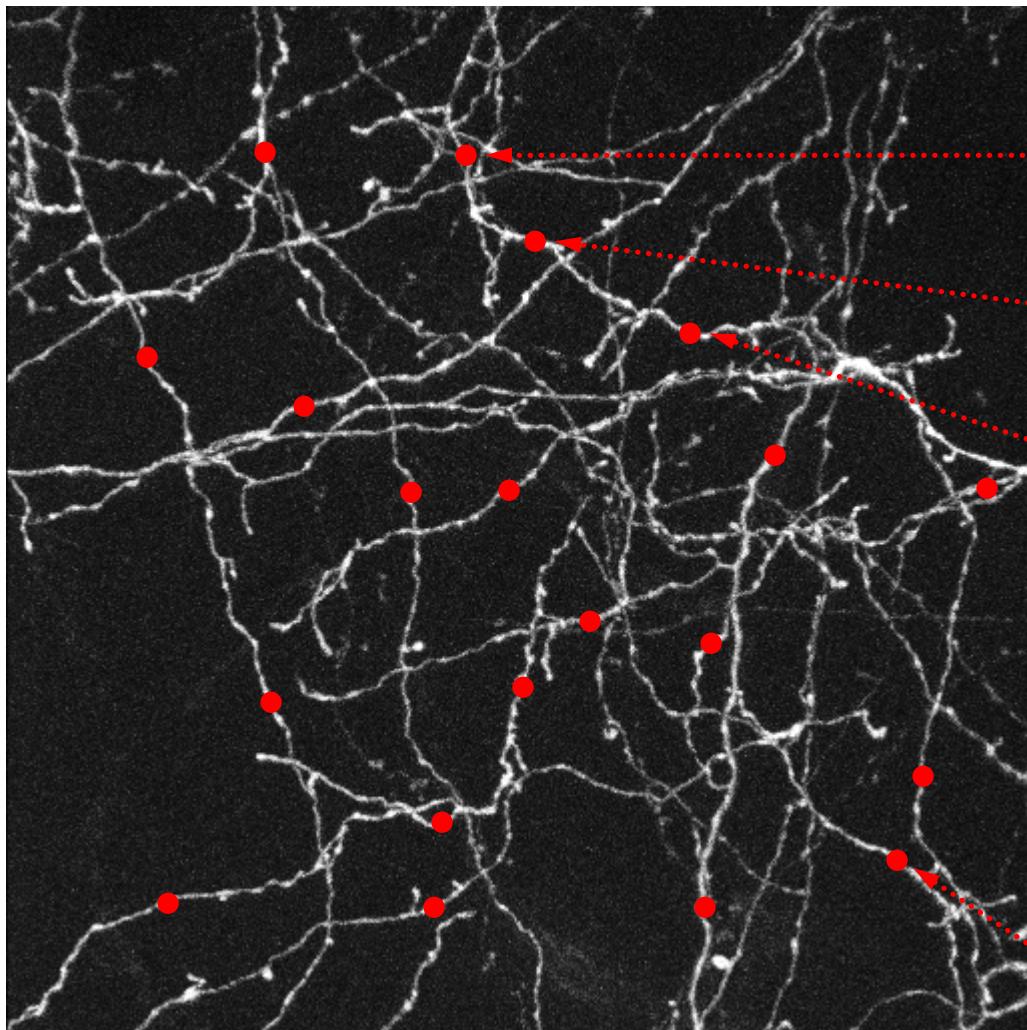
Neuron Reconstruction



$$\mathbf{H} = \begin{pmatrix} I_{xx} & I_{xy} & I_{xz} \\ I_{yx} & I_{yy} & I_{yz} \\ I_{zx} & I_{zy} & I_{zz} \end{pmatrix} = \mathbf{V}^T \cdot \boldsymbol{\Lambda} \cdot \mathbf{V}$$

Seed points: $\lambda_3 \ll \lambda_2 \approx \lambda_1$

Neuron Reconstruction



Target states

$$\mathbf{x}_{1;k} = (x_{1;k}, y_{1;k}, z_{1;k}, v_{1;k}^x, v_{1;k}^y, v_{1;k}^z)$$

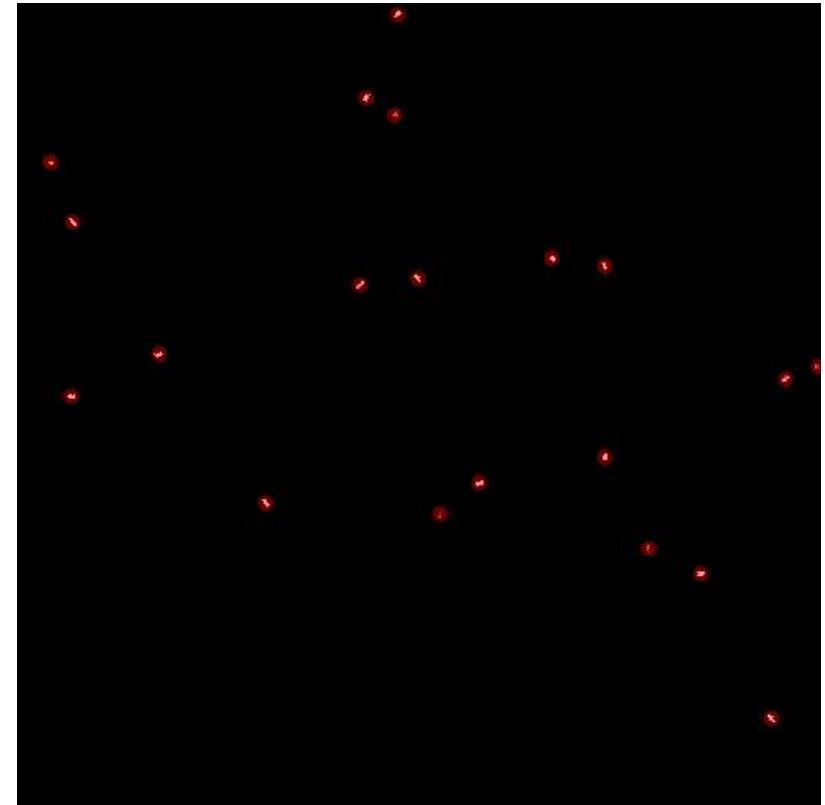
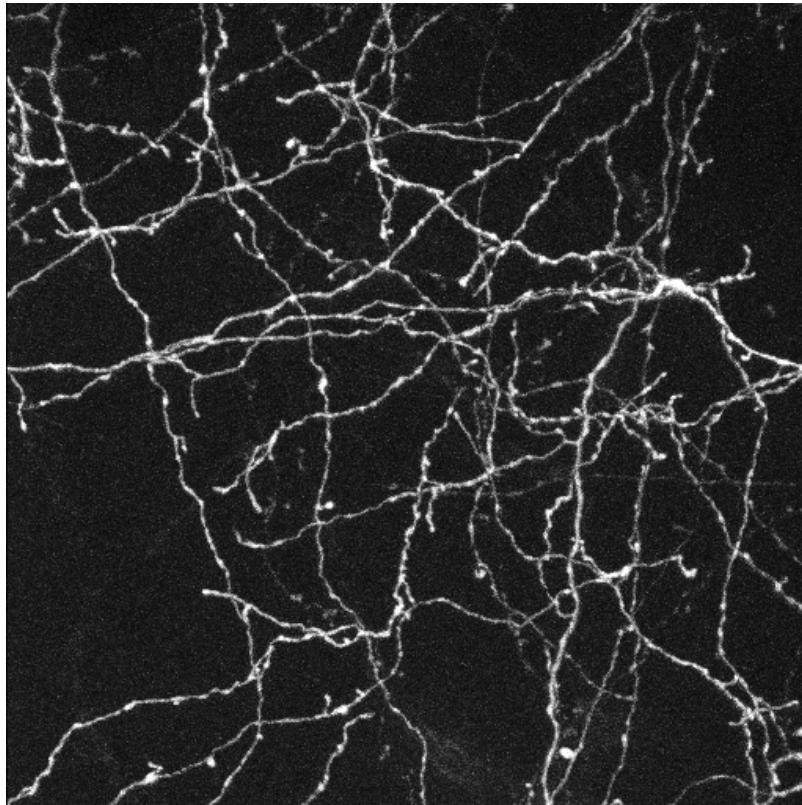
$$\mathbf{x}_{2;k} = (x_{2;k}, y_{2;k}, z_{2;k}, v_{2;k}^x, v_{2;k}^y, v_{2;k}^z)$$

$$\mathbf{x}_{3;k} = (x_{3;k}, y_{3;k}, z_{3;k}, v_{3;k}^x, v_{3;k}^y, v_{3;k}^z)$$

⋮

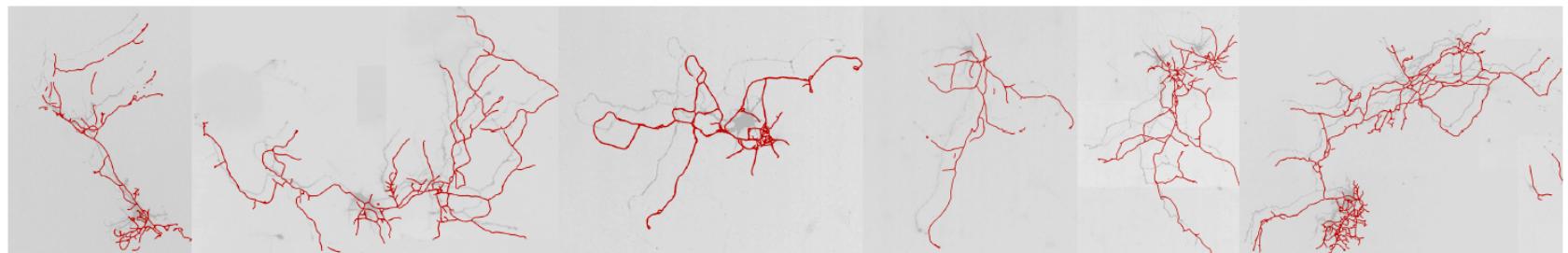
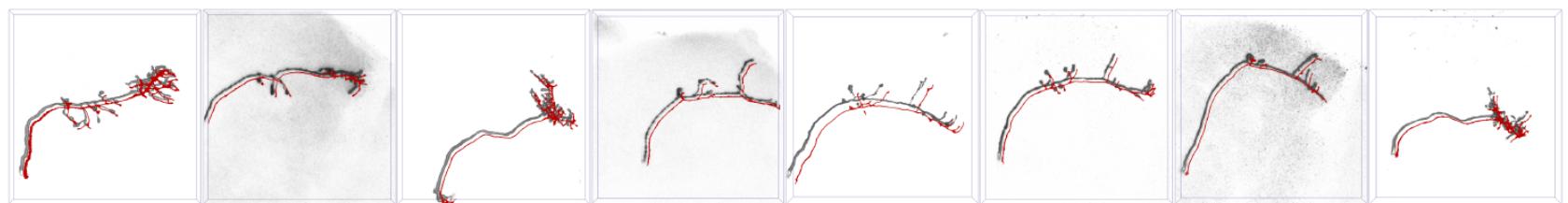
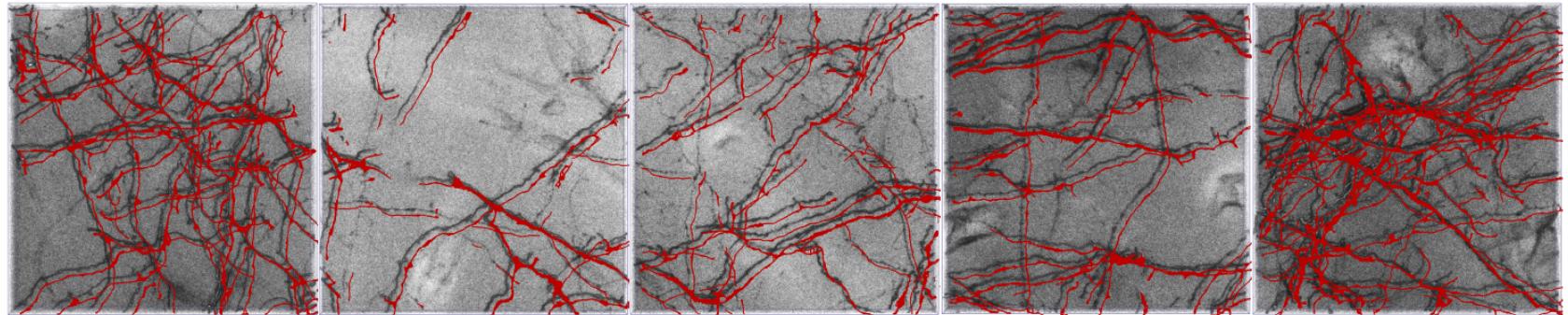
$$\mathbf{x}_{N;k} = (x_{N;k}, y_{N;k}, z_{N;k}, v_{N;k}^x, v_{N;k}^y, v_{N;k}^z)$$

Tracking for Neuron Reconstruction



[Radojevic & Meijering, Neuroinformatics, 2019](#)

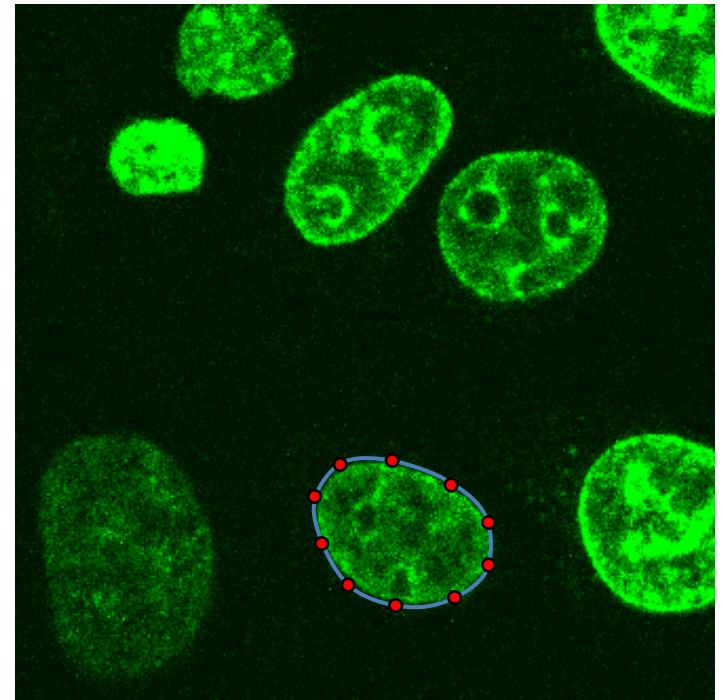
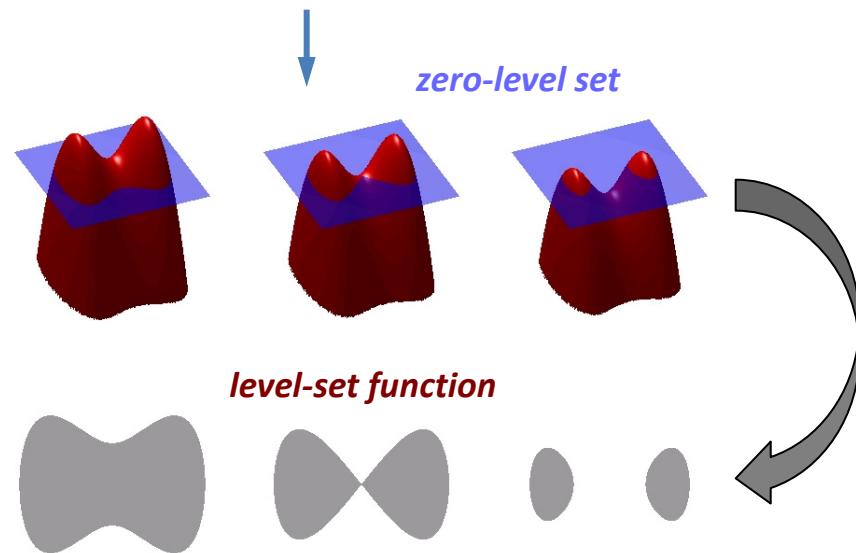
Neuron Reconstruction Results



Cell Tracking

Popular segmentation methods

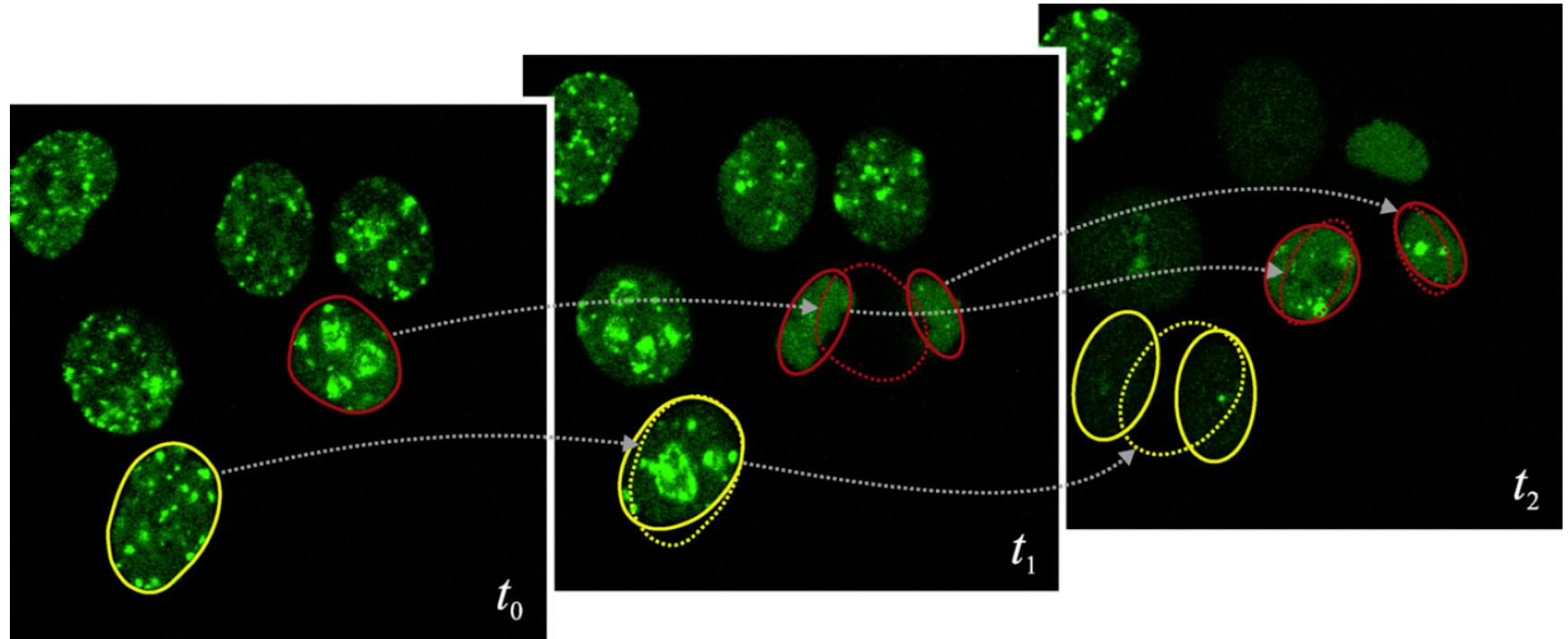
- Intensity thresholding
- Watershed segmentation
- Active contour fitting
- Level-set segmentation



$$\text{Model: } C(r) = \sum_n \mathbf{P}_n B(r - n)$$
$$\text{Fitting: } \hat{C} = \arg \min E(C)$$

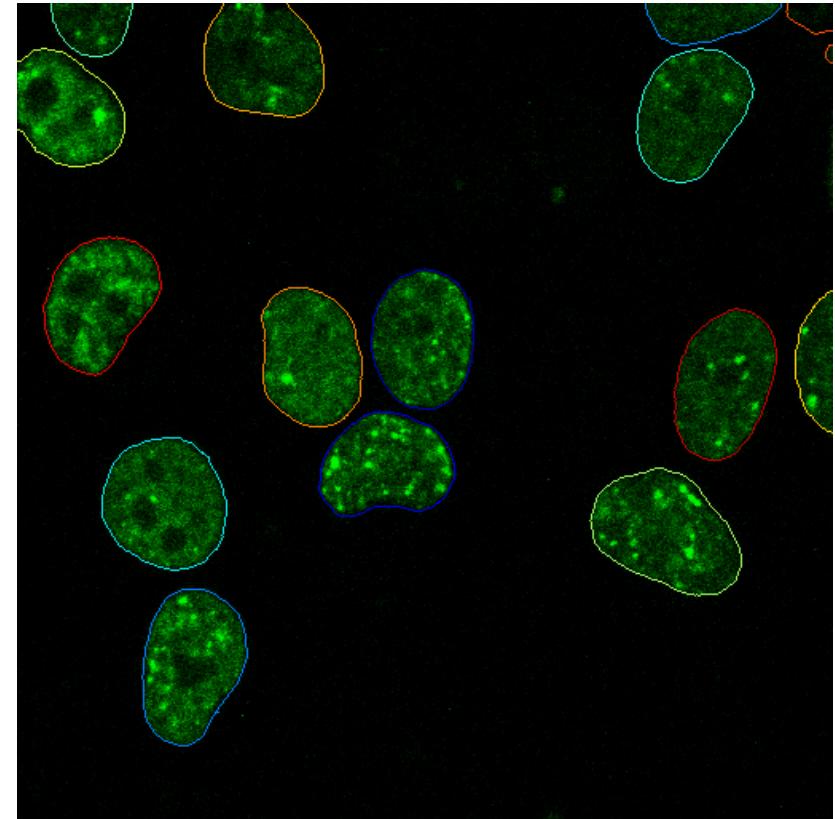
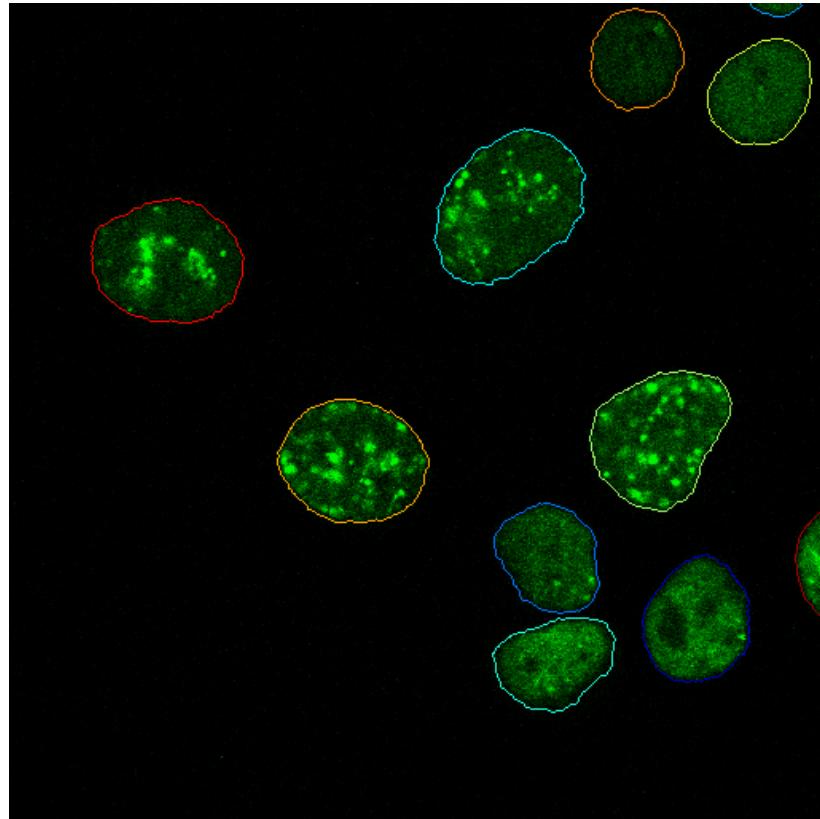
Cell Tracking

Linking by contour model evolution



[Dzyubachyk & Meijering, IEEE Transactions on Medical Imaging, 2010](#)

Cell Tracking



Coloured contours indicate the results of cell segmentation and identification

[Ulman et al., Nature Methods, 2017](#)

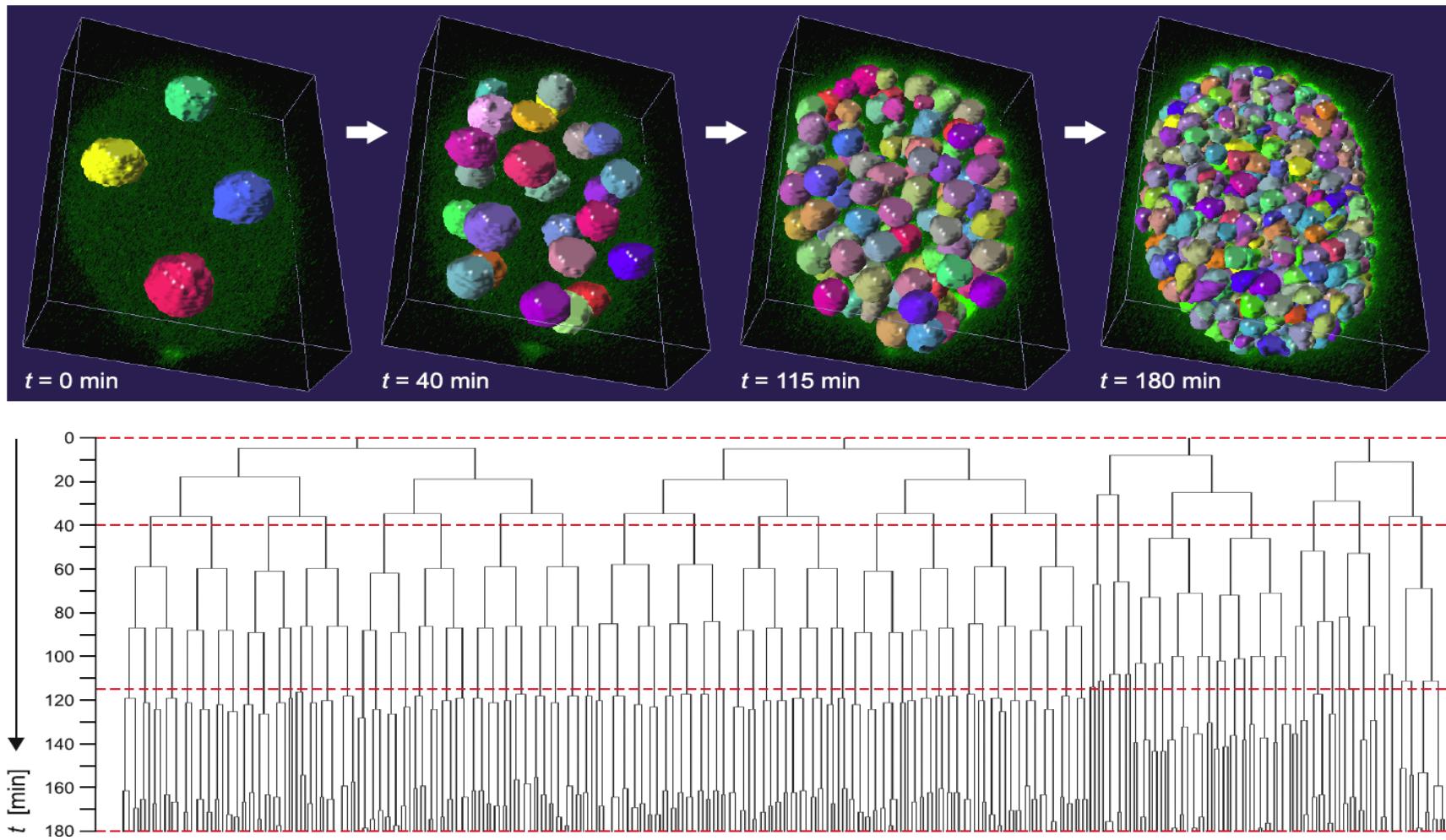
An objective comparison of cell-tracking algorithms

Vladimír Ulman^{1,24,25} , Martin Maška^{1,25}, Klas E G Magnusson², Olaf Ronneberger^{3,24}, Carsten Haubold⁴, Nathalie Harder^{5,24} , Pavel Matula¹, Petr Matula¹, David Svoboda¹ , Miroslav Radojevic⁶, Ihor Smal⁶, Karl Rohr⁵, Joakim Jaldén², Helen M Blau⁷, Oleh Dzyubachyk⁸, Boudewijn Lelieveldt^{8,9}, Pengdong Xiao^{10,24} , Yuexiang Li^{11,24}, Siu-Yeung Cho¹², Alexandre C Dufour¹³ , Jean-Christophe Olivo-Marin¹³ , Constantino C Reyes-Aldasoro¹⁴, Jose A Solis-Lemus¹⁴, Robert Bensch³ , Thomas Brox³, Johannes Stegmaier¹⁵, Ralf Mikut¹⁵ , Steffen Wolf⁴, Fred A Hamprecht⁴, Tiago Esteves^{16,17} , Pedro Quelhas¹⁶, Ömer Demirel¹⁸, Lars Malmström¹⁸ , Florian Jug¹⁹, Pavel Tomancak¹⁹ , Erik Meijering⁶, Arrate Muñoz-Barrutia^{20,21} , Michal Kozubek¹ & Carlos Ortiz-de-Solorzano^{22,23} 

We present a combined report on the results of three editions of the Cell Tracking Challenge, an ongoing initiative aimed at promoting the development and objective evaluation of cell segmentation and tracking algorithms. With 21 participating algorithms and a data repository consisting of 13 data sets from various microscopy modalities, the challenge displays today's state-of-the-art methodology in the field. We analyzed the challenge results using performance measures

these processes. Imaging techniques, such as phase contrast (PhC) or differential interference contrast (DIC) microscopy, make cells visible without the need of exogenous markers. Fluorescence microscopy, on the other hand, relies on fluorescent reporters to specifically label cell components such as nuclei, cytoplasm or membranes. These labeled structures are then imaged in two or three dimensions by various imaging modalities, including widefield, confocal, multiphoton or light-sheet fluorescence microscopy.

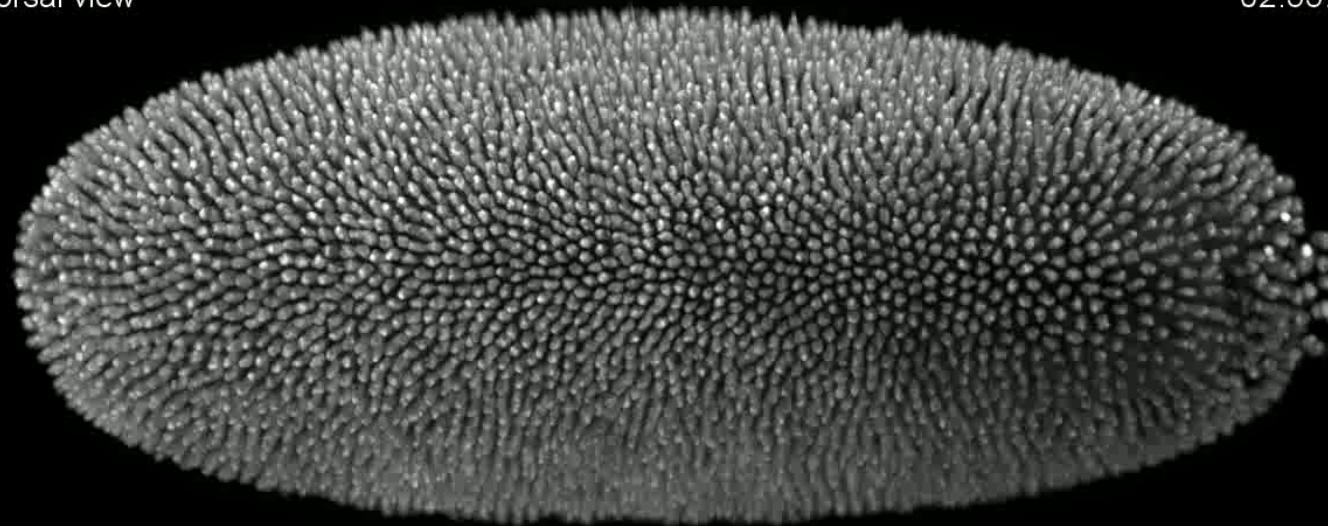
Cell Lineage Reconstruction



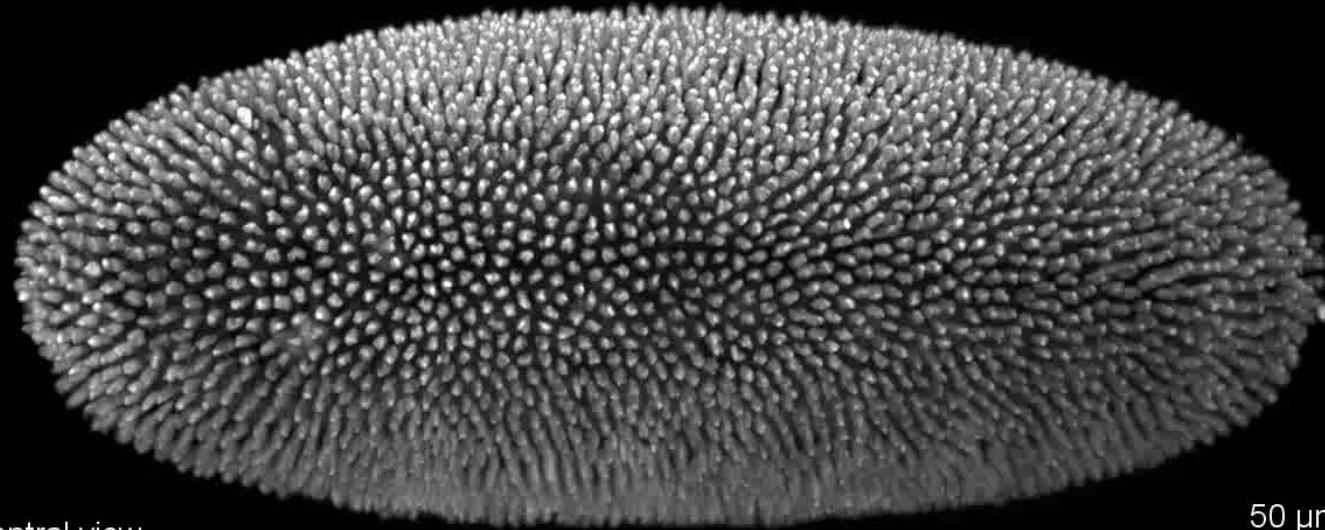
Drosophila embryogenesis

dorsal view

02:55:00



Keller et al. 2014

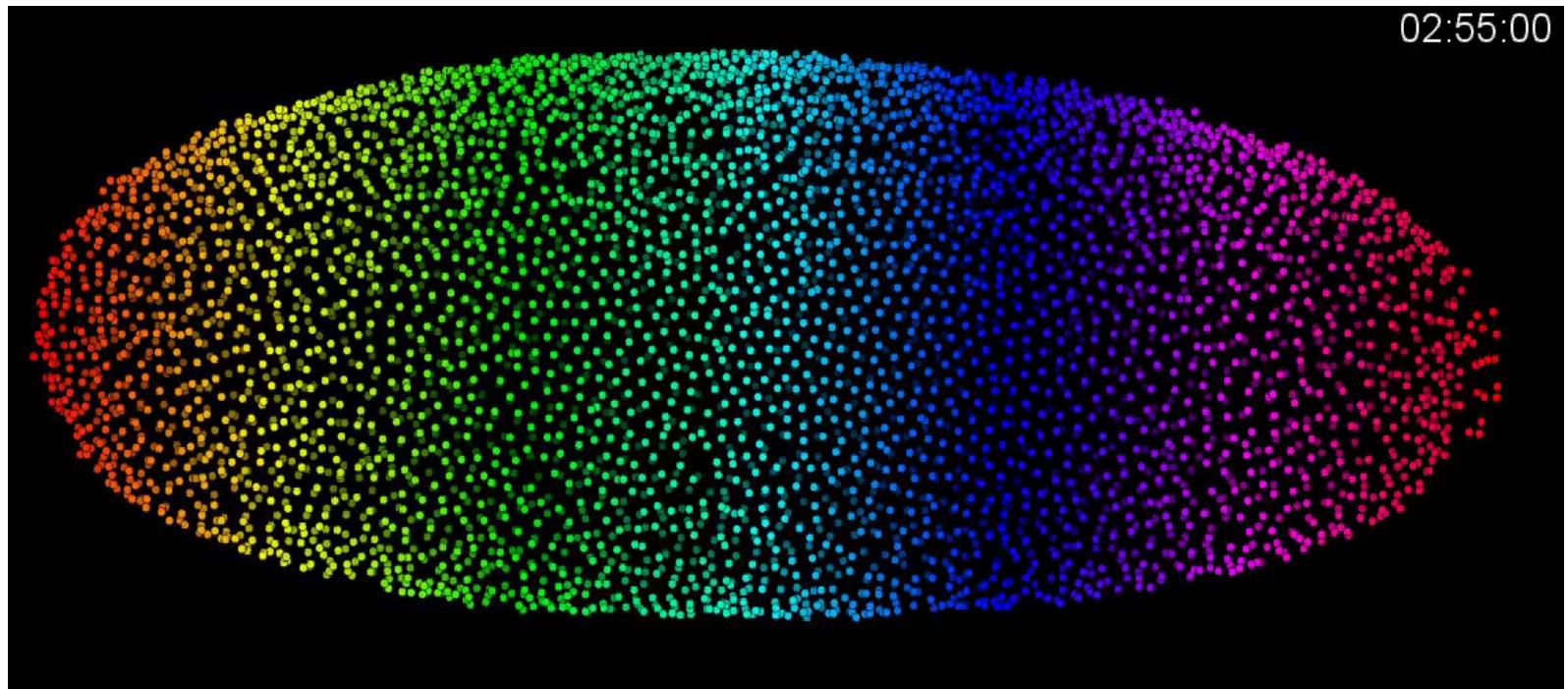


ventral view

50 μm

Cell Lineage Reconstruction

Tracking each cell during Drosophila embryonic development



[Keller et al., Nature Methods, 2014](#)

References and Acknowledgements

Further information on the presented applications can be found in the following papers:

- [Image Registration for Digital Subtraction Angiography](#)
- [Advanced Level-Set Based Cell Tracking in Time-Lapse Fluorescence Microscopy](#)
- [Multimodal Volume Registration by Maximization of Mutual Information](#)
- [Optical-Flow Based Non-Invasive Analysis of Cardiomyocyte Contractility](#)
- [Multiple Object Tracking in Molecular Bioimaging by RBM Particle Filtering](#)
- [Objective Comparison of Particle Tracking Methods](#)
- [Reversible Jump MCMC Methods for Fully Automatic Motion Analysis in Tagged MRI](#)
- [Automated Neuron Tracing Using Probability Hypothesis Density Filtering](#)
- [An Objective Comparison of Cell-Tracking Algorithms](#)
- [Methods for Cell and Particle Tracking](#)
- [Reconstruction of Cell Lineages From Large-Scale Fluorescence Microscopy Data](#)
- [A Tutorial on Particle Filters for Online Nonlinear/Non-Gaussian Bayesian Tracking](#)