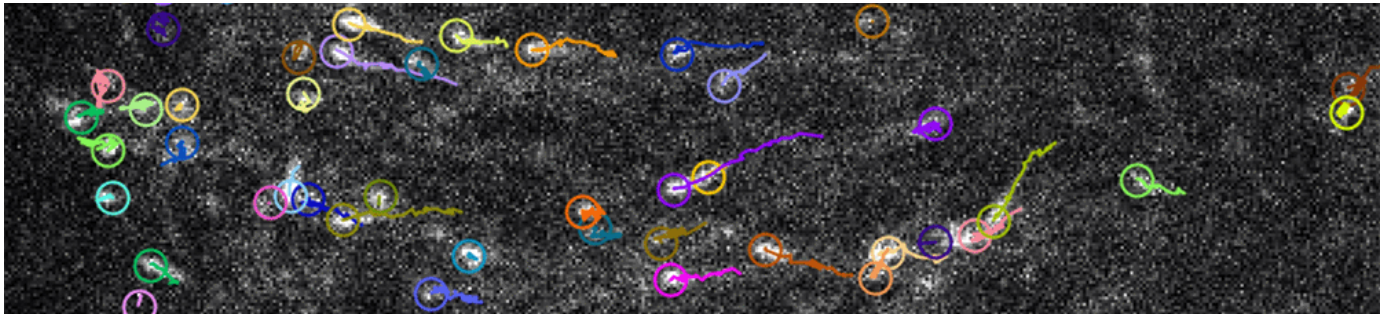


COMP9517: Computer Vision

Motion Tracking Applications in Biomedical Computer Vision

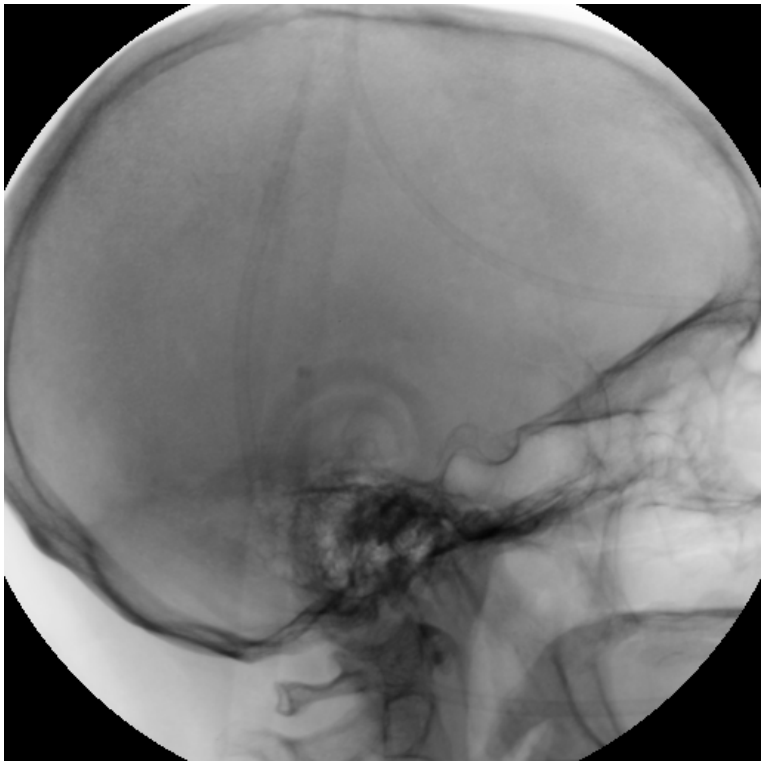
Topics

- 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

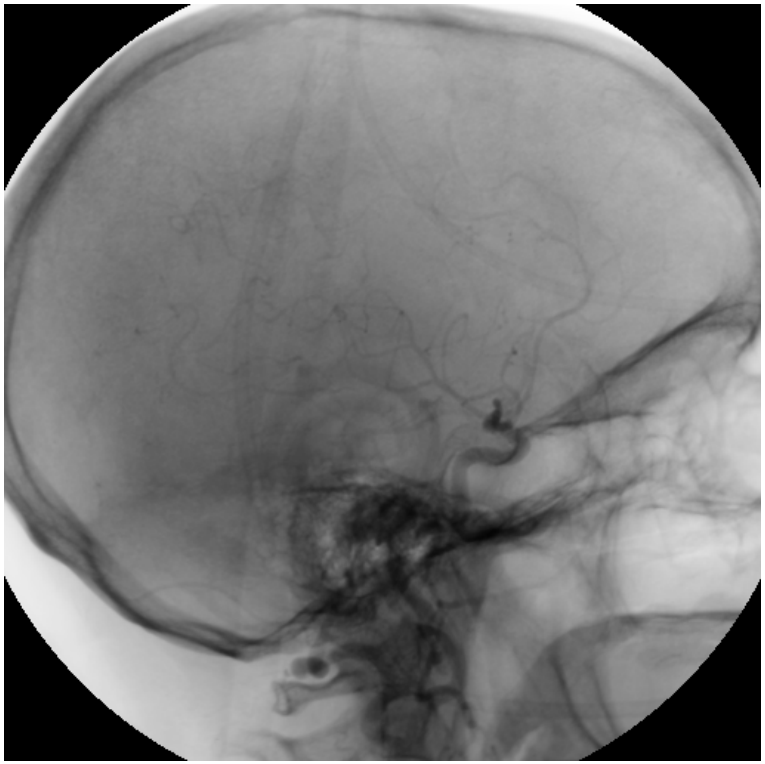
Digital Subtraction Angiography

X-ray at time t_0



Mask Image

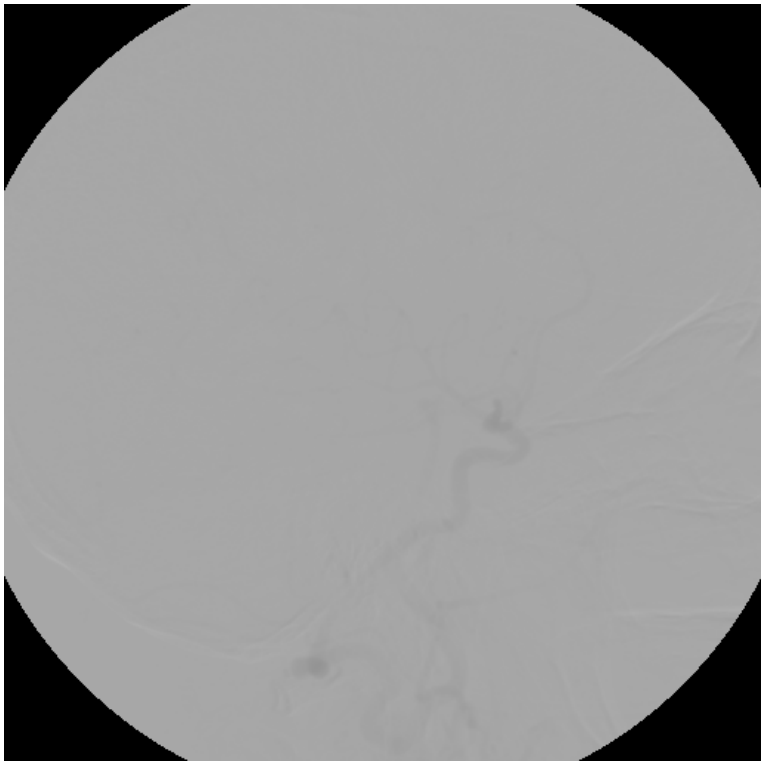
X-ray at time $t_0 + \Delta t$



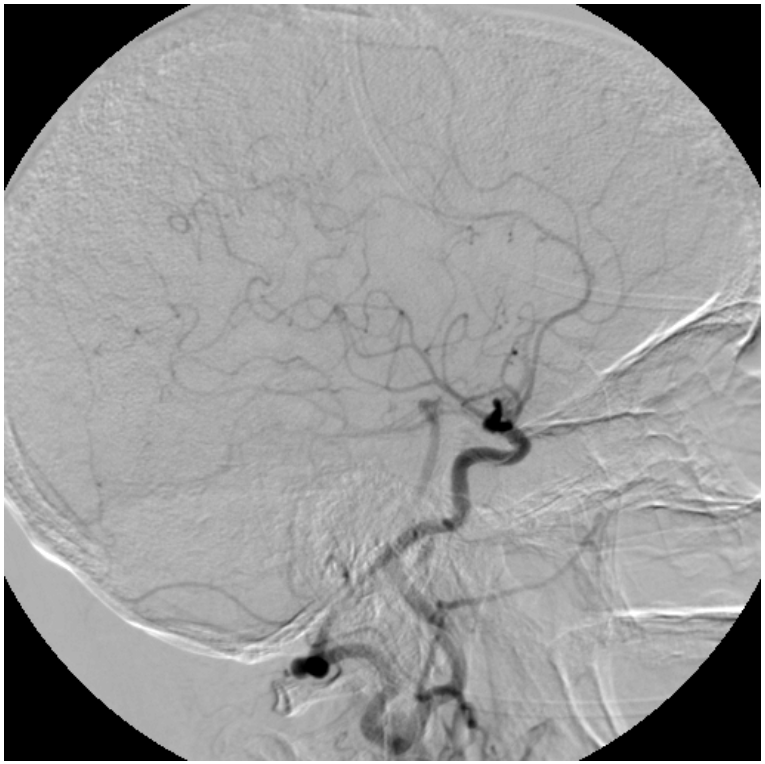
Live Image

Digital Subtraction Angiography

Live – Mask



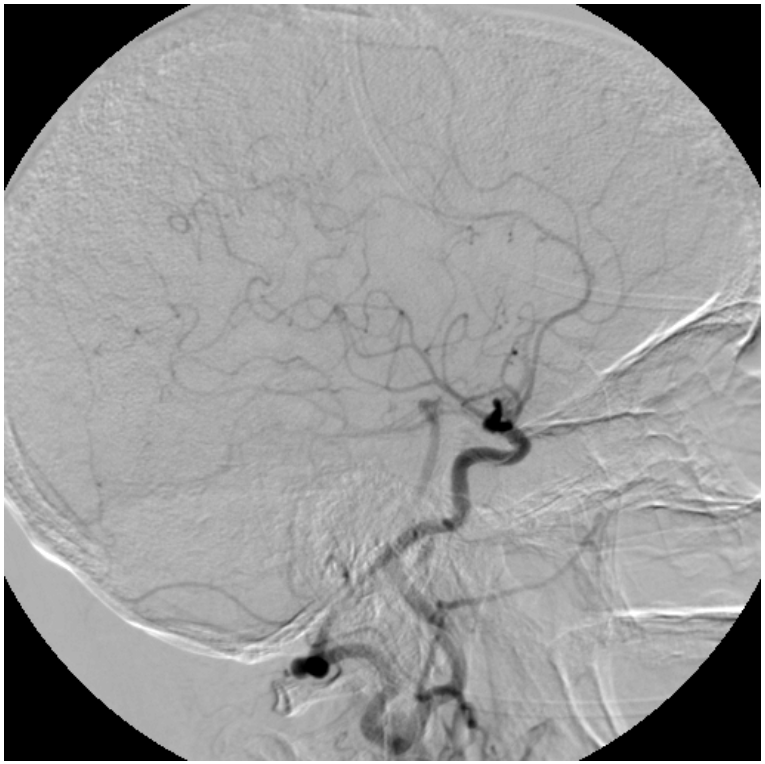
Contrast Stretched



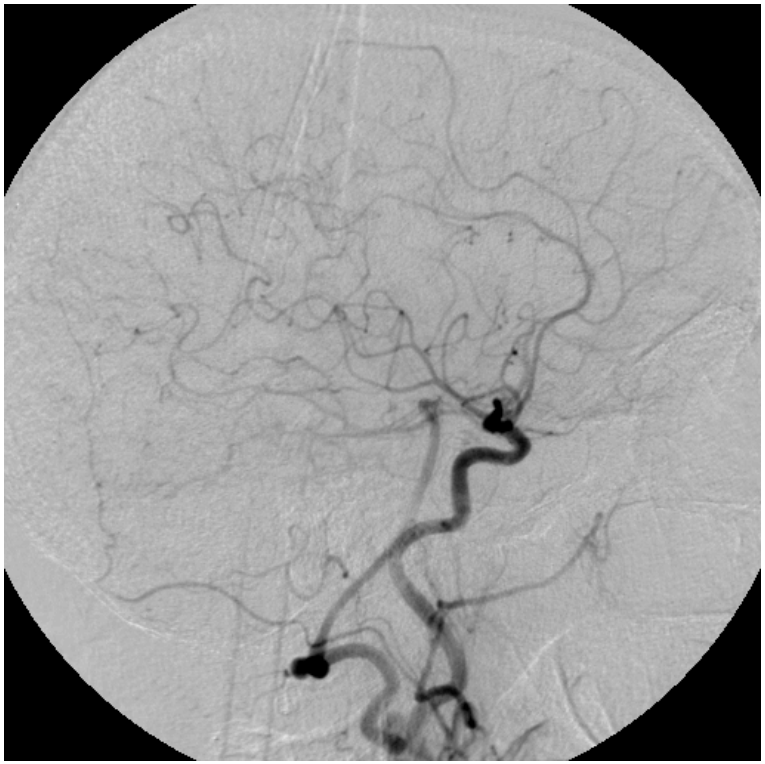
Meijering et al., *Radiology*, 2001

Digital Subtraction Angiography

Contrast Stretched



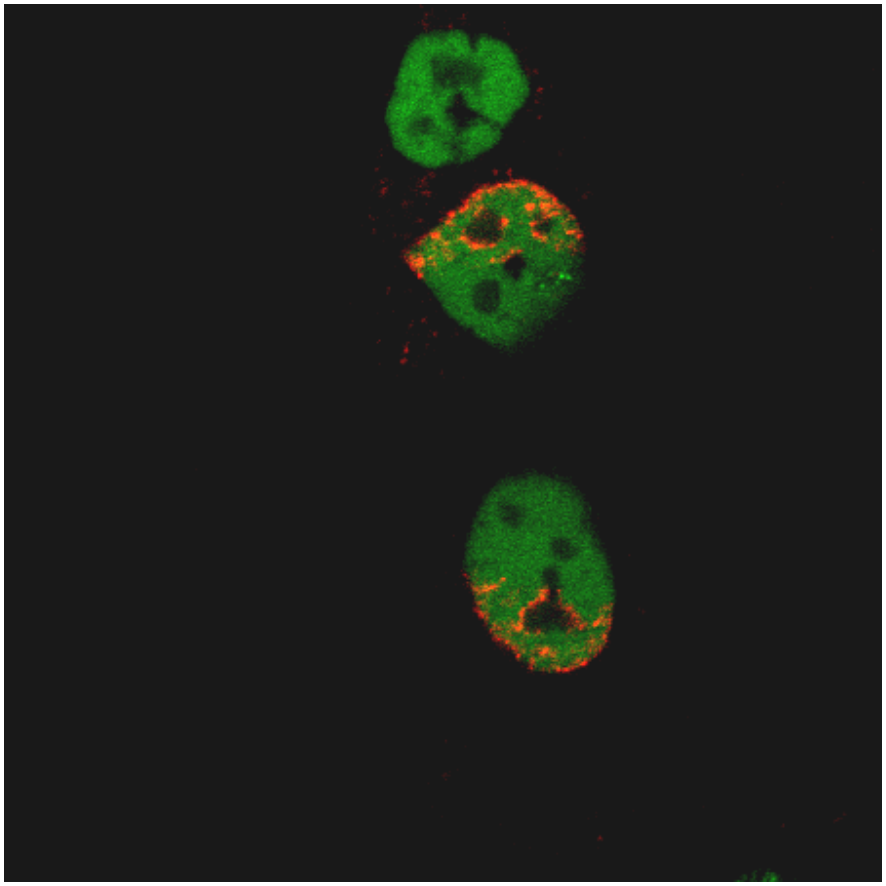
Motion Corrected

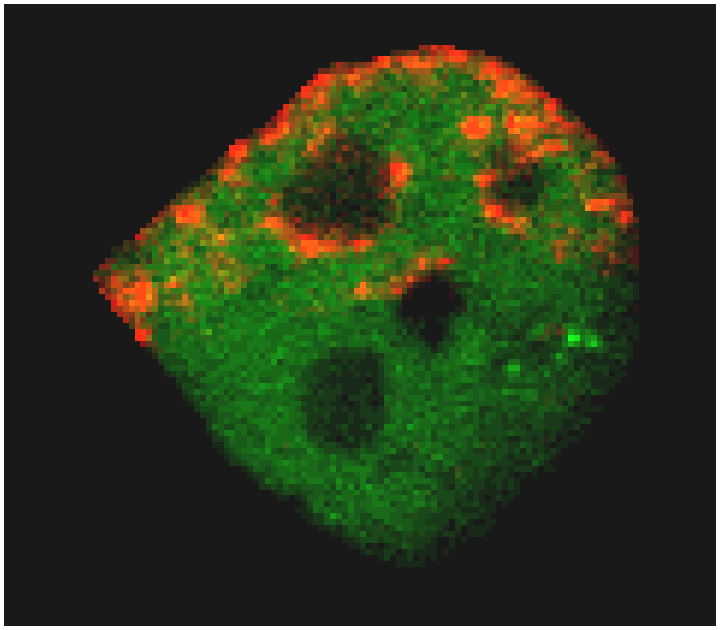


Automatic motion correction here is a form of template matching

Examples of Template Matching

Cell Motion Correction

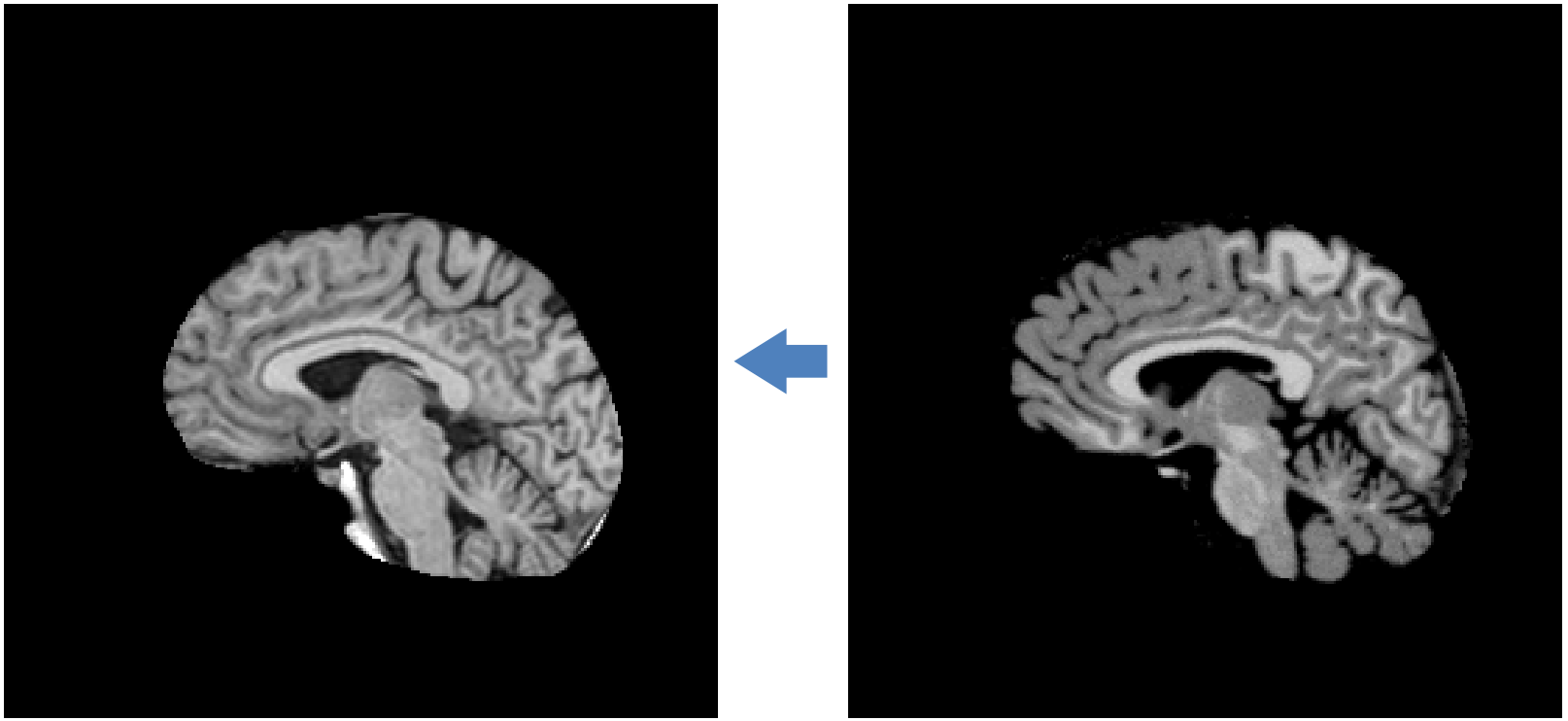




Cell fixation by image post-processing allows analysis of the internal changes over time

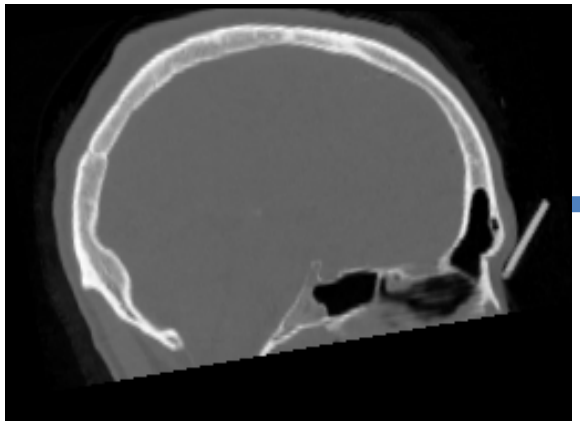
Brain Image Registration

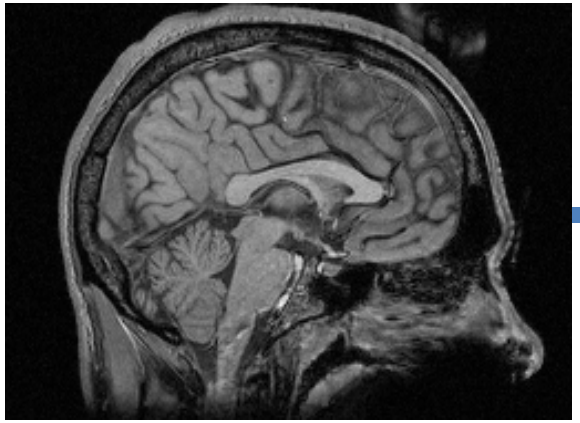
To understand how the human brain develops from childhood to adulthood and to study developmental disorders we can use magnetic resonance imaging (MRI) at different ages and match the images to a template using automatic image registration techniques



Multimodal Image Registration

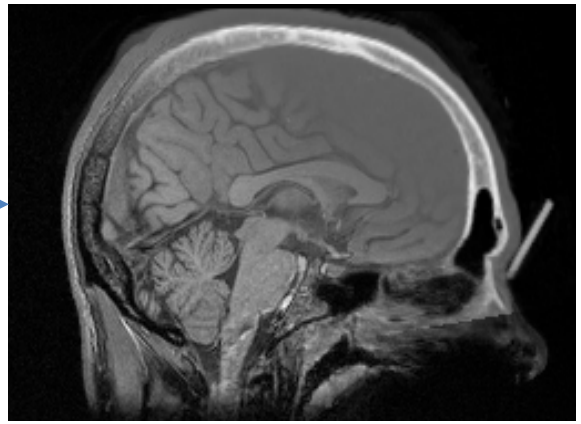
Computed Tomography (CT)





Magnetic Resonance (MR)

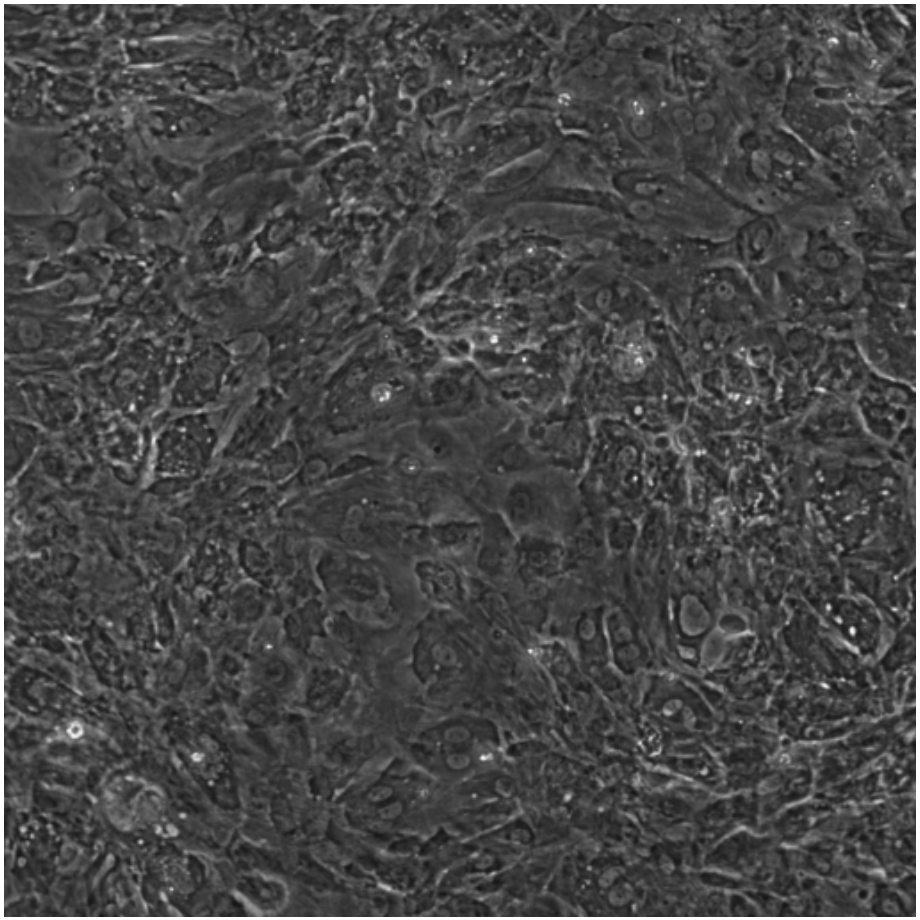
Joint Visualization



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

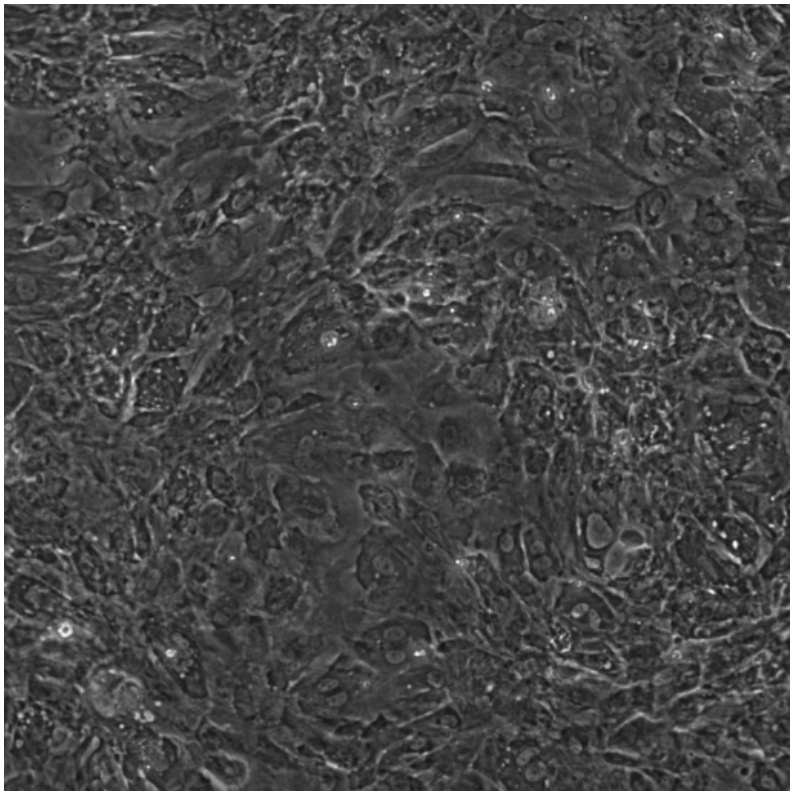


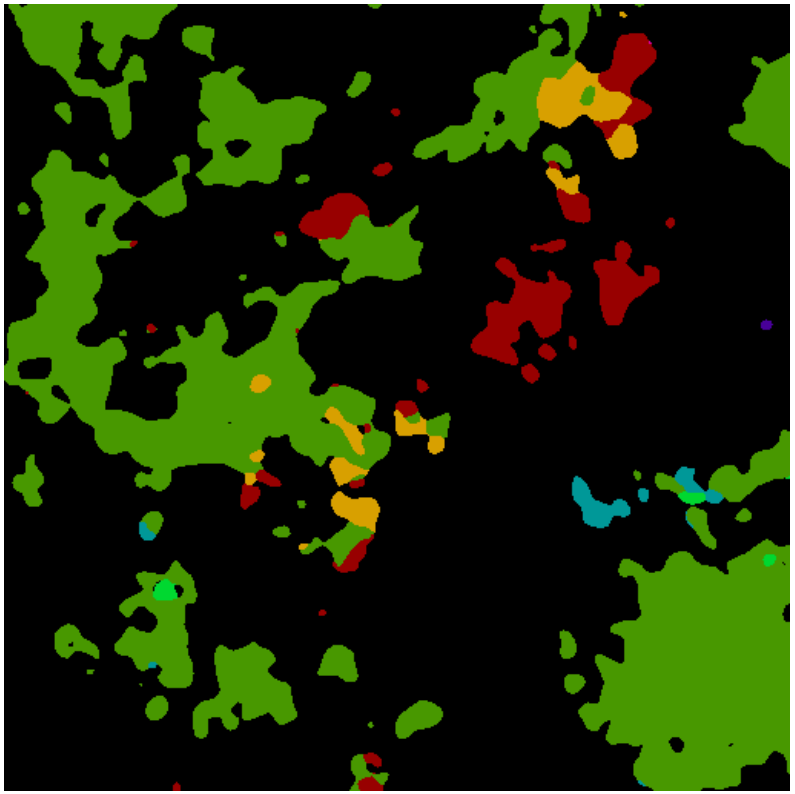
- Heart tissue cultured 6 days
- Mono-layer cardiomyocytes
- Phase-contrast microscopy
- Real-time imaging 24 fps

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

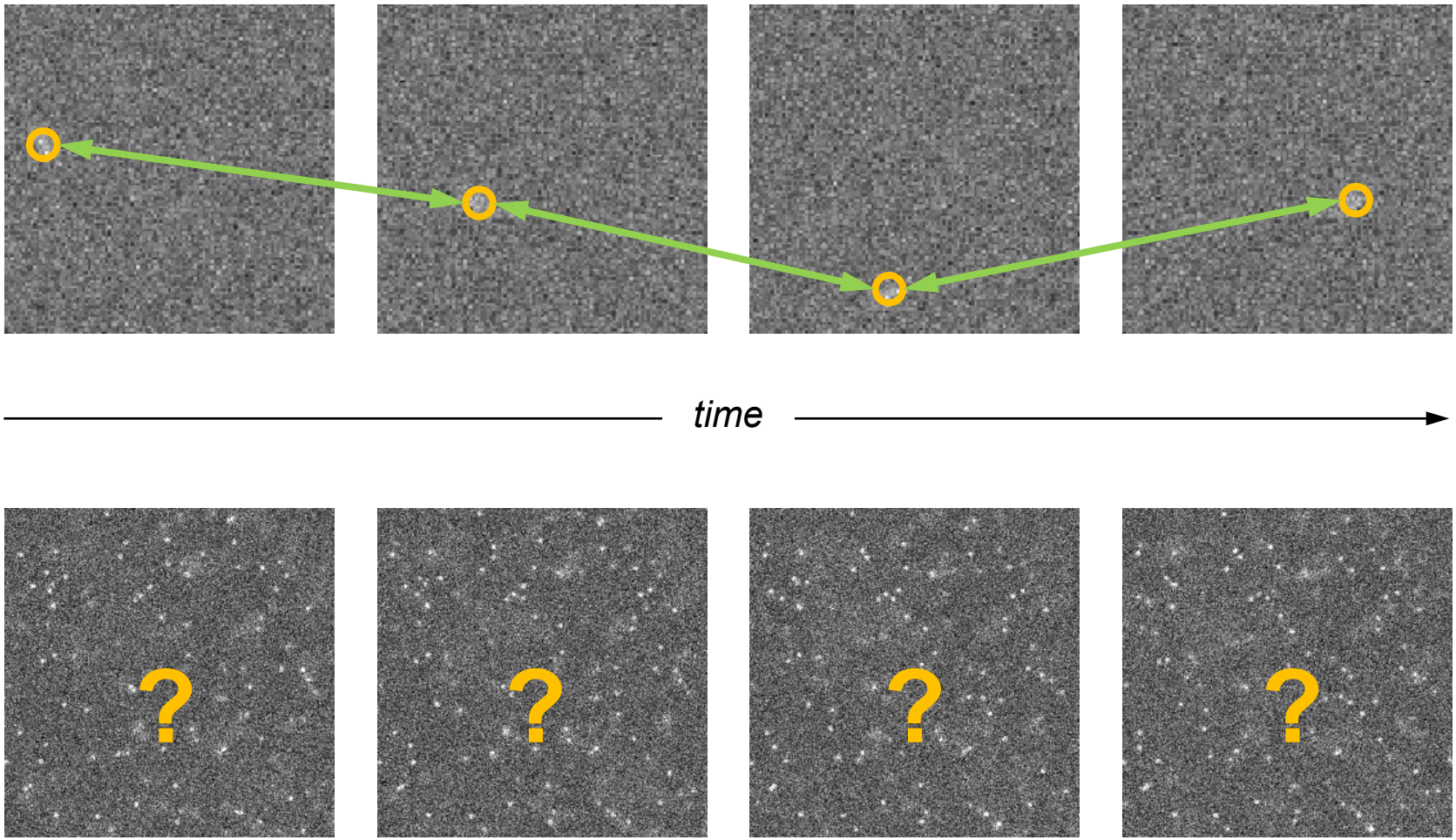




Motion vectors visualised by direction (color) and magnitude (intensity)

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

Position, velocity, acceleration, shape, intensity, …

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

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

Prior, Transition Model, Posterior

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

Posterior, Observation Model, Prior

Bayesian Multitarget Tracking

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

$$X_t = (X_{1;t}, X_{2;t}, \ldots, X_{N;t})$$

$$X_{1;t} = (r_{1;t}, v_{1;t}, a_{1;t}, s_{1;t}, I_{1;t}, \ldots) \qquad X_{N;t} = (r_{N;t}, v_{N;t}, a_{N;t}, s_{N;t}, I_{N;t}, \ldots)$$

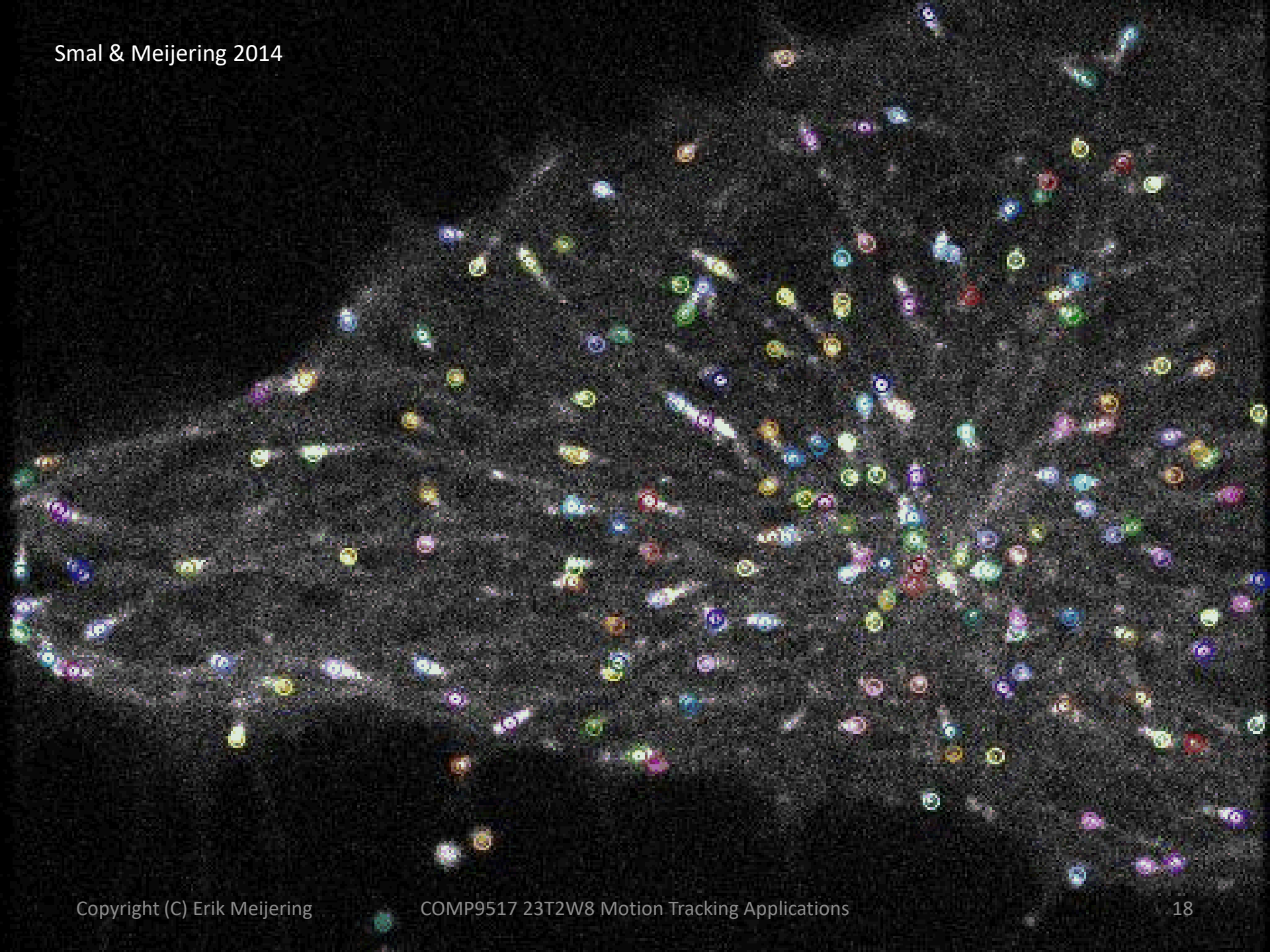
Computational cost grows exponentially with the number of targets

- Use a mixture model of single-target probability densities

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

Requires heuristics to keep track of number of targets and identities

Smal & Meijering 2014



NATURE METHODS | VOL.11 NO.3 | MARCH 2014 | 281-289

ANALYSIS

OPEN

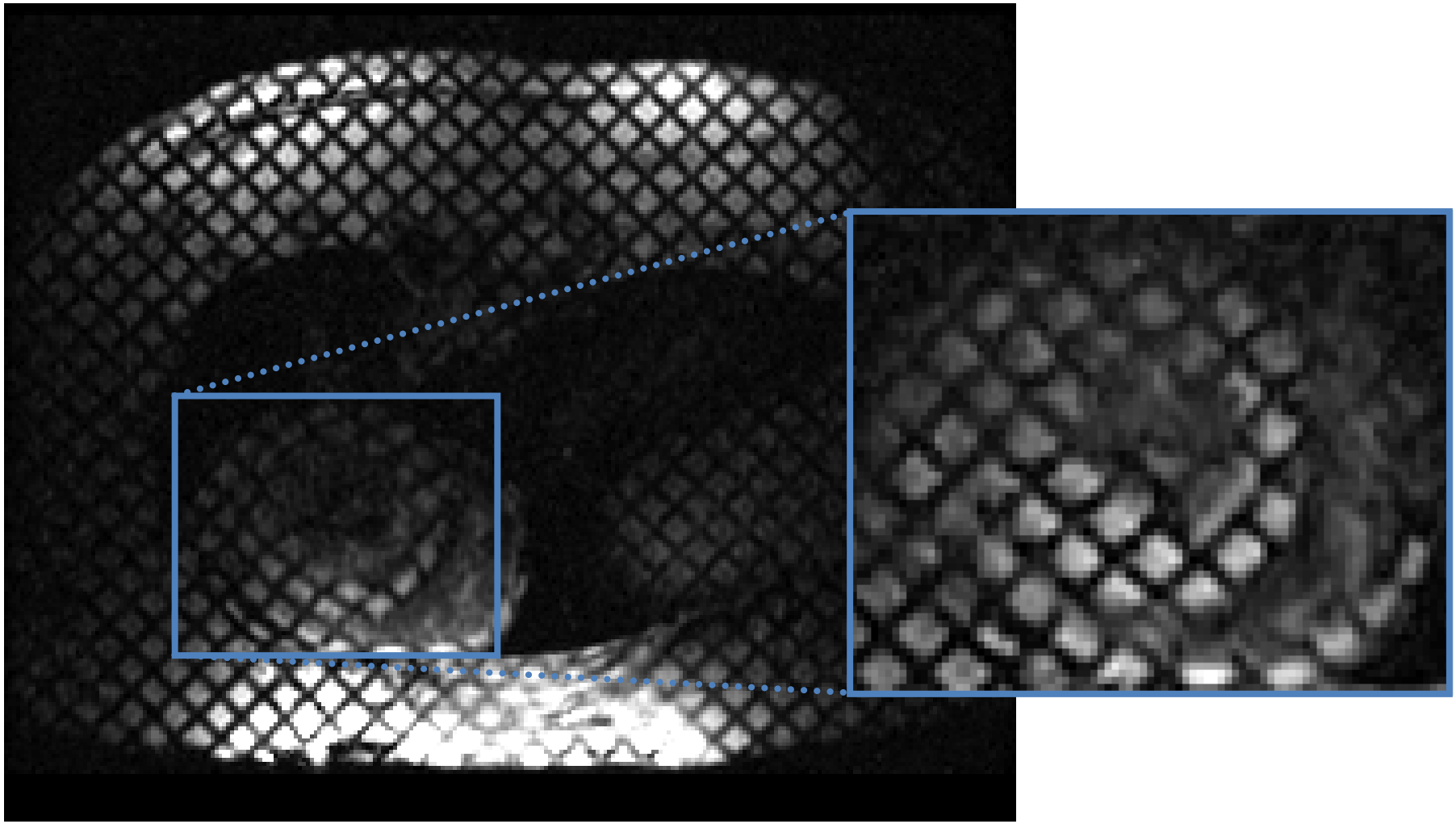
Objective comparison of particle tracking methods

Nicolas Chenouard[1–3,25], Ihor Smal[4,5,25], Fabrice de Chaumont[1,25], Martin Maška[6,7,25], Ivo F Sbalzarini[8], Yuanhao Gong[8], Janick Cardinale[8], Craig Carthel[9], Stefano Coraluppi[9], Mark Winter[10], Andrew R Cohen[10], William J Godinez[11,12], Karl Rohr[11,12], Yannis Kalaidzidis[13,14], Liang Liang[15], James Duncan[15], Hongying Shen[16], Yingke Xu[17], Klas E G Magnusson[18], Joakim Jaldén[18], Helen M Blau[19], Perrine Paul-Gilloteaux[20], Philippe Roudot[21], Charles Kervrann[21], François Waharte[20], Jean-Yves Tinevez[22], Spencer L Shorte[22], Joost Willemse[23], Katherine Celler[23], Gilles P van Wezel[23], Han-Wei Dan[24], Yuh-Show Tsai[24], Carlos Ortiz de Solórzano[6], 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

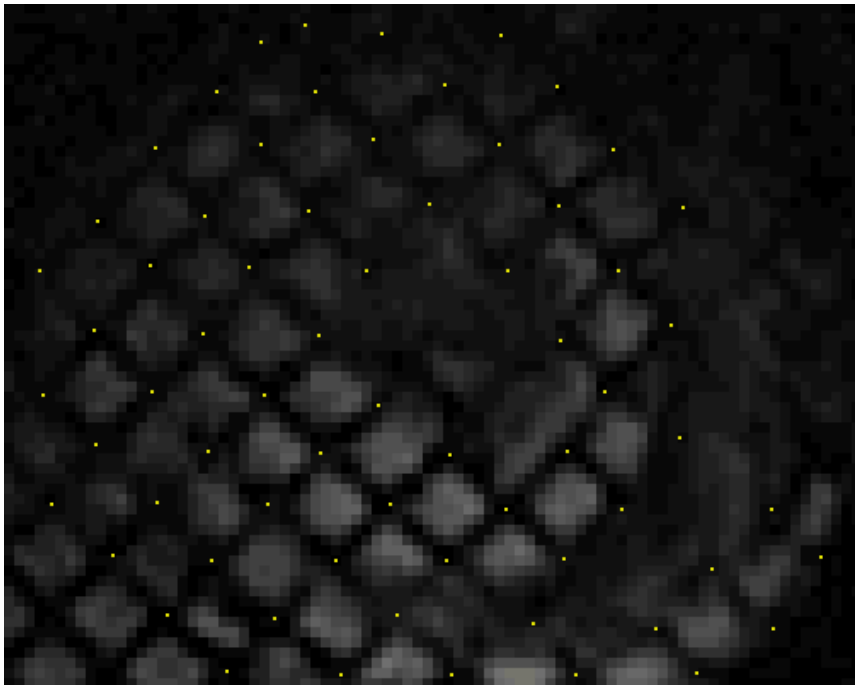
processes is particle tracking. Here, a 'particle' may be anything from a single molecule to a macromolecular complex, organelle, virus or microsphere[12], and the task of detecting and following individual particles in a time series of images is often (somewhat confusingly) referred to as 'single-particle 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

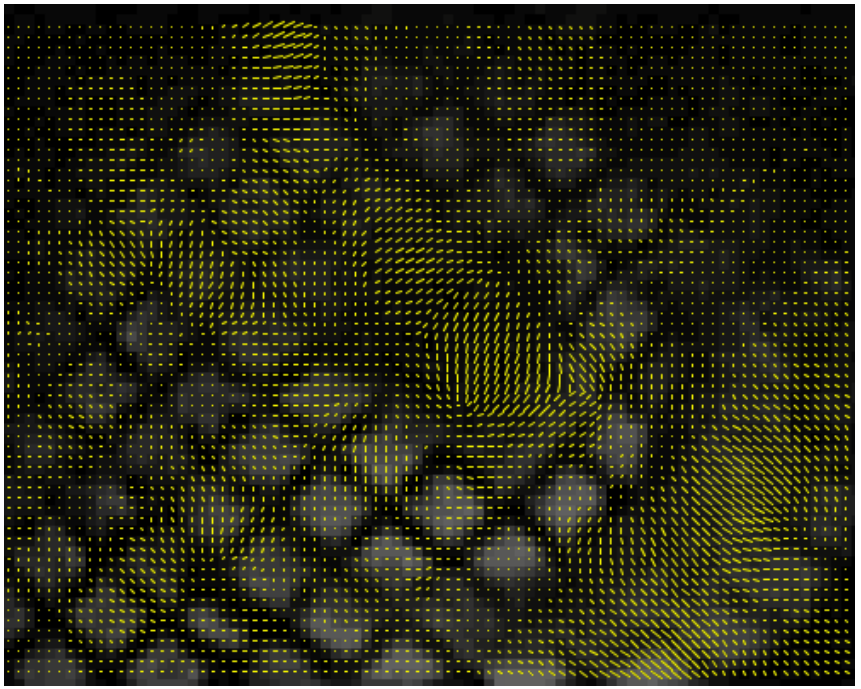


Tracking Heart Motion in MRI

Tracks

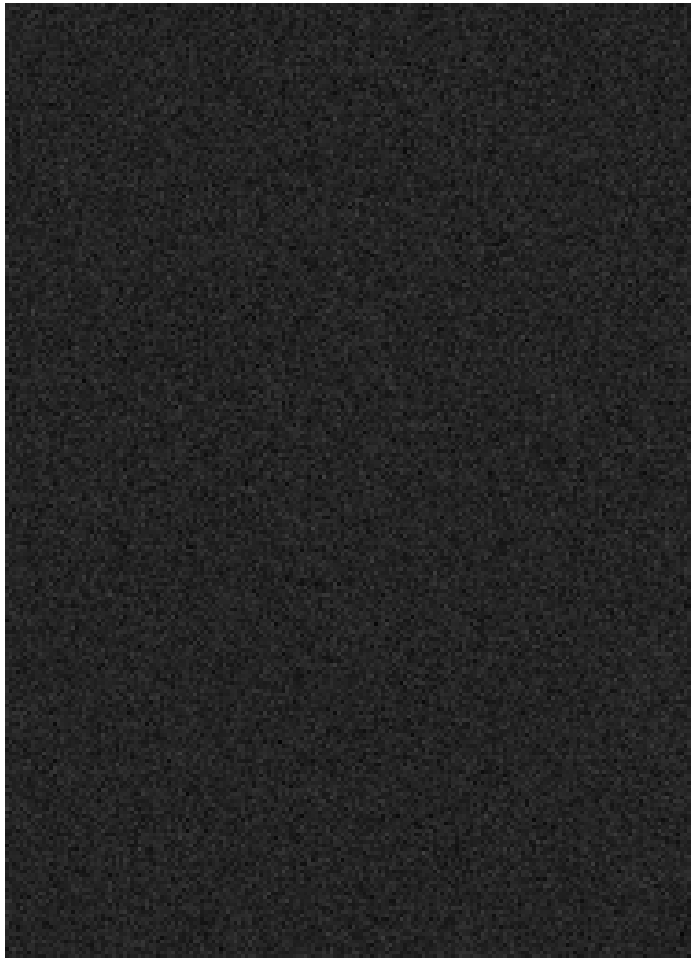


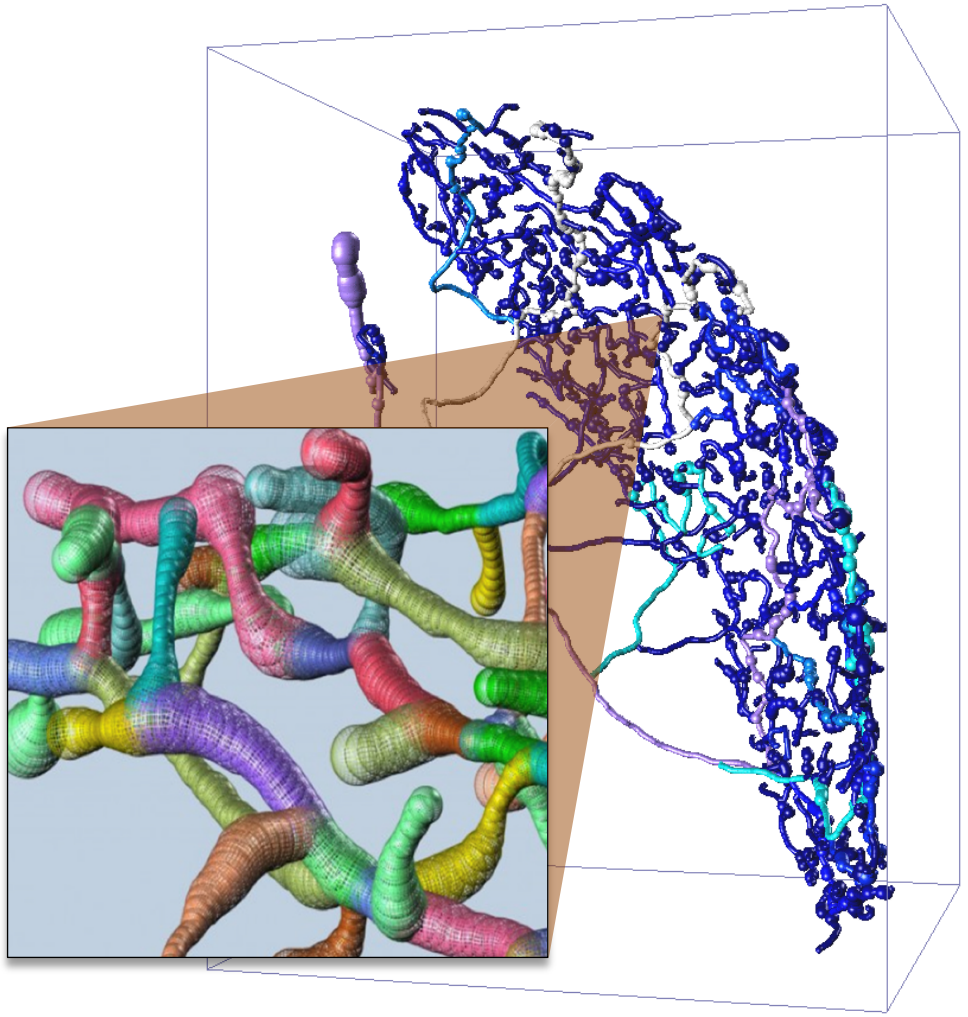
Strain



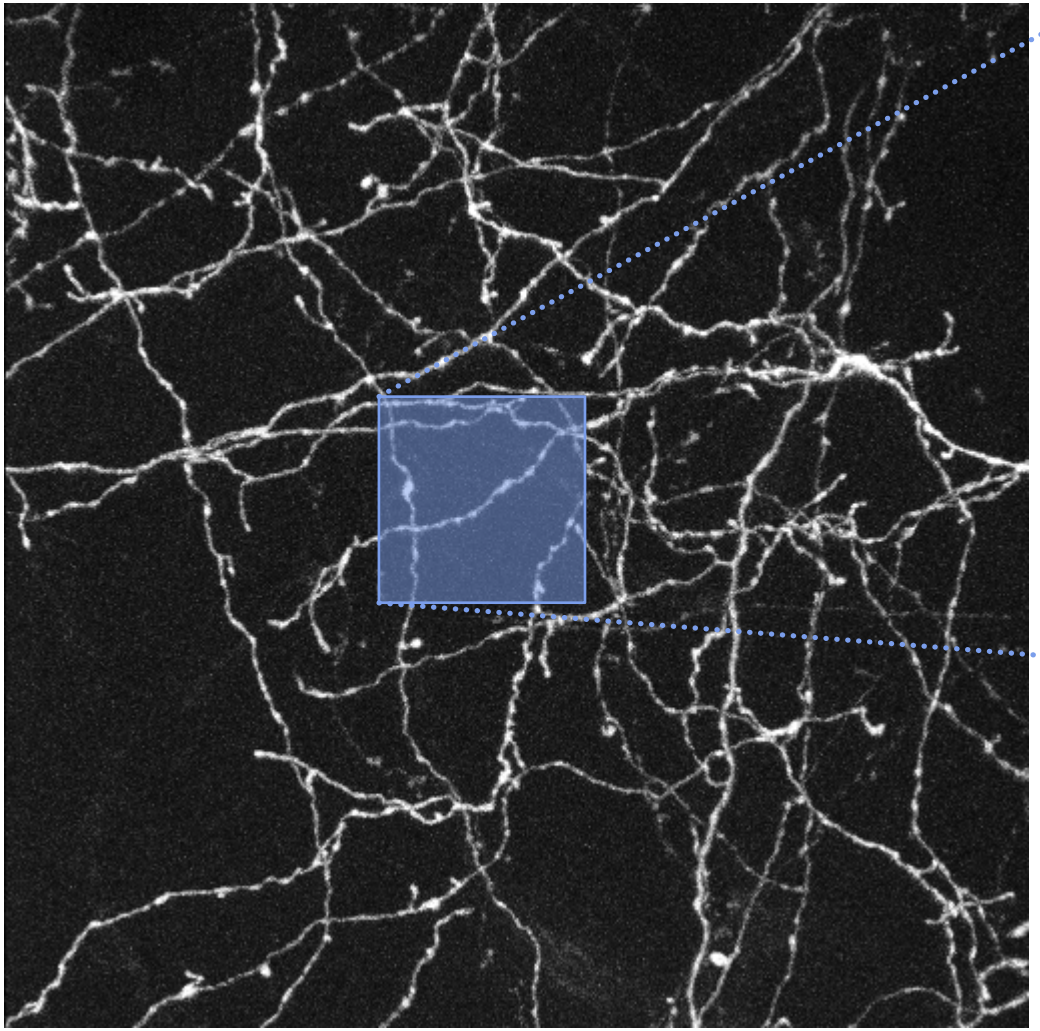
Smal & Meijering, *Medical Image Analysis*, 2012

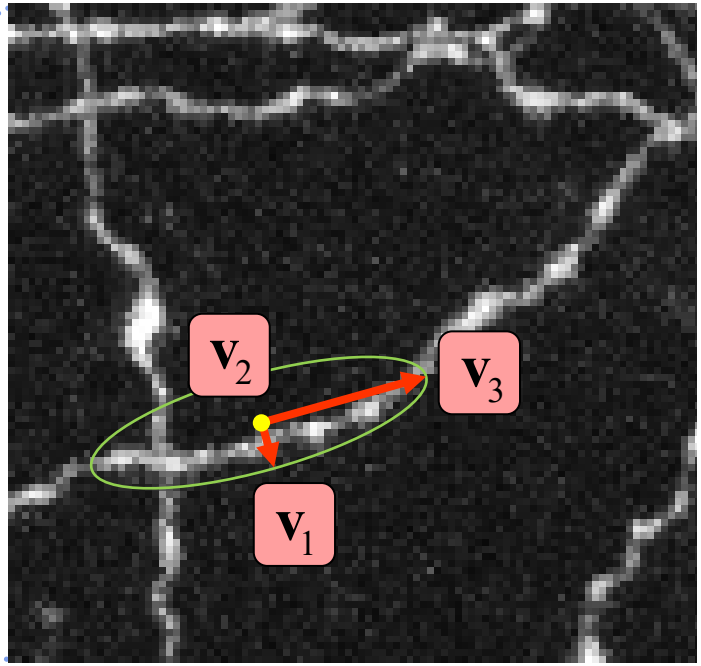
Neuron Reconstruction





Neuron Reconstruction

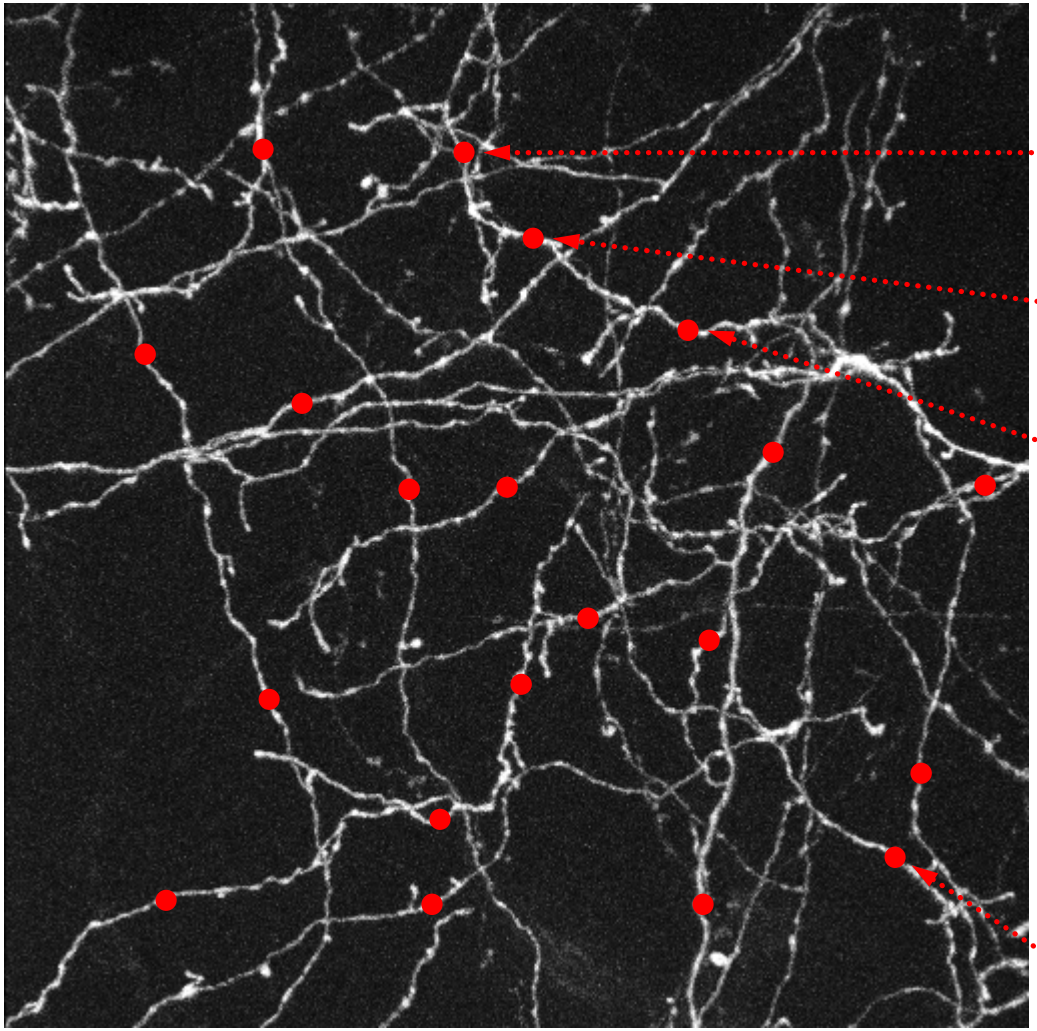




$$\mathbf{H} = \begin{pmatrix} I_{xx} & I_{xy} & I_{xz} \\ I_{yx} & I_{yy} & I_{yz} \\ I_{zx} & I_{zy} & I_{zz} \end{pmatrix} = \mathbf{V}^{\mathrm{T}} \cdot \mathbf{\Lambda} \cdot \mathbf{V}$$

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

Neuron Reconstruction



Target states

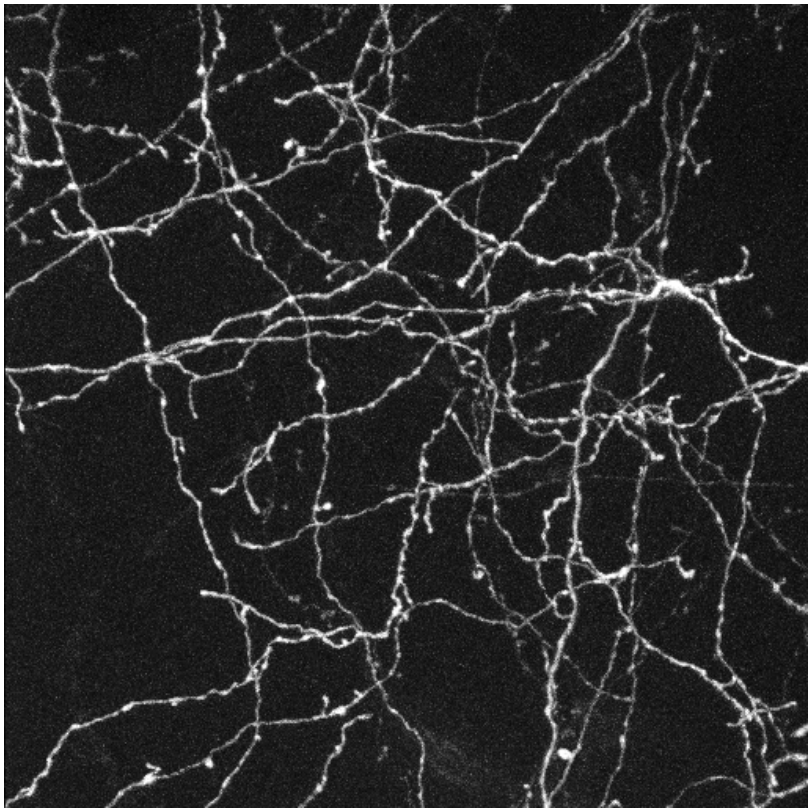
$$\mathbf{x}_{1;k} = \left(x_{1;k}, y_{1;k}, z_{1;k}, v^x_{1;k}, v^y_{1;k}, v^z_{1;k}\right)$$

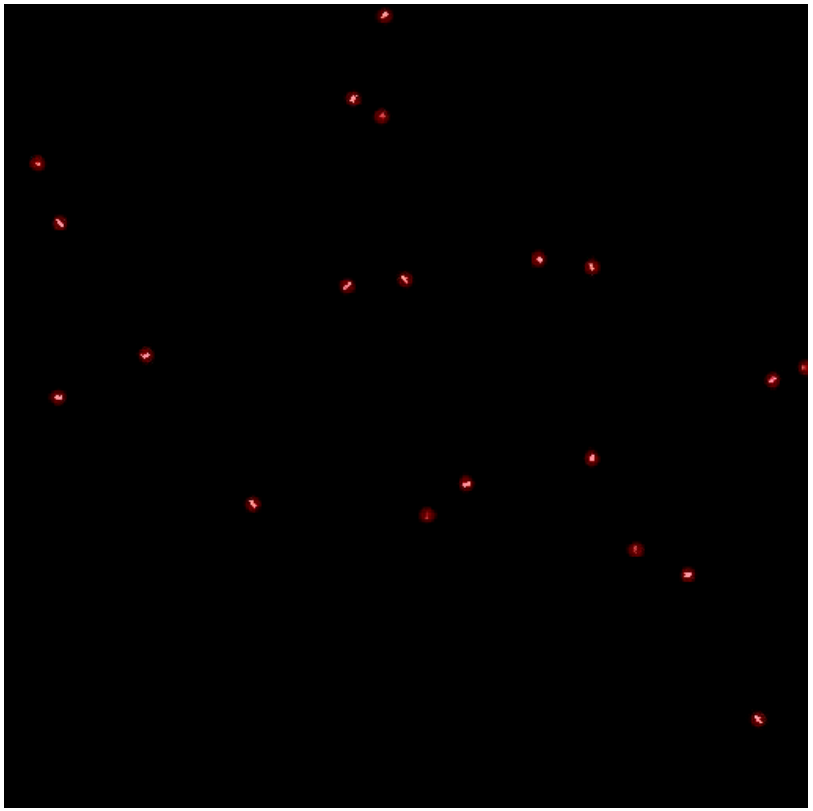
$$\mathbf{x}_{2;k} = \left(x_{2;k}, y_{2;k}, z_{2;k}, v^x_{2;k}, v^y_{2;k}, v^z_{2;k}\right)$$

$$\mathbf{x}_{3;k} = \left(x_{3;k}, y_{3;k}, z_{3;k}, v^x_{3;k}, v^y_{3;k}, v^z_{3;k}\right)$$

$$\mathbf{x}_{N;k} = \left(x_{N;k}, y_{N;k}, z_{N;k}, v^x_{N;k}, v^y_{N;k}, v^z_{N;k}\right)$$

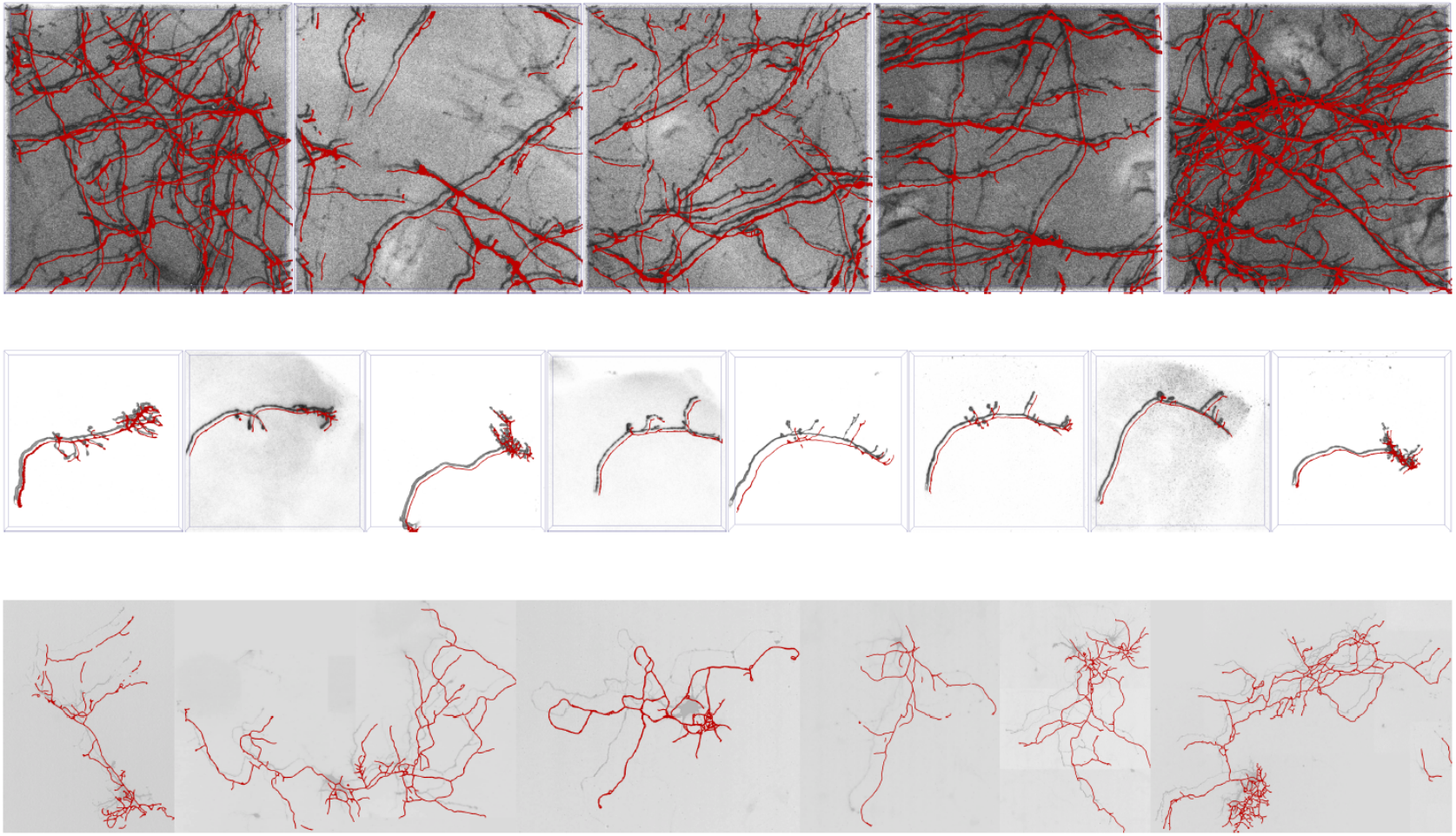
Tracking for Neuron Reconstruction





Radojevic & Meijering, *Neuroinformatics*, 2019

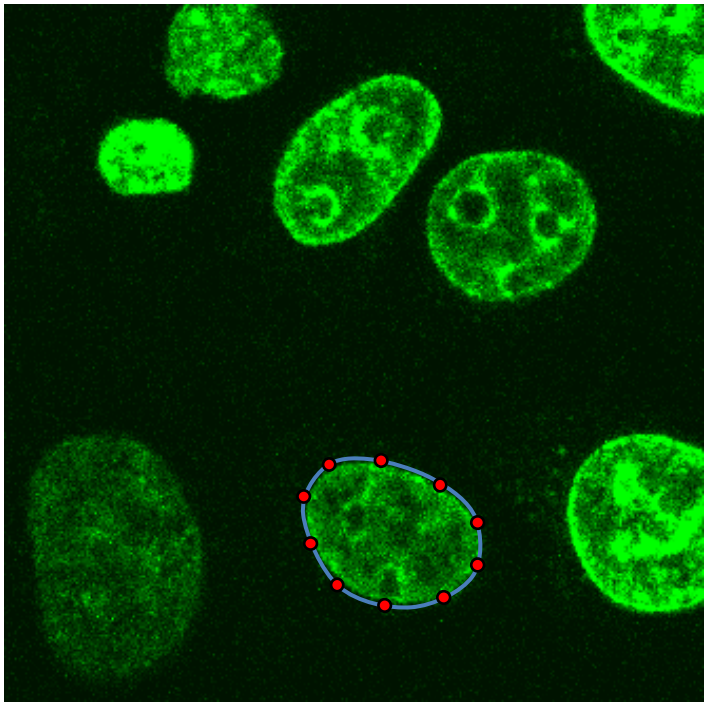
Neuron Reconstruction Results

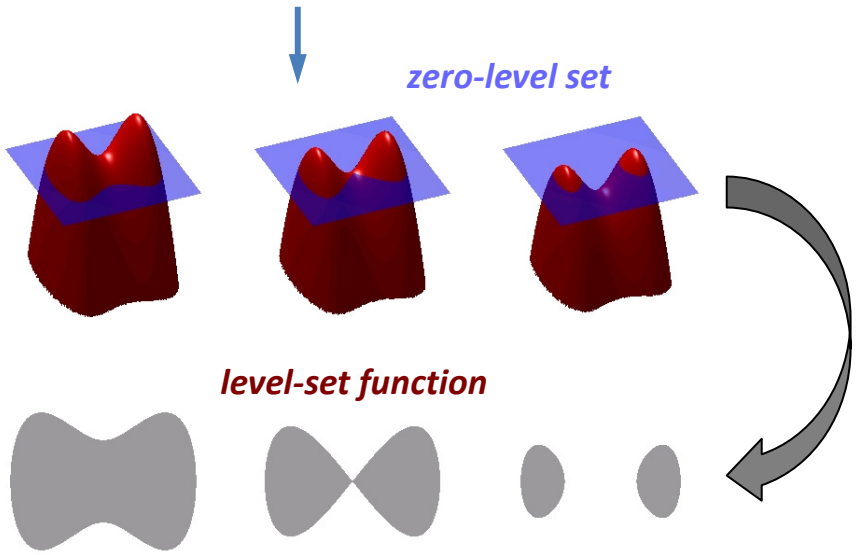


Cell Tracking

Popular segmentation methods

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



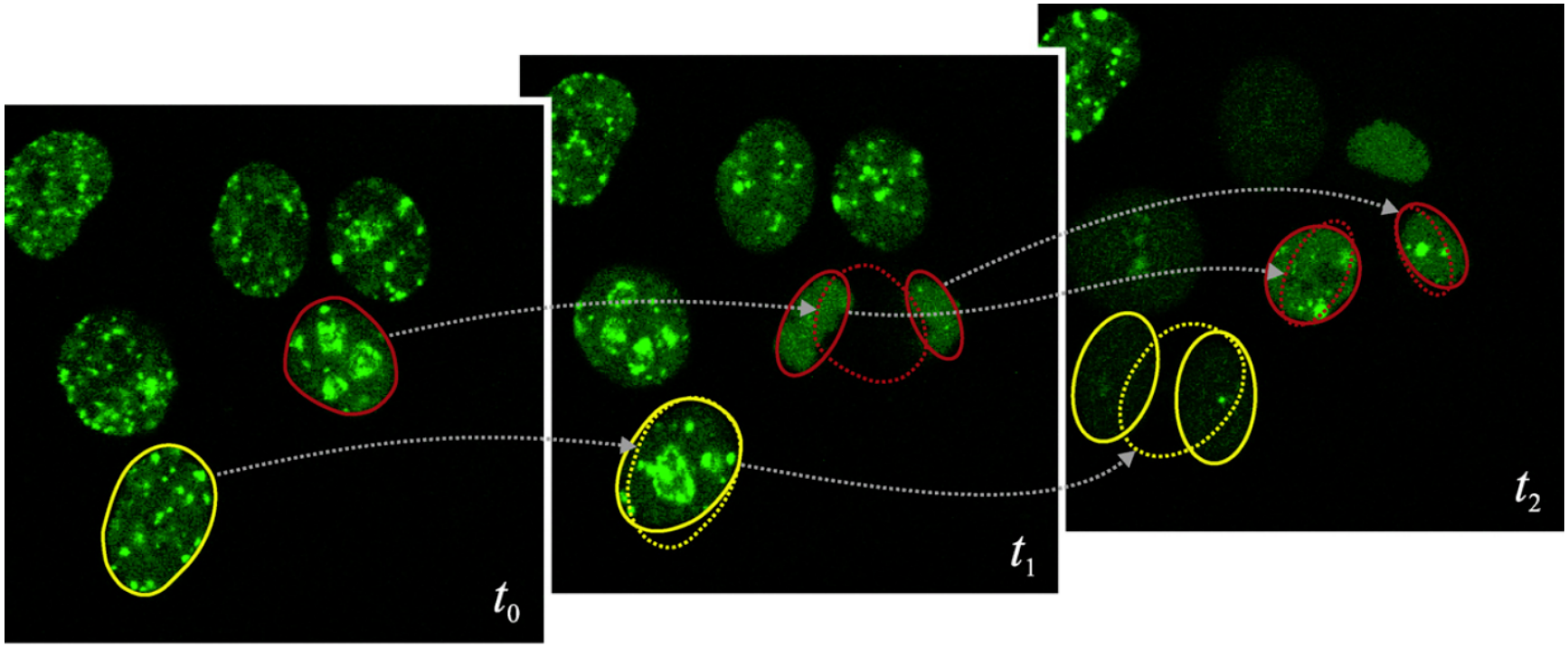


Model: $C(r) = \sum_n \mathbf{P}_n B(r-n)$

Fitting: $\hat{C} = \arg\min E(C)$

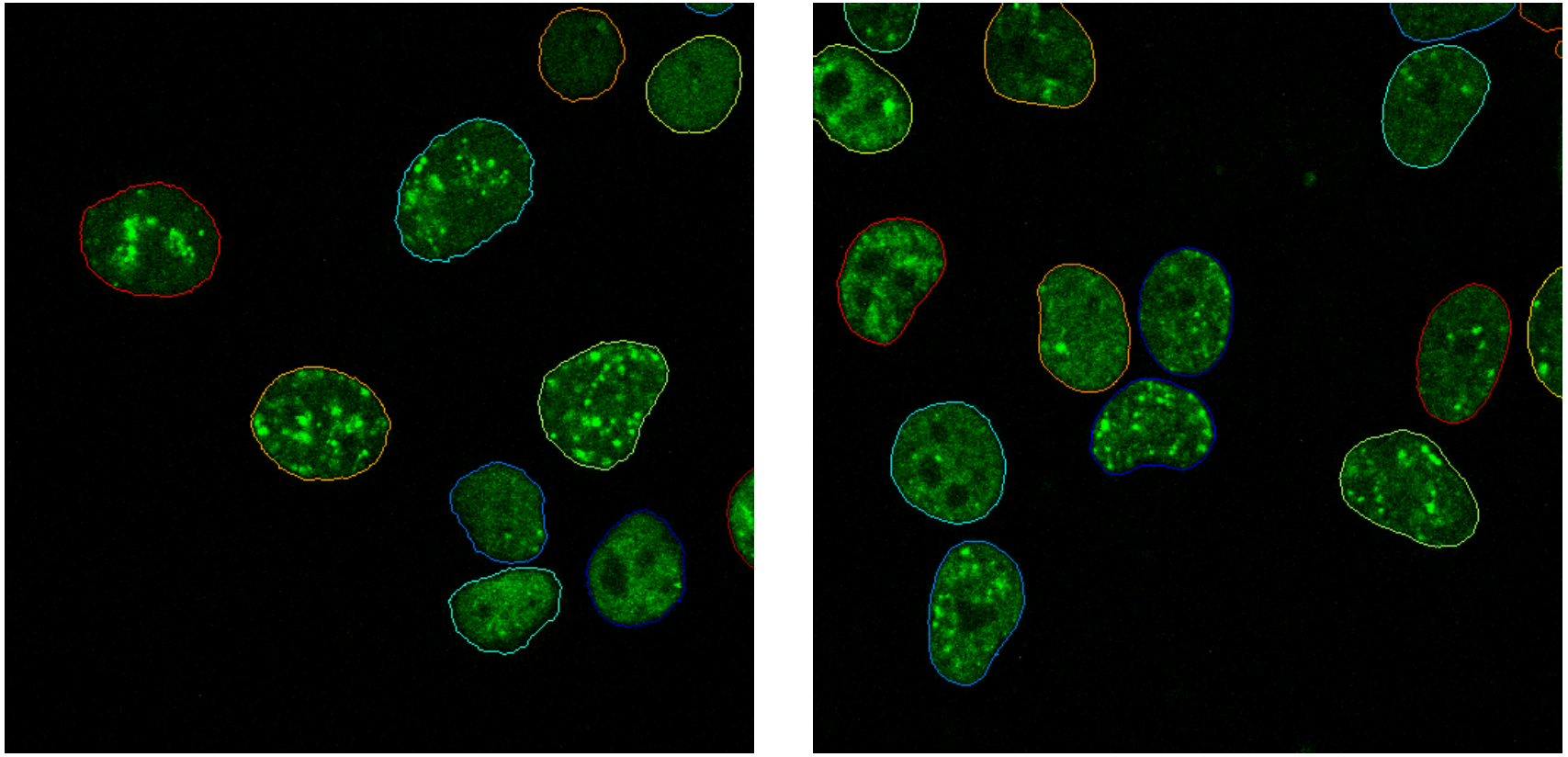
Cell Tracking

Linking by contour model evolution



Dzyubachyk & Meijering, *IEEE Transactions on Medical Imaging*, 2010

Cell Tracking



Coloured contours indicate the results of cell segmentation and indentification

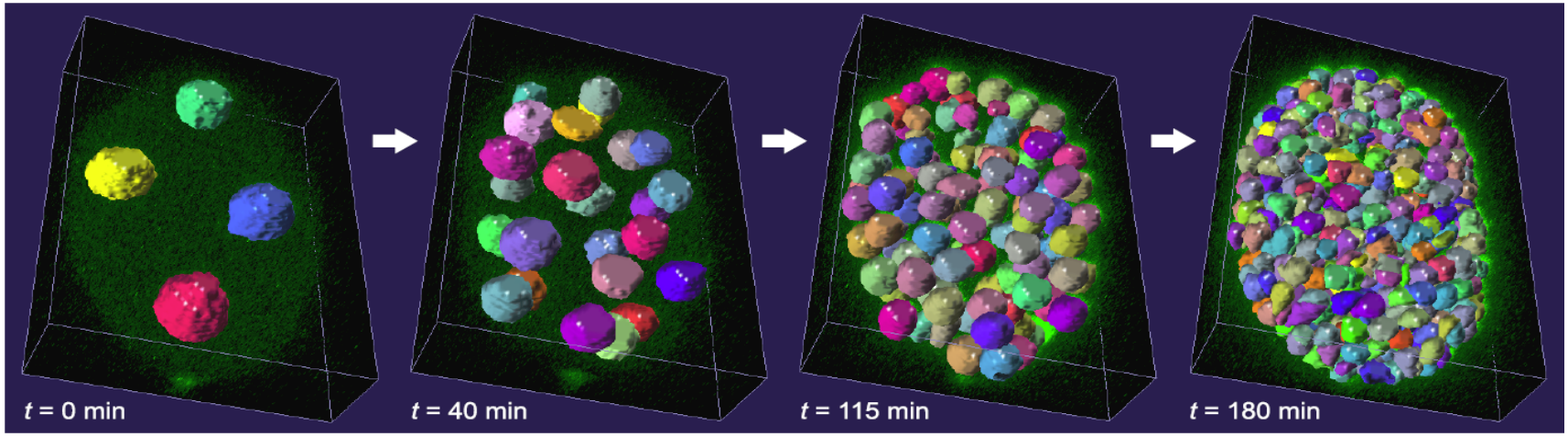
An objective comparison of cell-tracking algorithms

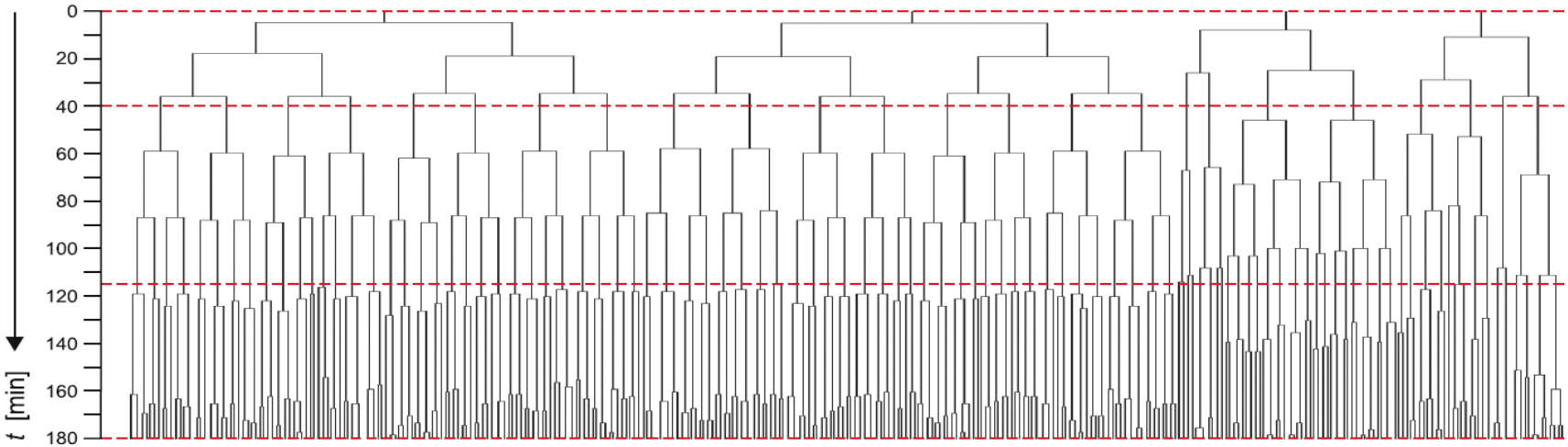
Vladimír Ulman[1,24,25], Martin Maška[1,25], Klas E G Magnusson[2], Olaf Ronneberger[3,24], Carsten Haubold[4], Nathalie Harder[5,24], Pavel Matula[1], Petr Matula[1], David Svoboda[1], Miroslav Radojevic[6], Ihor Smal[6], Karl Rohr[5], Joakim Jaldén[2], Helen M Blau[7], Oleh Dzyubachyk[8], Boudewijn Lelieveldt[8,9], Pengdong Xiao[10,24], Yuexiang Li[11,24], Siu-Yeung Cho[12], Alexandre C Dufour[13], Jean-Christophe Olivo-Marin[13], Constantino C Reyes-Aldasoro[14], Jose A Solis-Lemus[14], Robert Bensch[3], Thomas Brox[3], Johannes Stegmaier[15], Ralf Mikut[15], Steffen Wolf[4], Fred A Hamprecht[4], Tiago Esteves[16,17], Pedro Quelhas[16], Ömer Demirel[18], Lars Malmström[18], Florian Jug[19], Pavel Tomancak[19], Erik Meijering[6], Arrate Muñoz-Barrutia[20,21], Michal Kozubek[1] & 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

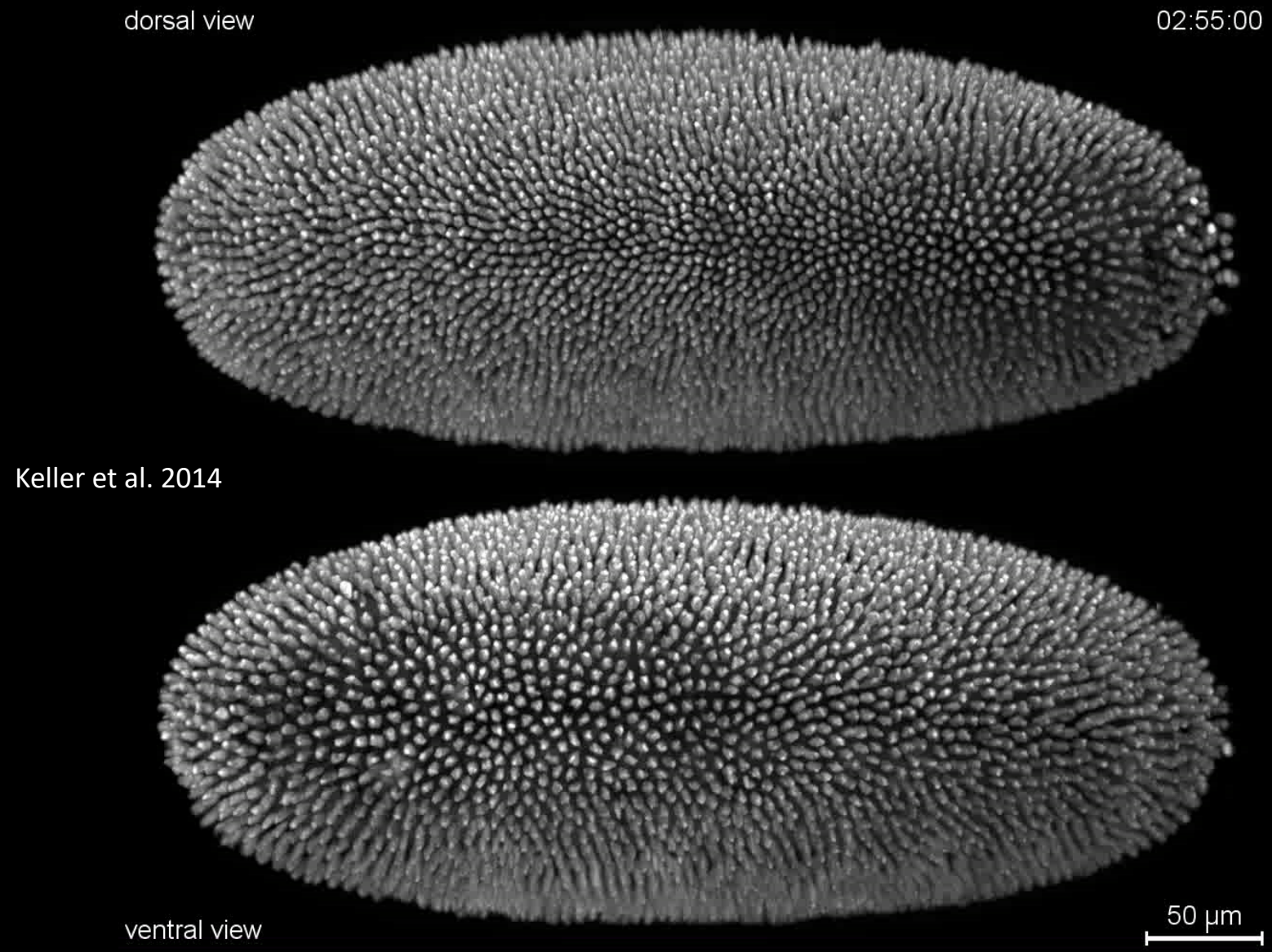
these processes. Imaging techniques, such as phase contrast (PhC) or differential interference contrast (DIC) microscopy, make cells visible without the need of exogenous markers. Fluorescence microscopy, on the other hand, relies on fluorescent reporters to specifically label cell components such as 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





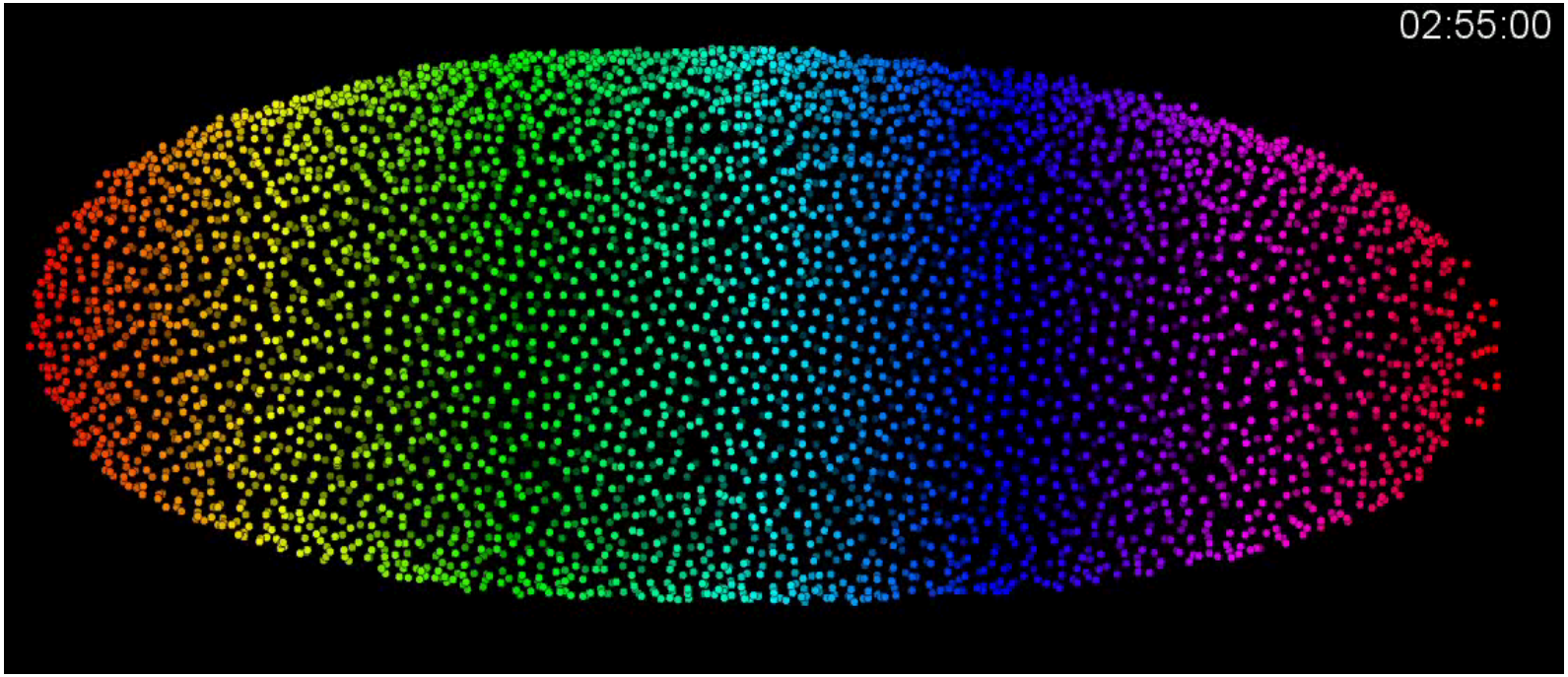
Drosophila embryogenesis



Keller et al. 2014

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