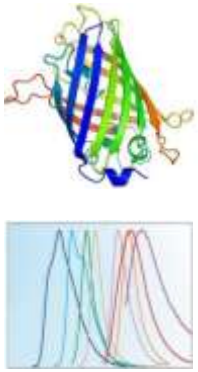
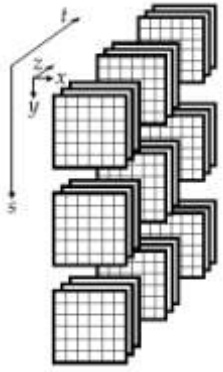
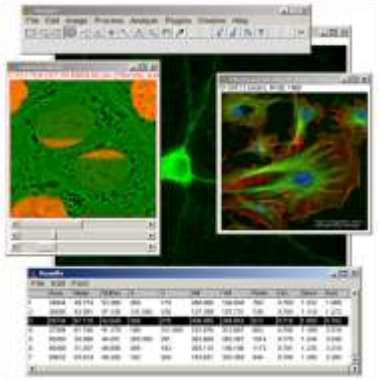
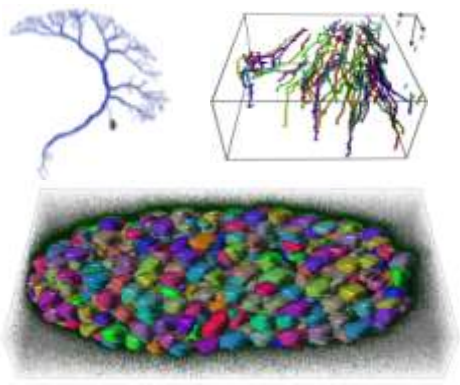
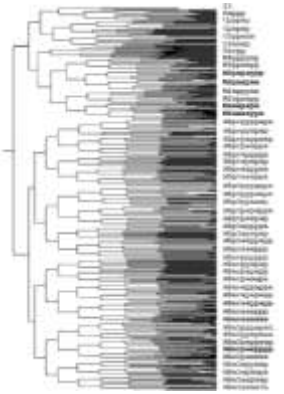
Advances and Challenges in Dynamic Bioimage Analysis

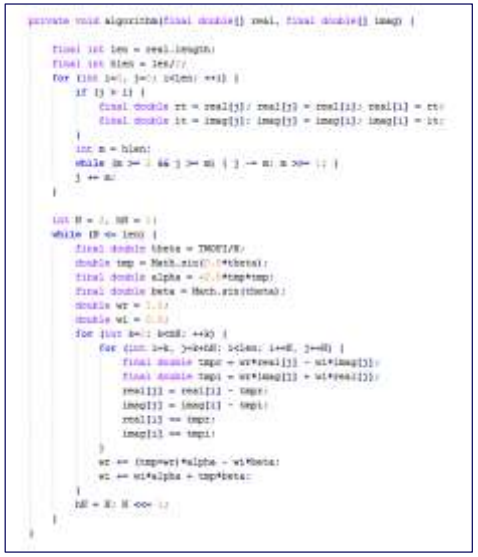
Erik Meijering

Erasmus University Medical Center
Departments of Medical Informatics and Radiology
Biomedical Imaging Group Rotterdam
Rotterdam, The Netherlands
meijering@imagescience.org

Bioimage analysis ingredients

Microscope

Computer



Software

Developments in light microscopy

Resolution improvements

- **1670:** Leeuwenhoek ~ 1 µm
- **1930:** Phase-Contrast
- **1950:** Differential Interference Contrast
- **1980:** Confocal ~ 250 nm
- **1994:** STED ~ 40 nm
- **1997:** 4Pi ~ 100 nm
- **1999:** I^nM ~ 70-90 nm
- **2000:** SIM ~ 100 nm
- **2005:** SSIM ~ 50 nm
- **2006:** PALM/STORM ~ 2-25 nm

MICRO

NANO

Nobel Prizes and Laureates

Chemistry Prizes 2014

▼ About the Nobel Prize in Chemistry 2014
- Summary
- Prize Announcement
- Press Release
- Advanced Information
- Popular Information
- Greetings
- Award Ceremony Video
- Award Ceremony Speech

▶ Eric Betzig
▶ Stefan W. Hell
▶ William E. Moerner

All Nobel Prizes in Chemistry
All Nobel Prizes in 2014

The Nobel Prize in Chemistry 2014
Eric Betzig, Stefan W. Hell, William E. Moerner

Share this:

The Nobel Prize in Chemistry 2014

Photo: A. Mahmoud
Eric Betzig
Prize share: 1/3

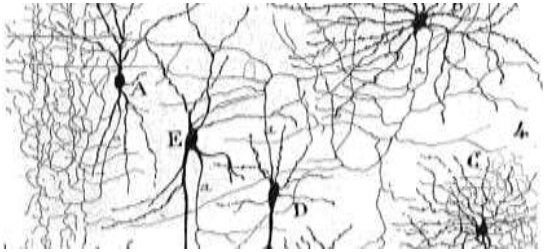
Photo: A. Mahmoud
Stefan W. Hell
Prize share: 1/3

Photo: A. Mahmoud
William E. Moerner
Prize share: 1/3

The Nobel Prize in Chemistry 2014 was awarded jointly to Eric Betzig, Stefan W. Hell and William E. Moerner *"for the development of super-resolved fluorescence microscopy"*.

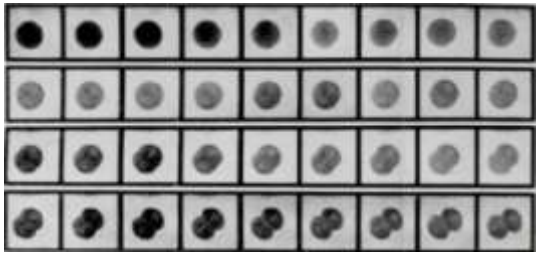
Share this:

Developments in light microscopy



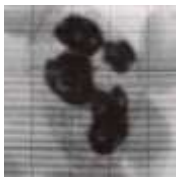
Hand drawn

1670



Photography and cinematography

1900



128^2 pixels

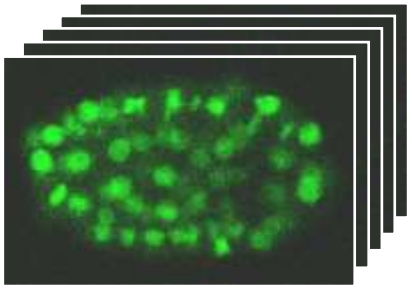
~ 16 KB

Digital scanners

CCD cameras

1960

DATA EXPLOSION



10^{10} pixels

~ 10 GB

Fully automated

Today

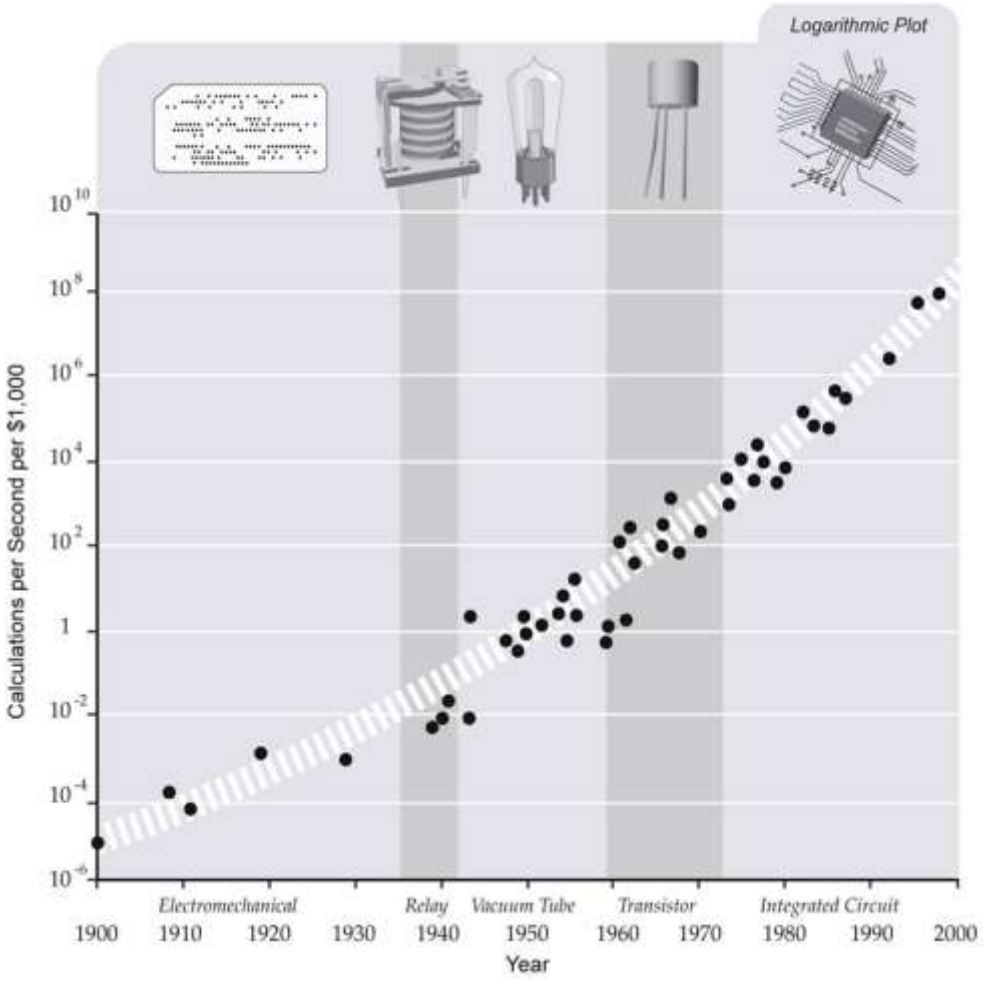
Developments in computer hardware

Electronics, Volume 38, Number 8, April 19, 1965

Cramming more components onto integrated circuits

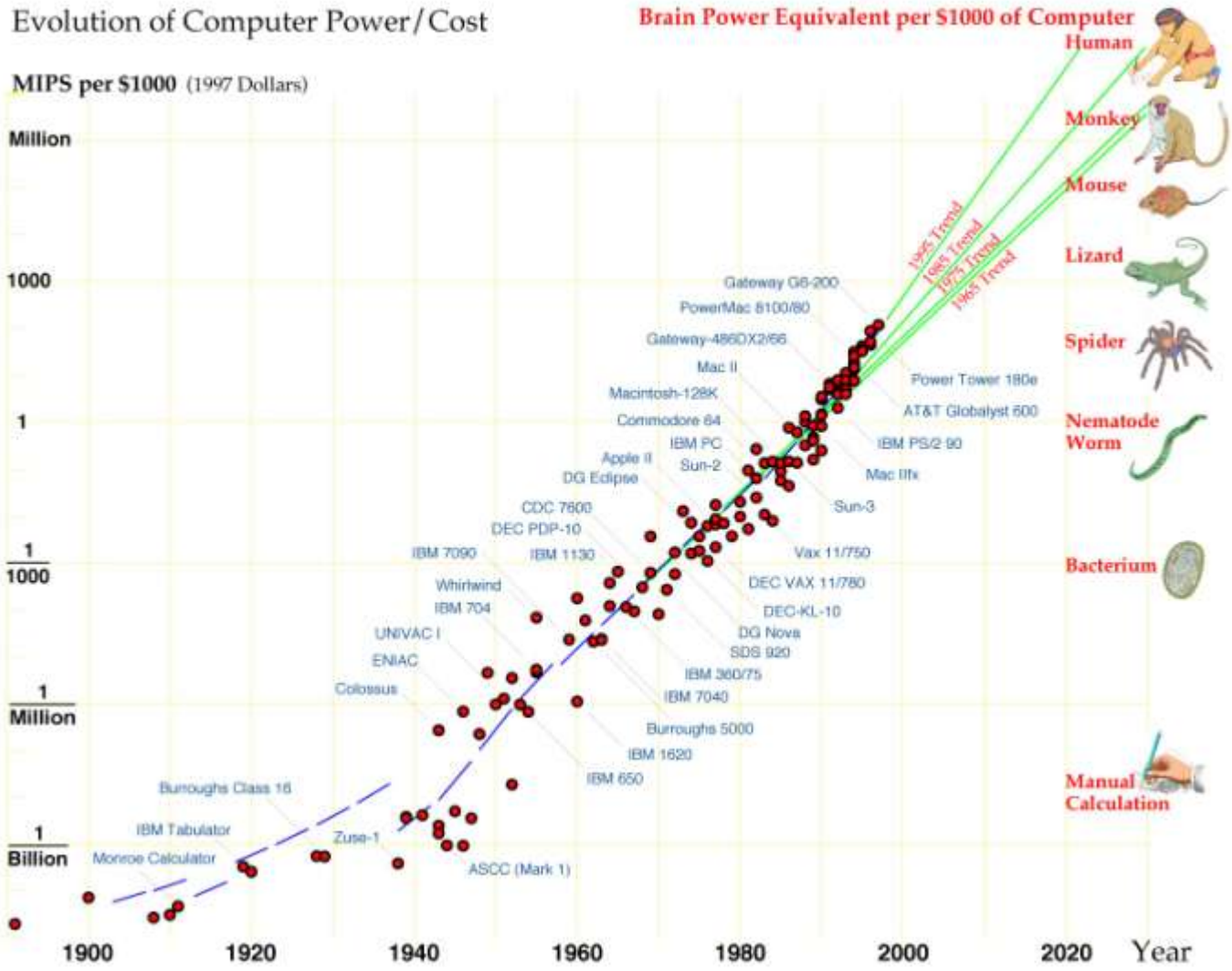
By Gordon E. Moore

"The complexity for minimum component costs has increased at a rate of roughly a factor of two per year (see graph on next page). Certainly over the short term this rate can be expected to continue, if not to increase. Over the longer term, the rate of increase is a bit more uncertain, although there is no reason to believe it will not remain nearly constant for at least 10 years."



singularity.com

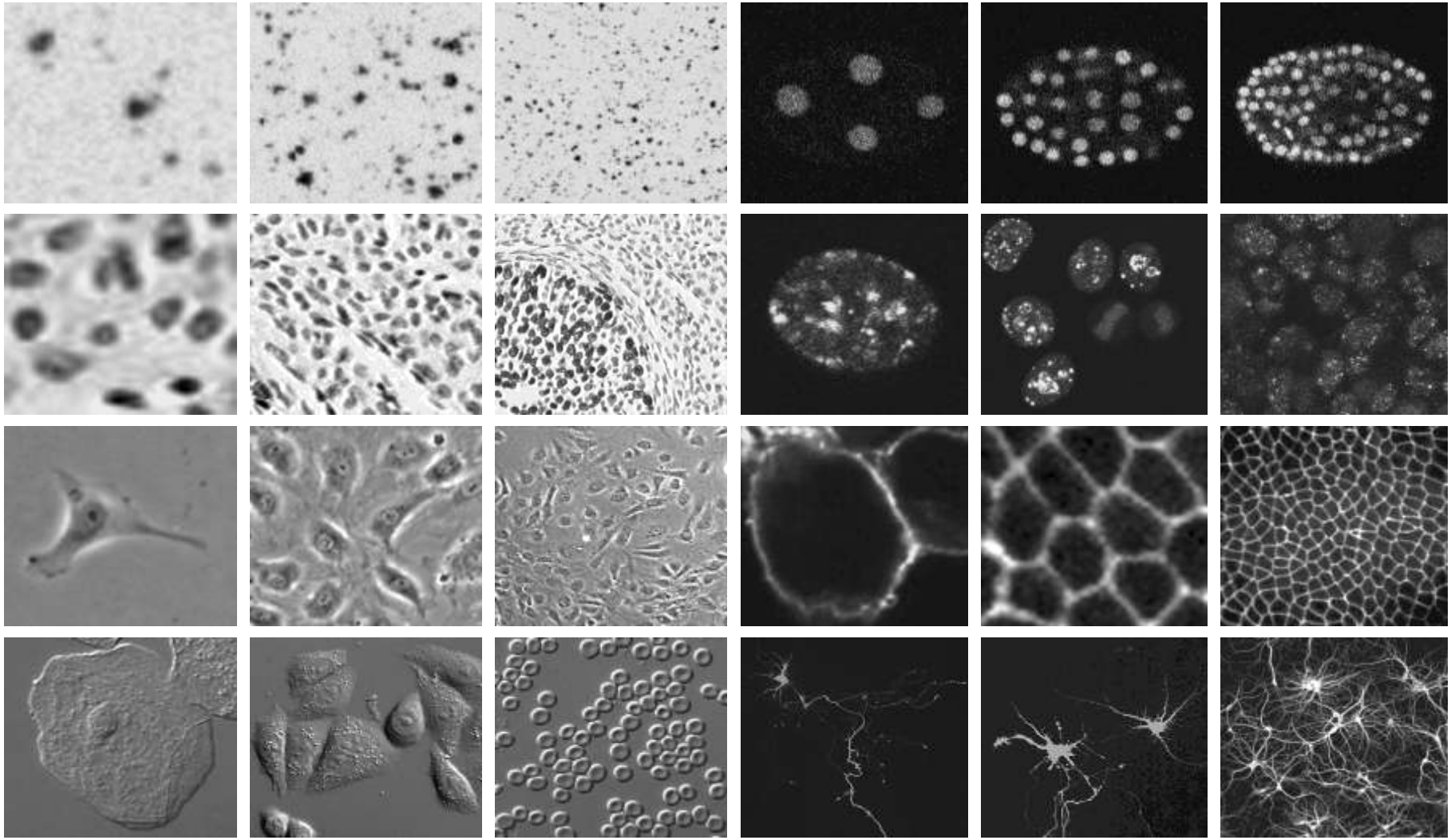
Developments in computer hardware



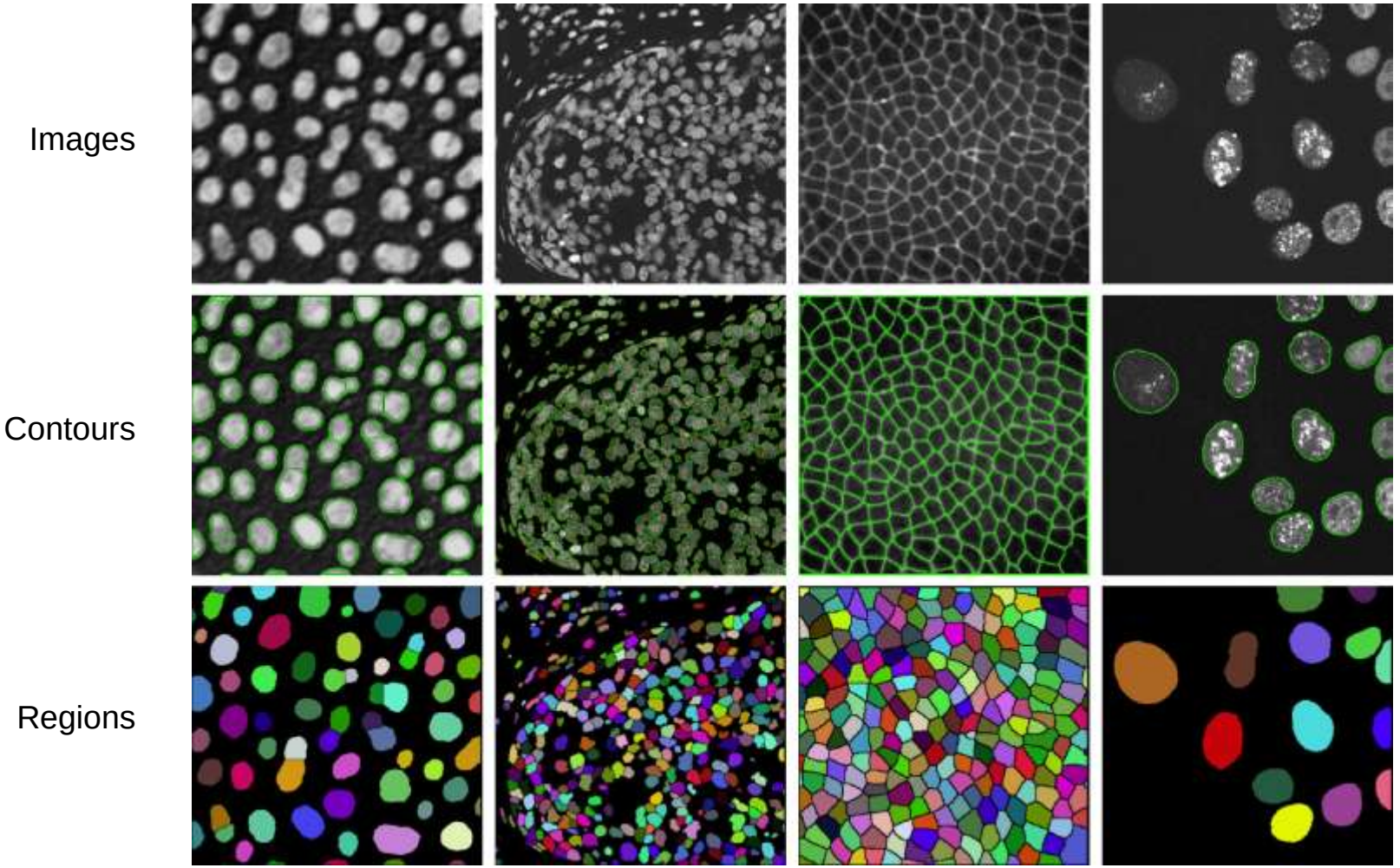
Hans Moravec

Developments in computer software?

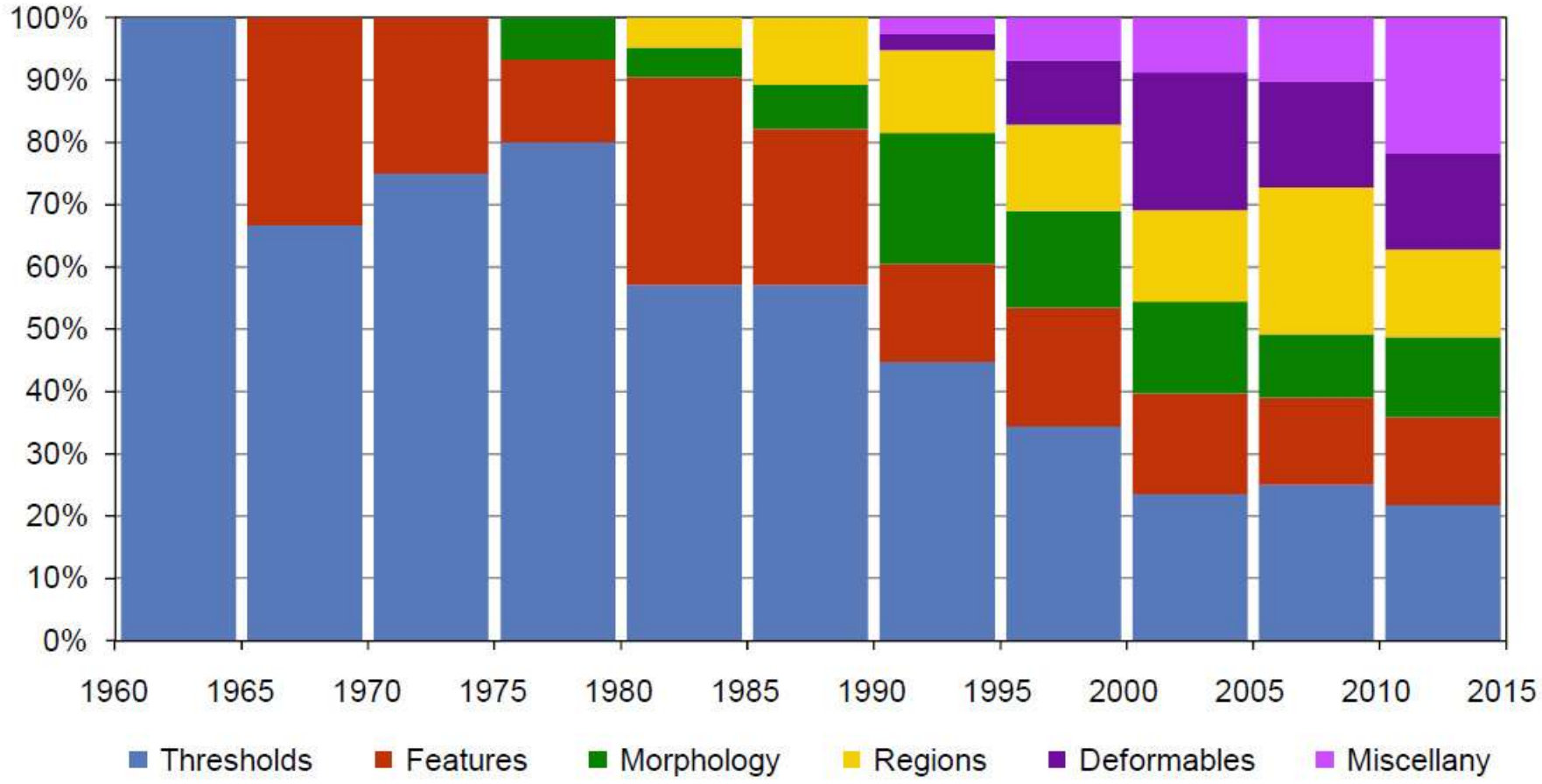
Diversity of cell images



Cell segmentation examples



Cell segmentation approaches over time



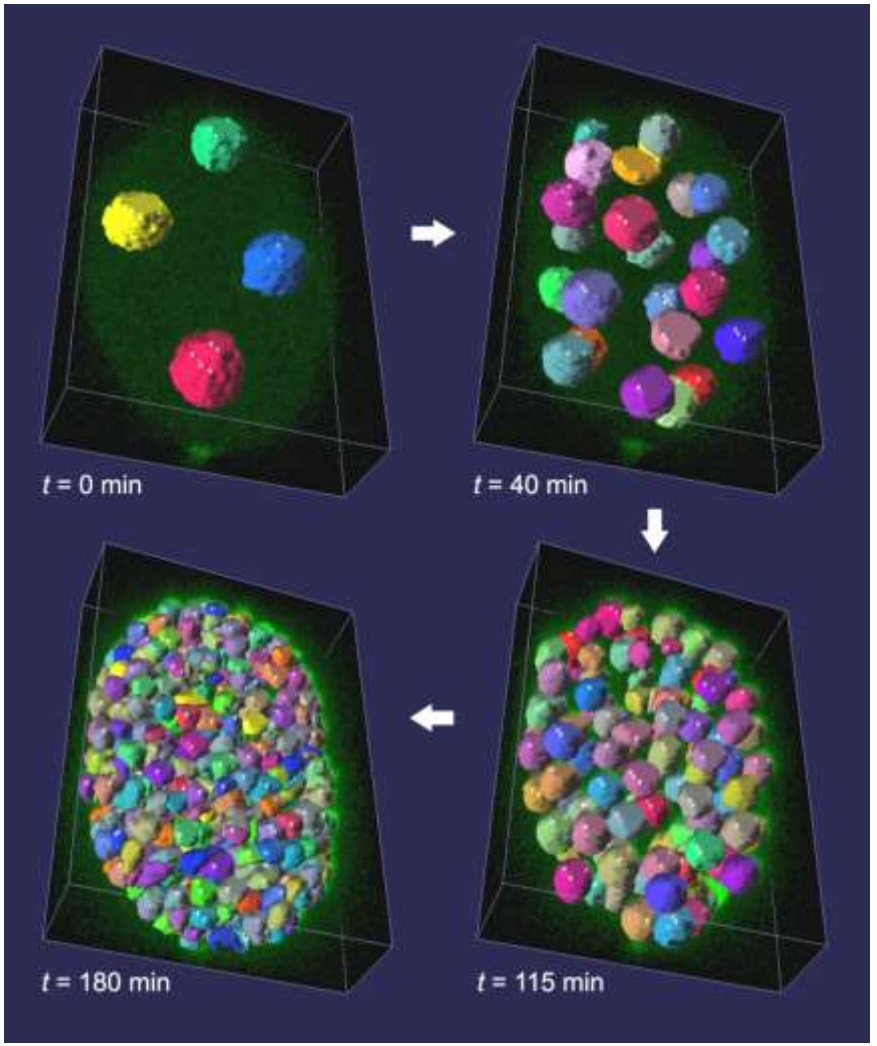
From 250 technical journal papers describing cell segmentation methods

Meijering, *IEEE Signal Processing Magazine*, 2012

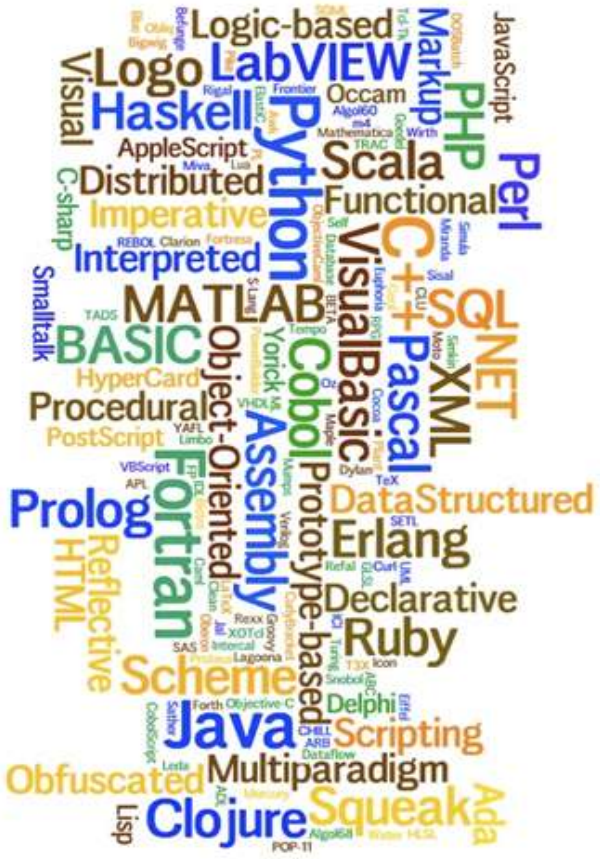
More powerful methods are needed

Recently proposed concepts

- Graph cuts
- Active masks
- Dynamic programming
- Support vector machines
- Tensor voting schemes
- Bayesian estimation
- Particle filtering
- Markov random fields
- Neural networks



Catalysts for future method development



- **Improved *availability***

  Community supported software platforms

- **Improved *testability***

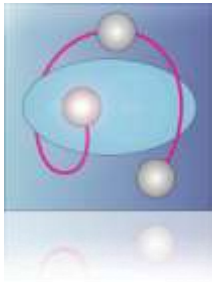
  Standardized test images and measures

- **Improved *comparability***

  Organization of objective challenges

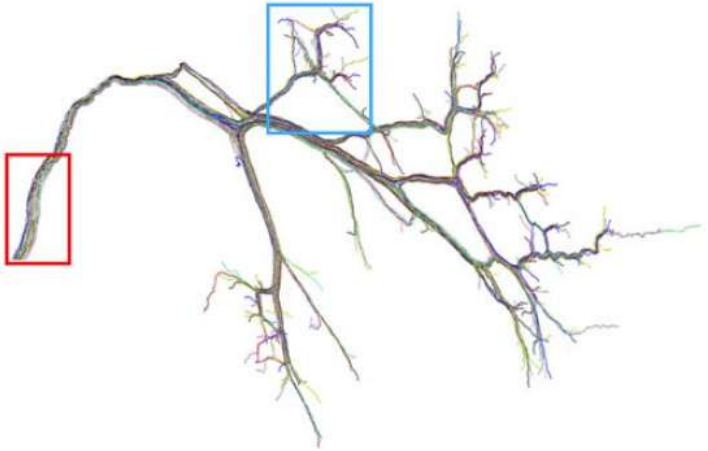
Community supported software

Once upon a time…



Standardized test images and measures

Images with expert annotation to serve as gold standard



- **DIADEM Data Sets**
  http://www.diademchallenge.org/
- **Broad Bioimage Benchmark Collection**
  http://www.broadinstitute.org/bbbc/
- **UCSB Bio-Segmentation Benchmarking**
  http://bioimage.ucsb.edu/research/bio-segmentation
- **Cell Centered Database**
  http://ccdb.ucsd.edu/
- **Cell Image Library**
  http://www.cellimagelibrary.org/

Need for objective comparison

COMPUTER VISION, GRAPHICS, AND IMAGE PROCESSING 36, 387–391 (1986)

Anything You Can Do, I Can Do Better (No You Can't)...*

KEITH PRICE

Powell Hall MC-0273, Intelligent Systems Group, University of Southern California, Los Angeles, California 90089-0273

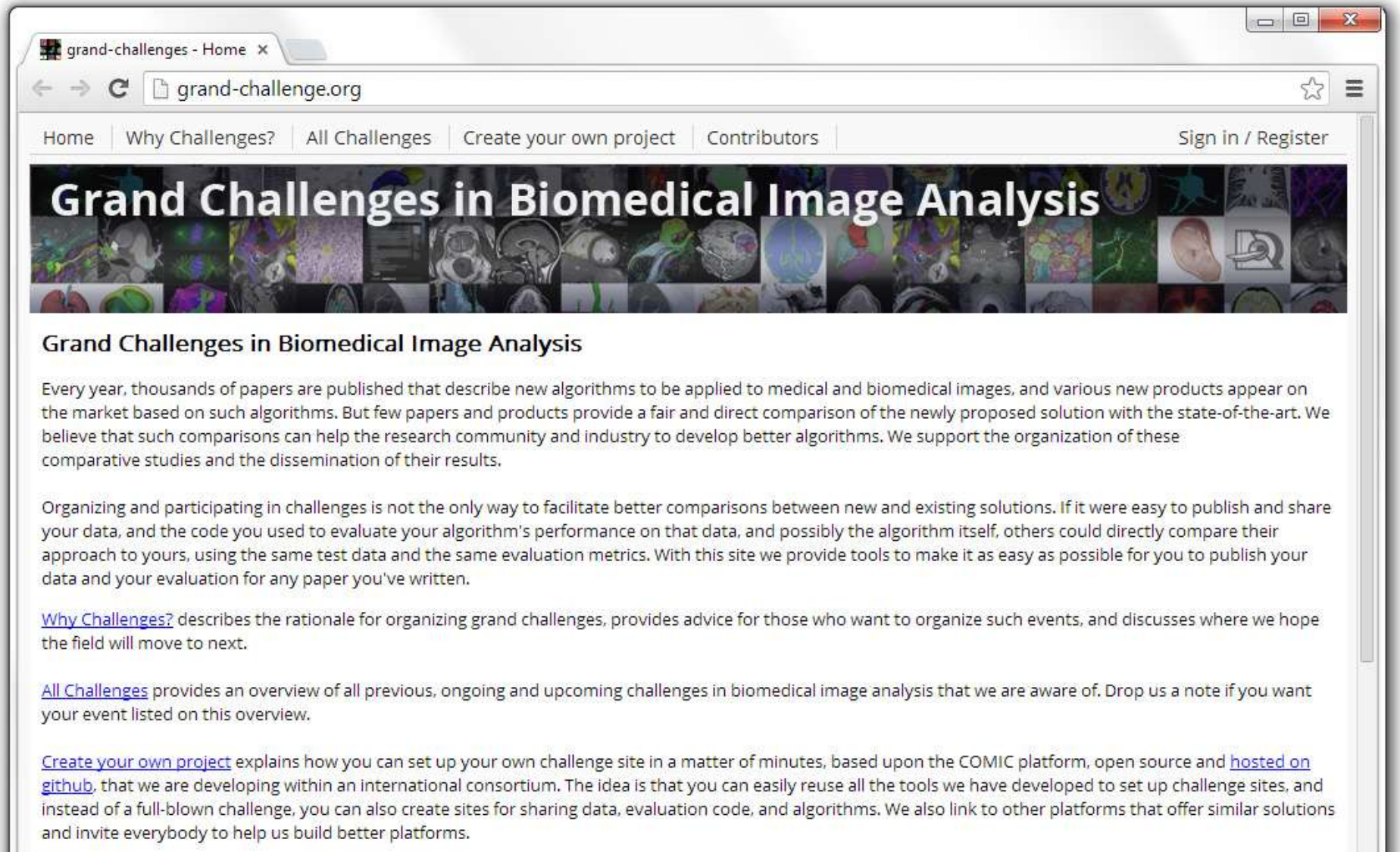
Received February 3, 1986; revised March 5, 1986

Computer vision suffers from an overload of written information but a dearth of good evaluations and comparisons. This paper discusses why some of the problems arise and offers some guidelines we should all follow.

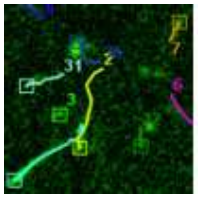
INTRODUCTION

Many of the comments in this paper apply to any scientific domain and are not unique to computer vision, but some other research domains have well-defined methods for evaluating research (e.g., in medical research, does it help the patient?).

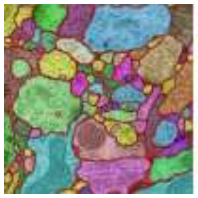
Organization of objective challenges



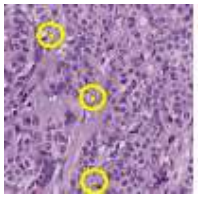
Bioimage analysis challenges



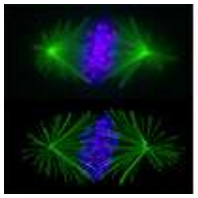
Particle tracking challenge 2012
Website: http://www.biomedicalimaging.org/2012/ind
Event: ISBI, May 2, 2012
Number of submissions: 14, Latest result: Apr 1, 201



Segmentation of neuronal structures in EM stacks 20
Website: http://www.biomedicalimaging.org/2012/ind
challenges/49-contest-workshop-segmentation-of-ne
Event: ISBI, May 2, 2012
Overview article: http://ieeexplore.ieee.org/xpl/articl
Number of submissions: 20

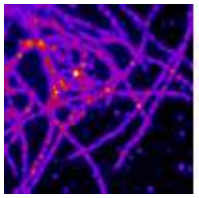


Mitosis Detection in Breast Cancer Histological Image
Website: http://ipal.cnrs.fr/ICPR2012/
Event: ICPR 2012
Number of submissions: 17, Latest result: Apr 16, 20

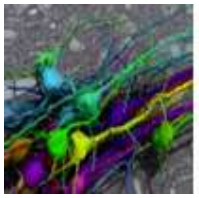


3D Deconvolution Microscopy
Website: http://bigwww.epfl.ch/deconvolution/challe
Event: ISBI, April 11, 2013
Number of submissions: 10

Cell Tracking Challenge
Website:
http://www.codesolorzano.com/celltrackingchallenge/
Event: ISBI, April 11, 2013



Localization Microscopy Challenge
Website: http://bigwww.epfl.ch/smlm/challenge/
Event: ISBI, April 11, 2013
Number of submissions: 25

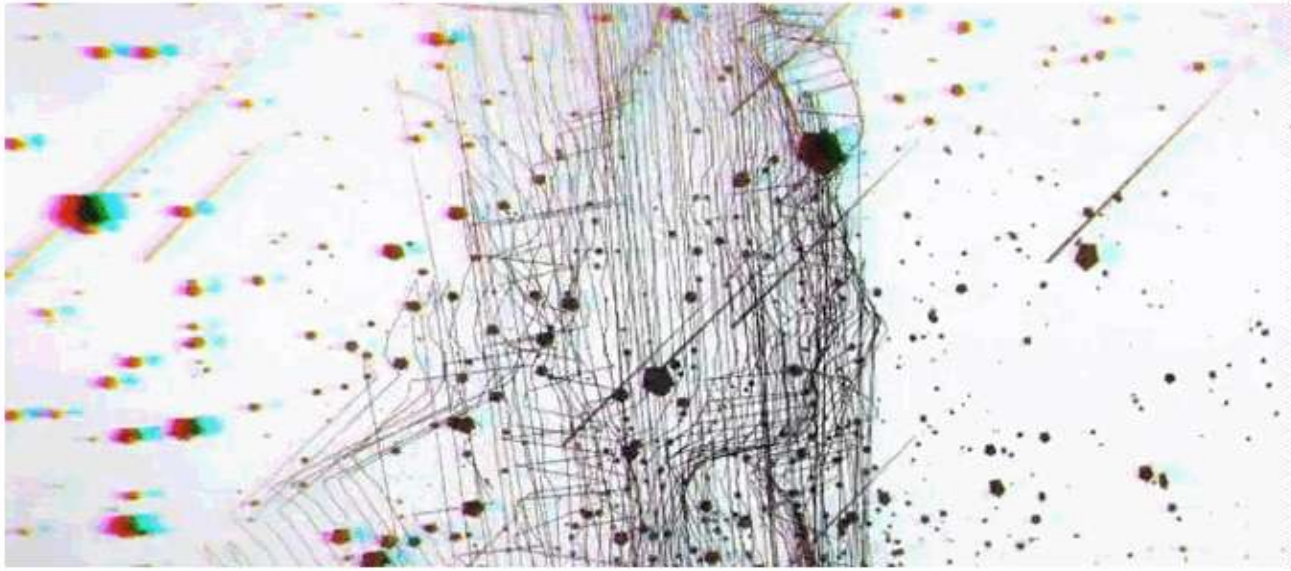


3D Segmentation of Neurites in EM Images
Website: http://brainiac.mit.edu/SNEMI3D/
Event: ISBI, April 11, 2013

Assessment of Mitosis Detection Algorithms 2013
Website: http://amida13.isi.uu.nl/
Event: MICCAI, September 22, 2013

Particle Tracking Challenge
Contest Workshop

http://bioimageanalysis.org/track/



Particle Tracking Challenge

Contest Workshop

ISBI 2012

Summary

Quantitative analysis of dynamic processes in biological cells requires accurate tracking of large numbers of particles in time-lapse microscopy images. The aim of this challenge is to objectively compare the performance of existing and newly developed particle tracking algorithms for this purpose.

The evaluation will be based on synthetic image sequences (with known ground truth) simulating real fluorescence microscopy image data from a range of biological applications. The accuracy and robustness of the algorithms will be evaluated using various particle localization and trajectory consistency error measures.

ISBI 2012 Challenges

This challenge is organized as part of the ISBI 2012 Challenges. It is open to all groups (academic or corporate) developing their own particle tracking methods.

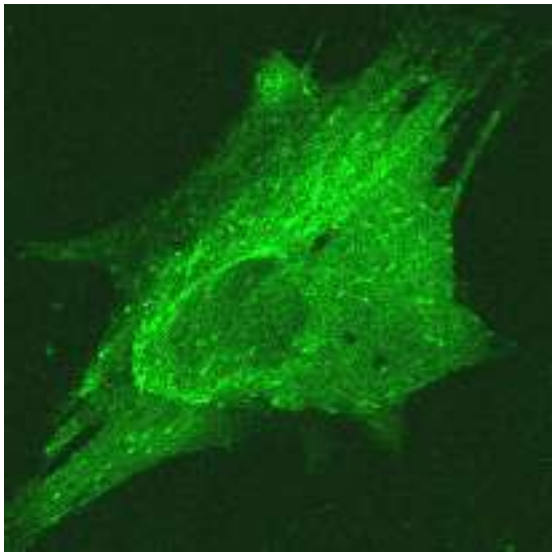
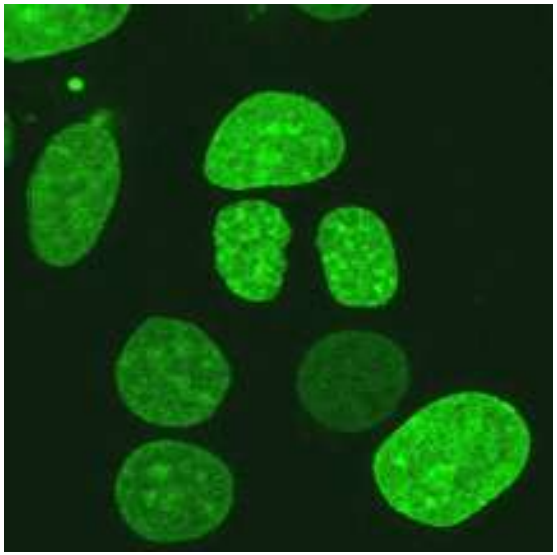
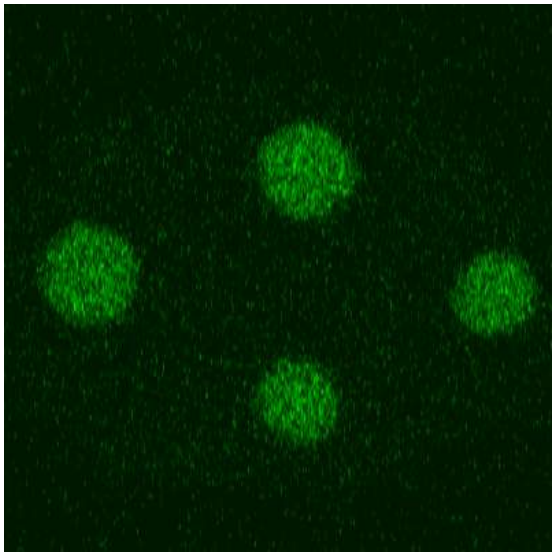
Organizers

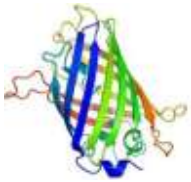
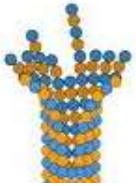
Erik Meijering
Erasmus MC – University Medical Center Rotterdam, The Netherlands

Jean-Christophe Olivo-Marin
Institut Pasteur, Paris, France

INTERNATIONAL SYMPOSIUM ON BIOMEDICAL IMAGING ISBI

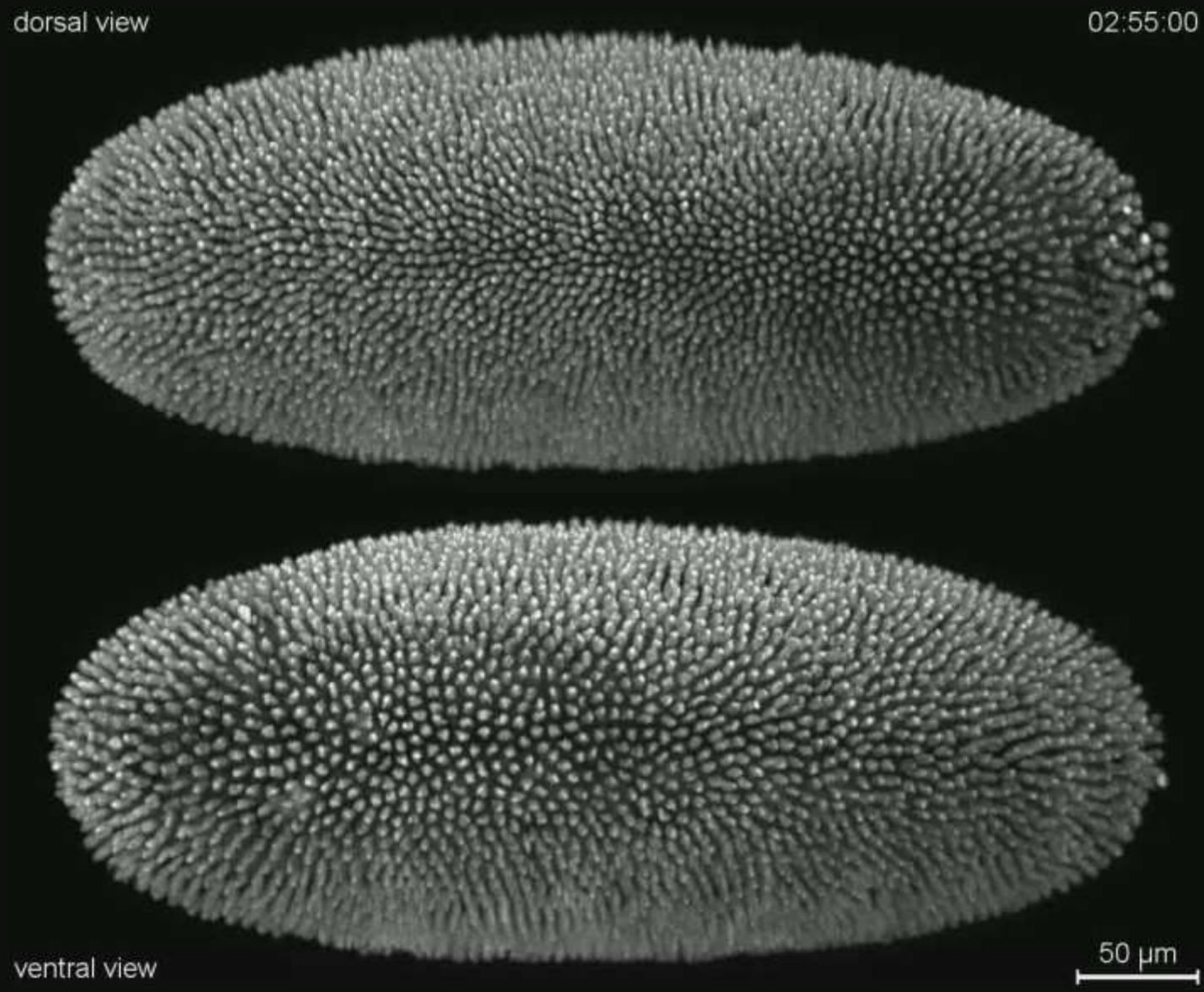
Life is dynamic…

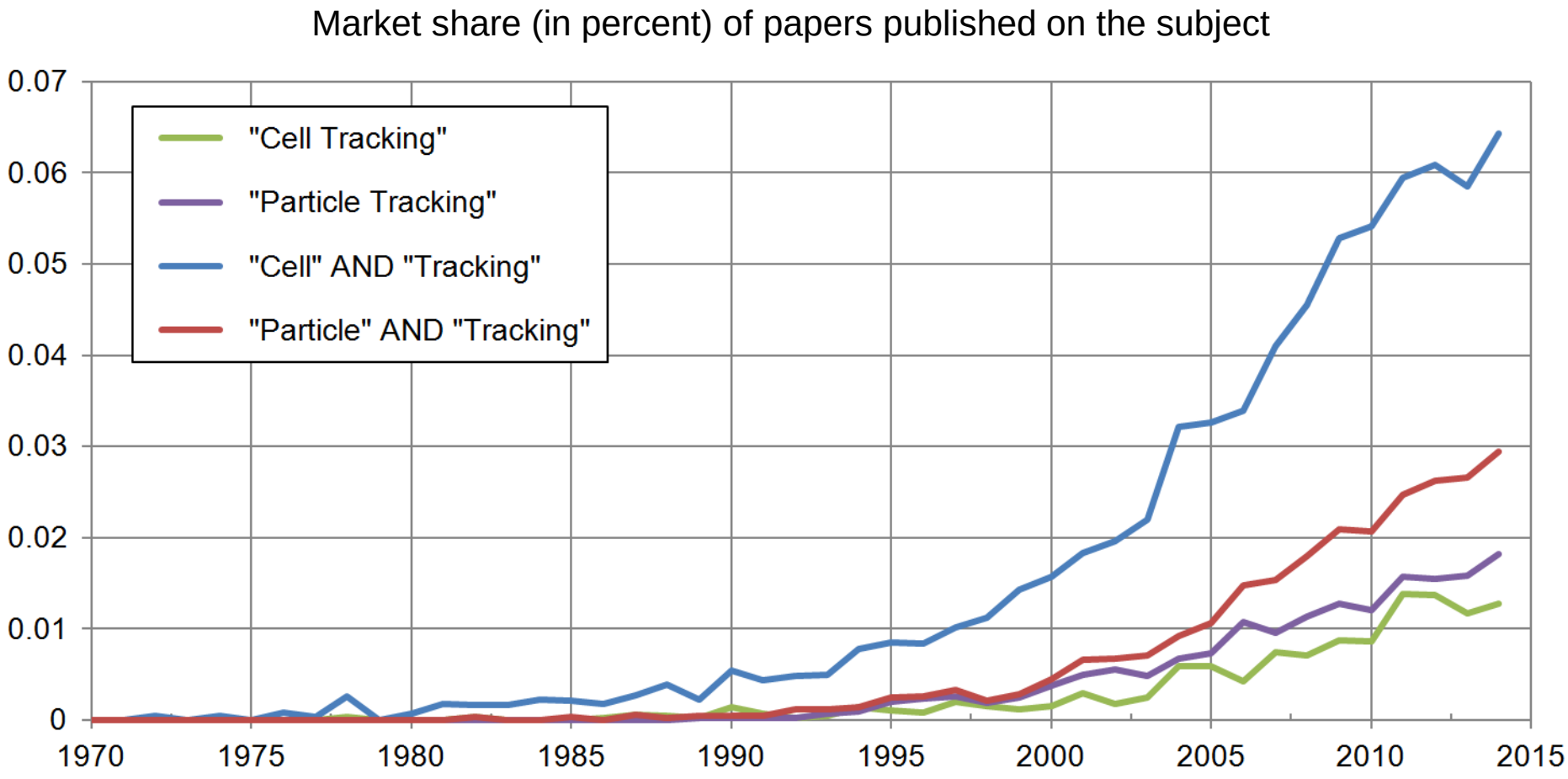
1nm 10nm 100nm 1μm 10μm 100μm 1mm

Drosophila embryogenesis



Keller et al. 2014

Increasing interest in tracking



PubMed, NLM, USA, January 2015

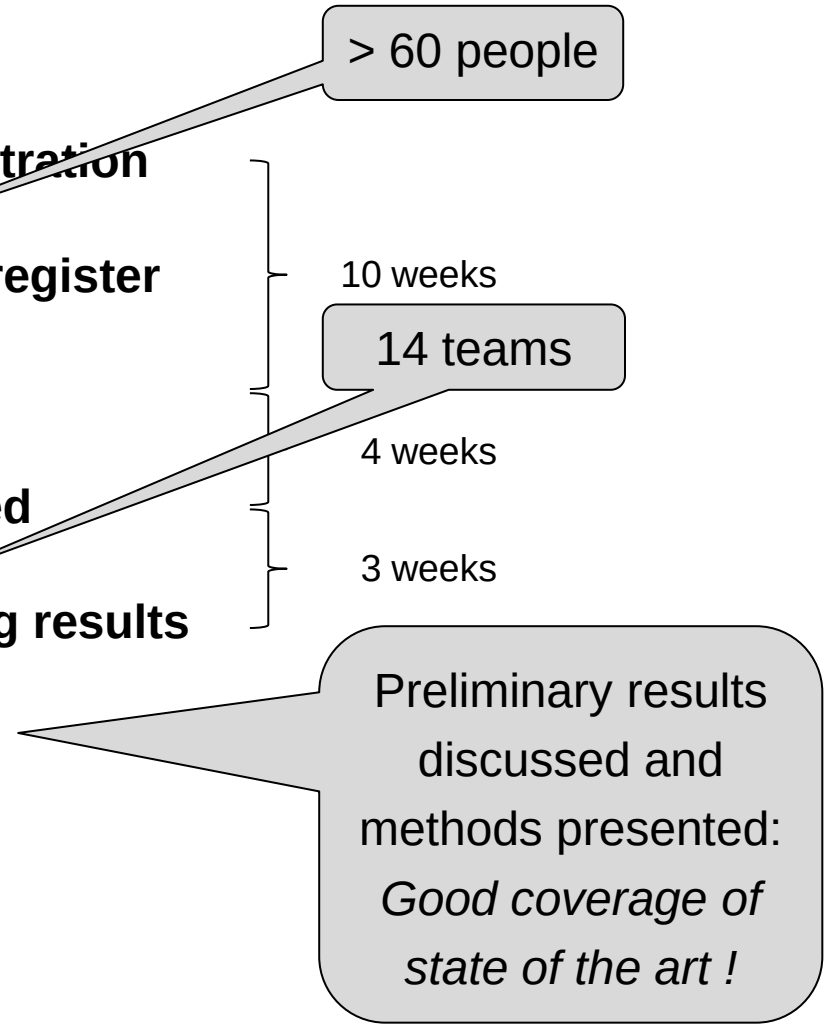
Many tools already available

Meijering et al. 2012
Methods in Enzymology

Name	Available	Platform	Source	Cell	Particle	Multiple	Dimensions	Automation	Author or Reference	Website
Braincells	Free	Win		√		√	2D	Manual	Gabor Ivancsy	http://pearl.elte.hu/~kyd/
CellProfiler	Free	Win/Lin/Mac	√	√	√	√	2D	Auto	Carpenter et al. (2006)	http://www.cellprofiler.org/
CellTrack	Free	Win	√	√		√	2D	Auto	Sacan et al. (2008)	http://db.cse.ohio-state.edu/CellTrack/
CellTracker	Free	Win		√		√	2D	Semi	Shen et al. (2006)	http://go.warwick.ac.uk/bretschneider/celltracker/
ClusterTrack	Free	Matlab	√		√	√	2D	Auto	Matov et al. (2010)	http://lccb.hms.harvard.edu/software.html
DCellIQ	Free	Matlab	√	√		√	2D	Auto	Li et al. (2010)	http://www.cbi-tmhs.org/Dcelliq/
DIAS	Paid	Win/Mac		√		√	3D	Auto	Wessels et al. (2006)	http://keck.biology.uiowa.edu/
DiaTrack	Paid	Win		√	√	√	3D	Auto	Semasopht (Switzerland)	http://www.semasopht.com/
DYNAMIK	Free	Matlab	√	√		√	2D	Auto	Mosig et al. (2009)	http://www.picb.ac.cn/sysbio/DYNAMIK/
FARSIGHT	Free	Win/Lin/Mac	√	√		√	3D	Auto	Bjornsson et al. (2008)	http://www.farsight-toolkit.org/
GMinPro	Free	Win			√	√	2D	Auto	Mashanov & Molloy (2007)	http://www.nimr.mrc.ac.uk/gmimpro/
ICY	Free	Java	√	√	√	√	3D	Auto	de Chaumont et al. (2011)	http://icy.bioimageanalysis.org/
Image-Pro Plus	Paid	Win		√	√	√	3D	Auto	Media Cybernetics (USA)	http://www.mediacy.com/index.aspx?page=IPP
ImarisTrack	Paid	Win/Mac		√	√	√	3D	Auto	Bitplane (Switzerland)	http://www.bitplane.com/go/products/imaristrack
LevelSetTracker	Free	Matlab	√	√		√	3D	Auto	Dzyubachyk et al. (2010)	http://celmia.bigr.nl/
LineageTracker	Free	ImageJ		√		√	2D	Auto	Till Bretschneider	http://go.warwick.ac.uk/bretschneider/lineagetracker/
ManualTracking	Free	ImageJ	√		√	√	3D	Manual	Fabrice Cordelières	http://rsb.info.nih.gov/ij/plugins/track/track.html
MetaMorph	Paid	Win		√	√	√	3D	Auto	Molecular Devices (USA)	http://www.moleculardevices.com/Products/Software.html
MTrack2	Free	ImageJ	√		√	√	2D	Auto	Nico Stuurman	http://valelab.ucsf.edu/~nico/IJplugins/MTrack2.html
MTrackJ	Free	ImageJ	√		√	√	3D	Manual	Erik Meijering	http://www.imagescience.org/meijering/software/mtrackj/
MTT	Free	Matlab	√		√	√	2D	Auto	Sergé et al. (2008)	http://www.ciml.univ-mrs.fr/lab/he-marguet.htm
Octane	Free	ImageJ	√		√	√	2D	Auto	Ji Yu lab	http://www.ccam.uchc.edu/yu/Software.shtml
Oko-Vision	Paid	Win		√		√	2D	Semi	Okolab (Italy)	http://www.oko-lab.com/cell_tracking.page
ParticleTracker	Free	ImageJ	√		√	√	3D	Auto	Sbalzarini et al. (2005)	http://weeman.inf.ethz.ch/ParticleTracker/
ParticleTracking	Free	IDL	√		√	√	2D	Auto	Crocker & Grier (1996)	http://physics.nyu.edu/grierlab/software.html
plusTipTracker	Free	Matlab	√		√	√	2D	Auto	Danuser lab	http://lccb.hms.harvard.edu/software.html
PolyParticleTracker	Free	Matlab	√		√	√	2D	Auto	Rogers et al. (2007)	http://personalpages.manchester.ac.uk/staff/david.kenwright/software.html
QuimP	Free	ImageJ		√			2D	Auto	Bosgraaf et al. (2009)	http://go.warwick.ac.uk/bretschneider/quimp/
SpeckleTrackerJ	Free	ImageJ	√		√	√	2D	Semi	Smith et al. (2011)	http://athena.physics.lehigh.edu/speckletrackerj/
SpotTracker	Free	ImageJ			√		2D	Auto	Sage et al. (2005)	http://bigwww.epfl.ch/sage/soft/spottracker/
StarryNite	Free	Win/Lin		√		√	3D	Auto	Murray et al. (2006)	http://waterston.gs.washington.edu/
TIKAL	Request	Win/Lin			√	√	3D	Auto	Bacher et al. (2004)	http://ibios.dkfz.de/tbi/
TLA	Free	Matlab	√	√		√	2D	Auto	Huth et al. (2011)	http://www.informatik.uni-ulm.de/ni/staff/HKestler/tla/
u-track	Free	Matlab	√		√	√	2D	Auto	Jaqaman et al. (2008)	http://lccb.hms.harvard.edu/software.html
Volocity	Paid	Win/Mac		√	√	√	3D	Auto	Perkin Elmer (USA)	http://cellularimaging.perkinelmer.com/products/volocity/demo/

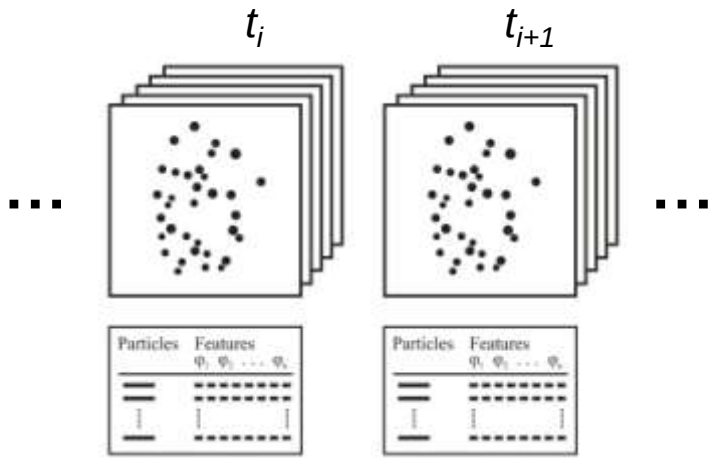
Objective comparison of algorithms

- 1 April 2011 **Idea born at ISBI 2011**
- 1 December 2011 **Website open for registration**
- 1 February 2012 **Deadline for teams to register**
- 15 February 2012 **Training data released**
- 15 March 2012 **Challenge data released**
- 6 April 2012 **Deadline for submitting results**
- 2 May 2012 **Workshop at ISBI 2012**
- November 2012 **Verification of results**
- Present **Paper published !**



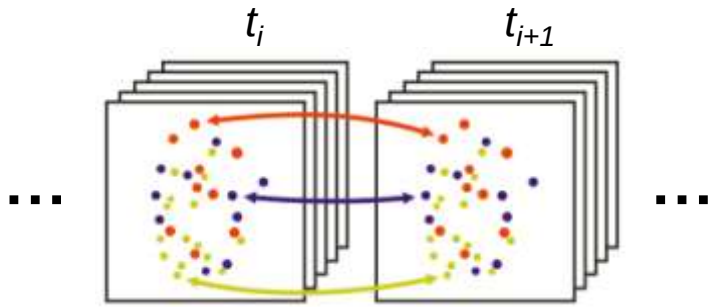
Participating methods

Particle detection



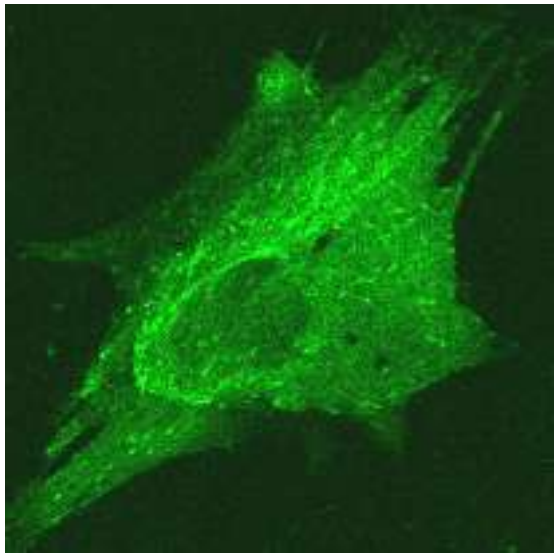
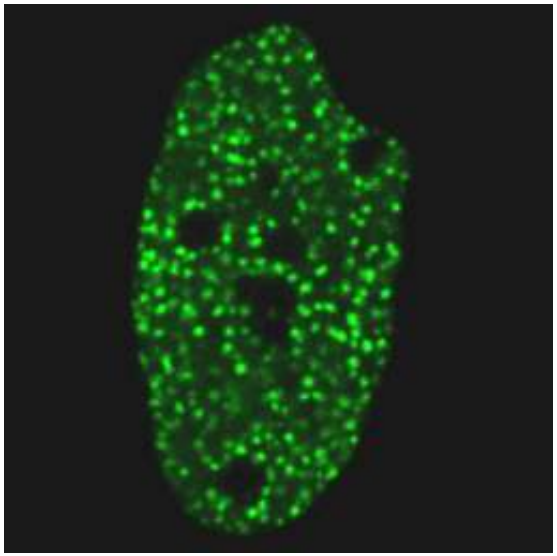
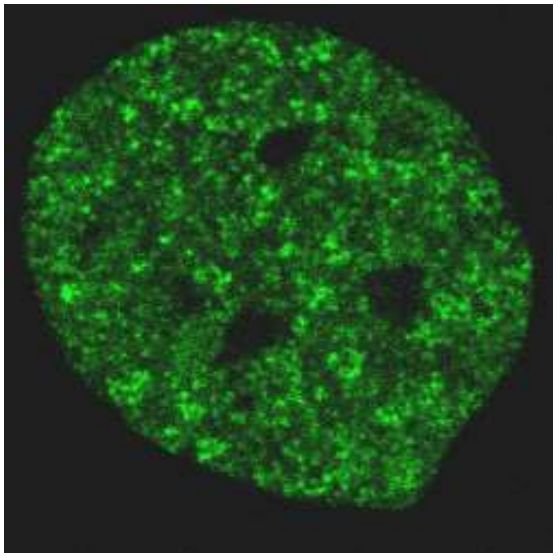
- Intensity thresholding
- Centroid calculation
- Convolution with disk
- Wavelet-based detection
- Local maxima finding
- Gaussian model fitting
- LoG / DoG filtering
- Morphological filtering

Particle linking



- Nearest-neighbor linking
- Multiple hypothesis tracking
- Viterbi path searching
- Multi-Kalman filtering
- Dynamic programming
- Interacting multiple motion models
- Simulated annealing energy minimization

Real image data…?

- Most realistic particle appearance and dynamics
- But… no ground truth available… manual annotation?
- Observer variability, subjectivity, incompleteness
- Known from previous evaluations to be inferior

Simulated image data

Most important factors affecting tracking performance?

Particle dynamics

- Random walk (2D)
- Near-constant velocity (2D)
- Switching random (2D)
- Switching directed (3D)

Particle density

- Low (≈ 100 particles)
- Medium (≈ 500 particles)
- High (≈ 1000 particles)

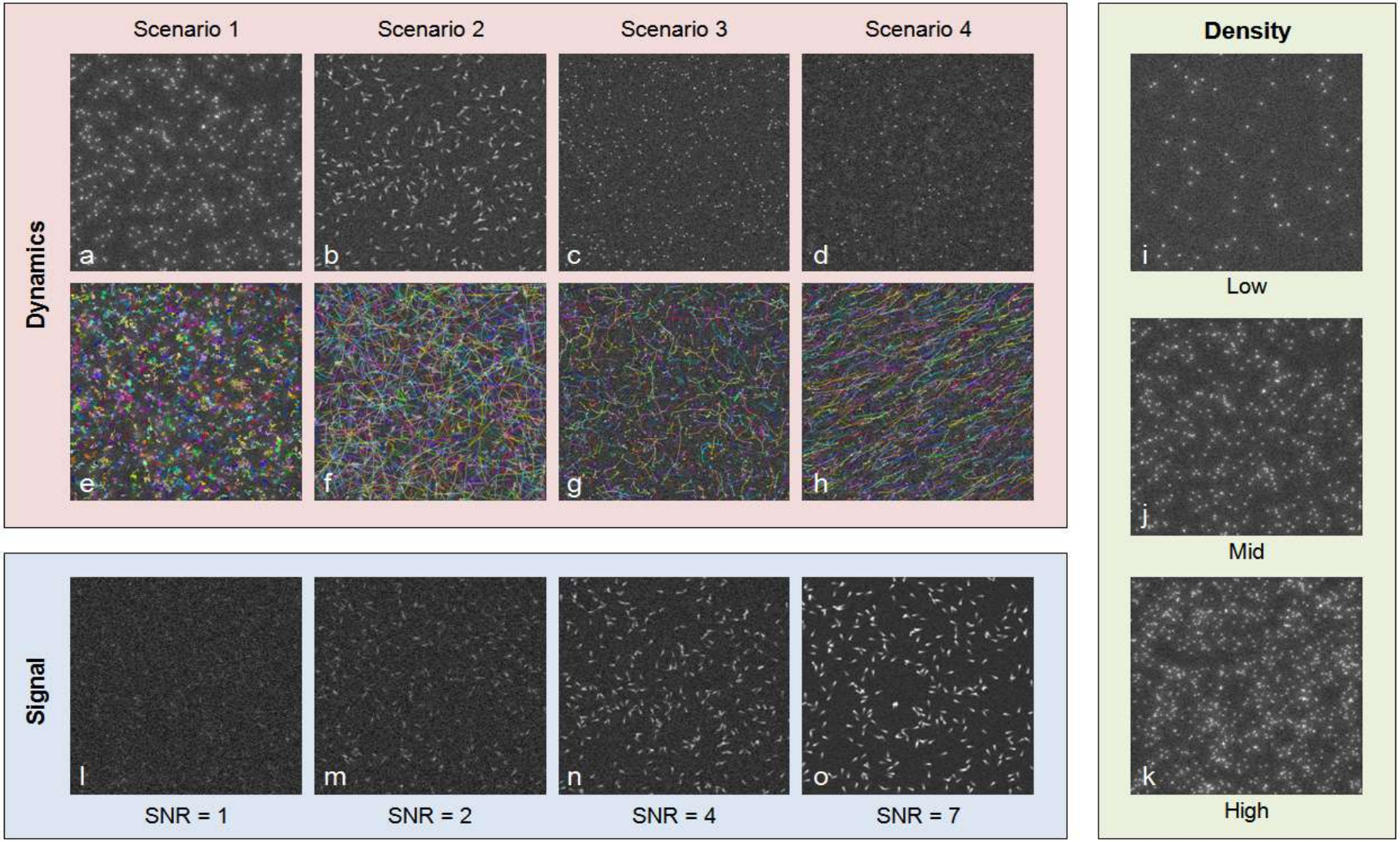
Particle signal

- Bad (SNR ≈ 1)
- Low (SNR ≈ 2)
- Critical (SNR ≈ 4)
- High (SNR ≈ 7)

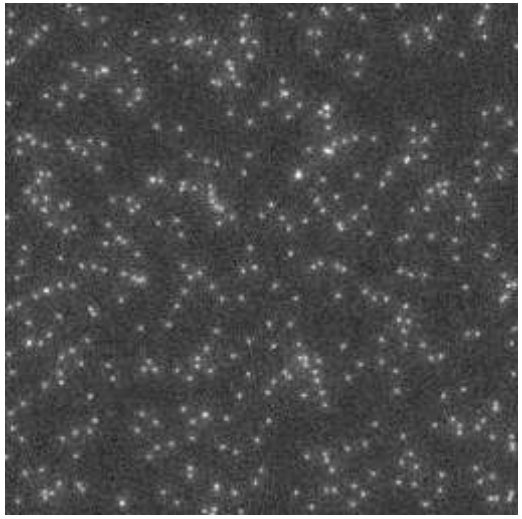
Total 48 sequences

- Fluorescence microscopy
- GFP-labeled particles
- Images 512 x 512 pixels
- Stacks of 10 slices
- Length 100 frames
- About 4 GB of data
- Airy or Gaussian PSF
- Poisson noise
- Random processes
- Track length ≥ 4 frames
- Mean length ≈ 15 frames
- No particle interaction
- Trajectory ambiguities
- Ground truth known

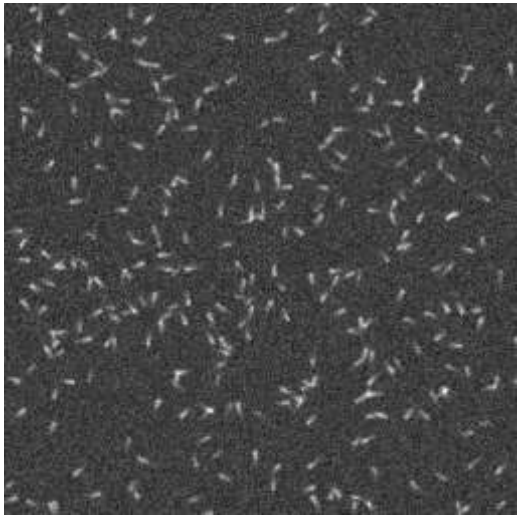
Simulated image data set



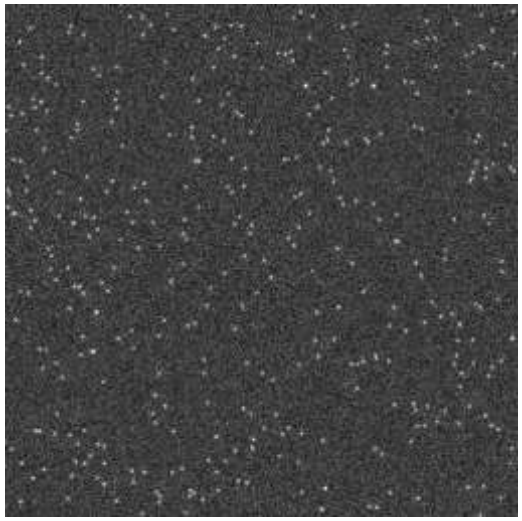
Simulated image data examples



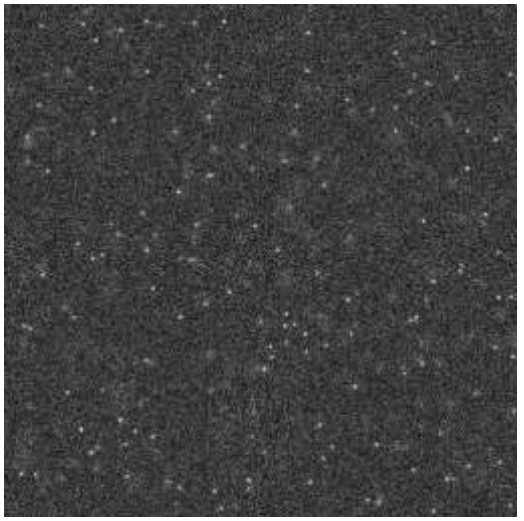
Scenario 1
Random
walk (2D)



Scenario 2
Near-constant
velocity (2D)



Scenario 3
Switching
random (2D)



Scenario 4
Switching
directed (3D)

Density = Medium
SNR = 4

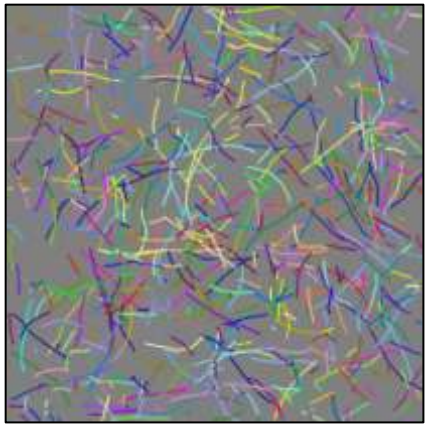
Quantitative performance measures

$$\alpha(X,Y) = 1 - \frac{d(X,Y)}{d(X,\varnothing)}$$

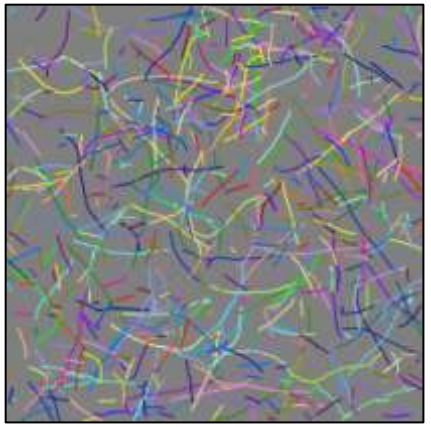
$$\beta(X,Y) = \frac{d(X,\varnothing) - d(X,Y)}{d(X,\varnothing) - d(S,\varnothing)}$$

X ⟷ Y Best possible match (OSPA and Munkres)

RMSE



Ground truth



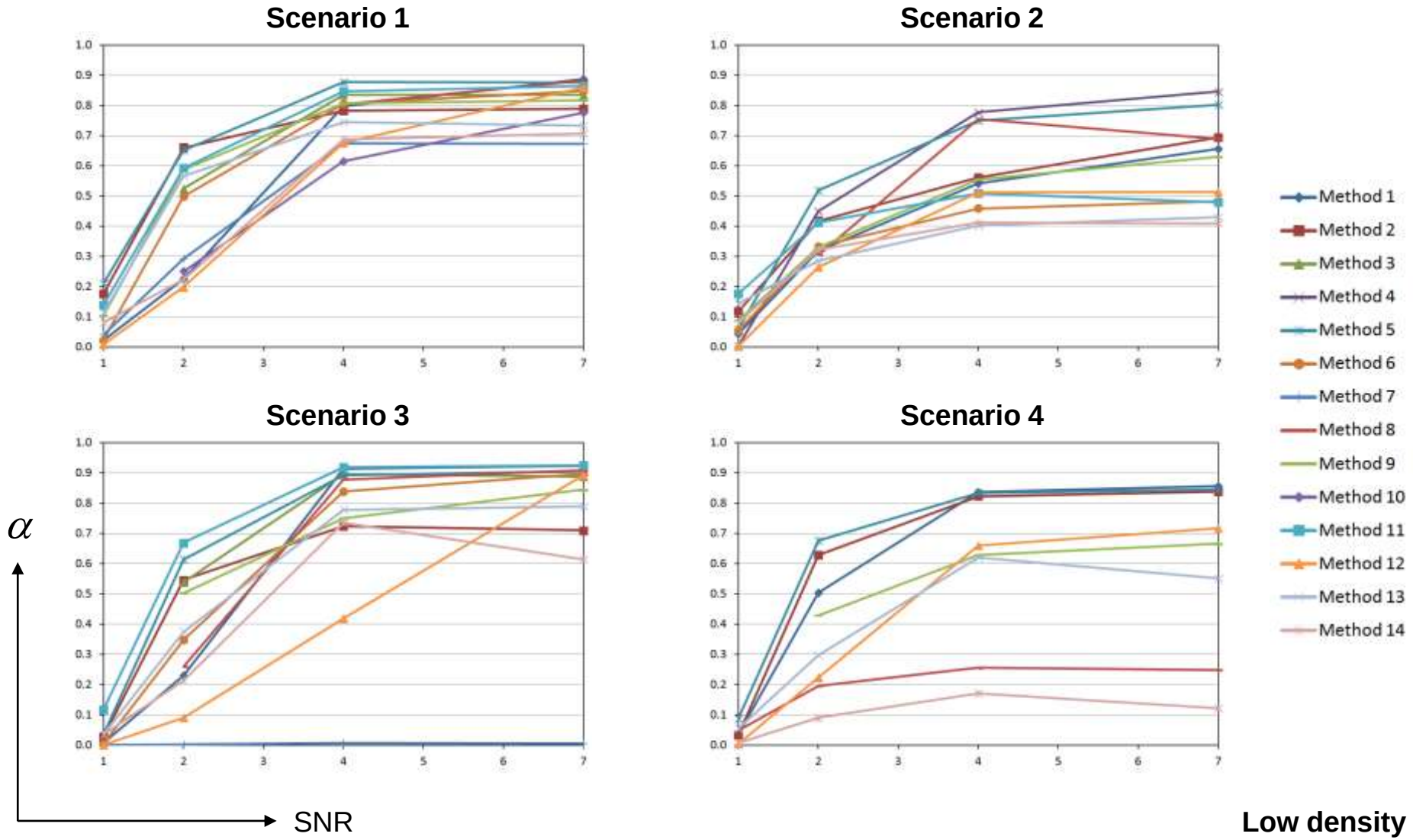
From tracker

Timing

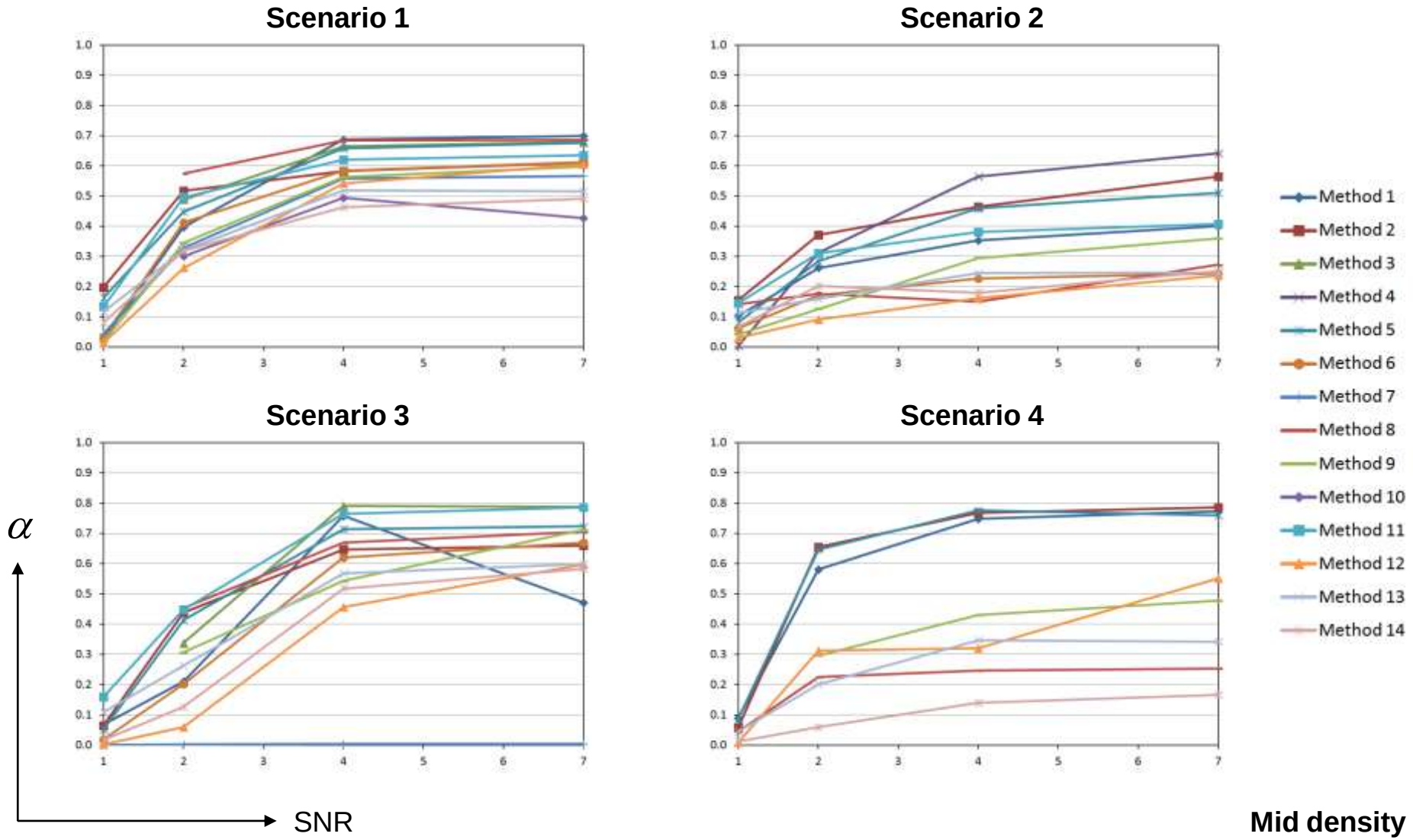
$$\text{JSC} = \frac{\text{MP}}{\text{MP} + \text{NMP} + \text{SP}}$$

$$\text{JSC}_\theta = \frac{\text{MT}}{\text{MT} + \text{NMT} + \text{ST}}$$

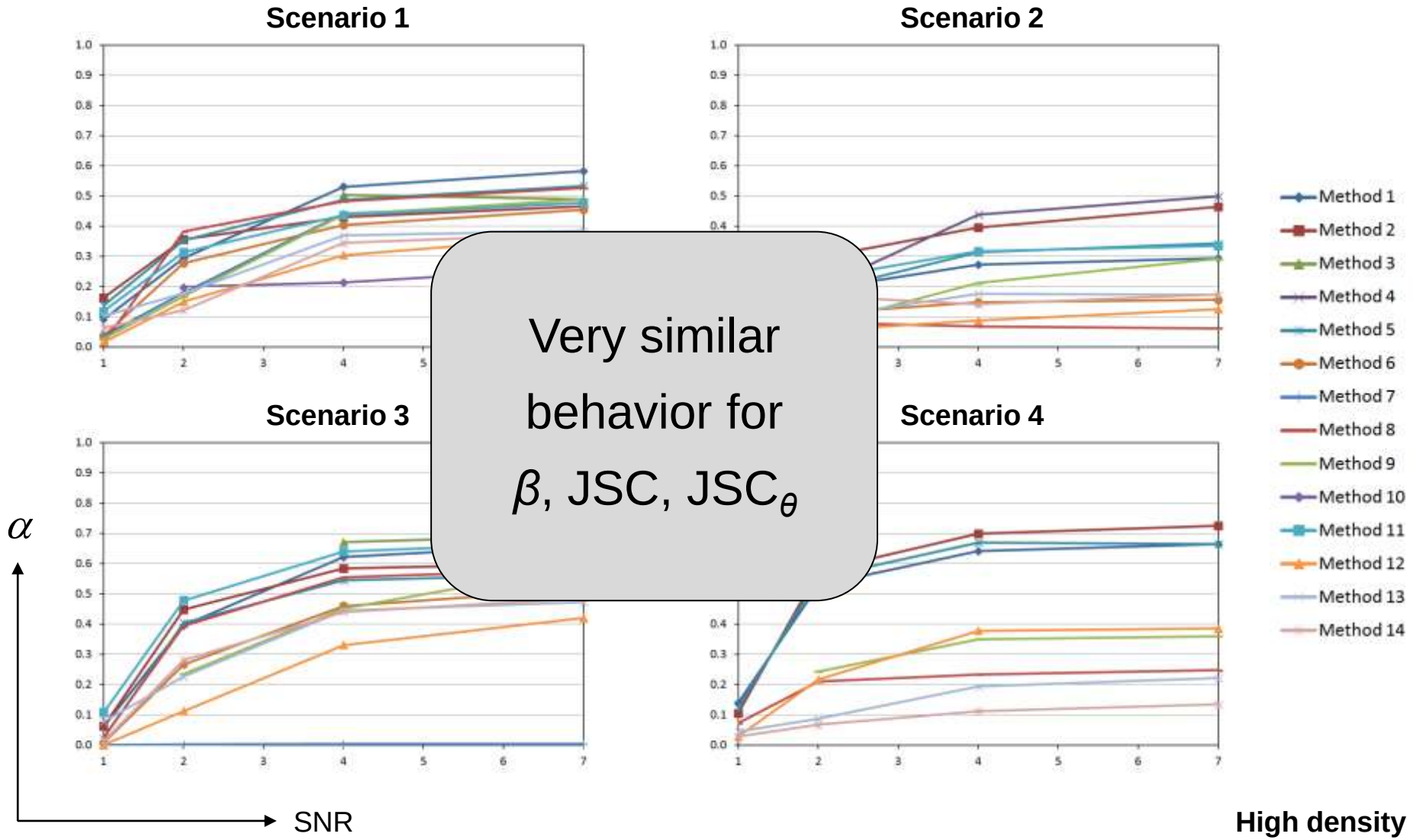
Selected challenge results



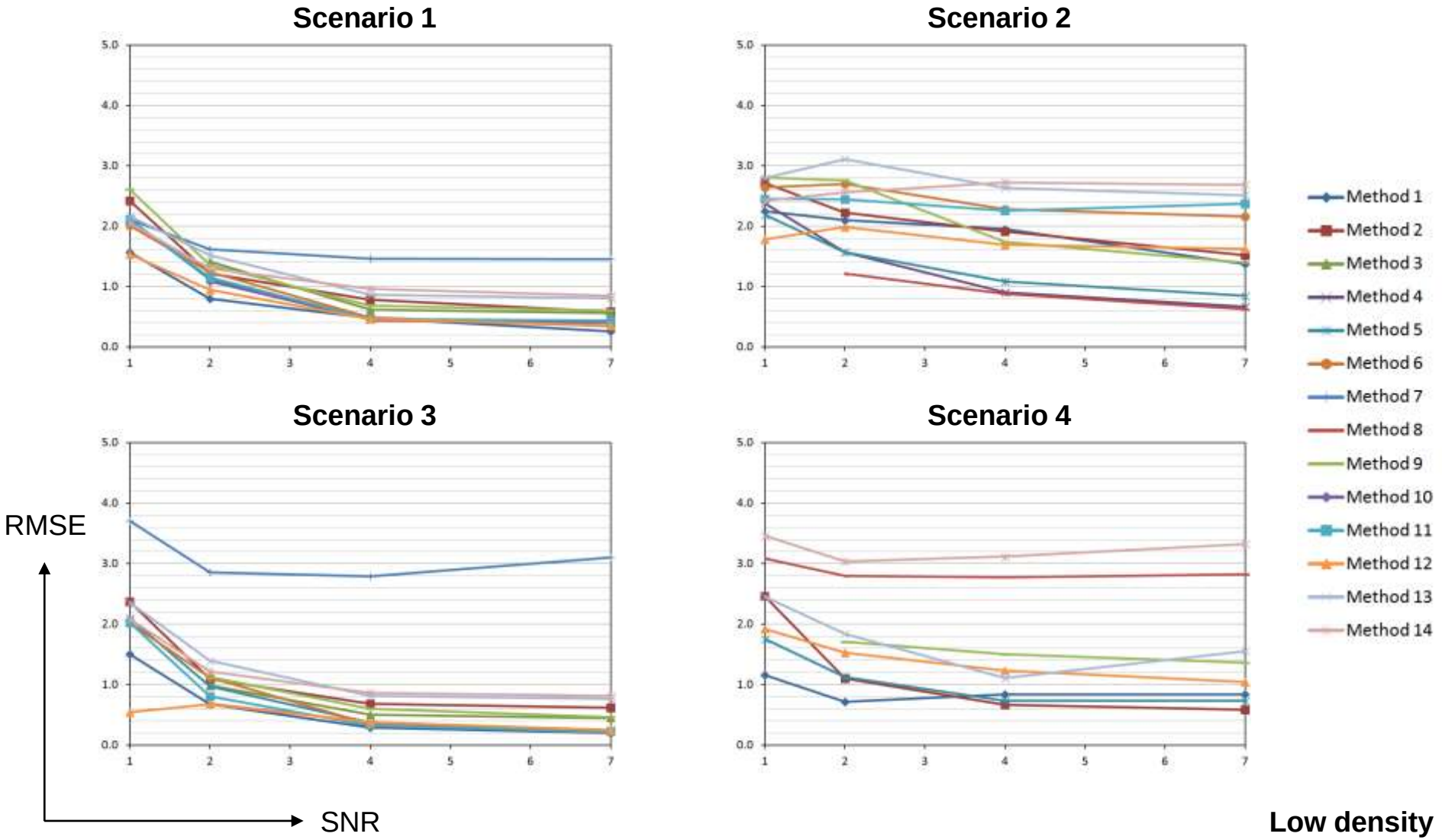
Selected challenge results



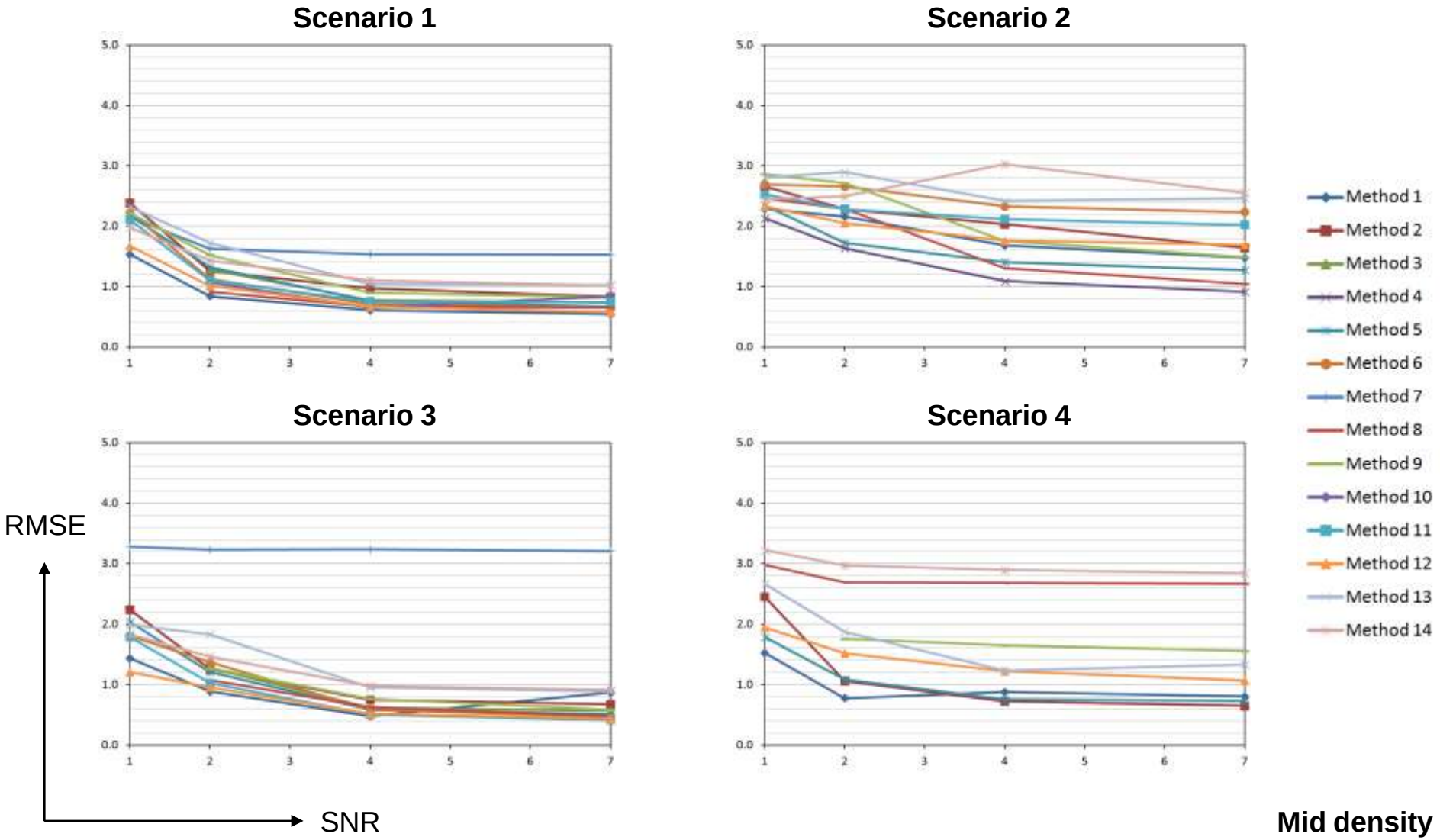
Selected challenge results



Selected challenge results

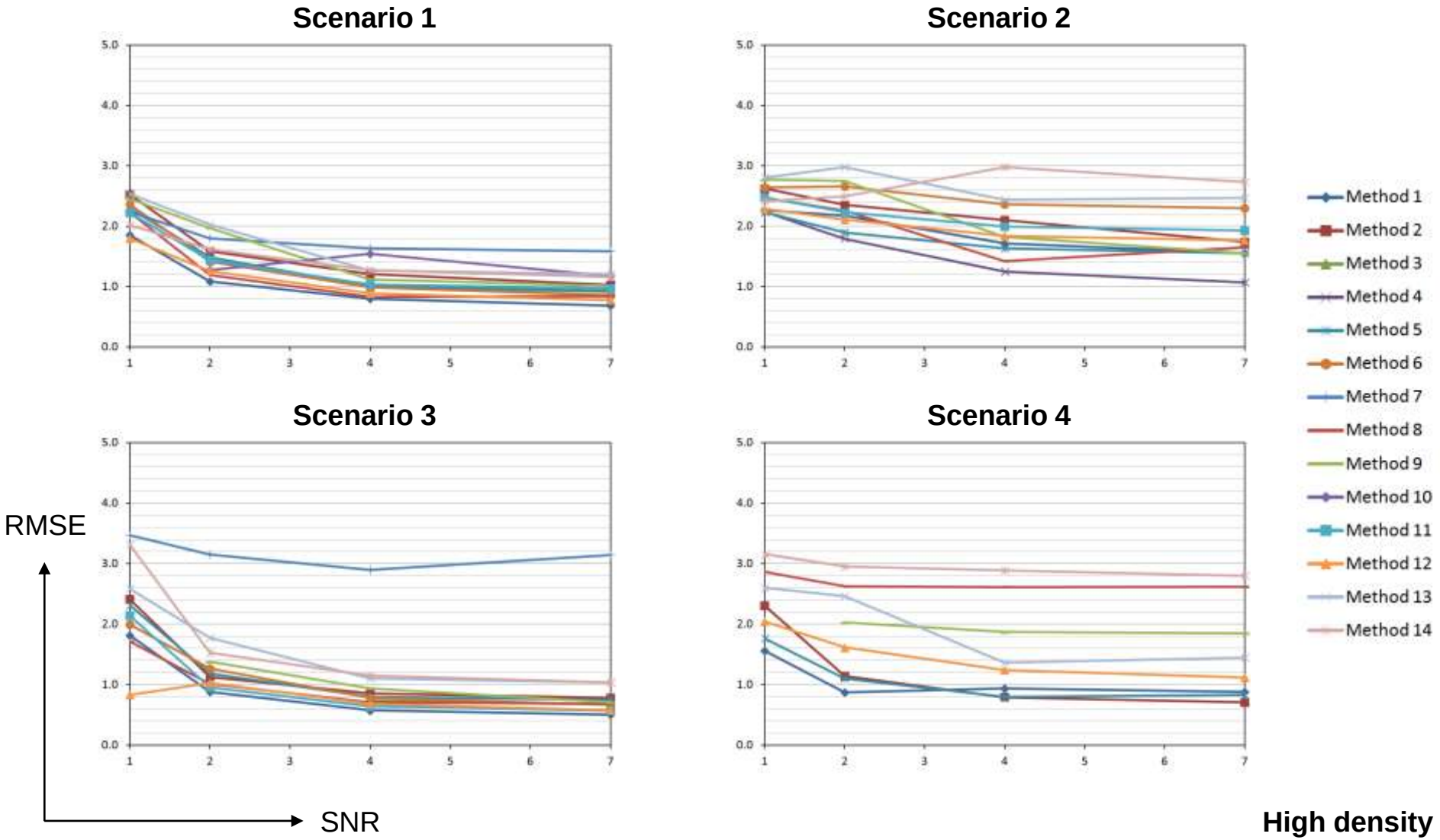


Selected challenge results



Mid density

Selected challenge results



General observations

- Overall trends in good agreement with expectations
- No single method best overall (dynamics, density, SNR)
- Best detection using Gaussian and centroid based methods
- Best linking using motion models and global optimization
- Best methods not necessarily computationally slowest
- Better methods are possible by different combinations
- Much room for improvement remains (detection + linking)
- Fundamentally new concepts (learning-based?) needed
- More detailed analyses in published challenge paper

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ANALYSIS

OPEN

Objective comparison of particle tracking methods

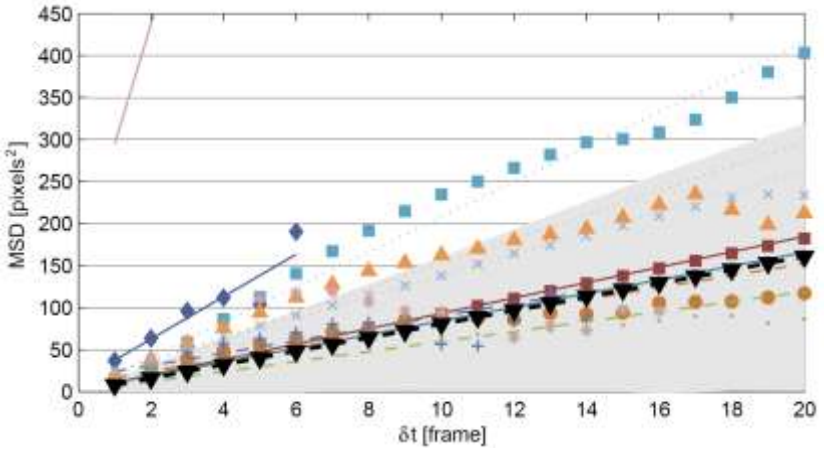
Nicolas Chenouard[1–3,25], Ihor Smal[4,5,25], Fabrice de Chaumont[1,25], Martin Maška[6,7,25], Ivo F Sbalzarini[8], Yuanhao Gong[8], Janick Cardinale[8], Craig Carthel[9], Stefano Coraluppi[9], Mark Winter[10], Andrew R Cohen[10], William J Godinez[11,12], Karl Rohr[11,12], Yannis Kalaidzidis[13,14], 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

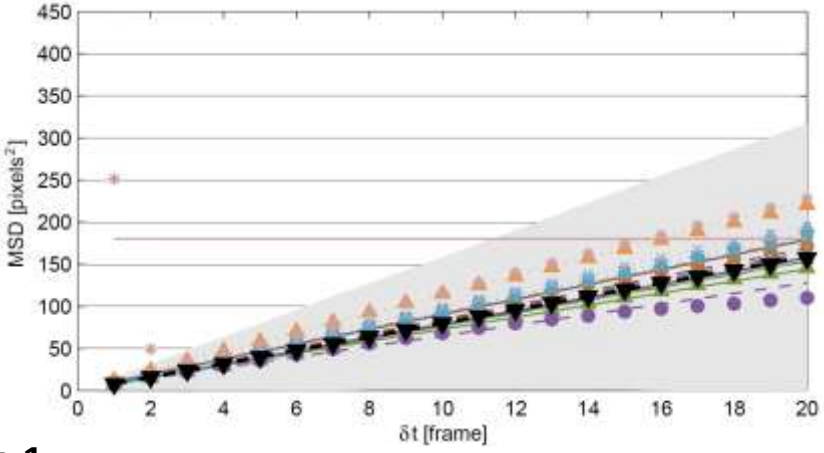
processes is particle tracking. Here, a 'particle' may be anything from a single molecule to a macromolecular complex, organelle, virus or microsphere[12], and the task of detecting and following individual particles in a time series of images is often (somewhat confusingly) referred to as 'single-particle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

Mean-squared displacement results

SNR = 1



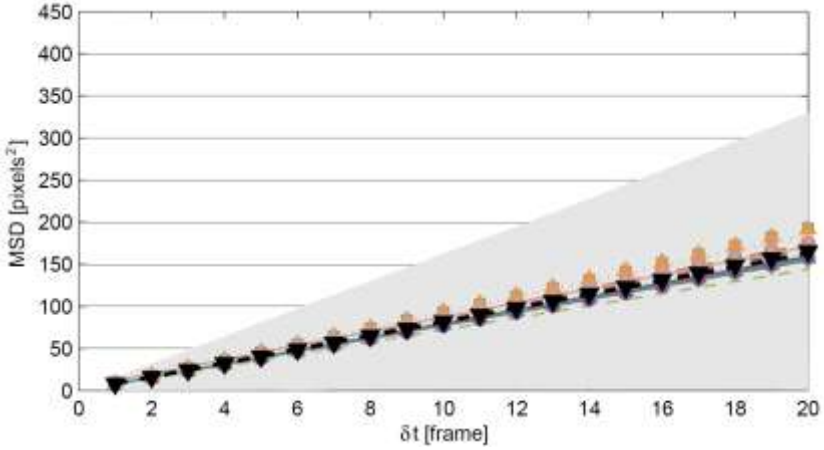
SNR = 2



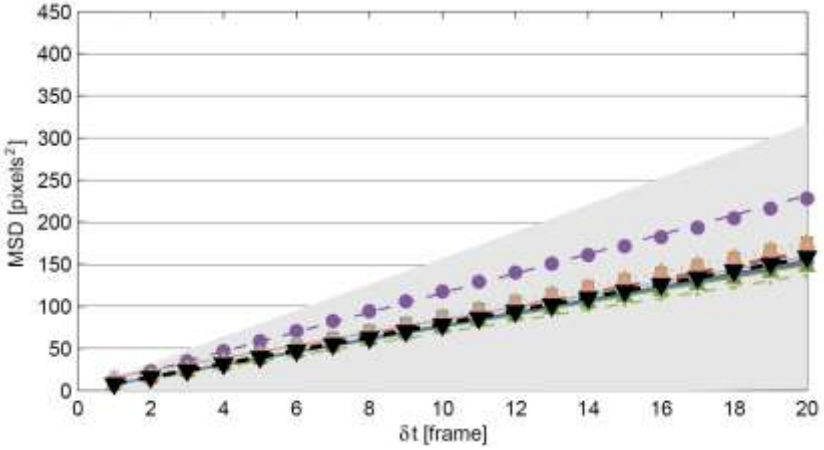
Scenario 1

Mid density

SNR = 4

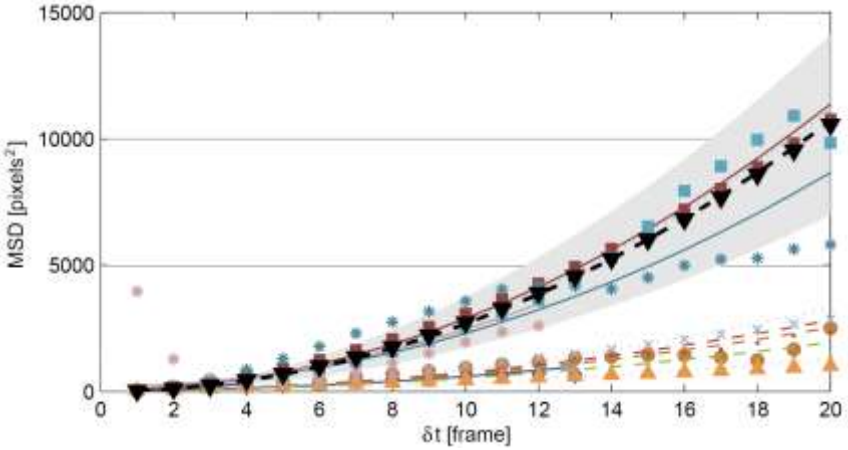


SNR = 7

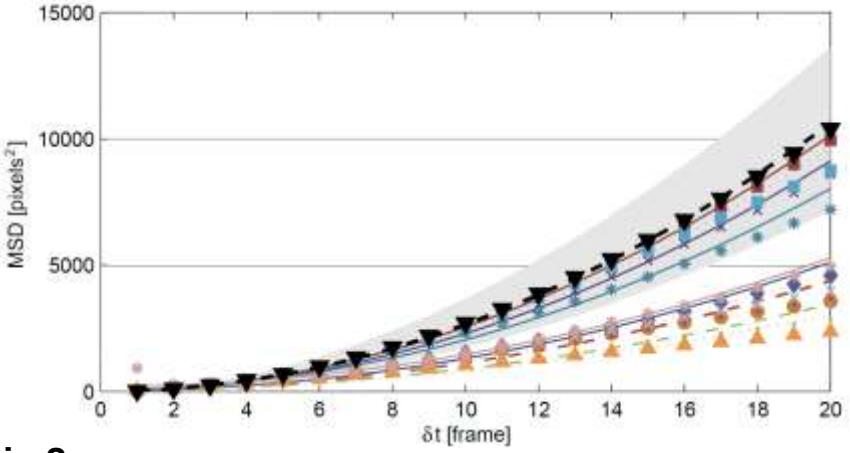


Mean-squared displacement results

SNR = 1



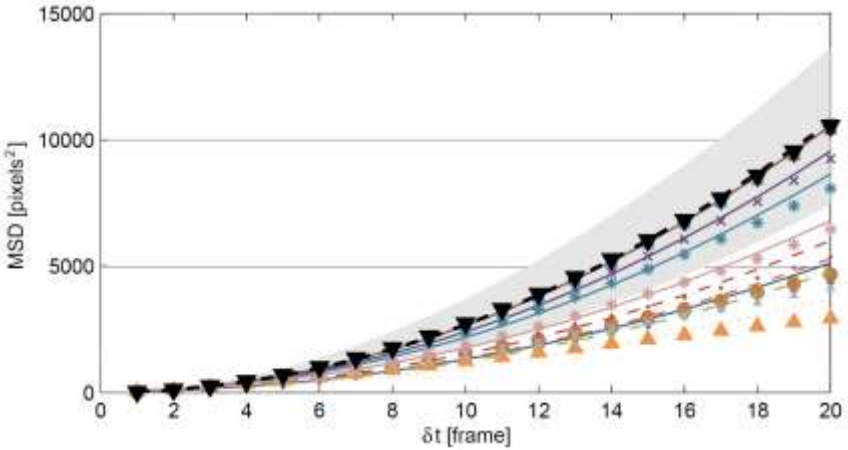
SNR = 2



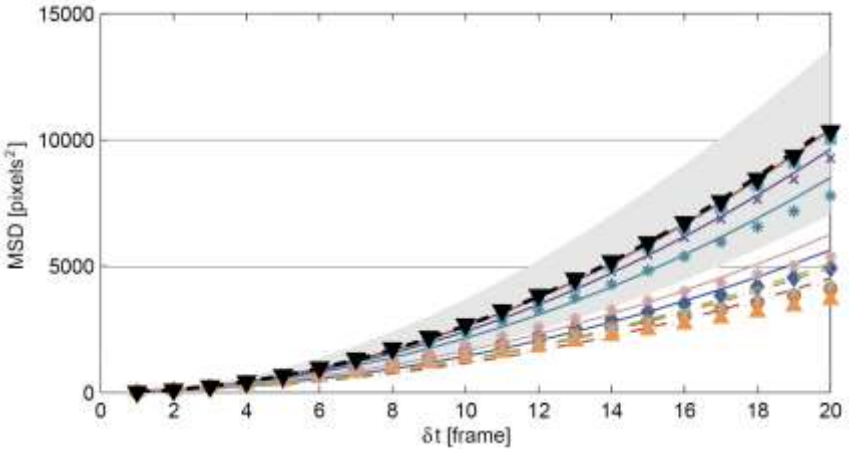
Scenario 2

Mid density

SNR = 4



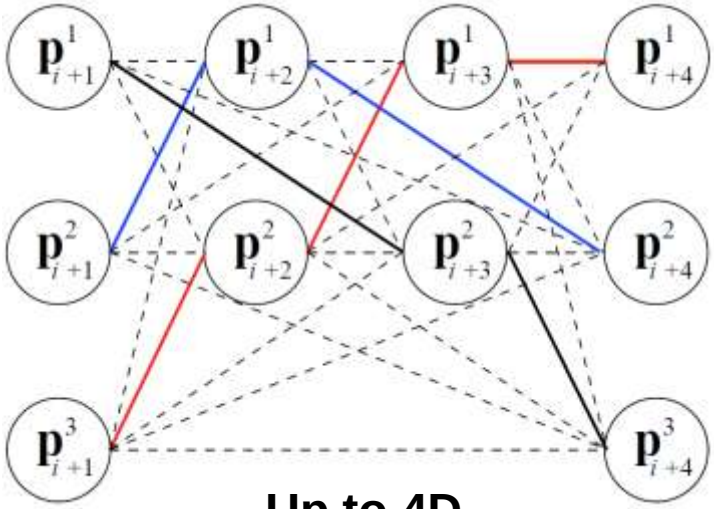
SNR = 7



Linking as a function of detection performance

Most common linking algorithms

- Multi-Dimensional Assignment (MDA)
- Noniterative Greedy Assignment (NGA)
- Interacting Multiple Models (IMM)
- Linear Assignment Procedure (LAP)
- Greedy Nearest-Neighbor (GNN)



Up to 4D

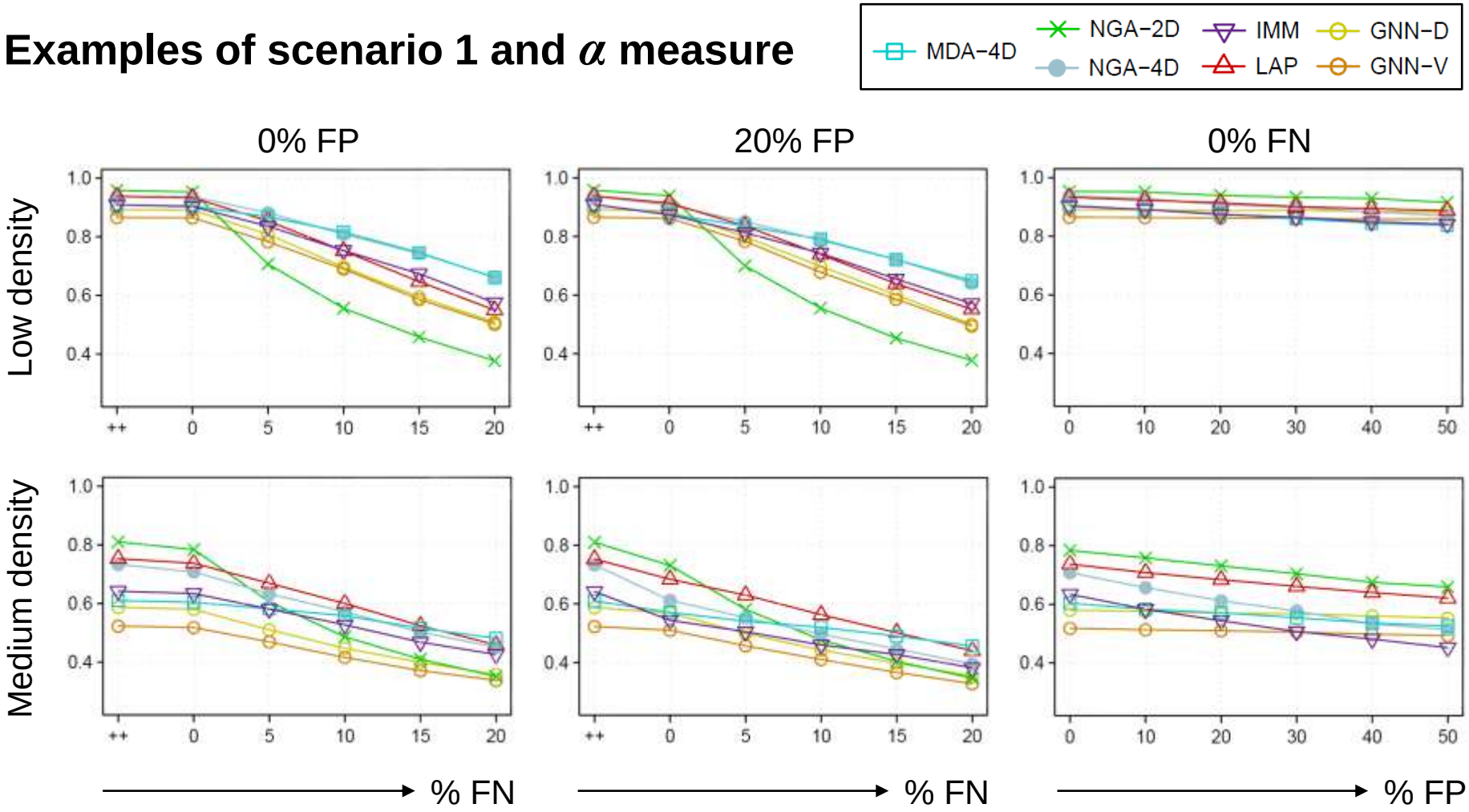
Enhanced ground-truth evaluation data set

- Four motion scenarios (random-walk, linear, mix 2D & 3D)
- Low (~100) and medium (~500 particles) density levels
- False-negative (FN) detection levels 0, 5, 10, 15, 20%
- False-positive (FP) detection levels 0, 10, 20, 30 ,40, 50%

240 cases

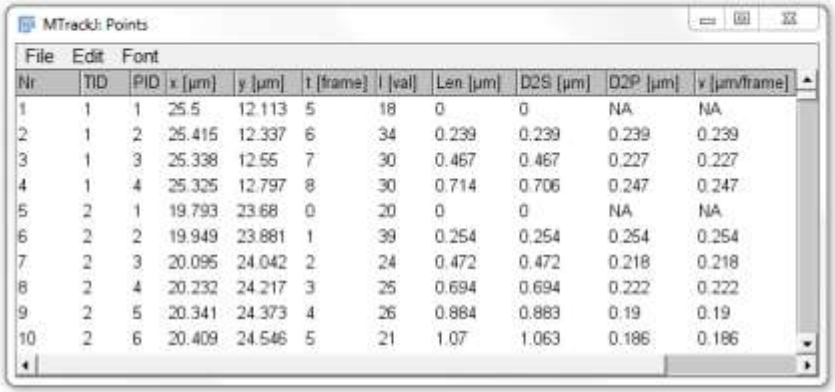
Linking as a function of detection performance

Examples of scenario 1 and α measure

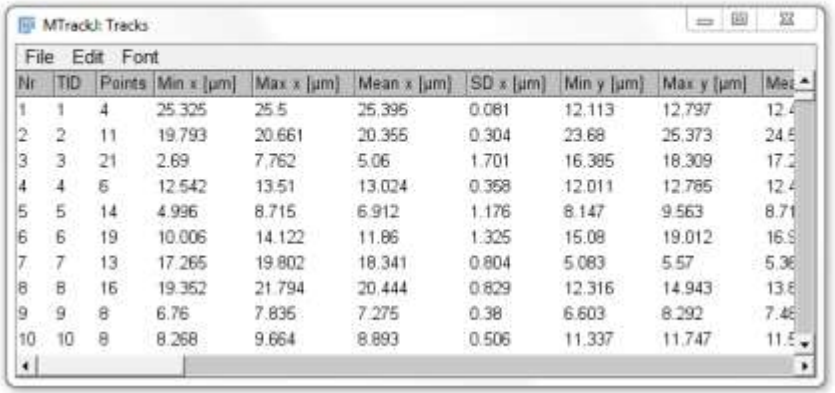


Linking is much more sensitive to missing than to spurious detections !

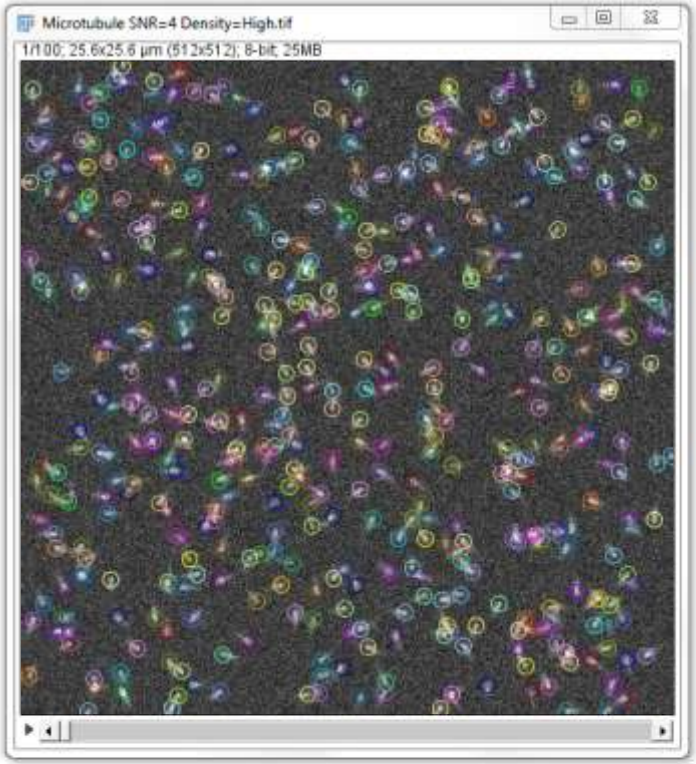
MTrackJ2 for advanced particle and cell tracking



Nr	TID	PID	x [µm]	y [µm]	t [frame]	I [val]	Len [µm]	D2S [µm]	D2P [µm]	v [µm/frame]
1	1	1	25.5	12.113	5	18	0	0	NA	NA
2	1	2	25.415	12.337	6	34	0.239	0.239	0.239	0.239
3	1	3	25.338	12.55	7	30	0.467	0.467	0.227	0.227
4	1	4	25.325	12.797	8	30	0.714	0.706	0.247	0.247
5	2	1	19.793	23.68	0	20	0	0	NA	NA
6	2	2	19.949	23.881	1	39	0.254	0.254	0.254	0.254
7	2	3	20.095	24.042	2	24	0.472	0.472	0.218	0.218
8	2	4	20.232	24.217	3	25	0.694	0.694	0.222	0.222
9	2	5	20.341	24.373	4	26	0.884	0.883	0.19	0.19
10	2	6	20.409	24.546	5	21	1.07	1.063	0.186	0.186



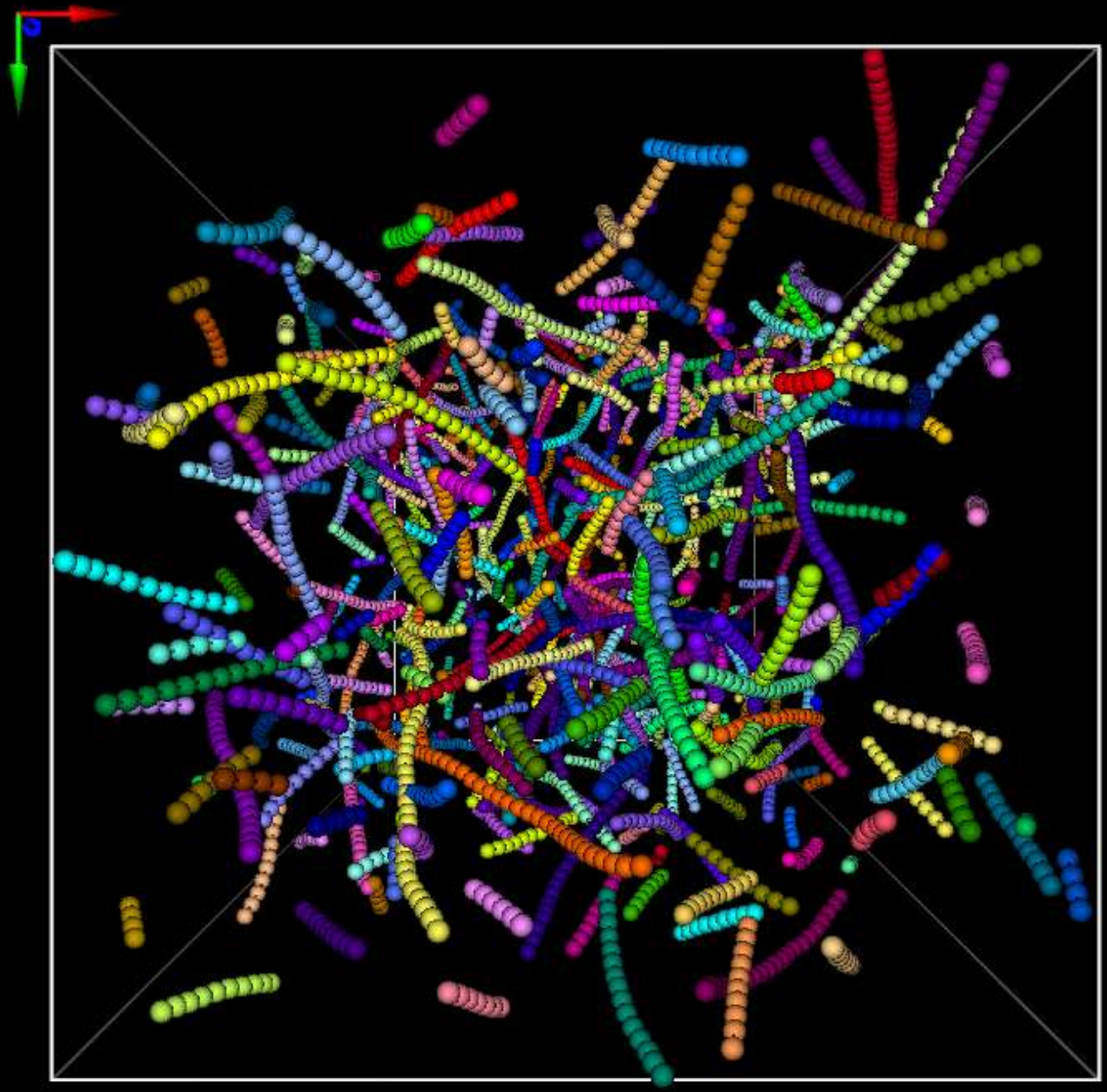
Nr	TID	Points	Min x [µm]	Max x [µm]	Mean x [µm]	SD x [µm]	Min y [µm]	Max y [µm]	Mea
1	1	4	25.325	25.5	25.395	0.081	12.113	12.797	12.4
2	2	11	19.793	20.661	20.355	0.304	23.68	25.373	24.5
3	3	21	2.69	7.762	5.06	1.701	16.385	18.309	17.2
4	4	6	12.542	13.51	13.024	0.368	12.011	12.785	12.4
5	5	14	4.996	8.715	6.912	1.176	8.147	9.563	8.71
6	6	19	10.006	14.122	11.86	1.325	15.08	19.012	16.9
7	7	13	17.265	19.802	18.341	0.804	5.083	5.57	5.36
8	8	16	19.352	21.794	20.444	0.829	12.316	14.943	13.6
9	9	8	6.76	7.835	7.275	0.38	6.603	8.292	7.46
10	10	8	8.268	9.664	8.893	0.506	11.337	11.747	11.5



To be released soon!

- Fully automated tracking solutions
- Fully manual tracking and track editing
- Customizable track visualization
- Support for multiple file formats

http://www.imagescience.org/meijering/software/mtrackj/



Bioinformatics

A benchmark for comparison of cell tracking algorithms

Martin Maška[1,2], Vladimír Ulman[1], David Svoboda[1], Pavel Matula[1], Petr Matula[1], Cristina Ederra[2], Ainhoa Urbiola[2], Tomás España[2], Subramanian Venkatesan[3], Deepak M.W. Balak[3], Pavel Karas[1], Tereza Bolcková[1], Markéta Štreitová[1], Craig Carthel[4], Stefano Coraluppi[4], Nathalie Harder[5], Karl Rohr[5], Klas E. G. Magnusson[6], Joakim Jaldén[6], Helen M. Blau[7], Oleh Dzyubachyk[8], Pavel Křížek[9], Guy M. Hagen[9], David Pastor-Escuredo[10], Daniel Jimenez-Carretero[10], Maria J. Ledesma-Carbayo[10], Arrate Muñoz-Barrutia[2], Erik Meijering[3], Michal Kozubek[1] and Carlos Ortiz-de-Solorzano[2,*]

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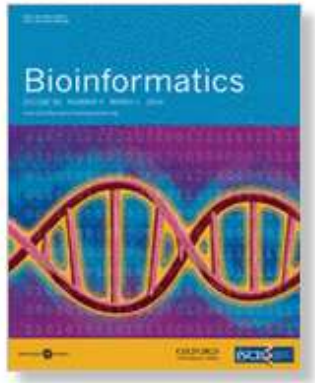
Abstract

Motivation: Automatic tracking of cells in multidimensional time-lapse fluorescence microscopy is an important task in many biomedical applications. A novel framework for objective evaluation of cell tracking algorithms has been established under the auspices of the IEEE International Symposium on Biomedical Imaging 2013 Cell Tracking Challenge. In this article, we present the logistics, datasets, methods and results of the challenge and lay down the principles for future uses of this benchmark.



NOV 29

Cell Tracking Challenge

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Erik Meijering
Erasmus Medical Center, Rotterdam, The Netherlands

Arrate Muñoz Barrutia
Carlos III University, Madrid, Spain

Third Edition at ISBI 2015 !

Website

http://www.codesolorzano.com/celltrackingchallenge/

Challenge Abstract

Tracking moving cells in time-lapse video sequences is a challenging task, required for many applications in both scientific and industrial settings. Properly characterizing how cells move as they interact with their surrounding environment is key to understanding the mechanobiology of cell migration and its multiple implications in both normal tissue development and many diseases. Our proposal is to leverage on the experience, methods and results of the ISBI'13 and ISBI'14 Cell Tracking Challenges to expand and enrich our comprehensive benchmark for comparison of cell tracking algorithms by attracting new participants, and new submissions. To this end will use our existing dataset repository, which includes 2D and 3D fluorescence, Phase Contrast and Differential Interference Contrast microscopy videos, and realistic simulations of moving nuclei both in 2D and 3D. Furthermore, we will provide new light-sheet microscopy 3D embryonic developmental data, probably the most challenging cell tracking problem existing today.

Summary

- **Bioimage analysis is a huge challenge!**
  - Rapid developments in microscopic imaging
  - Rapid developments in computer technology
  - To be matched by computer vision methods

- **Recent developments shaping the future**
  - Improved availability of bioimage analysis methods
  - Improved availability of image data and ground truth
  - Improved availability of objective comparison results