# INFO - H - 501

Pattern recognition and image analysis

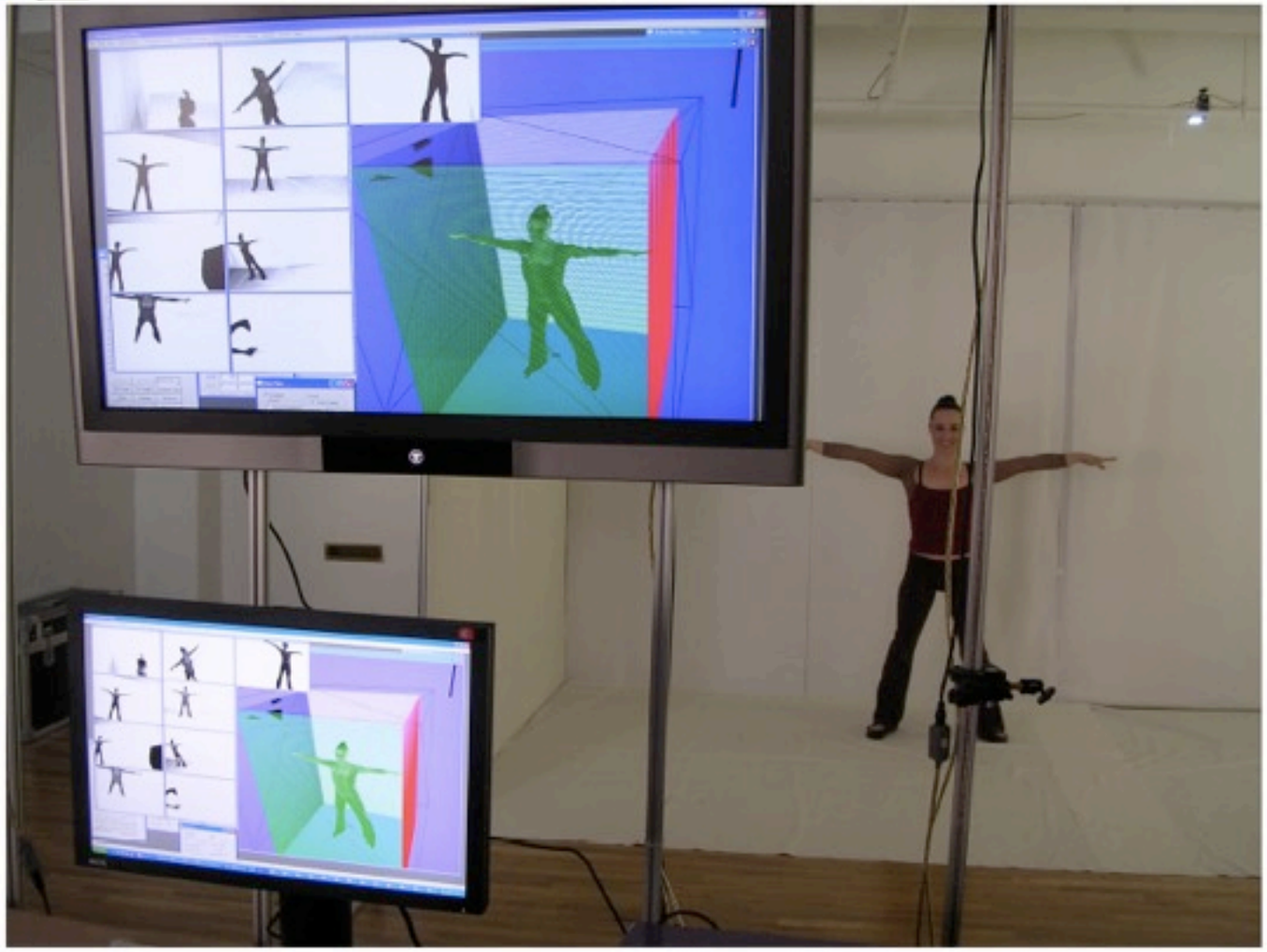
## Object Tracking

# Object tracking

- optical flow [HCVA] vol2 p310, [IPAMV] p512
- meanshift 2D/3D
- cell tracking
- particle filter
- body skeleton fitting on range data (particle filter)
- face tracking using color histogram
- 3D reconstruction from n-range images
-

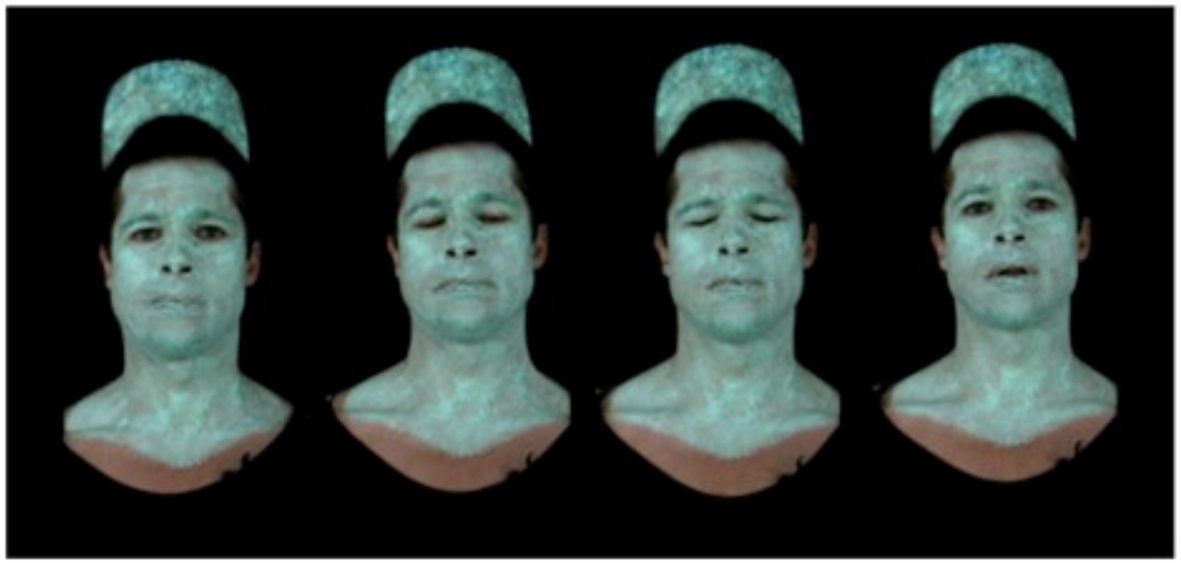
# Motion capture

http://sitemaker.umich.edu/pavelka/files/cunningham-dance.jpg



http://venturebeat.com/wp-content/uploads/2008/07/2-organic-motion-actor-and-outputcenter.jpg

# Face capture

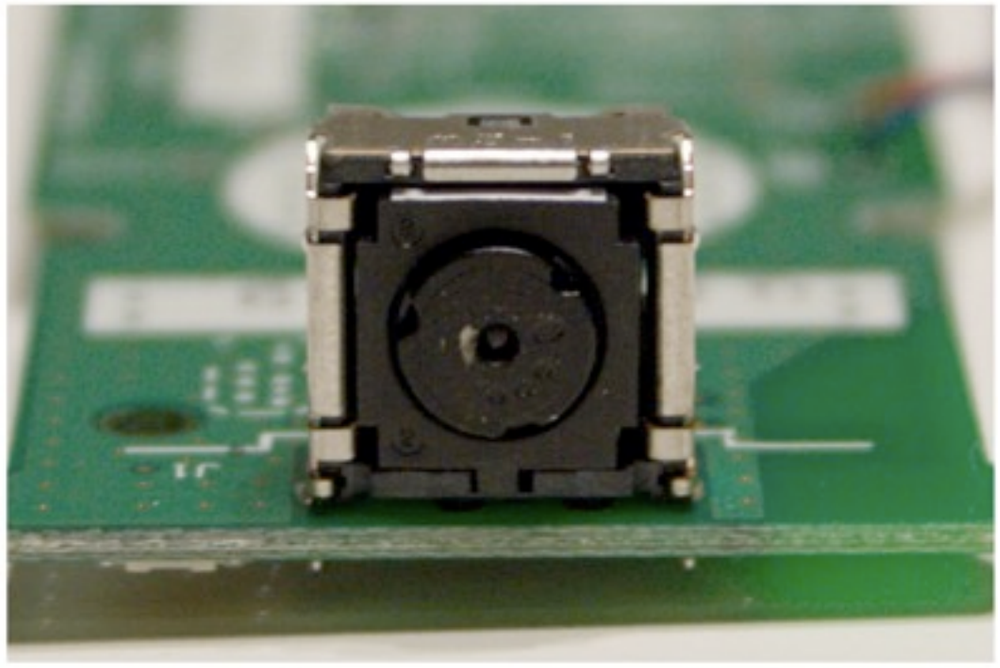


http://www.popularfront.com/wp-content/uploads/2009/03/ben_1.jpg

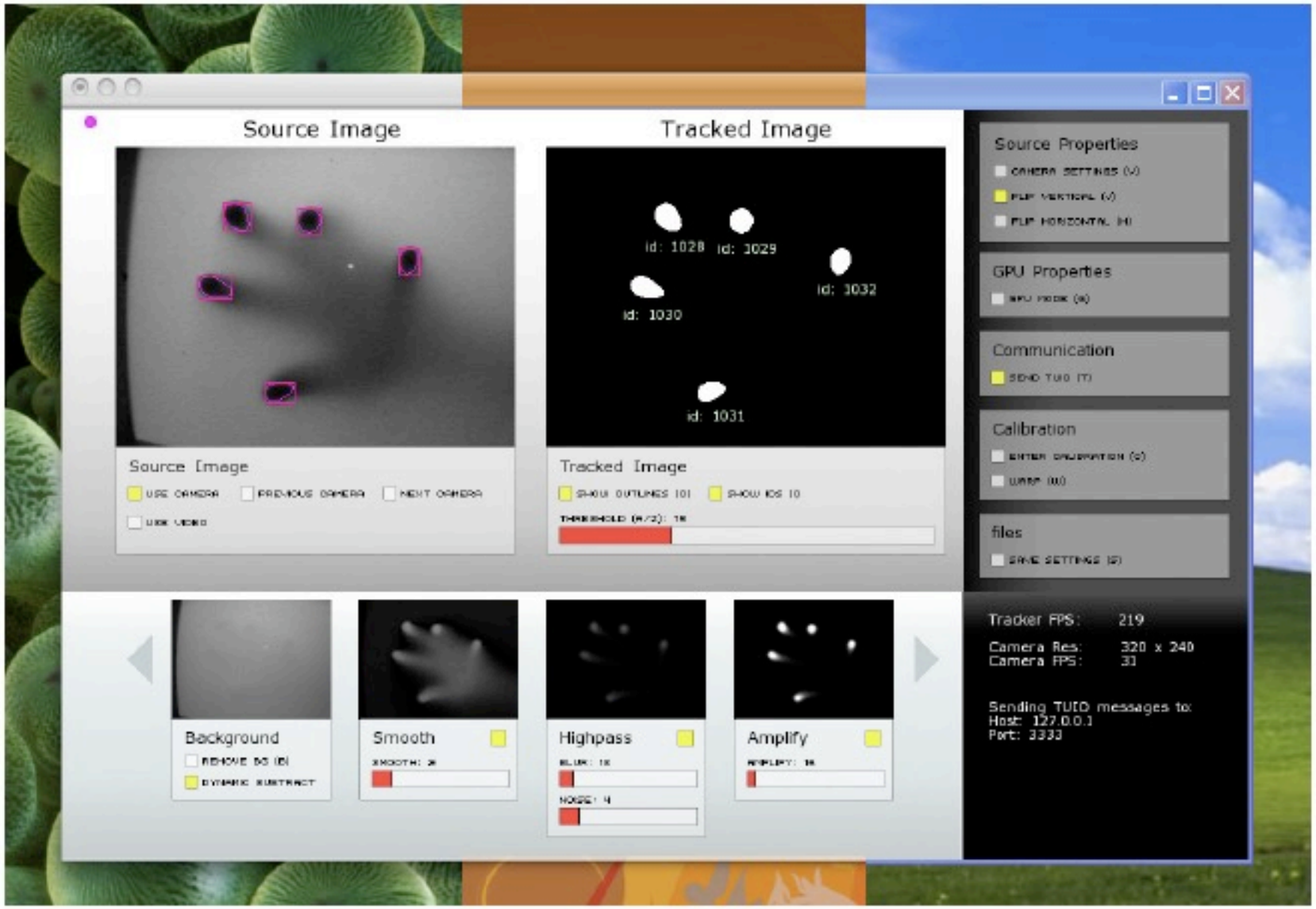
http://www.popularfront.com/wp-content/uploads/2009/03/ben_2.jpg

http://graphics8.nytimes.com/images/2006/07/31/business/31motion.large2.jpg

# HMI

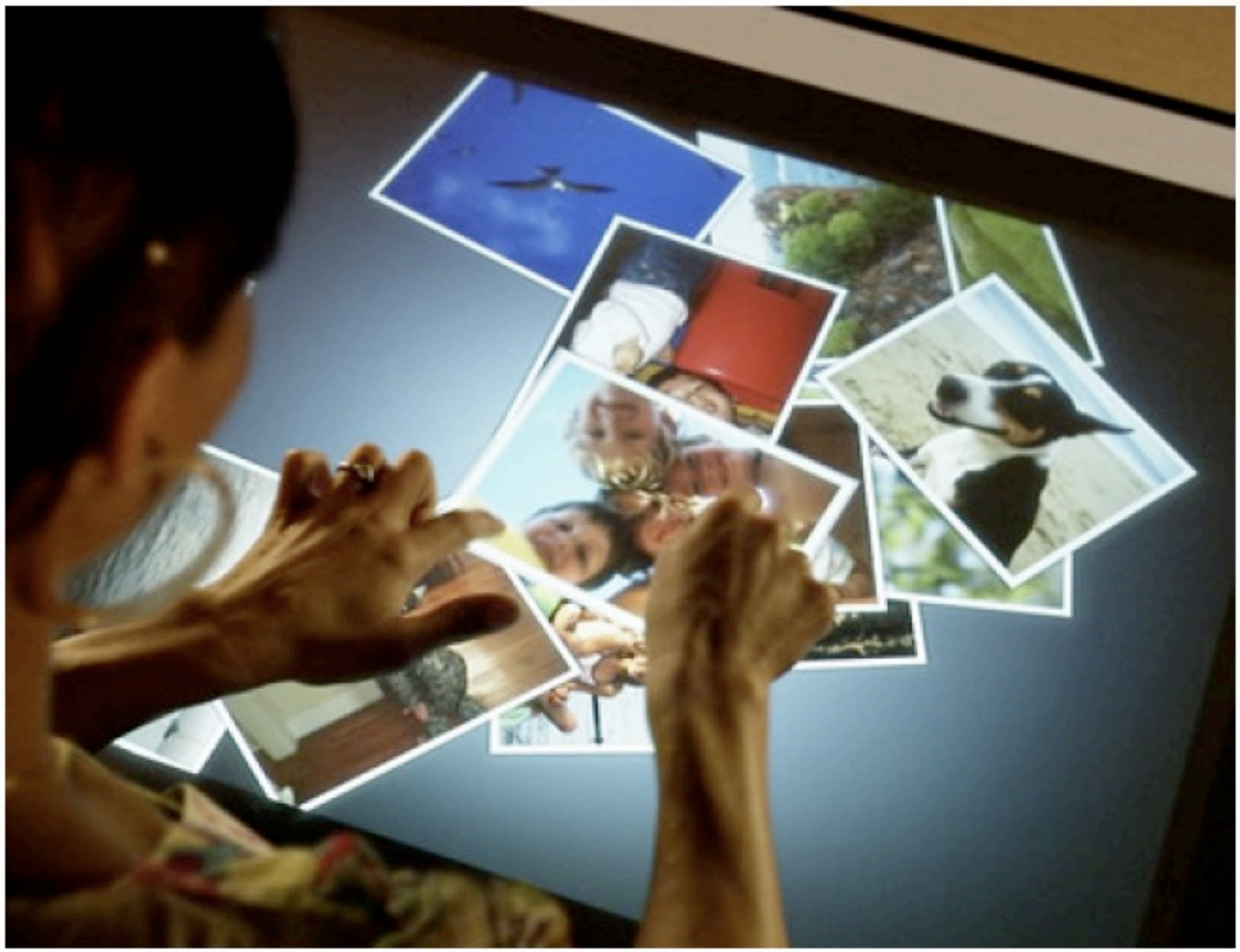



# HMI




http://www.nuigroup.com/uploads/cross.jpg

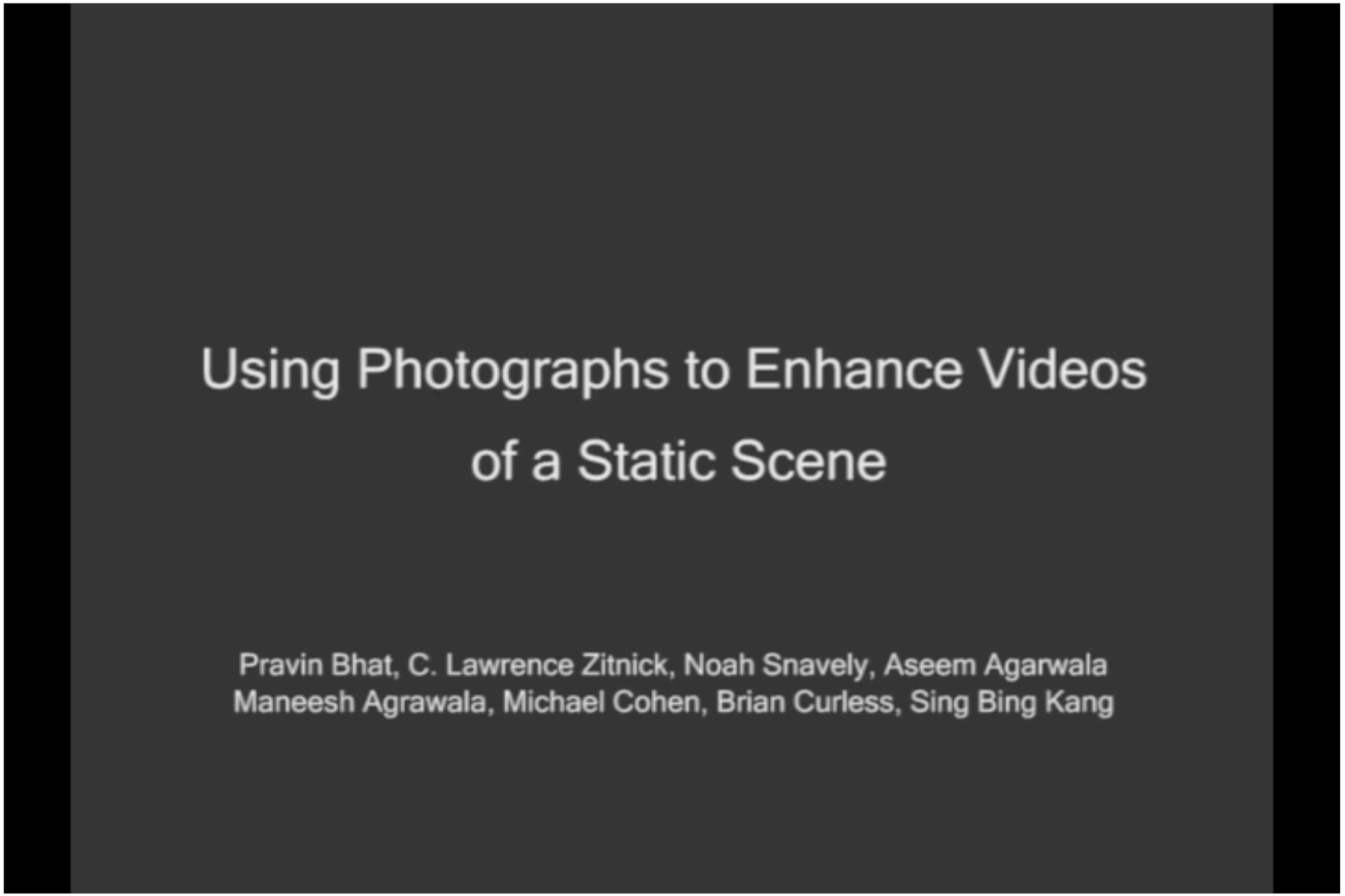
# HMI



http://www.globalgiants.com/archives/fotos/MICROSOFT-SURfaceComputer01.jpg

# Complex example: point detection

- video quality enhancement using high res pictures (http://grail.cs.washington.edu/projects/videoenhancement/videoEnhancement.htm)


Using Photographs to Enhance Videos of a Static Scene
Pravin Bhat, C. Lawrence Zitnick, Noah Snavely, Aseem Agarwala
Maneesh Agrawala, Michael Cohen, Brian Curless, Sing Bing Kang

# what are the different techniques involved ?

# what are the different techniques involved ?

- detection of specific points
- point pairing
- pose estimation
- 3D reconstruction
- structure from motion
- graph cut algorithm

# Demo

- Structure from motion

# Tracking

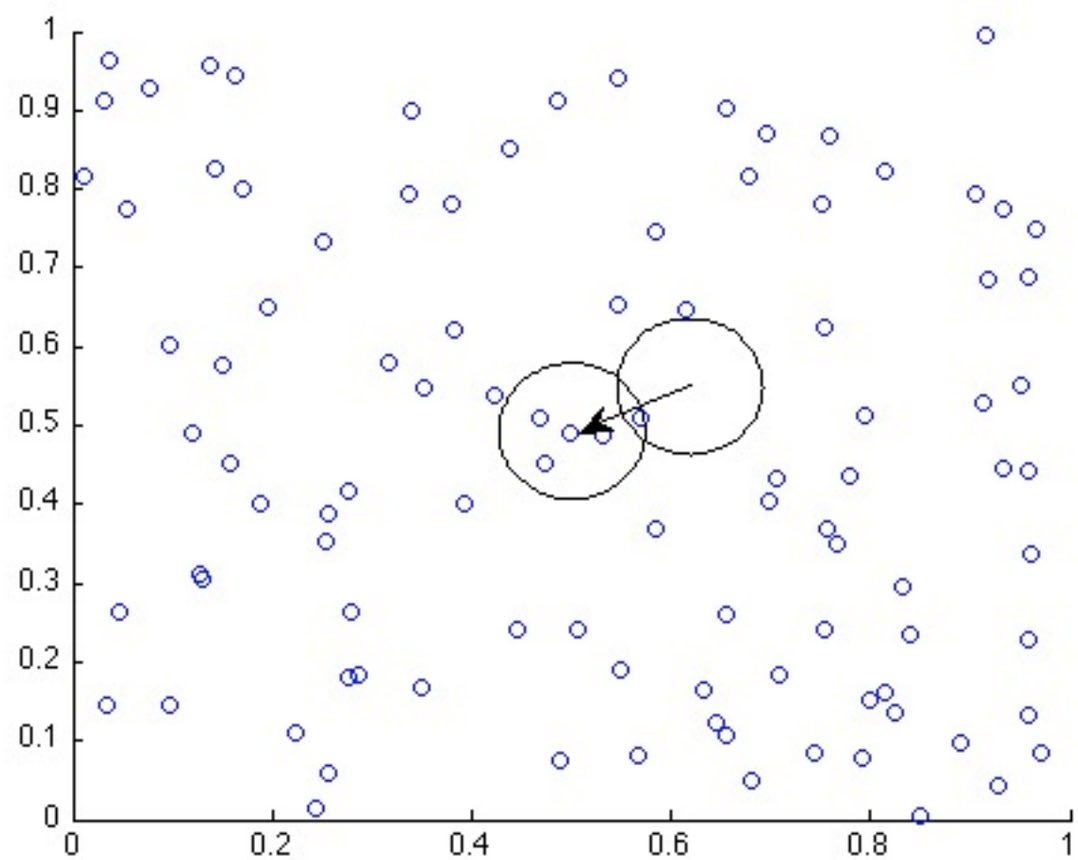
- object tracking (CCTV sequences, speed measurement)
- pose estimation
- co-registration
- stereo-vision
- 3D from motion
- object recognition
- robotic mapping and navigation (SLAM)
- image stitching
- 3D modeling
- gesture recognition,
- ...

# Mean shift

# Mean-shift

- non parametric clustering method (no hypothesis on the underlying distribution).
- Clustering of similar pixels <> segmentation

- *n* points defined in ***x***




D. Comaniciu and P. Meer. Mean shift: A robust approach toward feature space
analysis. IEEE Trans. Pattern Anal. Machine Intell., 24:603–619, 2002.

# Mean-shift

- local density estimator:

$$f(\mathbf{x}) = \frac{1}{nh^d} \sum_{i=1}^{n} K(\frac{\mathbf{x} - \mathbf{x_i}}{h})$$

- with *n* points, *d* dimensions, radius *h* and a kernel k *K*

- if *K* is central symmetric (only depends on the distance to c-the kernel center)

$$K(\mathbf{x}) = c_{k,d} k(||\mathbf{x}||^2)$$

# Mean-shift

- in order to find the mode of the f(***x***) distribution, one computes the zero of the gradient of f

$$\nabla f(\mathbf{x}) = 0$$

- for the radial estimator:

$$f_{h,K}(\mathbf{x}) = \frac{c_{k,d}}{nh^d} \sum_{i=1}^{n} k\left( \left\| \frac{\mathbf{x} - \mathbf{x}_i}{h} \right\|^2 \right)$$

$$\nabla f_{h,K}(\mathbf{x}) = \frac{2c_{k,d}}{nh^{d+2}} \sum_{i=1}^{n} (\mathbf{x} - \mathbf{x}_i) k'\left( \left\| \frac{\mathbf{x} - \mathbf{x}_i}{h} \right\|^2 \right)$$

# Mean-shift

- for

$$g(x) = -k'(x)$$

- we have:

$$\begin{aligned}
\nabla f_{h,K}(\mathbf{x}) &= \frac{2c_{k,d}}{nh^{d+2}} \sum_{i=1}^{n} (\mathbf{x}_i - \mathbf{x}) g\left( \left\| \frac{\mathbf{x} - \mathbf{x}_i}{h} \right\|^2 \right) \\
&= \frac{2c_{k,d}}{nh^{d+2}} \left[ \sum_{i=1}^{n} g\left( \left\| \frac{\mathbf{x} - \mathbf{x}_i}{h} \right\|^2 \right) \right] \left[ \frac{\sum_{i=1}^{n} \mathbf{x}_i g\left( \left\| \frac{\mathbf{x}-\mathbf{x}_i}{h} \right\|^2 \right)}{\sum_{i=1}^{n} g\left( \left\| \frac{\mathbf{x}-\mathbf{x}_i}{h} \right\|^2 \right)} - \mathbf{x} \right]
\end{aligned}$$

# Mean-shift

- first term is >= 0

- the second terme is the *mean-shift*

$$\mathbf{m}_h(\mathbf{x}) = \frac{\sum_{i=1}^{n} \mathbf{x}_i g\left(\left\| \frac{\mathbf{x}-\mathbf{x}_i}{h} \right\|^2\right)}{\sum_{i=1}^{n} g\left(\left\| \frac{\mathbf{x}-\mathbf{x}_i}{h} \right\|^2\right)} - \mathbf{x}$$

- heading toward the maximum of density

# Mean-shift

- iterative procedure
  - compute the mean-shift (itération *t)*

$$\mathbf{m}_h(\mathbf{x}^t)$$

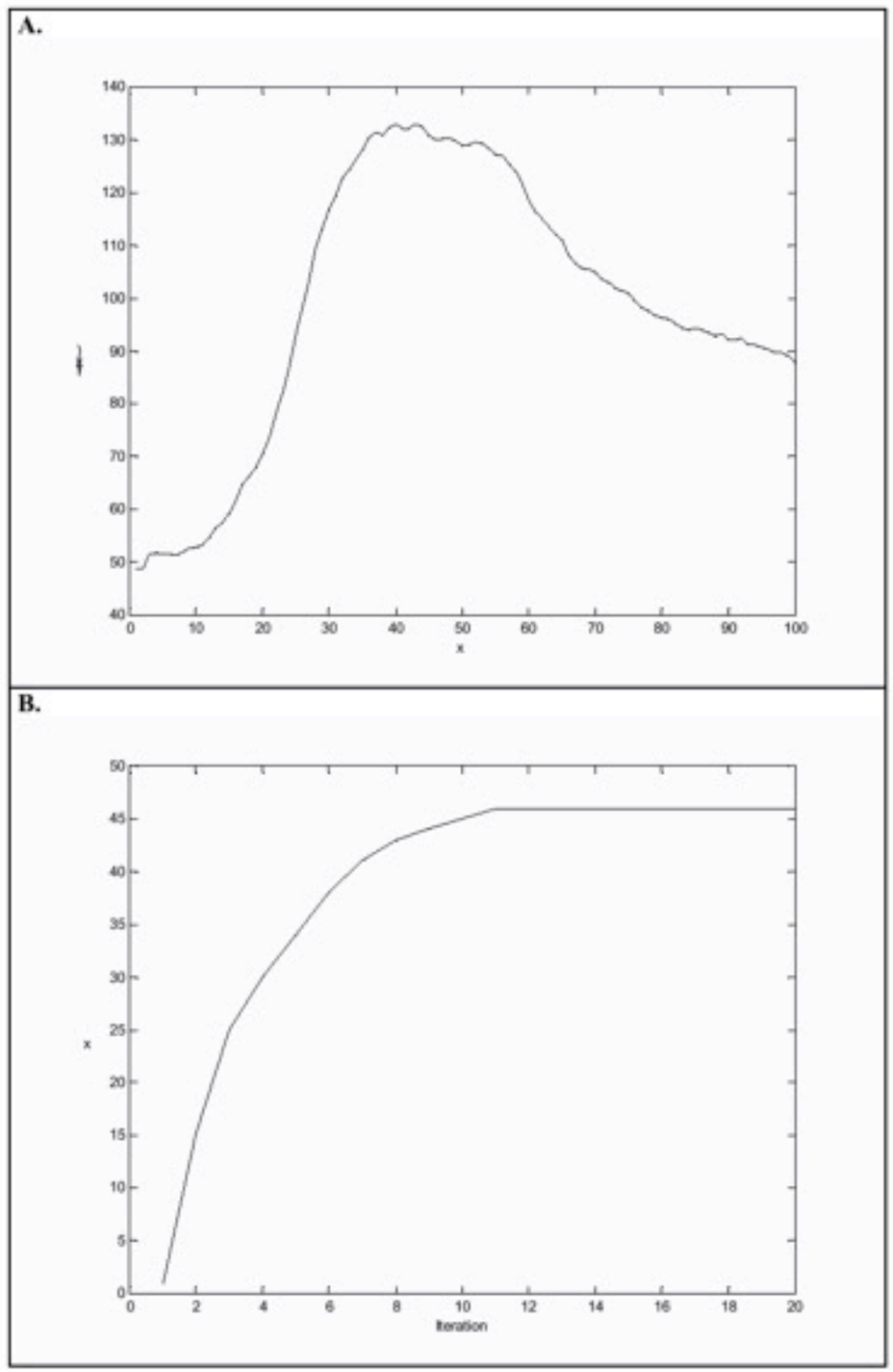
  - new neighboorhod position is computed by shifting **x** my **m**

$$\mathbf{x}^{t+1} = \mathbf{x}^t + \mathbf{m}_h(\mathbf{x}^t)$$

  - until convergence (gradient is nul)

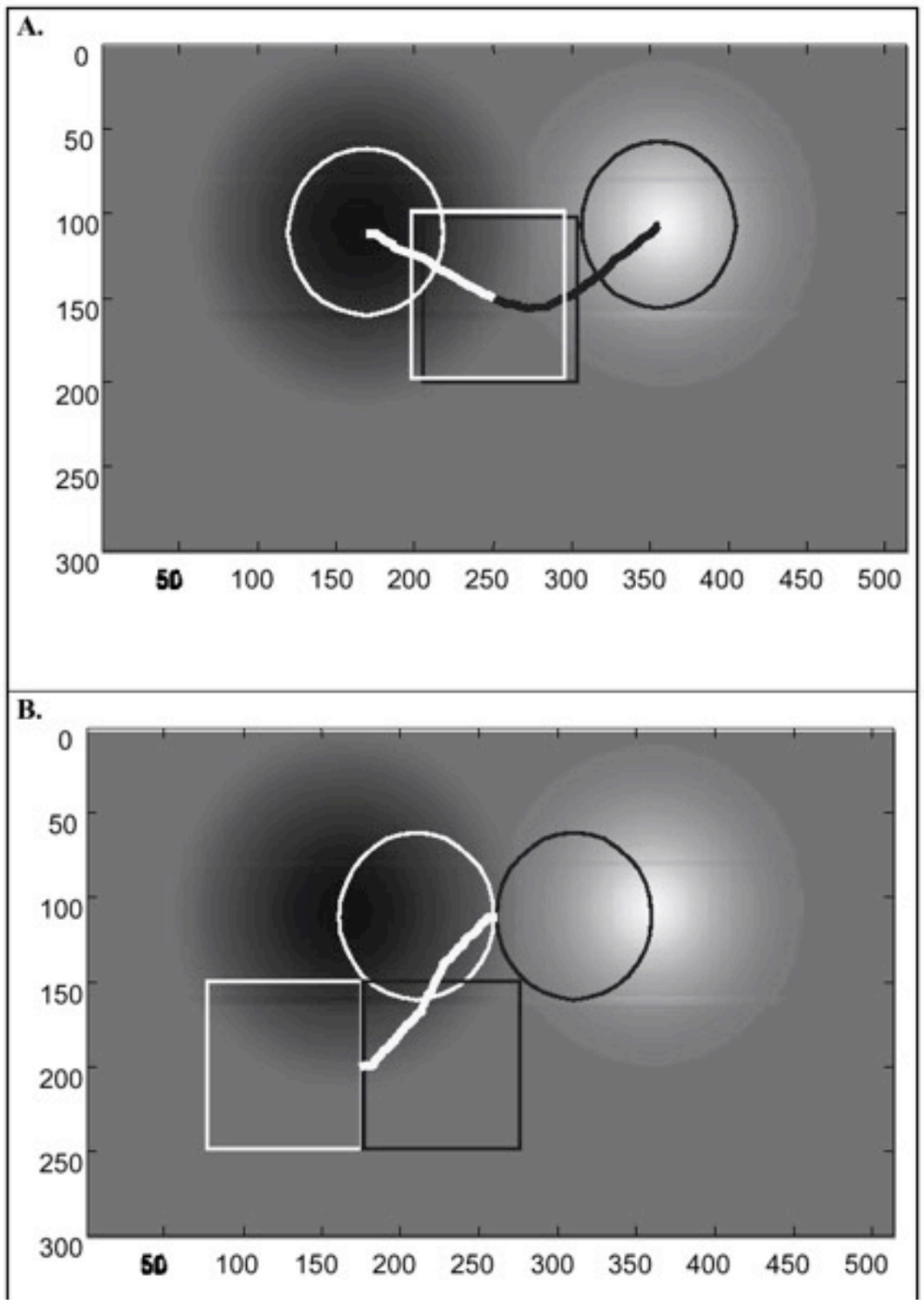
# Mean-shift

- Example in 1D

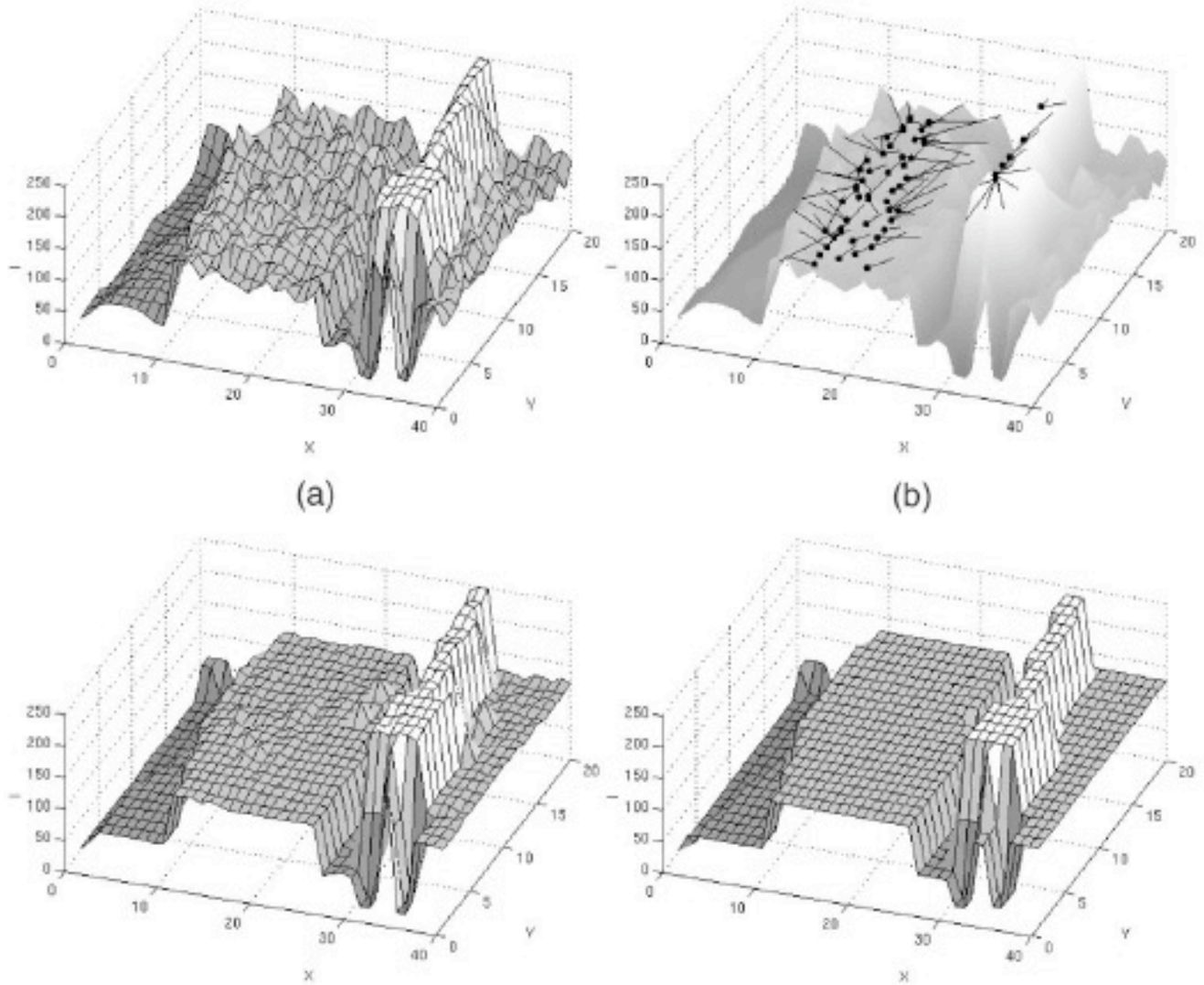


# Mean-shift

- Example in 2D



# Mean-shift




D. Comaniciu and P. Meer. Mean shift: A robust approach toward feature space
analysis. IEEE Trans. Pattern Anal. Machine Intell., 24:603–619, 2002.

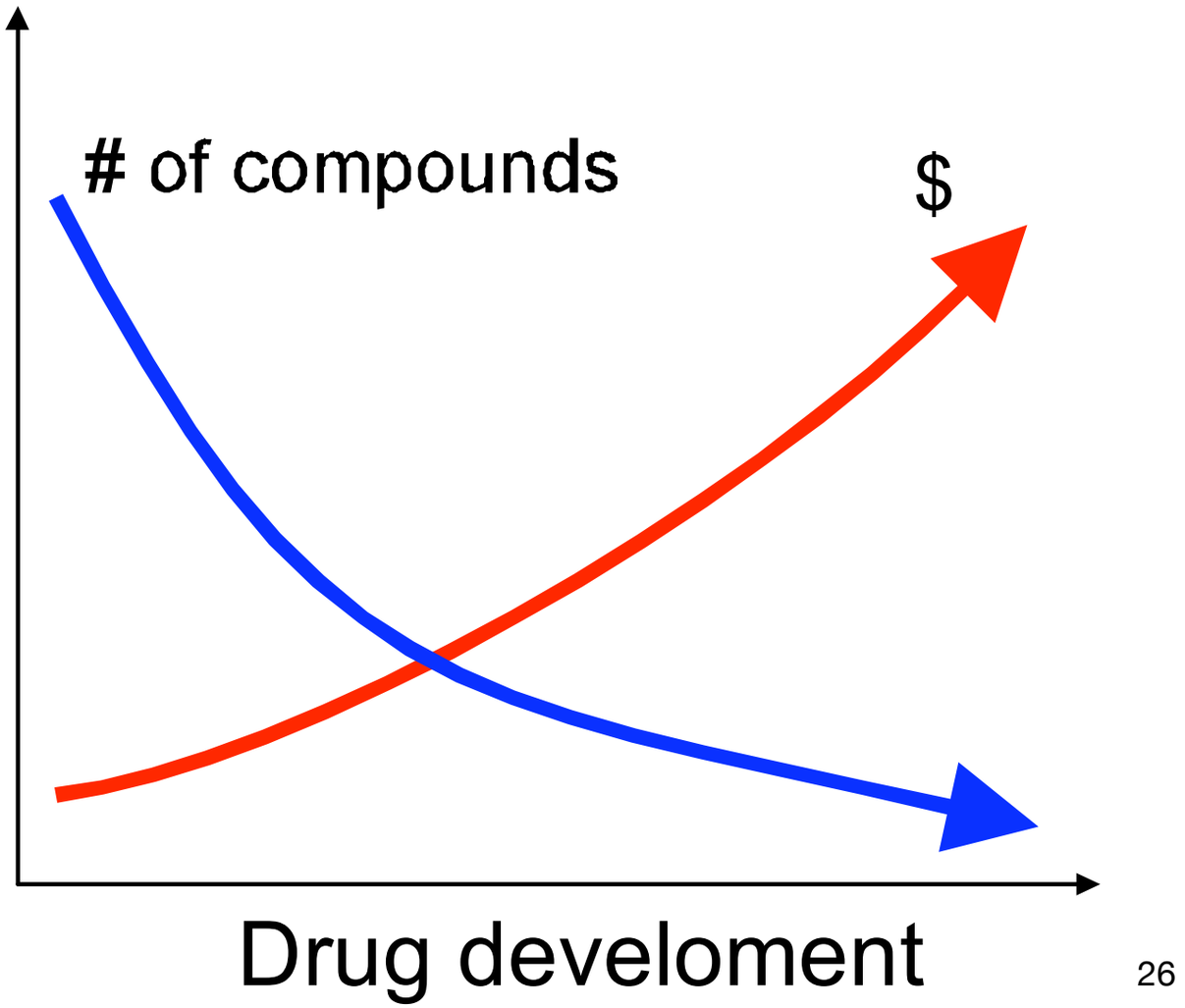
# application - in vitro cell tracking

# In vitro cell imaging

- In vitro cell observations have been extensively used for many years
- Wide range of applications
  - cell migration
  - drug testing
  - chemotactism
  - embryogenesis, ...
- Why in vitro ?
  - fast
  - cheap
  - versatile

# In vitro cell imaging

- Let’s focus on the drug testing (cancer)
    - Hundreds of new compounds are to be tested
    - Research costs are increasing with the study phase



# In vitro cell imaging

- Needs are :
- A fast potential activities detection of a drug on a cell line
- If possible a qualification of the effects of anticancer compounds on cell behavior
- The identification a subset of interesting candidates among dozens of compounds
- The detection of clues on the mechanism of drug action (MOA), and
- The optimization the selection of further time-consuming and expensive biological evaluations required to elucidate the true MOA

Decaestecker C. et al.
Can anti-migratory drugs be screened in vitro? A review of 2D and 3D assays for the quantitative analysis of cell migration.
Med Res Rev 27(2):149-76, Mar, 2007

# In vitro cell imaging

- Our unit :

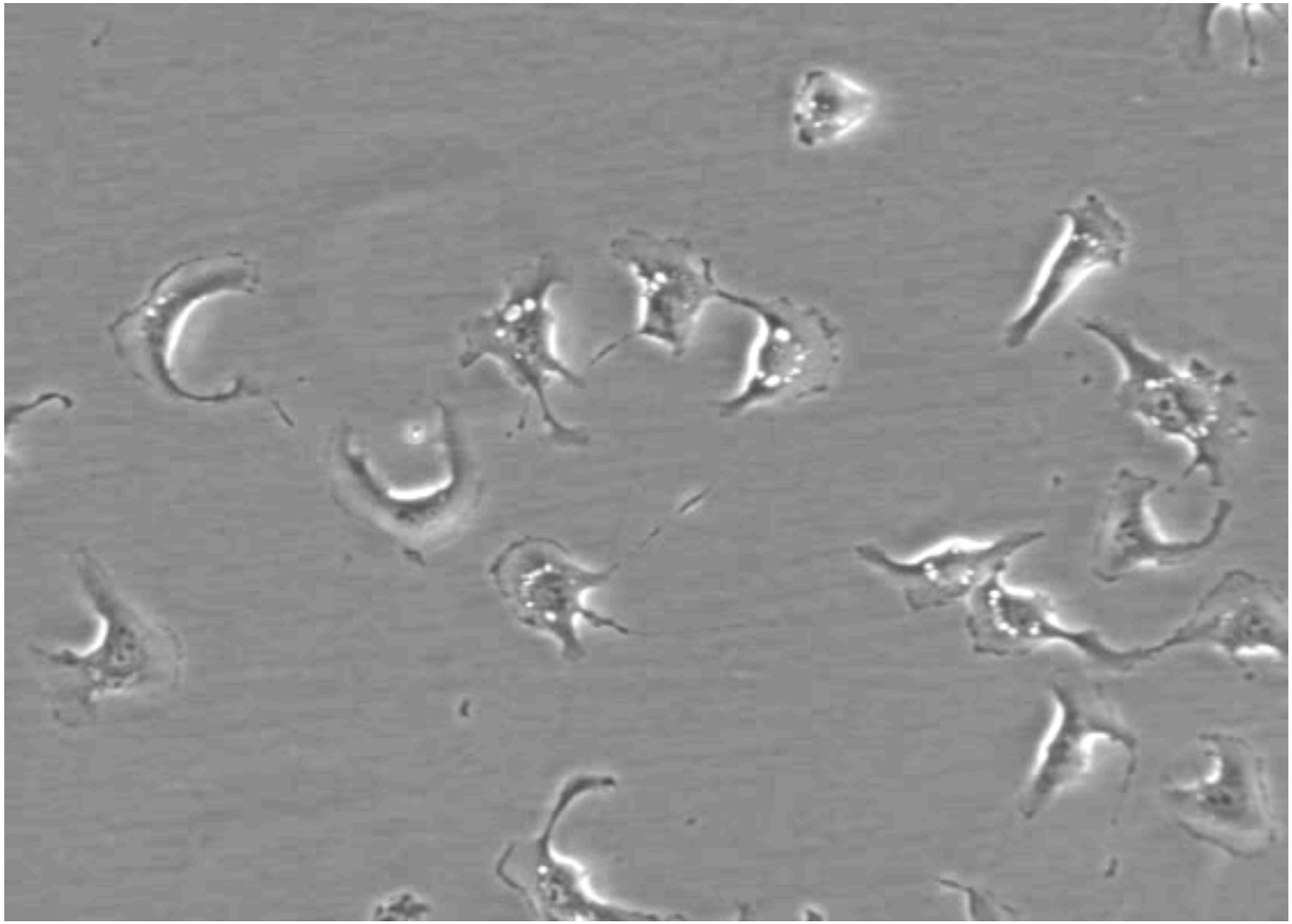
- 24 systems
  running in parallel

- Phase contrast microscopy

- Incubated at 37°c

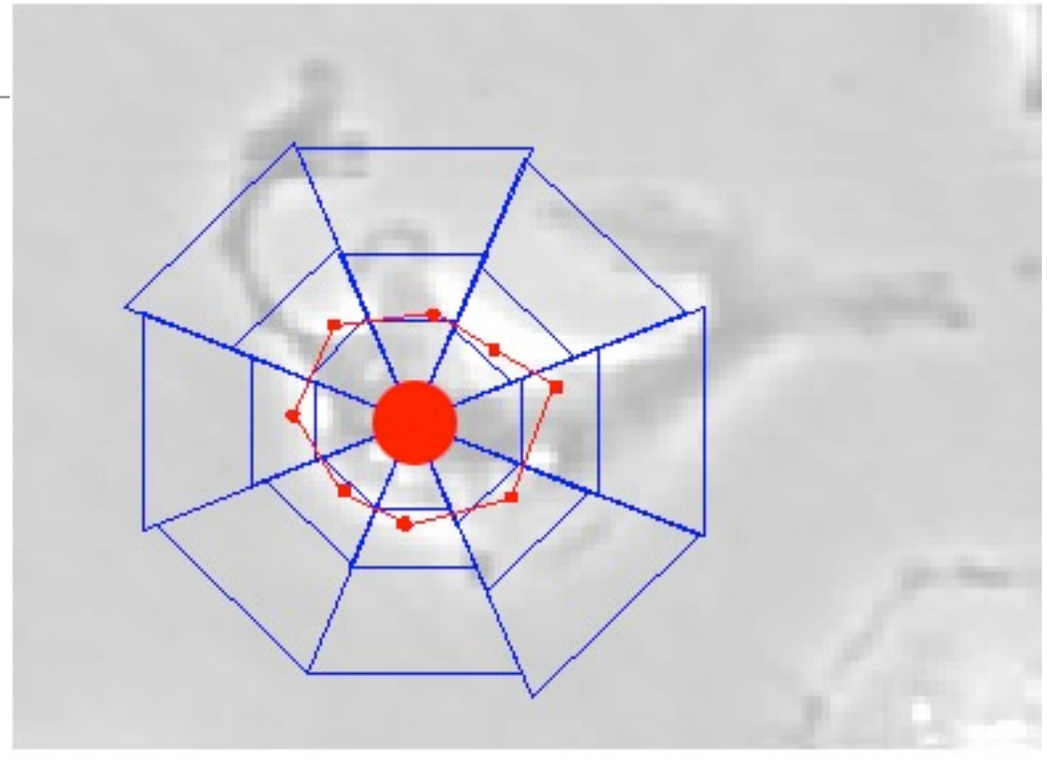

Unibioscreen S.A.
ULB spin-off

# In vitro cell imaging



# Automatic in vitro cell tracking

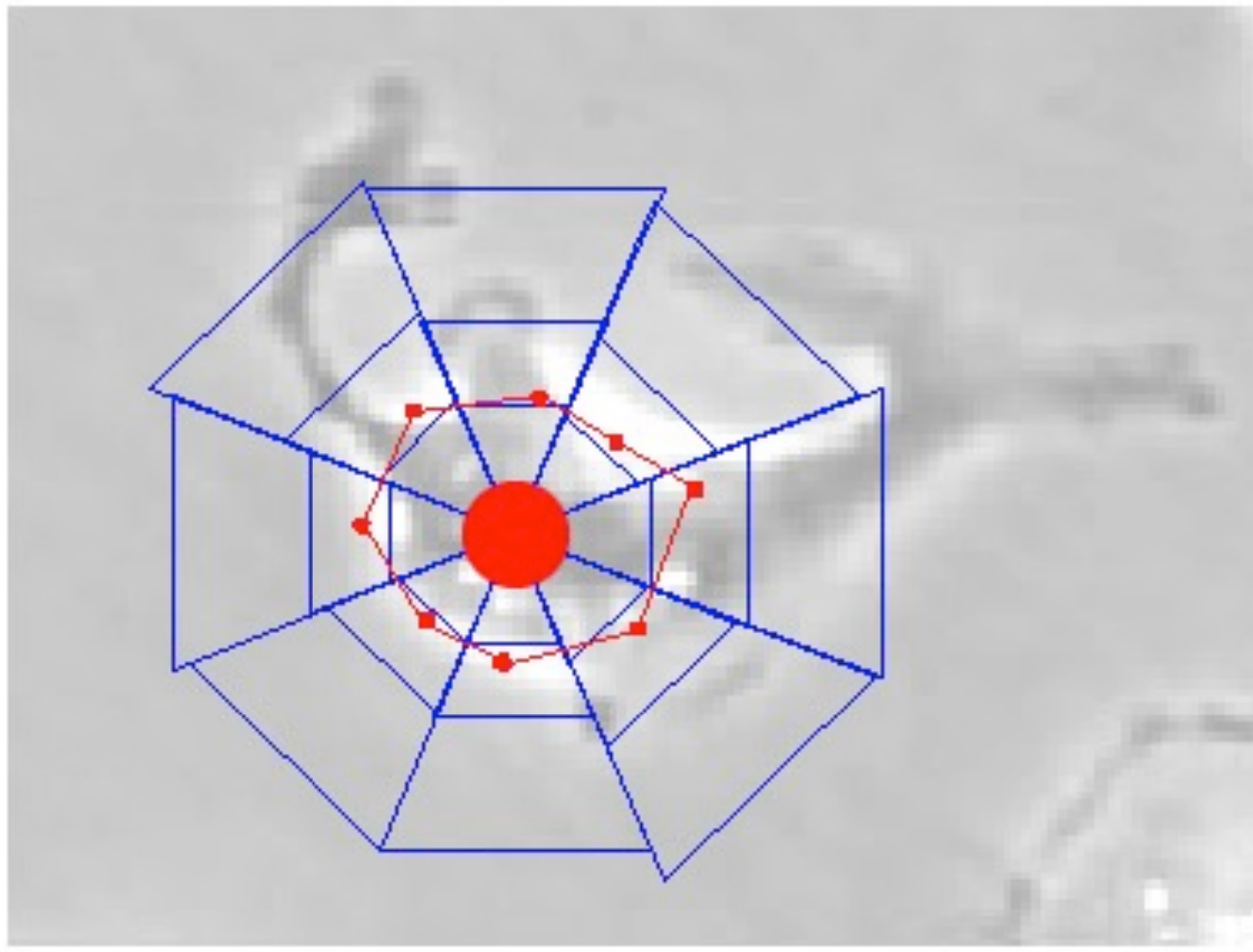
- Phase contrast microscopy
- Unmarked cells (No fluorescence (no bleaching, no toxicity, low cost)
- Automatic tracking
- Manual initialization
- Robust to shape changes
- Fast



O. Debeir et al. IEEE Transaction on Medical Imaging 24(6):697-711, june, 2005

# Mean-shift tracking

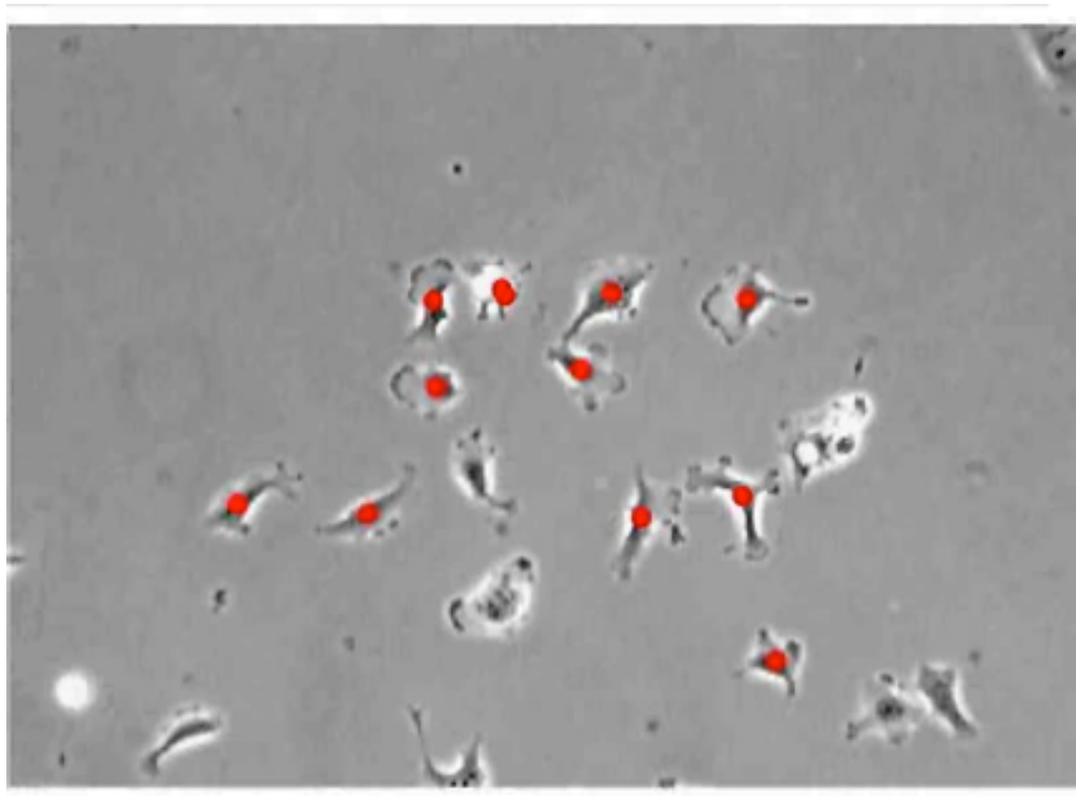
- Neighborhood cutted into pies
- Inner part attracted by dark pixels
- External part attracted by bright pixels
- The shape is adapted to the current cell size (robust to shape deformations)



# Automatic in vitro cell tracking

- Automatic cell Tracking from several hours to several days
  - Motility
  - Chemotactism
  - Event detection : cell division
  - Complex behaviour analysis

  ...



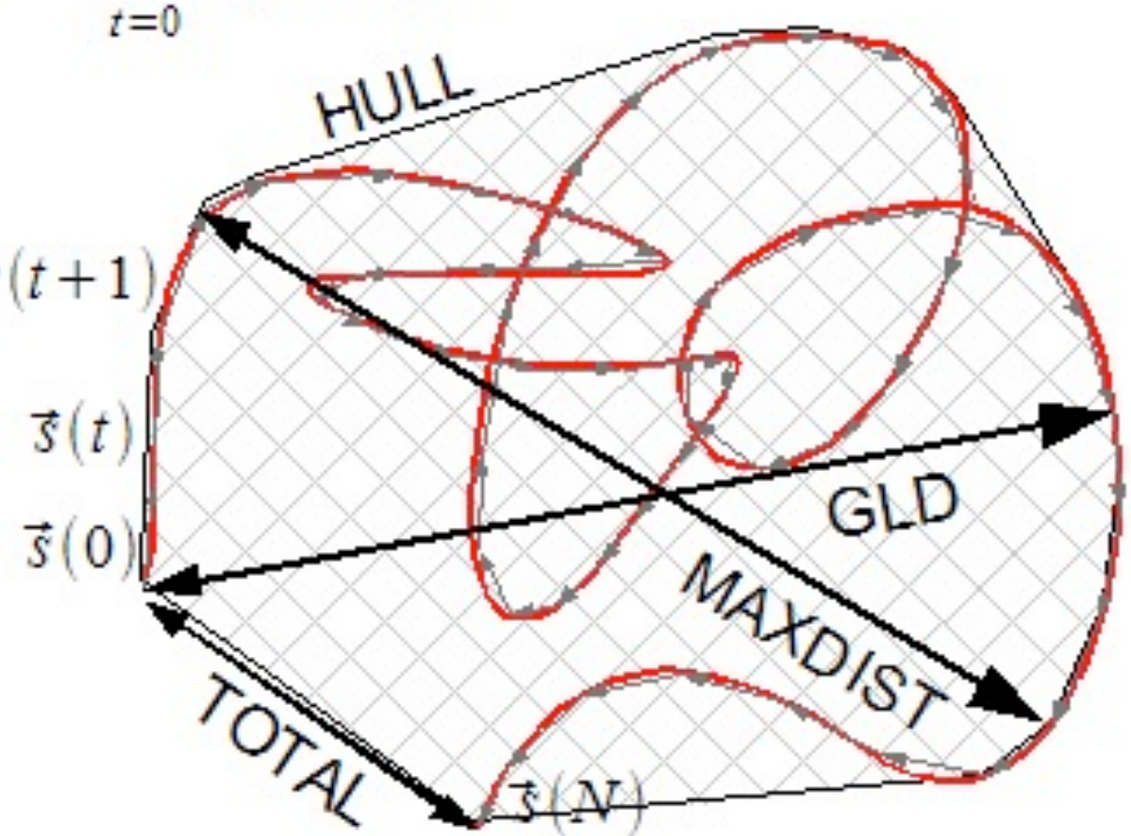
# Automatic in vitro cell tracking

- Cell motility

# Cell motility analysis

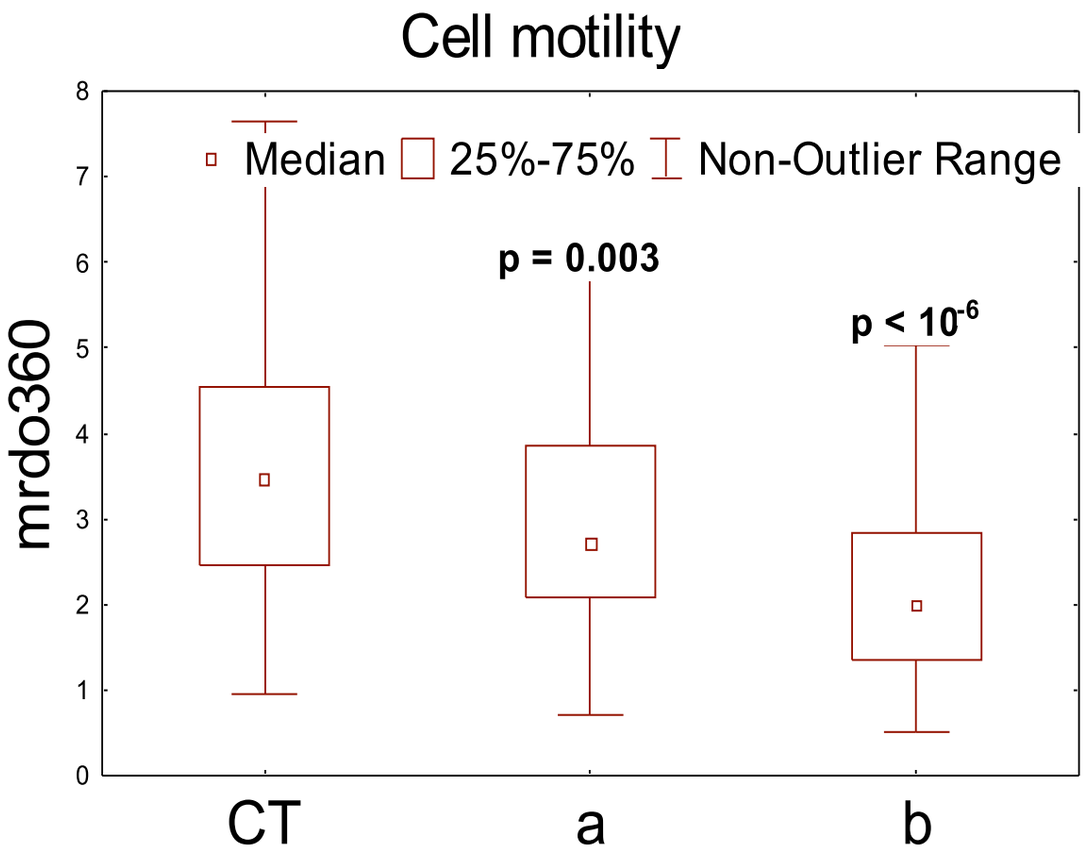
- Motility
- AS : Average Speed
- GLD :Greatest Linear Distance
- Total Distance
- Hull Area
- MAXDIST :
  Maximum Distance in Hull convex

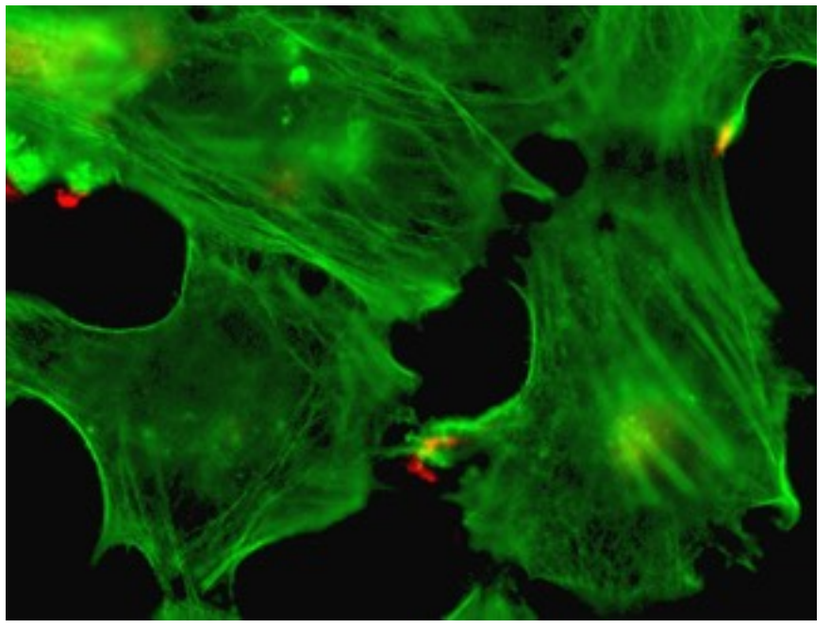
$$AS = \sum_{t=0}^{t=N-1} \left\| \vec{s}(t) \right\| / N$$



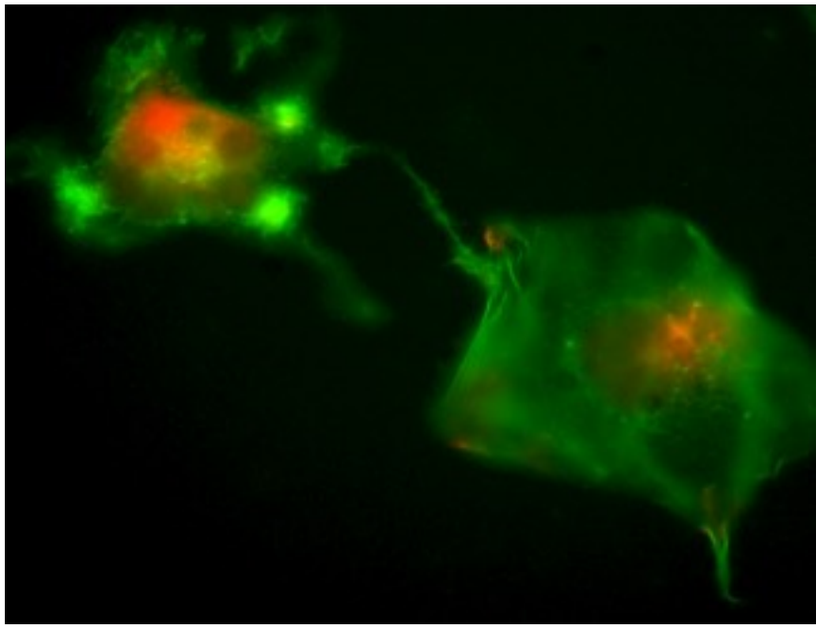
# Cell motility analysis

- The tested compound impairs U373 glioblastoma cell migration



Ct



UNBS1450 100nM

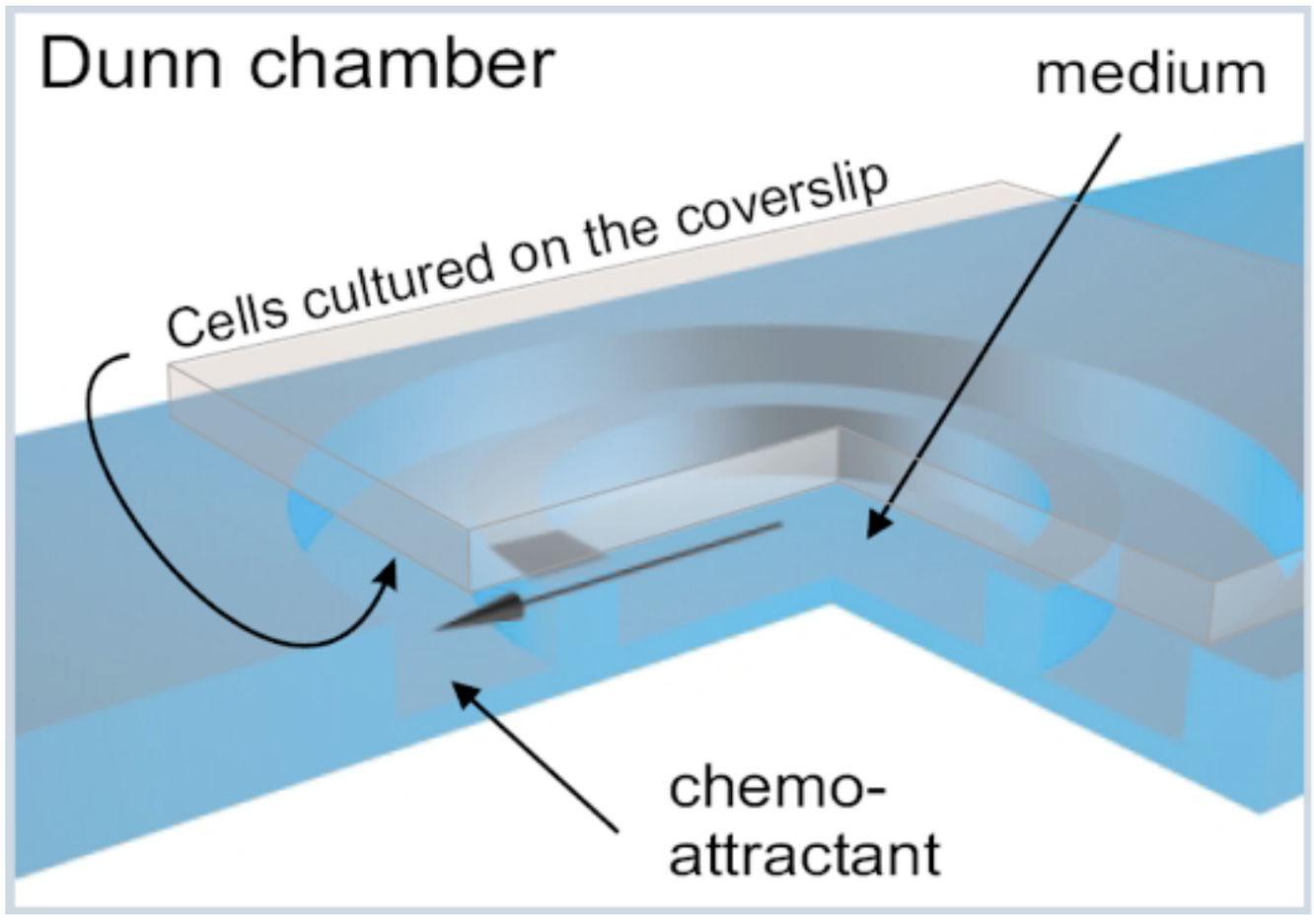
Debeir O. et al.
High throughput characterization of anti-cancer compounds by means of cellular imaging and automatic image analysis.
AACR, 2007

# Automatic in vitro cell tracking

- Cell chemotactism

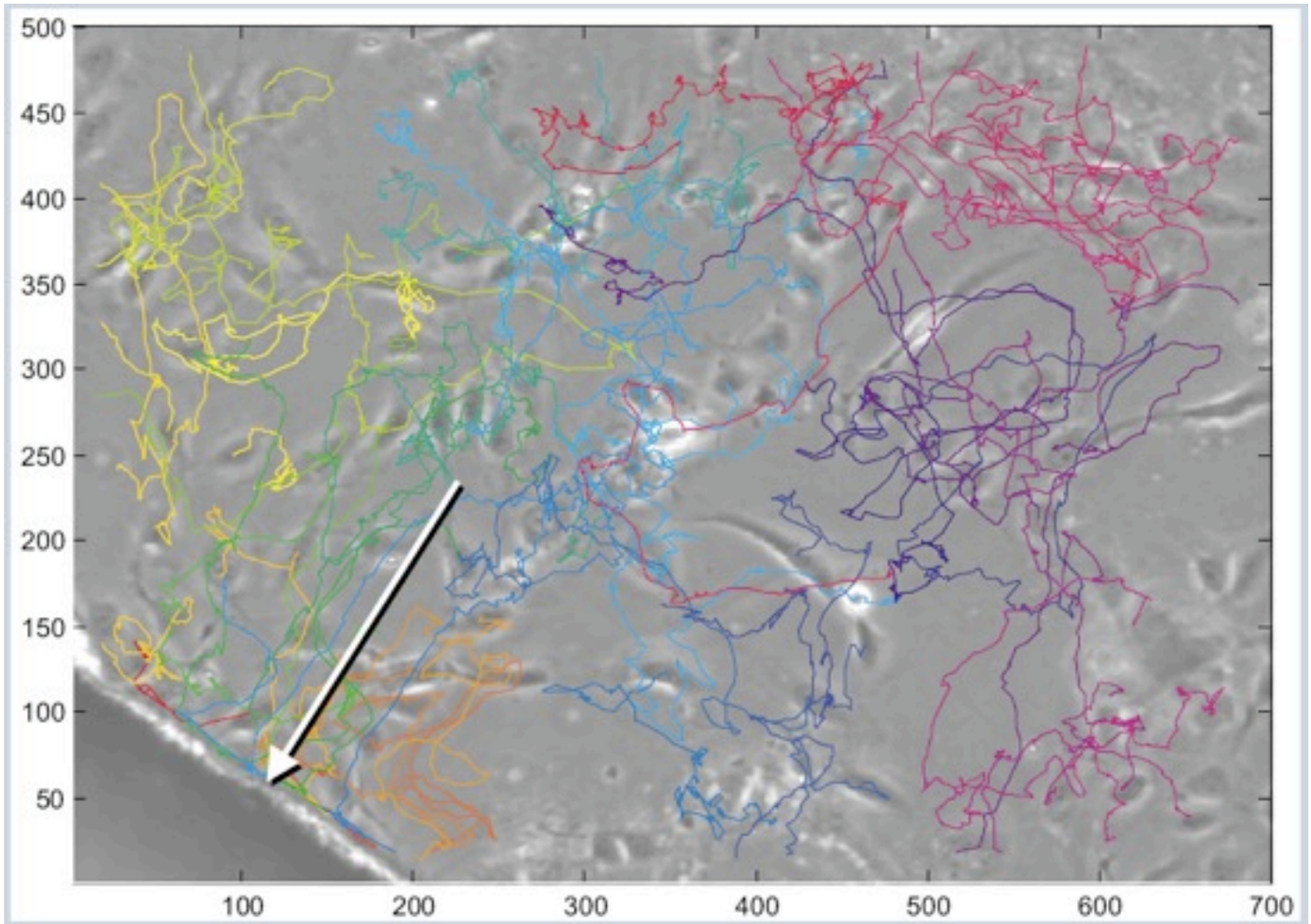
# Cell chemotactism analysis

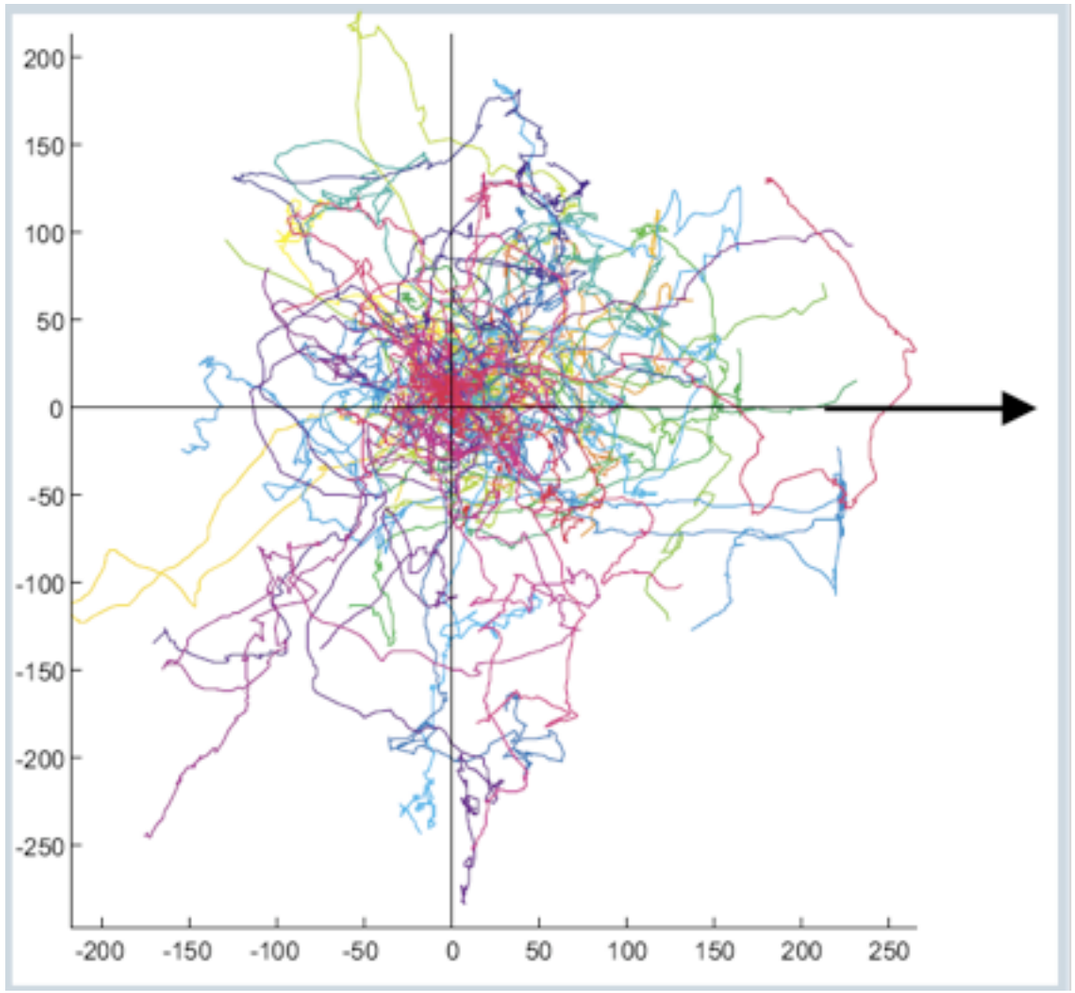
- Chemotactism
- Chemical gradient
- Dunn chamber



# Chemotactism

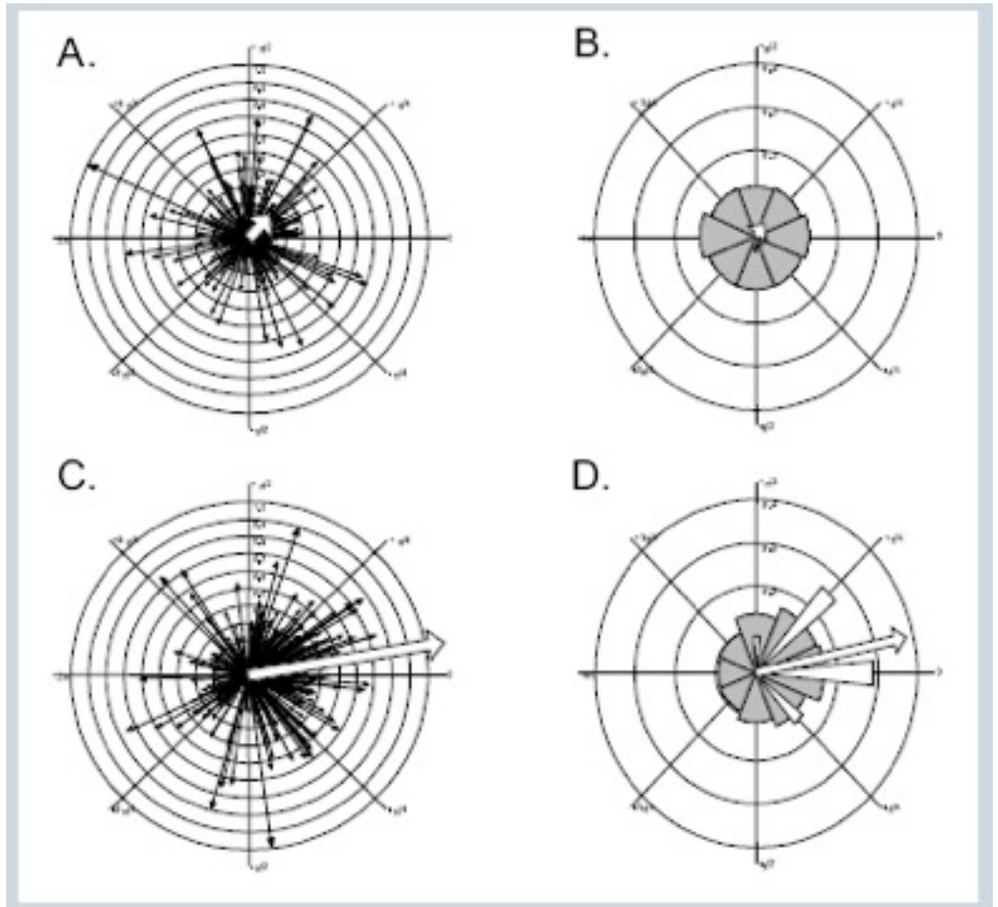
- Individual cell tracking
- Track orientation distribution



# Cell chemotactism analysis

- The tested compound exhibits a significant chemotactism activity on the cells with repect to control condition



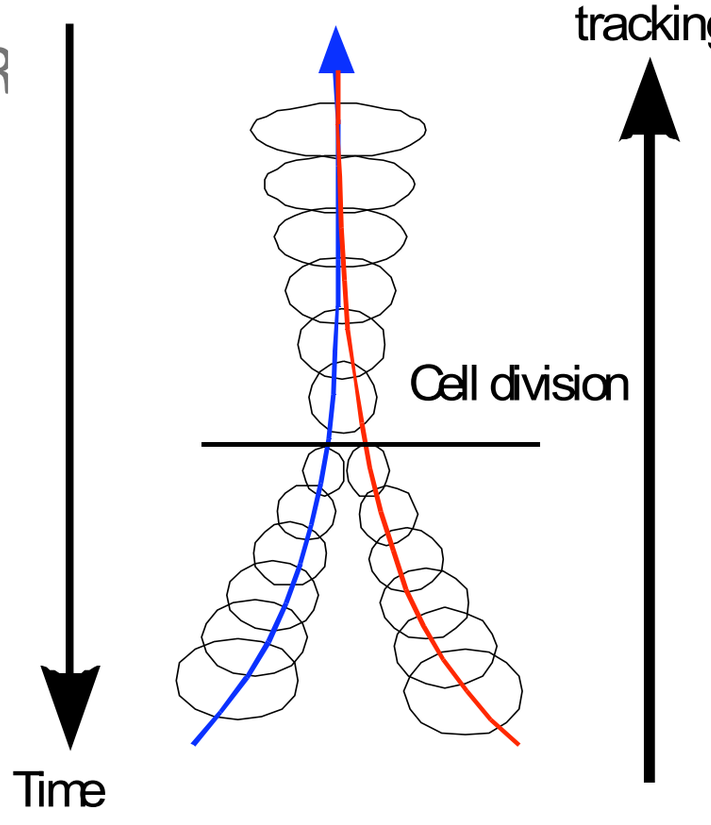

Debeir O. et al.
A Model-Based Approach For Automated In Vitro Cell Tracking And Chemotaxis Analyses.
CytometryA. 2004, 60(1):29-40.

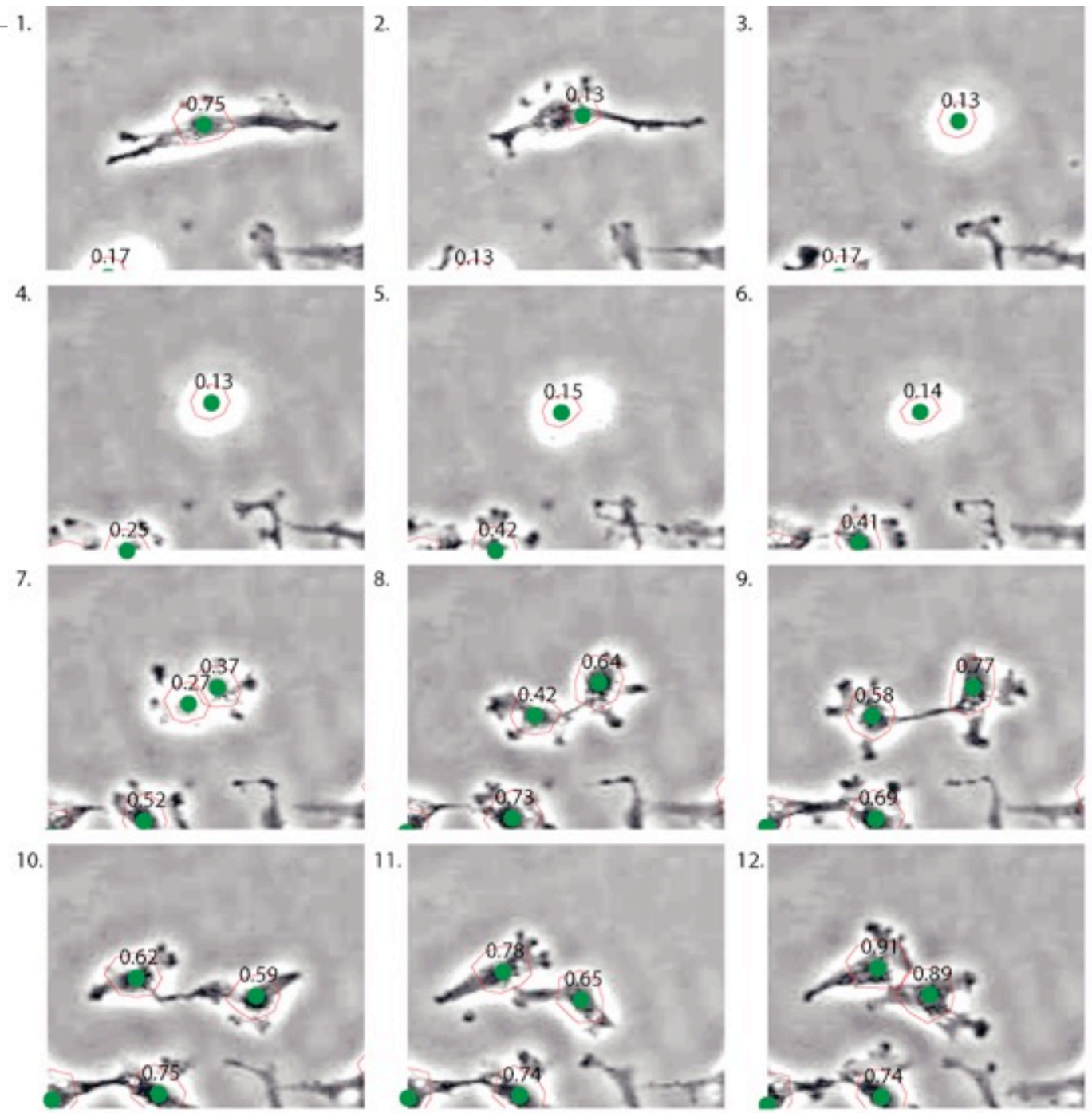
# Automatic in vitro cell tracking

- Cell division

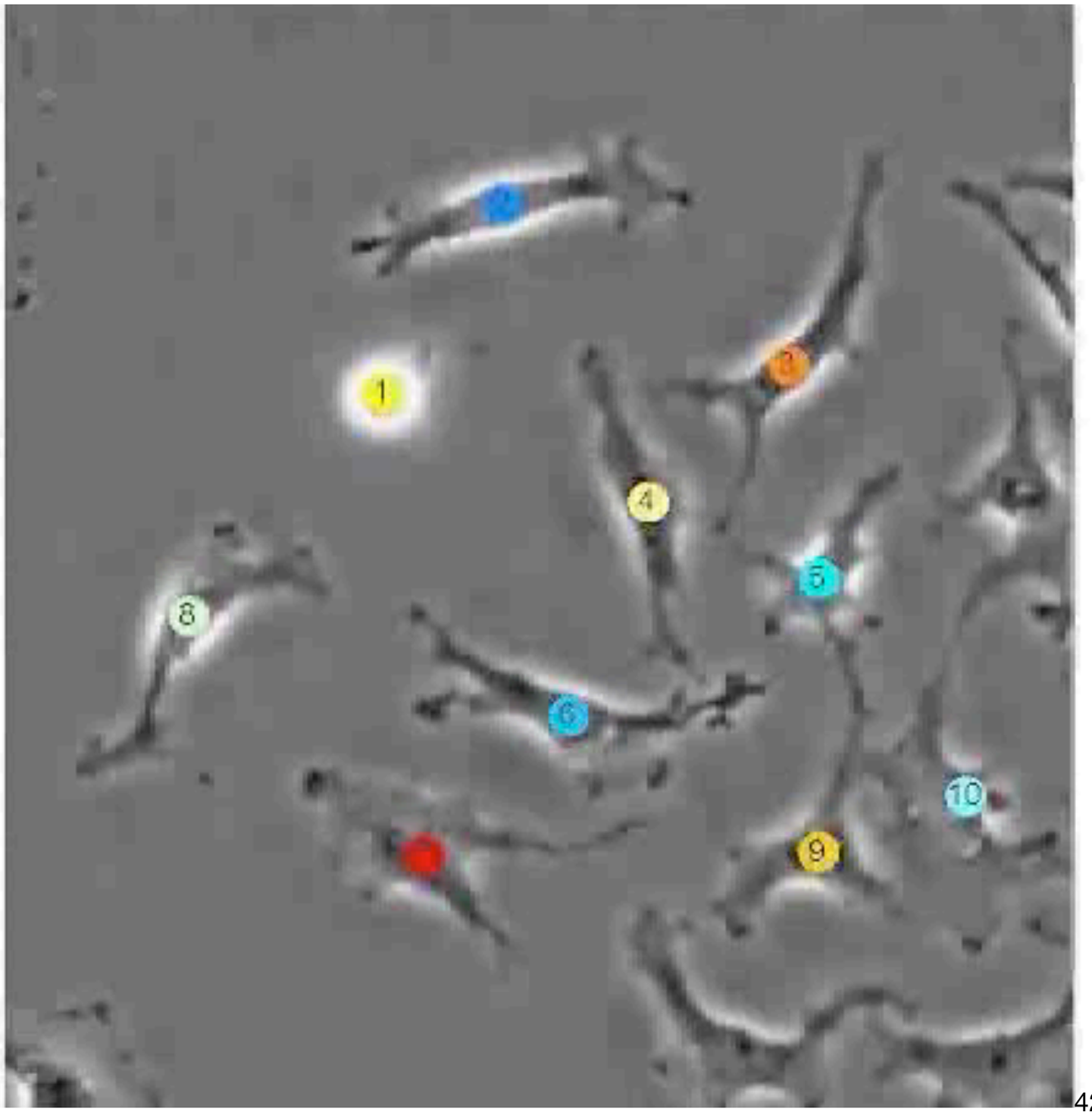
# Mitosis detection

- Tracking forward (red)
- Tracking reverse (red + blue)
- R

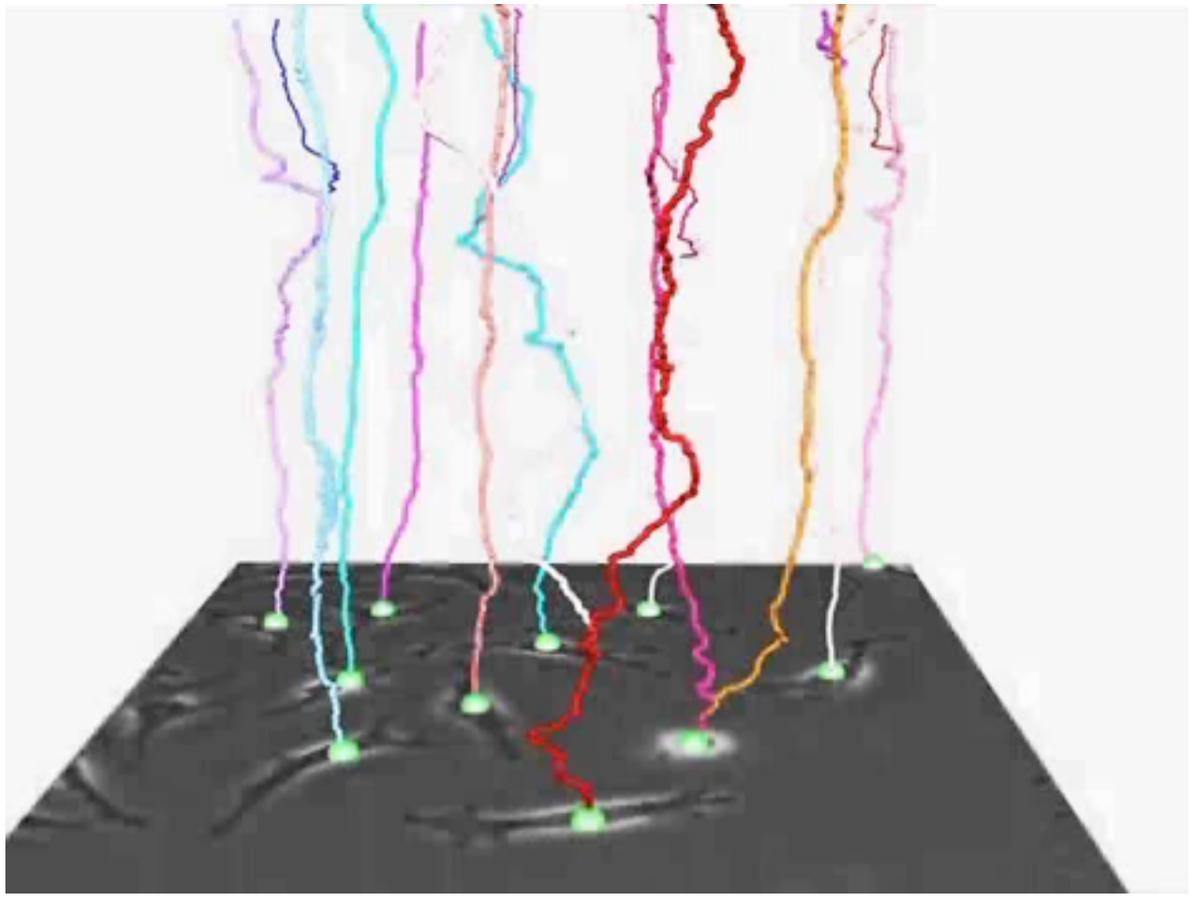


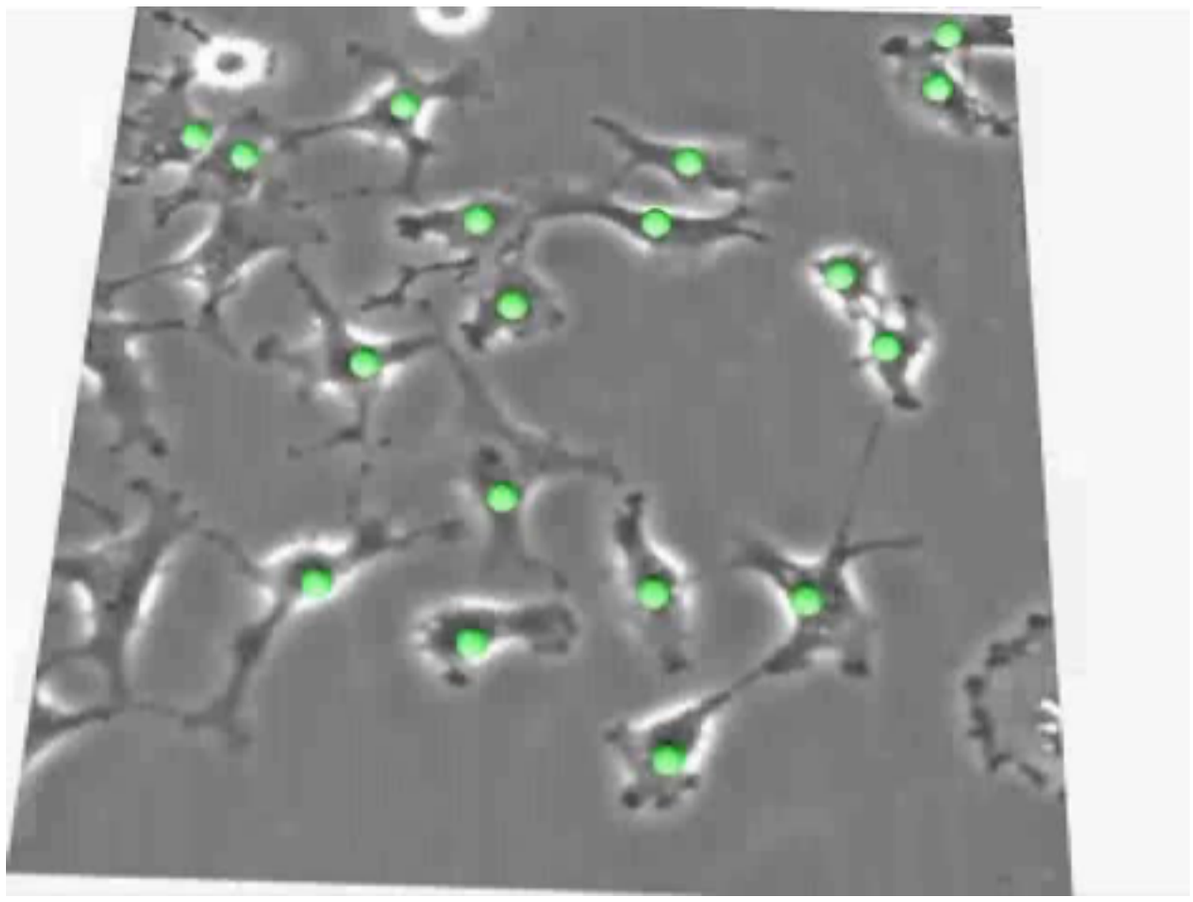



# Mitosis detection



# Mitosis detection

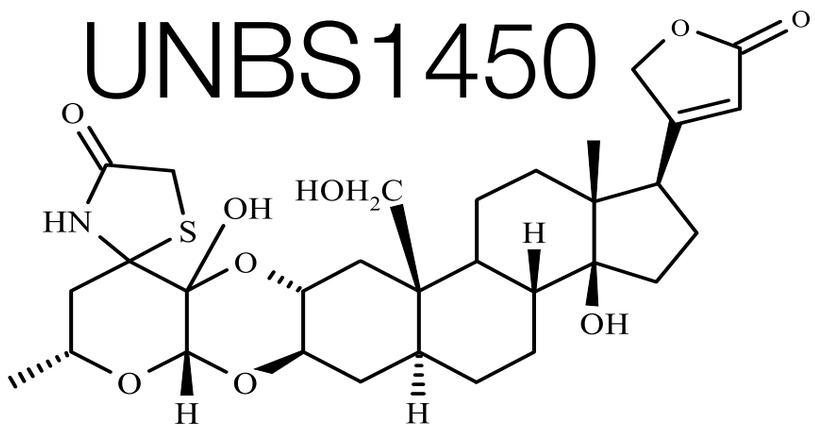




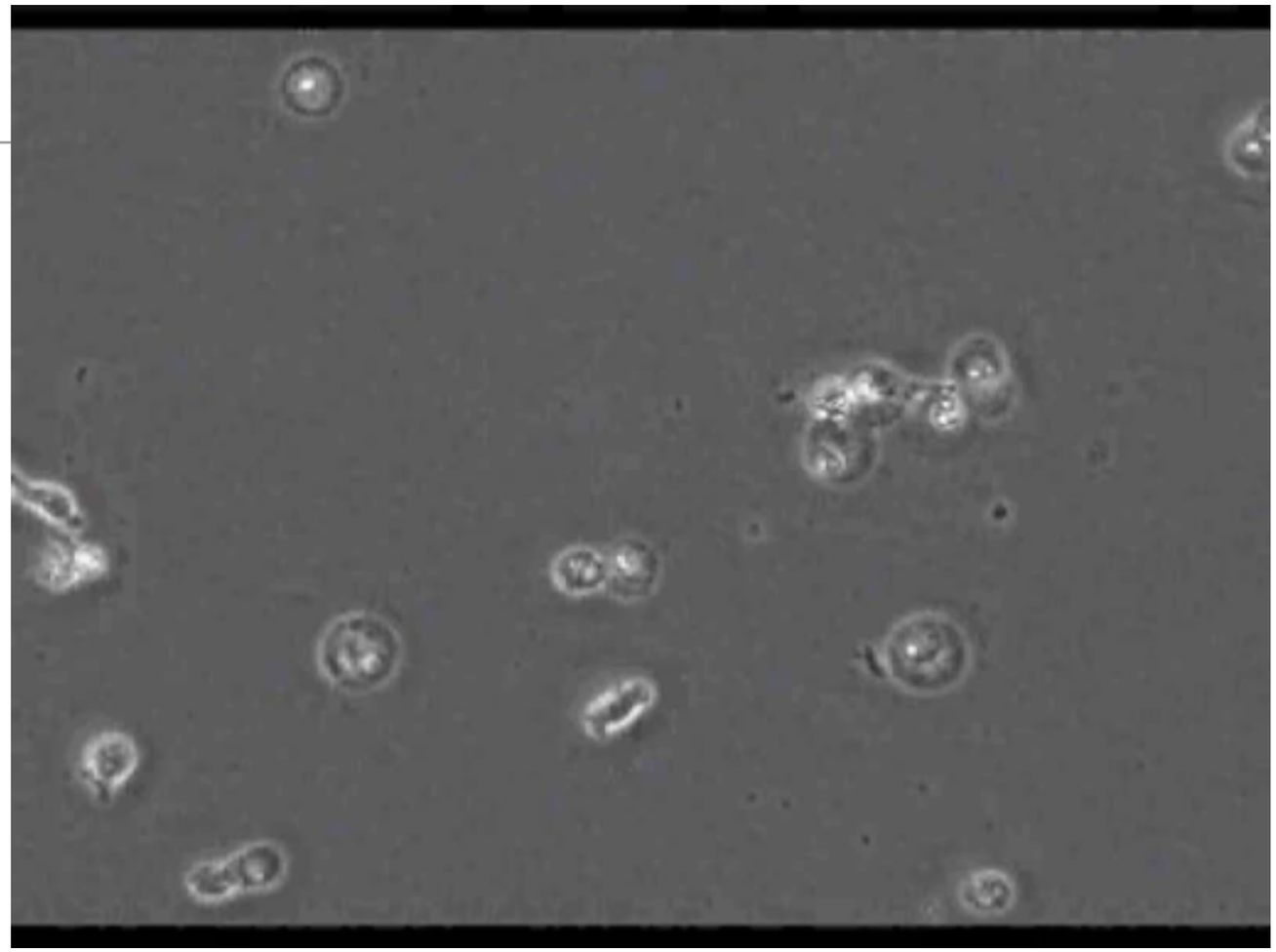
# Mitosis detection

- UNBS1450 compound has been selected amounf dozens of cardenolides thanks to our original approach

UNBS1450




Ligand to the sodium pump

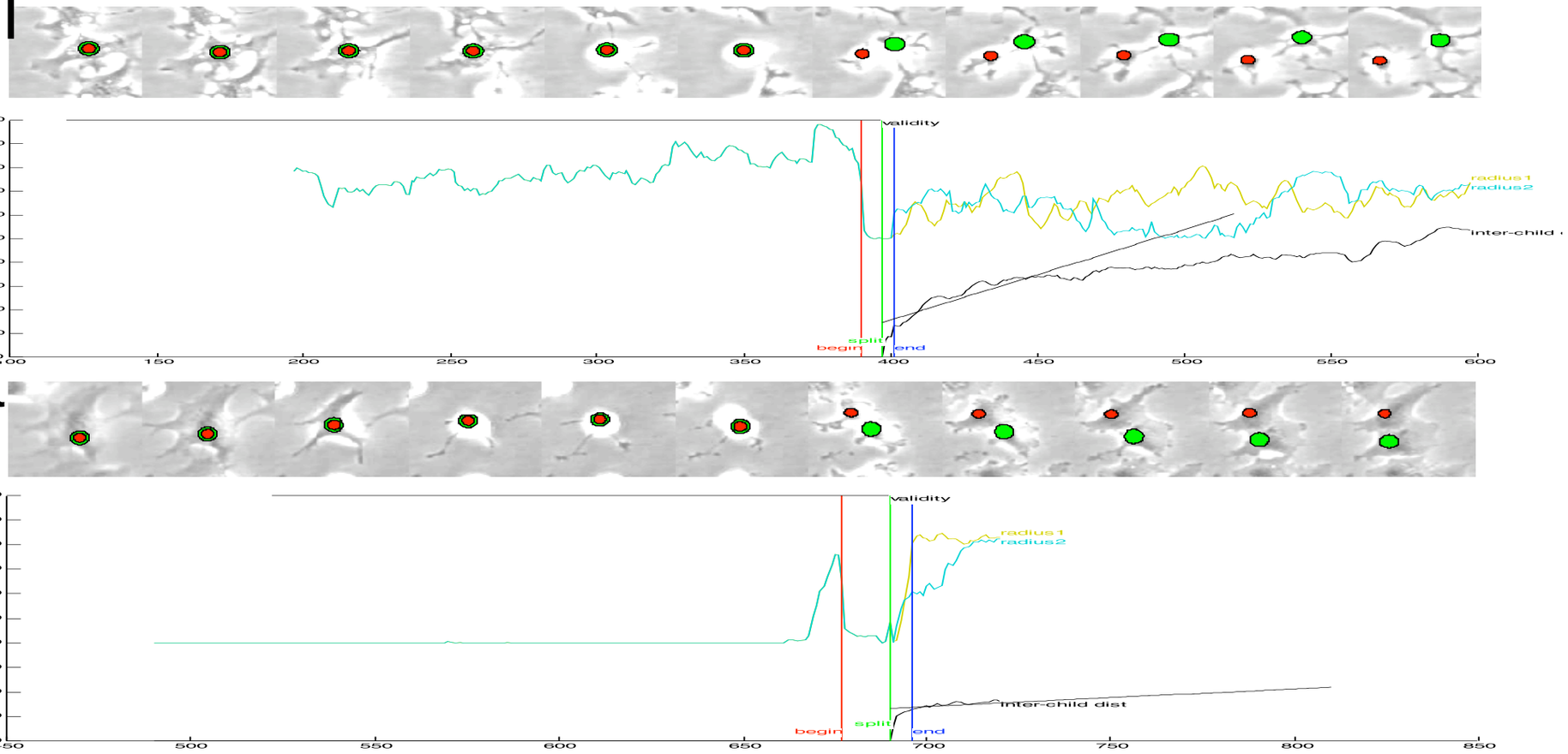


Event detection
Cell division
Cell death

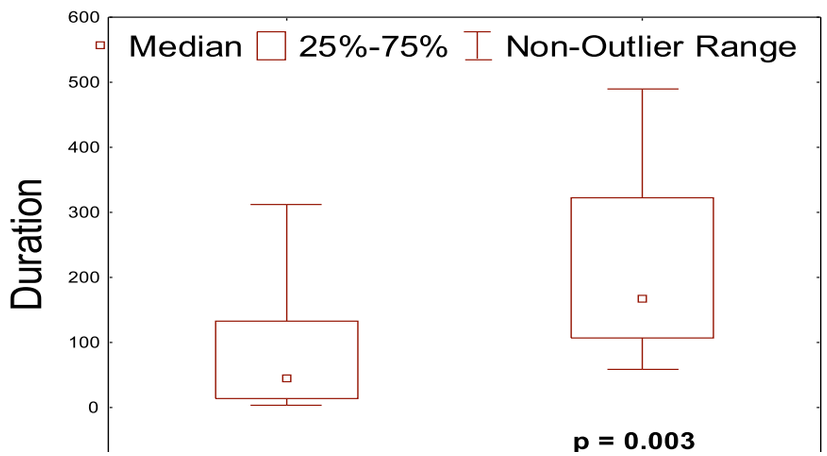
Debeir O. et al.
High throughput characterization of anti-cancer compounds by means of cellular imaging and automatic image analysis.
AACR, 2007

# Mitosis detection

CT




a



# Automatic in vitro cell tracking

- Complex cell behaviour

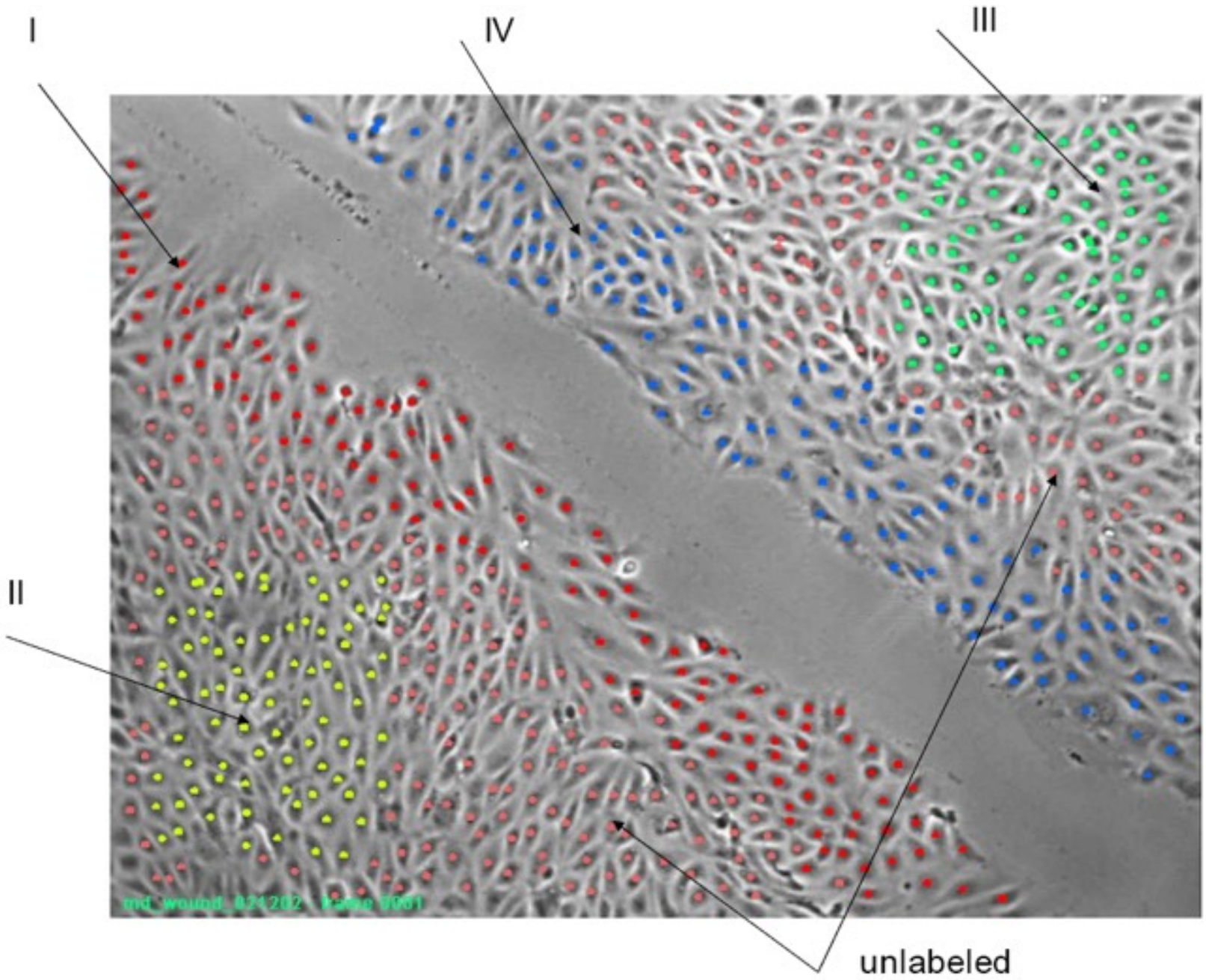
# Complex cell behaviour

- Scratch-wound setup
  - Confluence
  - Scratch with a tip
- Observation by in vitro phase contrast microscopy
- Cell submitted to a constant shear stress

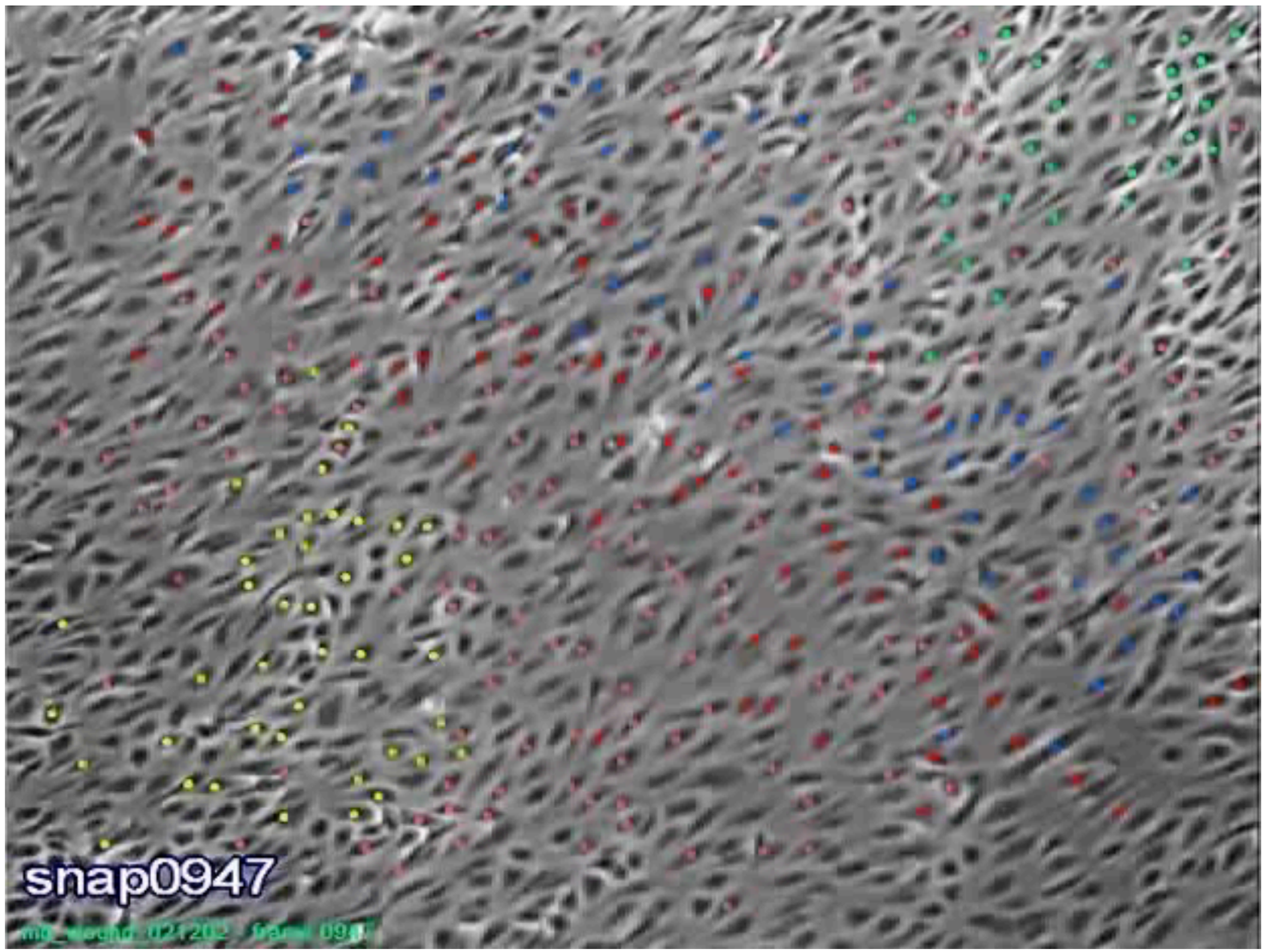
Work done in collaboration with Dr Marek Drab, Max-Planck Institute for Infection Biology.

# Complex cell behaviour

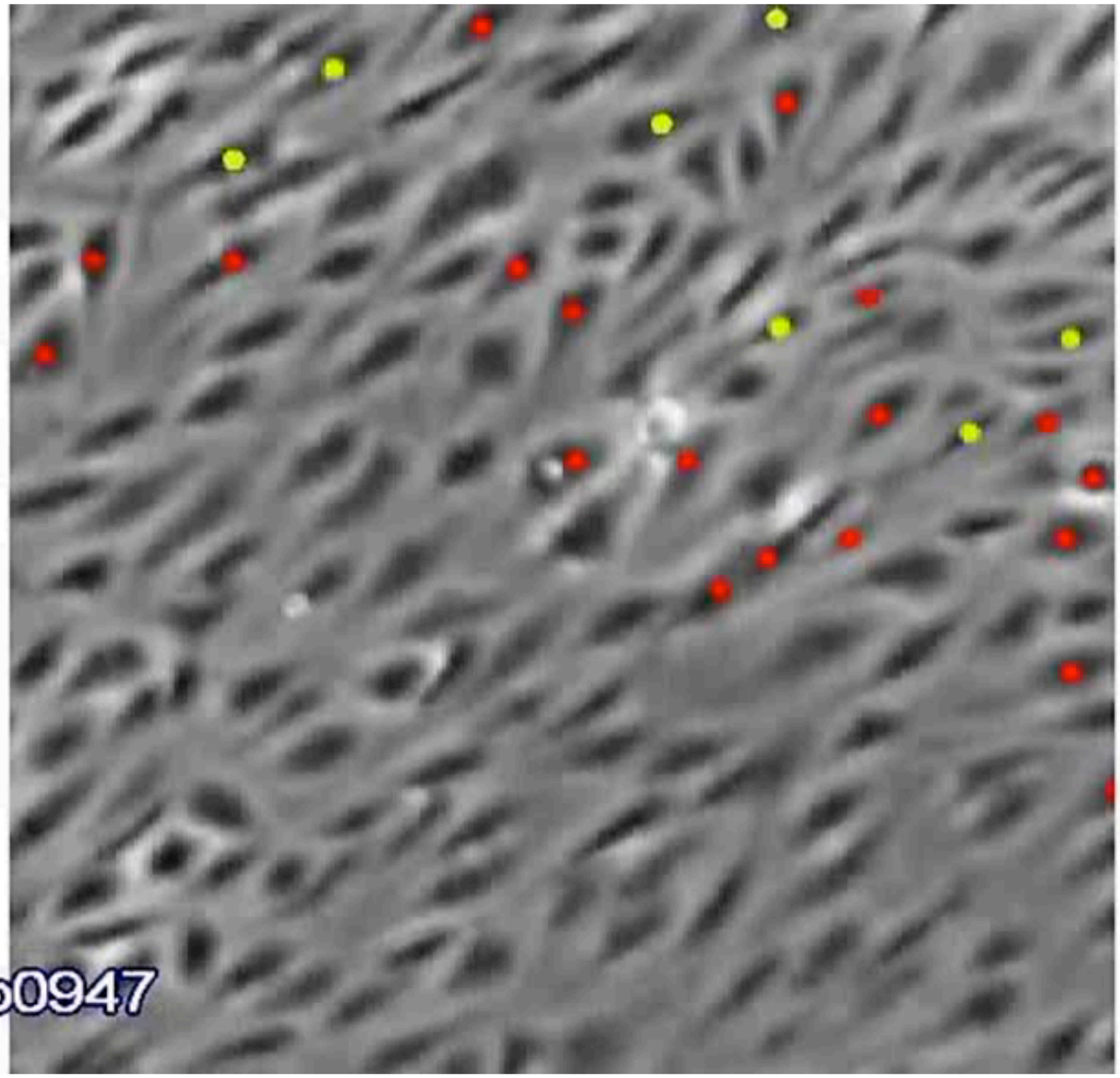
- 5 areas of interest
  - Inferior border (I)
  - Superior border (IV
  - Far inferior (II)
  - Far superior (III)
  - Others (unlabeled)



# Complex cell behaviour

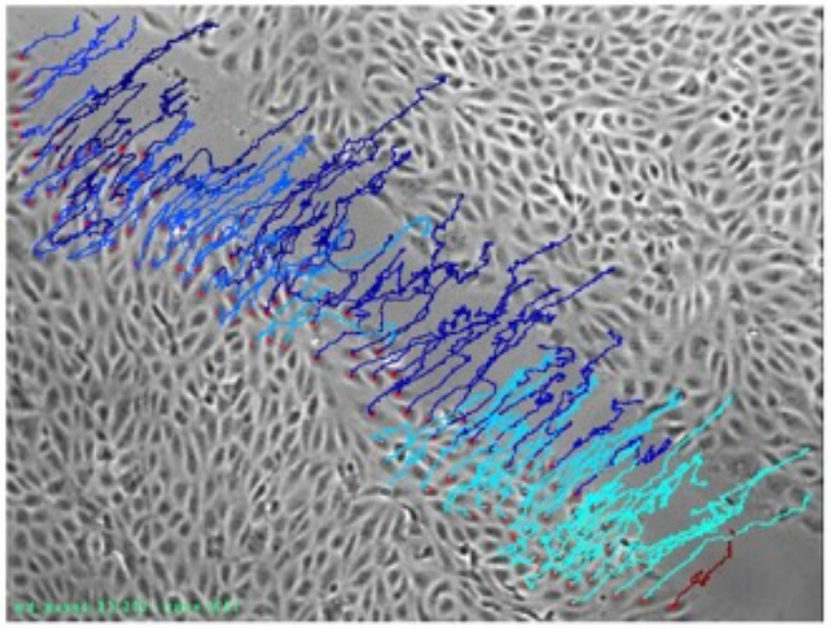


# Complex cell behaviour

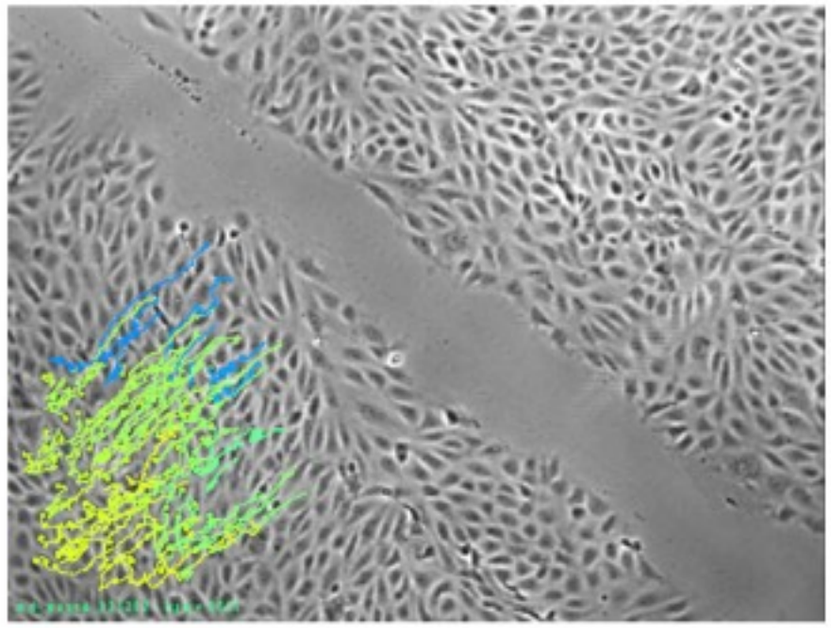


# Complex cell behaviour

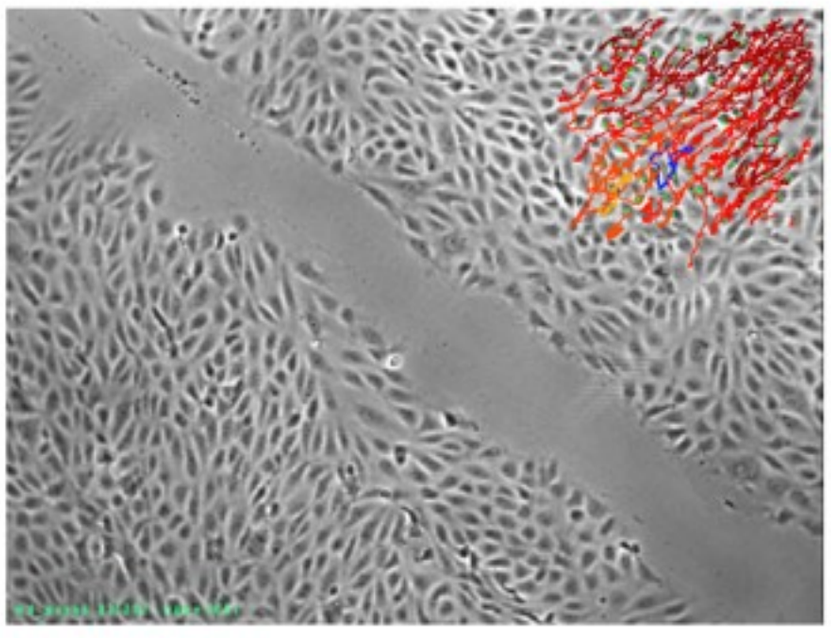
I



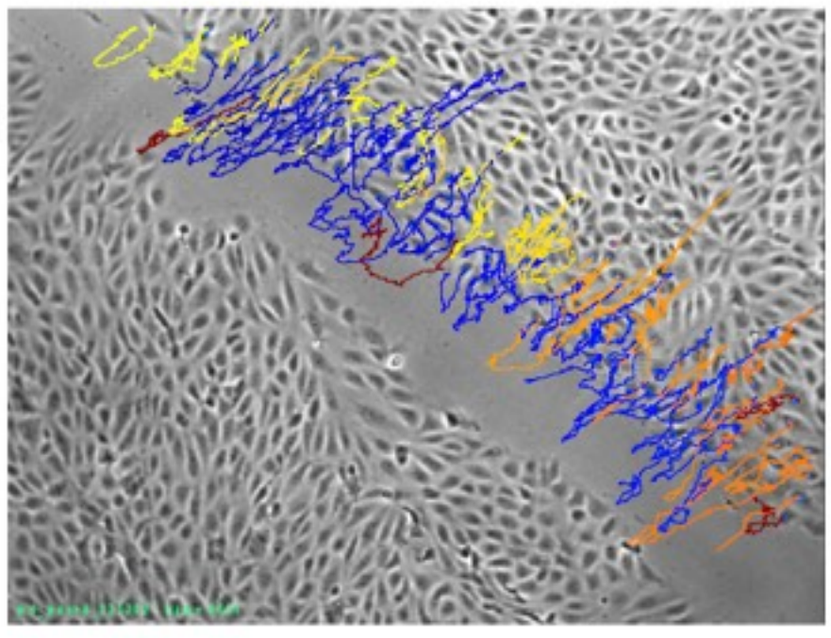
II



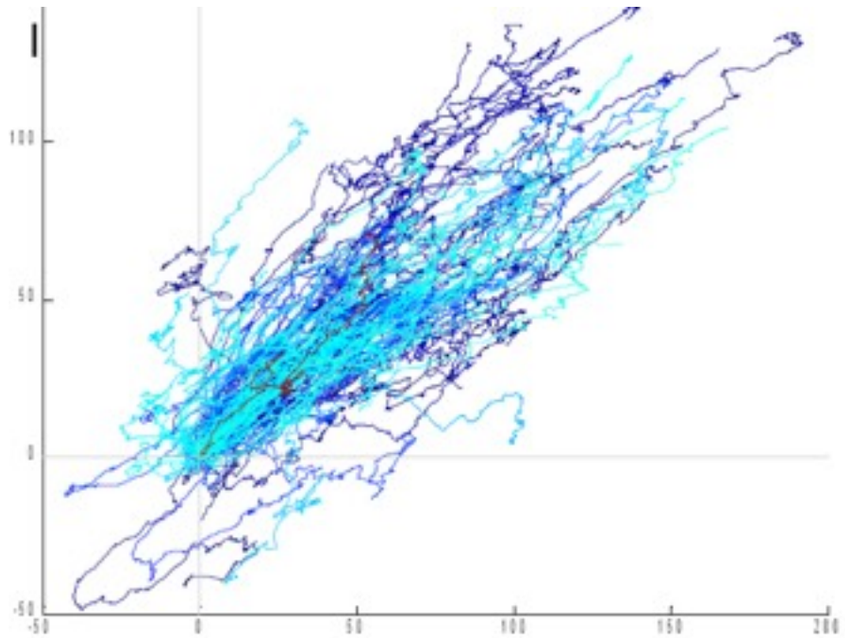
III

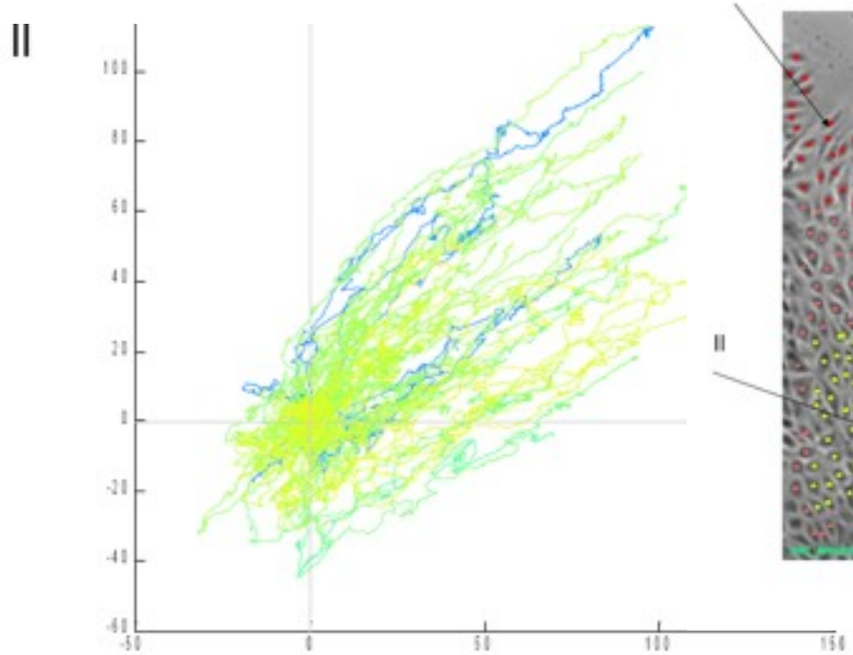


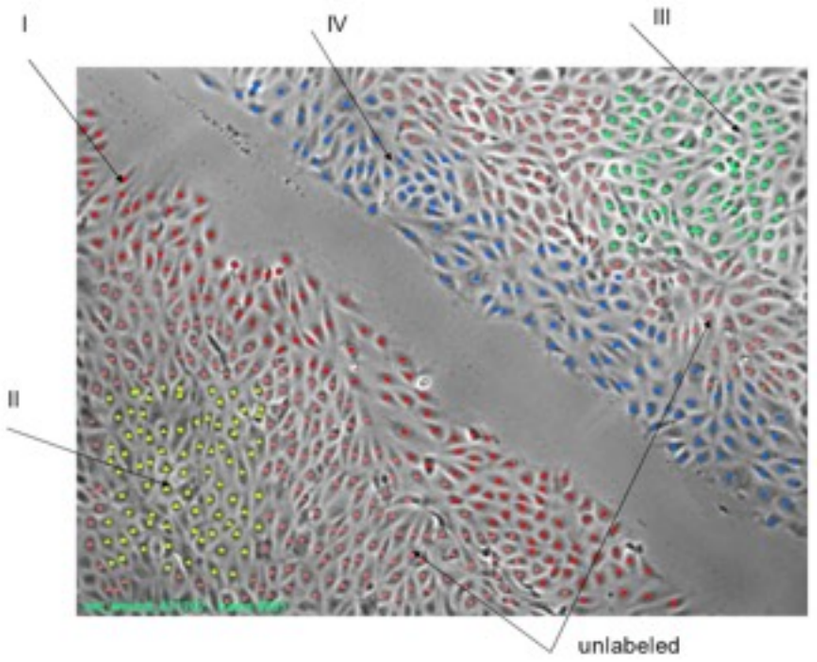
IV

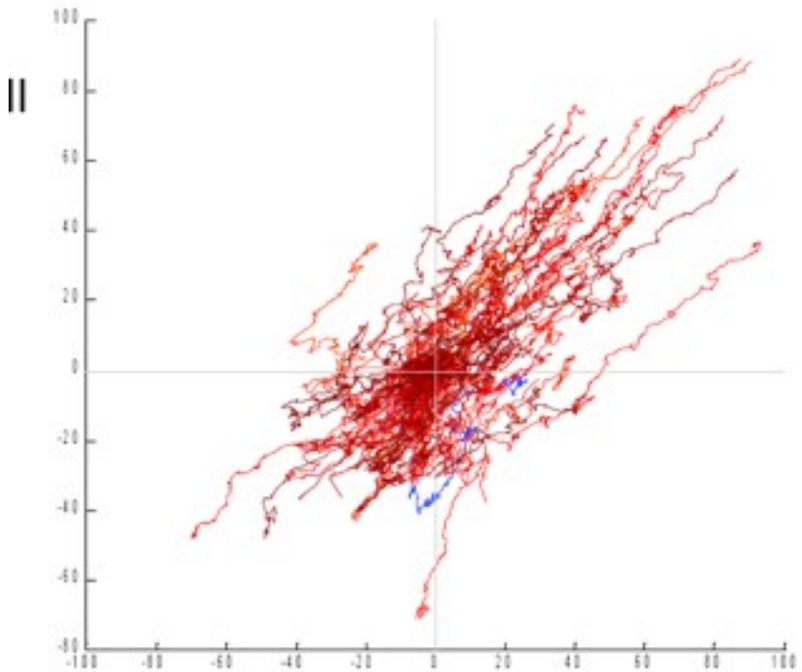


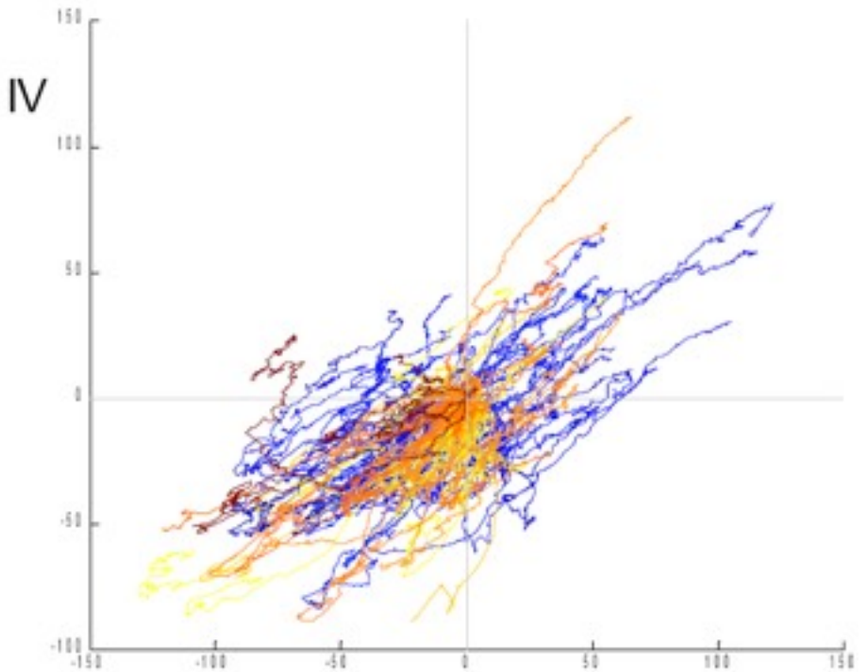
# Complex cell behaviour



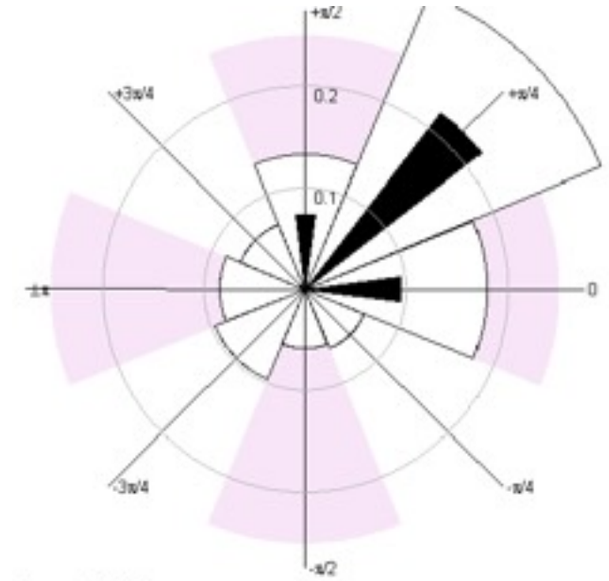



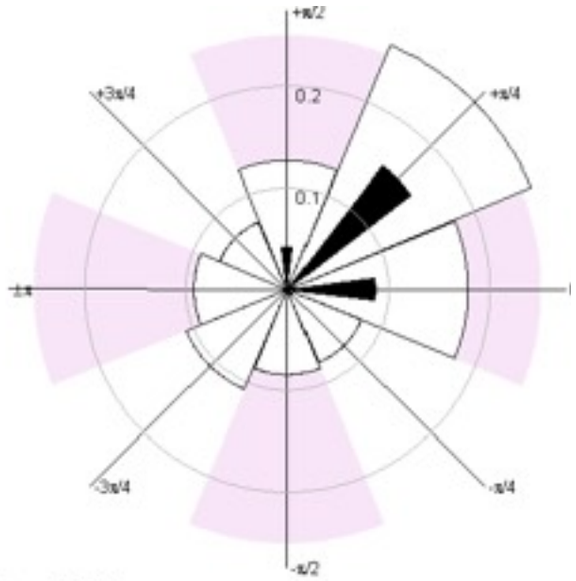



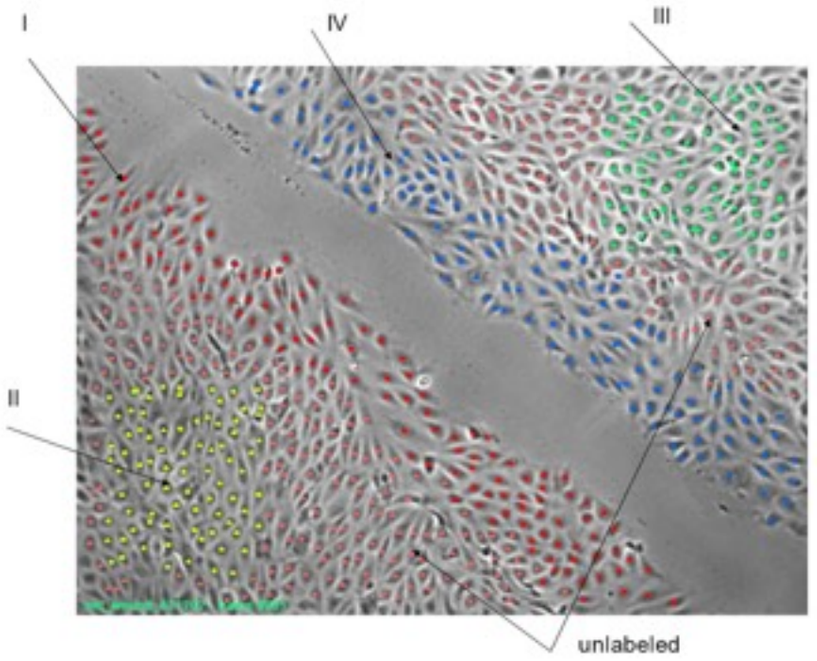
# Complex cell behaviour

I

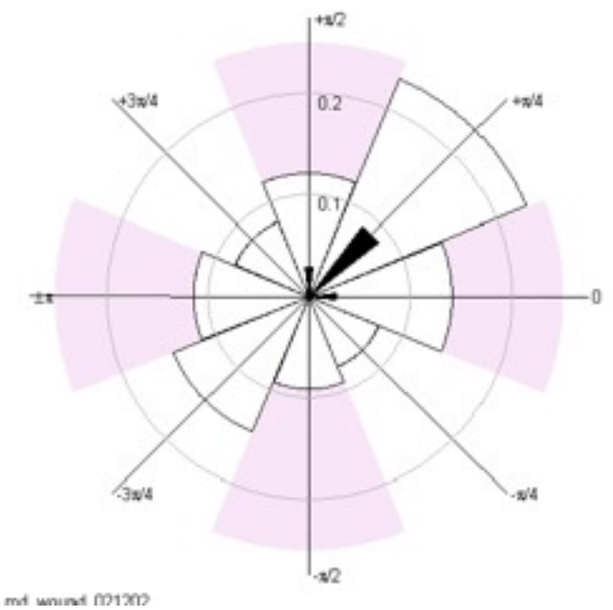



II

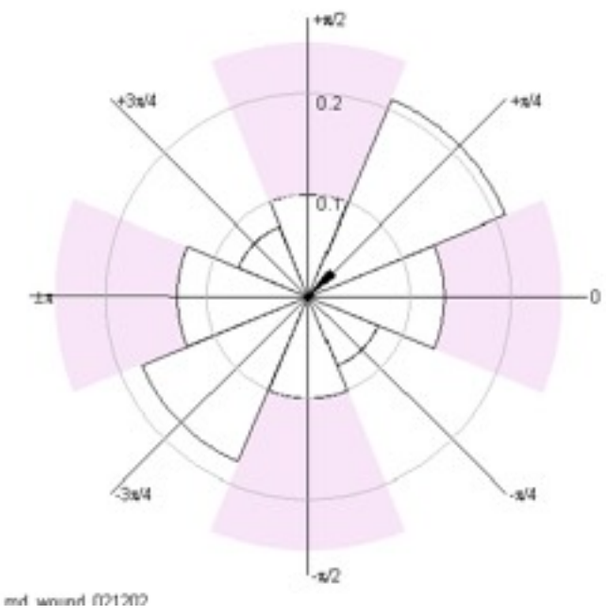



III

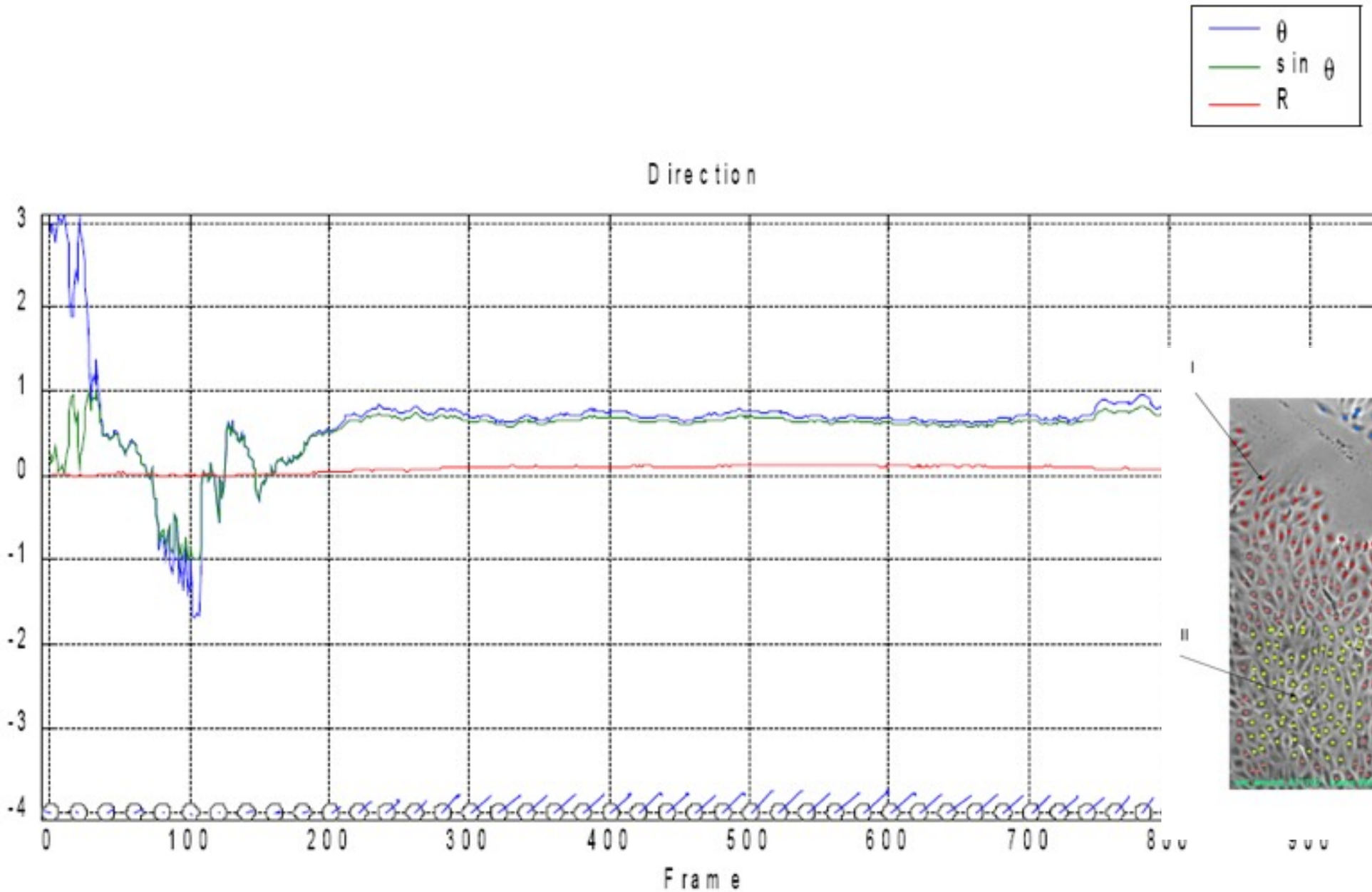


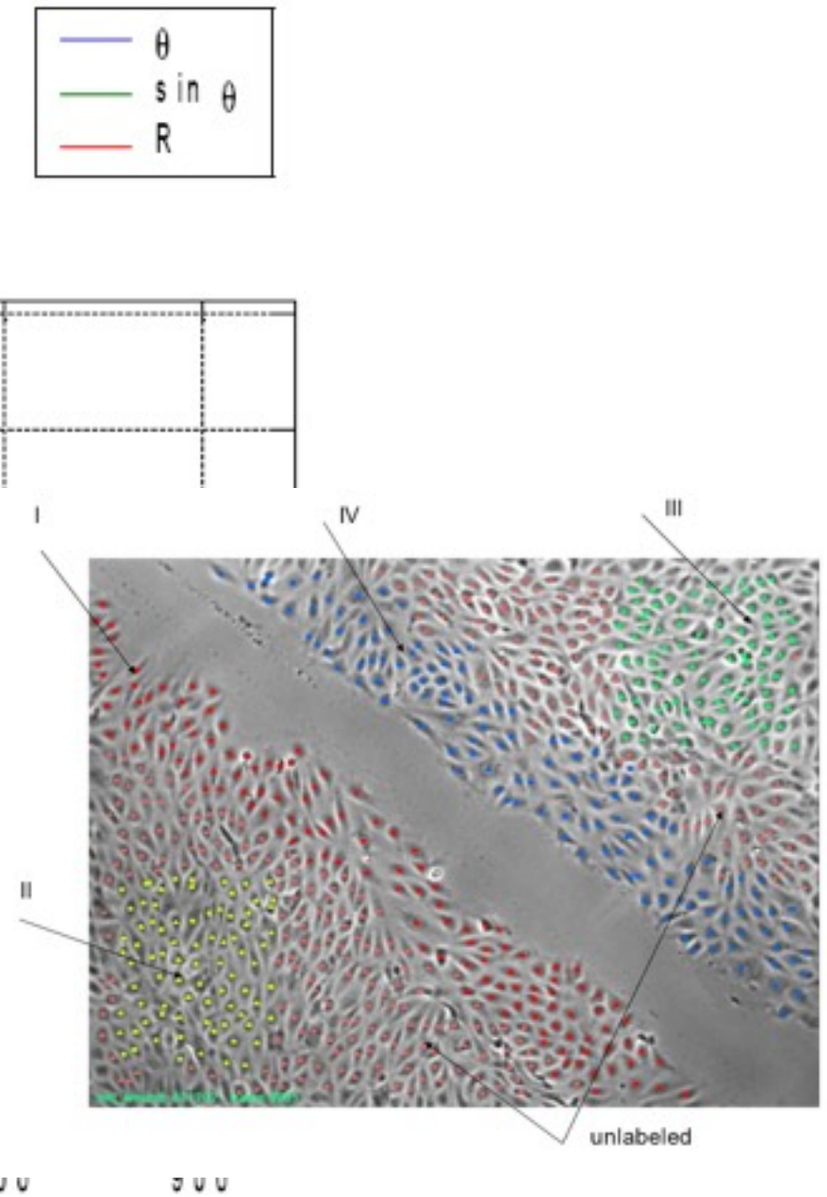

IV



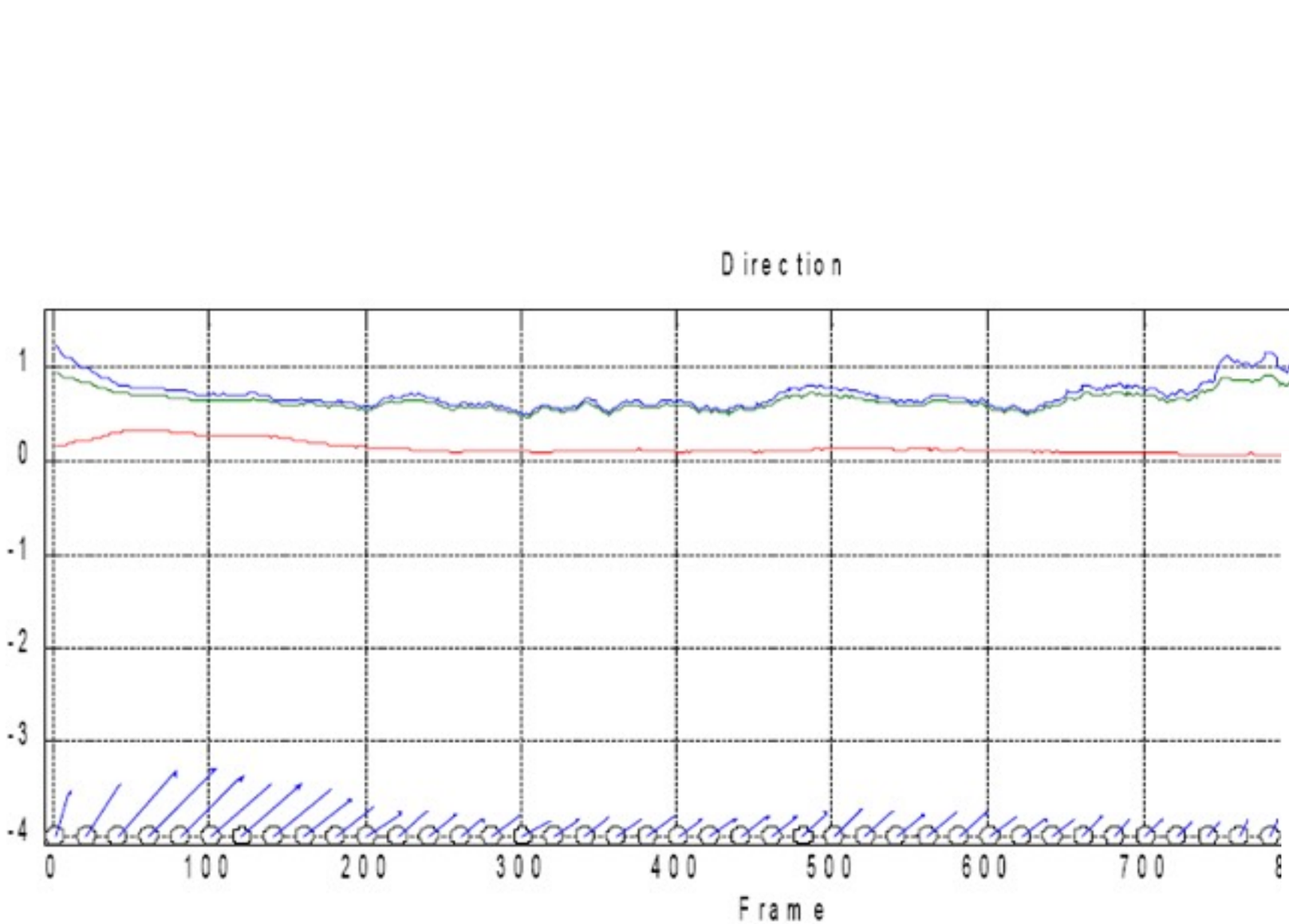
# Complex cell behaviour

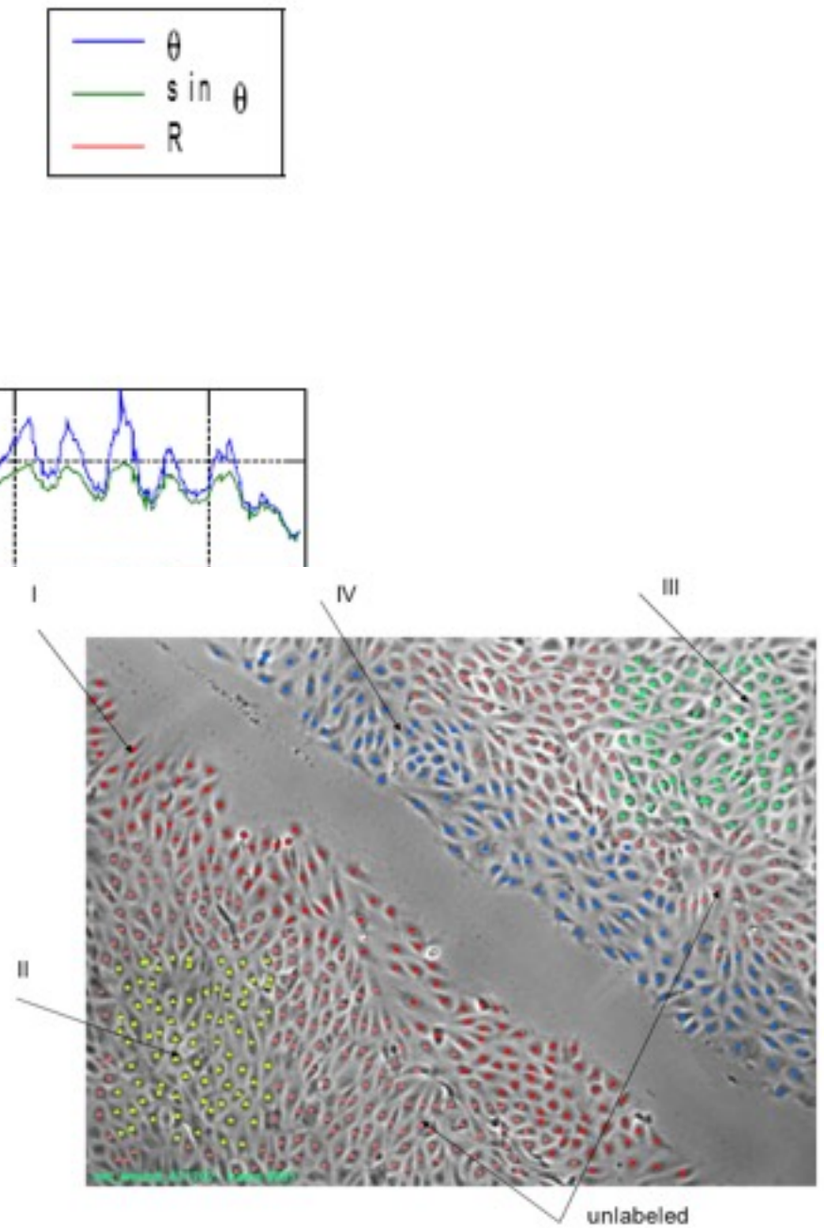
All



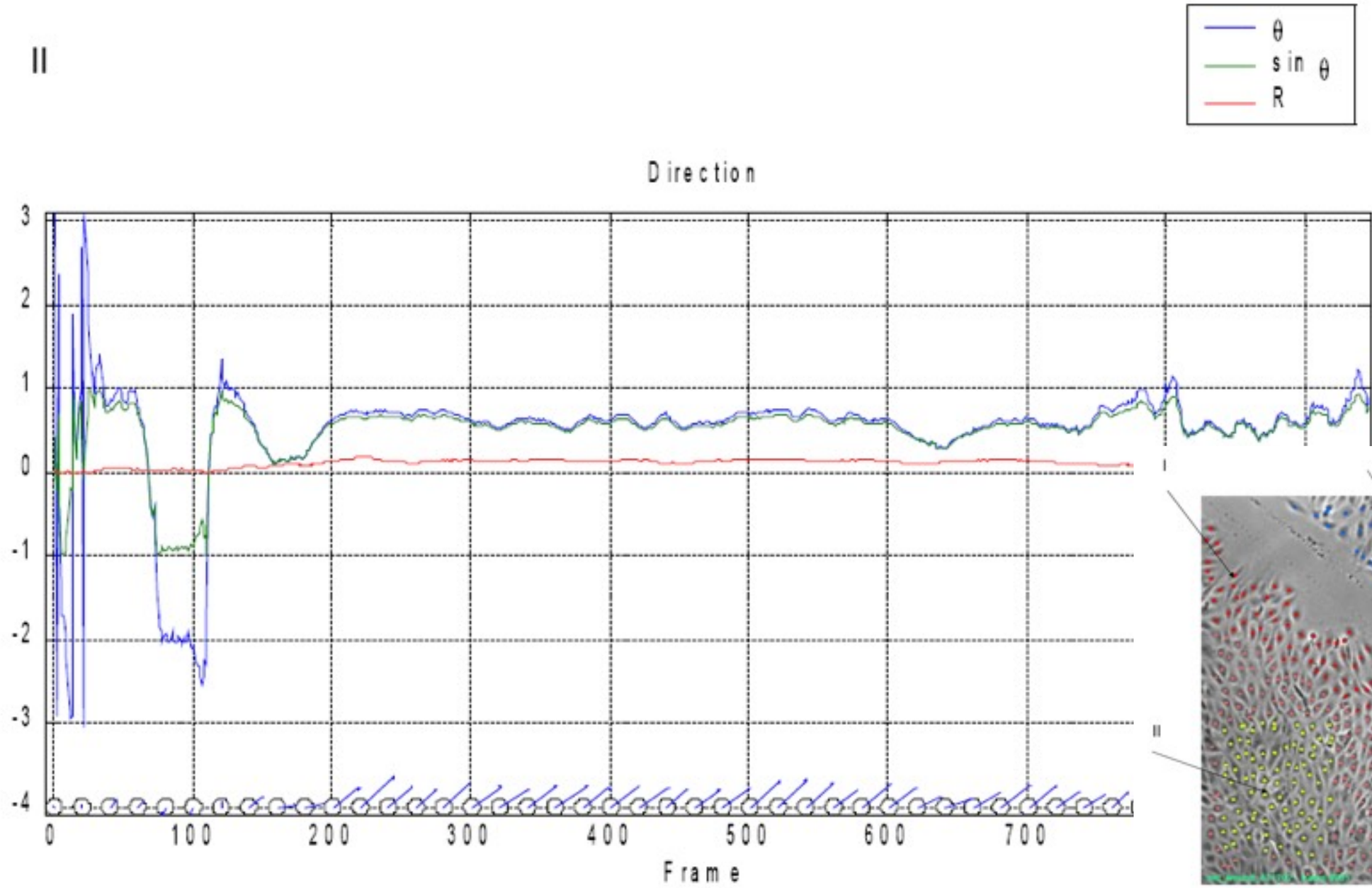



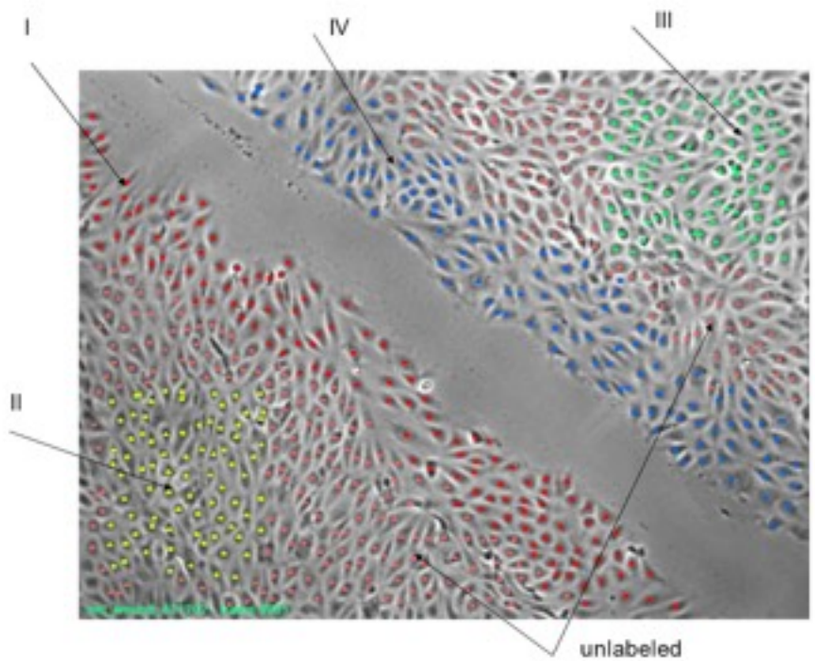
# Complex cell behaviour



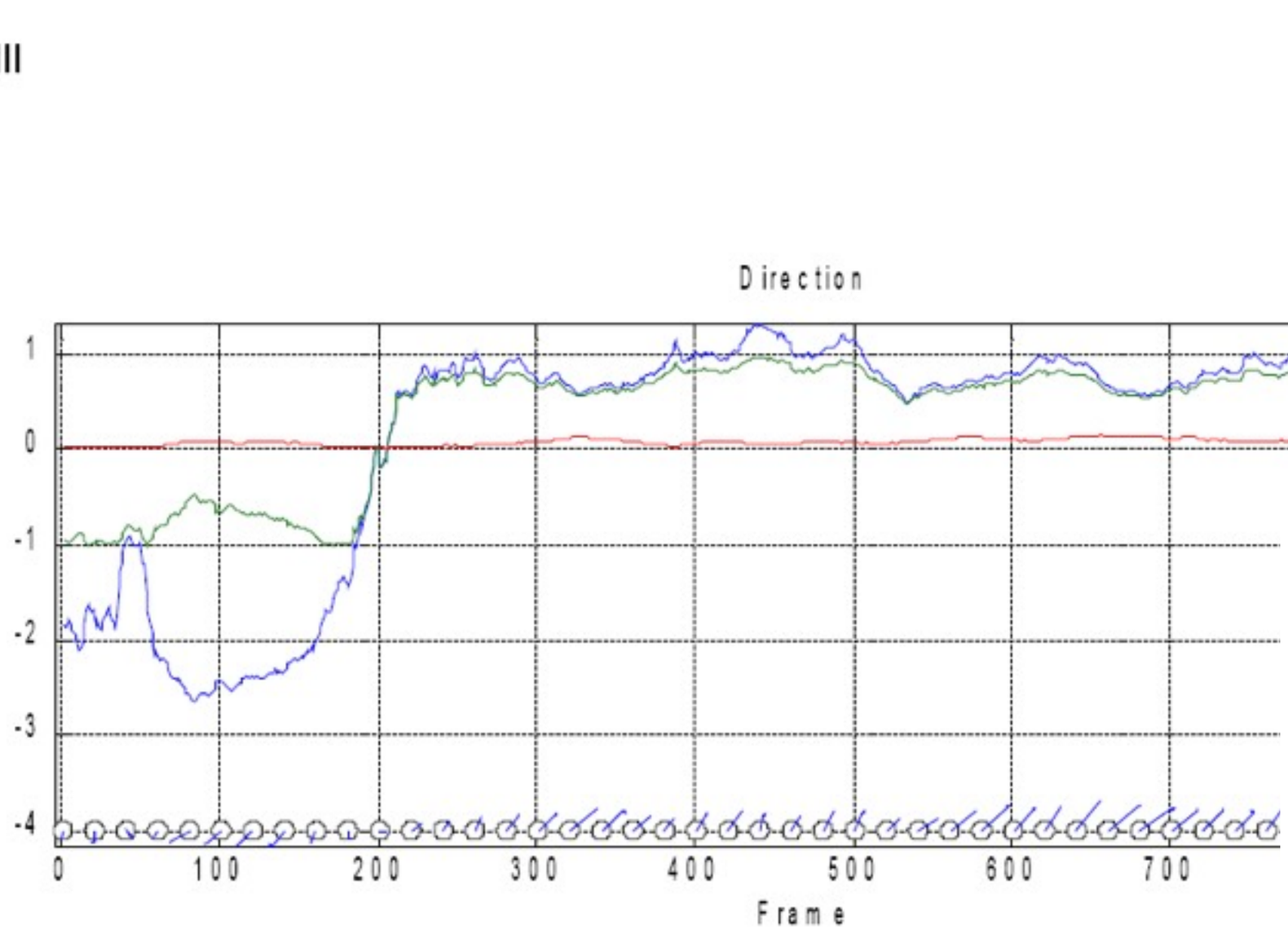
# Complex cell behaviour

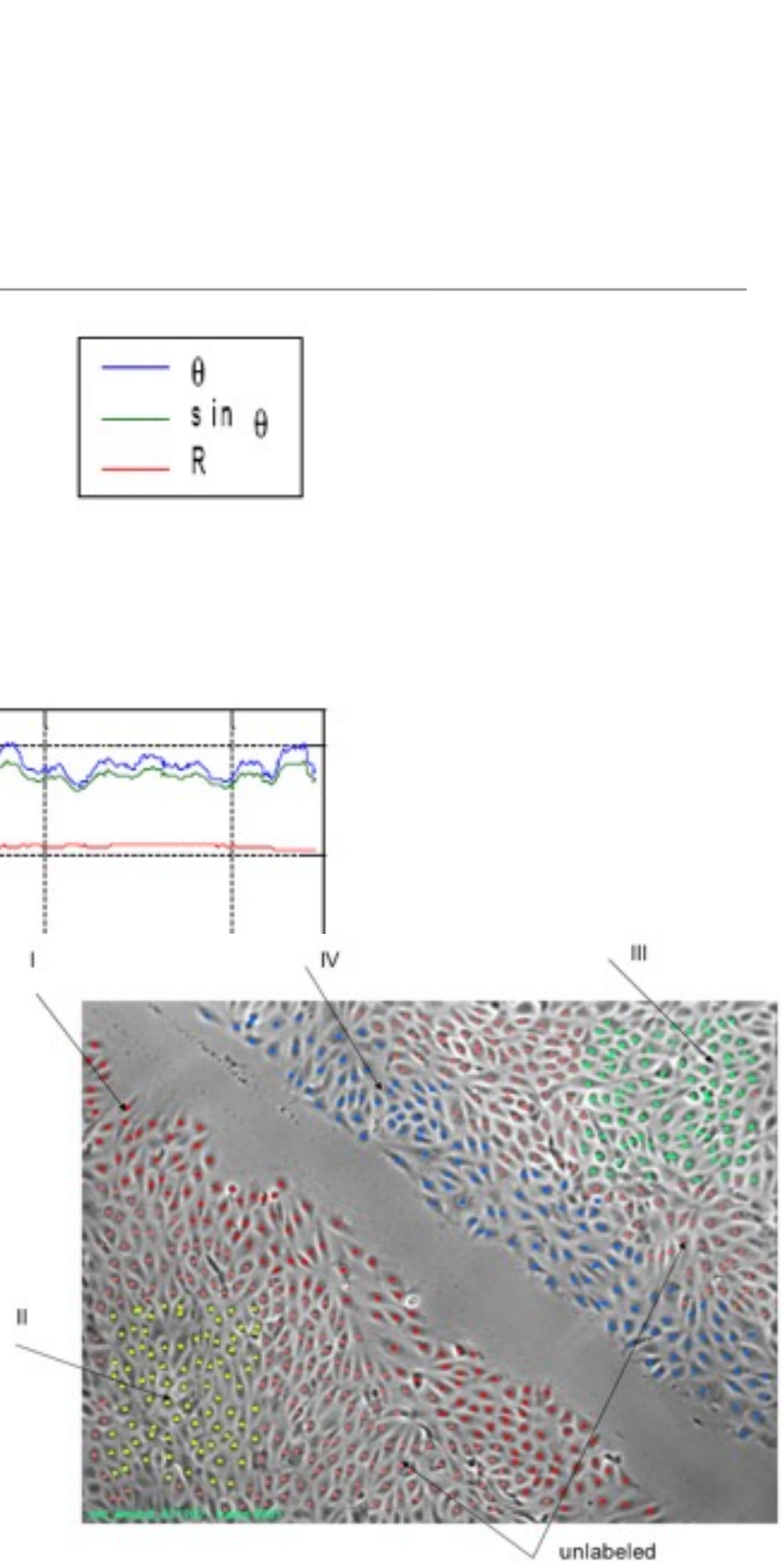


# Complex cell behaviour

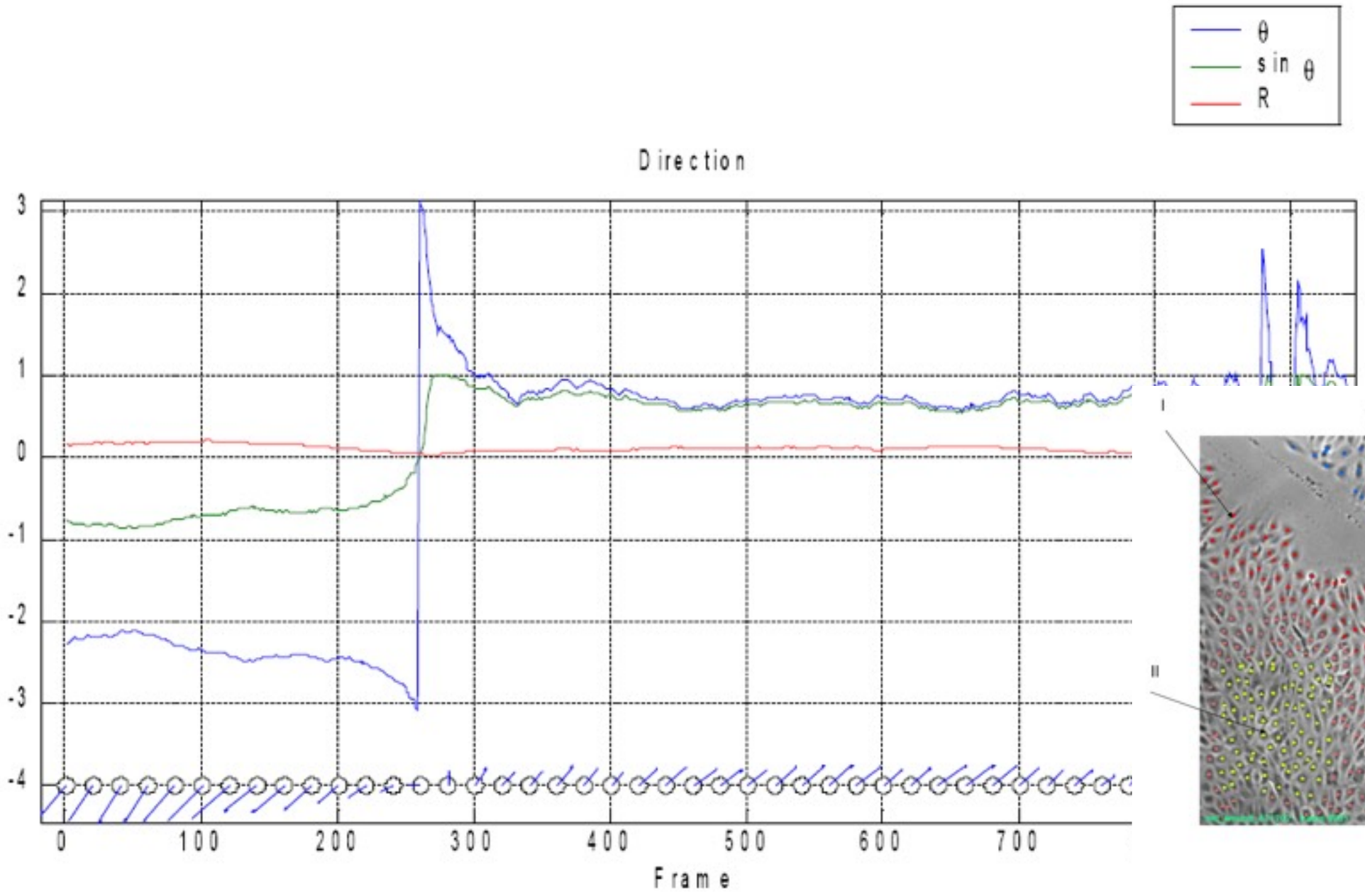
III

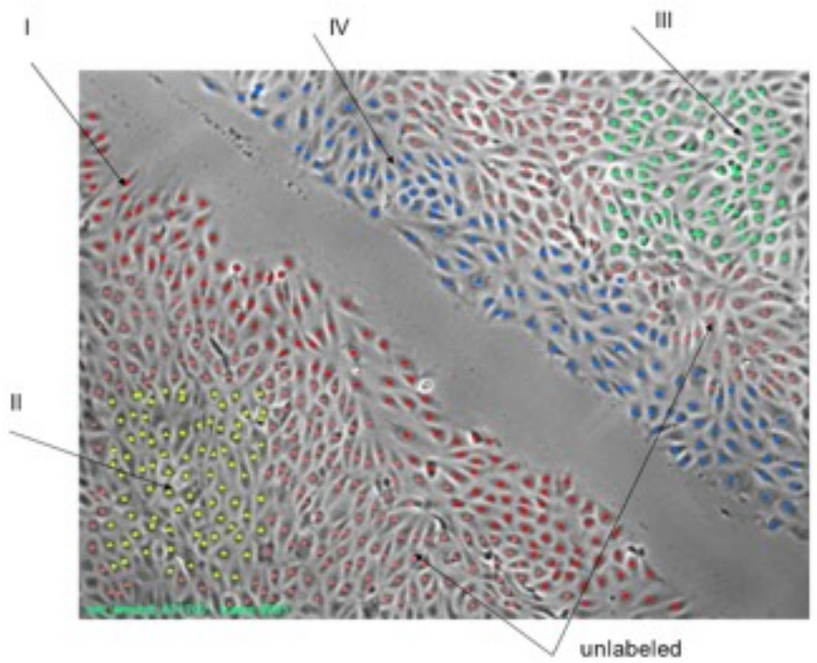


# Complex cell behaviour

IV



# Automatic in vitro cell tracking

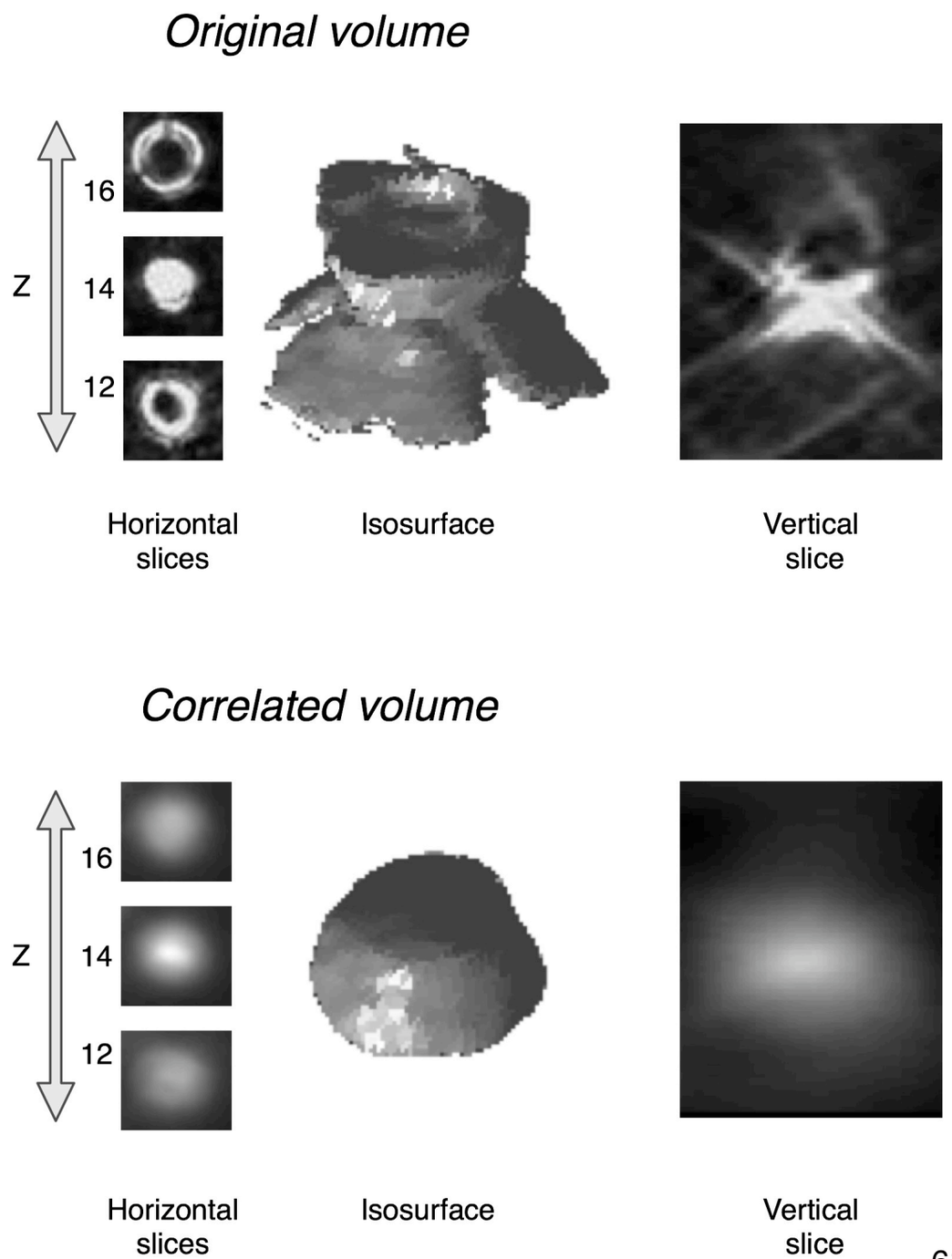
- Conclusions and future works

# Conclusions and future works

- In vitro cell imaging :
  - allows a fast observation and global observation (motility, proliferation, invasion, cell death, ...)
  - qualifies the effects of compounds on cell behavior
  - identifies a subset of interesting candidates among dozens of compounds
  - gives clues on the mechanism of drug action (MOA)
- Drug discovery

# Conclusions and future works

- Extension of the biological model
  - 3D gel observation
    - Fluorescence microscopy
      - Z-scanning phase contrast microscopy (I.Adanja)
- Refinement of the cell description



# Optical flow

# Motion estimation

- two approaches
  - corner based (e.g. Harris, Surf,...)
  - **pixel based direct method**
    - “dense” motion map

# Direct approach

- hypothesis
  - each pixel of image I “moves” ine the following image J
  - global image intensity remains constant

$$I(x, y) \approx J(x + u(x, y), y + v(x, y))$$

# Direct approach

$$I(x,y) \approx J(x + u(x,y), y + v(x,y))$$

| | | | |
|---|---|---|---|
| 1 | 2 | 3 | 4 |
| 5 | 6 | 7 | 8 |
| 9 | 10 | 11 | 12 |
| 15 | 16 | 13 | 14 |

I

| | | | |
|---|---|---|---|
| 5 | 6 | 7 | 8 |
| 1 | 2 | 3 | 4 |
| 12 | 11 | 10 | 9 |
| 13 | 14 | 15 | 16 |

J

| | | | |
|---|---|---|---|
| 0 | 0 | 0 | 0 |
| 0 | 0 | 0 | 0 |
| 3 | 1 | -1 | -3 |
| 2 | 2 | -2 | -2 |

u

| | | | |
|---|---|---|---|
| 1 | 1 | 1 | 1 |
| -1 | -1 | -1 | -1 |
| 0 | 0 | 0 | 0 |
| 0 | 0 | 0 | 0 |

v

# Constant intensity

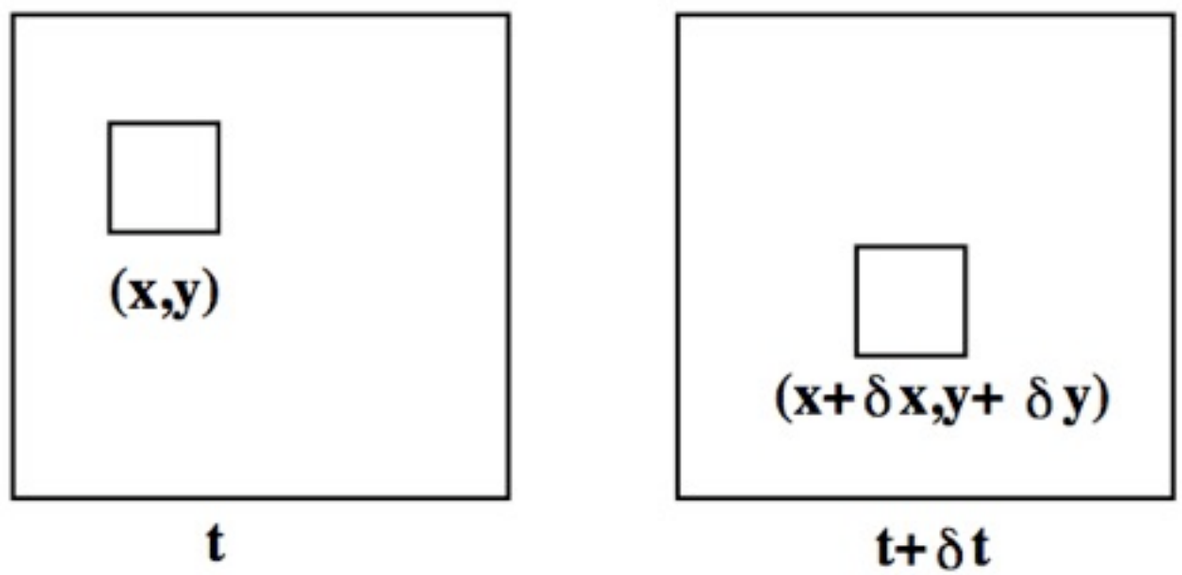
- let's

$$(u(x,y), v(x,y))$$

- such that

$$(I(x,y) - J(x + u(x,y), y + v(x,y)))^2$$

- is minimum
- ...



# Constant intensity

- practical approach using linear approximation
- linear approximation
  - motion linked to the gradient direction (gradient constraint)
  - only small u and v (e.g. 1 pixel)
  - using Taylor expension (1st term)

# Gradient constraint

- e.g. one dimension
  - let f(x) and g(x) = f(x-d)
  - f Taylor's expansion :
    f(x-d) = f(x) - d f'(x) + E with f' first f dérivative
  - f(x)-g(x) = d f'(x) + E
  - E is neglegted
    d = (f(x)-g(x)) / f'(x)

# Gradient constraint

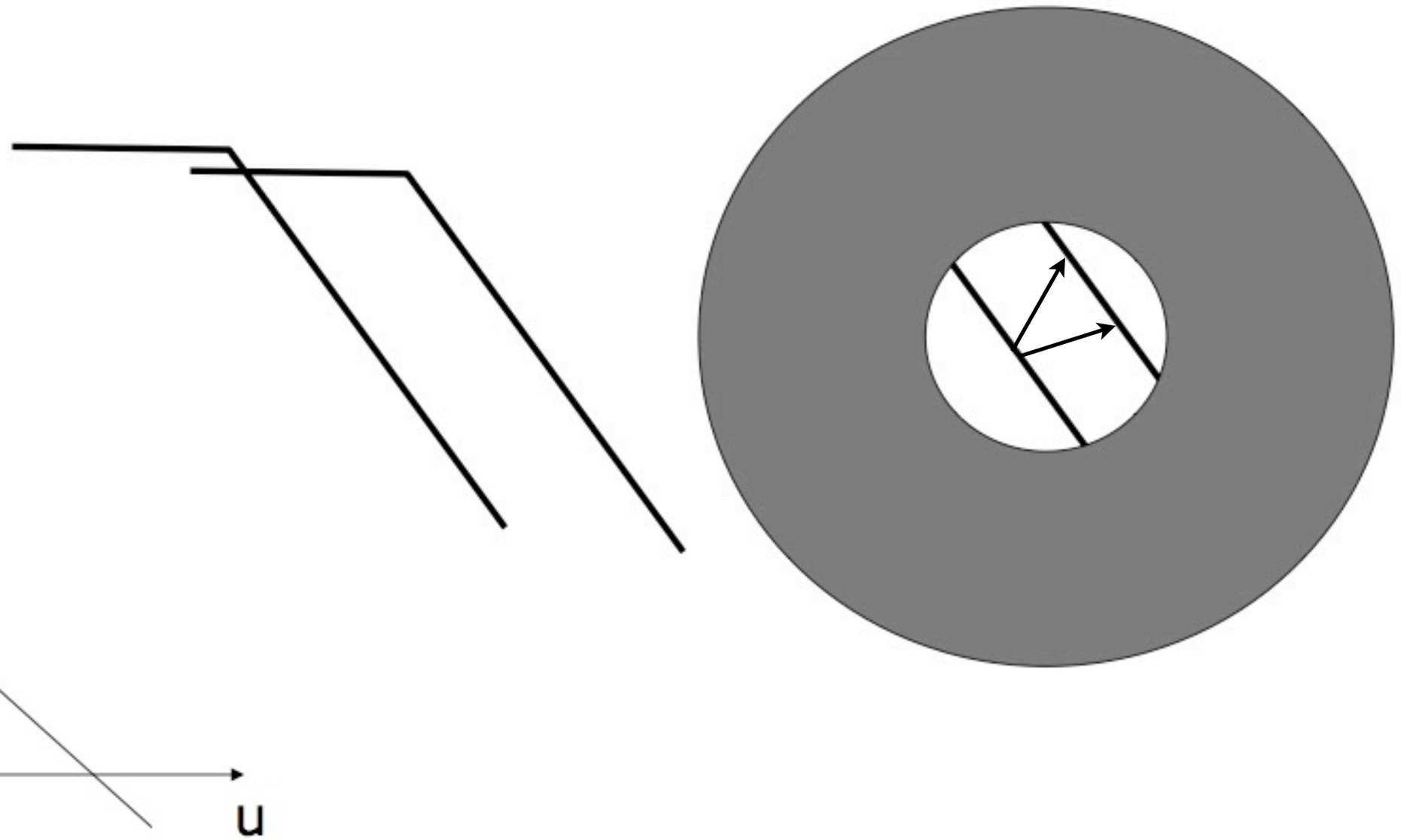
- two dimensions
  - I(x,y) ~ J(x+**u**,y+**v**), **u**=u(x,y), **v** = v(x,y)
  - J(x+**u**,y+**v**) ~ I(x,y) + Ix(x,y) **u** + Iy(x,y) **v** + It
    - Ix(x,y) u + Iy(x,y) v ~ -It
- gradient

$$\nabla I(u, v) \approx -I_t$$

- can not be solved (aperture problem)

# aperture problem

$$\nabla I(u, v) \approx -I_t$$



# Lucas-Kanade method

- filux is considered constant locally
- m x m window

$$(V_x, V_y) = cst$$

- n = m^2 equations such that

$$I_{x_1} V_x + I_{y_1} V_y = -I_{t_1}$$
$$I_{x_2} V_x + I_{y_2} V_y = -I_{t_2}$$
$$\vdots$$
$$I_{x_n} V_x + I_{y_n} V_y = -I_{t_n}$$

# Lucas-Kanade method

- too much equations (>2)

$$\begin{bmatrix} I_{x_1} & I_{y_1} \\ I_{x_2} & I_{y_2} \\ \vdots & \vdots \\ I_{x_n} & I_{y_n} \end{bmatrix} \begin{bmatrix} V_x \\ V_y \end{bmatrix} = \begin{bmatrix} -I_{t_1} \\ -I_{t_2} \\ \vdots \\ -I_{t_n} \end{bmatrix}$$

$$A\vec{v} = -b$$

- least squares optimization

# Lucas-Kanade method

- least squares optimization

$$
\begin{aligned}
A^T A\vec{v} &= A^T(-b) \\
\vec{v} &= (A^T A)^{-1} A^T(-b)
\end{aligned}
$$

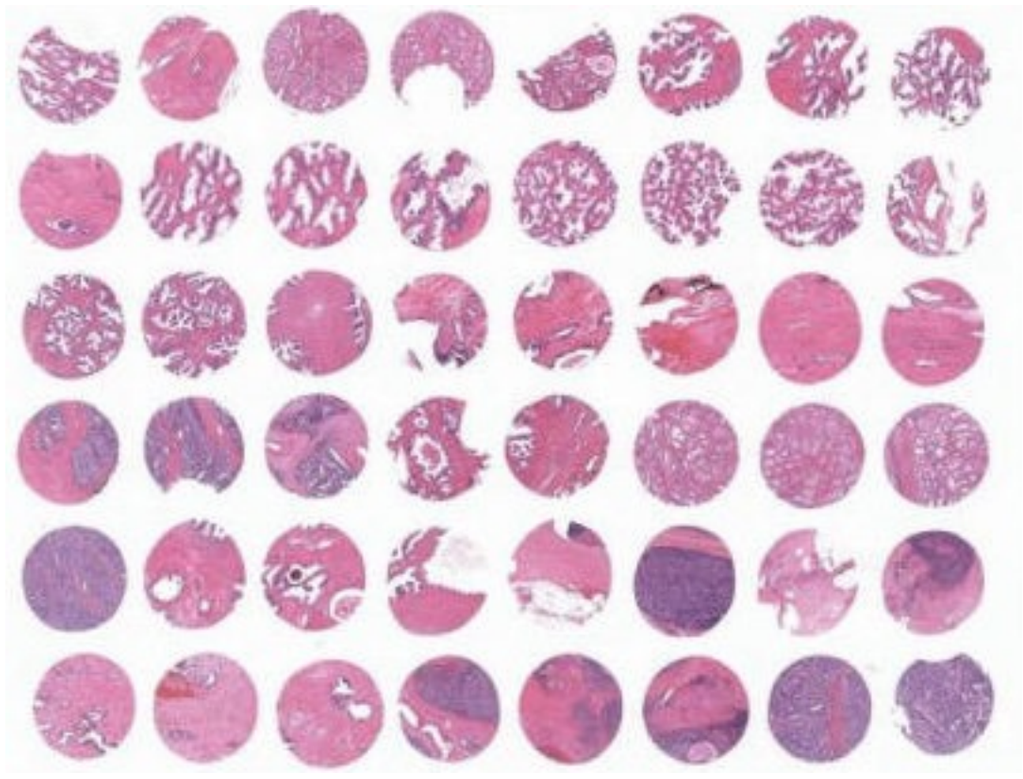
$$
\begin{bmatrix} V_x \\ V_y \end{bmatrix} = \begin{bmatrix} \sum I_{x_i}^2 & \sum I_{x_i} I_{y_i} \\ \sum I_{x_i} I_{y_i} & \sum I_{y_i}^2 \end{bmatrix}^{-1} \begin{bmatrix} -\sum I_{x_i} I_{t_i} \\ -\sum I_{y_i} I_{t_i} \end{bmatrix}
$$

# examples

- http://www.youtube.com/watch?v=0MtMxqJ6hF4 (opencv)
- http://www.youtube.com/watch?v=1D93RmW_eN4&feature=related (GPU)

# Particle filter

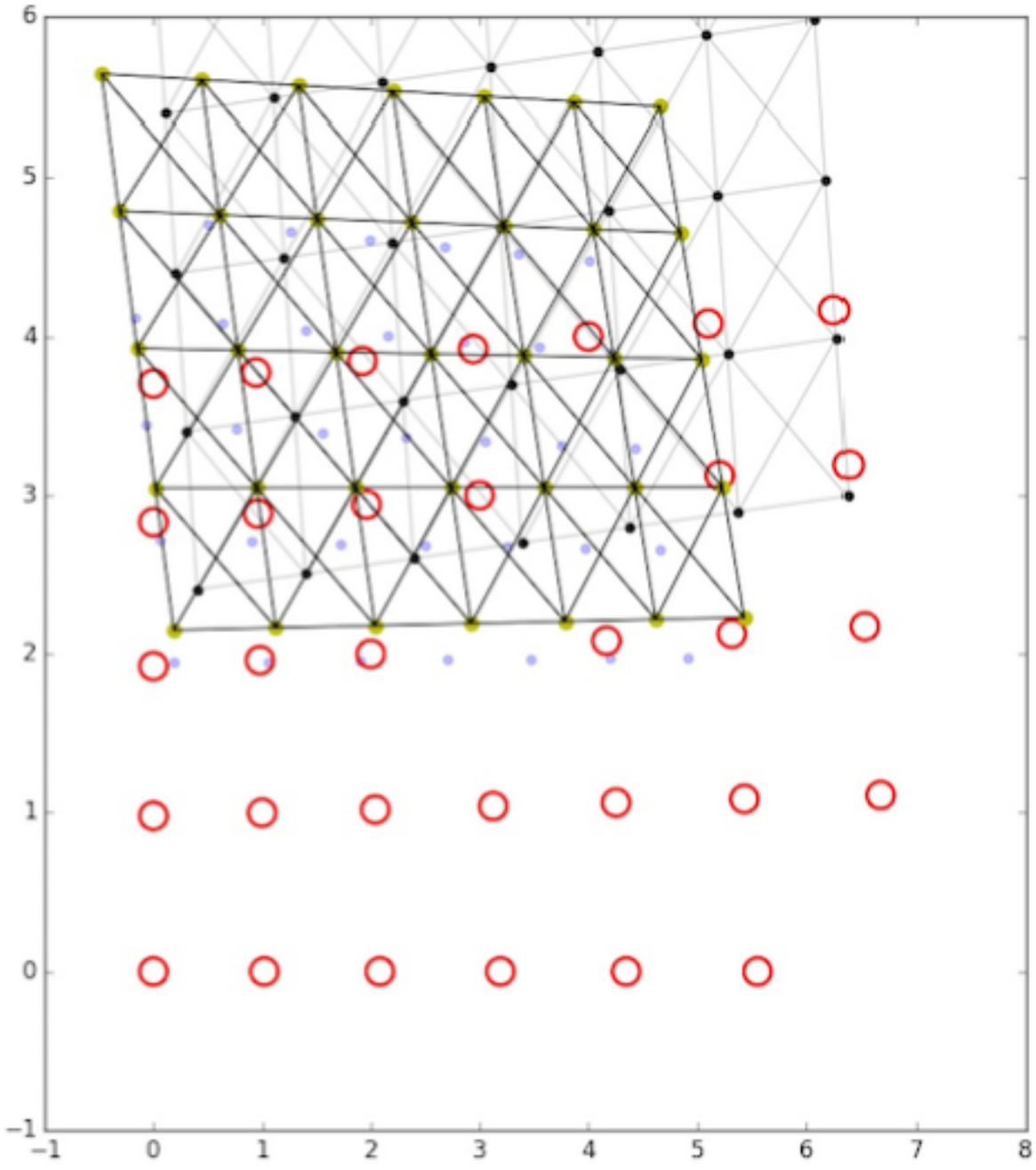
- example of application:
  TMA : tissue micro array



# Particle filter

# Particle filter

- Problem:
  - object detection
  - grid fitting



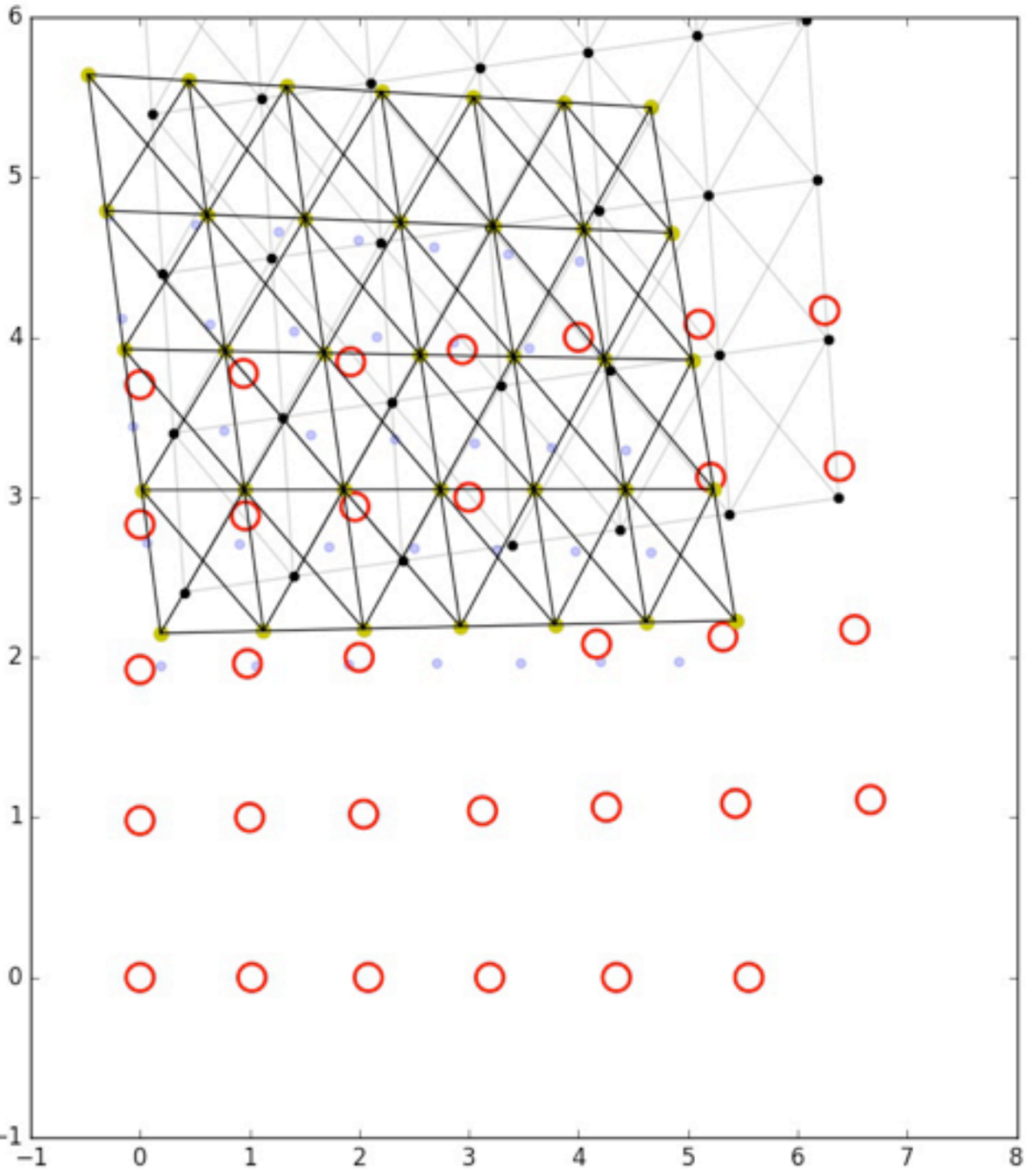
# Particle filter

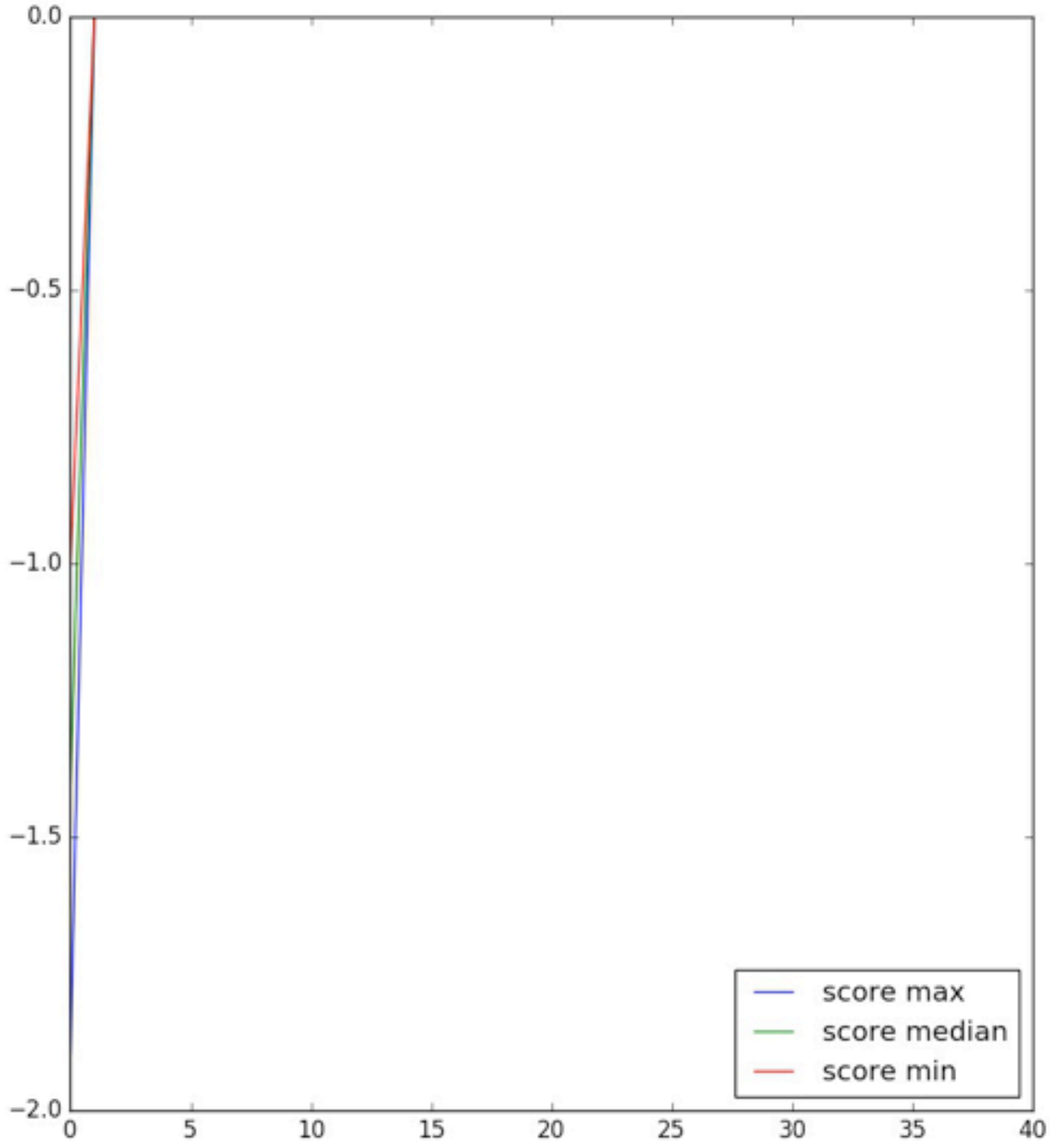
- Particule definition
  - one node (x,y) for each core + links between nodes
  - score = - (sum distance between cores and nodes)
- alternative definition
  - one single M affine matrix transform + fixed grid
  - score = id.

# Particle filter

- algorithm
  - initiate a set of particles
  - randomize particles
  - evaluate the score for each particle
  - resample particles with respect to their score
  - iterate

# Particle filter

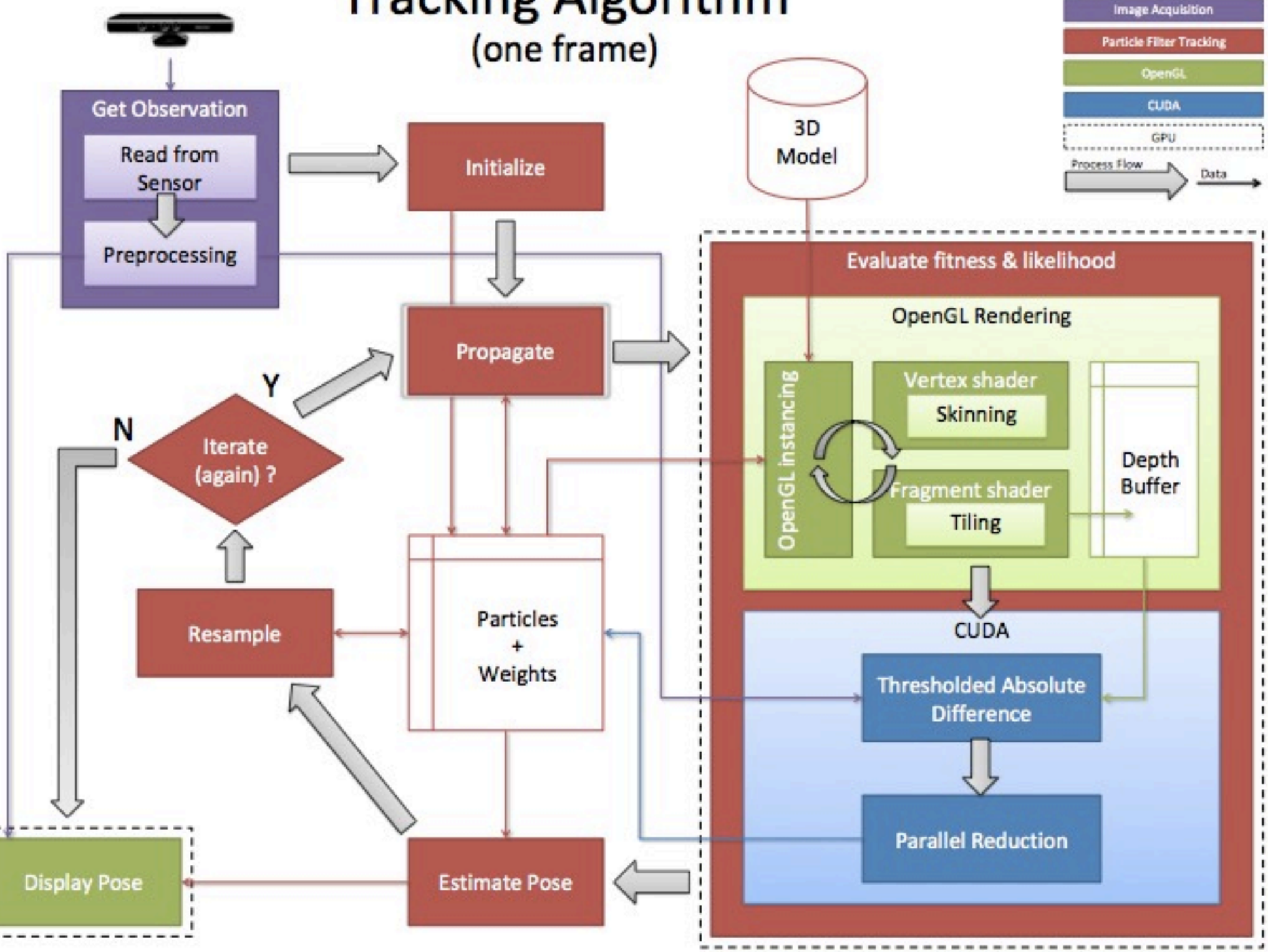


# Other example of particle filter use

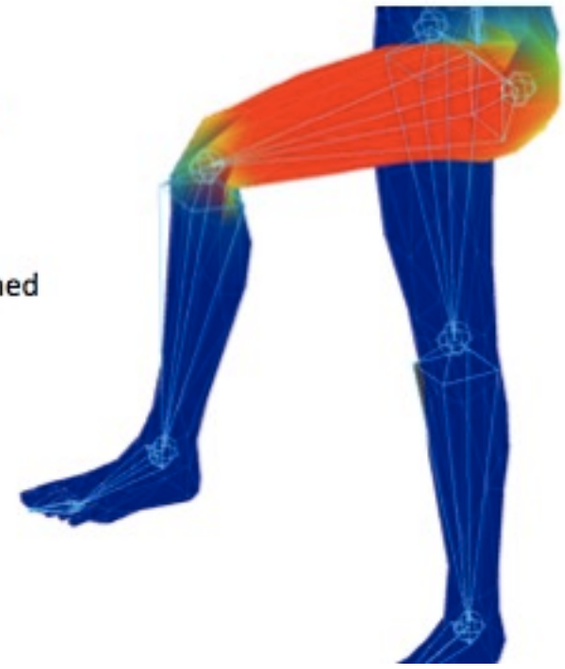
- Tracking of a body part using RGB+d camera

# Tracking Algorithm
(one frame)



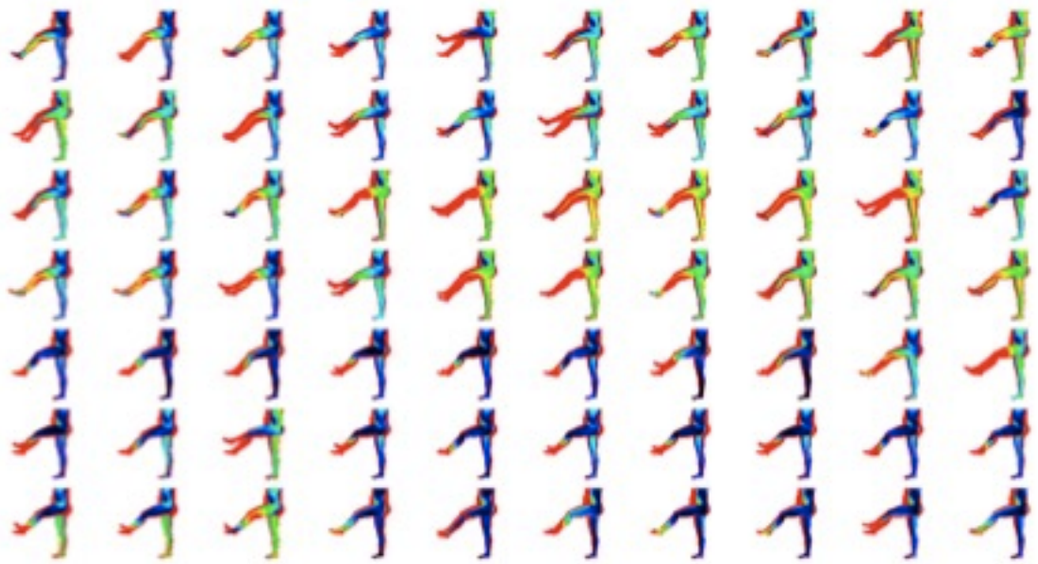
# Linear Blend Skinning

- Each vertex has a weight (see colors) for each skeleton segment.
- Vertex position transformed by weighted linear combination of bones transformations

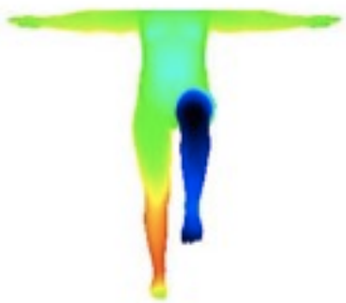


# Instancing & Tiling

N particles → N model instances → N tiles

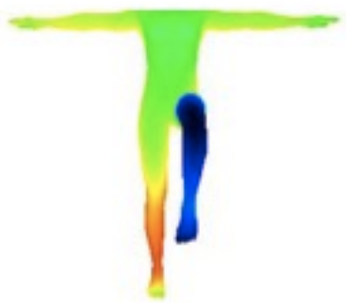


# Thresholded Absolute Difference



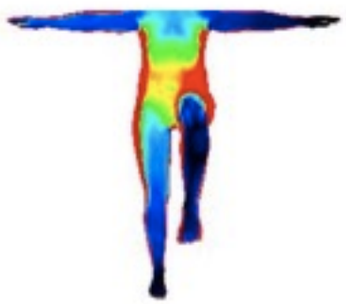
Observation

$D_O$



Posed Model

$D_M$



Thresholded
Absolute Difference

$$D_\Delta = \min(|D_O - D_M|, \tau)$$

# Estimate Pose

- Particles + weights → estimate of posterior pdf
- Optimal pose estimate may be computed as:
  - Minimum Mean Square Error (MMSE)

$$\hat{x}^{MMSE} = \sum_{i=1}^{N} f(x_i)x_i$$

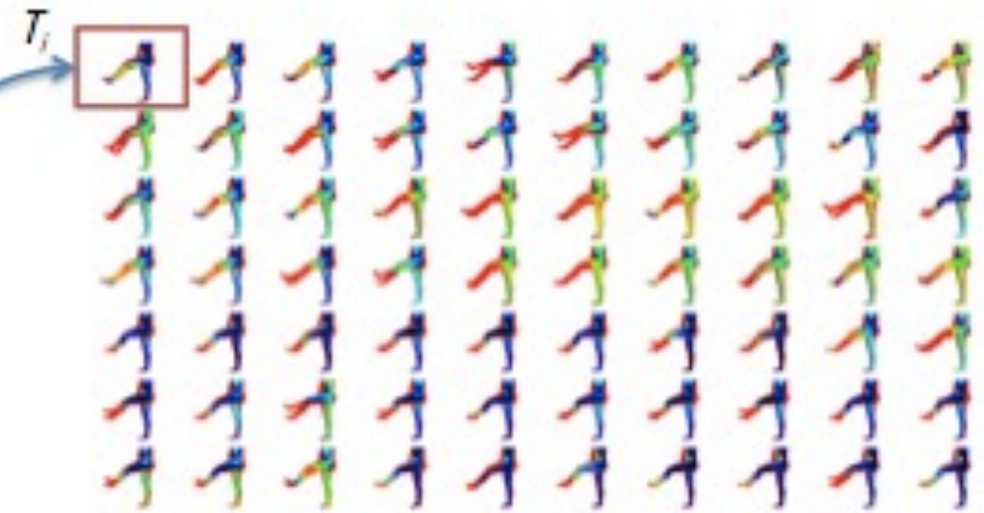
  - Maximum a-posteriori (MAP)

$$\hat{x}^{MAP} = \arg\max_{x_i}(f(x_i))$$

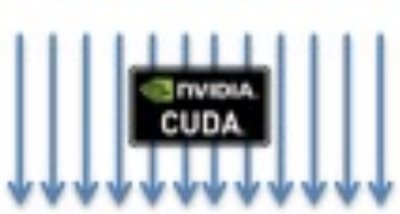
# Parallel Reduction

$x_i \equiv$ pose parameters for $i^{th}$ particle

$T_i \equiv$ tile for $i^{th}$ particle




$$\delta(x_i) = \sum_{j \in R_i} D_\Delta^j(x_i)$$

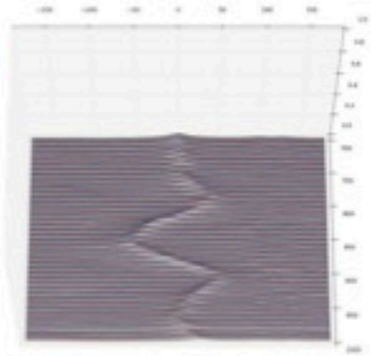



Particle's Fitness

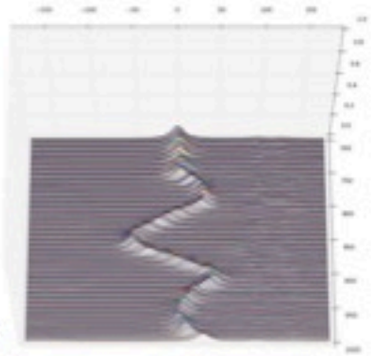
| | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| 0.0666 | 0.0020 | 0.0129 | 0.0244 | 0.0231 | 0.0094 | 0.0226 | 0.0321 | 0.0241 | 0.0164 |
| 0.0278 | 0.0065 | 0.0855 | 0.0876 | 0.0186 | 0.0253 | 0.0750 | 0.0133 | 0.0785 | 0.0229 |
| 0.0724 | 0.0498 | 0.0828 | 0.0632 | 0.0276 | 0.0165 | 0.0357 | 0.0428 | 0.0053 | 0.0239 |
| 0.0110 | 0.0160 | 0.0379 | 0.0561 | 0.0996 | 0.0544 | 0.0571 | 0.0828 | 0.0263 | 0.0947 |
| 0.0592 | 0.0516 | 0.0524 | 0.0745 | 0.0901 | 0.0954 | 0.0194 | 0.0792 | 0.0172 | 0.0022 |
| 0.0901 | 0.0516 | 0.0720 | 0.0476 | 0.0298 | 0.0639 | 0.0552 | 0.0634 | 0.0656 | 0.0557 |
| 0.0206 | 0.0904 | 0.0443 | 0.0685 | 0.0911 | 0.0699 | 0.0424 | 0.0408 | 0.0870 | 0.0756 |
| 0.0355 | 0.0074 | 0.0027 | 0.0708 | 0.0912 | 0.0515 | 0.0624 | 0.0740 | 0.0919 | 0.0937 |
| 0.0378 | 0.0732 | 0.0525 | 0.0990 | 0.0527 | 0.0033 | 0.0989 | 0.0075 | 0.0628 | 0.0295 |
| 0.0836 | 0.0436 | 0.0877 | 0.0618 | 0.0622 | 0.0398 | 0.0756 | 0.0639 | 0.0308 | 0.0305 |

# Likelihood

θ=1

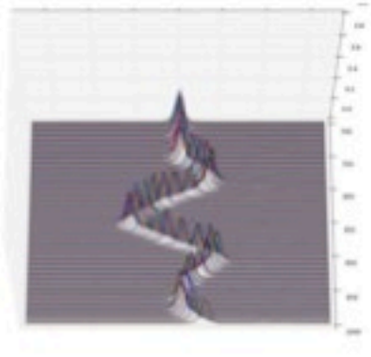


θ=2

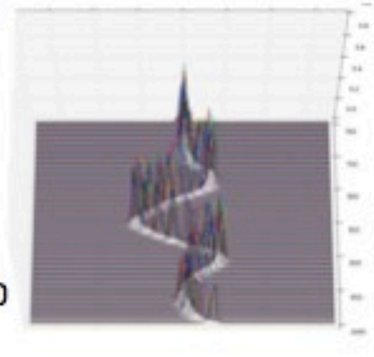


$$f(x_i) = \left( \frac{\max_j \delta(x_j) - \delta(x_i)}{\max_j \delta(x_j) - \min_j \delta(x_j)} \right)^{\theta}$$

θ=5



θ=10



# Propagate

| State Dynamics Model | |
|---|---|
| **No Model** | **Weak Model** |
| $x_{t+1} = x_t + w_t$ | $x_{t+1} = x_t + \alpha(x_t - x_{t-1}) + w_t$ |
| Zero mean Gaussian stochastic component $w_t = [N(0,\sigma_i)]$ | Velocity of the particle at current frame<br>Controls the velocity's influence |