# **Chapter 14**

# **Quantitative Motion Analysis in Two and Three Dimensions**

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#### Abstract

This chapter describes 2D quantitative methods for motion analysis as well as 3D motion analysis and reconstruction methods. Emphasis is placed on the analysis of dynamic cell shape changes that occur through extension and retraction of force generating structures such as pseudopodia and lamellipodia. Quantitative analysis of these structures is an underutilized tool in the field of cell migration. Our intent, therefore, is to present methods that we developed in an effort to elucidate mechanisms of basic cell motility, directed cell motion during chemotaxis, and metastasis. We hope to demonstrate how application of these methods can more clearly define alterations in motility that arise due to specific mutations or disease and hence, suggest mechanisms or pathways involved in normal cell crawling and treatment strategies in the case of disease. In addition, we present a 4D tumorigenesis model for high-resolution analysis of cancer cells from cell lines and human cancer tissue in a 3D matrix. Use of this model led to the discovery of the coalescence of cancer cell aggregates and unique cell behaviors not seen in normal cells or normal tissue. Graphic illustrations to visually display and quantify cell shape are presented along with algorithms and formulae for calculating select 2D and 3D motion analysis parameters.

Key words Cell motility, 2D motion analysis, 3D reconstruction, Cell migration, 3D data, 4D tumorigenesis model

# 1 Introduction

The importance of cell migration in developmental biology, immunity, and disease has oft been repeated [1-4]. Indeed, it is becoming increasingly apparent that basic cell motility, that is, crawling in the absence of chemoattractant or other directionally stimulatory signals, may be an inherent cellular property [5]. Molecular mechanisms that drive cell motility have been studied extensively in the model system *Dictyostelium discoideum* [6–10] as well as in the so-called professional migratory cells such as neutrophils [1, 11– 14] and macrophages [15, 16]. Considerable attention has also been focused on cell migration in the context of metastatic cancer [17–20] and understandably so since metastasis is the primary cause of death from this disease [21–23].

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Basic cell motility may be modulated by chemotactic and haptotactic signals [24]. Hence, the failure of certain mutants to respond to an exogenous signal may actually be due to a mutation in the basic motility apparatus rather than a mutation in a signal transduction pathway [25] and this important distinction can only be made using appropriate quantitative methods. In addition, different migratory behaviors are manifested on 1D [3], 2D [3, 26] and 3D surfaces [27] due to physical properties of the substrate [27, 28], interactions between the substrate components and cell adhesion receptors [29], and the activity of extracellular proteases such as the metalloproteinases that degrade or remodel the matrix [30]. Again, deciphering the underlying mechanisms responsible for these characteristics requires accurate quantitation. It likewise is important to know the specific motility defects of abnormally behaving immune cells [24, 31, 32] in order to accurately diagnose the disease and provide successful treatment. Finally, it should be noted that although transwell assays are widely used to assay motility and chemotactic defects [33-35], they may not distinguish between chemotaxis and chemokinesis, provide only a limited amount of all-or-none information and no quantitative information on cytoskeletal dynamics or mechanisms of cell migration.

The aforementioned points speak to the need for high resolution 2D and 3D quantitative methods in which cell shape changes mediated by pseudopod or lamellipod dynamics [24, 36, 37], invadopodia [38, 39], podosomes [40, 41] and/or filopodia [37, 42] are analyzed in order to distinguish normal from aberrant motility and normal chemotaxis or other forms of directed motility on one hand from directed crawling that has been dampened or obliterated by signal transduction deficiencies on the other. Here we will describe high-resolution 2D and 3D methods for motion analysis of individual cells. We include protocols for 2D motion analysis of basic cell motility as well as chemotaxis on a 2D substrate, 3D motion analysis of basic cell motility and reconstruction on a 2D substrate and finally, 3D motion analysis of basic cell motility and reconstruction in a 3D matrix (i.e., 4D). As an example of the validity of this approach, we will show how high-resolution quantitation of cell motility led to the discovery in the model system Dictyostelium discoideum that upregulation of lpten, a homolog of ptenA that is, in turn, an ortholog of the human PTEN mutated in many human cancers, rescues defects in ptenA<sup>-</sup> mutants, raising the possibility of a new stratagem for cancer therapy [43]. In addition, accurate quantitation of cell shape changes in basic cell motility as well as in chemotaxis has provided insights into human diseases [31, 44] and, as we show here, can be used to evaluate coalescence of cancer cells, cell-cell interactions within the tumor microenvironment as well as effects of potential cancer treatments [41].

#### 2 Materials

#### 2.1 Culturing 1. D. discoideum wild-type and mutant strains, as well as many plasmids, can be obtained from the Dictybase Stock Center. Dictyostelium (http://www.dictybase.org/StockCenter/StockCenter.html). discoideum 2. HL-5 nutrient growth media supplemented with the appropriate antibiotics for transformed strain selection (http://dictybase.org). 3. Amoebae maintained at the low-log phase of growth ( $\sim 2 \times 10^6$ cells/mL in HL-5) (see Note 1). 2.2 Development 1. BSS: 20 mM KCl, 2.5 mM MgCl<sub>2</sub>, 20 mM KH<sub>2</sub>PO<sub>4</sub>, 5 mM Na<sub>2</sub>HPO<sub>4</sub> (pH 6.4), 0.34 mM streptomycin sulfate, filter sterof D. discoideum for ilized [22, 23]. Basic Cell Motility and Chemotaxis Assays 2. HAB040700 nitrocellulose filters (Millipore, Billerica, MA, USA). 3. Millipore support filters (catalog AP1004700; www.millipore.com). 4. Humidified incubation chamber at 22 °C. 5. cAMP: 1 mM stock solution of adenosine 3',5'-cyclic monophosphate (cAMP; Sigma-Aldrich, Inc. http://www.sigmaaldrich.com) diluted in BSS and frozen until use. 1. 10 mL whole venous blood drawn from healthy donors using 2.3 Isolation of IRB-approved informed consent protocols into blood collec-Primary Human PMNs tion tubes coated with anticoagulant, preferably EDTA for use for Basic Cell Motility with Polymorphprep. Heparin-coated tubes are not recomand Chemotaxis mended for use with Polymorphprep. Assays 2. Polymorphprep Axis Shield Density Gradient Media (www. cosmobiousa.com) for separation of neutrophils from whole blood. 3. Hepes-buffered Hanks' balanced salt solution (H-HBSS) with 1.26 mM CaCl2 and 0.49 mM MgCl2 (Life Technologies, Carlsbad, CA), pH 7.4 and 10 mM Hepes. 4. Centrifuge capable of $400-900 \times g$ forces at room temperature with the option of no-brake deceleration. 5. N-formyl peptide (fMLP): 500 µM stock solution of N-formylmet-leu-phe (Sigma-Aldrich, Inc.) in DMSO frozen until use. 2.4 Culturing 1. Laboratory personnel who have contact with cells, tissue, and/ or blood products, particularly those of human origin, should **Cell Lines** be trained in the proper use of personal protective equipment (PPE) and the safe handling of material that may harbor bloodborne pathogens (see Note 2). 2. Certified biological safety cabinet, biohazardous waste decon-

tamination, and biohazardous waste disposal systems.

3. Cell culture media: Dulbecco's m	nodified	Eagle's	medium
(DMEM), RPMI 1640, (Life Tecl	hnologie	s, Carlsl	oad, CA,
http://www.lifetechnologies.com)	or su	applier's	media
recommendation.			

- 4. Fetal bovine serum (FBS, Atlanta Biologicals https://www.atlantabio.com/) (see Note 3).
- 5. Penicillin/streptomycin mixture (Life Technologies, Carlsbad, CA, http://www.lifetechnologies.com).
- 6. DPBS (Dulbecco's phosphate-buffered saline; Life Technologies, Carlsbad, CA http://www.lifetechnologies. com) without magnesium and without calcium for cell dissociation: 2.67 mM potassium chloride (KCl), 1.47 mM potassium phosphate monobasic (KH<sub>2</sub>PO<sub>4</sub>), sodium chloride (NaCl), and sodium phosphate dibasic (Na<sub>2</sub>HPO<sub>4</sub>·7H<sub>2</sub>O).
- 7. Trypsin-0.25 % EDTA with phenol red (Life Technologies, Carlsbad, CA, http://www.lifetechnologies.com).
- 8. CO<sub>2</sub> incubator at 37 °C and 5 % CO<sub>2</sub> (http://www.thermo-fisher.com/en/home.html).
- 9. Tissue culture flasks for cell culturing (http://www.usascientific.com/).
- 1. DMEM/F12, M199, and/or RPMI 1640 (Life Technologies, Carlsbad, CA, http://www.lifetechnologies.com).
- 2. Horse serum and fetal calf serum (Life Technologies, Carlsbad, CA, http://www.lifetechnologies.com).
- 3. Epidermal growth factor human (EGF) (Sigma-Aldrich, St. Louis, MO, http://www.sigmaaldrich.com).
- 4. Hydrocortisone (Sigma-Aldrich, St. Louis, MO, http://www.sigmaaldrich.com).
- 5. Insulin (Sigma-Aldrich, St. Louis, MO).
- 6. Cholera toxin (Sigma-Aldrich, St. Louis, MO).
- 7. Penicillin/streptomycin (Gemini Bio-products).
- 8. 6-Well plates (Fisher Scientific, http://www.fishersci.com).
- 9. Sterile scissors, scalpels, and forceps.
- 10. CO<sub>2</sub> incubator at 37 °C and 5 % CO<sub>2</sub>.
- 1. Aliquoted Matrigel matrix (Becton Dickinson Bioscience, Franklin Lakes, NJ) stored at -20 °C (*see* **Note 4**).
- 2. Chilled pipette tips.
- 3. Chilled 35 mm and/or 65 mm plastic Petri dishes with glass insert in dish bottom (InVitro Scientific, www.invitrosci.com).

2.6 Preparation of Matrigel Cultures in Petri Dishes

2.5 Culturing Cells

from Tissue

- 4. For 3D experiments, the Petri dishes may have to be modified. Modifications require sharp scissors sterilized in 100 % ethanol to trim the height of the dish bottom (*see* Note 5).
- 5. Modified Petri dish lid for use with DIC optics in 3D experiments (*see* **Note 6**).
- 1. Upright or inverted microscope (depending on the chamber used) equipped with phase or bright-field optics and 10–40× objectives.
  - 2. When working with cell lines, tissues, and/or long-term experiments with immune cells isolated from freshly drawn blood, the microscope should be fitted with environmental controls or contained within a CO<sub>2</sub> incubator at 37 °C and 5 % CO<sub>2</sub>.
  - 3. Sony XCD-V50 1/3-type Progressive Scan IT CCD camera (or comparable) with a IEEE1394B high-speed digital interface that operates at 60 fps and 640×480 resolution, with C-mount and controlled by FireWire compatible software such as FireI (www.unibrain.com), Adobe Premiere<sup>®</sup>, QuickTime Pro<sup>®</sup>, iStopMotion, or iMovie.
  - 4. Sykes-Moore perfusion chamber (Bellco Glass, Inc., http://www.bellcoglass.com) with 2.5 mm gasket, holder, and 25 mm #2 cover slips coupled to programmable pumps to assay basic cell motility, to assay response to global exposure to chemoattractant or to generate a dynamic gradient of temporal waves [46–48] (Fig. 1a).
  - 5. For perfusion with the Sykes-Moore chamber, two pieces of Tygon tubing (1/16 in. ID), each connected to a 21-gauge needle via a luer lock for inlet and outlet ports and a 60 cm<sup>3</sup> syringe connected to the other end of the inlet tubing via a luer fitting (Fig. 1a, b).
  - 6. For perfusion experiments, NE-1000 Multiphase Programmable Pumps (New Era Pump Systems, Farmingdale, NY) [49, 50] or other continuous pump system that does not introduce oscillations (Fig. 1b).
  - For quantifying the response of single cells to chemoattractant: Dunn chamber (http://www.hawksley.co.uk/), Zigmond chamber (Fig. 1c, d). (http://www.neuroprobe.com/products/zigmond.html), or modified Zigmond chamber [44, 51].
  - Single cells can also be imaged in gradients of chemoattractant generated in a microfluidic device [10, 52–54]. Various perfusion and chemotaxis chambers are also available from Ibidi (www.ibidi.com).
  - 9. Coated cover slip within a Petri dish for mammalian cells (Fig. 1e).
- An environmental chamber if pH and temperature need to be regulated; alternatively, microscope can be housed within a 37 °C, 5 % CO<sub>2</sub> incubator (Fig. 1f).

#### 2.7 2D Experiment on 2D substrate



**Fig. 1** Methods for 2D motion analysis of cells crawling on a 2D substrate. (*a*) The assembled Sykes-Moore perfusion chamber with inlet and out tubes inserted into their respective ports. (*b*) The Sykes-Moore perfusion chamber connected to a 60 cm<sup>3</sup> syringe containing the perfusion solution and placed in a programmable syringe pump. (*c*) Diagram of the gradient of chemoattractant that forms by diffusion across the bridge of the Zigmond chamber and the method for calculating the chemotactic index (CI). (*d*) Diagram of the Zigmond chemotaxis chamber. Cells are attached to the cover slip that is inverted over the bridge. Buffer is placed in the "sink" trough and buffer plus chemoattractant in the "source" trough. (*e*) Cells can be spread onto a thin coat of Matrigel or other matrix cast onto the glass window (cover slip) inserted into the bottom of a Petri dish for 2D analysis of mammalian cells crawling on a 2D substrate. (*f*) In cases requiring environmental regulation, image acquisition can be performed on a microscope with camera housed in an incubator

- 11. Dedicated acquisition computer capable of storing hundreds of gigabytes of data.
- 12. Motion analysis software such as ImageJ (http://imagej.nih. gov/ij/) or J3D-DIAS4.1 (*see* Note 7).
- 1. Short-working-distance perfusion chamber such as the one available from Harvard Apparatus (http://www.harvardappa-ratus.com) or from Life Imaging Services (http://www.lis.ch/download/LIS\_Ludin\_Chamber\_v8.pdf).
  - 2. Microscope equipped with differential interference (DIC) optics, high numerical aperture objectives, high numerical aperture condenser, and motorized stage capable of moving

# 2.8 3D Experiment on a 2D substrate

the focus through  $10-20 \ \mu m$  in  $2-3 \ s$  every  $4-5 \ s$  (*see* **Note 8**) for rapidly moving cells such as *D. discoideum* and PMNs.

- 3. Environmental chambers are required to maintain temperature and pH for long-term imaging of mammalian cells. Alternatively, a microscope may be housed within a 37 °C, 5 % CO<sub>2</sub> incubator (*see* Note 9).
- 4. Digital camera controlled by video acquisition software such as the Zeiss AxioCam MRc5 and Laser Vision 6 software as described in **item 3**, Subheading 2.7, synchronized with the LED light engine and motorized stage.
- 5. A computer capable of running Microsoft Windows XP, equipped with serial ports (RS-232) to control the microscope Z-axis stepper motor, a firewire port (IEEE 1394) to capture images from the AxioCam MRc5 camera, and a storage disk capable of storing hundreds of gigabytes of data.
- 6. Software for 3D reconstruction (see Note 7).

#### 2.9 3D Experiment on a 3D substrate

- 1. Cell cultures embedded in Matrigel in modified Petri dishes (Fig. 2a) as described in Subheading 2.6, Notes 5 and 6.
- Microscope equipped with differential interference contrast (DIC) optics, programmable motorized stage, 20× or 40× long-working-distance objectives and LED light engine (*see* **Note 10**) contained within a 37 °C, 5 % CO<sub>2</sub> incubator or other means of regulating temperature and pH for 30 days or more of continual imaging (Fig. 2b).
- 3. Digital camera controlled by video acquisition software such as the Zeiss AxioCam MRc5 and Laser Vision 6 software, synchronized with the LED light engine and motorized stage.
- 4. A computer capable of running Microsoft Windows XP, equipped with serial ports (RS-232) to control the microscope Z-axis stepper motor, a firewire port (IEEE 1394) to capture images from the AxioCam MRc5 camera, and a storage disk capable of storing hundreds of gigabytes of data.
- 5. Software for 3D reconstruction (see Note 7).

#### 3 Methods

3.1 Preparation of D. discoideum amoebae for 2D Analysis of Basic Motile Behavior and Chemotaxis 1. Harvest  $5 \times 10^7$  cells in the low log phase of growth (~2×10<sup>6</sup> cells/mL), wash three times in BSS, and disperse on a nitrocellulose filter supported by two Millipore pre-filters pre-saturated with BSS. Incubate in a humidified chamber at 22 °C until the onset of aggregation [55] when motility and chemotactic responsiveness peak [55, 56]. Wash cells from the filter pads and dilute to  $3 \times 10^4$  cells/mL (*see* **Note 10**) for inoculation into chamber.



**Fig. 2** Methods for 3D motion analysis of cells crawling on a 3D substrate. (*a*) Modified Petri dish for 3D analysis of cells embedded in a 3D matrix. Cells are mixed with Matrigel and plated onto a glass window in the bottom section of the Petri dish that has been trimmed to fit within the allowable working distance of the microscope. A glass window in the lid is necessary to achieve optical sections using DIC microscopy. (*b*) Microscope fitted with DIC optics and a motorized stage housed inside a 5 % CO<sub>2</sub>, 37 °C incubator for long-term imaging of living cells in 3D cultures. Camera and motor are synchronized by controlling software. A timer regulates the LED light so that the specimen is only illuminated during the 45 s in which the z-series is actively being acquired. The *white box* indicates the area of the stage that is diagrammed at a larger scale in (*c*). (*c*) Diagrammatical summary of optical sectioning using DIC microscopy. A typical z-series of 150 optical sections is acquired through 1.5 mm of Matrigel matrix at 5–10 µm increments. (*d*) Representative optical sections through a culture of aggregating cancer cells embedded in a 3D Matrigel matrix. The level of each section is given in the upper left hand corner of each panel

2. Mutant *Dictyostelium* strains may be defective in cAMP signaling and cAMP induced gene expression, and therefore require exogenously applied pulses of cAMP in order to become motile and/or chemoresponsive [48]. To exogenously pulse cells, harvest *D. discoideum* amoebae at the low log phase of growth, wash in BSS and resuspend at a density of  $2 \times 10^7$  cells/mL in BSS. Maintain the flask containing the cell suspension on a rotary shaker at 180 rpm for 1 h. Cells are then pulsed by programming the NE-1000 Pumps to deliver 80 nM cAMP (final) from a 10 cm<sup>3</sup> syringe every 6 min for 6 subsequent hours [43, 48, 57]. At the completion of pulsing, cells are pelleted, washed in BSS, and diluted to  $3 \times 10^4$  cells/mL for inoculation into a chamber.

- 3. For analysis of basic motile behavior, inoculate 1.1 mL of the dilute cell suspension into a Sykes-Moore perfusion chamber. Allow cells to adhere to the cover slip for 5–10 min, seal the chamber, and insert inlet and outlet needles into the respective ports. Connect inlet tube to a 60 cm<sup>3</sup> syringe filled with BSS and insert the syringe into a pump programmed to deliver 4 mL/min (Fig. 1a; see Notes 10 and 11).
- 4. For analysis of chemotaxis, streak 20  $\mu$ L of the dilute cell suspension across the center of a clean 24 × 30 mm cover slip and allow 5 min for the cells to adhere. Invert the cover slip so that the cells contact the bridge then lightly fasten the clamps. Carefully pipette 55–60  $\mu$ L of BSS into one trough (sink) and 55–60  $\mu$ L of 10<sup>-6</sup> M cAMP (source) into the other trough. Chamber assembly is diagrammed in Fig. 1d.
- Whole venous blood is drawn into a blood collection tube coated with anticoagulant. The tube is gently inverted several times, brought to room temperature by gently rocking for about 30 min and 5 mL of blood is layered onto the top of 5 mL of Polymorphprep, also at room temperature, in a 15 mL Falcon centrifuge tube according to the manufacturer's instructions [49].
- 2. Centrifuge at room temperature for 30-35 min at  $500 \times g$  with no brake.
- 3. The PMN band is collected, washed in H-HBSS by centrifugation at  $400 \times g$  for 10 min, and resuspended to a concentration of  $1.5 \times 10^6$  cells/mL in H-HBSS. Brake can be used during washing steps.
- 4. Inoculate into the Sykes-Moore perfusion chamber for motion analysis of basic motile behavior as described in Subheading 3.1, step 3, using H-HBSS as the perfusion buffer (Fig. 1a, b).
- 5. Inoculate into a chemotaxis chamber for motion analysis of chemotaxis as described in Subheading 3.1, step 4, using H-HBSS as the sink buffer and H-HBSS plus 0.1  $\mu$ M fMLP as the chemoattractant in the source trough as illustrated in Fig. 1d.

3.2 Preparation of Human Primary Polymorphonuclear Neutrophils (PMNs) for 2D Analysis of Basic Motile Behavior and Chemotaxis on a 2D Substrate

1. Using a sterile, pre-chilled pipet tip, distribute 50  $\mu$ L/cm<sup>2</sup> of 3.3 Preparation ice-cold Matrigel onto the glass insert of a pre-chilled Petri of Cell Lines for 2D dish, taking care not to introduce bubbles. Analysis of Basic Motile Behavior 2. Incubate the Petri dish for 30 min at 37 °C. on a 2D Substrate 3. Dissociate cells from tissue culture flask, resuspend in media, wash, resuspend in fresh media, and count. 4. Withdraw the volume required to yield  $5 \times 10^5$  cells, adjust to 100 µL, and spread onto the pre-coated, gelled Matrigel coat. 5. Incubate for 30 min to allow cells to attach. 6. Add 1–3 mL of appropriate media to the dish. 7. Place preparation on the stage of the 2D microscope and begin image acquisition. 3.4 Image Capture 1. For *D. discoideum* or for short-term recording of PMNs, place and Outlining in 2D cells in the appropriate chamber on the stage of microscope equipped with phase optics and a camera controlled by software. Set the time interval and duration of experiment. 2. For mammalian cells, place the chamber on a microscope within a 37 °C, CO<sub>2</sub> incubator or in an environmental chamber. 3. Images are saved as a series of sequential JPEG files that can be opened in J3D-DIAS4.1 and saved in native format (Fig. 3a). 4. Imaging processing can facilitate automatic outlining (Fig. 3b) (see Note 12). 5. The edge of cells can be automatically detected in each frame employing a grayscale threshold algorithm (Fig. 3c). 6. The perimeter is converted to a mathematically precise betaspline replacement image [58-61] and the centroid, or geometric center [59-61], at each time point (Fig. 3d) is determined (see Note 13). 1. Cell motility parameters can be computed over time based on 3.5 2D Cell the changing position of the centroid [59–62] (Table 1a; Figs. Movement and Shape 4d and 5b) and cell shape parameters can be quantified from **Parameters** the beta spline replacement images (Table 1b; see Notes 14-16). 2. The "chemotactic index" is computed as the net distance moved towards the source of chemoattractant divided by the total distance the cell migrated [63, 64] (Fig. 1c). 3. Cell shape changes can be evaluated by "unwrapping" and stacking. (Fig. 3b) Polar coordinates are converted to rectangular coordinates and stacked with each unwrapped perimeter having a lower offset than the previous one. This display accentuates the position and frequency of protrusions over time and therefore is particularly useful in determining cytoskeletal con-

tributions to lamellipodial behavior [24, 36]



**Fig. 3** 2D automatic outlining, path and shape generation in cancer cells crawling on top of a 2D, thin coat of matrix. (*a*) Original phase image. (*b*) The image can be processed to facilitate automatic outlining. (*c*) Automatic outlining. (*d*) Centroid tracks and shapes generated from the outlines. (*e*) Stacked perimeter plots of coalescing cancer cells. Time is indicated in the *upper left hand corner* 

Axis tilt (deg)	28.0	333.0	329.0	339.6	331.0	347.5	337.1	342.5	20.9	332.6
Persist. (μm/ min deg)	0.15	0.13	0.0	0.22	0.11	0.17	0.31	0.16	0.48	0.16
Accel. (µm/sq min)	0.14	0.19	0.13	0.06	0.06	0.21	0.07	0.18	0.22	0.13
Direction change (deg)	48.0	40.8	48.9	70.5	54.2	51.7	74.3	50.0	58.1	49.6
Direction (deg)	228.2	297.7	225.8	135.5	259.1	203.8	292.1	210.5	282.9	148.4
peed (µm∕ min)	.80	69.	.42	.76	.58	66.	.15	.83	.67	.74
Direct. S right	0.12 0	0.12 0	0.08 0	-0.41 0	0.18 0	0.10 0	0.63 1	0.08 0	0.12 1	-0.08 0
Direct. upward	0.04	-0.08	-0.02	0.40	-0.04	0.17	-0.19	0.14	-0.18	-0.05
Direct. total	0.12	0.14	0.08	0.58	0.18	0.20	0.65	0.16	0.22	0.09
Net path length (µm)	8.48	15.56	10.80	18.88	3.78	57.39	23.98	36.95	13.43	17.87
Total path length (µm)	68.63	110.66	137.61	32.86	21.19	287.43	36.69	237.02	61.53	199.59
Total elapsed time (min)	64	102	202	38	30	202	30	202	30	202
Time (min)	0.000– 64.000	0.000 - 102.000	0.000- 202.000	0.000- 38.000	0.000 - 30.000	0.000- 202.000	0.000 - 30.000	0.000- 202.000	0.000 - 30.000	0.000- 202.000
Frames	1–33	1-52	1-102	1–20	l-16	1-102	l-16	1-102	l-16	1-102
Object	1	5	6	4	2 2	6		8	6	10
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Table 12D motility and shape parameters

319.3	318.7	318.6	345.2	326.4	342.4	312.5	7.1	316.1	355.9	326.8	331.0	289.1	110.6	(continued)
0.16	0.12	0.16	0.23	0.10	0.22	0.20	0.07	0.13	0.24	0.22	0.16	0.2	0.1	
0.17	0.13	0.09	0.41	0.16	0.08	0.05	0.07	0.10	0.11	0.08	0.11	0.1	0.1	
49.4	50.7	59.9	38.4	44.0	60.9	68.1	55.0	56.2	61.8	61.1	52.5	54.7	9.1	
49.1	142.0	311.3	276.8	41.4	284.2	274.8	21.7	49.1	143.3	9.5	301.9	190.4	102.7	
0.80	0.57	0.67	0.93	0.65	0.84	0.74	0.41	0.52	0.95	0.73	0.58	0.8	0.3	
-0.06	-0.02	0.06	0.15	-0.17	0.23	0.76	-0.14	-0.08	-0.01	-0.02	0.06	0.1	0.2	
0.07	0.05	-0.09	-0.14	-0.21	0.00	-0.07	-0.23	-0.08	0.07	0.05	0.00	0.0	0.1	
0.09	0.05	0.11	0.20	0.27	0.23	0.76	0.27	0.12	0.07	0.06	0.06	0.2	0.2	
14.98	8.74	18.15	6.56	13.43	36.84	47.64	24.27	12.85	12.32	5.06	2.44	18.7	14.3	
165.17	165.93	171.37	32.73	49.23	161.33	62.32	90.32	110.23	178.85	88.20	44.57	114.2	73.6	
144	202	202	20	50	162	76	162	154	154	100	56	MEAN	± S.D.	
0.000 - 144.000	0.000- 202.000	0.000 - 202.000	0.000- 20.000	0.000- 50.000	0.000- 162.000	0.000- 76.000	40.000- 202.000	48.000- 202.000	48.000- 202.000	102.000 - 202.000	146.000 - 202.000			
1–73	1-102	1-102	1-11	1–26	1-82	1–39	21-102	25-102	25-102	52-102	74–102			
11	12	13	14	15	16	17	19	20	21	23	26			

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B. 2D sha	ıpe paran	neters								
Object	Frames	Time (min)	Total elapsed time (min)	Maximum length (µm)	Mean width (µm)	Area (sq µm)	Per. (µm)	Rnd (%)	Mean radial length (µm)	Radial deviati (%)
1	1-33	0.000-	64	41.8	19.6	823.4	119.9	71.9	16.4	18.9

Neg. flow (%)	13.0	10.5	11.8	15.2	12.0	20.5	19.4	25.1	24.2	10.7	9.7
Pos. flow (%)	12.8	9.4	10.4	12.7	9.9	18.2	20.3	20.3	20.8	9.9	6.6
Mean Conc. (deg)	365.5	698.0	1585	203.4	241.8	260.2	113.7	136.8	265.3	466.7	762.7
Mean Conv. (deg)	725.5	1058.0	518.5	563.4	601.8	620.2	473.7	493.2	625.3	819.5	1117.7
Radial deviation (%)	18.9	31.2	18.8	19.0	17.1	19.7	17.0	18.3	20.0	25.1	33.6
Mean radial length (µm)	16.4	23.3	10.8	12.3	14.4	12.4	9.0	9.2	13.8	19.7	28.8
Rnd (%)	71.9	52.3	78.1	75.1	77.7	72.2	81.9	79.8	71.4	65.8	49.1
Per. (µm)	119.9	189.9	75.1	87.2	101.9	90.2	61.9	63.6	100.5	148.8	236.4
Arca (sq µm)	823.4	1493.9	344.1	439.5	640.4	451.8	243.4	254.2	571.1	1117.9	2152.7
Mean width (µm)	19.6	21.6	12.4	13.9	18.3	13.9	10.7	10.7	16.0	20.4	24.5
Maximum length (µm)	41.8	69.2	28.1	31.9	35.2	32.9	22.8	23.6	35.7	54.9	88.2
Total elapsed time (min)	64	102	202	38	30	202	30	202	30	202	144
Time (min)	0.000 - 64.000	0.000- 102.000	0.000- 202.000	0.000 - 38.000	0.000 - 30.000	0.000- 202.000	0.000 - 30.000	0.000- 202.000	0.000 - 30.000	0.000- 202.000	0.000 - 144.000
Frames	1–33	1-52	1-102	1–20	1-16	1-102	1-16	1-102	1-16	1-102	1–73
Object	1	5	33	4	ŝ	6		∞	6	10	11

16.8	18.0	15.2	17.3	20.4	17.5	7.8	12.9	18.9	17.0	6.1	15.5	5.0
14.5	15.3	13.6	12.6	17.7	14.3	7.3	12.3	17.8	14.9	5.2	13.6	4.3
205.4	106.2	655.5	80.0	207.8	114.0	225.9	160.8	193.8	143.6	1239.7	318.4	284.7
565.4	466.2	1015.5	440.0	567.8	474.0	585.9	520.8	553.8	503.6	1599.7	677.7	284.3
15.4	15.7	30.2	9.2	19.5	17.1	17.5	20.1	17.9	14.1	51.1	21.2	8.8
11.3	10.0	17.5	1.11	10.3	9.6	14.2	11.2	10.8	10.5	44.0	15.0	8.1
78.8	84.2	41.5	92.0	75.7	81.2	81.4	76.3	77.1	83.9	32.4	71.8	14.9
78.8	67.4	165.0	72.6	74.3	66.7	98.5	78.3	76.1	70.8	395.0	114.5	77.4
394.2	307.0	862.4	387.5	314.3	286.0	621.8	373.5	357.8	337.1	4017.7	763.3	861.5
14.1	12.2	16.9	15.0	11.8	11.8	17.5	12.5	12.9	13.1	26.3	15.7	4.4
27.7	24.8	51.2	25.7	26.8	24.2	35.6	29.5	27.5	25.5	152.7	41.6	29.7
202	202	20	50	162	76	162	154	154	100	56	MEAN	±S.D.
0.000- 202.000	0.000- 202.000	0.000- 20.000	0.000 - 50.000	0.000- 162.000	0.000- 76.000	40.000- 202.000	48.000- 202.000	48.000- 202.000	102.000 - 202.000	146.000 - 202.000		
1-102	1-102	1-11	1–26	1-82	1–39	21-102	25-102	25-102	52-102	74–102		
12	13	14	15	16	17	19	20	21	23	26		

- 4. Stacked perimeter plots (Figs. 3e, 4c and 5a) are another means of displaying dynamic cell shapes over time and are useful in evaluating the frequency of lateral pseudopod extension and directional persistence, especially in the comparison of mutant or defective cells with their normal counterparts (Figs. 4d and 5b) [10, 65, 66].
- 5. Cytoskeletal defects can often be detected in measurements of membrane protrusions [24, 36]. This information can be visualized quickly and effectively on large numbers of cells through the use of "difference pictures" [60, 61, 63] (Fig. 4a). Difference pictures are constructed by overlaying the outline of the cell at frame n-x with the outline of the current frame n where x is the user-specified interval. Expansion zones are regions into which the cell expanded during the specified interval (black areas in Fig. 4a) and retraction zones are regions from which the cell retracted (hatched areas in Fig. 4a). Areas shared in the two images are color-coded gray.
- 6. The area contained within expansion and retraction zones as determined from differencing can be quantified in J3D-DIAS4.1. This measurement can be used to determine if cyto-skeletal mutants are defective in force generation required to extend lamellipodia or pseudopod or to retract the uropod [67–69]. The user windows the localized expansion or retraction zone from a series of difference pictures (Fig. 4a). The percent of the total area within the window is then calculated.

3.6 Sample Preparation for 3D Analysis of 3D Culture

- 1. Modify the Petri dish for use with DIC optics and to fit within the allowable working distance of the microscope (*see* **Notes 6** and 7).
- 2. Using a sterile, pre-chilled pipet tip, apply 100  $\mu$ L of ice cold Matrigel onto the 30 mm glass insert of a pre-chilled 65 mm Petri dish, taking care not to introduce bubbles.
- 3. Incubate the Petri dish for 30 min at 37 °C.

**Fig. 4** (continued) (*black*) and retraction zones (*hatched*) can be visualized in difference pictures. Relative flow is measured from a difference picture by windowing the area of interest (*boxes*) at 0, 4, and 14 min. The percent of the total area contained within the window is calculated and displayed alongside the window. (*b*) Unwrapping and stacking the cell perimeter over time provides a history of expansions and can be used to detect cyclical shape changes. (*c*) Comparison of stacked perimeter plots of control, *ptenA*<sup>-</sup>, *lpten*<sup>-</sup>, and *ptenA*<sup>-</sup> cells overexpressing *lpten* (*ptenA*<sup>-</sup>/*lpten*<sup>oe</sup>) in the model system *D. discoideum* reveal significant defects in instantaneous velocity in *ptenA*<sup>-</sup> cells and increased lateral pseudopod extension in *lpten*<sup>-</sup> cells [43]. The final shape in the time series of the stacked perimeter plots is shaded *dark gray*. Interestingly, overexpression of *lpten* in *ptenA*<sup>-</sup> background rescues the velocity and shape defects in *ptenA*<sup>-</sup>, conclusions confirmed by quantitative parameters (*d*). (*e*) 3D reconstructions of control and *lpten*<sup>-</sup> cells migrating on a 2D substrate reveal that the majority of lateral pseudopods extended by *lpten*<sup>-</sup> cells (*arrows*) are off the surface and therefore do not produce turns [71]



# e 3D reconstruction of cells migrating on 2D substrate



**Fig. 4** 2D cell shape parameters available in J3D-DIAS4.1 provide dynamical information. (*a*) Difference pictures at 2 min intervals of a cell from a human cancer cell line migrating on a 2D Matrigel substrate. Expansion zones

lpten<sup>-</sup>

ptenA<sup>-</sup>

/lpten<sup>oe</sup>

9.8 ± 3.0

 $7.6 \pm 2.4$ 

51%

27%



**Fig. 5** Comparison of 2D cell shape and motion parameters in control, *ptenA*<sup>-</sup>, *lpten*<sup>-</sup>, and *ptenA*<sup>-</sup>/*lpten*<sup>oe</sup> strains in *D. discoideum* demonstrates that cells from all strains, with the exception of *ptenA*<sup>-</sup>, are capable of efficient chemotaxis. (a) Stacked perimeter plots of control, *ptenA*<sup>-</sup>, *lpten*<sup>-</sup>, and *ptenA*<sup>-</sup>/*lpten*<sup>oe</sup> migrating in a Zigmond chamber in the presence of a spatial gradient of cAMP. The source of the gradient is to the *right*, as indicated by the direction of the *large arrow* at the *bottom* of *each panel*. The final shape in the time series of the stacked perimeter plots is shaded *dark gray*. (b) Sample motion analysis parameters computed by J3D-DIAS4.1 demonstrate that *ptenA*<sup>-</sup> defects in velocity and later pseudopod suppression in a spatial gradient of cAMP are rescued by over-expression of *lpten* in *ptenA*<sup>-</sup> background

 $+0.63 \pm 0.33$ 

 $+0.66 \pm 0.16$ 

4. Dissociate cells from tissue culture flask, resuspend in media, wash, resuspend in fresh media, and count.

99%

100%

100%

96%

 $5.2 \pm 1.4$ 

 $1.1 \pm 0.6$ 

- 5. Withdraw the volume required to yield  $5 \times 10^5$  cells, bring the total volume up to 250  $\mu$ L and chill.
- 6. Add 500  $\mu$ L of ice cold Matrigel to the 100  $\mu$ L of chilled cell suspension and mix by gently pipetting up and down. Distribute the entire 750  $\mu$ L onto the Matrigel-coated cover slip (*see* Fig. 2a).

- 7. Incubate for 30 min to allow gelation.
- 8. Add 2–3 mL of media to the dish.
- 9. Place preparation on the stage of the 3D microscope and begin image acquisition (Fig. 2b).
- 1. For 3D analysis of basic motile behavior on a 2D substrate, samples are inoculated into a perfusion chamber. The chamber is connected to a perfusion pump and positioned on the stage of an inverted microscope equipped with DIC optics and a high numerical aperture objective such as the Zeiss 63× Planapochromat.
  - 2. To obtain optical sections of single cells such as *D. discoideum* amoebae or human PMNs migrating on a 2D substrate, program the motor to move through the z-axis height, generally  $10-20 \mu m$ , in 2-3 s and repeat the process every 4-5 s for  $5-10 \min$  per cell (Fig. 4e) (*see* Note 17).
  - 3. For 3D analysis of cells embedded in a 3D matrix, place the 3D culture on the stage of a microscope with environmental controls or contained within a 5 % CO<sub>2</sub>, 37 °C incubator. Set the top and bottom of the z range, the z increment, the time interval between acquisition of each z-series, and the length of the experiment as shown in Fig. 2c (see Note 18).
  - 4. The acquisition software typically generates a numbered JPEG image stack that can be played and saved as a movie (Fig. 2c). Objects are then detected from this movie as described below.
  - 1. Bitmapping is a rapid and accurate method to detect objects (Fig. 6a). This method distinguishes a cell or group of cells based on the fact that they exhibit a higher grayscale variation than the background. More specifically, bitmapping assigns a 0-256 gray scale value to individual pixels within a user-defined kernel; i.e., a  $3 \times 3$ ,  $5 \times 5$  or  $7 \times 7$  pixel matrix. The gray scale values within the kernel are averaged, the standard deviation (sd) computed and that sd is assigned to a reference pixel within the kernel. If the referenced sd is above the user-determined threshold value, then the pixel is considered part of the object and is retained as such. The kernel moves by one pixel and the process is repeated until every pixel within the field is scanned. Background or out of focus objects in each optical section will have more uniform gray scale values, lower sd values and thus be discarded. One advantage of bitmap tracing over outlining is that holes, gaps or concave indentations present within the real image are maintained.
  - 2. Manual outlining can be used for single cells and fine structures such as filopodia (Fig. 6b).

# 3.8 Object Detection and Reconstruction in 4D Experiment

3.7 Optical

Sectioning



**Fig. 6** Examples of automatic bitmap object detection, manual outlining of single cells, and 3D reconstruction methods. (*a*) Fields of cells and aggregates within a 3D matrix optically sectioned at 30-min intervals for 30 days generates movies comprised of over 100,000 frames. Cells and aggregates can be identified in these movies by complexity based automatic bitmap detection. (*b*) Single cells and organelles can be manually traced in optical sections. (*c*-*e*) Methods for 3D reconstructions combining automatically detected and manually detected objects. Coalescing aggregates in preparations of cancer cells are color-coded gray, facilitator cell and filopodia are color-coded green and yellow, respectively, and probe cells, *red* 

- 3. Overlapping traces are stacked into a 3D z-series, either as a complexity stack in the case of bitmap tracings or as a series of beta-spline replacements (*see* **Note 19**), in the case of outlines.
- 4. Outlines are filled with voxels (3D pixels) and bitmap pixels are expanded into voxels. In both cases, the *x*, *y*, and *z* scales determine the voxel dimensions.
- 5. Java OpenGL (JOGL) implemented in J3D-DIAS4.1 performs 4D reconstructions using the "adaptive skeleton climbing isoform extraction" method [70], a variation of the "marching cubes" algorithm (Fig. 6c; *see* **Note 20**).
- 6. Vertices are smoothed three times to attenuate the sharp edges in the surface of the object (Fig. 6d) (*see* **Note 21**). DIC texture overlay can be added to restore details present in the original image (Fig. 6e).
- Manually and automatically traced cells can be combined into a single movie file, reconstructed as wireframe images or as solid, shaded nontransparent objects, such as the cells shown in Fig. 6d, e. Filopodia, lamellipodia, and nuclei or other organelles can be independently color-coded.
- 8. Images can be rotated and viewed from different angles and saved as a movie.
- 9. Mechanisms of coalescence and the presence of different cell types can be analyzed in 4D in preparations of cancer cells. In Fig. 6c a facilitator cell (color-coded green) that emerged from an aggregate of a tumorigenic cell line contacted a probe cell (color-coded red) that emerged from another aggregate. The facilitator and probe then pulled the two aggregates together, resulting in coalescence.
- 10. The effects of potential anticancer therapies including monoclonal antibodies can be evaluated in 4D as shown in Fig. 7.
- 1. The 3D cell center (3D centroid) can be determined by averaging the *x*-, *y*-, and *z*-coordinates of the interior points of the faceted object and used to generate 4D paths.
- 2. Instantaneous velocity is calculated from the 3D position of the centroid by the central difference method [62] using the 2D formulae described earlier [60] (*see* Note 14). Other 2D parameters calculated from the centroid position can likewise be extrapolated to 3D.
- 3. The triangularized faceted surface is a polyhedron. *See*http:// wwwf.imperial.ac.uk/~rn/centroid.pdf to find the standard calculus formulae to determine the volume of a polyhedron.
- 4. The "surface complexity" function was introduced into J3D-DIAS4.1 as a means to quantify the activity around the periph-

3.9 4D Motility and Dynamic Morphology Parameters



**Fig. 7** J3D-DIAS4.1 generated 3D reconstructions of cancer cells and aggregates embedded in a 3D Matrigel matrix reveal effects of potential anticancer treatments such as monoclonal antibodies on cell growth, coalescence and single cell behavior. (*a*) Untreated cancer cells coalesce into aggregates in a 3D matrix as indicated by the *white arrows*. (*b*) Aggregate coalescence is inhibited in identical cultures treated with anti- $\beta$ -1 integrin monoclonal antibody (AllB2). (*c*) Aggregate coalescence and rapid exit of single cells from the aggregates (color-coded *blue*) are stimulated in identical cultures treated with anti- $\alpha$ -3 integrin monoclonal antibody (P1B5), demonstrating that differential effects of different treatments are detected in the 4D analysis

ery of aggregates formed in cancer cell cultures (Scherer et al. submitted). The surface complexity parameter is the reciprocal of 3D roundness (*see* **Note 22**).

# 4 Notes

- 1. To insure that experiments are performed on exponentially dividing populations of cells and to minimize accumulation of spontaneous mutations, *D. discoideum* cells should be routinely passaged before reaching stationary phase (~1×10<sup>7</sup> cells/mL). In addition, fresh cultures should be reconstituted from frozen stocks every 4–6 weeks.
- 2. Protocols can be found at the web site for the Center for Disease Control http://www.cdc.gov/biosafety/publications/bmbl5/ index.htm and/or through the Research Office at the institution where the work is being performed. All human tissues

and/or blood products must be obtained under informed consent using protocols approved by the institution's IRB.

- 3. Heat inactivation of serum is no longer recommended for most cell culture applications (http://www.sigmaaldrich. com/technical-documents/protocols/biology/the-cell-environment.html).
- 4. Matrigel matrix will gel quickly, so care must be taken during preparation to keep it, as well as the surfaces and media that it contacts, chilled.
- 5. If the height of the dish exceeds the working distance of the optics, then approximately 5 mm can be trimmed from the dish bottom with sterile scissors before media is added.
- 6. For optical sectioning using DIC, a glass window should replace the plastic in the light path through the lid of the dish. An area with a diameter of 20–30 mm can be removed from the center of the plastic lid with a drill bit or laser cutter. A glass cover slip of larger dimensions can then be placed over the hole and sealed with Vaseline. The lid with the glass window is sterilized with ethanol and/or UV exposure within the biosafety cabinet.
- J3D-DIAS4.1 can be accessed by collaboration at the W.M. Keck Dynamic Image Analysis Facility, David R. Soll, director, Biology Department, University of Iowa, Iowa City, IA 52245 USA.
- 8. The z-height is empirically determined and depends on the cells being studied. The acquisition time for an individual z-series and the interval between each z-series can be increased for slower moving cells.
- 9. LED light significantly reduces phototoxicity during longterm imaging but is generally not necessary for *D. discoideum* and PMNs.
- 10. Inoculation of a dilute cell suspension along with continual perfusion prevents accumulation of cAMP in the chamber, thereby eliminating its effects on cell behavior.
- 11. Pre-fill syringe, inlet tube, and needle with appropriate solution so as to avoid air bubbles.
- 12. Image processing algorithms such as differencing, black filtering and white filtering can facilitate automatic edge detection, particularly in images with a "phase halo." Differencing copies the image, shifts the copy by one pixel in the horizontal direction, one pixel in the vertical direction, and then subtracts the two images. Neutral gray (128) is added to the resulting intensities. To black filter, pixels darker than a user determined threshold are detected and removed from a bitmap outline. Conversely, to white filter, pixels lighter than user-determined threshold are detected and removed from the bitmap outline.

- 13. The initial outline is a connected circuit of pixels determine by the threshold setting. Beta splines replace the outline with curves approximating the original pixels. Because the original pixel outline is likely to be jagged, "spline resolution" functions can be applied. These functions remove some of the pixels, allowing the calculation of splines and generation of a smooth, rather than stair-stepped, final outline. Bias and tension functions also can be applied to adjust the accuracy of the final outline.
- 14. The speed of cellular translocation (instantaneous velocity) is calculated by the central difference method [62] as follows [60]:

- $\begin{array}{l} \textbf{Speed}[f] = (\textbf{scale } x \ \textbf{frate}) x \ \textbf{sqrt}(((\textbf{x}[f+\textbf{I}]\textbf{-x}[f])/\textbf{I})^2 + ((\textbf{y}[f+\textbf{I}]\textbf{-y}[f])/\textbf{I})^2 + ((\textbf{z}f+\textbf{I}]\textbf{-z}[f\textbf{-I}])/2\textbf{I})^2))) \ \textbf{when} \ f\textbf{-I} < 1 \ \textbf{and} \ f\textbf{+I} < = \textbf{F} \ (\textbf{first frame}) \end{array}$
- $\begin{array}{l} \textbf{Speed } [f] = (\textbf{scale x frate}) x \ \textbf{sqrt}(((\textbf{x}[f] \textbf{x}[f \textbf{I}]) / \textbf{I})^2 + ((\textbf{y}[f] \textbf{y}[f \textbf{I}]) / \textbf{I})^2 + ((\textbf{z}f + \textbf{I}] \textbf{z}[f \textbf{I}]) / 2\textbf{I})^2))) \ \textbf{when} \ \textbf{l} < = \textbf{f} \textbf{I} \ \textbf{and} \ \textbf{f} + \textbf{I} > \textbf{F} \ (\textbf{last frame}), \end{array}$

where **F** is the total number of frames,

f is the "current" frame,

(x[f],y[f]) are the coordinates of the centroid of an object in frame f, 1<=f<=F,</pre>

I is the centroid increment,

frate is the frame rate in # of frames per unit time,

scale is the scale factor in distance units per pixel,

sqrt is the square root function, and

x denotes multiplication.

Speed [f] = 0

15. Direction of travel using the central difference method is calculated as follows:

Dir[f] = angle((x[f+I]-x[f-I]), (y[f+I]-y[f-I]))

when  $1 \le f - I$  and  $f + I \le F$ 

- Dir[f] = angle((x[f+I]-x[f]), (y[f+I]-y[f])) when f-I<1 and f+I<=F
- Dir[f] = angle((x[f]-x[f-I]), (y[f]-y[f-I])) when  $l < =f{-}I$  and f + I > F

**Dir**[f] = 0 otherwise

Multiples of  $\pm 360^{\circ}$  are added to the direction to make the graph continuous.

16. Direction change using the central difference method is calculated as follows:

DirCh[f] = 0 when f-I < 1 DirCh[f] = abs(Dir[f]-Dir[f-I])otherwise

- If the direction change is greater than 180°, it is subtracted from 360. This always gives values between 0 and 180°
- 17. 3D movies of single cells migrating on a 2D substrate are typically comprised of 30–60 optical sections per individual z-series. The height is due to the fact that these cells often lift the anterior off the substrate and can extend pseudopodia in the z plane [71–73]. Ten minutes of optical sectioning, therefore, will generate a movie that is 3600–7200 individual frames.
- 18. We typically optically section cells and cell aggregates through 1 mm of Matrigel at 5–10 μm increments every 30 min over a period of 14–30 days or longer if media is refreshed. This process can therefore yield 122,000 optical sections per preparation per period of analysis.
- Beta-splines replace the pixels in the outline with curves that approximate the original pixels [58]. In essence, beta-splines smooth the outline by applying bias, tension, and resolution [60] and generate a mathematical model from which data can then be calculated [59, 60, 63, 74].
- 20. Descriptively, in adaptive skeleton climbing a triangular facet is assigned to the raw voxel block in the most stable possible configuration. The user determines the size of the facet; the smaller the size, the greater the complexity of the surface. The remaining facets are then placed in the most stable possible configuration. Finally, irregularly shaped facets are added to any spaces between facets.
- 21. The *x*, *y*, and *z* coordinates of each vertex are averaged with neighboring *x*, *y*, and *z* coordinates [75].
- 22. 1/(6x sqrt xVol/(surface area<sup>3/2</sup>)) where sqrt is the square root, Vol is the volume and surface area is the sum of the area of all facets. This yields a value for surface complexity that increases, rather than decreases, with increasing complexity.

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