Patch Classification Measures

- 1 patch volume
- 2 patch surface area
- 3 patch perimeter
- 4 patch radius
- 5 patch closure surface area
- 6 patch volume / (patch closure surface area) $^{3/2}$
- 7 patch surface area / patch closure surface area
- 8 patch radius / (patch surface area) $^{1/2}$
- 9 patch surface area / $(patch perimeter)^2$
- 10 patch variation from a sphere
- 11 patch shape diameter function
- 12 maximum mean curvature on patch
- 13 average of mean curvature on patch
- 14 standard deviation of mean curvature on patch
- 15 average Gaussian curvature on patch
- 16 average of mean curvature on patch edge
- 17 |patch closure center average patch position|
- 18 |weighted average patch position average patch position| / patch radius
- 19 |patch closure center average patch position| / patch radius
- 20 |patch closure center weighted average patch position| / patch radius
- 21 cell volume
- 22 cell surface area
- 23 patch count

Supplementary Table 1

Geometric patch features used for SVM-based patch classification.

Patch Merging Measures

- 1 average of the mean curvature at the interface between the two patches
- 2 average of the Gaussian curvature at the interface
- 3 average of the mean curvature at the interface the average curvature of the two patches
- 4 maximum of the mean curvature at the interface
- 5 maximum of the mean curvature at the interface the maximum curvature of the two patches
- 6 standard deviation of the mean curvature at the interface
- 7 standard deviation of the Gaussian curvature at the interface
- 8 fraction of mean curvature at the interface that is above 80th percentile for the cell
- 9 fraction of mean curvature at the interface that is below 20th percentile for the cell
- 10 fraction of mean curvature at the interface that is above 80th percentile for the two patches
- 11 fraction of mean curvature at the interface that is below 20th percentile for the two patches
- 12 fraction of Gaussian curvature at the interface that is above 80th percentile for the cell
- 13 fraction of Gaussian curvature at the interface that is below 20th percentile for the cell
- 14 fraction of Gaussian curvature at the interface that is above 80th percentile for the two patches
- 15 fraction of Gaussian curvature at the interface that is below 20th percentile for the two patches
- 16 fraction of mean curvature at the interface that is above 90th percentile for the cell
- 17 fraction of mean curvature at the interface that is below 10th percentile for the cell
- 18 twice interface length / (perimeter patch 1 + perimeter patch 2)
- 19 difference in the averages of the mean curvature for the two patches
- 20 difference in the maxima of the mean curvature for the two patches
- 21 difference in the (patch closure surface area) / (patch perimeter)² for the two patches
- 22 difference in the (patch volume) / (patch surface area)^{1.5} for the two patches
- 23 difference in the (patch volume) / (patch closure surface area)^{1.5} for the two patches
- 24 average of the averages of the mean curvature for the two patches
- 25 average of the maxima of the mean curvature for the two patches
- 26 average of the (patch closure surface area) / (patch perimeter)² for the two patches
- 27 average of the (patch volume) / (patch surface area)^{1.5} for the two patches
- 28 average of the (patch volume) / (patch closure surface area)^{1.5} for the two patches
- 29 fraction of the interface that is ridged
- 30 fraction of the interface that is very ridged
- 31 fraction of the interface that is valley-like
- 32 fraction of the interface that is very valley-like
- 33 fraction of the interface that is domed
- 34 fraction of the interface that is cratered
- 35 fraction of the interface that is flat
- 36 fraction of the interface that is saddle-like

Supplementary Table 2

Geometric features of adjacent patch pairs used for SVM-based patch merging.

Distinguishing Features

Blebs vs. Non-Blebs

- 1 patch volume / (patch closure surface area) $^{3/2}$
- 2 average of mean curvature on patch edge

Filopodia vs. Non-Filopodia

- 1 |patch closure center average patch position|
- 2 patch surface area
- 3 |weighted average patch position average patch position | / patch radius
- 4 patch surface area / patch closure surface area
- 5 cell volume
- 6 average of mean curvature on patch edge
- 7 patch perimeter

Lamellipodia vs. Non-Lamellipodia

- 1 |patch closure center average patch position|
- 2 patch volume
- 3 |weighted average patch position average patch position | / patch radius
- 4 patch radius / (patch surface area)^{1/2}

Supplementary Table 3

Geometric patch features that best distinguish morphological motifs from non-motifs.

	Feature Selection Iterations	Precision	Recall	F1
Linear SVM	0	0.904	0.965	0.934
Linear SVM	1	0.917	0.955	0.936
Linear SVM	10	0.913	0.960	0.936
Radial SVM	1	0.924	0.874	0.898
Radial SVM	10	0.926	0.949	0.937
Random forest, 30 trees	0	0.950	0.938	0.944
Random forest, 300 trees	0	0.949	0.939	0.944
Random forest, 30 trees	1	0.950	0.938	0.944
Random forest, 30 trees	10	0.954	0.925	0.939

Supplementary Table 4

The precision, recall, and F_1 score of various machine-learning models used for filopodia detection on 13 HBEC cells.

Dataset				Deconvolution parameters		Surface extraction parameters							
Dataset						mode	one paran	ne parameters		mode <i>two</i> parameters			
cell	label	scope	motif	mode	param.	apo. height	mode	image smooth	image gamma	mesh smooth	inside gamma	dilate radius	erode radius
dendritic	Lifeact	meSPIM	lamellipodia	Wiener	0.018	0.06	three	0	1	6	0.6	5	6.5
melanoma	tractin	meSPIM	blebs	Wiener	0.018	0.04	one	0	1	0			
HBEC	tractin	meSPIM	filopodia	Wiener	0.015	0	one	0.6	1	0			
melanoma	Kras	meSPIM	blebs	Wiener	0.018	0.06	one	0	0.7	0			
melanoma	PIP ₂	meSPIM	blebs	Wiener	0.018	0.06	two	0	0.7	0	0.6	4	6
melanoma	tractin	meSPIM	blebs & filopodia	Wiener	0.015	0	one	0.6	1	2			
melanoma	tractin	meSPIM	filopodia	Wiener	0.015	0	one	0.6	1	2			
U2OS	tractin	meSPIM	blebs	RL	8	0.08	two	0	0.5	0	0.6	5	6
melanoma	PI3K	ASLM	blebs	RL	7	0.06	two	0	0.7	0	0.6	4	6
melanoma	tractin	confocal	blebs	RL	10	0	two	1	0.6	6	0.6	5	6
microglia	P2Y12	light sheet	extensions	RL	10	0.06	three	0	1	6	0.5	5	6.5
melanoma	cytosol	ASLM	blebs	RL	10	0.04	one	0	1	6			
T cell	Lifeact	lattice	lamellipodia	RL	10	0.06	three	0	0.8	6	0.3	5	6
breast cancer	CAAX	AO lattice	extensions	none			one	0.8	0.45	30			
melanoma	cytosol & tractin	meSPIM	blebs	Wiener	auto	0.055	one	0	1	0			
melanoma	cytosol	meSPIM	blebs	Wiener	auto	0.04	one	0	1	0			

Supplementary Table 5

Deconvolution and surface extraction parameters for all described datasets.

In the deconvolution parameters section, RL refers to Richardson-Lucy deconvolution. For Wiener deconvolution, the *param* column shows the Wiener parameter, whereas for Richardson-Lucy deconvolution it shows the number of iterations. In the surface extraction parameters section, in mode *one* an isosurface is created directly from the Otsu-normalized deconvolved image, in mode *two*, it is created from the combination of the Otsu-normalized image and an "inside" image, and in mode *three*, it is created from the combination of the Otsu-normalized image and an "inside" image, and in mode *three*, it is created from the combination of the Otsu-normalized image.

Features Selected

User 1

patch radius / (patch surface area)^{1/2} average of mean curvature on patch edge patch shape diameter function |patch closure center – average patch position| |weighted average patch position – average patch position| / patch radius |patch closure center – average patch position| / patch radius |patch closure center – weighted average patch position| / patch radius cell volume cell surface area

User 2

patch closure surface area patch volume / (patch closure surface area)^{3/2} patch surface area / (patch perimeter)² patch shape diameter function average of mean curvature on patch average of mean curvature on patch edge

User 3

patch closure surface area patch radius / (patch surface area)^{1/2} maximum mean curvature on patch |patch closure center – average patch position|

Supplementary Table 6

Automatically selected features for bleb detection models generated from three different users training on the same four cells.