CLAIMS

What is claimed is:

1. An automated method for analyzing biological tissues and cells, comprising:

storing two or more models for cell classification, where each of the two or more models represents shape and size of constituents from known biological samples;

staining constituents of a biological sample, where the biological sample includes tissue or cell culture containing at least one cell;

receiving image data of the biological sample, where the image data provides a three-dimensional representation of the biological sample;

labeling constituents of the at least one cell in the image data;

for each labeled tissue biomarker or cell or sub-cellular organelle or component in the image data, constructing a mathematical representation of boundaries surface of defining a given cell nuclei from the image data, including by chromosome territories, topological associated domains (TADs), lamina associated domains (LADs), or telomeric boundaries;

extracting features for each of the labeled tissue biomarker or cell or sub-cellular organelle or component using the mathematical representation of the tissue biomarker or surface defining a given cell or sub-cellular organelle or componentnuclei, where the features are measures of shape and size of the labeled tissue biomarker or cell or sub-cellular organelle or component;

storing two or more models for cell classification; and and

classifying the biological sample by comparing the extracted features of the labeled tissue biomarker or cell or sub-cellular organelle or component to the stored models.

2. The method of claim 1 further comprises generating the image data using a three-dimensional image acquisition technique.

3. The method of claim 1 wherein labeling constituents further comprises segmenting the image data into volumes, which represent the constituents.

4. The method of claim 1 wherein constructing a mathematical representation further comprises using iterative Laplace-Beltrami eigen-projection and boundary deformation.

5. The method of claim 1 wherein the features extracted from the labeled tissue biomarker or cell or sub-cellular organelle or component include determining one or more of a volume of a labeled tissue biomarker or cell or sub-cellular organelle or component, a surface area of a labeled tissue biomarker or cell or sub-cellular organelle or component, mean curvature of a labeled tissue biomarker or cell or sub-cellular organelle or component, shape index of a labeled tissue biomarker or cell or sub-cellular organelle or component, curvedness index of a labeled tissue biomarker or cell or sub-cellular organelle or component, and fractal dimension of a labeled tissue biomarker or cell or sub-cellular organelle or component.

6. The method of claim 1 further comprises classifying the biological sample using a random forest classification method.

7. The method of claim 1 further comprises classifying the biological sample using a classification method selected from a group consisting of linear classifiers, k nearest neighbor method, decision tree methods, neural networks, and support vector machines.

8. The method of claim 1 further comprises classifying the biological sample only if the biological sample contains more than three cells.

9. The method of claim 1 wherein staining constituents of the biological sample using a label for a tissue biomarker or cell or sub-cellular organelle or component, such as fibrillarin antibody, ethidium bromide and 4',6-diamidino-2-phenylindole.

10. The method of claim 1 wherein the biological sample is from a cell culture or cell tissue.

~~10.~~11. The method of claim 1 wherein the surface of the given cell nuclei is represented by a polygon mesh.

~~11.~~12. An automated method for analyzing biological cells, comprising:

staining constituents of a biological sample, where the biological sample includes at least one cell;

receiving image data of the biological sample, where the image data provides a three-dimensional representation of the biological sample;

labeling constituents of the at least one cell in the image data;

for each labeled cell nuclei in the image data, constructing a mathematical representation of boundaries defining a given cell nuclei;

extracting features for each of the labeled cell nuclei using the mathematical representation of the cell nuclei, where the features are measures of shape and size of the labeled cell nuclei;

for each labeled cell nucleoli, constructing a mathematical representation of boundaries defining a given cell nucleoli;

extracting features from each of the labeled cell nucleoli using the mathematical representation of the cell nucleoli, where the features are measures of shape and size of the labeled cell nucleoli;

storing two or more models for cell classification; and

classifying the biological sample by comparing the extracted features of the labeled cell nucleus and the labeled cell nucleolus to the stored models.

~~12.~~13. The method of claim ~~11~~ 12 further comprises generating the image data using a confocal microscope.

~~13.~~14. The method of claim ~~11~~ 12 wherein labeling constituents further comprises segmenting the image data into volumes which represent the constituents.

~~14.~~15. The method of claim ~~11~~ 12 wherein constructing a mathematical representation further comprises using iterative Laplace-Beltrami eigen-projection and boundary deformation.

~~15.~~16. The method of claim ~~11~~ 12 wherein the features extracted from the labeled cell nucleus include determining one or more of a volume of a labeled cell nuclei, a surface area of a labeled cell nuclei, mean curvature of a labeled cell nuclei, shape index

of a labeled cell nuclei, curvedness index of a labeled cell nuclei, and fractal dimension of a labeled cell nuclei.

16.17. The method of claim 15 16 wherein the features extracted from the labeled cell nucleolus include determining one or more of a count of nucleoli in corresponding cell nuclei, a volume of a labeled cell nucleoli, surface area of a labeled cell nucleoli, mean curvature of a labeled cell nucleoli, shape index of a labeled cell nucleoli, curvedness index of a labeled cell nucleoli, and fractal dimension of a labeled cell nucleoli.

17.18. The method of claim 11 12 further comprises classifying the biological sample using a random forest classification method.

18.19. The method of claim 11 12 further comprises classifying the biological sample using a classification method selected from a group consisting of linear classifiers, k nearest neighbor method, decision tree methods, neural networks and support vector machines.

19.20. The method of claim 11 12 further comprises classifying the biological sample only if the biological sample contains more than three cells.

20.21. The method of claim 11 12 wherein staining constituents of the biological sample using fibrillarin antibody, ethidium bromide and 4’,6-diamidino-2-phenylindole.

21.22. The method of claim 11 12 wherein the biological sample is from a cell culture.