Polyfiberquant software tool for cell state perfection

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INRODUCTON

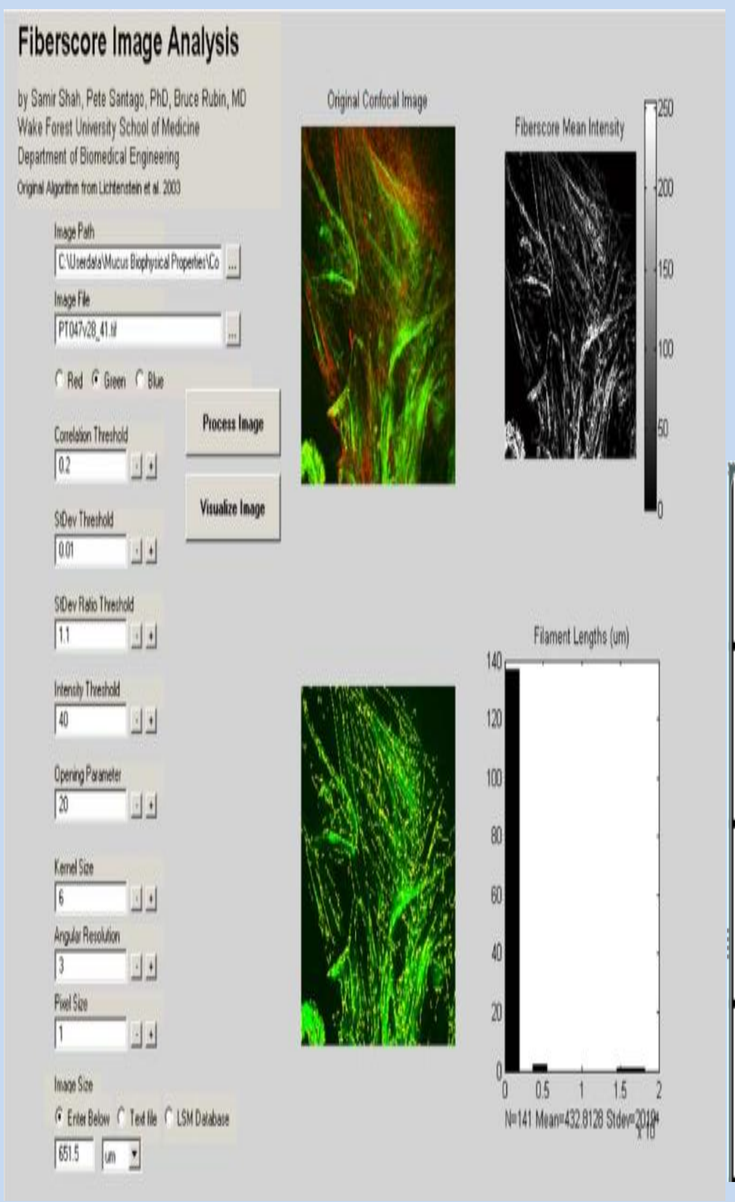
According to WHO, non-communicable diseases (NCDs) were responsible for 68% of all deaths globally in 2012, up from 60% in 2000. The four main NCDs are cardiovascular diseases, cancers, diabetes and chronic lung diseases. In most of the diseases, morphological and / or functional characteristics of cell facilitate researchers and clinicians to determine the cell state (i.e. diseased or healthy, disease state, etc).

In recent years, high-resolution imaging approaches (ex. confocal microscopy) are used to study and understand the morphological characteristics of the cell. In addition, there are few computational tools developed to process these high-resolution imaging images to identify the cell state. Polyfiberquant is one of the unique software tool for cell state prediction. But the sensitivity and specificity of the tool is primarily dependent on the parameters used in the prediction. Therefore, the primary goal of this study is to find the best parameters that can be used in Polyfiberquant tool that result in reliable cell state prediction using confocal microscopy images. Secondarily, the study will also determine the limitations of this tool.

CELL IMAGE TESTING

When laser confocal scanning images are loaded in the polyfiberquant which uses Matlab matrix convolution method to process and visualize images and are able to recognize and segment filaments in a 2 D images. The quantification description of the cell morphology is explained in this software tool whether the cell is a diseased state or healthy state or disease state could be explained with the computer resources that gives the cell filament length ,filament diameter ,filament orientation ,Euler number ,branch points and cross linking between the structure of any image. This tool can be used to characterize the cell morphology of various cell images of laser scanning confocal images and the data set can be prepared such that the quantified parameters of this tool can be utilized in later part for the concurrency and further cell morphology changes upon time. In order to ran the program, we set the thresholds to those recommended by Lichtenstein, a correlation coefficient threshold of at least 0.2,standard deviation threshold of at least 0.01 and intensity threshold of 100. We set our opening parameter of 20 and rod length of 6 pixels .

RESULTS



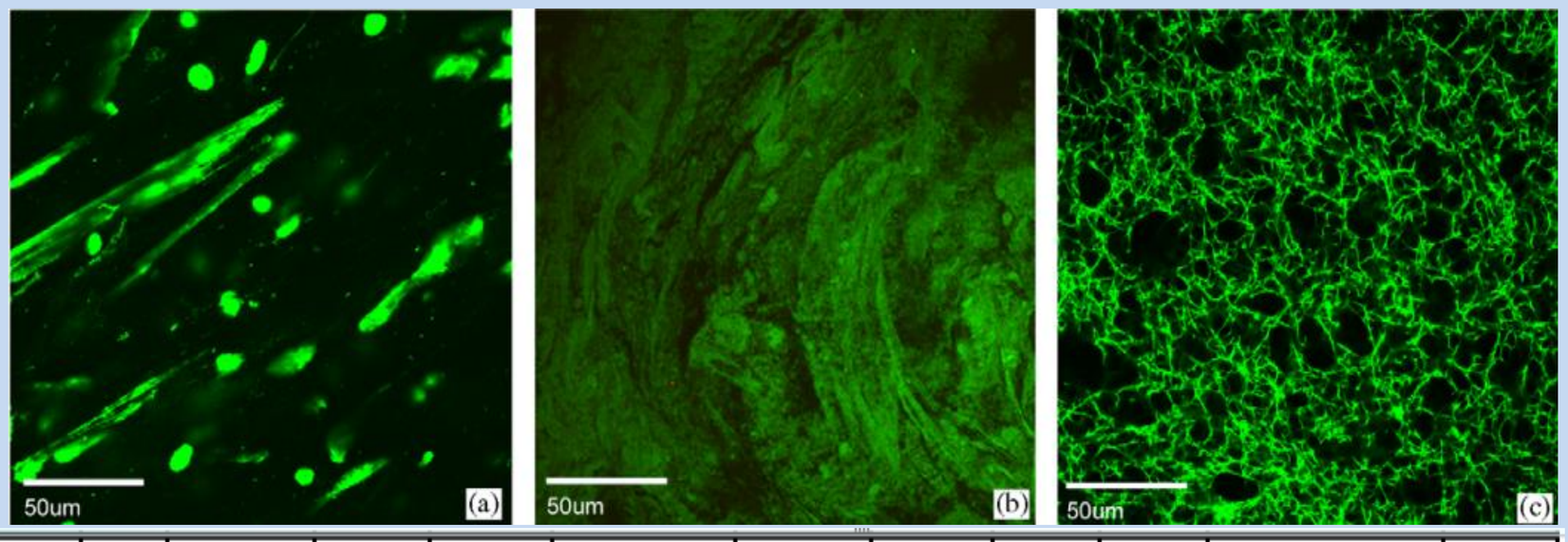


Image Name	N	Lichesten mean length	kulpa mean length	Kimura mean length	Length/1000	filament length	Branch points	End points	Euler	Fiberscore/length	Mean X length
normal	97	15.22	16.9	17	38.54	2.27	4.35	7.15	89	8.99E+02	4.23
CF	227	48.76	59	59.06	313.4	5.31	52.11	49.3	-24	4.61E+02	2.3
Fibrin	82	137.8	167	167.2	320.4	1.92	49.67	40	-312	4.47E+02	2.31

CONCLUSION

The table lists the filament length statistics by three methods .It shows cystic fibrosis and fibrin as higher length and normal mucus as lesser length. However, the Euler number was much more negative for the fibrin network, somewhat less negative for the DNA network of the CF airway secretion, and positive for the normal airway secretion. Hence it shows the diseased cell has more negative Euler number and higher filament length than the healthy cell .Basing on the above table results we can Understand how these networks affect the structure and function of living organizations.

FUTURE WORKS

To identify the best applicable parameters (eg. Pixel density, image resolution etc) in the software that results in more accurate cell state predictions.

To delineate the detailed correlation of individual contributing image quantification values such as Filament length, endpoints etc to the cell state.

To study precision/tolerance (P/T) of the software.

CITATIONS

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