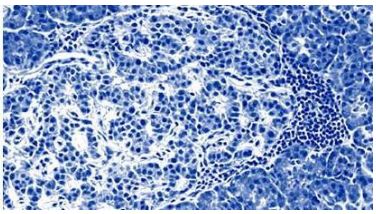

Automated human islet cell CD3+ lymphocyte quantification in multiplex IHC-stained whole slide scans using computer vision algorithms

AUTHORS

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PURPOSE

Around 100 million adults in the United States of America suffer from diabetes. This disease is characterized by its high complexity and disruption of the quality of life in the patients. Due to these factors, a significant amount of effort has been made to acquire datasets that can help lead to further understand pathogenic mechanisms for future treatment development. Multiplex immunohistochemistry (mIHC) whole slide scans are one of the growing datasets available to study this disease. Currently, analyses performed on mIHC slide scans are based on mixture of qualitative analysis made by a pathologist and manual tracing of the structures for further quantitative analysis. These methods are characterized by long processing times and the presence of human factor including error and biases.

METHODS

To assess these problems, we developed a computer vision algorithm that can extract structural and shape descriptors such as total area of the islet, total area of glucagon and insulin, distribution across the tissue, etc. from single cell to entire islet structures. In addition, we provide the capability of quantifying CD3+ cells to determine the presence of inflammation in the islet (<20um islet periphery) and as single cell counts.

SUMMARY OF RESULTS

We provide an algorithm that automates the analysis of mIHC whole slide scans of the pancreas. This algorithm was tested in 154 images of different pancreas regions with a range of 8 patients with type 1 diabetes. Additionally, this algorithm is capable of quantifying CD3+ cells to determine the presence of inflammation on the islet (insulitis) and single cells. Moreover, we were able to accelerate the processing time to an approximate of 20 minutes for a 3-stain (glucagon, insulin and CD3) mIHC pancreas image of size 250Mb.

CONCLUSIONS

By providing this standardized method we offer an opportunity to reduce the presence of human error or bias across the analysis. Furthermore, we were able to develop an automated detection and quantification algorithm that aims to reduce the processing time while greatly increasing the data that can be extracted for these images compared with previous methods.

This algorithm was developed on Python using a mixture of image processing and machine learning algorithms. The future goal is to improve the capabilities of the algorithm by introducing the possibility of analyzing immunofluorescence images and increasing the number of mIHC chromogens that can be determined on a given section.