Deep convolutional neural network-based method for quantification of the pancreatic β-cell mass in mice

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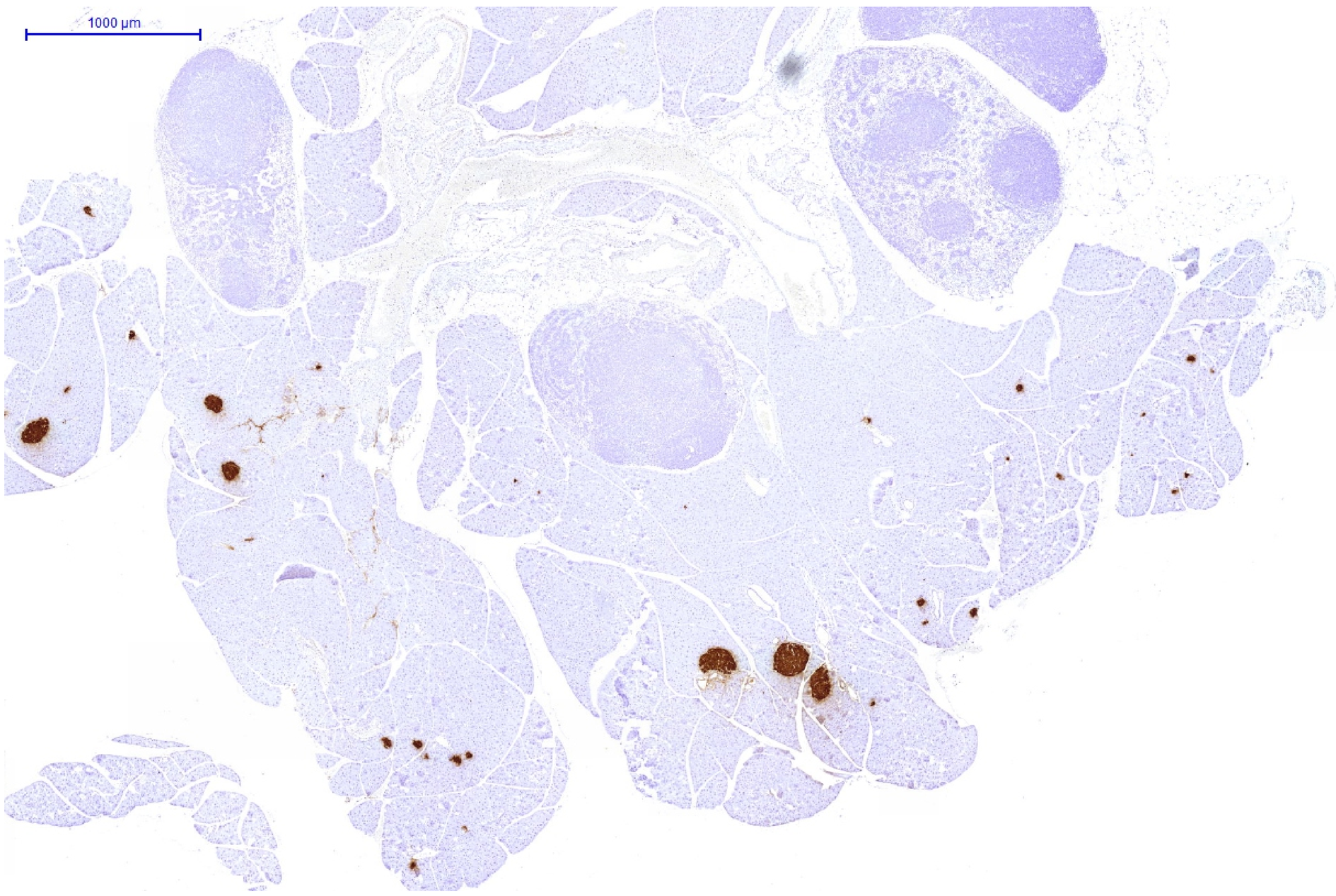
1. Backround

Functional pancreatic β-cell mass is an important parameter in diabetes research as it correlates with the insulin secretion in pancreas. Traditionally, image captures are acquired from insulin-stained pancreatic sections and analyzed using the low-throughput software platforms. However, accurate image analysis of high-resolution captures of pancreatic β-cell mass using established morphological methods is technically challenging and time-consuming. In contrast, low-resolution imaging solves the throughput issue, but performs poorly in identifying small islets, individual β-cells, and even pancreatic tissue. Thus, there is a need for image analytics “next-gen” methods enabling high-resolution whole-slide image analysis for accurate measurements of β-cell mass.

2. Methods

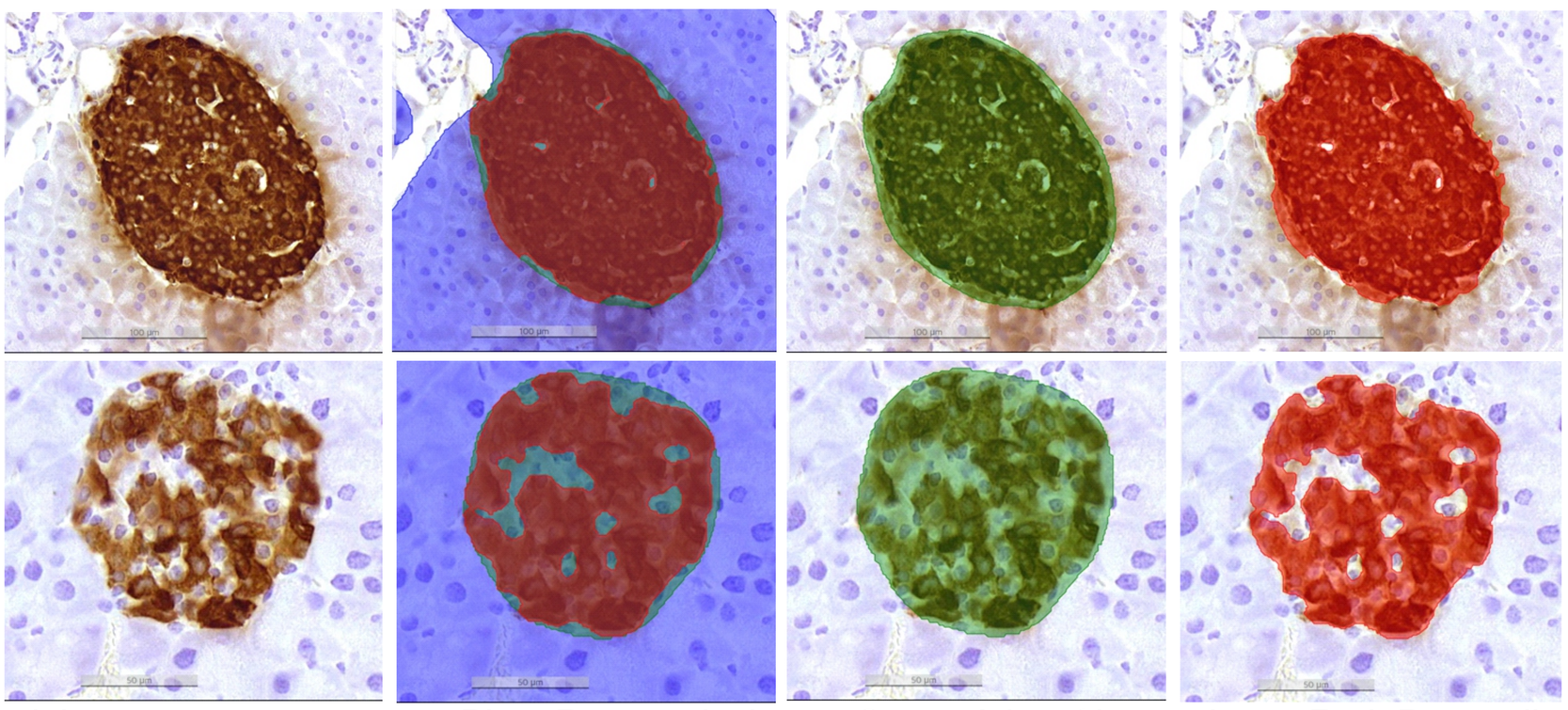
Machine learning methods based on deep convolutional neural networks (dCNN)-are highly efficient in classification of images and increasingly used in medical and biological research. We employed dCNNs for the analysis of β-cell mass measurement as well as quantification of individual β-cells on whole-slide digital images of mouse pancreatic sections stained with anti-insulin antibody from normal wild-type and MANF-deficient mice, which develop insulin-dependent diabetes due to progressive postnatal decrease in the β-cell mass.

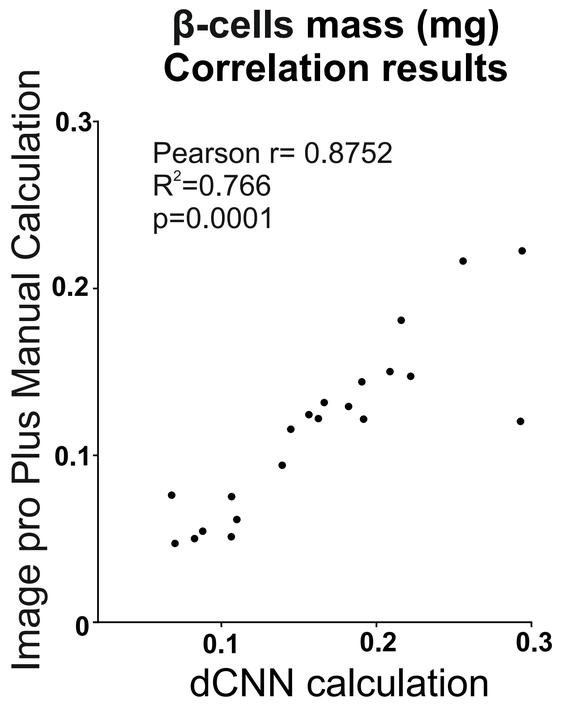
3. Results



Control mouse normal wild-type

Diabetic mouse MANF-deficient





Insulin staining on mouse pancreas, Blue=Pancreatic tissue, Green=Islet of Langerhans, Red=Beta-cells.

4. Conclusion

The established algorithms overcome current limitations in β-cell mass analysis and yield reliable and consistent data.The 112 slides were analyzed <2 hours (approx 1 min per slide).
Our algorithms were developed and run on a fully cloud-embedded Aiforia® Cloud Platform.

5. Acknowledgments

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