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COMMENTARY



# IsletLab: an application to reconstruct and analyze islet architectures

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**ABSTRACT**

The continuous interaction between experimental and theoretical work has proven to be extremely useful for the study of pancreatic cells and, recently, of pancreatic islets. This prolific interaction relies on the capability of implementing computational models and methods to derive quantitative data for the analysis and interpretation of experimental observations. In this addendum I introduce Isletlab, a multiplatform application developed to provide the research community with a user-friendly interface for the implementation of computational algorithms for the characterization and simulation of pancreatic islets.

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In a previous work, we proposed a computational algorithm to reconstruct islet architectures using computational optimization.[1] As a result, quantitative information related to the structural and morphological properties of the reconstructed islet such as cell radii, volume, position and connectivity (i.e. cell-to-cell contacts) is obtained. In a related article,[2] we used the properties obtained from the islet reconstruction process to quantitatively characterize the connectivity network formed in normal and perturbed islets. On the other hand, Hoang et al.[3] proposed a computational approach to evaluate the functional implications of the islet composition, organization and connectivity, using the Kuramoto model of coupled oscillators to simulate the pulsatile nature of hormone secretion. In all cases, although described in detail in the respective articles, the algorithms involved require a somewhat advanced computational knowledge in order to be adequately implemented. For this reason, and with the aim of making these tools available for the interested reader, Isletlab, a multiplatform application for the reconstruction, analysis and simulation of islet architectures, was developed.

Isletlab is a single-window application (see Figure 1) that allows the user to implement the workflow described schematically in Figure 2. In the following, a step-by-step example is briefly described with the objective of guiding the user throughout the process, from the reconstruction of the islet to the functional simulation. The whole process is based on the reconstruction of the islet architecture from experimental data (i.e. cell type and nucleus coordinates), that is first loaded in order to generate an initial islet for the optimization procedure (Figure 2a). Next, an iterative optimization process is performed until an islet composed of non-overlapped cells is obtained (Figure 2b). Once the islet has been reconstructed, cell-to-cell contacts are identified and quantified to determine the islet connectivity properties (Figure 2c), used afterward to generate the associated network and to calculate the corresponding metrics (Figure 2d). At every step of the process, all the statistics and metrics are automatically calculated and displayed in the statistics panel to give the reader a quantitative description of the islet under study. Also based on the connectivity properties of the reconstructed islet is the functional simulation

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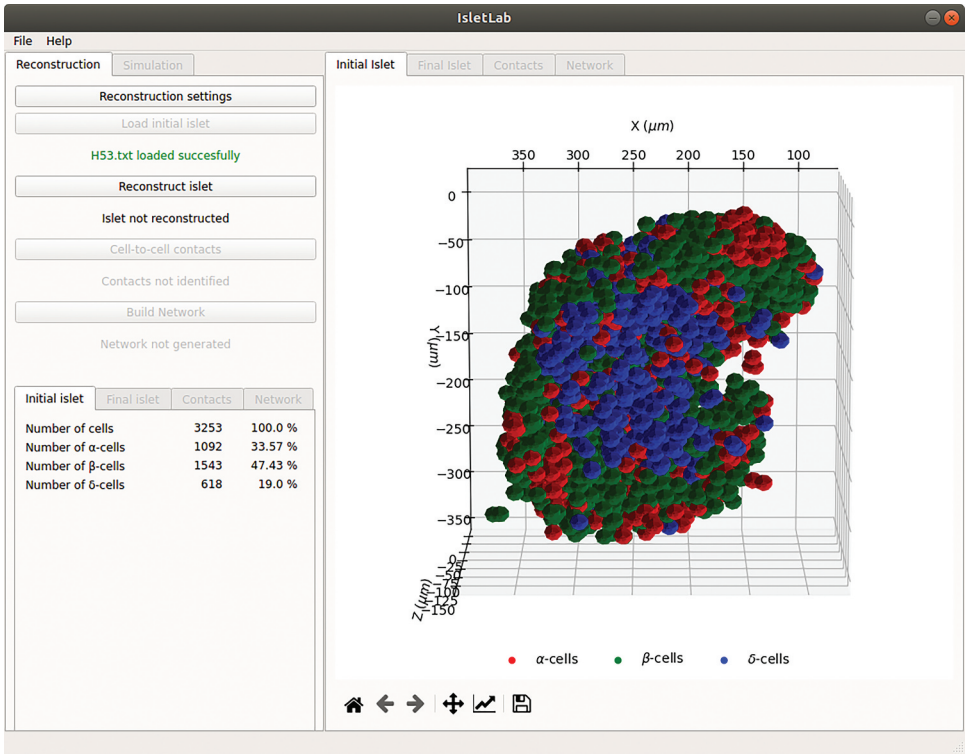


**Figure 1.** Isletlab user interface divided in configuration (top left), statistics (bottom left) and graphics (right) panel.

in which the synchronization index and phase differences between islet cells can be evaluated in different conditions (Figure 2e).

While the main objective of Isletlab is to serve as a tool for the analysis of islet architectures through quantitative metrics, it is also our intention to promote the use of computational modeling as a complement to the experimental work. For instance, reconstructed architectures could be exported and used for the development of computational models based on detailed mathematical descriptions of the cellular mechanisms involved in the secretion of pancreatic hormones and intercellular communication within the islets as in previous works on the subject.[4–6] Moreover, given that cell size can be correlated with function/transcriptome of each cell,[7] additional layers of information could be further incorporated. Similarly, structural and network properties of the reconstructed islets, along with functional simulations could be used to gain a better understanding of how functional networks observed experimentally could be formed.[8–10]

Computational models and methods have become routinely used tools for the study of pancreatic cells and islets and, in my opinion, increasing their usability will potentiate the already productive interaction between the experimental and theoretical work. Hopefully, in the near future Isletlab will become a collaborative environment in which both experimentalists and modelers could share their expertise for the advance of the field.

This addendum should be taken as a call for all the researchers in the field to contribute with new ideas, algorithms and models to further grow Isletlab. The interested reader can obtain Isletlab and the associated documentation from https://github.com/gjfelix/IsletLab.

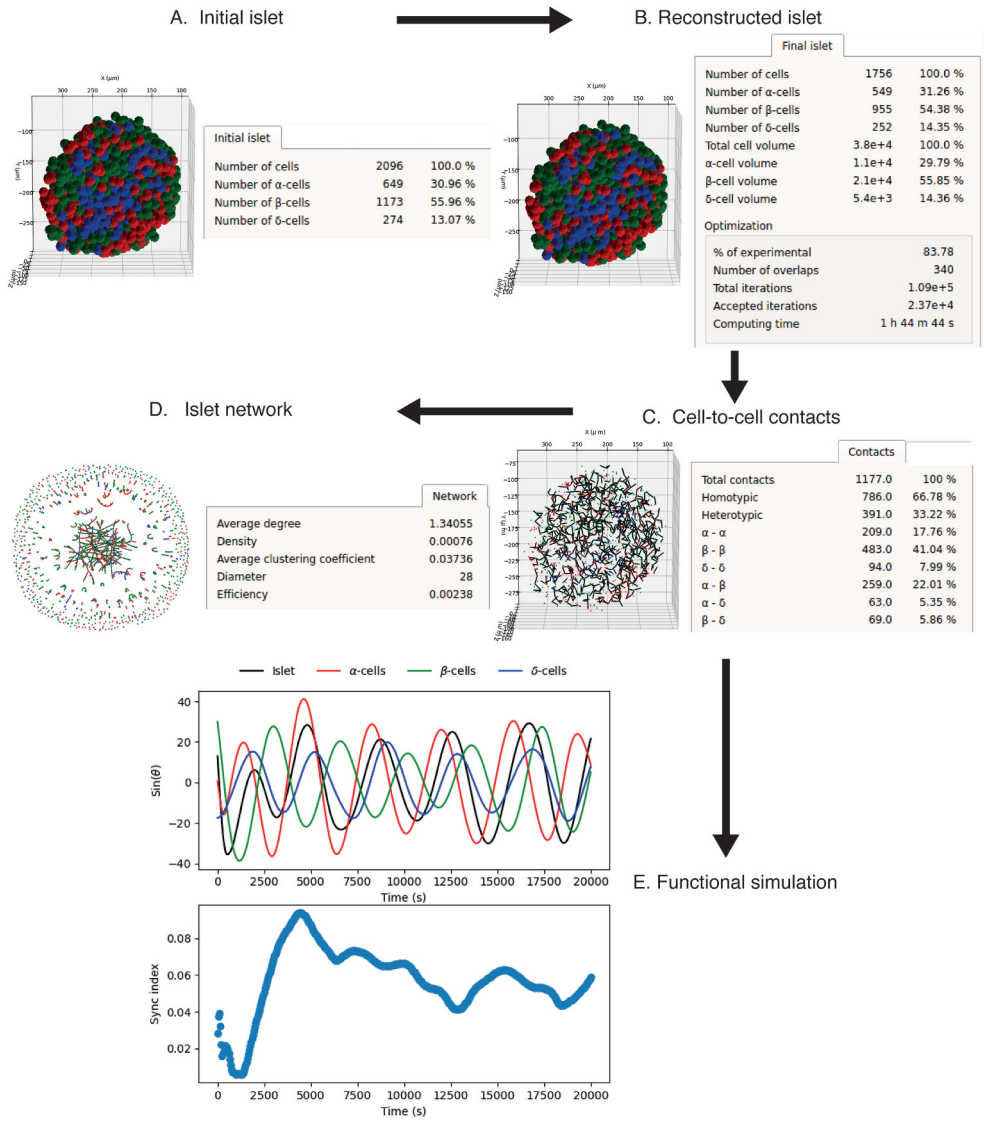


**Figure 2.** Workflow in Isletlab. Based on the data given by the user, an initial islet is proposed (a) to perform the reconstruction process (b). Afterwards, cell-to-cell contacts are found and identified (c). Based on the islet connectivity, the associated network is generated (d) and functional simulations are performed (e).

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## Disclosure statement

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