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AN INTEGRATED ENVIRONMENT FOR TISSUE MORPHOMETRICS AND ANALYTICS

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Introduction/ Background

Attaining high reproducibility in cancer diagnosis is still one of the main challenges in modern pathology due to subjectivity [1, 2, 3]. An integrated framework to extract quantitative morphological features from histology images and perform analytics that can lead to the identification of outcome-related features will provide a more accurate and reproducible means to assess cancer [4, 5].

Aims

We propose an integrated environment which enables analytics of whole-slide tissue morphometry for a selected cohort of cancer patients. The proposed integrated environment includes three main components [Figure 1]: (1) core module comprising of visualization of WSIs at multiple magnification levels, enabling display of clinical and imaging data for multiple cases simultaneously, (2) analytical module contains an interactive tool for measuring dimensions of tissue components and interactive annotation module <Figure 2>, and (3) analytics module applied to data from a selected subset of cases or all the cases using quantitative morphological measurements including those derived from automatic phenotyping of cells [6]<Figure 3>. The proposed environment can be further extended by adding new analytical modules and it can directly bring the benefits of quantitative analysis into pathological practices, thereby increasing reproducibility of cancer diagnosis. Furthermore, it can facilitate the studies of prognostic models, in which morphometric features strongly correlated with the outcome of cancers can be identified and used as image-based markers.

Methods

Our integrated environment for tissue analytics consists of core and analytical modules. The core module is a main portal to assess the already available imaging and clinical data, as well as a nalytical data which comes from integrated analytical modules. These data are interconnected, allowing the users to query imaging data according to available variables in clinical and/or analytical data. It also enables the examination of the clinical and imaging data at the same time. We developed a WSI viewer for exploring the tissue components at different magnification levels by supporting multi-threaded architecture for decompressing the image regions. The state-of-the-art algorithm for automatic phenotyping of all cells in WSIs [6] is the analytic module that makes our interface different from other existing software. The algorithm is capable of identifying multiple classes of cells with high accuracy both in terms of quantitative <Figure 3a, 3b> and quantitative <Figure 3c> validation. This tool offers a fully automated analysis at the cell population level, in terms of the number and the spatial distribution of different cell types. This can, consequently reduce subjectivity and tediousness of the routine semi-quantitative analyses performed by pathologists. This analytical tool is applicable to many prognostic applications such as identifying incidence of metastasis in sentinel lymph nodes, measuring the number of as well as locating tumor-infiltrating lymphocytes, etc.

Results

In this study, we have presented a fully customizable interactive environment for tissue analytics, equipped with measuring, annotating, and automatically cell phenotyping tools. The proposed integrated environment

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has remarkable potential to assist researchers and pathologists to reduce the human errors (if any) in diagnosing cancers. Further, this environment can serve as a benchmark to develop other morphometric measuring tools.

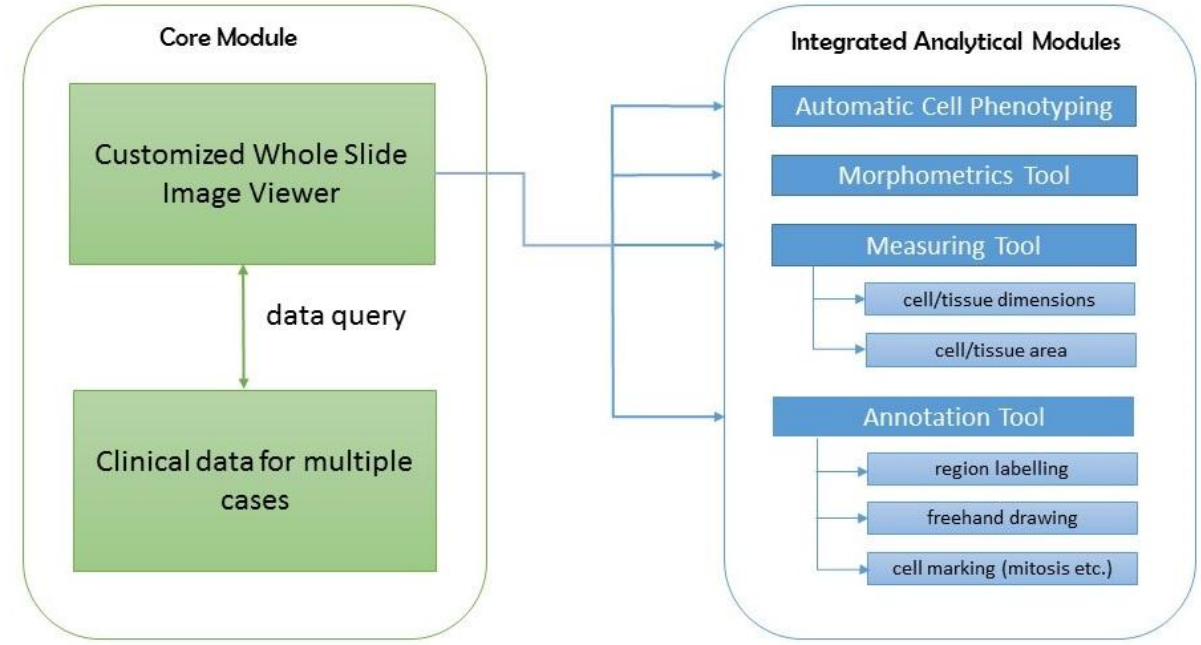

Figure 1.

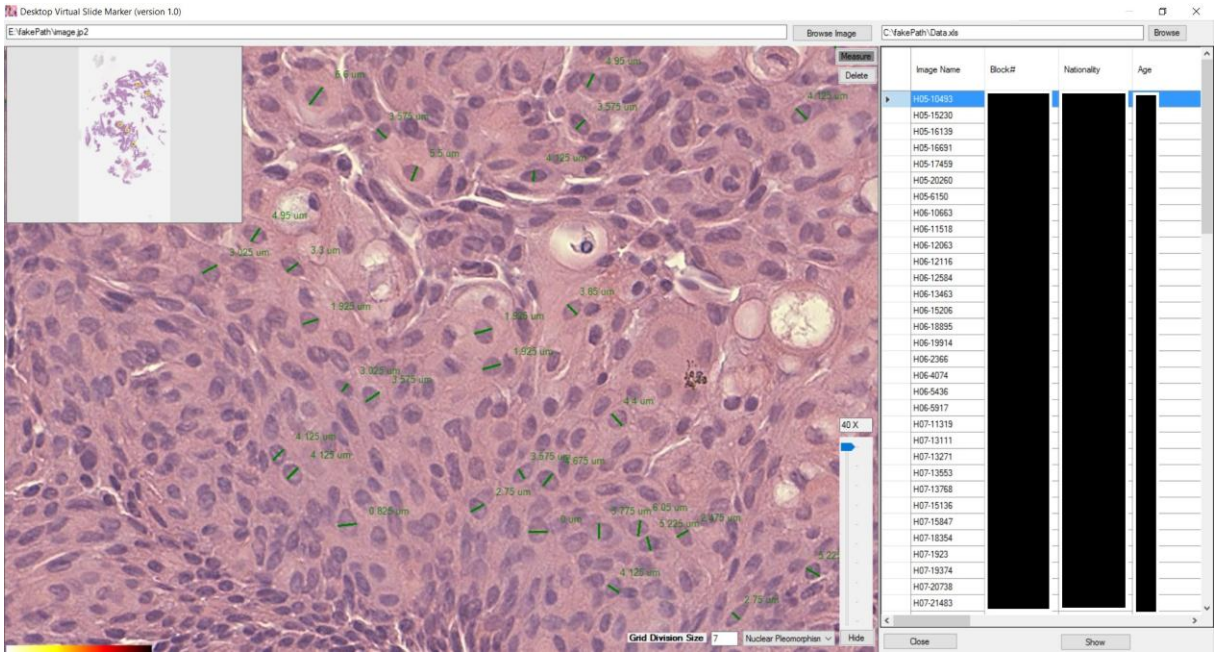

Figure 2.

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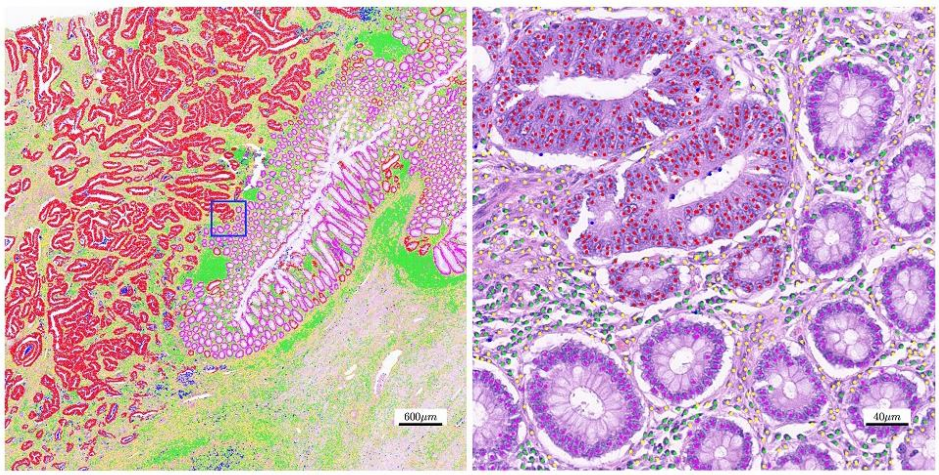

(a) (b)

Nuclear Class	Precision	Recall	F1 score
Benign Epithelial Nucleus	0.902	0.922	0.912
Malignant Epithelial Nucleus	0.921	0.866	0.893
Inflammatory Nucleus	0.805	0.815	0.810
Fibroblast	0.689	0.756	0.721
Necrosis	0.603	0.649	0.625
Miscellaneous	0.372	0.346	0.358

(c)

Figure 3.

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