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An Integrated Framework For Histological Image Data Analytics

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Introduction/ Background

Automated image analysis enables the mining of rich information from digitized histological slides. A major challenge is the complexity and large size of the images. Whole-slide images contain a multitude of different structures, like sections, regions of different tissue types and the contained cells. To make sense of these structures, often multiple analysis solutions must be combined. A common example is the initial identification of regions-of-interest and the subsequent evaluation of cellular structures with respect to these regions.

Aims

There is no general standard for representing image analysis data. Different analysis solutions may represent analysis data as either XML or JSON documents, spreadsheets or images. When combining multiple analysis solutions, the inconsistent data representation makes it necessary to convert information between different formats and to match related entities. This complicates data analytics considerably. To overcome this problem, we describe an integrated framework for histological image data analytics.

Methods

The framework represents image analysis data in an open relational data model. Image regions and cellular structures are represented as individual entities with properties and mutual relations. The framework incorporates multiple image analysis solutions for identifying image regions or cellular structures with machine-learning methods. The solutions are executed sequentially and populate the data model with more and more information from the image. Every step can take advantage of data generated in previous steps in order to target image processing operations to specific regions, or in order to reuse previously computed image features.

Results

The relational data model greatly simplifies data analytics in histological images. Region-specific statistics about cellular structures, or heat-maps of their spatial distribution can simply be computed by database queries. Furthermore, the relational data model enables the efficient management of the huge amounts of data generated by histological image analysis. We demonstrate the generic applicability of the framework by three example applications for the region-specific analysis of nuclear positivity, steatosis and inflammation in whole-slide images.