Gigapixel Software for Histology and Pathology

Category: Research

Abstract—Software development is key for advancing computational pathology imaging; a value proposition that includes more than just diagnostics. Currently available software tools for histology and pathology are slow and cumbersome for large data sets, restricted in their ability to annotate whole slide images, and rarely provide standard computational photography algorithms, such as image segmentation or point operations. In order to obtain the level of annotation and image manipulation required, pathologists often use several applications in their workflow. The combination of software programs and formats, and even simply the physical distance between workstations may result in the loss of data and therefore less optimal patient care. A high performance viewer combined with a streamlined management system and efficient image analysis tools would provide several advantages and advance the field of pathology. These advantages include, but are not limited to, a reduction in the amount of health care providers time required to process, analyze, and store histology data. This will be reflected into significant savings in healthcare costs. In addition, such a system will provide a permanent record for the original source histology slide, that otherwise could fade, brake or be lost during transfer and handling when evaluation by a pathologist in remote location is needed. In working closely with pathologists and histologists, we are developing a software to provide the ability to combine gigapixel histology scans with their annotations and a hierarchical scene graph of image manipulations in a single application, removing the need to transfer datasets between applications. Our gigapixel image viewing software has applications in clinical, research, and educational domains. We are testing our new software tools for histology educational applications and have received positive feedback from 122 medical students at the medical school at University of Utah.

Index Terms—Gigapixel, Data streaming, Image manipulation, Image segmentation, Point operations, Electronic health records, Histology, Pathology.

1 INTRODUCTION

As data acquisition advances and data sizes increase, the need for tools to process and visualize the results in an effective and efficient manner is becoming increasingly important. However, the reliance on supercomputers for scientific visualization and analysis of large data sets has already proven a hindrance for many researchers and scientists who lack easy access to such equipment. Additionally, having multiple users, such as students, trying to annotate a single image on a server creates challenges.

The Scientific Computing and Imaging (SCI) Institute, the Center for Extreme Data Management, Analysis, and Visualization (CED-MAV), and ViSUS (Visualization Streams for Ultimate Scalability) [4, 5] in collaboration with ARUP Laboratories and the University of Utah, Department of Neurobiology and Anatomy, have developed ViSOAR: ViSUS Scalable Output Annotation and Rendering viewer, a multi platform visualization application for accessing and processing very large imaging data.

A single slide scan can produce multi-gigapixel images requiring tens of gigabytes of raw data—thus the need for a tool that can process this data is essential. ViSOAR builds upon the ViSUS technology that allows for large-scale data to be streamed over a network, off of a disc, or on the cloud with extreme efficiency. Furthermore, the technology behind ViSUS allows the application to run on a variety of platforms—from mobile devices to desktops to large, multi-display walls. With this approach physicians and investigators are liberated from the physical constraints of traditional professional and educational environments. A mobile process would allow an efficient interactive teaching in a classroom and can provide remote access to their highly qualified expertise for diagnosing diseases and training the next generation of physicians. It also provides a physician or researcher the ability to review and make diagnoses from anywhere, as opposed to the confines of the lab.

Although the impetus for the collaboration was to build a tool used in clinical, research, and education application, we focused our initial development of the technology in the classroom setting. Our goals include replacing the traditional use of viewing histology slides on microscopes and providing the ability for annotation on the image. As class sizes increase and scanning devices improve in quality, it has become impractical to rely on microscopes for teaching. Additionally, with the use of mobile devices in the hands of everyone in a classroom, instructors want students to actively participate in analyzing and discussing the information presented, such as interactively exploring and annotating the same histology slide presented by an instructor.

A video showing the research in action is available at: http://www.cedmav.org/research/highlights/19-highlights/49-visoar.html.
2 BACKGROUND

We are creating software tools for imaging histology and pathology in order to make such tools easier to use for educational purposes, without losing sight of the potential for a clinical or research usages. Current most commercially available software typically have methods for importing slide data, annotation, image manipulation and image analysis. However, these state-of-the-art commercial tools are expensive and often difficult to use in an educational setting and by non-technical users.

Additionally, we’ve found in the classroom setting most of these tools cannot handle the server load of +100 students accessing data at the same time. Before using our software, histology classes used a Google Maps API viewer on histology slides [1, 7]. The software was restrictive, the only annotation available is text labeling. Our software allows medical students to access a library of slides either on device or stored remotely on a server and provides measuring and annotation features.

3 NEW HISTOLOGY WORKFLOW

After physical histology slides have been prepared, the slides are scanned into SVS file format (Compressed TIFF), storing data at several levels of resolution in a single file. Each slide varies in the amount of data from about 0.5 gigabyte to multiple gigabytes per slide. Previously, the researchers worked with had to import the files to ESlide data management tool and then launch Aperio Imaging software or other systems. The classroom setting used a Google Map API viewer, but the only annotations it provided were simple labels. Upon seeing a demonstration of our software, ViSOAR, and its interaction mechanisms, the pathologists wanted to see their data in ViSOAR’s workflow with in research environment and in the classroom.

With our software framework, it was easy to convert the SVS file format to our proprietary IDX file format. ViSOAR’s IDX file format is part of a high-performance I/O library that writes data in a multiresolution, Hierarchical-Z (HZ) order layout [2, 3]. Our ViSUS framework [4, 5], upon which ViSOAR is built, has converters for SVS, TIFF, or JPEG and many other file formats. Due to the I/O workflow of IDX, ViSOAR enables interactive visualization of gigapixel and terapixel data, lessening the gap between the compute and storage capabilities of common desktop and portable devices.

ViSOAR easily allows researchers and students to view and annotate data with a multiresolution approach. Our software includes polyline, polygon, text and image point of interest annotations, as well as controls for adding scale to the images in pixel, inches, mm, or cm. ViSOAR includes measurement tools, a ruler showing resolution, and a picture-in-picture box to keep the user oriented within the dataset. Image analysis and annotations can happen at any resolution while maintaining the position of the annotations at screen resolution. ViSOAR’s user interface is simple, intuitive and fast, allowing novice users, like students, to quickly interact with the image data without the heavy workflow of typical slide imaging software. ViSUS provides a single platform agnostic code base that compiles on multiple platforms allows users to be on Macs, Windows, or iOS operating systems.

3.1 Into the future

In our collaboration, we will be working on adding the ability to handle multiple user annotations on a server, all referencing the same data set. Additionally, we are exploring adding functionality for a scene graph like hierarchy of image processing methods.

Multiple User Annotation. A current bottleneck in the use of digital slide exploration is the annotation of histopathology data across multiple users. Users desire a streamlined process with active communication between multiple viewers of the data and their annotations, without difficulty in sharing the data. ViSOAR allows users on different platforms (such as an iPad and a Windows laptop) to view the same data, seamlessly, regardless of computation power or operating system. We are currently adding to our system the ability to allow multiple users to see the annotations on a dataset made by fellow observers. Annotations will be able to be grouped by time, user, or tag and viewed in an image layer like browser to provide a more interactive learning environment and hand on experience in histology classes and in the research lab.

Hierarchy of Image Manipulations. Additionally, we’ve found that users, especially in research, would like to explore their own image processing methods, such as computing histograms, point operations, and image segmentation. We seek to build a system that allows users access to simple defaults as well as the controls to change system preferences and to be able to apply these operations in sequence. The sequence of operations can be maintained in a visually editable scene graph, enabling ease of use as well as instant feedback on operations applied to the entire visible image, not just a narrow window on the dataset.

4 USER TESTING

We tested ViSOAR on a 122 students at the University of Utah Medical Center Histology course. Students explored data from high-resolution micrographs on iPads and laptops using ViSOAR allowing them to examine the full range of image resolutions and add annotations. With ViSOAR, students do not need to wait in line for microscope; each student can take the time they need to learn the material without the pressure due to number of people waiting in line for microscope. ViSOAR combines the traditional techniques that used to be done via microscopes and printed copies into one continuous workflow. Instructors liked ViSOAR’s ability to be more quantitative, while maintaining the microscope metaphors of pan and zoom via slide movement and focus operations. Instructors found that teaching via ViSOAR was potentially more effective and definitely easier with ViSOAR as well.

Students reported that they found it easier to learn the material provided by the software, rather than using a slide atlas (printed copy) or a microscope, because the digital slides provide context for the image with a simultaneous low and high resolution view. Digital image manipulations save the time normally required to adjust the microscopes focus and change lenses for different magnifications.

In the process of our testing, instructors were able to ask students to do homework and lab work via a more interactive and hands on experience. Students were discovering structures by carefully examining slides instead of looking at what was presented on a limited, static image. Instructors commented that eventually they would like to provide tests on the digital data to evaluate student comprehension.

5 CONCLUSION

We are developing ViSOAR: ViSUS Scalable Output Annotation and Rendering viewer for histology and pathology applications in research and education. Our software provides a simple interface for viewing, interacting, and annotating gigabyte histopathology datasets at continuous levels of resolution. Our software is able to run locally or off of servers and is platform agnostic. Working closely with domain researchers and educators, we are providing access to data such that +100 clients can attach to our servers and interact with the same data.

In the future, we will allow all these users to add annotations, see each other’s annotation thereby increasing the ability of students, instructors, and clinical researchers to become active participants in the exploration of histology data. Additionally, we would like to add features to allow clinical researchers the ability to explore state of the art computational photography image manipulations for performing analysis.

REFERENCES


