Image Analysis Tool for Oncology

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ONCOLOGY RESEARCH

- One determinant of an effective cancer therapy is the **diffusion of drugs** within the tumor from the vasculature.
- Diffusion can be quantified by analyzing imported **fluorescence microscopy images**, seen in Figure 1.

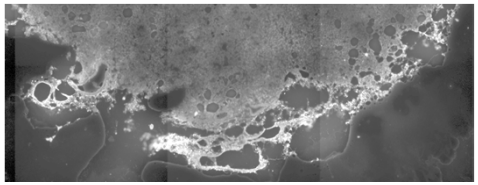


Figure 1: Fluorescence microscopy image of tumor.

CURRENT CHALLENGES AND PROBLEMS

- Full tumor images are large (hundreds of megabytes and tens of millions of pixels).
- Currently used programs use brute force algorithms and are difficult to use.
- **Problems:**
  - Analysis is **time** and **labor** intensive
  - Potential for selection **bias**

GOALS

- Develop a software tool that can:
  - **Analyze** large fluorescence microscopy images.
  - **Quantify** and **Visualize** the drug diffusion.

OBJECTIVES

- Develop algorithms to **determine drug diffusion** within tumor and cell nuclei.
- Order of magnitude **improvement in speed** compared to current programs.
- **User friendly** and intuitive interface that minimizes user involvement and visualizes data.

MODULAR SYSTEM DESIGN

Three Modules

- Data Analysis – Algorithms
- Data Visualization – Plotting
- User Interface

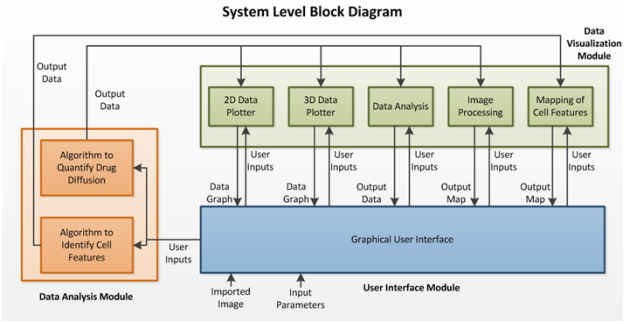


Figure 2: System Block Diagram of Final Design displaying the three modules.

ALGORITHM DESIGN

Drug Distribution

- Compiles frequency histogram of pixels for every drug intensity and distance to closest blood vessel location
- Incorporates image partitioning and blood vessel location caching for localized search (See Figure 3)

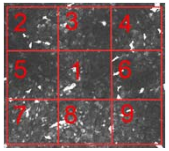


Figure 3: Step by step traversal for localized blood vessel search.

Cell Feature Identification

- Assumes DNA in nuclei act as sinks for drugs
- Determines intensity range of nuclei at each distance position
- Cluster formation and shape recognition to find nuclei (See Figure 4)

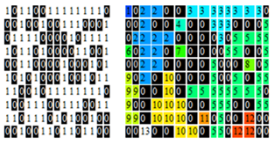
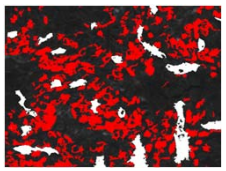


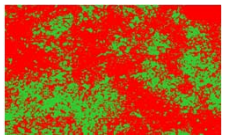
Figure 4: Binary and cluster matrix to identify cell nuclei.

USER INTERFACE DESIGN

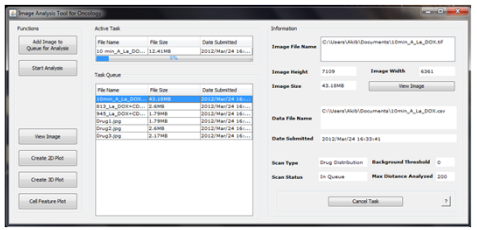
Cell Feature Map of Nuclei



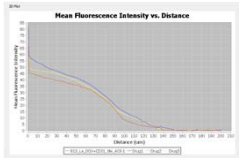
Dynamic Area of Analysis Preview



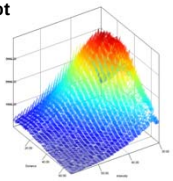
Main Graphical User Interface



2D Plot



3D Plot



PERFORMANCE RESULTS

Orders of magnitude performance improvement achieved:

- **22** times faster for small images (2MB)
- **3865** times faster for larger images (>40MB)

Image Size (Pixel Resolution)	Current Design Runtime (s)	New Design Runtime (s)
2501 x 2501	820	38
6361 x 7109	398055 (est.)	103
8901 x 9137	N/A	191
11441 x 11165	N/A	358

Table 1: Performance runtime testing results

USABILITY RESULTS

- Rated by actual users as **very easy to use**
- Average score of **4.7/5**
- Design minimized number of steps required to complete a task and the number of errors

	Current Design	New Design
Modular Interface	☒	☑
Built-in Data Visualization	☒	☑
Support for 2D/3D Plots	☒	☑
Task Queuing for Automatic Analysis	☒	☑

Table 2: Comparison of current and new tool features

FUTURE WORK

- Additional memory optimization
- Further testing and refinement of cell feature identification
- GPU implementation of massively parallel analysis algorithms

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