

ESTD

Engineering Science &
Technology Division

Biomedical Imaging

Telomere Quantification by Florescence in-situ Hybridization

Telomere Quantification

Telomeres, which are the end pieces of linear chromosomes in eukaryotes, serve important roles in the protection, stabilization, and replication of the chromosome ends and are related to aging and cancer. Shortening of the telomeres can promote chromosome rearrangement that may contribute to cancerous transformation of the cell. Although direct imaging of the telomeres with conventional microscopy is limited by the resolution of optical systems, the size of the telomeres can be estimated by measuring the intensity of the telomere structures in images.

Technology

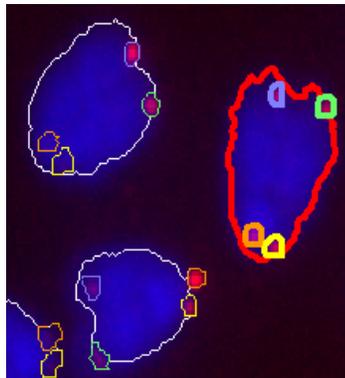


Figure 2. Segmented chromosomes and telomeres from the ORNL telomere analysis software.

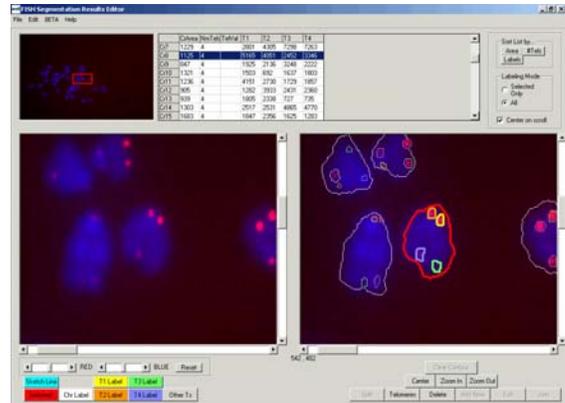


Figure 1. ORNL FISH graphical user interface. Chromosomes (blue) and telomeres (red) are shown with segmentation boundaries and size estimates..

ORNL has developed image processing algorithms and user-friendly software for the automated analysis of telomere imagery (see Fig. 1). This software detects, segments, and quantifies (see Fig. 2) the amount of telomere material for each chromosome. The software can process a large batch of images automatically, allows manual interaction with the results, and allows cross-platform data export. The high-throughput nature of the software will permit life science researchers to perform more statistically robust experiments.

The software emphasizes ease-of-use for manually “correcting” automated image segmentation procedures, such as erroneously joining two or more chromosomes together (Fig. 3). Although additional research is being performed involving the application of Bayesian Belief Networks and probabilistic techniques to perform the segmentation in a more robust manner, the usability of the manual segmentation software methods is invaluable since errors

are likely with any kind of automated segmentation technique.

Specifications and Features

- Windows interface, built with C++ and Visual Basic
- Batch processing and user-interactive modes
- Cross-platform (CSV) data export

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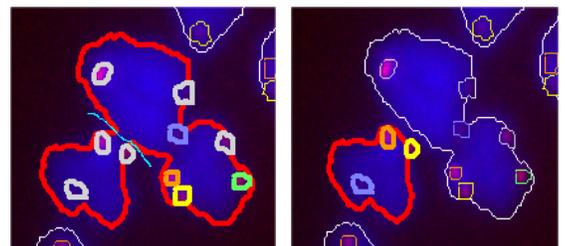


Figure 3. Software is designed for ease of use. Manually editing segmentation results (for example, splitting a region into component chromosomes) is as simple as drawing a line and pushing a button.