



CALIFORNIA STATE SCIENCE FAIR

2010 PROJECT SUMMARY

Name(s) Eric V. Jang	Project Number S1405
Project Title 4D Telomere Modeling: Studying Morphological Differences of Cancerous Telomeres	
Objectives/Goals Telomeres and their interactions with other structures within the cell is currently the subject of active research in the study of genomic stability. Cells undergoing tumorigenesis exhibit irregular telomere behavior in the nucleus, and thus it is important to study the spatial organization of telomeres in a cell over time to characterize these genomic changes. However, no method currently exists to visually compare telomere distributions in 3D space and over time. This project presents a novel, unique way to visualize dynamics of telomeres by displaying the convex hull that describes the shape of telomere organization as changing over time.	Abstract The Laboratory of Dr. Yuval Garini provided confocal microscopy data of U2OS osteosarcoma nuclei and healthy 3t3 fibroblast nuclei. The images were segmented by binarization, mask filtering and flood-filled algorithms that were extended specifically to operate in 3D. These functions were implemented through a Telomere Analyzer Tool written in C++ using the Visual Studio IDE. Segmentation results were passed through the Quickhull convex hull algorithm. Convex hull polytopes and telomeres in each frame were calculated and displayed over time in the Blender software through an importer script written in Python. The resulting animations were observed at different angles. Segmentation error was validated through variable noise applied to phantom data.
Methods/Materials The Laboratory of Dr. Yuval Garini provided confocal microscopy data of U2OS osteosarcoma nuclei and healthy 3t3 fibroblast nuclei. The images were segmented by binarization, mask filtering and flood-filled algorithms that were extended specifically to operate in 3D. These functions were implemented through a Telomere Analyzer Tool written in C++ using the Visual Studio IDE. Segmentation results were passed through the Quickhull convex hull algorithm. Convex hull polytopes and telomeres in each frame were calculated and displayed over time in the Blender software through an importer script written in Python. The resulting animations were observed at different angles. Segmentation error was validated through variable noise applied to phantom data.	Results Telomere clustering is more prevalent in the U2OS nuclei. U2OS telomere convex hulls and ellipsoid models take on an oblate shape, and have gradually increasing volume and surface area over time. The volume and surface area of the U2OS models are greater than their 3t3 counterparts. Segmentation error for telomere locations does not change when the S/N ratio exceeds 16.5 (min error = 0.078 um).
Conclusions/Discussion A novel method of studying telomere dynamics and organization is presented in this study. Observations of generated animations suggest that cancerous telomeres are organized in a more clustered, oblate fashion. Understanding telomere organization in cancer cells leads to improvements in therapeutic medicine and treatment strategy. This project has can be used to intuitively study of quantitative and qualitative differences in telomere dynamics between healthy and diseased cells, as well as the role of telomeres in signaling pathways.	
Summary Statement Comparing healthy/cancerous telomere dynamics by using a novel time-lapse 3D visualization algorithm.	
Help Received Lab data provided by Dr. Yuval Garini; father introduced the basics of image processing.	