SYNOPSYS CHAMPIONSHIP 2016 PROJECT ABSTRACT

THE ABSTRACT IS A REQUIRED PART OF YOUR PROJECT
Bring your abstract with you to project check-in on Wednesday, March 16, 2016.

PROJECT NUMBER: 111-530-42 STUDENT NAMES(s): Nathan Wong and Mahesh Murag

You should bring at least ten copies of your abstract with you when you come to the Championship. One copy should remain on display with your project during the Championship. You will want others to give to the judges. Your abstract should be written after you finish your research and experimentation and should include:

- Your project title, the full name(s) of all team members, and your school (all centered)
- The purpose of your project
- Your hypothesis or evaluation criteria
- A brief statement about the procedures and equipment you used
- Your results (analysis of data)
- Your conclusions

Type or print neatly using 10- or 12- point black type. Single space throughou
Center your project title, your name(s), and school.
You must use this form. Your abstract should be less than 500 words, and it should fit within the lines on this form.

NGSomics (Next-Gen Sequencing Genomics): A Mobile-optimized, Cloud-based NGS Pipeline that Utilizes Docker Containers for Parallelization and Automation

Research conducted by: Nathan Wong & Mahesh Murag
Mentor: Renee Fallon
School: Monta Vista High School

Personalized medicine achieved through individualized analysis of genetic data is the future that connects bioinformatics and biomedicine. This field posits solutions to previously incurable diseases and opens up pathways towards better treatment options. A hallmark of bioinformatics research is the massive amount of data collected and generated from raw sequences of DNA which the genomic analysis software seeks to efficiently analyze. Even though many different genomic analysis programs are currently used by professionals to find mutations within a sequence, most of these tools are inaccessible for public use. This issue is caused by both a lack of practical interpretation of the resulting data and an absence of a platform capable of running intense operations while also being convenient and easy-to-use. A full-scale, parallelized and automated genomic analysis pipeline, NGSomics, is a solution which offers not only accurate variant calls, efficient processing speeds, and easy-to-replace bioinformatics tools, but also directly connects the user with applicable information through its responsive platform. NGSomics is hosted on a public domain and offers digestible and applicable data interpretations. Built on Docker, NGSomics is primed for seamless updating of currently integrated tools, such as the BWA aligner and SAMtools variant caller, as well as for the implementation of newly-developed genomic analysis tools. With the standardized Human Genome 19 data set used in the comparative GCAT test, it is asserted that NGSomics is an equally suitable option for DNA variants-based studies, as it is able to yield reliable outputs when compared with other genomic analysis pipelines. Future improvements to NGSomics would include implementing the concepts of one discarded design, a prototype which added WGCNA for identifying gene modules across specific biological conditions. Nevertheless, current developments in personalized medicine reveal high demands for the feature set of NGSomics. Its ability to branch lengthy bioinformatics data with clinically relevant information for the public is vital, especially as personal DNA sequencing becomes more affordable and commonplace.

More information (Application): http://ngsomics.com & http://app.ngsomics.com