The International System Safety Society

Tennessee Valley Chapter

ALABAMA - MISSISSIPPI - TENNESSEE

http://www.isss-tvc.org/

May 2016 Newsletter

Tennessee Valley Chapter Officers

President: Christopher Trumble, 256-847-3247

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Secretary: Jason Rupert, 256-313-8650

Immediate Past President: Ken Rose, 256-645-1621,

Special Events Coordinator: Open

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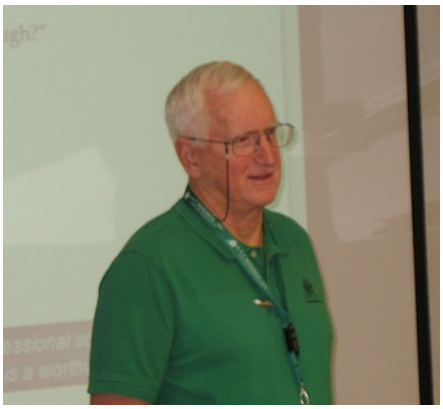
President's Corner

Election – I know many of you are probably sick of hearing about elections of any kind but the ISSS-TVC one will not drag on and on and it is important. It's that time again, it's time to vote! The ballots are being sent out for positions in the Chapter. I strongly urge you to throw your name into the hat and run for a position in this respected Society. You can write in a name if it is not on the ballot. If you choose not to run for one of the Chapter Officer positions, I remind you of the importance of voting for someone for each of the Chapter Officer positions. Remember that during the Chapter Officer Elections, your vote matters.

Awards - During the May and June meetings I plan on recognizing some of our members for their contributions to the Chapter and others will be receiving awards. I hope you will support your peers and attend the meetings. You get the added benefit of some excellent presentations by our guest presenters.

Meetings – The May meeting will be an excellent opportunity to learn about FPGA Safety. You may want to refresh your memory concerning international standard RTCA/DO-254 and have your questions regarding verification and validation (V&V) ready. This will be your chance to get answers regarding the significant challenges associated with V&V due to the strict adherence necessary to stringent and complex design assurance guidelines defined by DO-254. Looking forward to seeing our membership well represented at this meeting.

News



April 20th we were fortunate to have Tom Pfitzer of A-P-T Research provide a presentation regarding universal risk scales (URS), a method of comparing risks with multiple known risks. URS is useful for communicating risk and explaining levels of concern and orders of magnitude. It is a method for selecting acceptable risks, i.e., determining "How safe is safe enough?" It is also useful for calibrating RAC matrices. The presentation was very well received. The presentation is on the web at http://www.isss-tvc.org/Pfitzer-Universal_Risk_Scales.pdf. Those who want additional details should contact Tom at APT. The meeting was attended by 17 members and 7 guests.

The Chapter of the Year award has transferred in April 2016 from the Dynetics to APT Research. APT has many ISSS-TVC members and has supported the Chapter and the Society for many years. The Award has been on the walls at APT before and I'm sure it's beginning to feel like it's back home while it is gracing one of their walls. If your business would like to display the award at their facility just email a request and we will be happy to try to coordinate a period of time for you to display it.

Upcoming Meetings

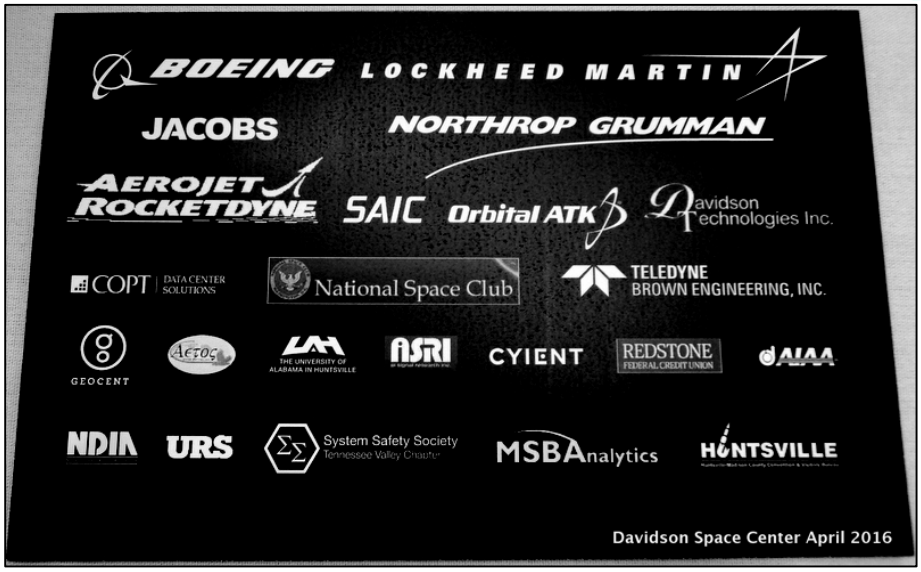
18 May 2016 Intuitive Research and Technology 5030 Bradford Blvd NW # 205, Huntsville, AL 35805 will be hosting the meeting. Dr. Bruce Peters from Intuitive will be providing a presentation on Field-Programmable Gate Array (FPGA) Safety. Many within the manufacturing industry today are turning to FPGA devices in systems that are critical for safety to mitigate risks, control cost and ensure speed. This presentation should be of interest to and valuable for all our membership to attend.

15 June 2016 Eric Bale, System Safety Engineer at Bastion Technologies, working with NASA Marshall Space Flight Center as part of the SLS integrated hazard team, will be providing a presentation on Experimental Amateur Built (EAB) aircraft vs Federal Aviation Administration (FAA) part 23 aircraft. Our members who are involved with

manned and unmanned aviation systems will have a particular interest in this presentation but all are encouraged to attend.

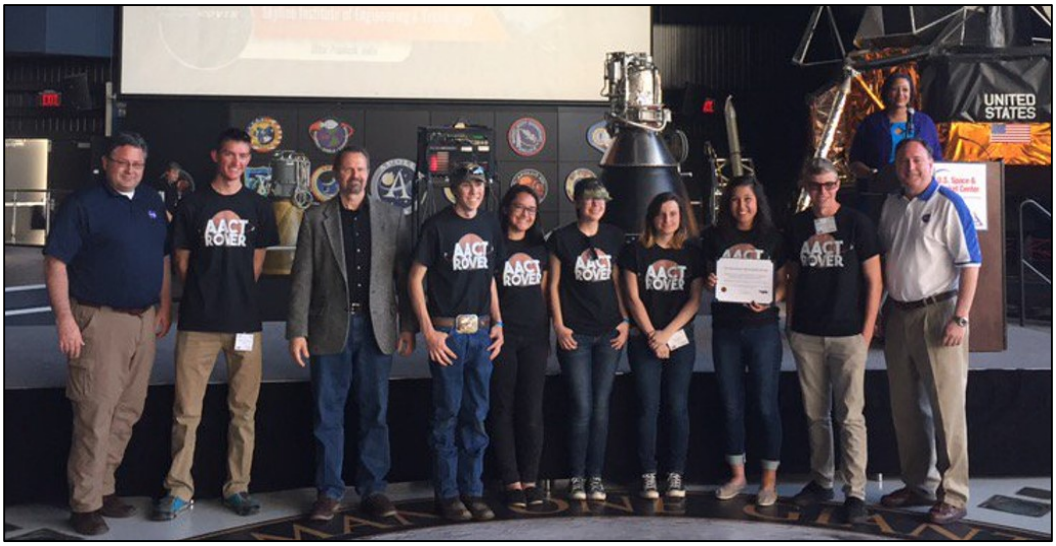
Special Events

The Chapter was happy to assist with NASA Rover Challenge April 7-9, 2016. Awards were presented on the final day of the race at 5:00 pm. The ISSS-TVC selected two teams to present awards to, one high school and a University. Our logo was proudly displayed along with other companies and organizations who assisted with the event by the event coordinators.



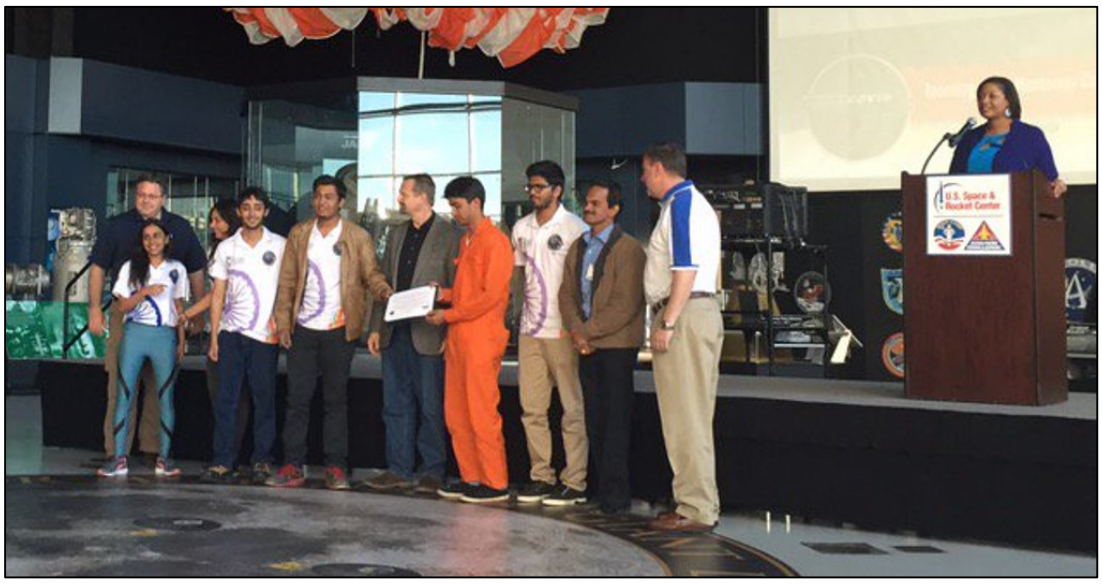
Some action photos taken during the race over a demanding course

The High school winner was Academy of Arts, Careers & Technology from Reno Nevada. The judges were impressed with their submission when compared with some university entries theirs shined.



Academy of Arts, Careers & Technology – Reno, Nevada

The University winner was SVKM'S NMIMS Mukesh Patel School of Technology Management and Engineering, from India. The ISSS being an International Society, it is nice to receive submissions for consideration from other countries and this University's submission rose to the top and snatched the first place award for the best use of System Safety in the NASA Human Exploration Rover Challenge.



SVKM'S NMIMS Mukesh Patel School of Technology Management and Engineering - India

Awards

We are excited to announce there have been submissions and very proud that members are recognizing the efforts of their peers. The chapter will be presenting awards during the May and June meetings.

Fun stuff

HudsonAlpha Institute for Biotechnology is a rapidly growing company in the Huntsville, AL research park that is involved in Genomics. Here is a brief overview of Genomics from the National Human Genome Research Institute (https://www.genome.gov/18016863/a-brief-guide-to-genomics/):

Deoxyribonucleic acid (DNA) is the chemical compound that contains the instructions needed to develop and direct the activities of nearly all living organisms. DNA molecules are made of two twisting, paired strands, often referred to as a double helix.

Each DNA strand is made of four chemical units, called nucleotide bases, which comprise the genetic "alphabet." The bases are adenine (A), thymine (T), guanine (G), and cytosine (C). Bases on opposite strands pair specifically: an A always pairs with a T; a C always pairs with a G. The order of the As, Ts, Cs and Gs determines the meaning of the information encoded in that part of the DNA molecule just as the order of letters determines the meaning of a word.

An organism's complete set of DNA is called its genome. Virtually every single cell in the body contains a complete copy of the approximately 3 billion DNA base pairs, or letters, that make up the human genome.
With its four-letter language, DNA contains the information needed to build the entire human body. A gene traditionally refers to the unit of DNA that carries the instructions for making a specific protein or set of proteins. Each of the estimated 20,000 to 25,000 genes in the human genome codes for an average of three proteins.

Located on 23 pairs of chromosomes packed into the nucleus of a human cell, genes direct the production of proteins with the assistance of enzymes and messenger molecules. Specifically, an enzyme copies the information in a gene's DNA into a molecule called messenger ribonucleic acid (mRNA). The mRNA travels out of the nucleus and into the cell's cytoplasm, where the mRNA is read by a tiny molecular machine called a ribosome, and the information is used to link together small molecules called amino acids in the right order to form a specific protein.

Proteins make up body structures like organs and tissue, as well as control chemical reactions and carry signals between cells. If a cell's DNA is mutated, an abnormal protein may be produced, which can disrupt the body's usual processes and lead to a disease such as cancer.

DNA Sequencing
Sequencing simply means determining the exact order of the bases in a strand of DNA.

Because bases exist as pairs, and the identity of one of the bases in the pair determines the other member of the pair, researchers do not have to report both bases of the pair.

In the most common type of sequencing used today, called sequencing by synthesis, DNA polymerase (the enzyme in cells that synthesizes DNA) is used to generate a new strand of DNA from a strand of interest. In the sequencing reaction, the enzyme incorporates into the new DNA strand individual nucleotides that have been chemically tagged with a fluorescent label. As this happens, the nucleotide is excited by a light source, and a fluorescent signal is emitted and detected. The signal is different depending on which of the four nucleotides was incorporated. This method can generate 'reads' of 125 nucleotides in a row and billions of reads at a time.

To assemble the sequence of all the bases in a large piece of DNA such as a gene, researchers need to read the sequence of overlapping segments. This allows the longer sequence to be assembled from shorter pieces, somewhat like putting together a linear jigsaw puzzle. In this process, each base has to be read not just once, but at least several times in the overlapping segments to ensure accuracy.

Researchers can use DNA sequencing to search for genetic variations and/or mutations that may play a role in the development or progression of a disease. The disease-causing change may be as small as the substitution, deletion, or addition of a single base pair or as large as a deletion of thousands of bases.

The Human Genome Project

The Human Genome Project, which was led at the National Institutes of Health (NIH) by the National Human Genome Research Institute, produced a very high-quality version of the human genome sequence that is freely available in public databases. That international project was successfully completed in April 2003, under budget and more than two years ahead of schedule.

The sequence is not that of one person, but is a composite derived from several individuals. Therefore, it is a "representative" or generic sequence. To ensure anonymity of the DNA donors, more blood samples (nearly 100) were collected from volunteers than were used, and no names were attached to the samples that were analyzed. Thus, not even the donors knew whether their samples were actually used.

The Human Genome Project was designed to generate a resource that could be used for a broad range of biomedical studies. One such use is to look for the genetic variations that increase risk of specific diseases, such as cancer, or to look for the type of genetic mutations frequently seen in cancerous cells. More research can then be done to fully understand how the genome functions and to discover the genetic basis for health and disease.

Implications of Genomics for Medical Science

Virtually every human ailment has some basis in our genes. Until recently, doctors were

able to take the study of genes, or genetics, into consideration only in cases of birth defects and a limited set of other diseases. These were conditions, such as sickle cell anemia, which have very simple, predictable inheritance patterns because each is caused by a change in a single gene.
With the vast trove of data about human DNA generated by the Human Genome Project and other genomic research, scientists and clinicians have more powerful tools to study the role that multiple genetic factors acting together and with the environment play in much more complex diseases.

These diseases, such as cancer, diabetes, and cardiovascular disease constitute the majority of health problems in the United States. Genome-based research is already enabling medical researchers to develop improved diagnostics, more effective therapeutic strategies, evidence-based approaches for demonstrating clinical efficacy, and better decision-making tools for patients and providers. Ultimately, it appears inevitable that treatments will be tailored to a patient's particular genomic makeup. Thus, the role of genetics in health care is starting to change profoundly and the first examples of the era of genomic medicine are upon us.

It is important to realize, however, that it often takes considerable time, effort, and funding to move discoveries from the scientific laboratory into the medical clinic. Most new drugs based on genome-based research are estimated to be at least 10 to 15 years away, though recent genome-driven efforts in lipid-lowering therapy have considerably shortened that interval. According to biotechnology experts, it usually takes more than a decade for a company to conduct the kinds of clinical studies needed to receive approval from the Food and Drug Administration.

Screening and diagnostic tests, however, are here. Rapid progress is also being made in the emerging field of pharmacogenomics, which involves using information about a patient's genetic make-up to better tailor drug therapy to their individual needs.

Clearly, genetics remains just one of several factors that contribute to people's risk of developing most common diseases. Diet, lifestyle, and environmental exposures also come into play for many conditions, including many types of cancer. Still, a deeper understanding of genetics will shed light on more than just hereditary risks by revealing the basic components of cells and, ultimately, explaining how all the various elements work together to affect the human body in both health and disease.

To the chapter's membership, keep expanding your knowledge and thanks for all that you do!