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[Academics] America's Bioinformatics Expert Gave Keynote Speech on Cancer at GIW2012
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NCKU News (2012/12/14) Cancer genomics research expert Ilya SHMULEVICH, a professor of the Institute for Systems Biology (ISB) was invited by National Cheng Kung University (NCKU), southern Taiwan, as a keynote speaker for GIW 2012 -- the 23rd International Conference on Genome Informatics – giving a talk on "Integrative Analysis and Interactive Exploration of Data from The Cancer Genome Atlas (TCGA)," Dec. 13.

In ISB, Prof. SHMULEVICH directs a Genome Data Analysis Center as part of TCGA project, a comprehensive and coordinated effort to accelerate our understanding of the molecular basis of cancer through the application of genome analysis technologies, including large-scale genome sequencing.

Dr. SHMULEVICH elaborated, "TCGA data is large scale molecular measurement data from different cancer. So they measure DNA, RNA and protein and so they generate lots of data from individual cancer patient from individual tumor, and they do that for approximately 25 different tumor types and then we computation and analyze all of these data and to learn about the cancer."

Dr. SHMULEVICH's team in ISB uses genome analysis to decide how gene's function and to find the relationship between the genes that signals the potential for new cancer drugs.

His work in cancer genomics research spans multiple cancers, with published work in glioma, lymphoma, leukemia, breast cancer, ovarian cancer, and sarcoma. "Overall will be 10 thousand cancer patients included in the project," said SHMULEVICH.

However, "TCGA project was not design to do clinical research because we don't have enough information to make new clinical discovery," Dr. SHMULEVICH responded to the inquiry of the possibility of TCGA data to help with medical breakthrough.

He added, "the goal of the project is to provide molecular characterization of the cancer and these data will be used by other studies to make new clinical discoveries, new follow-up studies probably clinical trials."

"TCGA is so powerful because it's unprecedented in its scope, and in its scope it turns out how much data it generates for different cancer." Dr. SHMULEVICH said, "there's never been a project including so much different kind of data for these cancers."

"What's unique about the project is that for each tumor sample, they generate all of these data, DNA, RNA, protein, and that will give the potential power of the data analysis."

Dr. SHMULEVICH offered his advice for students who are interested in the field, "For students of Computer Science and Engineering or Bioinformatics, I would strongly advice working collaboratively projects with biologists."

He said, "You cannot just sit there analyzing those data without really understanding what they mean and that's the major limitation have been in the field. The important breakthrough is going to happen when people are working with interdisciplinary teams."

As for GIW2012 hosted by NCKU, he noted, "I think it's a very exciting program with a lot of new contribution and there's really a need for this kind of computational method and analysis."

Further Information:
NCKU News 2012/12/14

National Science Council International Cooperation Sci-Tech Newsbrief

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