This work was recognized as first prize winner for excellent research at ISMB/ECCB CAMDA 2013 Conference. I am giving a talk at CAMDA 2013 Conference, which runs as a satellite meeting of ISMB/ECCB 2013 Conference.&#65533;CAMDA focuses on challenges in the analysis of the massive data sets that are increasingly produced in several fields of the life sciences. The conference offers researchers from the computer sciences, statistics, molecular biology, and other fields a unique opportunity to benefit from a critical comparative evaluation of the latest approaches in the analysis of life sciences' &#65533;Big Data&#65533;. Currently, the Big Data explosion is the grand challenge in life sciences. Analysing large data sets is emerging to one of the scientific key techniques in the post genomic era. Still the data analysis bottleneck prevents new biotechnologies from providing new medical and biological insights in a larger scale. This trend towards the need for analysing massive data sets is further accelerated by novel high throughput sequencing technologies and the increasing size of biomedical studies. CAMDA provides new approaches and solutions to the big data problem, presents new techniques in the field of bioinformatics, data analysis, and statistics for handling and processing large data sets. This year, CAMDA's scientific committee set up two challenges; the prediction of drug compatibility from an extremely large toxicogenomic data set, and the decoding of genomes from the Korean Personal Genome Project. The keynote talks were given by&#65533;Atul Butte from Stanford University School of Medicine and Nikolaus Rajewsky from Max-Delbr&#65533;ck-Center for Molecular Medicine in Berlin. Atul Butte talked about translational bioinformatics and emphasized the importance of converting molecular, clinical and epidemiological data into diagnostics and therapeutics to ease the bench-to-bedsize translation. Nikolaus Rajewsky presented his group work on circular RNAs and findings on RNA-protein interactions. I was involved in the prediction of drug compatibility from an extremely large toxicogenomic data set to answer two most important questions in toxicology. We investigated whether animal studies can be replaced with in vitro assays and if liver injuries in humans can be predicted using toxicogenomics data from animals. In this work, we demonstrate that data fusion allows us to simultaneously consider the available data for outcome prediction of drug-induced liver injury. Its models can surpass accuracy of standard machine learning approaches. Our results also indicate that future prediction models should exploit circumstantial evidence from related data sources in addition to standard toxicogenomics data sets. We anticipate that efforts in data analysis have the promise to replace animal studies with in vitro assays and predict the outcome of liver injuries in humans using toxicogenomics data from animals.   &#65533;