

# The 14th Annual International Conference On Critical Assessment of Massive Data Analysis (CAMDA)

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CAMDA focuses on the analysis of massive data in life sciences. The conference presents new techniques in the field of bioinformatics, data analysis, and statistics for the handling and processing large data sets, the combination of multiple data sources, and computational inference. An essential part of CAMDA is its open-ended data analysis challenge which focuses on big heterogeneous data sets. The winners of the annual challenges are voted by the delegates at the end of the conference. CAMDA has a track record as a well-recognized annual conference going back to the year 2000, and it has become an ISMB Satellite Meeting since 2011.

<http://www.camda.info>



## **Keynote Speakers**

### **Des Higgins, PhD - Making and using extremely large multiple sequence alignments.**

**Short Bio:** Des Higgins is professor of Bioinformatics in University College Dublin, Ireland and has been working on sequence alignment and molecular evolution since the mid 1980s. He originated the widely used Clustal package and continues to develop and maintain multiple sequence alignment algorithms and software. He also works on the analysis of high throughput genomics data, especially in the application of multivariate analysis methods for data integration. He has published more than 130 peer-reviewed articles in bioinformatics, sequence alignment and genomics with an h-index of 54.

### **Christopher E. Mason, PhD - Leveraging short and long reads for optimal RNA-Sequencing with CAMDA data set #1.**

**Short Bio:** Dr. Mason founded his laboratory as an assistant professor at Weill Cornell Medical College in the Department of Physiology and Biophysics and at the Institute for Computational Biomedicine. Professor Mason also holds an appointment in the Tri-Institutional Program on Computational Biology and Medicine between Cornell, Memorial Sloan-Kettering Cancer Center and Rockefeller University and he also has an appointment at the Weill Cornell Cancer Center and the Brain and Mind Research Institute. In 2013, he won the Hirschl-Weill-Caulier Career Scientist Award. In 2014, he won the Vallee Foundation Young Investigator Award, the CDC Honor Award for Standardization of Clinical Testing, and he was just named as one of the “Brilliant Ten” Scientists in the world by Popular Science magazine.

## Friday July 10<sup>th</sup> 2015

07:30 - 09:00	ISMB / CAMDA Registration
09:00 - 09:15	CAMDA Welcome
09:15 - 10:15	<b>Keynote: Des Higgins, University College Dublin, Ireland</b> Making and using extremely large multiple sequence alignments
10:15 - 10:45	<i>Morning break</i>
10:45 - 11:10	<b>Djork-Arné Clevert, Johannes Kepler University Linz, Austria</b> Setting the context
11:10 - 11:50	<b>Hubert Rehrauer, ETH Zurich and University of Zurich, Switzerland</b> Prognostic value of cross-omics screening for cancer survival
11:50 - 12:30	<b>Marta R. Hidalgo, Centro de Investigación Príncipe Felipe (CIPF), Spain</b> Functional hallmarks in clear cell renal cell carcinoma grade and stage progression revealed by changes in signalling circuit activities
12:30 - 13:30	<i>Lunch break</i>
13:30 - 14:10	<b>Jari Björne, University of Turku, Finland</b> Cancer progression classification for mutation analysis
14:10 - 14:50	<b>Sinjini Sikdar, University of Louisville, USA</b> Exploring the importance of cancer pathways by meta-analysis of differential protein expression networks in three different cancers
14:50 - 15:30	<b>Pramila Tata, Agilent Technologies, USA</b> Multi-Omics analysis for understanding the molecular basis of Lung Adenocarcinoma
15:30 - 16:00	<i>Afternoon break</i>
16:00 - 16:40	<b>Alejandra Cervera, University of Helsinki, Finland</b> A pipeline for exploratory and pathway analysis of NGS data
16:40 - 17:20	<b>Jose Carbonell, Centro de Investigación Príncipe Felipe (CIPF), Spain</b> Integrative Gene Set Analysis of mRNA and miRNA expression data
17:20 - 18:00	<b>Olivier Gevaert, Stanford University, USA</b> Multi-omics fusion for cancer data
19:00	CAMDA Dinner. Tickets are available via ISMB website!

## Saturday July 11<sup>th</sup> 2015

09:05 - 09:15	CAMDA Welcome
09:15 - 10:15	<b>Keynote: Christopher E. Mason, Weill Cornell Medical College, USA</b> Leveraging short and long reads for optimal RNA-Sequencing with CAMDA data set #1
10:15 - 10:45	<i>Morning break</i>
10:45 - 11:10	<b>Weida Tong, US Food and Drug Administration, USA</b> Setting the context
11:10 - 11:50	<b>Cankut Cubuk, Centro de Investigación Príncipe Felipe (CIPF), Spain</b> Signalling circuit activities as mechanism-based features to predict mode of action of chemicals
11:50 - 12:30	<b>Chathura Siriwardhana, University of Louisville, USA</b> Inter-platform concordance of gene expression data for the prediction of chemical mode of action
12:30 - 13:30	<i>Lunch break</i>
13:30 - 13:50	<b>Sergei Mangul, UCLA, USA</b> Examining lost reads to survey the microbiome and immune components of the human body across 43 human sites from 175 individuals
13:50 - 14:30	<b>Pawel P. Labaj, Boku University Vienna, Austria</b> Sensitivity, specificity and reproducibility of RNA-Seq differential expression calls
14:30 - 14:50	<b>Najmeh Abiri, Lund University, Sweden</b> Unbiased Optimization of Microarray Pre-processing.
14:50 - 15:30	<b>Udo Gieraths, ETH Zurich, Switzerland</b> Genome-wide detection of intervals of genetic heterogeneity associated with complex traits
15:30 - 16:00	<i>Afternoon break</i>
16:00 - 16:20	<b>Aleksandra Gruca, Silesian University of Technology, Poland</b> New Gene Ontology term similarity measure - comparison and performance evaluation based on DNA microarray data
16:20 - 17:00	<b>Menno J. Witteveen, ETH Zurich, Switzerland</b> In silico phenotyping via co-training for improved phenotype prediction from genotype
17:00 - 17:30	Closing address and CAMDA contest awards