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24-26 April | San Francisco
www.rna-seqsummit.com

Applied RNA Seq Summit
For Drug Discovery & Development

Harness the Next Generation of RNA Seq to Power Drug Discovery, Biomarker & Clinical Applications

- Overcome Analytical & Bioinformatics challenges in your RNA Seq Computational Pipeline to Optimize Your Drug Discovery, Biomarker Validation & Clinical Development
- Uncover the Key Information Within the Transcriptome By Harnessing the Power of Single-Cell Sequencing

Expert Speakers Including:

Thomas Wu
Principal Scientist, Bioinformatics & Computational Biology
Genentech

Bin Tian
Professor & Director of Genome Informatics
Rutgers New Jersey Medical School

Tae Lee
Scientist
GSK

Jin Jen
Co-Director, Genome Analysis Core
Mayo Clinic

Paul Kayne
Director, Genomics
Bristol-Myers Squibb

Aparna Bhaduri
Scientist
UCSF

Hosting Partner: QIAGEN

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Spotlight Partner: CELLECTA

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Welcome back to the 6th RNA Seq Summit 2018

Applied RNA Seq for Drug Discovery & Development 2018 returns dedicated to helping you overcome the bioinformatics and computational challenges in RNA sequencing to power your application of the technology in your drug discovery, biomarker validation and in your clinical applications.

Learn & network with the leaders utilizing the next generation of single cell RNA sequencing to fine tune your knowledge of the transcriptome and unlock the information within.

This year's agenda has been designed specifically for the RNA-Seq community by fore-thinkers in the industry with a greater focus on single-cell RNA-Seq, bioinformatics approaches and the clinical applications of RNA-Seq.

What Hanson Wade's attendees have said about our meetings

"Great discussions with a key high profile researchers on potential collaboration"

Roche, past attendee, RNA Seq Summit 2017

"Great informative conference"

Biogen, past attendee, RNA Seq Summit 2017

5 Key Takeaways from the RNA Seq Summit this year

1.
Discover how **BMS** are carrying out integrated analysis by co-extraction of RNA, DNA and protein from FFPE Tumour samples.

2.
Learn how **GSK** are leveraging Single Cell RNA-Seq as a rapid and comprehensive method for target validation and for disease understanding to help forward your drug discovery

3.
Understand how **Genentech** are overcoming the longstanding challenge that is RNA-Seq analysis of aligning to either a transcriptome or a genome by utilizing the transcriptome as a guide in performing genomic alignment

4.
Discover how **The Mayo Clinic** is implementing RNA-Seq as a test for gene fusion identification and beyond RNA-Seq

5.
Learn how the **UCSC Genome Browser** is optimizing Data Visualization in RNA-Seq

Your Expert Speakers

Thomas Wu
Principal Scientist, Bioinformatics & Computational Biology
Genentech

Bin Tian
Professor & Director of Genome Informatics
Rutgers New Jersey Medical School

Tae Lee
Scientist
GSK

Jin Jen
Co-Director, Genome Analysis Core
Mayo Clinic

Paul Kayne
Director, Genomics
Bristol-Myers Squibb

Aparna Bhaduri
Scientist
UCSF

Timothy Mercer
Principal
Garvan Institute of Medical Research

Piotr Mieczkowski,
Research Associate Professor, Director of High Throughput Sequencing Facility
UNC

Rob Currie
CTO
UCSC Genomics Institute

Eric Klee
Associate Professor
Mayo Clinic

Joost Groot
Computational Biology Scientist
Biogen

Robert Kuhn
Associate Director
Genome Browser UCSC

Christopher Vollmers
Assistant Professor, Biomolecular Engineering
UCSC

Paul Diehl
COO
Cellecta

Jean-Noel Billaud
Senior Principal Scientist
QIAGEN

Samuel Rulli
Global Product Manager
Qiagen

Speaker to be confirmed
Biorad

Jun Yin
Scientist, Computational Biology
Amgen

Conference Day One | Wednesday, April 25th 2018

8.00 Registration

9.00 Chairperson's Opening Remarks

Moving RNA-Seq Into The Clinic

Jin Jen
Co-Director, Genome Analysis Core
The Mayo Clinic

9.10 RNA-Seq as a CLIA Test for Gene Fusion Identification and Beyond
- Current clinical needs for an NGS based whole transcriptome test
- Critical elements required to develop a CLIA test for RNA-Seq
- Novel discoveries and new applications using RNA-Seq in clinical settings

9.40 Presentation in Collaboration with Qiagen: Presentation details TBC

Bin Tian
Professor & Director of Genome Informatics
Rutgers New Jersey Medical School

10.10 RNA Sequencing From the 3' end: Methods and Implications
- Review of methods to sequence RNA from the 3' end
- Diversity of 3' end of RNA for biomedical and clinical research
- Data analysis of 3' end diversity using RNA-Seq and ScRNA-Seq

10.40 Speed Networking

11.10 Morning Refreshments

Piotr Mieczkowski
Research Associate Professor, Director of High Throughput Sequencing Facility
UNC

11.40 Detection of Virial Transcripts or Genomes Using RNA-Seq
- Analysis of viral transcription or viral RNA genomes is becoming standard practice using RNA-Seq application
- Sensitivity of new RNA library preparation chemistries for low input, or low-quality RNA from the FFPE fixed samples is under investigation and testing
- I will introduce technologies applied to projects focused on analysis of polyomavirus mediated disease (oncogenesis) in immunocompromised patients and Dengue virus genotype testing using RNA extracted from plasma

Robert Kuhn
Associate Director
Genome Browser
UCSC

12.10 Optimising Data Visualization in RNA-Seq
- The Genome Browser allows users to load their RNA-seq data and view it in the context of other large projects that mayhave similar or complementary data

Paul Diehl
COO
Cellecta

12.40 Sensitive & Comprehensive Genome-Wide Expression Profiling Directly from Total RNA
- Gene expression analysis of target model systems is required to understand the genetic changes associated with biological responses
- We show that the combination of RT-PCR amplification with next generation deep sequencing provides a more sensitive and robust approach for transcriptome profiling than standard RNA-Seq
- The RT-PCR step with targeted primers enables the profiling assay to generate highly specific data, even with mouse xenograft models, directly from total RNA

12.55 Lunch

Advancing Basic Research Through Harnessing Next Generation Sequencing Techniques

Thomas Wu
Principal Scientist, Bioinformatics & Computational Biology
Genentech

13.55 Transcriptome-Guided Genomic Alignment

- A longstanding problem in RNA-Seq analysis has been whether to align to a transcriptome (useful for measuring expression) or to a genome (useful for analyzing splicing)
- We have implemented a strategy that uses the transcriptome as a guide in performing genomic alignment, addressing the needs for both expression and splicing analysis
- This strategy speeds up alignment significantly, and also improves accuracy, especially at the ends of reads

14.25 Presentation in Collaboration with Biorad: Presentation details TBC

14.55 Afternoon Refreshments & Poster Session

15.30 Interactive Roundtable Sessions

This will be an hour long interactive session dedicated to discussing the common challenges, solutions and advancements within the field, with the opportunity to learn and share from and with your colleagues on the following topics:

1. Data processing and informatics management

2. The utility of non-coding RNA in Drug Development

3. Standardizing RNA-sequencing data analysis: Is it Achievable?

4. What's necessary for clinical validation: controlling the statistical variables

5. RNA Based Modifications: Exploring a potential role in Drug Development

17.00 Chair's Closing Remarks and End of Day 1

17.10 QIAGEN Hosted Drinks Reception

Conference Day Two | Thursday, April 26th 2018

8.30 Registration

9.00 Chair's Opening Remarks

Utilising RNA-Seq to Forward Drug Discovery and Development

Paul Kayne
Director, Genomics
Bristol-Myers Squibb

9.10 Integrated Analysis of Colorectal Carcinoma by Co-Extraction of RNA, DNA and Protein From FFPE Tumor Samples

- Method development to isolate high quality mRNA, DNA, and proteins from a single FFPE sample
- Comparison of protein expression and transcript levels, mapping differential expression onto pathways
- Evaluation of RTP (RNA-to-Protein) conversion factors

Eric Klee
Associate Professor
The Mayo Clinic

9.40 RNAseq in Blood for Diagnostic Odyssey Patients

- Exome and genome DNA sequencing have provided diagnosis for 25-30% of patients with Rare and previously undiagnosed disease
- Germline RNA sequencing is proving to significantly complement DNA sequencing, providing resolution of a genetic diagnosis in many of these patients that previously had ambiguous or absent pertinent genetic findings
- We will present findings from a pilot study looking at RNA sequencing of blood to clarify splice-site variants of uncertain significance, report previously undetected structural events, and identify other cryptic splicing events that may have disease relevance.

Timothy Mercer
Principal
Garvan Institute of Medical Research

10.10 Diagnosis of Fusion Genes in Cancer using Targeted RNA Sequencing

- The utilisation of targeted RNA-Seq methods to diagnose fusion genes present in tumors

10.40 Morning Refreshments

Joost Groot
Computational Biology Scientist
Biogen

11.20 Translating Next-Generation Sequencing and Omics Technologies for Drug Discovery and Manufacturing Development

- RNA-Seq and Gene Set Analysis approaches for translation in drug discovery
- Targeted RNA-Seq for transgene QC in protein manufacturing - an application update

Jun Yin
Scientist, Computational Biology
Amgen

11.50 A Comprehensive RNA-Seq Computational Pipeline for Investigation of Gene Differential Expression and Alternative Splicing for Target Discovery and Validation

- Target oriented drug discovery strategy at Amgen
- Implementation of a RNA-Seq computational pipeline to provide comprehensive evaluation on gene expression, alternative splicing and expression/splicing QTL analysis
- Integrated genomics resources and network analysis to enable target discovery and elucidate mechanism of action

Zooming into The Untapped World Of Single Cell Sequencing: Utilising Single-Cell RNA-Seq to Forward Drug Discovery and Development

Tae Lee
Scientist
GSK

12.20 Leveraging Single Cell RNA-Seq in Target Validation and Disease Understanding

- Single cell RNA sequencing can serve as a rapid and comprehensive method for target validation and for disease understanding in drug discovery
- For target validation, we have studied gene functions directly in a heterogenous pool of genome-edited cells via single cell RNA sequencing
- To combat the drastic differences in response between cell types within a patient and between patients; we have performed single cell RNA sequencing in murine tumor models to profile the immune composition and to analyze drug responses in individual cell types

12.50 Lunch and Networking

 **Aparna Bhaduri** Scientist **UCSF**	**13.50 Using Single-Cell RNA Sequencing to Understand Brain Development** • We are using single cell RNA sequencing to atlas the developing brain • Using network analysis we can identify key developmental trajectories • These analyses illuminate crucial early distinctions that lay the foundation for later brain area development
 **Christopher Vollmers** Assistant Professor, Biomolecular Engineering **UCSC**	**14.20 Using Nanopore Technology to Improve Single Cell RNA-Seq** • Recent advances in molecular biology protocols and sequencing technology have made it possible to analyze the entire transcriptomes of single cells • Applying this single cell RNAseq technology to B and T cells has the potential to uncover the true diversity of the adaptive immune system • We have implemented both library preparation protocols and computational tools to use Oxford Nanopore Technology sequencing for the analysis of single cells transcriptomes. This has allowed us to identify high diversity among B cell surface receptor isoforms that Illumina sequencing failed to resolve.
	14.50 Chair's Closing Remarks
	15.00 Close of the RNA Seq Summit 2018

"As a result of the meeting we currently are involved in active negotiations with three companies we met there and are in question-answering stage with others. Almost too much interest for us to handle!"

Washington University School of Medicine

Post-Conference Workshop Day | 24th April 2018

Workshop A

Understanding Innate Resistance to Anti-PD-1 Therapy in Melanoma Through Transcriptomics

9:00am – 12:00pm

Immunotherapy consisting of blocking immune checkpoints, such as PD-1, has shown promise in treating melanoma. However, innate and acquired resistance to anti-PD-1 therapy often results in recurrence after initial successful treatment leading to advanced Metastatic melanoma.

This workshop will include in-depth coverage of the bioinformatics solutions from QIAGEN used to analyze and interpret whole transcriptome and targeted RNA sequencing results from pretreatment mRNAs of patients with advanced metastatic melanoma and with respect to their subsequent immunotherapy treatment outcomes. We will show how to optimize the transcriptome data and will provide highlights into the biological signatures that determine non-responder versus responder status using Ingenuity Pathway Analysis (IPA).

Workshop Leader

Dr. Jean-Noel Billaud, Senior Principal Scientist, **QIAGEN**

Workshop Leader

Dr. Samuel Rulli, Global Product Manager, **QIAGEN**

Workshop B

RNA-Seq data in the UCSC Genome Browser - New Display Modes

13:00pm – 16:00pm

The workshop will be a hands-on demonstration of the UCSC Genome Browser, a widely used visualization tool that offers myriad resident datasets to aid in the interpretation of your own uploaded data. Exon-only display mode allows narrowing the view to show only the relevant parts of the genome.

A preview of a soon-to-be released feature that allow users to group datasets into composite tracks that can be configured together, subtracted or added to each other, and displayed as “transparent overlay” -- together on the same axes. Data can be combined across multiple data sources, from user-uploaded private data, track data hubs all over the internet and from UCSC.

In this workshop you will learn:

- Learn some useful navigation features of the Genome Browser, including exon-only display.
- Upload RNA-seq data to the UCSC Genome Browser and visualize in the context of UCSC-resident data such as GTEx.
- Configure data tracks from multiple sources for co-visualization.
- Display sum and difference datasets by subtracting controls from experimental in real time on-screen.

Workshop Leader

Robert Kuhn, Associate Director, **Genome Browser UCSC**

Robert Kuhn received his PhD at the University of California, Santa Barbara in Biochemistry and Molecular Biology, where he studied the centromeres of yeast. Following a postdoctoral at UC Berkeley/USDA Plant Gene Expression Center, he taught biochemistry, molecular biology and genetics at UC Santa Cruz. He joined the UCSC Genome Browser project in 2003, where he is now Associate Director, helping bring the fruits of the Human (and other) Genome Project(s) to scientists worldwide

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www.cellecta.com

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1. Discover emerging trends beyond single cell sequencing and how they are being applied to drug development, research and clinic environments
2. Evaluate and validate analytical tools being utilized for enhanced transcriptome data interpretation in both basic research and clinical applications
3. Engage in debate with bioinformaticians and biologists to streamline the RNA-Seq process from the bench to the computer

Team Discounts*

- **15% discount – 3 delegates**
- **20% discount – 4 delegates**
- **25% discount – 6 or more delegates**

Please note that discounts are only valid when three or more delegates from one company book and pay at the same time.
Contact: register@hansonwade.com

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