ROCKY 2022

Bioinformatics Conference

20th Anniversary

ROCKY MOUNTAIN BIOINFORMATICS CONFERENCE

DECEMBER 8 TO 10, 2022

VIEWLINE RESORT SNOWMASS,
SNOWMASS VILLAGE
COLORADO

iSCB
INTERNATIONAL SOCIETY FOR COMPUTATIONAL BIOLOGY
OFFICIAL CONFERENCE

Conference Chair
Lawrence Hunter, PhD
University of Colorado
Anschutz Medical Campus

Welcome to the 20th Rocky Mountain Bioinformatics Conference.

We are excited about this big anniversary year and have put together a program that reflects both 20 years of Rocky meetings and the 20th anniversary of the University of Colorado's Computational Bioscience Program, which was the genesis of this conference. Over the last 20 years, it has been my privilege to see the blossoming of many successful careers in biomedical informatics that were launched here. We have a few special moments where we will reflect on our history and look forward to our future. Please feel free to offer your own reminiscences and future hopes during those events.

We hope that you enjoy the scientific program as well and find the meeting a productive opportunity to meet researchers, students and industrial users of bioinformatics technology. We are grateful for your interest in the meeting. We are also grateful for the support of our sponsors.

We want to thank and acknowledge the support of our major sponsors over the years. Kirk Jordan of IBM has been a tireless champion of this meeting, and is now enjoying a happy retirement. We are grateful to Larry Gold and SomaLogic who have also been enthusiastic supporters. We are so fortunate to have. It is only with the help of these sponsors that we can make this meeting as affordable as it is. Thank you from the bottom of my heart. Please seek out attendees from all the sponsoring organizations and let them know that their participation is important to you!

Finally, I want to thank my partner in organizing for the last 20 years, Stephanie Hagstrom. She has taken care of everything organizational from the largest decisions to the smallest details. Her skills in insulating me and the rest of us from all the headaches and tough choices that putting on such a meeting entails have made the last 20 years wonderfully enjoyable. We all owe her a huge debt of gratitude. Thank you also to the many students and staff members who have helped in the organization and operations of the meeting.

We hope you enjoy the science, the people, and the spectacular environment of the Rocky Mountains. Happy 20th anniversary to all!

Larry Hunter
Conference Chair

20th
ROCKY 2022
Bionformatics Conference
Anniversary

See Full detailed schedule, keynote and oral presentation abstracts and links to the Poster Abstracts by logging into the Sched.com Application here: https://rocky2022.sched.com/

GENERAL INFORMATION

Registration Hours

THURSDAY, DECEMBER 8	**8:00 AM TO 5:00 PM**
FRIDAY, DECEMBER 9	**8:00 AM TO 5:00 PM**
SATURDAY, DECEMBER 10	**8:00 AM TO 11:00 AM**

Schedule and Information

The most up-to-date Rocky 2022 schedule and information are posted in the online "SCHED" App. All pre-registered Rocky attendees have been added to the App. Please log in at this link here https://rocky2022.sched.com and update your profile information.

Communications App

We are using the SLACK app for Rocky2022 announcements. If you have joined already, please see the top of the "General" channel for 'pinned' announcements and for instructions on how to use SLACK. If you have not already joined, please send a request to 'rocky@iscb.org' and we will send you an invitation.

Ski Lift Tickets

Lift tickets may be used from Thursday, Dec. 1 to Sunday, Dec. 15. You may pick up your pre-ordered lift tickets at the Rocky Registration desk during all open registration desk hours. Additional tickets may be available for purchase at the desk on a first-come basis.

Every lift ticket is loaded with Mountain Advantages, which entitles you to discounts at select Aspen Snowmass locations, such as Four Mountain Sports, Ski and Snowboard Schools, and select on-mountain restaurants. You must present the group lift ticket to receive discounts.

CAUTION, PLEASE READ: Please take a picture of your lift ticket showing the ticket(s) identifier (ASP#). A ticket cannot be replaced without this ASP#.

If you purchased multiple lift tickets, please only place one ticket in your pocket per day. If you put more than one ticket in your pocket you will risk activating all of them at the lift gates on the same day rendering them void for use on the following days.

High Altitude Sickness

Aspen/Snowmass are 9,100 feet above sea level and altitude sickness is something that visitors to Colorado commonly experience. Read tips for helping ease altitude sickness www.aspenchamber.org/blog/tips-getting-adjusted-to-altitude

Hydrate: You need to drink twice the amount of water here as you would at home.

Help Desk

If you need any assistance, please check with the Rocky team at the registration desk during published hours or post your question on the SLACK channel "help desk" or email 'rocky@iscb.org' and we will respond as soon as possible.

We are aware there may be some attending Rocky without sleeping accommodations at the Viewline hotel. For those attendees, we have a secure room available to store personal items while attending the Rocky conference. Please inquire at the Rocky registration desk during registration hours.

Thank you for attending Rocky 2022.

AGENDA AT-A-GLANCE

All sessions are in the Snowmass Conference Center - outside and next to the Viewline Resort

WEDNESDAY – DECEMBER 7, 2022

4:00 PM - 6:00 PM	**REGISTRATION**

THURSDAY – DECEMBER 8, 2022

08:00 AM - 05:00 PM	**REGISTRATION**
08:00 AM - 09:00 AM	**BREAKFAST**
09:00 AM - 09:15 AM	**OPENING SESSION**
09:15 AM - 10:00 AM	**KEYNOTE 1 • ZHIYONG LU, PhD** **PubTator: 10 Years of Growth and Innovation**
10:00 AM - 10:10 AM	**OP 01**
10:10 AM - 10:20 AM	**OP 02**
10:20 AM - 10:30 AM	**OP 03**
10:30 AM - 10:40 AM	**OP 04**
10:40 AM - 11:00 AM	**BREAK**
11:00 AM - 11:10 AM	**OP 05**
11:10 AM - 11:20 AM	**OP 06**
11:20 AM - 11:30 AM	**OP 07**
11:30 AM - 11:40 AM	**OP 08**
11:40 AM - 11:50 AM	**OP 09**
11:50 AM - 04:00 PM	**SKI BREAK**
04:00 PM - 04:30 PM	**KEYNOTE 2 • BLAKE WILLIAMS** **Topic Modeling: Unsupervised Learning and Drivers of the Human Serum Proteome**
04:30 PM - 04:40 PM	**OP 10**
04:40 PM - 04:50 PM	**OP 11**
04:50 PM - 05:00 PM	**OP 12**
05:00 PM - 05:10 PM	**OP 13**
05:10 PM - 05:30 PM	**BREAK**
05:30 PM - 05:40 PM	**OP 14**
05:40 PM - 05:50 PM	**OP 15**
05:50 PM - 06:00 PM	**OP 16**
06:00 PM - 06:10 PM	**OP 17**
06:30 PM - 09:00 PM	**IL POGGIO RESTAURANT** • *57 Elbert Ln, Snowmass Village* *Tickets are required for entry. Please see registration to purchase tickets.*

See Full detailed schedule, keynote and oral presentation abstracts and links to the Poster Abstracts by logging into the Sched.com Application here: https://rocky2022.sched.com/

AGENDA AT-A-GLANCE

All sessions are in the Snowmass Conference Center - outside and next to the Viewline Resort

FRIDAY – DECEMBER 9, 2022

08:00 AM - 05:00 PM	**REGISTRATION**
08:00 AM - 09:00 AM	**BREAKFAST**
09:00 AM - 09:45 AM	**KEYNOTE 3 • DAVID NICHOLSON, PhD** **Changing Word Meanings in Biomedical Literature Reveal Pandemics and New Technologies**
09:45 AM - 09:55 AM	**OP 18**
09:55 AM - 10:05 AM	**OP 19**
10:05 AM - 10:15 AM	**OP 20**
10:15 AM - 10:25 AM	**OP 21**
10:25 AM - 10:45 AM	**BREAK**
10:45 AM - 10:55 AM	**OP 22**
10:55 AM - 11:05 AM	**OP 23**
11:05 AM - 11:15 AM	**OP 24**
11:15 AM - 11:25 AM	**OP 25**
11:25 AM - 11:35 AM	**OP 26**
11:35 AM - 04:00 PM	**SKI BREAK**
04:00 PM - 04:30 PM	**KEYNOTE 4 • ZHONGMING ZHAO, PhD** **Deep Generative Neural Network for Accurate Drug Response Prediction**
04:30 PM - 04:40 PM	**OP 27**
04:40 PM - 04:50 PM	**OP 28**
04:50 PM - 05:00 PM	**OP 29**
05:00 PM - 05:10 PM	**OP 30**
05:10 PM - 05:30 PM	**BREAK**
05:30 PM - 05:40 PM	**OP 31**
05:40 PM - 05:50 PM	**OP 32**
05:50 PM - 06:00 PM	**OP 33**
06:00 PM - 06:10 PM	**OP 34**
06:10 PM - 06:30 PM	**20 YEAR CELEBRATION**
06:30 PM - 08:30 PM	**POSTER SESSION**

See Full detailed schedule, keynote and oral presentation abstracts and links to the Poster Abstracts by logging into the Sched.com Application here: https://rocky2022.sched.com/

AGENDA AT-A-GLANCE

All sessions are in the Snowmass Conference Center - outside and next to the Viewline Resort

---

SATURDAY – DECEMBER 10, 2022

08:00 AM - 11:00 AM	**REGISTRATION**
08:00 AM - 09:00 AM	**BREAKFAST**
09:00 AM - 09:30 AM	**KEYNOTE 5 • TIFFANY J. CALLAHAN, PhD** **The Future of Translational Informatics: Leveraging Knowledge to Enable Causal Explanations at Scale**
09:30 AM - 09:40 AM	**OP 35**
09:40 AM - 09:50 AM	**OP 36**
09:50 AM - 10:00 AM	**OP 37**
10:00 AM - 10:10 AM	**OP 38**
10:10 AM - 10:30 AM	**BREAK**
10:30 AM - 10:40 AM	**OP 39**
10:40 AM - 10:50 AM	**OP 40**
10:50 AM - 11:00 AM	**OP 41**
11:00 AM - 11:45 AM	**KEYNOTE 6 • ROBYN L. BALL, PhD** **Traversing the Mouse-human Interface: An Integrative Bioinformatics Approach to Identify Preclinical Models and Identify Genes and Variants with Shared Roles in Complex Disease**
11:45 AM - 12:00 PM	**CLOSING RAFFLE AND BEST POSTER AWARDS**

See Full detailed schedule, keynote and oral presentation abstracts and links to the Poster Abstracts by logging into the Sched.com Application here: https://rocky2022.sched.com/

KEYNOTE SPEAKERS

ROBYN L. BALL, PhD

Computational Scientist, The Jackson Laboratory

Traversing the Mouse-human Interface: An Integrative Bioinformatics Approach to Identify Preclinical Models and Identify Genes and Variants with Shared Roles in Complex Disease

TIFFANY J. CALLAHAN, PhD

Postdoctoral Research Fellow, Department of Biomedical Informatics, Columbia University

The Future of Translational Informatics: Leveraging Knowledge to Enable Causal Explanations at Scale

ZHIYONG LU, PhD

FACMI Deputy Director
Literature Search, National Center for Biotechnology (NCBI)

PubTator: 10 Years of Growth and Innovation

DAVID NICHOLSON, PhD

Data Scientist, Digital Science & Research Solutions Ltd.

Changing Word Meanings in Biomedical Literature Reveal Pandemics and New Technologies

BLAKE WILLIAMS

Bioinformatics Analyst III, SomaLogic

Topic Modeling: Unsupervised Learning and Drivers of the Human Serum Proteome

ZHONGMING ZHAO, PhD

Professor and Chair, School of Biomedical Informatics and School of Public Health, University of Texas Health Science Center at Houston

Deep Generative Neural Network for Accurate Drug Response Prediction

See Full detailed schedule, keynote and oral presentation abstracts and links to the Poster Abstracts by logging into the Sched.com Application here: https://rocky2022.sched.com/

ORAL PRESENTATION LIST

OP-01 **Goals, Roles, and Watering holes: A playbook for the leading edge of team science** • *Presenting Author: Julie McMurry, University of Colorado, Anschutz Medical Campus*

OP-02 **Realizing the potential of secure and decentralized harmonization of clinical and genomics data for precision medicine** • *Presenting Author: Ahmed Elhussein, Columbia University*

OP-03 **iAtlas: an Open-Source, Interactive Portal and Platform for Immuno-Oncology Research** • *Presenting Author: James Eddy, Sage Bionetworks*

OP-04 **Tissue-adjusted pathway analysis of cancer** • *Presenting Author: Rob Frost, Dartmouth College*

OP-05 **Alignment-free phylogenetic method unveils the pan-mammalian regulatory motif adaptations underlying extended lifespan** • *Presenting Author: Elysia Saputra, University of Pittsburgh*

OP-06 **A robust computational framework to benchmark spatiotemporal trajectory association analysis in single-cell spatial transcriptomics** • *Presenting Author: Fan Zhang, University of Colorado School of Medicine*

OP-07 **LochNESS: a novel statistic to quantify sample specific effects in single-cell data based on k-NN graphs** • *Presenting Author: Xingfan Huang, University of Washington*

OP-08 **C3PO: Combined polygenic protein prediction in oncology** • *Presenting Author: Matthew Bailey, Brigham Young University*

OP-09 **Sex specific genetic architecture of childhood asthma** • *Presenting Author: Amelie Fritz, Technical University Denmark*

OP-10 **An efficient not-only-linear correlation coefficient based on machine learning** • *Presenting Author: Milton Pividori, University of Pennsylvania*

OP-11 **Survival-based Gene Set Enrichment Analysis** • *Presenting Author: Jeffrey Thompson, University of Kansas Medical Center*

OP-12 **How do you build a data commons? A case study for Down Syndrome** • *Presenting Author: Monica Munoz-Torres, University of Colorado Anschutz Medical Campus*

OP-13 **Leveraging edge computing for workflow tracking and management to improve academic and healthcare security, efficiency, and auditability** • *Presenting Author: Caylin Hickey, University of Kentucky*

OP-14 **Systematic study of human diseases using graph signal processing on gene expression datasets** • *Presenting Author: Renming Liu, Michigan State University*

OP-15 **GeneplexusZoo: Utilizing network information across species to improve supervised gene classification** • *Presenting Author: Christopher Mancuso, University of Colorado-Denver Anschutz Medical Campus*

OP-16 **Privacy-preserving prediction of phenotypes from genotypes using homomorphic encryption** • *Presenting Author: Annie Choi, Columbia University*

OP-17 **Leveraging public transcriptome data with ML to infer pan-body age- and sex-specific molecular phenomena** • *Presenting Author: Kayla Johnson, Michigan State University*

See Full detailed schedule, keynote and oral presentation abstracts and links to the Poster Abstracts by logging into the Sched.com Application here: https://rocky2022.sched.com/

ORAL PRESENTATION LIST

OP-18 **A comprehensive knowledgebase of known and predicted genetic variants associated with COVID-19 severity** • *Presenting Author: Meltem Ece Kars, Icahn School of Medicine at Mount Sinai*

OP-19 **Abyssinian to Zebu: Classifying Animal Breeds with the Vertebrate Breed Ontology (VBO)** • *Presenting Author: Kathleen Mullen, University of Colorado Anschutz Medical Campus*

OP-20 **Binding sites prediction of proteins** • *Presenting Author: Zhong-Ru Xie, University of Georgia*

OP-21 **On Language Models, Medicine, and Factuality** • *Presenting Author: Sagi Shaier, University of Colorado, Boulder*

OP-22 **Metabolites and Markers of Endothelial Dysfunction Help Understand Sepsis Mortality Risk** • *Presenting Author: Sarah McGarrity, Brigham and Women's Hospital and Harvard Medical School*

OP-23 **A comprehensive analysis of the reusability of public omics data across 2.8 million research publications** • *Presenting Author: Mohammad Vahed, University of Southern California*

OP-24 **Creating an Ignorance-Base: Exploring known unknowns in the scientific literature** • *Presenting Author: Mayla Boguslav, University of Colorado Anschutz Medical Campus*

OP-25 **Identify genes associated with gastrointestinal tract adaptation using Evolink** • *Presenting Author: Xiaofang Jiang, NIH/NLM*

OP-26 **Development and validation of an explainable machine learning-based prediction model for drug-food constituent interactions from chemical structures** • *Presenting Author: Quang Hien Kha, Taipei Medical University*

OP-27 **Metrics and software for assessing microbiota engraftment following Fecal Microbiota Transplant** • *Presenting Author: Chloe Herman, Northern Arizona University*

OP-28 **Exploration of 5'UTR Variation in a Clinical Workflow Evaluating Undiagnosed Rare Disease Patients** • *Presenting Author: Eric Klee, Mayo Clinic*

OP-29 **An ML framework for precision medicine: from patient-specific gene networks to translational animal models** • *Presenting Author: Hao Yuan, Michigan State University*

OP-30 **Identifying alterations associated with aggressiveness in prostate cancer molecular subtypes** • *Presenting Author: Michael Orman, University of Colorado*

OP-31 **Rigorous benchmarking of T cell receptor repertoire profiling methods for cancer RNA sequencing** • *Presenting Author: Serghei Mangul, University of Southern California*

OP-32 **How tRNA pools and ramp sequences regulate protein and transcript levels associated with disease** • *Presenting Author: Justin Miller, University of Kentucky*

OP-33 **Finding Long COVID: Topic modeling of post-infection trends in patient EHR profiles** • *Presenting Author: Shawn ONeil, University of Colorado*

See Full detailed schedule, keynote and oral presentation abstracts and links to the Poster Abstracts by logging into the Sched.com Application here: https://rocky2022.sched.com/

ORAL PRESENTATION LIST

OP-34 **Language representation models based on metadata identify relevant datasets in Gene Expression Omnibus** • *Presenting Author: Grace Salmons, Brigham Young University*

OP-35 **Using knowledge graphs to infer gene expression in plants** • *Presenting Author: Anne Thessen, University of Colorado Anschutz*

OP-36 **Fast, flexible and safe sequence assembly for RNA and beyond** • *Presenting Author: Brendan Mumey, Montana State University*

OP-37 **Visualization and Exploration of Survival Prediction Model Explanations** • *Presenting Author: Cartsen Görg, Colorado School of Public Health*

OP-38 **Double-strand DNA breaks: Quantitative mapping and computational modeling of mechanisms.** • *Presenting Author: Maga Rowicka, University of Texas Medical Branch*

OP-39 **Novel enzyme families among artificial intelligence-based protein structure models** • *Presenting Author: Krzysztof Pawlowski, University of Texas Southwestern Medical Center*

OP-40 **The Mondo Disease Ontology: A Standardized Disease Terminology of Human and Animal Diseases** • *Presenting Author: Sabrina Toro, University of Colorado, Anschutz Medical Campus*

OP-41 **The ability to classify patients based on gene-expression data varies by algorithm and performance metric** • *Presenting Author: Stephen Piccolo, Brigham Young University*

POSTER PRESENTATIONS

LOCATION

Snowmass Convention Center Ballroom

POSTER SESSION HOURS

The Poster Session with authors present will be on Friday evening. Poster Presenters must be available for presentation during the scheduled poster session.

POSTER NUMBER ASSIGNMENTS

Posters are assigned odd and even numbers and will present during those assigned times.

SCHEDULE

Friday, December 3

12:00 pm – 6:00 pm	**SET UP POSTERS**

Friday, December 3

6:30 pm – 8:30 pm	**POSTER SESSION**
6:30 pm – 7:30 pm	**Authors with Even Number Posters Present**
7:30 pm – 8:30 pm	**Authors with Odd Number Posters Present**
8:30 pm	**Authors please remove posters from boards at end of this session**

POSTER PRESENTATION LIST

P01 **Effects of Rurality on Cancer Risk Factors Using Multiscale-Geographical-Weighted-Regression-Model** • *Presenting Author: Jonah Amponsah, University of Kansas Medical Center*

P02 **Highly accurate merging of overlapping paired-end next-generation sequencing reads** • *Presenting Author: Shofi Andari, Iowa State University*

P03 **Development of SpliceCluster: A New Tool to Discriminate Complexity in Similar Immune Cell Subsets in Single-Cell RNA Sequencing** • *Presenting Author: Jared Andersen, University of Utah*

P04 **A convolutional neural network based tool for predicting protein AMPylation sites from binary profile representation** • *Presenting Author: Sayed Mehedi Azim, Rutgers University*

P05 **Survival outcomes based on T-cell receptor CDR3 chemical complementarity in ovarian serous cystadenocarcinoma** • *Presenting Author: Vayda Barker, University of South Florida, Morsani College of Medicine*

P06 **Identifying Technical Variation Between Replicate Samples of 16S rRNA Sequencing Data** • *Presenting Author: Angela Sofia Burkhart Colorado, University of Colorado at Anschutz Medical Campus*

See Full detailed schedule, keynote and oral presentation abstracts and links to the Poster Abstracts by logging into the Sched.com Application here: https://rocky2022.sched.com/

POSTER PRESENTATION LIST

P07 Using Huffman codes and n-grams to compress tabular data • *Presenting Author: Maren Callaway, Brigham Young University*

P08 Metformin is Associated with Reduced COVID-19 Severity in Patients with Prediabetes • *Presenting Author: Lauren Chan, Oregon State University*

P09 Privacy-preserving prediction of phenotypes from genotypes using homomorphic encryption • *Presenting Author: Annie Choi, Columbia University*

P10 Easy NanoString Gene Expression Analysis with the NanoTube • *Presenting Author: Caleb Class, Butler University*

P11 ExtCodonIslands: a tool for identifying and visualizing regions vulnerable to deleterious synonymous codon mutations • *Presenting Author: Matthew Cloward, Brigham Young University*

P12 REVEALING POTENTIAL MECHANISMS FOR EHLERS DANLOS SYNDROME USING KNOWLEDGE GRAPHS • *Presenting Author: Katherina Cortes, University of Colorado Anschutz*

P13 Domain generalization for prediction from pan-cancer gene expression • *Presenting Author: Jake Crawford, University of Pennsylvania*

P14 Inference of bacterial pathogen load in US rivers from landscape-scale shotgun metagenomic sequencing • *Presenting Author: Alyssa Cruz, University of Colorado Denver*

P15 Equine tissue atlas of small non-coding RNA expression • *Presenting Author: Jonah Cullen, University of Minnesota*

P16 Non-model de novo assemblies: the complexities of sequencing and assembling a marine invertebrate genome and transcriptome • *Presenting Author: Benjamin Daniels, California Polytechnic State University*

P17 Prediction of gene expression using interpretable chromatin accessibility features • *Presenting Author: Natalie Davidson, CU Anschutz*

P18 Accurately Predicting AntiCancer Peptide using an ensemble of heterogeneously Trained Classifiers • *Presenting Author: Iman Dehzangi, Rutgers University*

P19 PROSTIMATE: A prostate cancer-specific predictor of tumor purity • *Presenting Author: Cailin Deiter, University of Colorado*

P20 iAtlas: an Open-Source, Interactive Portal and Platform for Immuno-Oncology Research • *Presenting Author: James Eddy, Sage Bionetworks*

P21 Realizing the potential of secure and decentralized harmonization of clinical and genomics data for precision medicine • *Presenting Author: Ahmed Elhussein, Columbia University*

P22 Prioritizing mechanistic targets in chemotherapy resistant muscle-invasive bladder cancer • *Presenting Author: Lily Elizabeth Feldman, University of Colorado Anschutz Medical Campus*

P23 Disentangling Information Flow in the Visual System • *Presenting Author: Nicholas Garcia, University of Colorado*

P24 Integrating Molecular Data into Knowledge Graph Embeddings to Predict Adverse Drug Reactions in Trisomy 21 • *Presenting Author: Lucas Gillenwater, University of Colorado Anschutz Medical Campus*

See Full detailed schedule, keynote and oral presentation abstracts and links to the Poster Abstracts by logging into the Sched.com Application here: https://rocky2022.sched.com/

POSTER PRESENTATION LIST

P25 Kable: A tool for bacterial genome comparison with metadata • *Presenting Author: Jo Hendrix, University of Colorado at Anschutz*

P26 Deconvolution of cancer data: best practices for bulk and single-cell RNA-seq • *Presenting Author: Ariel Hippen, University of Pennsylvania*

P27 Tradeoffs between predictive performance and execution for multiple classifier systems • *Presenting Author: Eliza Homer, Brigham Young University*

P28 Interactive web-based exploration of single-cell atlases of millions of cells • *Presenting Author: Xingfan Huang, University of Washington*

P29 Identify genes associated with gastrointestinal tract adaptation using Evolink • *Presenting Author: Xiaofang Jiang, NIH/NLM*

P30 Leveraging public transcriptome data with ML to infer pan-body age- and sex-specific molecular phenomena • *Presenting Author: Kayla Johnson, Michigan State University*

P31 Exploring the Feasibility of Automating Biocuration for Neuropharmacology • *Presenting Author: Indika Kahanda, University of North Florida*

P32 Do Custom Regional DNA Barcode Databases Lead to More Efficient Specimen ID? • *Presenting Author: Michael Kerr, Brigham Young University*

P33 OrbiSeq-L: an Aid to Diagnosis to Confirm a Positive Low Dose CT Scan • *Presenting Author: Nicholas Kinney, Orbit Genomics*

P34 Exploration of 5'UTR Variation in a Clinical Workflow Evaluating Undiagnosed Rare Disease Patients • *Presenting Author: Eric Klee, Mayo Clinic*

P35 Discover Higher-order Relationship between Molecular Profiles in COPD Patients with Novel Multi-omics Network Inference Pipeline for Hypergraph • *Presenting Author: Weixuan Liu, University of Colorado Anschutz Medical Campus*

P36 Systematic study of human diseases using graph signal processing on gene expression datasets • *Presenting Author: Renming Liu, Michigan State University*

P37 GeneplexusZoo: Utilizing network information across species to improve supervised gene classification • *Presenting Author: Christopher Mancuso, University of Colorado-Denver Anschutz Medical Campus*

P38 Rigorous benchmarking of T cell receptor repertoire profiling methods for cancer RNA sequencing • *Presenting Author: Serghei Mangul, University of Southern California*

P39 Metabolites and Markers of Endothelial Dysfunction Help Understand Sepsis Mortality Risk • *Presenting Author: Sarah McGarrity, Brigham and Women's Hospital and Harvard Medical School*

P40 Integrative omic profiling of human pulmonary vascular cells in response to hypoxia • *Presenting Author: Sarah McGarrity, Brigham and Women's Hospital and Harvard Medical School*

P41 Goals, Roles, and Watering holes: A playbook for the leading edge of team science • *Presenting Author: Julie McMurry, University of Colorado, Anschutz Medical Campus*

P42 How tRNA pools and ramp sequences regulate protein and transcript levels associated with disease • *Presenting Author: Justin Miller, University of Kentucky*

See Full detailed schedule, keynote and oral presentation abstracts and links to the Poster Abstracts by logging into the Sched.com Application here: https://rocky2022.sched.com/

POSTER PRESENTATION LIST

P43 Abyssinian to Zebu: Classifying Animal Breeds with the Vertebrate Breed Ontology (VBO) • *Presenting Author: Kathleen Mullen, University of Colorado Anschutz Medical Campus*

P44 How do you build a data commons? A case study for Down Syndrome • *Presenting Author: Monica Munoz-Torres, University of Colorado Anschutz Medical Campus*

P45 Safety Signal Detection with Bayesian Hierarchical Models • *Presenting Author: Lisa Neums, Boehringer Ingelheim Pharmaceuticals, Inc.*

P46 Speciel: A New Tool to Identify Species-Defining SNPs and its Application in Cutthroat Trout • *Presenting Author: Alyssa Nitz, Brigham Young University*

P47 Detection of outlier methylation in rare genetic disease with novel Bioconductor package BOREALIS • *Presenting Author: Gavin Oliver, Mayo Clinic*

P48 Finding Long COVID: Topic modeling of post-infection trends in patient EHR profiles • *Presenting Author: Shawn ONeil, University of Colorado*

P49 A Comprehensive Bioinformatics Pipeline for Preparing Observational Data for Machine Learning Analysis • *Presenting Author: Alena Orlenko, Cedars Sinai Medical Center*

P50 Identifying alterations associated with aggressiveness in prostate cancer molecular subtypes • *Presenting Author: Michael Orman, University of Colorado*

P51 Evaluating the effectiveness of restoration efforts in island ecosystems via UAV obtained imagery and manual classification • *Presenting Author: Haden Penrod, Brigham Young University*

P52 An efficient not-only-linear correlation coefficient based on machine learning • *Presenting Author: Milton Pividori, University of Pennsylvania*

P53 Comparison of Liver Enzyme Models for Polygenic Risk Score • *Presenting Author: Robert Plant, Galatea Bio*

P54 A trans ancestry genomics based approach to study the interplay between the immune system, infectious type, and HLA type, ancestry and sepsis outcome • *Presenting Author: Tejasvene Ramesh, University of Southern California*

P55 Language representation models based on metadata identify relevant datasets in Gene Expression Omnibus • *Presenting Author: Grace Salmons, Brigham Young University*

P56 Using knowledge graphs to understand microbe-mediated diseases • *Presenting Author: Brook Santangelo, University of Colorado Anschutz Medical Campus*

P57 Alignment-free phylogenetic method unveils the pan-mammalian regulatory motif adaptations underlying extended lifespan • *Presenting Author: Elysia Saputra, University of Pittsburgh*

P58 SVPred: An integrated framework for structural variant discovery • *Presenting Author: Varuni Sarwal, UCLA*

P59 CytoSnake: Reproducible workflow software for processing cell morphology features fast • *Presenting Author: Erik Serrano, University of Colorado, Anschutz Medical Campus*

P60 On Language Models, Medicine, and Factuality • *Presenting Author: Sagi Shaier, University of Colorado, Boulder*

See Full detailed schedule, keynote and oral presentation abstracts and links to the Poster Abstracts by logging into the Sched.com Application here: https://rocky2022.sched.com/

POSTER PRESENTATION LIST

P61 Integrated regulatory and metabolic networks for the prioritization of therapeutic targets in the tumor microenvironment • *Presenting Author: Tiange Shi, University at Buffalo*

P62 Using Computer vision pipeline to quantify behavior in cichlids • *Presenting Author: Breanna Shi, Georgia Institute of Technology*

P63 Breast cancer patients from the Midwest region of the United States have reduced levels of short-chain fatty acid-producing gut bacteria • *Presenting Author: Rachel Shrode, Department of Informatics, University of Iowa*

P64 Methylation Site Prediction Using a Deep Convolutional Neural Network • *Presenting Author: Austin Spadaro, Rutgers University*

P65 Figures in biological journal articles are often unfriendly to people with color vision deficiencies • *Presenting Author: Harlan Stevens, Brigham Young University*

P67 Reducing underspecification in breast cancer subtyping by ranking performance on unshifted versus shifted datasets. • *Presenting Author: Ella Thomas, Cal Poly, San Luis Obispo*

P68 Survival-based Gene Set Enrichment Analysis • *Presenting Author: Jeffrey Thompson, University of Kansas Medical Center*

P69 Benchmarking image analysis pipelines to discover an NF1 genotype biomarker from Schwann cell morphology • *Presenting Author: Jenna Tomkinson, University of Colorado Anschutz Medical Campus*

P70 The Mondo Disease Ontology: A Standardized Disease Terminology of Human and Animal Diseases • *Presenting Author: Sabrina Toro, University of Colorado, Anschutz Medical Campus*

P71 A machine learning approach incorporating germline information improves genotyping of CRISPR-Cas9 gene editing events at single cell resolution • *Presenting Author: Matthew Ung, Vor Biopharma*

P72 A comprehensive analysis of the reusability of public omics data across 2.8 million research publications • *Presenting Author: Mohammad Vahed, University of Southern California*

P73 CNV assessments in Neuroblastoma: Loss of MAPT correlates with lower survival probability • *Presenting Author: Mallika Varkhedi, University of South Florida College of Medicine*

P74 Private information leakage in single-cell omics data • *Presenting Author: Conor Walker, Columbia University & New York Genome Center*

P75 Automating microbial taxonomy workflows with PHANTASM: PHylogenomic ANalyses for the TAxonomy and Systematics of Microbes • *Presenting Author: Joe Wirth, Harvey Mudd College*

P76 Ramp Sequences Affected by Single Nucleotide Polymorphisms • *Presenting Author: Joseph Wride, Brigham Young University*

P77 Chromosomal structures reveals cell-to-cell variability in single-cell Hi-C data analysis • *Presenting Author: Tianchun Xue, University of Tennessee*

P78 Comparison of differential co-expression networks • *Presenting Author: Kuranosuke Yamada, The Jackson Laboratory and Colby College*

See Full detailed schedule, keynote and oral presentation abstracts and links to the Poster Abstracts by logging into the Sched.com Application here: https://rocky2022.sched.com/

POSTER PRESENTATION LIST

P79 An ML framework for precision medicine: from patient-specific gene networks to translational animal models • *Presenting Author: Hao Yuan, Michigan State University*

P80 Exploring the Genetic Effects of Investigational Drugs that Block Anticancer Immunity in Mice • *Presenting Author: Juliana Yue, Brigham Young University*

P81 A robust computational framework to benchmark spatiotemporal trajectory association analysis in single-cell spatial transcriptomics • *Presenting Author: Fan Zhang, University of Colorado School of Medicine*

P82 Sex specific genetic architecture of childhood asthma • *Presenting Author: Amelie Fritz, Technical University Denmark*

P83 spongEffects: ceRNA modules offer patient-specific insights into the miRNA regulatory landscape • *Presenting Author: Markus Hoffmann, Technical University of Munich*

P84 Hyper-methylation of ABCG1 as an Epigenetic Biomarker in Non-small Cell Lung Cancer • *Presenting Author: Thi-Oanh Tran, Ph.D. student/ Taipei Medical University*

P85 The Metazoan Transcription Factors • *Presenting Author: Diego A Rosado-Tristani, University of Puerto Rico, Rio Piedras Campus*

P86 ClaID: a Rapid Method of Clade-Level Identification of the Multidrug Resistant Human Fungal Pathogen Candida auris • *Presenting Author: Pavitra S, The Institute of Mathematical Sciences*

P87 Network propagation deciphers the pathogenesis of inflammatory bowel disease in a patient-specific way • *Presenting Author: Dezso Modos, Quadram Institute Bioscience*

P88 Development and validation of an explainable machine learning-based prediction model for drug-food constituent interactions from chemical structures • *Presenting Author: Quang Hien Kha, Taipei Medical University*

P89 Connecting Research Results with Biomedical Ignorance-Base to Resolve Literature Knowledge Goals • *Presenting Author: Nourah Salem, University of Colorado, Anschutz Medical Campus*

Notes

CONFERENCE SPONSOR

somalogic

HTTPS://SOMALOGIC.COM

GoldLab FOUNDATION

HTTPS://GOLDLABFOUNDATION.ORG

Rocky 2022 is supported
by the Hunter Lab at the
University of Colorado
Anschutz Medical Campus

iSCB
INTERNATIONAL SOCIETY FOR
COMPUTATIONAL BIOLOGY
OFFICIAL CONFERENCE