

Digital Tools & Resources Schedule

Saturday - January 12, 2019

- 1:30pm - 3:40pm** **Digital Tools and Resources Session 1 - CALIFORNIA**
Organizer: Brian Smith-White, National Center for Biotechnology Information (NCBI/NLM/NIH)
- 1:30pm Yuxuan Yuan, University of Western Australia
 "Bionano Data Analysis on the Command Line and Genome Assembly Quality Assessment using a GUI" (C01)
- 1:50pm Joelle Amselem, URGI, INRA, Université Paris-Saclay
 "RepetDB: A Resource for Unified Transposable Element References with Classification" (C02)
- 2:10pm Kristina Gruden, National Institute of Biology,
 "DiNAR: Revealing Hidden Patterns of Plant Signalling Dynamics using Differential Network Analysis in R" (C03)
- 2:30pm Sheri Sanders, National Center for Genome Analysis Support, Pervasive Technology Institute
 "NCGAS Makes Robust Transcriptome Assembly even easier with Added Features to an Accessible *de novo* Transcriptome Assembly Workflow" (C04)
- 2:50pm Jorge Duitama, Universidad de los Andes
 "Efficient Ortholog Identification and Interactive Web-Based Whole Genome Alignment with NGSEP" (C05)
- 3:10pm John A. Hadish, Washington State University
 "GEMmaker, a Nextflow Workflow for Large Scale RNA-Seq Processing" (C06)

Monday - January 14, 2019

- 12:50pm - 3:00pm** **Digital Tools and Resources Session 2 - CALIFORNIA**
Organizer: Brian Smith-White, National Center for Biotechnology Information (NCBI/NLM/NIH)
- 12:50pm Amanda J Burridge, University of Bristol
 "CerealsDB Version 4.0 - A Review of Tools and Data for Wheat Breeders and Research Scientists" (C07)
- 1:10pm Jodi L. Humann, Washington State University
 "GenSAS v6.0: A Web-Based Platform for Structural and Functional Annotation of Model and Non-Model Organisms" (C08)
- 1:30pm Ido Bar, Griffith University
 "Shinotate: An R-Based Shiny Server for Annotation and Analysis of RNA-Seq Transcriptome Assemblies" (C09)
- 1:50pm Erin Haskell, EMBL-EBI
 "Exploring Your Data in Ensembl" (C10)
- 2:10pm Emily Grau, University of Connecticut
 "TreeGenes and CartograTree: Tools for Forest Tree Genomics" (C11)
- 2:30pm Patrick X. Zhao, Noble Research Institute
 "MtSSPdb: The *Medicago truncatula* Small Signaling Peptide Database" (C12)

Tuesday - January 15, 2019

- 10:30am - 12:40pm** **Digital Tools and Resources Session 3 - CALIFORNIA**
Organizer: Brian Smith-White, National Center for Biotechnology Information (NCBI/NLM/NIH)
- 10:30am Zhonglin Tang, Agricultural genomics Institute, CAAS
 "An Atlas of *Sus scrofa* RNA Editome in Developmental Skeletal Muscle" (C13)
- 10:45am Yannick De Oliveira, INRA
 "SHiNeMaS : A Database and its Web Interfaces dedicated to Seed Lots History, Phenotyping and Cultural Practices" (C14)
- 11:00am Xinbin Dai, Noble Research Institute
 "psRNATarget V2: A High-Performance Plant Small RNA Target Analysis Server" (C15)
- 11:15am Star Yanxin Gao, Genomic Open-Source Breeding Informatics Initiative Project
 "Integrated Genomic Selection Galaxy Analysis Pipeline and Workflows" (C16)
- 11:30am Mirella Flores-Gonzalez, Boyce Thompson Institute
 "A Tissue and Host-Specific Expression Atlas for *Citrus sinensis* and *Diaphorina citri* for Exploring the Citrusgreening Disease Complex" (C17)
- 11:45am Ben Busby, NIH/NCBI
 "GeneHummus: A Computational Pipeline to Define Gene Families and their Expression in Legumes and other Plant Species" (C18)
- 12:00pm Yaw A. Nti-Addae, Genomic Open-Source Breeding Informatics Initiative Project
 "Genomic Data Manager - a Scalable Open-Source Genomics Database for Breeding Applications" (C19)

Wednesday - January 16, 2019

- 10:30am - 12:40pm** **Digital Tools and Resources Session 4 - CALIFORNIA**
Organizer: Brian Smith-White, National Center for Biotechnology Information (NCBI/NLM/NIH)
- 10:30am Dong-Ha Oh, Louisiana State University
 "CLfinder-OrthNet: Encoding Evolutionary History of a Gene Locus as Network Topology" (C20)
- 10:45am Xiangchao Gan, Max Planck Institute for Plant Breeding Research
 "Irisas: A Framework for Genome Wide Association with Structure Variants in *Arabidopsis thaliana* and *Drosophila melanogaster*" (C21)
- 11:00am Bhavya Papudeshi, Indiana University
 "Compute Resources Available to the Research Community for Microbiome Analysis" (C22)
- 11:15am Chunpeng James Chen, Washington State University
 "iPat: A Genomics Analysis Tool for Everyone" (C23)
- 11:30am Anthony Greenberg, Bayesic Research
 "Methods for Robust Bayesian Analyses of Complex Genetic Experiments" (C24)
- 11:45am Sumaira Zaman, University of Connecticut
 "OrthoQuery: A Tripal Database Module to Assess and Visualize Gene Family Evolution" (C25)
- 12:00pm Samuel Taler Westreich, DNAnexus
 "Exploring a Landscape of Genetic Variation in Virtual Reality" (C26)