

BOSC 2017 Posters

Poster	Authors	Title
A-107	Ismail Moghul, Suresh Hewapathirana, Nazrath Nawaz, Anisatu Rashid, Marian Priebe, Bruno Vieira, Fabrizio Smeraldi and Conrad Bessant	GeoDiver: Differential Gene Expression Analysis & Gene-Set Analysis for GEO Datasets
A-108	Alberto Riva, Richard L Bennett and Jonathan D Licht	DAMON, an open source framework for reliable and reproducible analysis pipelines
A-109	Uros Sipetic	Workflow for processing standard bioinformatics formats with SciClone to infer tumor heterogeneity
A-110	Nikola Tesic and Marko Kalinic	Microsatellite instability profiling of TCGA colorectal adenocarcinomas using a Common Workflow Language pipeline
A-111	Monica-Andreea Drăgan, Ismail Moghul, Anurag Priyam, Claudio Bustos and Yannick Wurm	GeneValidator: identify problems with protein-coding gene predictions
A-112	Sanja Mijalkovic, Milan Domazet	Somatic Variant Calling Benchmarking
A-114	Wei Wang, Yichao Zhou, Patrick Tan, Vincent Kyi, Xinxin Huang, Chelsea Ju, Justin Wood and Peipei Ping	Aztec: Automated Biomedical Tool Index with Improved Information Retrieval System
A-115	Malvika Sharan, Toby Hodges, Julia Ritzerfeld and Georg Zeller	Building a local bioinformatics community: challenges and efforts
A-116	Aleksandra Gruca	CHARME - harmonising standardisation strategies to increase efficiency and competitiveness of European life-science research
A-117	Vincenzo Belcastro, Stephane Cano, Diego Marescotti, Carine Poussin, Ignacio Gonzales-Suarez, Florian Martin, Filipe Bonjour, Nikolai Ivanov, Julia Hoeng	High Content Screening data storage and analysis platform - An open source solution
A-118	Laura Huerta, Elisabet Barrera, Wojciech Bazant, Nuno A. Fonseca, Anja Fullgrabe, Maria Keays, Suhaib Mohammed, Alfonso Munoz-Pomer Fuentes, Amy Tang, Irene Papatheodorou, Robert Petryszak, Ugis Sarkans and Alvis Brazma	Expression Atlas: exploring gene expression results across species under different biological conditions
A-119	Jorge Miguel Martins Boucas	Microservices in data, code, and project management.
A-120	Pieter Lukasse, Fedde Schaeffer, Oleguer Plantalech Casals, Sander Tan and Sjoerd van Hagen	Gene Set Variation Analysis in cBioPortal

A-121	Tazro Ohta	Databases to support reanalysis of public high-throughput DNA sequencing data
A-122	Chunlei Wu, Cyrus Afrasiabi, Sebastien Lelong, Jiwen Xin, Ginger Tsueng and Andrew I. Su	BioThings SDK: a toolkit for building high-performance data APIs in biology
A-123	Evanthia Kaimaklioti, Robert P Davey and Ian Mulvany	Reproducing computational experiments in situ as an interactive figure in a journal article
A-124	Mark Robinson, Stian Soiland-Reyes, Michael Crusoe and Carole Goble	CWL Viewer: The Common Workflow Language Viewer
A-125	Thomas Cokelaer, Dimitri Desvillechabrol, Rachel Legendre and Mélissa Cardon	Sequanix: a standalone application to expose Snakemake pipelines to end-users
A-126	Rickard Hammarén, Philip Ewels and Max Käller	NGI-RNAseq - a best practice analysis pipeline in Nextflow
A-127	Ngoc-Vinh Tran, Bastian Greshake and Ingo Ebersberger	PhyloProfile: an interactive and dynamic visualization tool for multi-layered phylogenetic profiles
A-128	Nikita Moshkov, Daria Iakovishina and Dimitri Nikogosov	CueSea: quality control tool for Illumina genotyping microarray data, with correction on intensity, clusterization and biological specificity.
A-129	Rishi Nag	Bio::DB::HTS – accessing HTSlib from Perl
A-130	Luis Pedro Coelho, Paulo Monteiro, Renato Alves, A.T. Freitas and Peer Bork	NGLESS: Perfectly understandable and reproducible metagenomics pipelines using a domain-specific language
A-131	Keiran Raine, Adam Butler, Peter Clapham, Jon Teague, Peter Campbell	CGP as a Service (CGPaaS) - From data submission to results using your web-browser
A-132	Lacey-Anne Sanderson, Reynold Tan, Carolyn Caron, Kirstin Bett	Large-scale genotypic and phenotypic data support for Tripal: Chado optimization by utilizing modern PostgreSQL functionality
A-133	Michael Reich, Thorin Tabor, Helga Thorvaldsdóttir, Barbara Hill, Ted Liefeld, Jill Mesirov, Pablo Tamayo	GenePattern Notebooks: An integrative analytical environment for genomics research
A-134	John Fonner, Rion Dooley, Jacquelyn Turcinovic and Matthew Vaughn	BioContainers for supercomputers: 2,000+ accessible, discoverable Singularity apps

A-135	Felix Shaw, Anthony Etuk, Rob Davey, Alejandra Gonzalez-Beltran, David Johnson, Phillipe Rocca-Serra and Susanna Sansone	Collaborative Open Plant Omics: A platform for “FAIR” data for plant science
A-136	Farah Khan, Andrew Lonie, Richard Sinnott and Stian Soiland-Reyes	CWL+Research Object == Complete Provenance
A-137	Steffen Moeller	Workflow-ready bioinformatics packages for Debian-based distributions and this Linux distribution’s infrastructure for low-friction reproducible research
A-138	Yo Yehudi, Daniela Butano, Matthew Chadwick, Justin Clark-Casey, Sergio Contrino, Josh Heimbach, Rachel Lyne, Julie Sullivan and Gos Micklem	Forever in BlueGenes: a next-generation genomic data interface powered by InterMine
A-139	Silvia Di Giorgio and Konrad Förstner Dr.	GRADitude: A computational tool for the analysis of Grad-seq data
A-140	Stefan Popa and Radu Dobrescu	Enabling the optimization of open-source biological computational tools with scripting languages
A-141	Rabie Saidi, Hanna Papkova, Tunca Dogan and Maria Martin	Protein Inpainter: a Message-Passing-based Predictor using Spark GraphX
A-142	Ricardo Wurmus and Altuna Akalin	Reproducible and user-controlled software management in HPC with GNU Guix
A-143	Monther Alhamdoosh, Milica Ng and Matthew Ritchie	An ensemble approach for gene set testing analysis with reporting capabilities
A-144	Julia Kurps, Maxim Moinat, Joris Borgdorff, Fanscesco Nobilia, Maximilian Kerz, Nivethika Mahasivam, Irina Pulyakhina, Matthias Dümpelmann, Herculano Campos, Mark Begale, Richard Dobson and Amos Folarin	RADAR-CNS - Research Infrastructure for processing wearable data to improve health
A-145	Kevin Sayers, Paolo Di Tommaso, Maria Chatzou, Evan Floden and Cedric Notredame	Workflows interoperability with Nextflow and Common WL
A-146	Carole Goble, Rafael Jimenez, Alasdair Gray, Niall Beard, Giuseppe Profiti and Norman Morrison	Bioschemas for life science data
A-147	Denis Yuen, Brian O'Connor, Andrew Duncan, Solomon Shorser, Vincent Chung, Xiang Kun Liu, Janice Patricia, Han Yuan Cao, Gary Luu, Vincent Ferretti and Lincoln Stein	The GA4GH Tool Registry Service (TRS) and Dockstore - Year One

A-148	Annemarie H. Eckes, Tomasz Gubała, Piotr Nowakowski, Tomasz Szymczyszyn, Rachel Wells, Judith A. Irwin, Carlos Horro, John M. Hancock, Graham King, Sarah C. Dyer and Wiktor Jurkowski	Introducing the Brassica Information Portal: Towards integrating genotypic and phenotypic Brassica crop data
A-149	Anil S. Thanki, Nicola Soranzo, Wilfried Haerty and Robert P. Davey	Discovery and visualisation of homologous genes and gene families using Galaxy
A-150	Olga Vrousadou, Simon Jupp, Thomas Liener, Tony Burdett and Helen Parkinson	The SPOT ontology toolkit : semantics as a service
A-151	Aditya Bharadwaj, Divit P. Singh, Anna Ritz, Allison N. Tegge, Christopher L. Poirel, Pavel Kraikivski, Neil Adames, Kurt Luther, Shiv D. Kale, Jean Peccoud, John J. Tyson and T. M. Murali	GRAPHSPACE: Stimulating interdisciplinary collaborations in network biology
A-152	Keiichiro Ono, Eric Sage and Barry Demchak	Revitalizing a classic bioinformatics tool using modern technologies: the case of the Cytoscape Project
A-153	Kieran O'Neill, Benjamin Decato, Alexander Goncarenko, Azhar Khandekar, Benjamin Busby and Aly Karsan	Screw: tools for building reproducible single-cell epigenomics workflows
A-154	Stephen Lincoln, Shan Yang, Benedict Paten, Melissa Cline, Yuya Kobayashi, Scott Topper, Can Zhang, David Haussler and Robert Nussbaum	Emerging public databases of clinical genetic test results: Implications for large scale deployment of precision medicine
A-155	Alexander S. Rose and Stephen K. Burley	NGL – a molecular graphics library for the web
A-156	Kenzo-Hugo Hillion, Ivan Kuzmin, Hedi Peterson, Jon Ison and Hervé Ménager	ToolDog - generating tool descriptors from the ELIXIR tool registry
A-157	Ted Liefeld, Marco Ocana, Michael Reich, Helga Thorvaldsdottir and Jill P Mesirov	Integrating cloud storage providers for genomic analyses
A-159	Kate Voss, Jeff Gentry and Geraldine Van der Auwera	Full-stack genomics pipelining with GATK4 + WDL + Cromwell
A-160	Matúš Kalaš, Sveinung Gundersen, László Kaján, Hervé Ménager, Jon Ison, Steve Pettifer, Christophe Blanchet, Rodrigo Lopez, Kristoffer Rapacki and Inge Jonassen	BioXSD BioJSON BioYAML - Towards unified formats for sequences, alignments, features, and annotations
A-161	Matúš Kalaš, Hervé Ménager, Veit Schwämmle, Jon Ison and Edam Contributors	EDAM - The ontology of bioinformatics operations, types of data, topics, and data formats (2017 lightning update)