



Portland 2018

Galaxy Community Conference (GCC2018) and
Bioinformatics Open Source Conference (BOSC2018)

June 25 - July 2, 2018

Reed College, Portland, Oregon, United States

<https://gccbosc2018.sched.com/>

#GCCBOSC gitter.im/GCC-BOSC-2018

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Welcome to GCCBOSC 2018!

GCCBOSC 2018 is a new bioinformatics community conference that includes both the Galaxy Community Conference (GCC) and the Bioinformatics Open Source Conference (BOSC). There are joint and parallel sessions as well as shared keynotes, poster & demo sessions, birds-of-a-feather, and social events. The main meeting is preceded by two days of training workshops, and followed by several days of collaborative work.

The Galaxy Community Conference (GCC) is all about high-throughput biology and tools that support it. Galaxy is an open web-based platform for data integration and analysis in the life sciences and is deployed around the world.

The Bioinformatics Open Source Conference (BOSC) is organized by the Open Bioinformatics Foundation (OBF), a non-profit group dedicated to promoting the practice and philosophy of open source software development and open science within the biological research community. Since its inception in 2000, BOSC has provided a forum for developers and users to interact and share ideas and results in open source bioinformatics. BOSC was part of the annual ISMB conference until this year, when BOSC decided to try co-locating with GCC.

Cheers,

GCCBOSC 2018 Organizing Committee

Co-Chairs: Nomi Harris, Heather Wiencko, Nicole Vasilevsky, Dave Clements



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Wi-Fi Access

1. Select ReedXenia from your list of wireless networks.
2. Members outside the Reed community should click "Register as Guest" and enter a name and e-mail address or phone number. You can then log in using your e-mail address as the username, *and the numerical password e-mailed/texted to that address or phone number.*
3. After registering, you may be warned by your browser that you're being redirected; this is normal as we redirect you to Reed's homepage, and you can ignore any such warning.

Having problems? Talk to the registration desk or see bit.ly/reedwireless.

Swipe cards

At registration you will receive a swipe card that works for your dorm and laundry access, and your meal card (for included meals that are served in the Gray Campus Center Commons). If you are staying on campus, you will also receive a key to your dorm room. You will need to return the room key when you check out (swipe cards need not be returned). Talk to the help desk if you lose your card or key during GCCBOSC. Replacement keys are \$75 each.

Meals

If you are staying on campus then breakfast at the Commons in the Gray Campus Center is included with your lodging (bring your swipe card). If you aren't staying on campus then grab something before you get here, or you can buy breakfast at the Commons too. The Commons is open for breakfast from 8-9 every morning. Breakfast has hot and continental options including hot cereal, muffins and scones.

Lunch is also included as part of training, the meetings, and CollaborationFest: Core (but not during CollaborationFest: Encore). Lunch is in the Performing Arts Building (PAB) lobby or the Commons (see map at back). All breaks are in the PAB Atrium.

The conference dinner will be outside on Thursday at 7pm. Dinner on other nights can be purchased at the Commons, if you want to stay on campus, or in the nearby Woodstock neighborhood.

Code of Conduct

GCCBOSC has a code of conduct that describes what is expected of conference participants. Please give it a read and help make GCCBOSC a welcoming and safe environment for all participants. [**bit.ly/gccbosc2018-conduct**](http://bit.ly/gccbosc2018-conduct)

There's more online

The list of posters and demos, and the full author lists for accepted talks are online at [**gccbosc2018.sched.com**](http://gccbosc2018.sched.com).

Monday, June 25: Galaxy Training Day

Time	Using Galaxy PAB 104	Galaxy Admin PAB 320
8:00	Conference Desk Open, PAB Atrium	
9:00	Galaxy 101: A Gentle Introduction to Using Galaxy Bérénice Batut, Joachim Wolff	Intro to Galaxy Admin I Martin Čech, Enis Afgan, Marius van den Beek, John Chilton, Nate Coraor, Carrie Ganote, Simon Gladman, Nuwan Goonasekera
11:30	Lunch, Gray Campus Center Commons Cafe	
12:30	RNA-Seq Analysis with Galaxy Anton Nekrutenko	Intro to Galaxy Admin II Čech, <i>et al.</i>
3:00	Break, PAB Atrium	
3:30	Galaxy for Proteogenomics! Tim Griffin, Pratik Jagtap, JJ Johnson, Praveen Kumar, Subina Mehta	Intro to Galaxy Admin III Čech, <i>et al.</i>
6:00	Dinner on your own in Woodstock or the Commons Cafe	
7:30	Bioinformatics Training and Education with the Galaxy Training Network Bérénice Batut, PAB 320	

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Tuesday, June 26: All Topics Training Day

Time	PAB 104	PAB 131	PAB 320	PAB 332	Vollum Lounge
8:00 AM	Registration Desk Open, PAB Atrium				
9:00 AM	Handling integrated biological data using Python (or R) & InterMine Daniela Butano, Leyla Ruzicka, Yo Yehudi	Data Carpentry Genomics Workshop: Data Organization and Automation with Shell I Tracy K. Teal	Conda and Containers Martin Čech, John Chilton, Björn Grüning	Community built analyses that run everywhere with bcbio Brad Chapman, Radhika S. Khetani, Lorena Pantano Rubino	WDL: the Workflow Description Language Geraldine Van der Auwera, Jeff Gentry, Chris Lianwarne
11:30 AM	Lunch, Gray Campus Center, Commons Cafe				
12:30 PM	Setting up for success: Everything you need to know when planning for an RNA-seq analysis I Radhika S. Khetani, Meeta Mistry, Mary Piper	Data Carpentry Genomics Workshop: Data Organization and Automation with Shell II Tracy K. Teal	Introduction to Common Workflow Language Michael R. Crusoe, Hervé Ménager, Kenzo-Hugo Hillion	Galaxy Interactive Environments Björn Grüning	Practical use of the Galaxy API command line tools Dannon Baker, Marius van den Beek, Nicola Soranzo
3:00 PM	Break, PAB Atrium				
3:30 PM	Setting up for success: Everything you need to know when planning for an RNA-seq analysis II Radhika S. Khetani, Meeta Mistry, Mary Piper	Data Carpentry Genomics Workshop: Data Organization and Automation with Shell III Tracy K. Teal	Galaxy Architecture John Chilton, Nate Coraor	GATK4: What's new and how to run it Geraldine Van der Auwera, Kate Noblett	Command line workflow management systems: Snakemake & Nextflow Johannes Köster, Paolo Di Tommaso
6:00 PM	Dinner on your own in Woodstock, or the Commons Cafe or BoFs with Dinner (see bit.ly/gccbosc2018-bofs)				
8:00 PM	GCCBOSC 2018 Meeting: Joint Opening Session (see below)				

Tuesday, June 26: GCCBOSC Meeting Day 0

6:15 PM	Conference Desk Open, PAB Atrium Dinner on your own, or with a Birds of a Feather
8:00 PM	Joint Session 0: GCCBOSC 2018 Welcome Chairs: Heather Wiencko and Nicole Vasilevsky Vollum Lecture Hall
8:00 PM	Opening & Welcome <i>Nomi Harris and Dave Clements</i>
8:10 PM	Keynote: Democratizing Data <i>Tracy K. Teal</i>
9:10 PM	Done Conference Desk remains open until 10pm, PAB Atrium

Birds of a Feather

There is no better place than GCCBOSC 2018 to meet and learn from others doing bioinformatics. GCCBOSC includes Birds of a Feather (BoF) meetups, informal gatherings based on participants' shared interests. Times are set aside for Birds of a Feather gatherings on Tuesday through Thursday.

If you are interested in a BoF then just show up. See bit.ly/gccbosc2018-bofs.

If you want to organize a BoF, submit it here: bit.ly/gccbosc2018-bofs-call. It's never too late to launch a BoF, and organizers will help get the word out as soon as it's posted on the schedule.

Publish your articles, presentations and posters in our dedicated community spaces.

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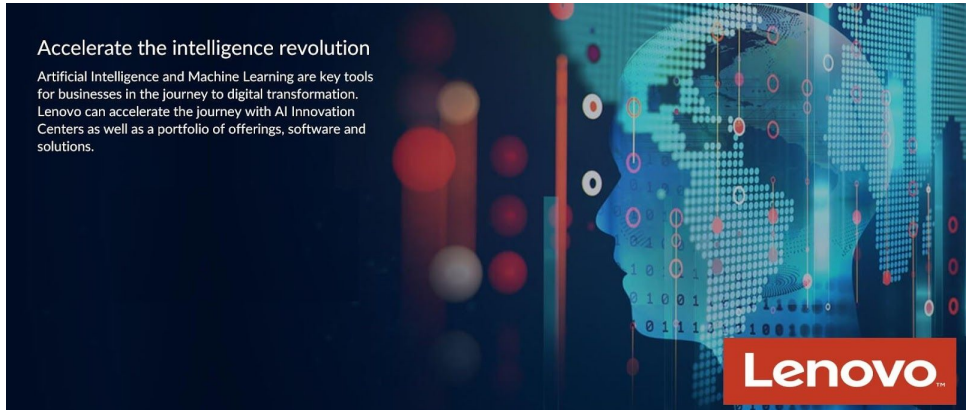
Wednesday, June 27: GCCBOSC Meeting Day 1

Session 1

8:00 AM	Conference Desk open, PAB Atrium
9:00 AM	Joint Session 1: GCCBOSC 2018 Chair: Nomi Harris Vollum Lecture Hall
9:00 AM	Keynote: Sustainable development of scientific open source tools: A view from Jupyter <i>Fernando Pérez</i>
10:00 AM	The journey of a team of engineers in learning packaging technology <i>Patrick Durand, Valentin Marcon, Laure Quintrie</i>
10:20 AM	Break, PAB Atrium

Accelerate the intelligence revolution

Artificial Intelligence and Machine Learning are key tools for businesses in the journey to digital transformation. Lenovo can accelerate the journey with AI Innovation Centers as well as a portfolio of offerings, software and solutions.



Got feedback? We want it: bit.ly/gccbosc2018-feedback

Session 2 (Wednesday, June 27: GCCBOSC Meeting Day 1)

10:50 AM	BOSC Session 2 Translational & Medical Informatics Chair: Hilmar Lapp Vollum Lecture Hall	GCC Session 2 Galaxy Infrastructure Chair: Simon Gladman Eliot Chapel
	<div>10:50 The Human Cell Atlas Data Coordination Platform: an open source, cloud-based system for ingesting, storing, analyzing, discovering, and exploring single-cell data, <i>Brian O'Connor</i></div> <div>11:05 Cloud-based data ingest for the Human Cell Atlas, <i>Daniel Vaughn</i></div> <div>11:20 Open Humans - connecting, sharing and analyzing personal data that enables community-driven research, <i>Bastian Greshake Tzovaras</i></div> <div>11:40 Enabling Machine Learning at Scale with "Tiled" Human Genomes, <i>Sarah Wait Zaranek</i></div> <div>11:45 JASS: a free and open source software for the joint analysis and interactive analysis of GWAS results, <i>Hervé Ménager</i></div> <div>11:50 Building a community menagerie of automated variant validations, <i>Brad Chapman</i></div> <div>11:55 Variant Transforms: Loading VCF files into BigQuery for large scale data analysis, <i>Asha Rostamianfar</i></div> <div>12:00 Q&A for lightning talks in this session</div>	<div>10:50 Storage Media Federation for Galaxy, <i>Vahid Jalili</i></div> <div>11:10 From laptop to super-computer: standardizing installation and management of Galaxy, <i>Nuwan Goonasekera</i></div> <div>11:30 Testing Wide-Area Lustre File Systems for Sharing load in Galaxy, <i>Carrie Ganote</i></div> <div>11:50 Galaxy for AnswerALS on Microsoft Azure and Kubernetes, <i>RC Carter</i></div> <div>11:56 Adding Python 3 support to Galaxy: a status report, <i>Nicola Soranzo</i></div> <div>12:02 Aurora Galaxy Tools: Using R Markdown as a framework to build interactive Galaxy tool output reports, <i>Ming Chen</i></div>

Campus Safety and Parking

Dial 911 for police, fire, or ambulance. For all other emergencies, call community safety at 503/788-6666 or dial 0 (zero) on a campus extension. Community safety officers are on duty 24 hours a day, seven days a week.

Parking is *free* in all campus lots. Please refrain from parking on neighboring streets. Reed is not liable for theft or damage to vehicles.

Got feedback? We need it: bit.ly/gccbosc2018-feedback

Sessions 3+4 (Wednesday, June 27: GCCBOSC Meeting Day 1)

12:10 PM	Lunch, PAB 12:30 BoFs with your Lunch , PAB (see bit.ly/gccbosc2018-bofs)	
1:40 PM	BOSC Session 3 All About Data Chair: Bastian Greshake Tzovaras Vollum Lecture Hall 1:40 miRTop: An open source community project for the development of a unified format file for miRNA data, <i>Lorena Pantano Rubino</i> 2:00 Reproducible big data science: A case study in continuous FAIRness, <i>Ravi K. Madduri</i> 2:20 InterMine 2.0: More than fifteen years of open biological data integration, <i>Yo Yehudi</i> 2:40 GRADitude: A computational tool for the analysis of Grad-seq data. <i>Silvia Di Giorgio</i> 2:45 NIH Data Commons Pilot Phase leverages the cloud to access, analyze, and share FAIR biomedical data, <i>David Siedzik</i> 2:50 Reproducible data analysis with Snakemake, <i>Johannes Köster</i> 2:55 Q&A for lightning talks in this session	GCC Session 3 Challenges & Opportunities Chair: Eliot Chapel 1:40 Galaksio, a more user friendly interface for Galaxy using workflows, <i>Tomas Klingström</i> 2:00 Large scale analyses with improved dataset collections, <i>Marius van den Beek</i> 2:20 A fruitful year for the Galaxy Training materials, <i>Bérénice Batut</i> 2:40 The usegalaxy.* servers: democratizing computational resources for life sciences at a new level, <i>Simon Gladman</i>
3:00 PM	Poster, Demo and Sponsor Session I PAB Atrium	
4:00 PM	Joint Session 4: GCCBOSC 2018 Chair: Brad Chapman Vollum Lecture Hall	
4:00 PM	Improving the Bioinformatics Curriculum <i>Jason Williams</i>	
4:20 PM	Panel: Training and Documentation in Bioinformatics <i>Bérénice Batut, Fernando Pérez, Tracy K. Teal, Jason Williams</i>	
5:20 PM	End of Talks	
5:40 PM	Dinner on your own in Woodstock or the Commons Cafe, or BoFs with Dinner (see bit.ly/gccbosc2018-bofs), or BOSC & GCC Social Mixer by Lifebit	
8:00 PM	Late Night BoFs (see bit.ly/gccbosc2018-bofs), or BOSC & GCC Social Mixer by Lifebit	

Icebreaker!

You should have received an icebreaker card with instructions on the back, and a sheet of stickers with your name on them when you checked in. Your goal is to fill and hand in your card, *no later than the start of Session 7*. A prize winner will be drawn randomly from all completed entries at the end of Session 8.

Got feedback? We want it: bit.ly/gccbosc2018-feedback

Thursday, June 28: GCCBOSC Meeting Day 2

Session 5

8:00 AM	Conference Desk Open, PAB Atrium	
9:00 AM	BOSC Session 5 Developer Tools and Libraries Chair: Peter Cock Vollum Lecture Hall 9:00 iMADS: A sustainable software collaboration for predicting transcription factor binding specificity, <i>Dan Leehr</i> 9:20 The Funnel Task Execution Server, <i>Alexander Buchanan</i> 9:40 Distributed execution of bioinformatics tools on Apache Spark with ADAM and Cannoli, <i>Michael Heuer</i> 9:45 Extended Extraction Transform Load: A novel framework for batch jobs on cloud computing resources, <i>Hiromu Ochiai</i> 9:50 Plugging Docker-based visualizations into Django with django_docker_engine, <i>Chuck McCallum</i> 9:55 The Arachne Graph Database Server. <i>Kyle Ellrott</i> 10:00 Owlery: An easily deployable web service for making reasoning queries over OWL ontologies web-native, <i>Hilmar Lapp</i> 10:05 taxa: taxonomic data standards and methods for R and Python, <i>Scott Chamberlain</i> 10:10 Q&A for lightning talks in this session	GCC Session 5 Galaxy in situ Chair: Laure Quintrie Eliot Chapel 9:00 Galaxy Enables Integrated Analysis of Phenotypic, Genotypic, and Environmental Data for Geo-referenced Trees in CartograTree, <i>Nic Herndon</i> 9:20 G-OnRamp: Create UCSC Assembly Hubs and JBrowse/Apollo Archives for Collaborative Eukaryotic Genome Annotations, <i>Luke Sargent</i> 9:40 Canada's Integrated Rapid Infectious Disease Analysis Platform (IRIDA), <i>Thomas Matthews</i> 10:00 Galaxy in a proteomics core facility, <i>Jeremy Volkening</i>
10:20 AM	Break PAB Atrium	

Join the conversation

GCCBOSC is on both Twitter and Gitter. Join the conversation:

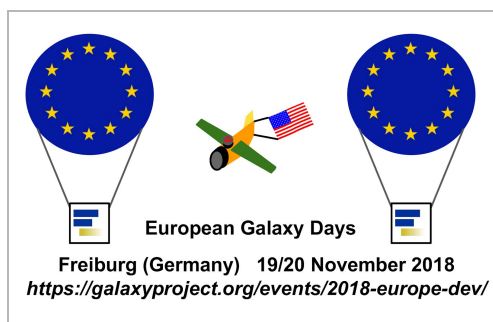
Hashtag: #GCCBOSC

Chat: gitter.im/GCC-BOSC-2018

Volunteers

Want to contribute an hour or two to GCCBOSC 2018? Then we would love to have your help. Most tasks involve helping session chairs - you won't even have to miss any presentations.

Contact an organizer or ask at the registration desk if you are interested.



Session 6 (Thursday, June 28: GCCBOSC Meeting Day 2)

10:50 AM	BOSC Session 6 Workflows Chair: Karsten Hokamp Vollum Lecture Hall	GCC Session 6 Galaxy <i>in situ</i> Chair: Maria Doyle Eliot Chapel
	<p>10:50 CWLProv - Interoperable retrospective provenance capture and its challenges, <i>Farah Zaib Khan</i></p> <p>11:10 Running portable workflow and container specifications at production scale in the cloud: strategy & best practices, <i>Geet Duggal</i></p> <p>11:30 The GA4GH/DREAM Workflow Execution Challenge, <i>James Eddy</i></p> <p>11:35 Bepin: An open source system to run reproducible computational workflows on cloud infrastructure, <i>Dan Leehr</i></p> <p>11:40 CWL-Airflow pipeline manager as a backend for BioWardrobe data analysis platform, <i>Andrey Kartashov</i></p> <p>11:45 Scaling bioinformatics analysis using Nextflow and AWS, <i>Francesco Strozzi</i></p> <p>11:50 One Week to 1,000 Whole Genomes with Open Source: Arvados, CWL, and bcbio, <i>Peter Amstutz</i></p> <p>11:55 Q&A for lightning talks in this session</p>	<p>10:50 Quantifying Functional Microbiomes: An integrated, quantitative metaproteomics approach reveals connections between taxa, function and protein expression in complex microbiomes, <i>Caleb Easterly, Pratik Jagtap</i></p> <p>11:10 GeneSeqToFamily: a Galaxy workflow to find gene families based on the Ensembl Compara GeneTrees pipeline, <i>Nicola Soranzo</i></p> <p>11:30 Galaxy HiCEXplorer: HiCEXplorer, deepTools3 and pyGenomeTracks, <i>Joachim Wolff</i></p> <p>11:50 Using Galaxy to analyze TCGA data: the experience of a Brazilian center, <i>Thais Talarico</i></p> <p>11:56 ImmPort Galaxy, facilitating analysis and meta-analysis of flow cytometry data, <i>Cristel Thomas</i></p> <p>12:02 Coloc-stats: a unified web interface to perform colocalization analysis of genomic features, <i>Sveinung Gundersen</i></p>

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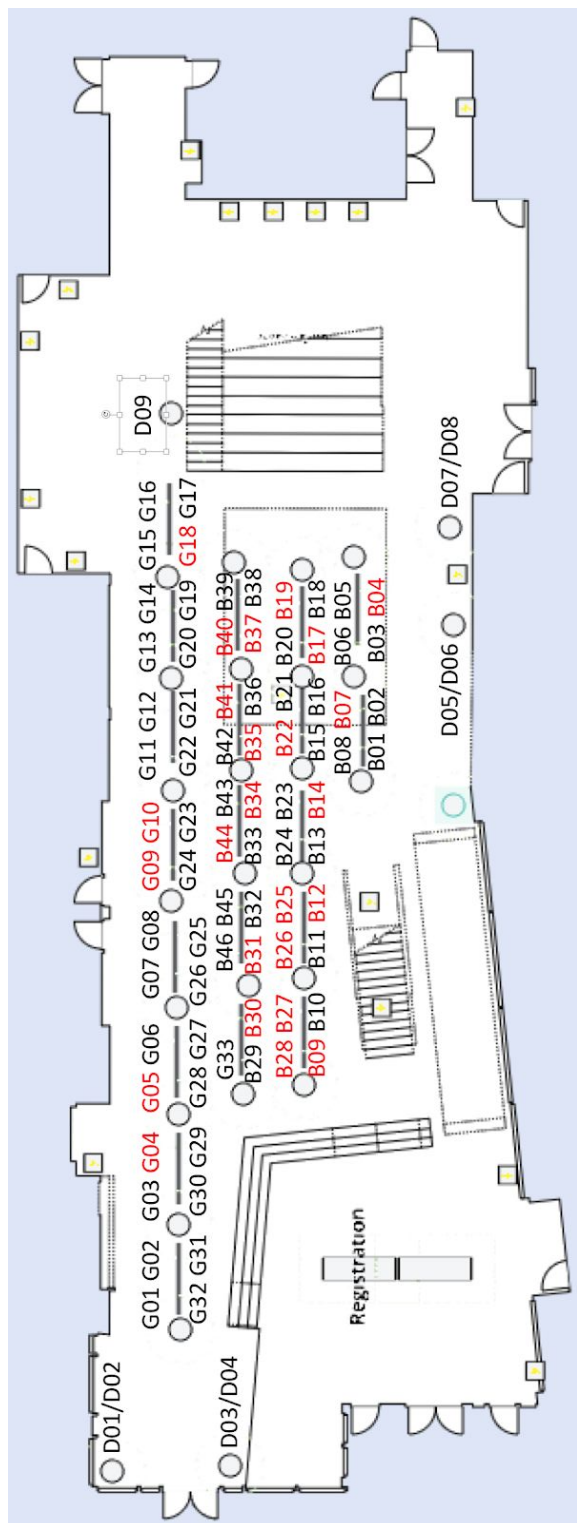


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Session 7+8 (Thursday, June 28: GCCBOSC Meeting Day 2)

12:10 PM	Lunch, PAB 12:30 BoFs with your Lunch , PAB (see bit.ly/gccbosc2018-bofs)	
1:40 PM	BOSC Session 7 Project Updates & Late-Breaking Research Chair: Chris Fields Vollum Lecture Hall 1:40 OBF update, <i>Hilmar Lapp</i> 1:50 GSOC update, <i>Michael R. Crusoe</i> 2:00 Biopython Project Update 2018, <i>Peter Cock</i> 2:07 Community Annotation with Apollo: Engaging the Collective in a Genome Annotation Workflow, <i>Nathan Dunn</i> 2:27 Late-Breaking Lightning Talks 2:52 Q&A for lightning talks in this session	GCC Session 7 Community Update(s) Chair: Frederik Coppens Eliot Chapel 1:40 Galaxy Community Update, <i>Dan Blankenberg, Jeremy Goecks, Anton Nekrutenko, James Taylor</i> 2:10 Integrative proteo-transcriptomics workflows within the Galaxy framework to explore the correlation between the expression of RNA and proteins, <i>Praveen Kumar</i> 2:16 A Galaxy Implementation of Next-Generation Clustered Heat Maps for Interactive Exploration of Large-Scale Molecular Profiling Data, <i>Bob Brown</i> 2:22 Candidate Gene Methylation quantification (CandiMeth) Within the Galaxy Bioinformatics Interface, <i>Sara-Jayne Thursby</i> 2:28 Making Immune Repertoire Sequence Analysis Accessible to Anyone via Galaxy, <i>Bradley W. Langhorst</i> 2:34 Galaxy Genome Annotation project: integrating Galaxy and GMOD for genome annotation, <i>Anthony Bretaudeau</i> 2:40 OrthoQuery: A Tripal Module to Assess Gene Family Evolution in Sequenced Gymnosperms, <i>Sumaira Zaman</i> 2:46 Galaxy-E, a first step towards collaborative data analysis by citizens, <i>Yvan Le Bras</i> 2:52 Galaxy2Shiny2Galaxy - Combining Galaxy with Shiny (and doing other bad things), <i>Hans-Rudolf Hotz</i>
3:00 PM	Poster, Demo and Sponsor Session II PAB Atrium	
4:00 PM	Joint Session 8: GCCBOSC 2018 Chair: Pratik Jagtap Vollum Lecture Hall	
4:00 PM	Keynote: Confound it! Reproducible biology from "omics" data analysis <i>Lucia Peixoto</i>	
5:00 PM	Conference Closing Nomi Harris, Heather Wiencko, Nicole Vasilevsky, Björn Grüning	
5:20 PM	Done	
5:40 PM	BoFs, the Final Flight! (see bit.ly/gccbosc2018-bofs)	
7:00 PM	Conference Dinner	

Got feedback? We want it: bit.ly/gccbosc2018-feedback



Posters & Demos

First Floor, PAB

Black: Poster or demo

Red: Poster and demo

Posters & demos are presented on Wednesday & Thursday from 3-4 PM in the PAB Atrium. Odd numbered posters/demos are presented Wednesday, even numbered Thursday.

CollaborationFest

OBf's *CodeFest*, Galaxy's *Hack the Galaxy*, and the NIH's *Data Commons Pilot Phase Consortium* are all converging at **CollaborationFest 2018**. CoFest starts at 9am on Friday morning, and features 2, 3, or 4 days of collaborative work on projects that matter to open source bioinformatics.

CoFest is in the Performing Arts Building (PAB) and will make extensive use of classrooms and the PAB Atrium, an ideal space for collaboration. CoFest participants will coalesce around shared interests and address common challenges related to those interests. These clusters form before, at the beginning of, and throughout CollaborationFest. These clusters will be fluid and highly interactive with each other.

Got something you want to address at CoFest 2018? Propose a cluster in advance: bit.ly/cofest2018-ideas

Posters & Demos

PD ID	Title	Black: Poster or demo Red: Poster and demo	Presenter
P B01	Association Mapping and Landscape Genomics of Georeferenced Forest Trees via CartograTree and TreeGenes		Taylor Falk
P B02	Tripal Sequence Similarity Search provides efficient protein sequence similarity search for Tripal sites		Sean Buehler
PD B03	CRI iAtlas: an interactive portal for immuno-oncology research		James Eddy
P B04	TreeGenes: enabling visualization and analysis in forest tree genomics		Emily Grau
PD B05	One Week to 1,000 Whole Genomes with Open Source: Arvados, CWL, and bcbio		Peter Amstutz
P B06	Bioinformatics in the age of AI and personalized medicine: an open source example		Michael Duncan
P B07	Classification of short read alignments from xenograft samples		Lawrence Heisler
PD B08	GRADitude: A computational tool for the analysis of Grad-seq data		Silvia Di Giorgio
PD B09	Enabling Machine Learning at Scale with "Tiled" Human Genomes		Sarah Wait ZaraneK
P B10	Debarcer2, De-Barcoding and Error Correction of sequencing data containing molecular barcodes designed to handle different library designs.		Lawrence Heisler
PD B11	flowDashboard: An Interactive Dashboard for Comparative Flow Analysis		Ted Laderas
PD B12	Plugging Docker-based visualizations into Django with django_docker_engine		Chuck McCallum
P B13	READemption - from reads to knowledge		Till Sauerwein
PD B14	Cirrus-NGS: Cloud-optimized compute infrastructure for next generation sequencing analysis		Guorong Xu
PD B15	RyuGoo-Saba: a CWL-based execution engine utilizing cloud resources for big data analysis in life science		HirotaKa Suetake
P B16	Infrastructure for coordinating multi-site clinical research projects via REDCap and Synapse		Xindi Guo
P B17	High-performance computing service in the Health Science and Human Services Library at University of Maryland Baltimore		Jean-Paul Courneya
P B18	NIH Data Commons Pilot Phase leverages the cloud to access, analyze, and share FAIR biomedical data		David Siedzik
PD B19	Reproducible big data science: A case study in continuous FAIRness		Ravi K. Madduri
P B20	Reproducible data analysis with Snakemake		Johannes Köster
P B21	FAIRsharing: Working with the community to map the landscape of		Massimiliano Izzo

standards, databases and data policies

PD ID	Title	Black: Poster or demo	Red: Poster and demo	Presenter
P B22	Code is Science: a manifesto for open source code in science			Yo Yehudi
P B23	Oxidizing Python: writing extensions in Rust			Luiz Irber
P B24	The Hypergraph Algorithms Package			Anna Ritz
PD B25	The GTrack ecosystem: expressive file formats for genomic track data and metadata - through compilation, exchange, storage and analysis			Sveinung Gundersen
P B26	Fast, sustainable, and secure bioinformatics with Rust-Bio and Rust-Htslib			Johannes Köster
P B27	JASS: a free and open source software for the joint analysis and interactive analysis of GWAS results			Hervé Ménager
PD B28	Community Annotation with Apollo: Engaging the Collective in a Genome Annotation Workflow			Nathan Dunn
PD B29	Extended Extraction Transform Load: A novel framework for batch jobs on cloud computing resources			Hiromu Ochiai
PD B30	The Funnel Task Execution Server			Alexander Buchanan
PD B31	The Arachne Graph Database Server			Kyle Ellrott
P B32	iMADS: A sustainable software collaboration for predicting transcription factor binding specificity			Dan Leehr
PD B33	BioThings Hub: An API Gateway for Biomedical Knowledge			Sébastien Lelong
P B34	Implementation of Nextflow for the automated processing of NovaSeq data sets			Netsanet (Net) Gebremedhin
P B35	Modernising somatic mutation calling pipelines with Open Source tools and Containers.			Mr Keiran M Raine
P B36	Understanding reproducibility of bioinformatics workflows			Sehrish Kanwal
PD B37	Accumulating computational resource usage of data analysis workflow to select suitable cloud instance			Tazro Ohta
PD B38	You can't spell Cromwell without CWL			Jeff Gentry
PD B39	CWL-Airflow pipeline manager as a backend for BioWardrobe data analysis platform			Andrey Kartashov
P B40	Running portable workflow and container specifications at production scale in the cloud: strategy & best practices			Geet Duggal
P B41	Scaling bioinformatics analysis using Nextflow and AWS			Francesco Strozzi
P B42	The GA4GH/DREAM Workflow Execution Challenge			James Eddy
P B43	CWLProv - Interoperable retrospective provenance capture and its challenges			Farah Zaib Khan
PD B44	A composable container system for genomic analysis pipelines			Yu Xang

PD ID	Title	Black: Poster or demo	Red: Poster and demo	Presenter
P B45	CWL Community Update			Michael R. Crusoe
P B46	Bespin: An open source system to run reproducible computational workflows on cloud infrastructure			John Bradley
D D01	From laptop to super-computer: standardizing installation and management of Galaxy			Nuwan Goonasekera
D D02	Adding R shiny apps as Galaxy interactive environment. A Galaxy-E demo			Valintin Chambon
D D03	Aurora Galaxy Tools: Using R Markdown as a framework to build interactive Galaxy tool output reports			Ming Chen
D D04	A Galaxy Implementation of Next-Generation Clustered Heat Maps for Interactive Exploration of Large-Scale Molecular Profiling Data			Bob Brown
D D05	Distributed execution of bioinformatics tools on Apache Spark with ADAM and Cannoli			Michael Heuer
D D06	Open Humans - connecting, sharing and analyzing personal data that enables community-driven research			Bastian Greshake Tzovaras
D D07	Building a community menagerie of automated variant validations			Brad Chapman
D D08	Owlery: An easily deployable web service for making reasoning queries over OWL ontologies web-native			Hilmar Lapp
D D09	taxa: taxonomic data standards and methods for R and Python			Scott Chamberlain
P G01	Galaxy-E, a first stage towards collaborative data analysis by citizens			Yvan Le Bras
P G02	Testing Wide-Area Lustre File Systems for Sharing load in Galaxy			Carrie Ganote
P G03	Predicting Galaxy Tool Runtimes with Random Forests			Anastasia Tyryshkina
PD G04	Galaxy for AnswerALS on Microsoft Azure and Kubernetes			RC Carter
PD G05	Galaksio, a more user friendly interface for Galaxy using workflows			Tomas Klingström
P G06	Galaxy2Shiny2Galaxy - Combining Galaxy with Shiny (and doing other bad things)			Hans-Rudolf Hotz
P G07	Identifying suitable spliced mapper and genomic assembly for variant detection			Akila Parvathy Dharshini
P G08	Collecting data for association genetics: Tripal Plant PopGen Submit pipeline			Peter Richter
PD G09	EWAS-Galaxy: a tool suite for population epigenetics integrated into the Galaxy			Krzysztof Poterłowicz
PD G10	Coloc-stats: a unified web interface to perform colocalization analysis of genomic features			Sveinung Gundersen
P G11	Candidate Gene Methylation quantification (CandiMeth) Within the Galaxy Bioinformatics Interface			Sara-Jayne Thursby

PD	ID	Title	Black: Poster or demo	Red: Poster and demo	Presenter
P	G12	Canada's Integrated Rapid Infectious Disease Analysis Platform (IRIDA)			Thomas Matthews
P	G13	Bacterial genomics in Galaxy			Delphine Larivière
P	G14	HIV transmission clustering in Galaxy			Dave Bouvier
P	G15	Galaxy in a proteomics core facility			Jeremy Volkening
P	G16	Integrative proteo-transcriptomics workflows within the Galaxy framework to explore the correlation between the expression of RNA and proteins			Praveen Kumar
P	G17	Evaluation of moFF and FlashLFQ for label-free peptide quantification in proteomic workflows within the Galaxy-P framework			Subina Mehta
PD	G18	CRAVAT (Cancer-Related Analysis of Variants Toolkit) integration into Galaxy-P and extension towards proteogenomic studies			Ray Sajulga
P	G19	Implementation of machine learning algorithms for medulloblastoma classification in a local galaxy server			Luciane Sussuchi Da Silva
P	G20	Using Galaxy to analyze TCGA data: the experience of a Brazilian center			Thais Hosokawa
P	G21	The Mammalian Ortholog and Annotation Database: enhanced ortholog information with an accurate identifier mapping between NCBI and Ensembl accessible from a Galaxy-server			Jochen Bick
P	G22	ARIAWeb: a structural bioinformatics web interface linked to galaxy			Fabien Mareuil
P	G23	SECIMTools: A suite of Metabolomics Data Analysis Tools			Oleksandr Moskalenko
P	G24	New tools to enhance the Galaxy-based metabolomics workbench			Arthur Eschenlauer
P	G25	VKMZ: Visualizing Metabolomics on a van Krevelen Diagram through Galaxy			Mark Esler
P	G26	ISAcree: a Galaxy tool for Prospective Data Management with ISA format support - Application to Metabolomics Datasets			Philippe Rocca-Serra
P	G27	BioXSD BioJSON BioYAML – towards unified formats for sequences, alignments, features, and annotations			Matus Kalas
P	G28	EDAM: the ontology of bioinformatics operations, types of data, topics, and data formats (2018 update)			Hervé Ménager
P	G29	ELIXIR contributions to the FAIRness of Bioinformatics resources, with bio.tools, Galaxy and CWL			Kenzo-Hugo HILLION
P	G30	Compliance? We don't need no stinking compliance!			Jeffrey Miller
P	G31	A fruitful year for the Galaxy Training materials			Bérénice Batut
P	G32	Results of an Extended Developer Support consultation with the CloudLaunch project			Marcus Christie
P	G33	Refinery: a data management, analysis, and visualization platform utilizing the Galaxy workbench			Scott Ouellette

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* Also reviewed late-breaking abstracts

Conference and project URLs

- GCCBOSC 2018
 - gccbosc2018.sched.com
 - gccbosc2018.sched.com/info
 - [gitter.im/GCC-BOSC-2018](https://git.im/GCC-BOSC-2018)
 - bit.ly/gccbosc2018-feedback
- Open Bioinformatics Foundation
 - www.open-bio.org
- Galaxy Project
 - galaxyproject.org



GCC 2019

Freiburg, DE

1-6 July

1-6 July, Konzerthaus, Freiburg
galaxyproject.org/gcc2019

See you next year!

