Welcome to BOSC 2019! The Bioinformatics Open Source Conference has been held annually since 2000, usually in conjunction with the Intelligent Systems for Molecular Biology (ISMB) Conference. BOSC is organized by the Open Bioinformatics Foundation (OBF), a non-profit group that promotes the practice and philosophy of Open Source software development and Open Science within the biological research community.

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Sponsorships from private companies and organizations help to defray some of our costs and enable us to grant more travel fellowships. We are grateful to our sponsors: Amazon Web Services (virtually unlimited infrastructure and fast networking for scalable HPC), Google Cloud (partnering with you to engineer a healthier world), eLife (cutting-edge technology for cutting-edge research), The Hyve (open source solutions for bioinformatics), GigaScience (an open access, open data, open peer-review journal), PLoS Computational Biology (making research open-access and freely available), and KNIME (software for end-to-end data science).

BOSC is a community effort. We thank all who made it possible, including the organizing committee, the review committee, the session chairs, our sponsors, the presenters and attendees, and the ISCB.

BOSC 2019 Organizing Committee

Nomi Harris (Chair)

Heather Wiencko (Co-Chair), Peter Cock, Chris Fields, Bastian Greshake Tzovaras, Michael Heuer, Karsten Hokamp, Monica Munoz-Torres, Bastian Rieck, Yo Yehudi

Review Committee

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* reviewed both rounds

If you are interested in reviewing abstracts next year, please email bosc@open-bio.org.

Program

BOSC includes two full days of talks, posters, and Birds of a Feather interest groups (BOFs). Session topics this year include Data Crunching, Data Modeling and Formats, Open Data, Containers, Workflows, Open Science, and Building Open Source Communities, as well as a session of late-breaking lightning talks. The longer talks this year are 17 minutes (plus 3 minutes for questions); lightning talks are 5 minutes, with a short time allocated for questions at the end of each group of lightning talks.

Keynote: Nicola Mulder

Building infrastructure for responsible open science in Africa

Due to a history of exploitation and inequitable scientific partnerships, many African researchers are reluctant to fully embrace open science practices. Recent investment in genomics research on the continent and associated capacity development initiatives have enabled the development of research infrastructures and data related skills. This is helping to narrow the gap in expertise and access to data analysis capacity and facilitate more equitable engagement in international collaboration or more importantly, more independent research. H3ABioNet is a Pan African bioinformatics network that has been instrumental in building capacity for genomics data analysis on the continent. The network has an ethos of openness and is promoting open science practices among its members. This is exercised through many different activities, including open source software and workflow development, open science *training, and efforts to make our data, tools and training materials FAIR. Though the genomic data we work with is controlled access, H3ABioNet is working to ensure the data is findable, harmonized and interoperable to increase the value for both data providers and users who are granted access for responsible secondary use. In this talk I will describe some of our activities in data, tool and training material curation, standardization and dissemination. Our approach considers past inequities and tries to promote responsible openness that ensures protection of privacy and recognition of scientific contributions.*

Prof. Nicola Mulder heads the Computational Biology Division at the University of Cape Town (UCT) in South Africa and leads H3ABioNet, a Pan-African Bioinformatics Network of 28 institutions in 16 African countries. H3ABioNet is developing bioinformatics capacity to enable genomic data analysis on the continent. Prior to her position at UCT, she worked at the European Bioinformatics Institute in Cambridge UK as a Team Leader for bioinformatics resources. At UCT her research focuses on genetic determinants of susceptibility to disease, African genome variation, microbiomes, genomics and infectious diseases from the host and pathogen perspectives. Prof Mulder is actively involved in training and education, including bioinformatics curriculum development. She is a member of the Board of Directors for the International Society for Computational Biology (ISCB); she co-chairs the Nominations and Education Committees.

Posters

Check https://www.open-bio.org/events/bosc/schedule/ for your poster number.

- Setup: Day 1 (Wednesday, 24-July), 7:30-10:00am
- Poster session: Day 1 (Wednesday, 24-July), 6:00-8:00pm
- Takedown: Posters should be removed by 2pm on the last day of BOSC/ISMB.

If you want to get some food before the poster session, some quick places nearby are listed on this map. The closest is Thai House (Clarastrasse 34), which is open for takeout even though the sit-down restaurant is closed. Note that many restaurants and stores in Basel are closed in July. The ISMB has a compiled a list of nearby restaurants, but they may not have checked whether they're open in July.

Birds of a Feather (BoFs)

BoFs are informal, self-organized meetups focused on specific topics. They're a great way to meet other like-minded community members and have in-depth discussions on a topic of interest.

Anyone is welcome to propose a BoF! All you need is a title, an organizer, and a brief description. BoFs are held during lunchtime each day as well as during an additional BOSC-only BoF session (4:40-5:40pm on the first day of BOSC, 24-July). Visit bit.ly/BOSC2019-bofs to see the schedule or propose your own BoF! Please note that last-minute BoFs will not get rooms; you will need to find a suitable lobby or cafe in which to meet.

Pay-your-own-way dinner

We invite you to join BOSC organizers and attendees at an optional pay-your-own-way dinner on the last evening of BOSC **(Thursday, 25 July) at 7:30pm**. We have reserved seating for 30 people at the Basel Markthalle at Steinentorberg 20 (the same place as the ISMB reception on Tuesday, July 23). The Markthalle is like a big food court: you order your food at one of the counters and then sit down. Our reserved seating area will be near the house bar--look for the BOSC sign.

Sign up to attend at http://bit.ly/BOSC2019-dinner. Dinner attendees are responsible for paying for their own food and drinks (cash preferred). Please order all drinks at the house bar.

OBF CollaborationFest (CoFest)

In conjunction with BOSC, the Open Bioinformatics Foundation runs a collaborative event (formerly called CodeFest, short for coding festival, and now called CollaborationFest, or CoFest for short). At these events, participants work together to contribute to bioinformatics software, documentation, training materials, and use cases.

This year's CoFest will take place the two days after BOSC, July 26-27, at The Swiss Innovation Hub for Personalized Medicine in Basel, Switzerland. Registration is free; sponsorships offset the cost of venue, coffee and snacks. Join the CoFest Gitter to be part of the action!

OBF Travel Fellowships

The Open Bioinformatics Foundation (OBF) sponsors a Travel Fellowship program aimed at increasing diverse participation at events (such as BOSC) that promote open source bioinformatics software development and open science in the biological research community. The next application deadline is August 15. You can apply for funding for events you plan to attend or that you recently attended.

Joining OBF

Anyone involved in open science or open source software or the life sciences is invited to join BOSC's parent organization, the Open Bioinformatics Foundation (OBF). You can find information on how to join OBF on our website, open-bio.org. Anyone who is involved in some way in open source or open science is welcome to join; there is no membership fee..

If you'd like to meet some of the OBF Directors and members, please join us at the "Welcome to BOSC" Birds of a Feather (BoF) session on the first day of the conference during lunch or the OBF Board Meeting BoF on the second day during lunch.

Stay in touch

Here are ways to stay in touch with the BOSC community before, during and after the meeting:

- Our website (https://www.open-bio.org/events/bosc/) -- check the schedule page for any updates to the program
- Our public Gitter room: https://gitter.im/OBF/BOSC_community
- Follow us on Twitter (@OBF_BOSC) and help us get the word out about BOSC by (re)tweeting (use hashtag #BOSC2019)
- Join the low-traffic bosc-announce mailing list

We look forward to meeting you in Basel! If you have any questions, you can contact the BOSC organizing committee at bosc@open-bio.org.

BOSC 2019 Schedule at a Glance

Day 1 (Wednesday, July 24)	
Time	**Session**
8:15-10:15	ISMB announcements & keynote; coffee break
10:15-12:40	*Session 1*
	BOSC opening remarks; OBF update; GSoC update
	Session: Data crunching
	Session: Data modeling and formats
12:40-14:00	Lunch, BoFs
14:00-16:00	*Session 2*
	Keynote: Nicola Mulder
	Session: Open data
16:00-16:40	Coffee break
16:40-17:50	*Session 3*
	Extra BoFs (bit.ly/BOSC2019-bofs)
18:00-20:00	Posters

Day 2 (Thursday, July 25)	
Time	**Session**
8:30-9:40	*Session 4*
	BOSC announcements
	Late-Breaking Lightning Talks
9:40-10:15	Coffee break
10:15-12:40	*Session 5*
	Session: Containers
	Session: Open science
12:40-14:00	Lunch, BoFs
14:00-16:40	Session 6
	Session: Workflows
	Session: Building Open Source Communities
	CoFest preview; BOSC closing remarks
16:40-18:00	Coffee break & ISMB keynote
19:30	BOSC dinner, Basel Markthalle

Complete schedule of talks

(Check https://www.open-bio.org/events/bosc/schedule/ for updates)

Day 1 (Wednesday, July 24, 2019)

Title	**Speaker**	**Start time**	**End time**	**Session**
Opening remarks	Nomi Harris	10:15	10:25	**Session: Introducing BOSC and the OBF**
The Open Bioinformatics Foundation	Heather Wiencko	10:25	10:33	**Session: Introducing BOSC and the OBF**
Google Summer of Code 2018	Kai Blin	10:33	10:40	**Session: Introducing BOSC and the OBF**
Session: Data crunching	Chair: Peter Cock	10:40	11:40	**Session: Data crunching**
elPrep 4: A multi-threaded tool for sequence analysis	Charlotte Herzeel	10:40	11:00	**Session: Data crunching**
Variant Transforms and BigQuery: Large scale data analytics in the cloud	Andrew Moschetti	11:00	11:05	**Session: Data crunching**
Forome Anfisa – an Open Source Variant Interpretation Tool	Michael Bouzinier	11:05	11:10	**Session: Data crunching**
Biotite: A comprehensive and efficient computational molecular biology library in Python	Patrick Kunzmann	11:10	11:15	**Session: Data crunching**
Q&A for lightning talks	-	11:15	11:20	**Session: Data crunching**
Portable Pipeline for Whole Exome and Genome Sequencing	Andrey Kokorev	11:20	11:25	**Session: Data crunching**
Epiviz File Server - Query, Compute and Interactive Exploration of data from Indexed Genomic Files	Jayaram Kancherla	11:25	11:30	**Session: Data crunching**
What does 1.0 take? MISO LIMS after 9 years of development	Morgan Taschuk	11:30	11:35	**Session: Data crunching**
Q&A for lightning talks	-	11:35	11:40	**Session: Data crunching**

Title	**Speaker**	**Start time**	**End time**	**Session**
Session: Data modeling and formats	Chair: Karsten Hokamp	11:40	12:25	**Session: Data modeling & formats**
BioLink Model - standardizing knowledge graphs and making them interoperable	Deepak Unni	11:40	12:00	**Session: Data modeling & formats**

pysradb: A Python package to query next-generation sequencing metadata and data from NCBI Sequence Read Archive	Saket Choudhary	12:00	12:05	**Session: Data modeling & formats**
Disq, a library for manipulating bioinformatics sequencing formats in Apache Spark.	Michael Heuer	12:05	12:10	**Session: Data modeling & formats**
A toolkit for semantic markup, exploration, comparison and merging of metadata models expressed as JSON-Schemas	Dominique Batista	12:10	12:15	**Session: Data modeling & formats**
A lightweight approach to research object data packaging	Stian Soiland-Reyes	12:15	12:20	**Session: Data modeling & formats**
Q&A for lightning talks	-	12:20	12:25	**Session: Data modeling & formats**
Lunch, BoFs, unofficial poster session		**12:40**	**14:00**	**ISMB and BOSC Birds of a Feather**

Title	**Speaker**	**Start time**	**End time**	**Session**
BOSC 2019 Keynote: Building infrastructure for responsible Open science in Africa	Nicola Mulder	14:00	15:00	**Keynote**
Session: Open data	Chair: Karsten Hokamp	15:00	16:00	**Session: Open data**
The (Re)usable Data Project	Seth Carbon	15:00	15:20	**Session: Open data**
The FAIR data principles and their practical implementation in InterMine	Sergio Contrino	15:20	15:40	**Session: Open data**
GA4GH: Developing Open Standards for Responsible Data Sharing	Rishi Nag	15:40	15:45	**Session: Open data**
The Commons Alliance: Building cloud-based infrastructure to support biomedical research in Data STAGE and AnVIL	Brian O'Connor	15:45	15:50	**Session: Open data**
Fake it 'til You Make It: Open Source Tool for Synthetic Data Generation to Support Reproducible Genomic Analyses	Adelaide Rhodes	15:50	15:55	**Session: Open data**
Q&A for lightning talks		15:55	16:00	**Session: Open data**
Coffee break		16:00	16:40	
BOSC Birds of a Feather (BoFs)		**16:40**	**17:40**	**Session: BOSC Birds of a Feather**
Poster Session		**18:00**	**20:00**	

Day 2 (Thursday, July 25, 2019)

Title	**Speaker**	**Start time**	**End time**	**Session**
Session: Late-Breaking Lightning Talks	Chair: Yo Yehudi	8:30	9:35	**Session: LBLTs**
BOSC announcements	Heather Wiencko	8:30	8:40	
Archaeopteryx.js: Web-based Visualization and Exploration of Annotated Phylogenetic Trees (JavaScript)	Christian Zmasek	8:40	8:45	**Session: LBLTs**
Sequenceserver: a modern graphical user interface for custom BLAST databases	Anurag Priyam	8:45	8:50	**Session: LBLTs**
Parallel, Scalable Single-cell Data Analysis	Ryan Williams	8:50	8:55	**Session: LBLTs**
Q&A for late-breaking lightning talks		8:55	9:00	**Session: LBLTs**
RAWG: RNA-Seq Analysis Workflow Generator	Zeyu Yang	9:00	9:05	**Session: LBLTs**
SAPPORO: workflow management system that supports continuous testing of workflows	Tazro Ohta	9:05	9:10	**Session: LBLTs**
Lazy representation and analysis of very large genomic data resources in R / Bioconductor	Qian Liu	9:10	9:15	**Session: LBLTs**
Q&A for late-breaking lightning talks		9:15	9:20	**Session: LBLTs**
The Monarch Initiative: Closing the knowledge gap with semantics-based tools	Monica Munoz-Torres	9:20	9:25	**Session: LBLTs**
DAISY: a tool for the accountability of Biomedical Research Data under the GDPR.	Pinar Alper.	9:25	9:30	**Session: LBLTs**
Q&A for late-breaking lightning talks		9:30	9:35	
Coffee break		9:40	10:15	

Title	**Speaker**	**Start time**	**End time**	**Session**
Session: Containers	Chair: Heather Wiencko	10:20	11:00	**Session: Containers**
Dockstore: Enhancing a community platform for sharing cloud-agnostic research tools	Louise Cabansay	10:20	10:40	**Session: Containers**
Bioconductor with Containers: Past, Present, and Future	Nitesh Turaga	10:40	11:00	**Session: Containers**
Mini-Break		11:00	11:15	
Session: Open science	Chair: Monica Munoz-Torres	11:15	12:22	**Session: Open science**

OpenEBench. The ELIXIR platform for benchmarking.	Salvador Capella-Gutierrez	11:15	11:35	**Session: Open science**
ELIXIR Europe on the Road to Sustainable Research Software	Mateusz Kuzak	11:35	11:55	**Session: Open science**
The Kipoi repository: accelerating the community exchange and reuse of predictive models for genomics	Julien Gagneur	11:55	12:15	**Session: Open science**
A method for systematically generating explorable visualization design spaces	Anamaria Crisan	12:15	12:22	**Session: Open science**
Lunch, BoFs, unofficial poster session		12:40	14:00	**ISMB and BOSC Birds of a Feather**

Title	**Speaker**	**Start time**	**End time**	**Session**
Session: Workflows	Chair: Michael Heuer	14:00	15:20	**Session: Workflows**
snakePipes enable flexible, scalable and integrative epigenomic analysis	Devon Ryan	14:00	14:20	**Session: Workflows**
nf-core: Community built bioinformatics pipelines	Alexander Peltzer	14:20	14:40	**Session: Workflows**
NGLess: a domain-specific language for NGS analysis (the NG-meta-profiler case study)	Luis Pedro Coelho	14:40	15:00	**Session: Workflows**
Benten: An experimental language server for the Common Workflow Language	Kaushik Ghose	15:00	15:05	**Session: Workflows**
Janis: an open source tool to machine generate type-safe CWL and WDL workflows	Richard Lupat	15:05	15:10	**Session: Workflows**
Collecting runtime metrics of genome analysis workflows by CWL-metrics	Tazro Ohta	15:10	15:15	**Session: Workflows**
Q&A for lightning talks		15:15	15:20	**Session: Workflows**
Mini-Break		15:20	15:30	
Session: Building Open Source Communities (BOSC)	Chair: Nomi Harris			**Session: BOSC**
Inclusiveness in Open Science Communities	Malvika Sharan	15:30	15:50	**Session: BOSC**
ECRcentral: An open-source platform to bring early-career researchers and funding opportunities together	Aziz Khan	15:50	16:10	**Session: BOSC**
The Data Carpentry Genomics Curriculum: Overview and Impact	Jason Williams	16:10	16:15	**Session: BOSC**

Impact of The African Genomic Medicine Training Initiative: a Community-Driven Genomic Medicine Competency-Based Training Model for Nurses in Africa	Vicky Nembaware	16:15	16:20	**Session: BOSC**
Biopython Project Update 2019	Peter Cock	16:20	16:25	**Session: BOSC**
Q&A for lightning talks		16:25	16:30	**Session: BOSC**
Introducing CoFest 2019 - the post-BOSC Collaboration Festival	Alexander Peltzer	16:30	16:35	**Session: CoFest 2019 and Closing Remarks**
Closing Remarks	Nomi Harris	16:35	16:40	**Session: CoFest 2019 and Closing Remarks**
Coffee break and ISMB closing keynote		16:40	18:20	
BOSC dinner (pay your own way)		19:30		

Any last-minute schedule updates will be posted at
https://www.open-bio.org/events/bosc/schedule/

Poster Numbers

#	Title	Talk / Poster	Poster Presenter	Talk Presenter
P-01	pysradb: A Python package to query next-generation sequencing metadata and data from NCBI Sequence Read Archive	Talk + Poster	Saket Choudhary	Saket Choudhary
P-02	snakePipes enable flexible, scalable and integrative epigenomic analysis	Talk + Poster	Devon Ryan	Devon Ryan
P-03	The FAIR data principles and their practical implementation in InterMine	Talk + Poster	Sergio Contrino	Sergio Contrino
P-04	Collecting runtime metrics of genome analysis workflows by CWL-metrics	Talk + Poster	Tazro Ohta	Tazro Ohta
P-05	GA4GH: Developing Open Standards for Responsible Data Sharing	Talk + Poster	Rishi Nag	Rishi Nag
P-07	ELIXIR Europe on the Road to Sustainable Research Software	Talk + Poster	Mateusz Kuzak	Mateusz Kuzak
P-09	A method for systematically generating explorable visualization design spaces	Talk + Poster	Anamaria Crisan	Anamaria Crisan
P-10	Biotite: A comprehensive and efficient computational molecular biology library in Python	Talk + Poster	Patrick Kunzmann	Patrick Kunzmann
P-14	NGLess: a domain-specific language for NGS analysis (the NG-meta-profiler case study)	Talk + Poster	Luis Pedro Coelho	Luis Pedro Coelho
P-16	Forome Anfisa – an Open Source Variant Interpretation Tool	Talk + Poster	Dmitry Etin	Michael Bouzinier
P-22	Janis: An open source tool to machine generate type-safe CWL and WDL workflows	Talk + Poster	Richard Lupat	Richard Lupat
P-25	Fake it 'til You Make It: Open Source Tool for Synthetic Data Generation to Support Reproducible Genomic Analyses	Talk + Poster	Adelaide Rhodes	Adelaide Rhodes
P-53	OpenEBench. The ELIXIR platform for benchmarking.	Talk + Poster	Salvador Capella-Gutiérrez	Salvador Capella-Gutiérrez
P-26	The Kipoi repository: accelerating the community exchange and reuse of predictive models for genomics	Talk + Poster	Ziga Avsec	Julien Gagneur
P-28	Dockstore: Enhancing a community platform for sharing cloud-agnostic research tools	Talk + Poster	Denis Yuen	Louise Cabansay

P-29	Disq, a library for manipulating bioinformatics sequencing formats in Apache Spark.	Talk + Poster	Michael Heuer	Michael Heuer
P-30	The Data Carpentry Genomics Curriculum: Overview and Impact	Talk + Poster	François Michonneau	François Michonneau
P-31	Epiviz File Server - Query, Compute and Interactive Exploration of data from Indexed Genomic Files	Talk + Poster	Jayaram Kancherla	Jayaram Kancherla
P-32	A lightweight approach to research object data packaging	Talk + Poster	Stian Soiland-Reyes	Stian Soiland-Reyes
P-34	ECRcentral: An open source platform to bring early career researchers and funding together	Talk + Poster	Aziz Khan	Aziz Khan
P-35	Impact of The African Genomic Medicine Training Initiative: a Community-Driven Genomic Medicine Competency-Based Training Model for Nurses in Africa	Talk + Poster	Victoria Nembaware	Victoria Nembaware
P-36	Parallel, Scalable Single-cell Data Analysis	Talk + Poster	Ryan Williams	Ryan Williams
P-40	RAWG: RNA-Seq Analysis Workflow Generator	Talk + Poster	Zeyu Yang	Zeyu Yang
P-42	What does 1.0 take? MISO LIMS after 9 years of development	Talk + Poster	Morgan Taschuk	Morgan Taschuk
P-44	SAPPORO: workflow management system that supports continuous testing of workflows	Talk + Poster	Hirotaka Suetake	Hirotaka Suetake
P-45	Lazy representation and analysis of very large genomic data resources in R / Bioconductor	Talk + Poster	Qian Liu	Qian Liu
P-47	Sequenceserver: a modern graphical user interface for custom BLAST databases	Talk + Poster	Anurag Priyam	Anurag Priyam
P-50	Archaeopteryx.js: Web-based Visualization and Exploration of Annotated Phylogenetic Trees (JavaScript)	Talk + Poster	Christian Zmasek	Christian Zmasek
P-51	The Monarch Initiative: Closing the knowledge gap with semantics-based tools	Talk + Poster	Monica C Munoz-Torres	Monica C Munoz-Torres
P-52	DAISY: a tool for the accountability of Biomedical Research Data under the GDPR.	Talk + Poster	Venkata Pardhasaradhi Satagopam	Venkata Pardhasaradhi Satagopam

#	Title	Talk / Poster	Poster Presenter
P-06	Creating a pluggable visualisation toolsuite with BlueGenes Tool API	Poster only	Yo Yehudi
P-08	Cellular Genetics Informatics support group: Nextflow and Jupyter on Kubernetes, Nextflow web interface	Poster only	Anton Khodak
P-11	OpenBio-C: An Online Social Workflow Management System and Research Object Repository	Poster only	Alexandros Kanterakis
P-12	CWLab: an open-source, platform-agnostic, and cloud-ready framework for simplified deployment of the Common Workflow Language using a graphical web interface	Poster only	Kersten Henrik Breuer
P-13	pdb-tools: a dependency-free cross-platform swiss army knife for PDB files.	Poster only	João Rodrigues
P-15	OmicsSIMLA: A multi-omics data simulation tool for complex disease studies	Poster only	Ren-Hua Chung
P-17	Tagging of disease names in biomedical literature	Poster only	Jeanette Prinz
P-18	WhatsHap: fast and accurate read-based phasing	Poster only	Peter Ebert
P-19	Recommendations and guidelines for tumor heterogeneity quantification using deconvolution of methylation data: data challenges as a tool for benchmarking studies	Poster only	Magali Richard
P-20	Sustainability of legacy software - Making the antiSMASH genome mining tool ready for the future	Poster only	Kai Blin
P-21	Methrix: An R package for efficient processing of bedGraph files from large-scale methylome cohorts	Poster only	Anand Mayakonda
P-23	Run Scanner: a tool for monitoring sequencer runs and accessing run information	Poster only	Morgan Taschuk
P-24	Ada Discovery Analytics: All-in-One Data Platform for Clinical and Translational Medicine with Scalable Machine Learning	Poster only	Peter Banda
P-27	CViTjs: Dynamic Whole Genome Visualisation	Poster only	Andrew Wilkey
P-33	Developing Python and Rust libraries to improve the ontology ecosystem	Poster only	Martin Larralde
P-37	Another point of view for the fast and accurate large MSA, the regressive approach	Poster only	Edgar Garriga Nogales
P-38	Analyzing protein structure and evolution using Julia with MIToS.jl	Poster only	Diego Zea
P-55	ImmPort: Ensuring FAIR Data through a Trustworthy Biomedical Data Repository	Poster only	Dawei Lin

P-39	Pedigree-based analysis pipeline version 2 (PBAP v.2): new features added	Poster only	Alejandro Nato
P-41	Crowdsourcing towards Antimicrobial Resistance & Open Source Drug Discovery	Poster only	Anshu Bhardwaj
P-43	10 recommendations to make your research software FAIRer	Poster only	Carlos Martinez Ortiz
P-46	Terra Open Science Contest	Poster only	Geraldine Van der Auwera
P-48	EDAM: the ontology of bioinformatics operations, types of data, topics, and data formats (2019 update)	Poster only	Hervé Ménager
P-49	Physlr: Construct a Physical Map from Linked Reads	Poster only	Shaun Jackman
P-56	java2script/SwingJS for bioinformatics: Reintroducing Jalview on the Web as JalviewJS	Poster only	Robert Hanson

The Open Bioinformatics Foundation

Heather Wiencko

The Open Bioinformatics Foundation (https://www.open-bio.org/) is a non-profit, volunteer-run group that promotes open source software development and Open Science within the biological research community. The OBF helps to provide support and publicity for a variety of member projects. It also runs the annual Bioinformatics Open Source Conference (BOSC) and the associated CollaborationFest. Since 2016, the OBF has sponsored a Travel Fellowship program aimed at increasing diversity at community events.

The OBF is open to anyone who is interested in promoting open source bioinformatics / open science, which includes everyone at BOSC! We invite you to learn more about the OBF and engage in a two-way dialog with OBF Board members at the OBF BoF on 25-July at 12:45pm, which will include a vote on a new candidate for the Board.

Google Summer of Code 2018

Kai Blin

Google's Summer of Code program is focused on introducing students to open source software development. Students are paired up with mentors from participating organisations and earn a stipend while spending their summer semester break getting an exposure to real-world software development practices. In the past years, the Open Bioinformatics Foundation has participated in the Google Summer of Code eight times. In 2018, the Open Bioinformatics Foundation has acted as an umbrella organisation for four projects from the open source bioinformatics community, and five students successfully finished the program. In 2019, OBF is an umbrella for five open source bioinformatics projects. This talk will present an overview of the projects hosted under the OBF umbrella in last year's round of Google Summer of Code, as well as present the projects in the current round.

Introducing CoFest 2019 - the post-BOSC Collaboration Festival

Alexander Peltzer

In conjunction with the Bioinformatics Open Source Conference (BOSC), the Open Bioinformatics Foundation (OBF) runs a welcoming, self-organizing, non-competitive, and highly productive collaborative event called the CollaborationFest, or CoFest.

Everyone is welcome to attend. We will have a mix of experienced developers, users, trainers, and researchers, newcomers to experienced bioinformaticians, and everything in between. Attendees will self-organize into working groups based on shared interests like programming languages, open source projects, or biological questions.

CollaborationFest is not a competition; there are no prizes. Rather its goals are to grow and foster the contributor community for open source bioinformatics projects, and to extend, enhance, and otherwise improve open-source bioinformatics code and non-code artefacts, such as documentation and training materials.

This will be the 10th such event since 2010, which we originally called the Coding Festival or CodeFest. Communities such as Galaxy, Common Workflow Language, Nextflow, and others have found CollaborationFest a fun, rewarding, and highly productive experience. As in previous years, a summary of the results of the event will be included in the BOSC meeting report.

CollaborationFest 2019 will take place the two days after BOSC, July 26-27, at The Swiss Innovation Hub for Personalized Medicine in Basel, Switzerland. Registration is free; sponsorships offset the cost of the venue, coffee and snacks.