

## DEMO & POSTER LIST BioSB 2023

### DEMO LIST

Nr	Authors	Title
1	Luca Gerhards, Vladimir Bacic and Ilia Solov'Yov	VIKING: An Online Platform for Multiscale Modeling
2	Xiaofeng Liao, Anna Niehues, Casper de Visser, Junda Huang, Thomas Ederveen, Purva Kulkarni, Joeri van der Velde, Morris Swertz, Martin Brandt, Alain van Gool and Peter-Bram Hoen	FAIR Data Cube, a data sovereignty solution for integrated multi-omics data analysis
3	Astrid van den Brandt, Folkert de Vries, Sander Vlugter, Roel van Esch, Huub van de Wetering, Anna Vilanova and Sandra Smit	PanVA: Visual Analytics for Pangenome Exploration
4	Hasan Balci, Ugur Dogrusoz, Yusuf Ziya Ozgul and Perman Atayev	SyBLaRS: Systems Biology Layout & Rendering Service
5	Tooba Abbassi-Dalooi, Denise Slenter, Ozan Cinar, Chris Evelo and Egon Willighagen	BridgeDb-Shiny: A User-Friendly Application for Seamless Data Interoperability in Biological Research

### POSTER LIST

Nr	Authors	Title	Topic
1	Lorena Bucur, Reza Haydarlou, Sergio Martinez Cuesta, Abel Sousa and Avid Afzal	Developing protein ML bioinformatics approaches for hit discovery projects	Artificial intelligence
2	Xiaoyun Liu, Stijn Meijnikman, Anne Linde Mak, Onno Holleboom, Natal van Riel, Peter Hilbers and Dragan Bosnacki	Machine Learning Based Clinical Scoring of Whole Slide Images for Nonalcoholic Fatty Liver Disease	Artificial intelligence
3	Lucia Barbadilla Martinez, Jeroen De Ridder and Jeremie Breda	Promoter activity prediction based on massively parallel characterization	Artificial intelligence
4	Merel van Lieverloo, Anna Niehues, Alain van Gool and Peter-Bram T Hoen	Uncovering patterns in multi-omics using deep learning techniques	Artificial intelligence
5	Inez den Hond, Lieke Michielsen and Ahmed Mahfouz	Fine-Tuning Existing Deep Learning Models To Predict Gene Expression From DNA Sequence For New Unseen Cell Types	Artificial intelligence

## DEMO & POSTER LIST BioSB 2023

Nr	Authors	Title	Topic
6	Gabriel Vogel, Paolo Sortino and Jana M. Weber	Variational autoencoders for the design of sustainable plastic	Artificial intelligence
7	Javier Millan Acosta and Egon Willighagen	The eNanoMapper Ontology v9.0: Semi-automated and Community-based Ontology Development	Artificial intelligence
8	Yasin Tepeli and Joana P. Gonçalves	Mitigating Selection Bias Using Diverse and Balanced Unlabelled Data	Artificial intelligence
9	Jie Ju, Ioannis Ntafoulis, Marcel Reinders, Martine Lamfers, Andrew Stubbs and Yunlei Li	Two-step transfer learning improves deep learning-based drug response prediction in small datasets	Artificial intelligence
10	Steven Wijnen, Ruben van Boxtel and Joske Ubels	Unraveling the male susceptibility to cancer: A bioinformatics perspective	Artificial intelligence
11	Katharina Waury, Renske De Wit, Inge Verberk, Charlotte Teunissen and Sanne Abeln	Deciphering protein secretion from the brain to cerebrospinal fluid for biomarker discovery	Artificial intelligence
12	Maryna Chepeleva, Sang-Yoon Kim, Vladimir Despotovic, Tony Kaoma, Reka Toth and Petr Nazarov	Multomics and digital histopathology data integration with a reference-free consICA deconvolution method	Artificial intelligence
13	Kimberley Zwiers	Building a strong multidisciplinary (national) platform to support the future of data driven health and life sciences in the Netherlands.	Artificial intelligence
14	Sander Goossens, Yasin Tepeli and Joana Gonçalves	Integrated learning of mutational signatures and prediction of DNA repair pathway deficiency using Supervised Non-negative Matrix Factorization (SNMF)	Artificial intelligence
15	Konstantina Tzavella, Wim Vranken and Catharina Olsen	Combining evolution and protein language models for cancer driver mutation prediction with D2D	Evolutionary systems biology & bioinformatics
16	F.J.M. van Workum, S.L. Mehrem, L.B. Snoek, D. de Ridder, M.E. Schranz and S. Smit	A Lactuca super-pangenome reveals importance of presence/absence variation for lettuce breeding	Evolutionary systems biology & bioinformatics
17	Hasan Balci and Martina Kutmon	From WikiPathways to Drug Repurposing for COVID-19: Utilizing Knowledge Graphs to Identify Novel Therapies	Evolutionary systems biology & bioinformatics

## DEMO & POSTER LIST BioSB 2023

Nr	Authors	Title	Topic
18	Christina Papastolopoulou, Ronald Nieuwenhuis, Sven Warris, Linda Bakker, Jan van Haarst, Jan Cordewener, Thamara Hesselink, Hetty van den Broeck, Willem van Dooijeweert, Hans de Jong, Julapark Chunwongse, Sara Diaz Trivino, Elio Schijlen, Dick de Ridder, Sandra Smit and Sander Peters	Towards a graph-based Capsicum pangenome including wild species	Evolutionary systems biology & bioinformatics
19	Giulia Crocioni, Dario F. Marzella, Daniil Lepikhov, Heleen Severin, Coos Baakman, Daniel T. Rademaker, Dani Bodor, Chiayu Lin and Li C. Xue	From Sequences, to Structures, to AI: Advancing Cancer Vaccine Design with DeepRank-Core	Evolutionary systems biology & bioinformatics
20	Yi Chen, Frank Takes, Fons Verbeek and Katy Wolstencroft	Understanding the impact of Gene Ontology evolution with temporal semantic similarity	Evolutionary systems biology & bioinformatics
21	Sebastian Höpfl and Nicole Radde	Bayesian estimation shows the merits of reproducible and reusable modeling in systems biology	ELIXIR-NL
22	Rob Hooft and Corinne Martin	Parallels between 'road' and 'research data' infrastructures	ELIXIR-NL
23	Jasper Ouwerkerk, Helena Rasche, Dylan Spalding, Saskia Hiltemann and Andrew Stubbs	FAIR Data Retrieval for Sensitive Clinical Analysis in Galaxy	ELIXIR-NL
24	Jose Gavalda-Garcia, Adrian Diaz and Wim Vranken	A roadmap to scientific software deployment: bio2Byte Tools as a use case	ELIXIR-NL
25	Casper de Visser, Lennart F. Johansson, Purva Kulkarni, Hailiang Mei, Pieter Neerincx, Joeri van der Velde, Morris Swertz, Péter Horvatovich, Alain J. van Gool, Peter-Bram T Hoen and Anna Niehues	Ten simple rules for building FAIR workflows	ELIXIR-NL
26	Daphne Wijnbergen, Rajaram Kaliyaperumal, Marco Roos and Eleni Mina	The FAIR Data Point Populator: collaborative FAIRification and population of FAIR Data Points	ELIXIR-NL
27	Jeaphianne van Rijn and Egon Willighagen	A network of causal relationships linking the chemistry of a nanomaterial to their toxicology	ELIXIR-NL
28	Julian Dekker, Niek Van Ulzen, Nuria Queralt Rosinach, Rajaram Kaliyaperumal, Aliya Aktau, Marco Roos, Marcel Reinders, Eline Slagboom and Marian Beekman	Pilot towards FAIRification of the Leiden Longevity Study data	ELIXIR-NL

## DEMO & POSTER LIST BioSB 2023

Nr	Authors	Title	Topic
29	Lifang Liu, Jan-Willem Boiten, Robin Verjans, Ruben Kok, Rob Hooft and Celia van Gelder	The Health-RI infrastructure: Umbrella for the Dutch ESFRI Nodes	ELIXIR-NL
30	Sam de Vos, Shashikant Badloe, Eugene Verwiël, Marcel Santoso, Alex Janse, John Baker-Hernandez, Marc van Tuil, Claudia van Hamersveld, Lennart Kester, Jayne Hehir-Kwa, H.H.D. Kerstens, Bastiaan Tops and Patrick Kemmeren	Facilitating FAIR data usage of cancer genomes from the Dutch childhood cancer biobank	ELIXIR-NL
31	Marvin Martens, Chris Evelo, Rob Stierum, Karine Audouze and Egon Willighagen	Accelerating toxicological research through collaboration and data reuse: The ELIXIR Toxicology Community	ELIXIR-NL
32	Karolis Cremers, Marco Roos, Katy Wolstencroft, Eleni Mina and Núria Queralt-Rosinach	Structured review of iron in Huntington's Disease	ELIXIR-NL
33	L.C. Suurenbroek, C.G. van der Ham, M. Yeong, M.L. den Boer, J.M. Boer, E. Sonneveld, J.L.C. Loeffen and R.P. Kuiper	UV-associated DNA damage in pediatric B-ALL	Cancer research
34	Ianthe A.E.M. van Belzen, Marc C. van Tuil, Shashi Badloe, Alex Janse, Eugène T.P. Verwiël, Marcel Santoso, Sam de Vos, John Baker-Hernandez, Hindrik H.D. Kerstens, Michael T. Meister, Claudia Y. Janda, Bas B.J. Tops, Frank C.P. Holstege, Patrick Kemmeren and Jayne Y. Hehir-Kwa	Complex structural variation patterns and mechanisms are shared across pediatric solid tumors	Cancer research
35	Stavros Makrodimitris, Mark van de Wiel, Teoman Deger, Maurice Jansen, Jaco Kraan, Corine Beaufort, Dirk Grunhagen, Ruben Boers, Joost Gribnau, Stefan Sleijfer, Kees Verhoef, John Martens and Saskia Wilting	A multi-omic model for non-invasive tumor load quantification from blood plasma	Cancer research
36	Bernard Evers and Barbara M. Bakker	The ACO <sub>2</sub> :CS ratio as a putative marker for lowering lactate production to sensitize melanoma patients to immune therapy	Cancer research
37	Daan Hazelaar, Youri Hoogstrate, Stavros Makrodimitris, Henk Verheul and John Martens	Localized enrichment of DNA breaks reveals possible driver events in metastatic prostate cancer	Cancer research
38	Famke Schulting, Jayne Hehir-Kwa, Patrick Kemmeren and Hinri Kerstens	Improving variant phasing in short-read data of the Princess Máxima Center Biobank	Cancer research

## DEMO & POSTER LIST BioSB 2023

Nr	Authors	Title	Topic
39	Joanna von Berg, Ianthe van Belzen, Fleur Wallis, Anastasia Spinou, Lennart Kester, John Baker-Hernandez, Richard Gremmen, Alex Janse, Shashi Badloe, Sam de Vos, Douwe van der Leest, Eugène Verwiel, Marc van Tuil, Hindrik Kerstens, Jayne Hehir-Kwa, Bastiaan Tops, Frank Holstege and Patrick Kemmeren	Identifying genomic and transcriptomic drivers in pediatric cancers	Cancer research
40	Charlotte Adang, Anastasia Spinou and Patrick Kemmeren	Investigating phenotypic plasticity through the detection of higher order genetic interactions in acute myeloid leukaemia	Cancer research
41	Marcel Santoso, John Baker-Hernandez, Hindrik H.D. Kerstens, Sam de Vos, Alex Janse, Shashi Badloe, Eugène T.P. Verwiel, Jayne Y. Hehir-Kwa and Patrick Kemmeren	Towards Cloud Bioinformatics: Leveraging Cloud Computing and Containerization to Address the Challenges of Large-Scale Genomic Data Analyses	Cancer research
42	Freerk van Dijk	Preliminary results of germline whole genome sequencing of 119 extremely early age of onset bladder cancer patients in the MOTIEF study	Cancer research
43	Christina Veltman, Jeroen Pennings, Anna-Melina Steinbach, Phillip Marx-Stoelting, Bob van de Water and Mirjam Luijten	Towards a quantitative adverse outcome pathway model for chemically-induced oxidative stress leading to liver cancer	Cancer research
44	Anastasia Spinou, Richard Gremmen, Puck Veen, Jarno Drost and Patrick Kemmeren	Abundant genetic interactions detected by the inference of pathway relationships in pediatric cancer	Cancer research
45	Carolina Pita Barros, Zeinab van Gestel-Fadaie, Nina U. Gelineau, Julia Sprokkerieft, Arjan Boltjes, Freerk van Dijk, Reno S. Bladergroen, Giovanna V. ter Huizen, Eugène T.P. Verwiel, Jayne Y. Hehir-Kwa, Patrick Kemmeren and Godelieve A.M. Tytgat	CNA detection in NBL liquid biopsy WES	Cancer research
46	Richard Gremmen, Josephine Daub and Patrick Kemmeren	Stratifying pediatric cancers by mutational signature results in new genetic interaction candidates	Cancer research
47	Renske de Wit, Soufyan Lakbir, Caterina Buranelli, Sanne Abeln and Remond J.A. Fijneman	Characterizing the Landscape of L1 Activity in Colorectal Cancer	Cancer research

## DEMO & POSTER LIST BioSB 2023

Nr	Authors	Title	Topic
48	Michelle Kleisman	The genomic landscape and expression patterns of pediatric T-cell lymphoblastic lymphoma and its similarities and differences to T-cell acute lymphoblastic leukemia	Cancer research
49	Alex Janse, Eugène Verwiel, Shashikant Badloe, Sam de Vos, Marcel Santoso, John Baker-Hernandez, H.H.D. Kerstens, Marc van Tuil, Eric Strengman, Lennart Kester, Marco Koudijs, Bastiaan Tops, Patrick Kemmeren and Jayne Hehir-Kwa	Using Next Generation Sequencing Analysis to Diagnose Childhood Cancer	Cancer research
50	Melanie Opperman, Soufyan Lakbir, Remond Fijneman and Sanne Abeln	Development of a robust pipeline to identify patients with a high tumor break load.	Cancer research
51	Pien Toebosch, Barbara Rentroia-Pacheco, Domenico Bellomo, Loes M Hollestein, Marlies Wakkee and Harmen J G van de Werken	Integration of the Pan-transcriptome of Squamous Cell Carcinoma.	Cancer research
52	Lara Pozza, Sena Zümürütçü, Lizanne Bosman, Ashley van der Spek, Dennie Tempel and Domenico Bellomo	Bridging gene expression signatures across qPCR platforms	Cancer research
53	Fatih Bogaards, Thies Gehrman, Marian Beekman, Lisette de Groot, Marcel Reinders and Eline Slagboom	Transcriptomic Response of Postprandial Blood, Fat and Muscle to a combined lifestyle intervention in older adults, the GOTO study	Mechanistic & Multiscale modelling
54	Jia-Xian Yin, Ming-Hsiu Hsieh, Shih-Che Sue and Jen-Shiang K. Yu	Investigation on the Binding Mechanism between CXCR3 and Chemokines	Mechanistic & Multiscale modelling
55	Ryan de Vries, Shauna O'Donovan and Natal van Riel	From Population to Personalized Physiological Models; Parameter Estimation Approaches in a Physiology-Constrained Simulation Study	Mechanistic & Multiscale modelling
56	Meine Boer, Chrats Melkonian, Andi Haas, Daniel Garza and Bas Dutilh	Deep learning improves the gap-filling of genome scale metabolic models.	Mechanistic & Multiscale modelling
57	Zeynep Efsun Duman Ozdamar, Jeroen Hugenholtz, Vitor A.P. Martins dos Santos and Maria Suarez Diez	Model-driven design of <i>Yarrowia lipolytica</i> as a cell factory for improved microbial oil production	Mechanistic & Multiscale modelling
58	Michiel Bexkens, Olivier Martin, Bas Teusink, Barbara Bakker, Jaap van Hellemond, Jurgen Haanstra and Aloysius Tielens	The unusual kinetics of lactate dehydrogenase of <i>Schistosoma mansoni</i> play a role in the rapid metabolic switch after penetration of the mammalian host	Mechanistic & Multiscale modelling

## DEMO & POSTER LIST BioSB 2023

Nr	Authors	Title	Topic
59	Max de Rooij, Balázs Erdos, Natal van Riel and Shauna O'Donovan	Accelerating Dynamic Modelling and Parameter Estimation in Biology using the Julia Programming Language	Mechanistic & Multiscale modelling
60	Cyriel Huijjer and Rosemary Yu	Using Metabolic Modeling to Identify New Therapeutic Targets for Triple-Negative Breast Cancer	Mechanistic & Multiscale modelling
61	Taras Lukashiv, Igor Malyk, Maryna Chepeleva, Bakhtiyor Nosirov, Atte Aalto, Anna Golebiewska and Petr V. Nazarov	A parametrized mathematical model of glioblastoma cell proliferation	Mechanistic & Multiscale modelling
62	Martin Elferink, Maria Zwartkruis, Paul Hop, Ramona Zwamborn, Ivo Renkens, Joke van Vugt, Leonard van den Berg, Patrick Vourc'H, Véronique Danel, Philippe Corcia, Hanneke van Deutekom, Ludo van der Pol, Gijs van Haften, Ewout Groen and Jan Veldink	Long-read sequencing including DNA methylation detection enables detailed characterization of the C9orf72 locus within amyotrophic lateral sclerosis patients.	Health research
63	Nils Steinz, Tjardo Maarseveen, Erik van den Akker, Yann Abraham and Rachel Knevel	Rheumatoid arthritis medication effects shown with data-driven approaches	Health research
64	Yaran Zhang	MotifScope: A tool to characterize motif composition in tandem repeats	EXTRA
65	Niccolò Tesi, Alex Salazar, Yaran Zhang, Sven van der Lee, Marc Hulsman, Marcel Reinders and Henne Holstege	TREAT: A toolbox to accurately genotype, characterize, and visualize tandem repeats from long-read sequencing data	Health research
66	Marie Corradi, Alyanne de Haan, Thomas Luechtefeld, Raymond Pieters and Marc Teunis	Facilitating modern toxicology with Natural Language Processing	Health research
67	Lucija Malinar	Development of computational pipeline to predict exon splicing events for gene augmentation therapy	Health research
68	Sanne Hartog, Melanie de Gier and Hailiang Mei	Interactive user-friendly interface for B-cell receptor repertoire analysis: extending the functionality of Antigen Receptor Galaxy	Health research
69	Ammar Ammar, Chris Evelo, Rachel Cavill and Egon Willighagen	PSnpBind-ML: predicting the effect of binding site mutations on protein-ligand binding affinity	Structural biology
70	Willem de Koning, Casper W.F. van Eijck, Fleur van der Sijde, Gaby J. Strijk, Astrid A.M. Oostvogels, Reno Debets, Casper H.J. van Eijck and Dana A.M. Mustafa	Analyzing flow cytometry or targeted gene expression data influences clinical discoveries; profiling blood samples of pancreatic ductal adenocarcinoma patients	Structural biology

## DEMO & POSTER LIST BioSB 2023

Nr	Authors	Title	Topic
71	Floris van der Flier, Sina Pricelius, Lydia Dankmeyer, Harm Mulder, Rei Otsuka, Frits Goedegebuur, Diego Staphorst, Dave Estell, Aalt-Jan van Dijk, Dick de Ridder and Henning Redestig	Why is the effect of certain mutations harder to predict than others?	Structural biology
72	Paolo Sortino, Salvatore Contino and Roberto Pirrone	Graph Convolutional Architecture for Virtual Screening	Structural biology
73	Qitong Huang	MAE-seq refines regulatory elements across the genome	Structural biology
74	Leron Kok, Jip van Dinter, Damon Hofman and Sebastiaan van Heesch	Predicting tumor-specific neoantigens for the identification of novel immunotherapeutic targets	Structural biology
75	Jan Aarts, Farzaneh Meimandi Parizi, Gayatri Ramakrishnan, Lars Melio and Li Xue	Efficient Computational Docking of TCR:pMHC Complexes Using Restricted Rotation Matrices and Distance Restraints	Structural biology
76	Amelia Villegas-Morcillo, Jana M. Weber and Marcel J.T. Reinders	Designing Antibody Sequence and Structure with Suitable Developability Properties for Therapeutics	Structural biology
77	Heleen Severin	From Sequences to Structures: Deep Learning for Peptide-MHC Binding Affinity Prediction	Structural biology
78	Arthur Goetzee and Janani Durairaj	Ligand Binding Site Comparison Using a Graph Variational Autoencoders	Structural biology
79	Lindy Visser, Margit Bleijs, Thanasis Margaritis, Marc van de Wetering, Frank Holstege and Hans Clevers	Ewing sarcoma single-cell transcriptome analysis reveals functionally impaired antigen-presenting cells	Single-cell techniques
80	Julian Arts, Jos Smits, Dulce Cunha, Janou Roubroeks and Jo Zhou	Characterizing Cell States in the Human Cornea with a Multi-Omics Meta-Atlas	Single-cell techniques
81	Lieke Michielsen, Justine Hsu, Marcel Reinders, Ahmed Mahfouz and Hagen Tilgner	Unraveling alternative splicing mechanisms in the brain by applying deep learning to long-read single-cell data	Single-cell techniques
82	Daniel Kaptijn, Maryna Korshevniuk, Roy Oelen, Lude Franke, Monique van der Wijst and Marc Jan Bonder	Single-cell consortium for federated PBMC data pipeline for cell-type specific eQTL mapping and downstream analyses	Single-cell techniques
83	Tim Stohn and Evert Bosdriesz	Single Cell Comparative Network Reconstruction	Single-cell techniques



## DEMO & POSTER LIST BioSB 2023

Nr	Authors	Title	Topic
84	Frank M. Riemers, Deepani W. Poramba-Liyanage, Peter Zeller, Xiaole Tong, Alexander van Oudenaarden and Marianna A. Tryfonidou	Single-cell understanding of nucleus pulposus degeneration to instruct new treatment strategies for intervertebral disc disease	Single-cell techniques
85	Daniel Rademaker	Quantifying the deformability of malaria-infected red blood cells using deep learning trained on synthetic cells	Single-cell techniques
86	Abdool Al-Khaledi and Onur Basak	Identifying cell-types enriched in ASD activity during brain development.	Single-cell techniques
87			
88	Sabine van Oossanen, Sarah D'Adamo, Vitor Martins dos Santos, Maria Suarez Diez and Maria Barbosa	Designing microalgal metabolism: Improving lipid productivity in <i>Nannochloropsis</i> through genome-scale metabolic modeling	Microbial genomics
89	Lakhansing Pardeshi, Eef M. Jonkheer, Dick de Ridder, Sandra Smit and Theo A. J. Van Der Lee	Pangenomics to understand the emergence of a new <i>Pectobacterium brasiliense</i> pathovar	Microbial genomics
90	Erin Jordan, Ramin Shirali Hossein Zade, Thomas Abeel and Oliver Kayser	<i>Saccharomyces cerevisiae</i> CEN.PK2-1C undergoes plasma membrane remodelling and ion transport overregulation in response to cannabidiol exposure	Microbial genomics
91	Marco Campos	Optimization of para-aminobenzoic acid production using Design of Experiments	Microbial genomics
92	Ernestina Hauptfeld, Bas E. Dutilh and Fa Bastiaan von Meijenfeldt	Putting the RAT into integRATed profiling: a new way to annotate shotgun metagenomes	Microbial communities
93	Chengyao Peng, Ali May and Thomas Abeel	Accelerating microbiome-based precision feed by machine learning: explaining methane emission variance in Holstein cows	Microbial communities
94	Stephanie Pillay, Ramin Shirali Hossein Zade, Paul van Lent and Thomas Abeel	Metagenomic analysis of antibiotic resistance through the waste water cycle	Microbial communities
95	Bastiaan von Meijenfeldt, Su Ding, Nicole Bale, Jaap Sinninghe Damste and Laura Villanueva	Metagenomic and metalipidomic exploration of unusual lipids in the Black Sea	Microbial communities
96	Hilde Stawski and Mirna Baak	Development and application of a pipeline for Functional Metagenomics using shotgun metagenome data	Microbial communities

## DEMO & POSTER LIST BioSB 2023

Nr	Authors	Title	Topic
97	Peter Schaap, Alette Langenhoff, Robbert Kleerebezem, Jasper Koehorst, Merve Atasoy, Gerben Stouten and Hauke Smidt	Unlock, a large-scale infrastructure for research on microbial communities.	Microbial communities
98	Leonardo Tenori, Alessia Vignoli, Emanuela Risi, Erica Moretti, Luca Livraghi, Laura Biganzoli and Claudio Luchinat	Identification of Breast Cancer Patients at Higher Risk of Disease Relapse in Middle-aged and Elderly Subjects using NMR-based Metabolomics	Algorithms for genomics
99	Ben Noordijk, Reindert Nijland, Victor Carrion, Jos Raaijmakers, Dick de Ridder and Carlos de Lannoy	baseLess: lightweight detection of sequences in raw MinION data	Algorithms for genomics
100	Sarah Mehrem, Matthijs Kon, Douwe ten Bulte, Justin J. D. Pelle and Basten L. Snoek	Anthocyanin in Lettuce: A kmer GWAS case study	Algorithms for genomics
101	Marcel van de Streek, Maarten Penning, Loes van de Pasch, Pascal van der Weele, Sjoerd Creutzburg, Sam Stokman, Anne Manders, Bart Valkenburg, Ioannis Nemparis and Joris Albers	Fast Oxford Nanopore sequencing for accurate genotyping of polymorphic HLA genes	Algorithms for genomics
102	Henk van Lingen, Maria Suarez-Diez and Edoardo Saccenti	Exploring RNA-seq data normalization methods using principal component analysis and KEGG pathway enrichment	Algorithms for genomics
103	Vincent de Boer and Anna Bekebrede	Accurate metabolic cellular phenotyping using extracellular flux analysis coupled with a dedicated image analysis pipeline in R	Algorithms for genomics
104	Hanneke Leegwater, Zhengzheng Zhang, Amy Harms, Annelien Zweemer, Sylvia Le Dévédec and Alida Kindt	Normalization strategies for lipidomics data to correct for differences in biological material for cell line panels	Algorithms for genomics
105	Fred White, Anna Heintz-Buschart, Lemeng Dong, Harro Bouwmeester, Age Smilde and Johan Westerhuis	MASCARA: coexpression analysis in data from designed experiments	Algorithms for genomics
106	Aishwarya Iyer, Friederike Ehrhart, Martina Kutmon, Cenna Doornbos, Eleni Mina, Juan Carlos García-Pagán, Virginia Hernández-Gea, Juanjo Lozano, Peter-Bram Hoen and Chris Evelo	GSEA and co-expression network analysis approach to identify molecular processes affected in Porto-sinusoidal Vascular Disease	Algorithms for genomics
107	Joeri van Strien, Felix Evers, Taco W.A. Kooij and Martijn A. Huynen	A Gaussian mixture modelling-based workflow for automated identification of protein complexes from complexome profiling data	Algorithms for genomics
108	Isabel Mathilde Houtkamp, Ryoji Yoshisada, Juami van Gils, Seino Jongkees, Sanne Abeln and Halima Mouhib	Mining high-throughput sequencing data from mRNA display	Algorithms for genomics

## DEMO & POSTER LIST BioSB 2023

<b>Nr</b>	<b>Authors</b>	<b>Title</b>	<b>Topic</b>
109	Felicia Wolters, Justin J. J. van der Hooft, Eric Schranz, Klaas Bouwmeester and Marnix H. Medema	Biosynthetic Pathway Discovery in Plants Based on Omics Data Integration	Algorithms for genomics
110	Roy Lardenoije, Angela Kruse, Morad Malek, Nathan Heath, Haichun Yang, Agnes Fogo, Diane Saunders, Al Powers, Jeffrey Spraggins and Joana Gonçalves	Spatial Transcriptomics in the Human BioMolecular Atlas Program	Algorithms for genomics
111	Colm Seale, Marco Barazas, Robin Van Schendel, Marcel Tijsterman and Joana P. Gonçalves	Compositional Analysis of Mutational Spectra Identifies Gene Associations with DNA Repair	Algorithms for genomics
112	Marvin Martens, Chris Evelo and Egon Willighagen	Molecular Adverse Outcome Pathways: towards the implementation of transcriptomics data in risk assessments	Algorithms for genomics