

Poster nr.	Authors	Title	Topic
1	Laura van Rooijen, Rachel Cavill and Lars Eijssen	Generating a workflow for multiple omics integration and assessing publicly available data	ELIXIR-NL FAIR data
2	Egon Willighagen, Alasdair Gray, Anders Riutta, Alex Pico, Ian Dunlop, Carole Goble, Marvin Martens, Friederike Ehrhart, Denise Slenter, Martina Kutmon and Chris Evelo	Identifier interoperability is only one R package away (or web service, or Java library, or ...)	ELIXIR-NL FAIR data
3	Alexey Kolodkin, Lilia Alberghina, Jacky L. Snoep, Gennaro Piccialli, Massimiliano Borsani and Hans V. Westerhoff	Infrastructure Systems Biology Europe (ISBE): Emergence of Innovative Systems Biology Servicing	ELIXIR-NL FAIR data
4	Celia van Gelder and Mateusz Kuzak	FAIR Data Training activities in the Dutch ELIXIR node	ELIXIR-NL FAIR data
5	K. Joeri van der Velde, Bart Charbon, Mark de Haan, Gert-Jan van de Geijn, Mateusz Kuzak and Morris Swertz	Implementation of BioSchema for multiple patient registries	ELIXIR-NL FAIR data
6	Mattias de Hollander and Fleur Gawehns	NIOO-KNAW Bioinformatics Unit	ELIXIR-NL FAIR data
7	Christian Groß, Dick De Ridder and Marcel Reinders	Predicting variant deleteriousness in non-human species: applying the CADD approach in mouse	Genetic Variants & Population Studies
8	Niek de Klein, Freerk van Dijk, Annique Claringboud, Patrick Deelen, Urmo Vösa, Joost Verlouw, Ramin Monajemi, Richard Sinke, Morris Swertz, Peter A.C. 't Hoen and Lude Franke	Allele specific expression identifies rare variants as cause for extreme allelic imbalance	Genetic Variants & Population Studies
9	Elisa Cirillo, Kyoko Watanabe, Niels Delahaije, Rik van Dael, Martina Kutmon, Michiel Adriaens, Laurence Pamell and Chris Evelo	A genetic reference network to better understand the non-coding variants in obesity	Genetic Variants & Population Studies
10	Olivier Bakker, Raul Aguirre Gamboa, Twan Spenkelink, Urmo Vösa, Martin Jaeger, Marije Oosting, Sanne Smeekens, Romana Netea-Maier, Ramnik Xavier, Iris Jonkers, Lude Franke, Leo Joosten,	Multivariate analysis of immune phenotypes reveals novel genetic and context specific genetic factors for cytokine production capacity	Genetic Variants & Population Studies
11	Hilmi Al-Shakhshir, Job Verdonschot, Kasper Derks, Stephane Heymans, Ilja Arts and Michiel Adriaens	Striking the allelic imbalance in dilated cardiomyopathy	Genetic Variants & Population Studies
12	Asli Kucukosmanoglu	Genetic complementation predicts convergent evolution in glioblastoma	Genetic Variants & Population Studies
13	Niccolo' Tesi, Sven van der Lee, Marc Hulsman, Iris Jansen, Najada Stringa, Natasja van Schoor, Hanne Meijers-Heijboer, Martijn Huisman, Philip Scheltens, Marcel Reinders, Wiesje van der Flier	Genetic case-control study with healthy centenarians as controls identifies PLCG2-variant as survival-associated and APOE alleles as Alzheimer's Disease-associated	Genetic Variants & Population Studies
14	Joanna von Berg, Sara Pulit and Jeroen de Ridder	What's in a name? Defining ischemic stroke phenotypes for Genome-Wide Association Studies	Genetic Variants & Population Studies
15	Roel Glas, Gerrit Meijer, Jaap Heringa, Remond Fijneman and Sanne Abeln	Detection of Chromosomal Breakpoints in TCGA Copy Number Data	Genomics
16	Ksenia Arkhipova and Bas E. Dutilh	Expanding knowledge of gene order conservation in viral genomes	Genomics
17	Rogier Stuger and Hans Westerhoff	Structural systems biology: forcing DNA into nucleoids	Genomics
18	Ronald de Jongh, Rita Volkens, Janine Verbokkem, Aalt-Jan van Dijk, Peter Schaap, Jan Springer, Vitor Martins Dos Santos, Gerrit Eggink and Dick de Ridder	Towards predictable, portable promoters	Genomics
19	Chiara Bortoluzzi, Mirte Bosse, Martien A.M Groenen and Hendrik-Jan Megens	The influence of demography and recombination on the homozygosity landscape in the poultry genome	Genomics
20	Luca Santuari, Sonja Georgievska, Carl Shneider, Arnold Kuzniar, Tilman Schaeffers, Wigard Kloosterman and Jeroen de Ridder	DeepSV: Somatic Structural Variant Detection with Deep Learning	Genomics
21	Siavash Sheikhezadeh Anari, Dick De Ridder, Eric Schranz and Sandra Smit	Multi-genome read mapping	Genomics
22	Eef Jonkheer	Pangenomic applications in plants and pathogens	Genomics
23	Mehmet Akdel and Dick De Ridder	Improving Optical Map Assemblies	Genomics
24	Marleen Nieboer and Jeroen de Ridder	Annotation and prioritization of structural variation	Genomics
25	Martijn Comans, Olav De Haas, Daan Oudejans, Alex Salazar and Thomas Abeel	Copy number variation analysis on genome graphs	Genomics
26	Alex Salazar and Thomas Abeel	Approximate, simultaneous comparison of microbial genome architectures via syntentic anchoring of quiver representations	Genomics
27	Dennie Hebels, Aurélie Carlier and Jan de Boer	cBIT: The Compendium for Biomaterial Transcriptomics	Integration of (omics) data sets
28	Nirupama Benis, Mari Smits, Jerry Wells, Soumya Kar, Bart van der Hee, Maria Suarez Diez and Dirkjan Schokker	High-level data integration: Pathway analysis of murine intestinal gene expression	Integration of (omics) data sets
29	Weiyang Tao, Sandra C. Silva-Cardoso, Chiara Angiolilli, Ana Pinheiro, Comelis Bekker, Abhinandan Devaprasad, Jaap van Laar, Marta Cossu, Erik Hack, Marianne Boes, Andaman Pandit and	Integration of transcriptomic and epigenetic profiling shows that CXCL4 induces novel gene regulatory networks and molecular pathways in dendritic cells	Integration of (omics) data sets
30	Benoît Carrères, G. Mitsue Leon-Saiki, Peter Schaap, Vitor Martins Dos Santos, Rene Wijffels, Dirk Martens and Maria Suarez-Diez	The diurnal transcriptional landscape of Tetrademus obliquus	Integration of (omics) data sets
31	Dennis Kuijpers, Rick Reijnders, Laurence de Nijs, Clara Snijders, Ghazi Al Jowf, Denise Slenter, Lars Eijssen and Bart Rutten	Molecular genetics of stress: regulatory mechanisms involved in PTSD	Integration of (omics) data sets
32	Rick Reijnders, Dennis Kuijpers, Laurence De Nijs, Clara Snijders, Ghazi Al Jowf, Yentl Van der Zee, Denise Slenter, Bart Rutten and Lars Eijssen	Molecular genetics of stress: regulatory mechanisms involved in chronic social defeat stress	Integration of (omics) data sets
33	Soufiane Mourragui, Marco Loog, Marcel Reinders and Lodewyk Wessels	Domain adaptation to transfer predictors of drug response from cell lines to tumors	Integration of (omics) data sets

Poster nr.	Authors	Title	Topic
34	Daniël Wijnbergen, Mohammed Charout, Eleni Mina, Roula Tsonaka, Annemieke Aartsma-Rus, Pietro Spitali and Kristina Hettne	Semantic interpretation of multi-omics data sets	Integration of (omics) data sets
35	Shauna O'Donovan, Michael Lenz, Aditya Krishna, Alexander Lukas, Jelmer Neeven, Tobias Stumm, Florian Wimmenauer, Evgueni Smimov, Gokhan Ertaylan, Rachel Cavill, Danyel Jennen,	Use of deep learning methods to translate drug-induced gene expression changes from rat to human hepatocytes	Integration of (omics) data sets
36	Giulia Mantini, Tessa Le Large, Tim Schellhorst, Sander Piersma, Jaco Knol, Thang Pham, Tom Wurdinger, Elisa Giovannetti and Connie Jimenez	Integration of omics data to prioritize drug targets and biomarkers in pancreatic cancer	Integration of (omics) data sets
37	Chaitra Sarathy, Michael Lenz, Maïke Aurich, Dominique Langin, Arne Astrup, Wim Saris, Gijss Goossens, Ellen Blaak, Ines Thiele, Chris Evelo and Ilja Arts	Integration of gene expression from human obese adipose tissue with plasma metabolomics data using genome-scale metabolic models	Integration of (omics) data sets
38	Gou-Tao Huang and Jen-Shiang K. Yu	Molecular Simulation on the Catalytic Mechanism of Sulfur Transfer in the Mercaptopyruvate Sulfurtransferase	Metabolic modelling
39	Erika Gaspari, Antoni Malachowski, Luis Garcia-Morales, Vitor Martins Dos Santos and Maria Suarez-Diez	How to Improve Mycoplasma Growth: Study of Mycoplasma pneumoniae Metabolism through Genome-Scale Modeling	Metabolic modelling
40	Rik van Rosmalen, Robert Smith, Christian Fleck and Vitor Martins Dos Santos	DMPy: A Python package for automated mathematical model construction of large-scale metabolic systems	Metabolic modelling
41	Yanfei Zhang, Theresa Kouril, Jacky Snoep, Bettina Siebers, Matteo Barberis and Hans V. Westerhoff	The Peculiar Glycolytic Pathway in Hyperthermophilic Archaea: Understanding Its Whims by Experimentation In Silico	Metabolic modelling
42	Bart van Sloun, Michael Lenz, Natal van Riel and Ilja Arts	Computational modelling of postprandial glucose and insulin dynamics: the role of amino acids	Metabolic modelling
43	David Lao Martil, Laura R Guilherme Luzia, Koen J A Verhagen, Johan H van Heerden, S Aljoscha Wahl, Joep P J Schmitz, Natal A W van Riel and Bas Teusink	Yeast 3M: Monitor, model and master the dynamics of yeast central metabolism	Metabolic modelling
44	Hester van Beers and Natal van Riel	The role of dopamine receptors in obesity: an in silico exploration	Metabolic modelling
45	Alina Doban and Mireoa Lazar	Stability and invariance in biomedical systems	Metabolic modelling
46	Camilo Suarez Mendez, Koen Verhagen and Aljoscha Wahl	Metabolic response upon repetitive substrate perturbations using dynamic 13C-tracing in yeast	Metabolic modelling
47	Joanna Wolthuis, Saskia van Mil and Jeroen de Ridder	MetaboShiny – identify each mass, en masse	Metabolomics
48	Martina Kutmon, Denise Slenter, Ryan Miller, Jonathan Melius, Chris T. Evelo and Egon Willighagen	Building directed networks from biological pathways to visualise and analyse metabolomics data	Metabolomics
49	Melany Rios Morales, Theo Boer, Rebecca Heiner-Fokkema, Albert Gerding, Fjodor Sluijs, Mara Van Trijp, Guido Hooiveld, Dirk-Jan Reijngoud and Barbara Bakker	Analytical methods to measure kinetics of fermentation of non-digestible carbohydrates inside the human gut	Metabolomics
50	Ilona den Hartog, Ewoudt van de Garde, Stefan Vestjens, Amy Hams, Paul Voom, Dylan de Lange, Willem Jan Bos, Thomas Hankemeier and Coen van Hasselt	Metabolomic fingerprint biomarkers to guide antibiotic therapy and reduce resistance development	Metabolomics
51	Bastian Homung, Jason Norman, Liz Terveer, Bruce Roberts, Josbert Keller and Ed Kuijper	Fecal Microbiota Transplant: The search for the basis of the cure	Microbiome and ecosystems
52	Hemando Suarez Duran, Zhenhua Liu, Mamix Medema and Anne Osbourn	A systematic analysis of dynamic genomic neighbourhoods reveals expansion of specialized metabolic diversity in Brassicaceae	Microbiome and ecosystems
53	Jonna van der Stam, Andrei Prodan, Annieke van Baar, Peter Hilbers, Bert Groen, Max Nieuwdorp, Evgeni Levin and Natal van Riel	Applications of Canonical Correlation Analysis to microbial and metabolite data of metabolic syndrome patients	Microbiome and ecosystems
54	Jesse J. Kerkvliet, Sofia I.F. Gomes, Rutger A. Vos and Vincent S.F.T Merckx	Evolutionary analysis of the interaction network of plants and arbuscular mycorrhizal fungi	Microbiome and ecosystems
55	Nila Servaas, Eleni Chouri, Rina Wichers, Alysya Affandi, Marta Cossu, Sandra Silva-Cardoso, Maarten van der Kroef, Tiago Carvalheiro, Nadia Vazirpanah, Lorenzo Beretta, Marzia Rossato,	Molecular stratification of systemic sclerosis patients based on gene co-expression networks from dendritic cells	Network biology
56	Abhinandan Devaprasad and Aridaman Pandit	Profiling regulatory networks of 40 distinct immune cells reveal progenitor plasticity and complex regulation of human hematopoietic cell lineages	Network biology
57	Tooba Abbassi-Daloui, Hermien Kan, Vered Raz and Peter-Bram T Hoen	Developing a pipeline to optimize the detection of co-expression gene modules with coherent molecular functions from expression data	Network biology
58	Josephine Daub, Saman Amini, Frank Holstege and Patrick Kemmeren	Genetic interactions in childhood cancer	Network biology
59	Christina Papastolopoulou, Josephine Daub, Frank Holstege and Patrick Kemmeren	Genetic interactions underlying mutational signatures in paediatric cancer	Network biology
60	Raju Prasad Sharma, Alexey Kolodkin, Hans V. Westerhoff, Marta Schuhmacher and Vikas Kumar	Systems biology Approach to All-in-One-Modeling: From organ-specific pharmacokinetics of Flutamide to predicting its personalised pharmacotoxic dynamic effects	Personalized Medicine
61	Zandra Félix Garza, Joerg Liebmann, Matthias Born, Peter Hilbers and Natal van Riel	In silico clinical studies on the efficacy of blue light for treating psoriasis	Personalized Medicine
62	Frans-Paul Ruzius, Raul Kooter, Job Geerligs, Erik Rozemuller and Joris Albers	Extrapolating incomplete HLA allele database entries improves identification of matching alleles using NGS	Personalized Medicine
63	Joske Ubels, Pieter Sonneveld, Annemiek Broijl, Erik H. van Beers, Martin H. van Vliet and Jeroen de Ridder	Predicting treatment benefit in Multiple Myeloma through simulation of alternative treatment effects	Personalized Medicine
64	Bas Jacobs, Eva E. Deinum and Jaap Molenaar	Modeling pattern formation in plant cells by ROP signalling	Regulation and signalling
65	Simone Lederer, Tjeerd Dijkstra and Tom Heskens	Additive Dose Response Models: Defining Synergy	Regulation and signalling
66	Marc Rullan, Dirk Benzinger, Gregor Schmidt, Andreas Miliás-Argeitis and Mustafa Khammash	Real-time, single-cell interrogation of yeast transcription using optogenetics	Regulation and signalling

Poster nr.	Authors	Title	Topic
67	Peter de Greef, Bram Geritsen, Benjamin Chain and Rob de Boer	VDJ-recombination shapes the clone-size distribution of naive T-cells	Regulation and signalling
68	Hans van Veen	Learning from nature to understand plant flooding tolerance	Regulation and signalling
69	Elena Merino, Xuefeng Gao, Philippe Robert, María Martínez, Fabien Crauste, Olivier Gandrillon, Michael Meyer-Hermann, Hubb Hoefsloot, Jeroen Guikema and Antoine van Kampen	Multiscale modeling of plasma cell differentiation in Germinal Centers	Regulation and signalling
70	Christ Leemans, Marloes van der Zwalm, Laura Brueckner, Tom van Schaik, Daan Peric Hupkes, Joris van Arensbergen and Bas van Steensel	Promoter-specific effects of Lamina-associated domains on gene expression	Regulation and signalling
71	K. Anton Feenstra, Qingzhen Hou, Paul De Geest, Christian Griffioen, Sanne Abeln and Jaap Heringa	Efficient generation of alignment profiles capture evolutionary information for fast and accurate predictions of PPI interface positions	RNA and protein diversity
72	Juani van Gils, Maryam Hashemi Shabestari, Halima Mouhib, Peter van Ulsen, Wouter Roos, Gijs Wuite and Sanne Abeln	The Mechanisms of Hbp Protein Folding	RNA and protein diversity
73	Laurène Picandet, Tony Kaoma, Francisco Azuaje and Petr Nazarov	Decomposition of transcriptional signals from tumours to improve classification of glioma patients	RNA and protein diversity
74	Miguel Correa Marrero, Richard G.H. Immink, Dick de Ridder and Aalt D.J van Dijk	Simultaneous unsupervised inference of protein-protein contacts and interactions	RNA and protein diversity
75	Teunis J. P. van Dam, Adam Soh and Chad. G. Pearson	Duplication order of SF-assemblins recapitulates substructure organization of the ciliary rootlet in the ciliate Tetrahymena thermophila	RNA and protein diversity
76	Jun Hou, Jose Debes, Zwier Groothuisink, Thomas Vanwolleghem and Andre Boonstra	Transcriptomic heterogeneity in hepatocytes of HCV patients revealed by single-cell RNA-sequencing	Single cell omics
77	Patrick van Den Berg and Stefan Semrau	Single-cell atlas of the human embryonic kidney reveals developmental role of disease-associated genes	Single cell omics
78	Nathalie Groen	Exploring human pancreatic $\beta$ -cell plasticity using single-cell RNA sequencing	Single cell omics
79	Tom van Schaik, Daan Peric-Hupkes, Ezequiel Miron and Bas van Steensel	Bridging the gap between ChIP and DamID to study protein-DNA interactions	Single cell omics
80	Tito Candelli, Philip Lijnzaad, Mauro Muraro, Hindrik Kerstens, Patrick Kemmeren, Alexander van Ourdenaarden, Thanasis Margaritis and Frank Holstege	Sharq: a versatile preprocessing and QC pipeline for Single Cell RNA-seq	Single cell omics
81	Jurian de Kanter, Philip Lijnzaad, Thanasis Margaritis, Tito Candelli and Frank Holstege	CHETAH: a robust and automated cell type identification method for single-cell RNA-seq data	Single cell omics
82	Tamim Abdelaal, Vincent van Unen, Thomas Höllt, Frits Koning, Marcel Reinders and Ahmed Mahfouz	Predicting cell types in single cell mass cytometry data	Single cell omics
83	Roy Straver, Alessio Marozzi, Wigard Kloosterman and Jeroen de Ridder	Consensus calling using raw nanopore data for Cyclomics	Single molecule sequencing
84	Carlos de Lannoy and Dick de Ridder	Sequence detection and quantification in MinION data without basecalling	Single molecule sequencing
85	Ward Weistra and Kees van Bochove	Glowing Bear: a new transSMART interface and a standalone cohort builder	Tools & resources
86	Mark Santcroos, Wibowo Arindrarto, Sander Bollen, Jonathan Vis and Jeroen Laros	Microservices for Automated End-to-end NGS Data Analysis	Tools & resources
87	Mark Santcroos, Matthijs Moed, Paul van Dijk, Raoul Teeuwen, Michiel Schok, Pieter Neerinx, Jeroen de Ridder, Christiaan Geertsma, Gerben Venekamp, Jeroen Belien, Jeroen Laros, Leon	Enabling collaborative access to data and resources in health research: Federated Identity and Access Management (FIAM)	Tools & resources
88	Paula Pérez Rubio, Claudio Lottaz and Julia C Engelmann	FastqPuri: high-performance preprocessing of RNA sequencing data	Tools & resources
89	Denise N. Sletter, Egon L. Willighagen and Chris T. Evelo	Chemistry Identifier Mapping to Pathway Databases using Ontologies: Expanding metabolomics analysis in WikiPathways with ChEBI	Tools & resources
90	Maurits Dijkstra, Punto Bawono, Sanne Abeln, K. Anton Feenstra, Wan Fokkink and Jaap Heringa	MA-PRALINE: improving the alignment of motif regions	Tools & resources
91	Marvin Martens, Egon Willighagen and Chris Evelo	Introducing WikiPathways as a data-source to support Adverse Outcome Pathways for regulatory risk assessment of chemicals.	Tools & resources
92	E. de Jong, E. Strengman, J.Y. Hehir-Kwa, W.B. Breunis, H.H.D. Kerstens, B.B.J. Tops, F.C.P. Holstege and P. Kemmeren	A DNA methylation pipeline for classifying pediatric tumor (sub)types	Tools & resources
93	Martin Brandt, Gabor Nyers and Ymke van den Berg	Demonstration of using the SURF National Research Cloud for setting up collaborative research environments	Tools & resources
94	Ángela Sedeño Cacciatore, Roy Straver and Jeroen de Ridder	Interactive visualization and clustering of multi-component circularized chromosome conformation capture data	Tools & resources
95	Yunlei Li, Wesley Ameling, Saskia Hiltmann, Rick Jansen, Folkert Kemenade and Andrew Stubbs	JUNIPER: A reproducible notebook with built-in machine learning functionality	Tools & resources
96	Kevin van Rooijen	A FAIR solution to a database containing data associated with exercise and training	Tools & resources
97	Stephen Pieterman	AVIDE - An interactive data visualization application for gene expression	Tools & resources
98	K. Joeri van der Velde, Bart Charbon, Mark de Haan, Gert-Jan van de Geijn, Mateusz Kuzak and Morris Swertz	Implementation of BioSchema for multiple patient registries	Tools & resources
99	Sven Warris, Steven Dijkxhoorn, Teije van Sloten and Bart van de Vossenber	Mining functional annotations using Cytoscape & Neo4J	Tools & resources

Poster nr.	Authors	Title	Topic
100	Nicola Bonzanni, Alvis Trevisan, Jorrit Posthuma, Jan Blom, Jos Lunenberg and Henk-Jan van den Ham	Scalable end-to-end immune repertoire analysis: the ImmunoGenomiX Platform	Tools & resources
101	Chris van Run, Hinri Kerstens and Patrick Kemmeren	Integrating MultiQC: quality control made elegant for next-generation sequencing	Tools & resources
102	Maarten Kooyman, Joke Van Vugt, Jan Veldink, Robert Griffioen, Matthijs Moed, Danielle Posthuma, Morris Swertz, Bas Heijmans, Leon Mei, Mark Santcroos, Pieter Neerincx, Marian Beekman, Eline	Co-creating ICT Tools and Data Processing Infrastructure for Cohort Studies	Tools & resources
103	Frans-Paul Ruzius, Raul Kooter, Job Geerlgs, Pieter Meulenberg, Joris Albers and Erik Rozemuller	Identifying homologous genes in pooled HLA NGS samples	Tools & resources
104	Pieter Lukasse, Fedde Schaeffer, Oleguer Plantalech Casals, Sander Tan, Dionne Zaal, Ersin Ciftci, Angelica Ochoa, Adam Abeshouse, Hongxin Zhang, Yichao Sun, Robert Sheridan,	Gene Set Variation Analysis in cBioPortal	Tools & resources
105	Cunliang Geng, Anna Vangone, Gert Folkers, Li Xue and Alexandre Bonvin	ISEE: Interface Structure, Evolution and Energy-based random forest predictor of binding affinity changes upon mutations	Tools & resources
106	Tim Kuijpers, Jos Kleinjans and Danyel Jennen	DynOVis: visualizing dynamic perturbations on biological networks	Tools & resources