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Nr	Authors	Title	Topic
1	Stavros Makrodimitris, Roeland van Ham and Marcel Reinders	Metric Learning on Expression Data for Gene Function Prediction	3D bioinformatics / Functional prediction
2	Halima Mouhib, Akiko Higuchi, Sanne Abeln, K. Anton Feenstra and Kei Yura	Exploring the effect of single amino acid variations on the function of the glucose transporter SLC2A by enhanced sampling coarse-grained simulation	3D bioinformatics / Functional prediction
3	Yan Wang, Miguel Correa Marrero, Aalt D.J. van Dijk and Marnix H. Medema	Machine Learning to Predict Protein-Protein Interactions in Polyketide Biosynthetic Assembly Lines	3D bioinformatics / Functional prediction
4	Hans de Ferrante, Reza Haydarlou, Jaap Heringa and K. Anton Feenstra	DeePpiS – towards Deep Learning for Predicting Protein-Protein Interface Positions from Sequence	3D bioinformatics / Functional prediction
5	Dei Elurbe, Laura Sanchez-Caballero, Fabian Baertling, Sergio Guerrero-Castillo, Mariel van den Brand, Joeri van Strien, Teunis J. P. van Dam, Richard Rodenburg, Ulrich Brandt, Martijn Huynen and Leo G. J. Nijtmans	Unraveling protein function through the integration of proteomics and evolutionary data	3D bioinformatics / Functional prediction
6	Danial Lashgari, Antoine van Kampen, Michael Meyer-Hermann, Marit van Gils and Rogier Sanders	A computational model of kinetic maturation in the germinal center	3D bioinformatics / Functional prediction
7	Bram Thijssen, Katarzyna Jastrzebski, Roderick Beijersbergen and Lodewyk Wessels	Creating robust models by fitting to multiple datasets -- correcting Bayesian inference for overconfident posteriors	Data integration & network biology
8	Anouk Verboven, Katrin Linda, Mark Hogeweg, Kees Albers, Bert de Vries, Peter-Bram 'T Hoen and Nael Nadif Kasri	MEA-seq for combined gene expression and neuronal network measurements in iPSC-derived neurons from Koolen-de Vries patients	Data integration & network biology
9	Laura Zwep, Kevin Duisters and Coen van Hasselt	Hierarchical group LASSO with random effects: identification of high-dimensional omics-drug interactions predictive of treatment response in patient-derived tumor growth data	Data integration & network biology
10	Tim Kuijpers, Jos Kleinjans and Danyel Jennen	Integration of omics data by applying new strategies for nonnegative matrix factorization	Data integration & network biology
11	Indu Khatri, Erik van den Akker, Cristina I. Teodosio, Marcel J.T. Reinders and Jacques J.M. van Dongen	Integration of cross-study and multi-omics datasets to identify cancer associated markers	Data integration & network biology

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Nr	Authors	Title	Topic
12	Renee Salz, Sven Degroeve, Seyed Yahya Anvar, Lennart Martens and Peter-Bram 'T Hoen	Personalized genome and transcriptomes for improved interpretation of personalized proteomes	Data integration & network biology
13	Margi Hartanto, Harm Nijveen and Dick de Ridder	Finding genes for traits using systems genetics	Data integration & network biology
14	Hernando Suarez Duran, Marnix Medema and Elizabeth Sattely	An Integrative Multi-omics Approach for Metabolic Pathway Prediction	Data integration & network biology
15	Elena Merino, Xuefeng Gao, Philippe A. Robert, María Rodríguez Martínez, Fabien Crauste, Olivier Gandrillon, Michael Meyer-Hermann, Huub Hoefsloot, Jeroen Guikema and Antoine van Kampen	Multiscale modeling of plasma cell differentiation in Germinal Centers	Data integration & network biology
16	Yi Chen, Katy Wolstencroft and Fons Verbeek	Analysing Cancer Hallmark Gene Mapping Methods	Data integration & network biology
17	Marvin Martens, Egon Willighagen and Chris Evelo	Expanding Adverse Outcome Pathway knowledge by creating AOP-Wiki RDF with semantic annotations to facilitate risk assessment of chemicals.	Data integration & network biology
18	Laura Luzia, Philipp Savakis, Johan van Heerden and Bas Teusink	Understanding pH dynamics in Saccharomyces cerevisiae - Population and Single cell approaches -	Data integration & network biology
19	Lauren J. Dupuis, Christine Staiger, Friederike Ehrhart, Alexander Botzki, Joke Baute, Dragan Bosnacki, Harold Weffers, Chris T. Evelo and Celia W.G. van Gelder	Helis Academy - Post-graduation teaching project for data analysis and data stewardship	Education/training
20	Celia van Gelder, Salome Scholtens, Petronella Anbeek, Jasmin Boehmer, Mirjam Mirjam Brullemans, Marije van der Geest, Mijke Jetten, Inge Slouwerhof and Christine Staiger	Towards a community-endorsed data steward profession for supporting life science research	Education/training
21	Mateusz Kuzak, Celia van Gelder, Shalini Kurapati, Carlos Martinez-Ortiz, Anita Schürch, Marta Teperek and Yasemin Turkyilmaz-van der Velden	Towards sustainable training in essential computing research skills in the Netherlands	Education/training
22	Celia van Gelder, Mateusz Kuzak and Christine Staiger	FAIR Data Training activities in the Netherlands	Education/training
23	Christine Anyansi and Thomas Abeel	Mixed Mycobacterium tuberculosis infections: an overlooked global phenomena	Genomics and genome bioinformatics

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24	Roos van der Donk, Sandra Jansen, Janneke Schuurs-Hoeijmakers, David Koolen, Alexander Hoischien, Han Brunner, Patrick Kemmeren, Christoffer Nellåker, Lisenka Vissers, Bert de Vries and Jayne Hehir-Kwa	Next generation phenotyping using computer vision algorithms in rare genomic neurodevelopmental disorders	Genomics and genome bioinformatics
25	Jasper Koehorst, Edoardo Saccenti, Vitor A.P. Martins Dos Santos, Maria Suarez Diez and Peter Schaap	Expected and observed genotype complexity in prokaryotes: correlation between 16S-rRNA phylogeny and protein domain content	Genomics and genome bioinformatics
26	Anna Maslowska-Gornicz, Melanie R.M. van den Bosch, Edoardo Saccenti and Maria Suarez Diez	Large -Scale Analysis of Codon Usage in Bacteria	Genomics and genome bioinformatics
27	Ramin Shirali Hossein Zade and Thomas Abeel	Improving de novo assembly by removing repeat induced overlaps	Genomics and genome bioinformatics
28	Bastian Hornung, Ed Kuijper and Wiep Klaas Smits	Comparative genomics and analysis of 1000 Clostridium difficile plasmids	Genomics and genome bioinformatics
29	Joanna von Berg, Sander van der Laan, Jeroen de Ridder and Sara Pulit	What's in a name? The importance of phenotype definitions for genetic discovery in ischemic stroke	Genomics and genome bioinformatics
30	Rodrigo Coutinho de Almeida, Ahmed Mahfouz, Yolande Fm Ramos, Wouter den Hollander, Hailiang Mei, Rob Ghh Nelissen, Marcel Reinders and Ingrid Meulenbelt	Transcriptome Clustering Analysis Identifies Two Subgroups of Osteoarthritis Patients	Genomics and genome bioinformatics
31	Petros Skiadas, Sandra Smit, Lidija Berke and Peter van Dam	Evolution of intron-exon structure in plants	Genomics and genome bioinformatics
32	Casey Cai, Marc van Tuil, Eric Strengman, Philip Lijnzaad, Ellen de Jong, Bastiaan Tops, Frank Holstege, Jayne Hehir-Kwa and Patrick Kemmeren	Gene Fusion Detection in Patient Whole-Genome versus RNA Sequencing Data	Genomics and genome bioinformatics
33	Muhammad Farooq, Aalt-Jan van Dijk, Harm Nijveen and Dick Ir de Ridder	Towards Biologically Informed Genotype-Phenotype Linking	Genomics and genome bioinformatics
34	Alexandra Danyi, Jeroen de Ridder and Alexandra Danyi	Cancer type classification based on somatic mutation profiles	Genomics and genome bioinformatics
35	Bryan van den Brand, Job Geerligs, Frans-Paul Ruzius, Hanneke van Deutekom, Joris Albers, Pieter Meulenberg and Erik Rozemuller	Combining NGS long and short reads to fully phase and unambiguously define new alleles for MHC and KIR genes	Genomics and genome bioinformatics

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36	Pooja Mandaviya, Jeroen van Rooij, Annique Claringbould, Janine Felix, Jenny van Dongen, Rick Jansen, Lude Franke, Peter 't Hoen, Bas Heijmans and Joyce van Meurs	Evaluation of commonly used analysis strategies for epigenome- and transcriptome-wide association studies through replication of large-scale population studies	Genomics and genome bioinformatics
37	Christian Groß, Martijn Derks, Marcel Reinders and Dick De Ridder	Predicting variant deleteriousness in non-human species: applying the CADD approach in pig	Genomics and genome bioinformatics
38	Thomas Ederveen	Cutaneous Staphylococcus profiling at species level in atopic dermatitis by Single Locus Sequence Typing (SLST) marker design and oligotyping for high-resolution sequencing-based microbial profiling	Genomics and genome bioinformatics
39	Zhen-Hua Zhang, Joeri van der Velde and Morris Swertz	Prediction of Allele-specific Expression via Genomic Annotations	Genomics and genome bioinformatics
40	Martijn Cordes	ImSpectR – R package to quantify immune repertoire diversity in spectratype data	Immunology
41	Arpit Swain and Rob Deboer	Homeostatic control of T cell memory pool	Immunology
42	Rodrigo García-Valiente, Danial Lashgari, Elena Merino Tejero, Barbera van Schaik, Michael Meyer-Hermann, Huub Hoefsloot, Jeroen Guikema, Rikard Holmdahl, Niek de Vries, Rochelle Vergroesen, Linda Slot, René Toes, Hans Scherer and Antoine van Kampen	Understanding Fab N-Glycosylation of ACPA B-cells and its relation to affinity maturation through modelling	Immunology
43	Ilona Den Hartog, Ewoudt van de Garde, Stefan Vestjens, Amy Harms, Paul Voorn, Dylan de Lange, Willem Jan Bos, Thomas Hankemeier and Coen van Hasselt	Predictive metabolite biomarker profiles for microbial aetiology in patients with community-acquired pneumonia	Immunology
44	Tamim Abdelaal, Vincent van Unen, Thomas Höllt, Frits Koning, Marcel Reinders and Ahmed Mahfouz	Predicting cell populations in single cell mass cytometry data	Immunology
45	DEMO - Seiler, Kronstad, Simpson, Le Gars, Vendrame, Blish and Holmes	Uncertainty Quantification in Multivariate Mixed Models for Mass Cytometry Data	Immunology
46	Pim Fuchs, Henk-Jan van den Ham, Nuray Nuray Akyüz, Donjete Simnica, Mascha Binder and Nicola Bonzanni	Repertoire analysis using the IGX platform: Monitoring the effect of immunomodulatory treatment in myelodysplastic syndrome patients	Immunology
47	Gizem Aktas and Yaman Barlas	The Biological Subsystem Interactions Underlying the Stress Response of the Human Body: A Dynamic Modeling Approach	Immunology

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Nr	Authors	Title	Topic
48	Joske Ubels, Pieter Sonneveld, Martin van Vliet and Jeroen de Ridder	Understanding treatment specific survival in Multiple Myeloma	Medical biology
49	Óscar Lapuente, Francesca Finotello and Federica Eduati	Mechanistic biomarkers of patient response to immunotherapy	Medical biology
50	Soufiane Mourragui, Marco Loog, Marcel Reinders and Lodewyk Wessels	PRECISE: A domain adaptation approach to transfer predictors of drug response from pre-clinical models to tumors	Medical biology
51	Freek Manders, Karlijn Hasaart, Rurika Oka and Ruben van Boxtel	Characterizing mutagenesis and developmental lineages in human fetal hematopoiesis	Medical biology
52	Petr Nazarov, Arnaud Muller, Thomas Eveno, Tony Kaoma and Francisco Azuaje	Independent Component Analysis Improves Chartacterization of Cancer Patients	Medical biology
53	Fianne Sips, Emma Meessen, Albert Groen, Maarten Soeters and Natal van Riel	Dynamic modeling of time-series metabolomics reveals physiological differences in intestinal bile acid handling between healthy men	Medical biology
54	Arlin Keo, Ahmed Mahfouz and Marcel Reinders	Transcriptomic signatures of brain regional vulnerability to Parkinson's disease	Medical biology
55	Renée Beekman, Helen E. Speedy, Vicente Chapaprieta, Giulia Orlando, Philip J. Law, David Martín-García, Jesús Gutiérrez-Abril, Daniel Catovsky, Sílvia Beà, Guillem Clot, Montserrat Puiggros, David Torrents, Xose S. Puente, James M. Allan, Carlos López-Otín, Elias Campo, Richard S. Houlston and José I. Martín-Subero	Integration of genomic and epigenomic data refines the regulatory mechanisms and biological significance of chronic lymphocytic leukemia risk loci	Medical biology
56	Diana Hendrickx and Enrico Glaab	Integrative analysis of molecular changes in the aging-related disorders Parkinson's disease and Hutchinson-Gilford progeria syndrome	Medical biology
57	Agnieszka B. Wegrzyn, Edinson Lucumi Moreno, Alida Kindt, Cornelius Willacey, German Preciat, Jennifer Modamio Chamarro, Zhi Zhang, Rashi Halder, Javier Jarazo, Paul Wilmes, Enrico Glaab, Jens Schwamborn, Amy Harms, Thomas Hankemeier and Ronan M.T. Fleming	The metabolic signature of PINK1 monogenic Parkinson's disease - multi-omics approach coupled with constraint-based modelling	Medical biology
58	Josephine Daub, Saman Amini, Frank Holstege and Patrick Kemmeren	Beyond synthetic lethality: Multiple mechanisms can explain genetic interactions within childhood cancer	Medical biology

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Nr	Authors	Title	Topic
59	Fentaw Abegaz, Ernst Wit and Barbara Bakker	Understanding Bistability in the Mitochondrial Fatty Acid β-Oxidation Pathway as a Physiological Switch in Fatty Acid Metabolism	Metabolism
60	Kazuhiro Maeda, Hans Westerhoff, Hiroyuki Kurata and Fred Boogerd	Ranking E. coli's ammonium transport and assimilation networks by how they fit diverse experiments	Metabolism
61	Jen-Shiang K. Yu and Gou-Tao Huang	Catalytic Roles of Histidine and Arginine in Pyruvate Class II Aldolase from Metadynamics Combined with Quantum Mechanics and Molecular Mechanics	Metabolism
62	Wenxuan Zhang, Anne-Claire Martines, Terry Derks, Robert Henning, Albert Gerding, Marcel de Vries, Maaike Goris, Barbara Bakker, Rainer Bischoff and Dirk-Jan Reijngoud	Untargeted lipidomics reveals glycerolipid compositional changes in fasted, cold-exposed MCAD KO mice	Metabolism
63	Maxime den Ridder, Carol de Ram, Pascale Daran-Lapujade and Martin Pabst	Comprehensive temporal analysis of the yeast glycolytic pathway under anaerobic conditions using high-resolution mass spectrometry	Metabolism
64	Koen Verhagen, Camilo Suarez-Mendez, Isabelle Duijnstee and Aljoscha Wahl	Dynamic metabolism of trehalose and its role in glucose recycling in Saccharomyces cerevisiae using 13C-labeling	Metabolism
65	Bart van Sloun, Michael Lenz, Gijs Goossens, Natal van Riel and Ilja Arts	Computational modelling of postprandial glucose and insulin dynamics in humans: the role of amino acids	Metabolism
66	Lotte de Graaf, Eleni Vasilakou, Giulia Giordano and Aljoscha Wahl	Analysis of the energy homeostasis by modeling substrate dynamics in E.coli	Metabolism
67	Tom Clement and Daan de Groot	Elementary Conversion Modes in large-scale metabolic analysis	Metabolism
68	Stefania Magnusdottir, Marc Pages Gallego, Saskia van Mil and Boudewijn Burgering	Metabolic modeling of colorectal cancer cells reveals metabolic differences among concensus molecular subtypes	Metabolism
69	Eunice van Pelt-Kleinjan, Yu Chen, Brett Olivier, Douwe Molenaar, Herwig Bachmann, Jens Nielsen and Bas Teusink	Genome-scale Proteome Constrained model of L. lactis	Metabolism
70	Sebastián N. Mendoza, Brett G. Olivier, Douwe Molenaar and Bas Teusink	A systematic assessment of current genome-scale metabolic reconstruction tools	Metabolism

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Nr	Authors	Title	Topic
71	David Lao Martil, Natal van Riel, Bas Teusink and Joep Schmitz	Divide and conquer parameter estimation and inclusion of biomass to improve fidelity in yeast kinetic metabolic models	Metabolism
72	Joan Sebastian Gallego Murillo, Marieke von Lindern, Aljoscha Wahl, Emile van den Akker, Luuk van der Wielen, Angelo D'alessandro and Nurcan Yagci	Metabolomics analysis of high cell density erythroblast cultures: Small molecules trigger cellular oxidative stress	Metabolism
73	Carlos de Lannoy, Victor Carrion, Mattias de Hollander and Dick de Ridder	Evaluation of the MinION as a field-deployable soil community analyzer	Microbial ecosystems
74	Wasin Poncheewin, Anne van Diepeningen, Theo van der Lee, Peter Schaap and Maria Suarez Diez	Microbiome Interactions Prediction using Genome-Scale Constraint-Based Metabolic Modeling.	Microbial ecosystems
75	Jeroen Meijer, Bram van Dijk and Paulien Hogeweg	Evolutionary contingency drives metabolic interactions and the emergence of ecological structure in microbial communities	Microbial ecosystems
76	Nomikos Skyllas and Julia Engelmann	Causal interactions between marine microbes and their environment in the Mediterranean Sea	Microbial ecosystems
77	Laurens Krah, Istvan Kleijn and Rutger Hermsen	Noise propagation in an integrated model of bacterial gene expression and growth	Single cell biology
78	Sieze Douwenga, Branco dos Santos, Teusink and Bachmann	Identification of trade-offs between growth rate and adaptation to new environments in Lactococcus lactis	Single cell biology
79	Age Tjalma and Frank Bruggeman	Information in phenotypic adaptation: it is not about looking closer but about looking wider	Single cell biology
80	Paul de Raadt, Tamim Abdelaal and Ahmed Mahfouz	Scalable clustering of high dimensional single cell data	Single cell biology
81	Stefania Astrologo, I Barozzi, Sp Hong, Thierry Mondeel, L Magnani, Pj Verschure and Hv Westerhoff	Chasing heterogeneity: exploring functional noise	Single cell biology
82	Sakshi Sakshi, Stefano Schivo, Kannan Govindaraj, Leilei Zhong, Xiaobin Huang, Marcel Karperien and Janine N. Post	DKK1, FRZB and GREM1 restore SOX9 transcriptional activity in osteoarthritic chondrocytes: a computational modeling study validated by primary human cell experiments	Single cell biology
83	DEMO - Joanna Wolthuis, Jeroen de Ridder and Saskia van Mil	MetaboShiny - identify each mass, en masse	Tools & resources

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84	Ruben Vorderman, Sander Bollen, Davy Cats, Guy Allard and Leon Mei	Pytest-workflow: a pytest based test framework for integration and functional testing of bioinformatics workflows	Tools & resources
85	Rob Hooft, Mateusz Kuzak, Marek Suchánek and Robert Pergl	“Data Stewardship Wizard”: bringing together Researchers, Data Stewards, and Data Experts around Data Management Planning	Tools & resources
86	Daniel Rademaker	Deep learning for optical chemical structure recognition.	Tools & resources
87	Daniel Rademaker	Deep learning for faster and better detection of malaria infected cells	Tools & resources
88	Juan Ochoteco, Jos Kleinjans and Florian Caiment	Evaluation of transcriptomic quantification tools	Tools & resources
89	Roy Straver, Alessio Marcozzi, Wigard Kloosterman and Jeroen de Ridder	Consensus calling using raw nanopore data for Cyclomics-seq	Tools & resources
90	Shuang Li, Joeri van der Velde, Morris Swertz, Dick de Ridder, Aalt-Jan van Dijk, Dimitrios Soudis and Leslie Zwerwer	A Machine Learning Approach to Variant Pathogenicity Estimation	Tools & resources
91	Christian Tönsing, Jens Timmer and Clemens Kreutz	Optimal paths between parameter estimates in nonlinear ODE systems	Tools & resources
92	Weiyang Tao, Timothy Radstake and Aridaman Pandit	RegEnrich: an R package for gene regulator enrichment analysis	Tools & resources
93	Maurits Dijkstra, Punto Bawono, Sanne Abeln, K. Anton Feenstra, Wan Fokkink and Jaap Heringa	MA-PRALINE: improving the alignment of motif regions	Tools & resources
94	Raúl Wijfjes, Sandra Smit and Dick De Ridder	Hecaton: a framework to reliably detect copy number variation in plant genomes	Tools & resources
95	Luca Santuari, Sonja Georgievska, Carl Shneider, Arnold Kuzniar, Tilman Schaefers, Wigard Kloosterman and Jeroen de Ridder	DeepSV: Somatic Structural Variant Detection using Deep Learning	Tools & resources
96	Laurène Picandet, Hindrik Kerstens, Van Tuil, Strengman, Eugène Verwiel, Frank Holstege, Tops, Jayne Hehir-Kwa and Patrick Kemmeren	Optimizing somatic variant calling on samples sequenced on NovaSeq	Tools & resources
97	Tjardo Maarseveen, Thomas Huizinga, Marcel Reinders, Erik Van den Akker and Rachel Knevel	Automated diagnosis extraction from Electronic Medical Records with Machine Learning classifiers.	Working with Data Resources (quality, future, access)

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Nr	Authors	Title	Topic
98	Eugène Verwiel, Hinri Kerstens, Chris van Run, Ellen de Jong, Bas Tops, Patrick Kemmeren and Jayne Hehir-Kwa	Workflow Manager, keeping track of daily operations with MOLGENIS and Cromwell	Working with Data Resources (quality, future, access)