GCB 2021

GERMAN CONFERENCE ON BIOINFORMATICS

6 – 9 SEPTEMBER
VIRTUAL CONFERENCE

PROGRAMME

gcb2021.de

CONTENTS

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EXHIBITOR | SUPPORTER

EXHIBITOR

The German Network for Bioinformatics Infrastructure (de.NBI)

The German Network for Bioinformatics Infrastructure (de.NBI) is a distributed bioinformatics infrastructure which started in March 2015 as an academic funding initiative of the German Ministry of Research and Education (BMBF). With its wide range of bioinformatics expertise and renowned partner institutions, the de.NBI network delivers high-standard bioinformatics services, comprehensive training, as well as powerful computing capacity (de.NBI Cloud) that contributes to the advancement of life sciences research in Germany and Europe.

SUPPORTER

Universität Leipzig/D

Leibniz-Institut für Pflanzenbiochemie (IPB), Halle (Saale)/D

Deutsches Zentrum für integrative Biodiversitätsforschung (iDiv) Halle-Jena-Leipzig/D

Julius Kühn-Institut – Bundesforschungsinstitut für Kulturpflanzen (JKI), Quedlinburg/D

Martin-Luther-Universität Halle-Wittenberg/D

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OntoChem GmbH, Halle (Saale), D

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GERMAN NETWORK FOR BIOINFORMATICS INFRASTRUCTURE

THE GERMAN NETWORK FOR BIOINFORMATICS INFRASTRUCTURE

Bioinformatics Solutions for Big Data Analysis in the Life Sciences

de.NBI offers training courses at GCB 2021

- *Cell segmentation using KNIME Analytics Platform and its Tensorflow2 Integration*
- *BioC++ - solving daily bioinformatic tasks with C++ efficiently*
- *Bioinformatics tools for analyzing clinical metaproteomics samples of the human gut*
- *Exploring Target Structures with ProteinsPlus*
- *Non-targeted label-free Proteomics*

INDUSTRIAL FORUM

Consulting, Networking, Software solutions

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Training courses, Summer schools, Hackathons, Webinars

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Workflows, Databases, Consulting, Tools
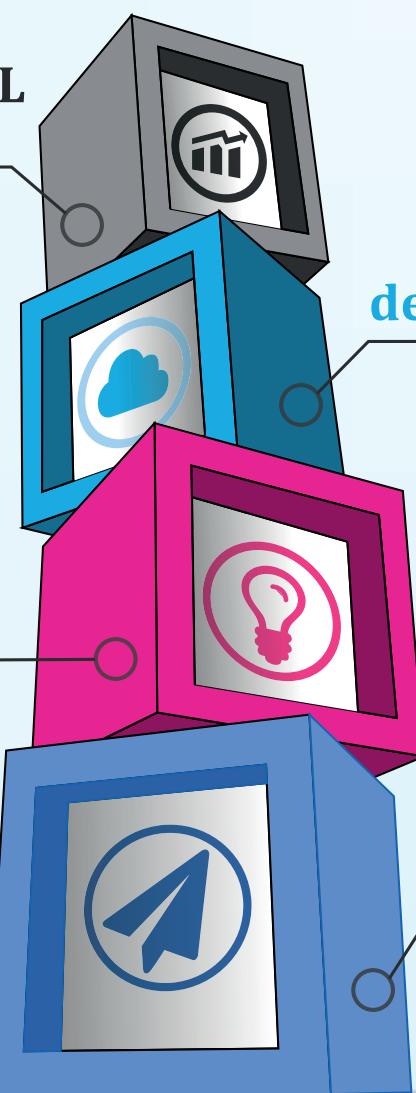
Find out more at: www.denbi.de

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Workshops/Tutorials (with registration only)

(Details available at https://gcb2021.de/workshops)

Wednesday, 08.09. 2021

Workshop/Tutorials	
	14:00 – 17:00
Room 1	**WS1:** Metabolic Reconstruction and Flux Modelling
Room 2	**WS2:** Cell segmentation using KNIME Analytics Platform and its Tensorflow2 Integration
Room 3	**WS3:** BioC++ - solving daily bioinformatic tasks with C++ efficiently

Thursday, 09.09. 2021

Workshop/Tutorials		
09:00 – 12:00	**12:00 – 14:00**	**14:00 – 17:00**
Room 1 — **WS4:** Modern hashing for alignment-free sequence analysis		**WS6:** How to build and analyse mathematical models of biological systems using Python & modelbase
Room 2 — **WS5:** Bioinformatics tools for analyzing clinical metaproteomics samples of the human gut	Lunch break	**WS7:** Non-targeted label-free proteomics
Room 3		**WS8:** Exploring Target Structures with ProteinsPlus

PROGRAMME

Monday, 6 September 2021

08:40 **OPENING**

Chair: I. Grosse - Martin Luther University Halle-Wittenberg/D

Welcome Address

Rector C. Tietje - Martin Luther University Halle-Wittenberg/

KEYNOTE SESSION

Chair: J. Grau - Martin Luther University Halle-Wittenberg/D

09:00 **Computational challenges in single cell regulatory genomics**
U. Ohler[1]; [1] Max Delbrück Center for Molecular Medicine, Berlin/D

09:40 *Discussion*

09:55 Short break

MACHINE LEARNING

Chair: D. Heider - Philipps-Universität Marburg/D

10:00 **Tailored Machine Learning Model training for functional RNA detection**
S. Findeiss[1]; C. Klapproth[1]; [1] Leipzig University, Leipzig/D

10:25 **Prediction of non-covalent protein-ligand interactions using an interpretable machine learning model**
M. Weber[1]; M. Kaden[1]; F. Kaiser[2]; C. Leberecht[2]; V. Haupt[2]; T. Villmann[1]
[1] University of Applied Sciences Mittweida, Mittweida/D; [2] PharmAI GmbH, Dresden/D

10:40 *Discussion*

10:55 Short break

MACHINE LEARNING

Chair: K. Jung - Tierärztliche Hochschule Hannover/D

11:00 **Deep Learning Improves Pancreatic Cancer Diagnosis Using RNA-Based Variants**
A. Al-Fatlawi[1]; M. Schroeder[1]; [1] TU Dresden, Dresden/D

11:25 **The impact of negative data sampling on antimicrobial peptide prediction**
M. Burdukiewicz[1]; K. Sidorczuk[2]; P. Gagat[2]; F. Pietluch[2]; J. Kała[3]; D. Rafacz[3]; M. Bakala[3]; J. Slowik[3]; R. Kolenda[4]; S. Rödiger[5];
P. Mackiewicz[2]; [1] Medical University of Białystok, Białystok/PL; [2] University of Wrocław, Wrocław/PL; [3] Warsaw University of
Technology, Warsaw/PL; [4] Wroclaw University of Environmental and Life Sciences, Wrocław/PL; [5] Brandenburg University of
Technology Cottbus-Senftenberg, Senftenberg/D

11:40 *Discussion*

12:00 Lunch break

13:00 **POSTERSESSION 1 P01 - P29**

STRUCTURES & IMAGES

Chair: A. Mosig - Ruhr-Universität Bochum/D

14:30 **Prediction of quadruplex secondary structure topologies by means of sequence mutual information functions and interpretable
machine learning models**
J. Abel[1]; K. Bohnsack[1]; M. Kaden[1]; T. Villmann[1]; T. Zok[2]; J. Miskiewicz[2]; M. Szachniuk[2]
[1] Hochschule Mittweida - University of Applied Sciences, Mittweida/D; [2] Poznan University of Technology, Poznan/PL

14:45 **3D investigations of the pathomic profiles of human macrophages in lymph nodes reveal typical diagnostic supersets**
A. Vladisavljevic[1]; P. Wurzel[2]; S. Scharf[2]; H. Schäfer[1]; J. Ackermann[1]; I. Koch[1]; M. Hansmann[1]; [1] Goethe University Frankfurt,
Frankfurt am Main/D; [2] Frankfurt Institute for Advanced Studies (FIAS) and Goethe University, Frankfurt am Main/D

15:10 *Discussion*

15:25 Short break

PROGRAMME

IMAGE ANALYSIS

Chair: K. Reinert - Freie Universität Berlin/D

15:30 **A deep learning-based all-in-one image analysis tool for cell quantification: Proof-of-concept using confocal images of immunostained cells on ECMO membranes**
Z. Görmez[1]; F. Hoeren[2]; M. Richter[3]; A. Krause[1]; K. Troidl[1]; [1] Technische Hochschule Bingen, Bingen/D; [2] Max Planck Institute for Heart and Lung Research, Bad Nauheim/D; [3] Justus-Liebig-Universität Giessen, Giessen/D

15:45 **Bioimage analysis with deep learning for everyone: Visual programming in JIPipe**
R. Gerst[1]; J. Praetorius[1]; Z. Cseresnyés[1]; M. Figge[1]
[1] Leibniz Institute for Natural Product Research and Infection Biology – Hans Knöll Institute (HKI), Jena/D

16:00 **INDUSTRY: APEER: A cloud-based digital microscopy platform to create image processing workflows.**
B. Fichtl, [1] Carl Zeiss Microscopy , München/D.

16:15 *Discussion*

KEYNOTE SESSION

Chair: E. Gladilin - Leibniz Institute of Plant Genetics and Crop Plant Research (IPK), Gatersleben/D

16:30 **Utilizing Natural Variation and High-Throughput Phenotyping with PlantCV For Crop Improvement**
M. Gehan[1], [1] Danforth Plant Science Center, St. Louis/USA   .

17:10 *Discussion*

17:25 End of day 1

Tuesday, 7 September 2021

KEYNOTE SESSION

Chair: M.-A. Blätke - Leibniz Institute of Plant Genetics and Crop Plant Research (IPK), Gatersleben/D

09:00 FAIR Computational Workflows
C. Goble[1], [1] University of Manchester, /UK

09:40 *Discussion*

09:55 Short break

GENES & METABOLITES

Chair: C. Kaleta - Kiel University (CAU)/D

10:00 Prediction of 3D gene expression profiles in the Arabidopsis Thaliana floral meristem using single nucleus RNA sequencing data
M. Neumann[1]; X. Xu[1]; C. Smaczniak[1]; J. Schumacher[1]; K. Kaufmann[1]; J. Muino[1], [1] Humboldt-Universität zu Berlin, Berlin/D

10:25 Tissue-specific reconstruction of constraint-based metabolic models based on ReconX
N. Leonidou[1]; A. Renz[1]; R. Mostolizadeh[1]; A. Dräger[1], [1] Eberhard Karls University of Tübingen, Tuebingen/D

10:40 *Discussion*

10:55 Short break

NETWORKS & MEDICINE

Chair T. Manke - Max-Planck-Institut für Immunbiologie und Epigenetik, Freiburg im Breisgau/D

11:00 Integrating multi-omics data into molecular networks enables differential predictions
K. Baum[1]; J. Hugo[2]; J. Zeinert[2]; N. Müller[2]; S. Kashyap[2]; J. Rajapakse[3]; F. Azuaje[4]; B. Renard[2]
[1] work initiated at: Luxembourg Institute of Health, Strassen/LU; current affiliation: Hasso Plattner Institute, Digital Engineering Faculty, University of Potsdam, Potsdam/D; [2] Hasso Plattner Institute, Digital Engineering Faculty, University of Potsdam, Potsdam/D; [3] School of Computer Science and Engineering, Nanyang Technological University, Singapore/SGP; [4] Luxembourg Institute of Health, Strassen/LU; current affiliation: Genomics England, London/UK

11:15 Network- and systems-based re-engineering of dendritic cells with microRNAs for cancer immunotherapy
X. Lai[1]; F. Dreyer[1]; M. Cantone[1]; M. Eberhardt[1]; K. Gerer[1]; T. Jaitly[1]; S. Uebe[1]; C. Lischer[1]; A. Ekici[1]; J. Wittmann[1]; H. Jäck[1]; N. Schaft[1]; J. Dörrie[1]; J. Vera[1], [1] Friedrich-Alexander-Universität Erlangen-Nürnberg (FAU) and Universitätsklinikum Erlangen, Erlangen/D

11:30 PEPTIDE REACToR – A tool for large-scale comparisons of peptide encodings for biomedical classification
S. Spänig[1]; S. Mohsen[1]; G. Hattab[1]; H. Anne-Christin[1]; D. Heider[1], [1] Uni Marburg, Marburg/D

11:45 *Discussion*

12:00 *Lunch break*

13:00 **POSTERSESSION 2 P30 - P58**

PANGENOMES

Chair: A. Korte (Julius-Maximilian Universität Würzburg)

14:30 ODGI: scalable tools for pangenome graphs
A. Guarracino[1]; S. Heumos[2]; P. Prins[3]; E. Garrison[3], [1] University of Rome Tor Vergata, Rome/I; [2] University of Tübingen, Tübingen/D; [3] University of Tennessee Health Science Center (UTHSC), Memphis/USA

FABI AWARD LECTURE

Chairs: T. Beißbarth - University of Göttingen/D, I. Koch - Goethe University Frankfurt/D

15:00 Network Inference from Perturbation Data: Robustness, Identifiability and Experimental Design
T. Groß[1], [1] Humboldt-Universität zu Berlin, Berlin/D

15:20 Short Break

15:30 *FaBi General Assembly*

16:15 Short Break

KEYNOTE SESSION

Chair: P. F. Stadler - University of Leipzig/D

16:30 Structural Bioinformatics with Rosetta
J. Meiler[1], [1] Universität Leipzig, Leipzig/D

17:10 *Discussion*

17:25 End of day 2

PROGRAMME

Wesnday, 8 September 2021

KEYNOTE SESSION

Chair: A. Heintz-Buschart - University of Amsterdam, Amsterdam/NL

09:00 **Orthology of virus proteins: challenges, approaches, applications**
T. Rattei[1], [1] Universität Wien, Wien/A

09:40 *Discussion*

09:55 Short break

MICROBES

Chair: M. Schulz - Saarland University, Saarbrücken/D

10:00 **Metabolic annotation of microbiomes**
J. Zimmermann[1], [1] Christian-Albrecht University of Kiel, Kiel/D

10:25 **Analyzing the metabolic diversity of environmental, biotechnical, and host microbiomes using the MPA Pathway Tool**
R. Heyer[1]; D. Walke[2]; E. Lange[3]; K. Schallert[4]; U. Reichl[5]; G. Saake[6]; D. Benndorf[4], [1] Otto von Guericke University of Magdeburg, Magdeburg/D; [2] Otto von Guericke University Magdeburg, Chair of Bioprocess Engineering/D; [3] Otto von Guericke University, Magdeburg/D; [4] Otto von Guericke University Magdeburg, Magdeburg/D; [5] Otto von Guericke University / Max Planck Institute for Dynamics of Complex Technical Systems, Magdeburg/D; [6] Otto von Guericke University, Magdeburg/D

10:40 *Discussion*

10:55 Short break

MICROBES & PATHOGENS

Chair: M. Nowrousian - Ruhr-University Bochum/D

11:00 **INDUSTRY: JSpeciesWS: Calculating the extent of identity between microbial genomes on the total DNA level in microbial systematics**
J. Peplies[1], [1] Ribocon GmbH, Bremen/D

11:15 **Comparative simulations of fungal infection dynamics in the human and murine lung**
C. Saffer[1]; S. Timme[1]; M. Figge[1], [1] Leibniz Institute for Natural Product Research and Infection Biology - Hans Knöll Institute, Jena, Germany, Jena/D

11:30 *Discussion*

CLOSING & BEST POSTER AWARD

11:40

Chair: I. Grosse - Martin Luther University Halle-Wittenberg/D

P 01 **Pathway enrichment, machine learning and causal reasoning analysis to deconvolute potential targets of a small-molecule tau aggregation inhibitor**
L. Hosseini-Gerami[1]; E. Ficulle[2]; N. Humphryes-Kirilov[3]; D. Airey[4]; J. Scherschel[4]; B. Eastwood[5]; S. Bose[5]; D. Collier[5]; E. Laing[6]; D. Evans[7]; H. Broughton[8]; A. Bender[1], [1] University of Cambridge, Cambridge/UK; [2] University College London, London/UK; [3] C4X Discovery, London/UK; [4] Eli Lilly and Company, Indiana/USA; [5] Eli Lilly and Company, Bracknell/UK; [6] GSK, Stevenage/UK; [7] Google DeepMind, London/UK; [8] Eli Lilly and Company, Alcobendas/E

P 02 **Selection of important and related variables utilizing surrogate variables in random forests**
S. Seifert[1], [1] Hamburg School of Food Science, Universität Hamburg, Hamburg /D

P 03 **Comparison of change point-detection algorithms for short time series of clustered gene expression data**
M. Sieg[1]; J. Kruppa[1], [1] Charité - Universitätsmedizin Berlin, Berlin/D

P 04 **A global survey of the secondary metabolite diversity and potential in bacteria**
A. Gavriilidou[1]; S. A. Kautsar2, Nestor Zaburannyi3; Daniel Krug3; Rolf Müller3; M. H. Medema2; N. Ziemert[1]
[1] Eberhard Karls University of Tübingen, Tübingen/D; 2Wageningen University, Wageningen/NL; 3Helmholtz Zentrum für Infektionsforschung, Barunschweig/D

P 05 **Automated prediction of modules and assembly of respiratory complex I using graphs of topology of protein structures**
J. Wolf[1]; M. Zunker[1]; J. Ackermann[1]; I. Koch[1]

P 06 **Comparative genomics of proteins involved in the electrical generation of prokaryotes and archaea**
A. Tsareva[1], [1] ITMO University, Saint Petersburg/RUS

P 07 **Investigation of transcription factor co-occurrence reveals protein complexes regulating gene expression**
M. Bentsen[1]; V. Heger[1]; M. Looso[1], [1] Max Planck Institute for Heart and Lung Research, Bad Nauheim/D

P 08 **De novo generation of binding motifs for unknown transcription factors from ATAC-seq data**
H. Schultheis[1]; M. Bentsen[1]; M. Looso[1], [1] Max-Planck-Institute for Heart and Lung Research, Bad Nauheim/D

P 09 **Network Analysis to Improve Tumor Mutational Signature Identification**
S. Sulaimany[1], [1] University of Kurdistan, Sanandaj/IR

P 10 **Virtual lymph node: A Petri net model of the adaptive immune response**
S. Scharf[1]; P. Wurzel[1]; J. Ackermann[2]; M. Hansmann[3]; I. Koch[2],[1] Frankfurt Institute of Advanced Studies (FIAS) and Goethe University, Frankfurt am Main/D; [2] Molecular Bioinformatics, Goethe-University, Frankfurt am Main/D; [3] Frankfurt Institute of Advanced Studies (FIAS), Frankfurt am Main/D

P 11 **Design of an optimal COVID-19 surveillance protocol for child care facilities using an infection spread model**
P. Rudolph[1]; S. Timme[1]; M. Figge[1], [1] Leibniz Institute for Natural Product Research and Infection Biology - Hans Knöll Institute, Jena, Germany, Jena/D

P 13 **Whole-genome comparison of Aspergillus fumigatus environmental and clinical isolates reveals triazole resistance-related genes**
T. Sae-Ong[1]; A. E. Barber[1]; K. Kang[1]; J. Li[2]; G. Walther[1]; G. Panagiotou[1]; O. Kurzai[1], [1] Hans Knöll Institute (HKI), Jena/D; [2] City University of Hong Kong, Hong Kong/CN

P 14 **From data deposition to visualising variants - how FAIR principles are facilitating flow between plant genomics resources**
G. Naamati[1]; A. Thormann[1]; S. Hunt[1]; S. Dyer[1]; B. Contreras Moreira[1]; E. ELIXIR consortium FONDUE[2], [1] European Bioinformatics Institute (EMBL-EBI), Cambridge/UK; [2] https://elixir-europe.org/about-us/commissioned-services/fondue, https://elixir-europe.org/about-us/commissioned-services/fondue/UK

P 15 **Pathogenic potential prediction of novel fungal DNA based on a newly curated fungi-host database**
F. Nasri[1]; J. Bartoszewicz[1]; M. Nowicka[1]; B. Renard[2], [1] Hasso Plattner Institute, Digital Engineering Faculty, University of Potsdam, 14482 Potsdam and Department of Mathematics and Computer Science, Free University of Berlin, 14195 Berlin, Potsdam and Berlin/D; [2] Hasso Plattner Institute, Digital Engineering Faculty, University of Potsdam, Potsdam/D

P 16 **DivBrowse - a web application for interactive visualization and analysis of SNP matrices**
P. König[1]; S. Beier[1]; M. Lange[1]; U. Scholz[1], [1] Leibniz Institute of Plant Genetics and Crop Plant Research (IPK), Seeland OT Gatersleben/D

P 17 **Lipoxygenases could facilitate pathogen host jumps between plants and humans**
G. Kurakin[1], [1] Tver State Medical University, Tver/RUS

P 18 **tidysq — tidy and efficient storage and processing of biological sequences**
M. Bąkała[1]; D. Rafacz[1]; J. Słowik[1]; M. Burdukiewicz[2], [1] Warsaw University of Technology, Warsaw/PL; [2] Medical University of Białystok, Białystok/PL

P 19 **DeePSIVal: Decoy-free peptide spectrum match validation using a deep learning approach**
K. Schallert[1]; D. Micheel[1]; R. Heyer[1]; G. Saake[1]; U. Reichl[2]; D. Benndorf[1], [1] Otto-von-Guericke University Magdeburg, Magdeburg/D; [2] Max Planck Institute for Dynamics of Complex Technical Systems Magdeburg, Magdeburg/D

P 20 **Local DNA shape is a general principle of transcription factor binding specificity in Arabidopsis thaliana**
J. Sielemann[1]; D. Wulf[2]; R. Schmidt[2]; A. Bräutigam[2], [1] Bielefeld University, Bielefeld/D; [2] Bielefeld University/CeBiTec, Bielefeld/D

P 21 **Transcriptomics to characterize the role of chromatin modifiers and transcription factors in multicellular development of fungi**
R. Lütkenhaus[1]; J. Breuer[1]; M. Nowrousian[1], [1] Ruhr-University Bochum, Bochum/D

P 22 **Evaluating Tools for Automatic Reconstruction of Clonal Evolution**
S. Sandmann[1]; S. Richter[1]; X. Jiang[2]; J. Varghese[1], [1] Westfälische Wilhelms-Universität Münster, Institut für Medizinische Informatik, Münster/D; [2] Westfälische Wilhelms-Universität Münster, Institut für Informatik, Münster/D

P 23 **Systems biology modelling in Cystic Fibrosis to predict possible drug targets and active compound combinations**
L. Vinhoven[1]; F. Stanke[2]; S. Hafkemeyer[3]; M. Nietert[1], [1] University Medical Center Göttingen, Göttingen/D; [2] Hannover Medical School, Hannover/D; [3] Mukoviszidose Institut gGmbH (MI), Bonn/D

P 24 **PepGM: A probabilistic graphical model for taxonomic profiling of viral proteomes**
T. Holstein[1]; L. Martens[2]; T. Muth[1], [1] Bundesanstalt für Materialforschung - und Prüfung, Berlin/D; [2] Ghent University (UGent), Ghent/B

P 25 **Molecular identification and phylogenetic analysis using COI gene of non-penaeid shrimps from Mumbai, India**
R. Kaur[1]; G. Uppal[1]; T. Sawant[1], [1] Mumbai University, Munmbai/IND

P 26 **InterCellar empowers lab-scientists in the downstream analysis of cell-cell communication from single-cell transcriptomics**
M. Interlandi[1]; K. Kerl[2]; M. Dugas[3], [1] University of Münster, Münster/D; [2] University Children's Hospital Münster, Münster/D; [3] Heidelberg University Hospital, Heidelberg/D

P 27 **Explainable modular Neural Network architecture to predict important pathways based on simulated expression dat**
J. Oldenburg[1]; S. Simm[1], [1] Institute of Bioinformatics, University Medicine Greifswald, Greifswald/D

P 28 **Bioinformatics analysis of periodicity in proteins with coiled-coil structure**
S. Schuster[1]; A. Then[1]; H. Zhang[1], [1] University of Jena, Jena/D

P 29 **Statistical analysis of 'stop-stop' ORFs in eukaryotes**
V. Wesp[1]; S. Schuster[1], [1] Friedrich-Schiller Universität Jena, Jena/D

P 30 **BugCube – A database for large microscopy datasets of embryonic development in insects**
A. Berghoff[1]; F. Krämer[1]; K. Trares[2]; F. Strobl[1]; E. Stelzer[1], [1] Goethe University, Frankfurt am Main/D; [2] Heidelberg University, Heidelberg/D

P 31 **Protein stability with respect to chemical modifications. Example: SARS-Cov 2**
H. Stark[1]; M. Fichtner[1]; S. Schuster[1], [1] Friedrich-Schiller-University Jena, Jena/D

P 32 **Prediction of Intrinsic Transcription Terminators using Deep Learning Methods**
V. Brandenburg[1]; F. Narberhaus[1]; A. Mosig[1], [1] Ruhr-University Bochum, Bochum/D

P 33 **Semi- and fully-automated root image analysis and phenotyping**
N. Narisetti[1]; C. Seiler[1]; J. Ostermann[2]; T. Altmann[1]; E. Gladilin[1], [1] Leibniz Institute of Plant Genetics and Crop Plant Research (IPK), Gatersleben/D; [2] Leibniz Universität Hannover, Hannover/D

P 34 **Comparison of wild and cultivated beets regarding repeats and transposon insertion polymorphisms.**
L. Blazek[1]; J. Dohm[1]; H. Himmelbauer[1], [1] DBT - University of Natural Resources and Life Sciences (BOKU), Vienna/A

P 35 **Patient-specific identification of genome-wide methylation differences between intra- and extracranial melanoma metastases**
T. Kraft[1]; K. Grützmann[1]; M. Meinhardt[2]; D. Westphal[2]; S. Michael[1], [1] TU Dresden, Dresden/D; [2], University Hospital Carl Gustav Carus, TU Dresden, Dresden/D

P 36 **Advancements of long-read sequencing and its application to decode a wild barley accession**
B. Thakkar[1]; S. Conert[1]; A. Maurer[1]; K. Pillen[1]; T. Schmutzer[1], [1] Martin Luther University Halle-Wittenberg, halle/D

P 37 **Assembling highly repetitive Xanthomonas TALomes**
A. Erkes[1]; R. Grove[2]; M. Žarković[3]; S. Krautwurst[3]; R. Koebnik[4]; M. Hölzer[5]; M. Marz[3]; J. Boch[2]; J. Grau[1]
[1] Martin Luther University Halle-Wittenberg, Halle/D; [2] Leibniz Universität Hannover, Hannover/D; [3] Friedrich Schiller University, Jena/D; [4] Plant Health Institute, Montpellier/F; [5] Robert Koch Institute, Berln/D

P 38 **Cancer Hallmarks-based Biomarkers**
C. Ozen[1], [1] Technical University Dresden, Dresden/D

P 39 **Understanding the sequence-specific dynamics of nucleosome positioning and transcription factor interaction using random forests**
M. Sahrhage[1]; M. Haubrock[1]; T. Beißbarth[1], [1] University Medical Center Göttingen, Göttingen/D

P 40 A Landscape of Single Amino Acid Variants in Melanoma
B. Szeitz[1]; M. Kuras[2]; J. Rodriguez[3]; J. Eriksson[2]; Z. Horvath[2]; A. Szász[1]; M. Rezeli[2]; P. Horvatovich[4]; L. Betancourt[2]; G. Marko-Varga[2], [1] Semmelweis University, Budapest/H; [2] Lund University, Lund/S; [3] Karolinska Institute, Stockholm/S; [4] University of Groningen, Groningen/NL

P 41 K-mer-based phylogeny of wild and cultivated beets
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P 42 Analysis of sugar beet and wild beet genomes to study relationships, origins, population dynamics and selection
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P 43 Correcting for NK Cells in Acute Myeloid Leukemia Cell Type Mixtures Using NNLS
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P 44 Implementation of a scalable SARS-CoV-2 NGS data processing, variant calling and correlation analysis pipeline with snakemake
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P 45 Interpretable deep learning for phage life cycle prediction
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P 46 De novo assembly of Humulus lupulus transcriptome comparing different bioinformatic tools
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P 47 Classification of TFBS based on position-specific evolutionary sequence information
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P 48 Experimental determination and data-driven prediction of homotypic transmembrane domain interfaces
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P 49 Benchmarking of single-cell trajectory inference methods
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P 50 Investigation of the Effect of Chromatin Accessibility on the Co-Regulation in Biological Pathways
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P 51 Towards a new taxonomic framework for decoding microbial communities from metagenomic data
K. Block[1]; J. Plewka[1]; T. Bornemann[1]; S. Eßer[1]; C. Moore[1]; A. Probst[1], [1] University Duisburg-Essen, Essen/D

P 52 Pattern recognition and reconstruction in Mouse ICM Organoids via Machine learning
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P 53 Statistical exploratory analysis of transposable element data
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P 54 EcoMetEoR
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P 55 Modeling and deciphering the regulation of microbial central metabolism by dynamic optimization
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P 56 Mantis: flexible and consensus-driven genome annotation
P. Queiros[1], [1] University of Luxembourg, Esch-sur-Alzette/L

P 57 A probabilistic framework for context-specific transcriptional regulation analysis of biosynthetic gene clusters
M. Banf[1], [1] EducatedGuess.ai, Siegen/D

P 58 binny: an automated binning algorithm to recover high-quality genomes from complex metagenomics datasets
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