



GCB 2023 Hamburg | 12-14 September

# GCB 2023

## GERMAN CONFERENCE ON BIOINFORMATICS

PROGRAMME

[gcb2023.de](http://gcb2023.de)



## VENUE | ORGANISER

## CONFERENCE VENUE

**Deutsches Elektronen-Synchrotron DESY**

Notkestraße 85  
22607 Hamburg

## WORKSHOP VENUE

**Computational Systems Biology**

University of Hamburg  
Notkestrasse 9  
22607 Hamburg

## ORGANISER



DECHEMA e.V.  
Theodor-Heuss-Allee 25  
60486 Frankfurt am Main  
Germany

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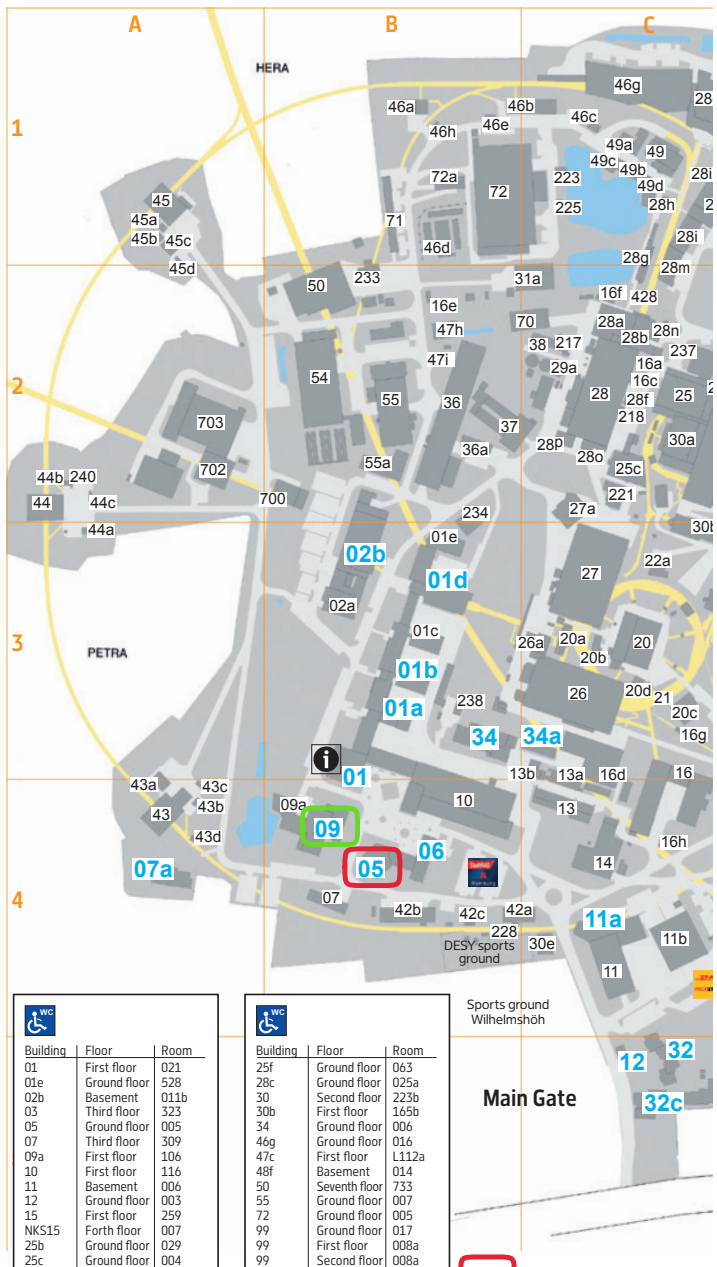
#GCB2023  
<https://twitter.com/gcb2023>

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SITE PLAN

- Laboratory building 1 01-01e (B3)
- Directorate 01 (B3)
- Press & Communications (Information) 01 (B3)
- Company medical officer, Social counselling 01a (B3)
- Seminar rooms 3-5 01b (B3)
- Library 01d (B3)
- Laboratory building 2a, Theory 02a (B3)
- Computer centre, UCO 02b (B3)
- Radiation Protection Department D3 03 (D4)
- Storage building 03b (D4)
- Auditorium (DESY)**, entrance bldg. 05 (B4)
- Administration building 06 (B4)
- Post, Guest services 06 (B4)
- Administration building 07 (B4)
- Guest house 8 07a (A4)
- Canteen, cafeteria, Cash machine** 09,09a (B4)
- Workshop 10 (B4)
- Purchasing department 11 (C4)
- Central warehouse 11a (C4)
- Works council 11a (C4)
- Gate lodge Notkestraße** (main gate) 12 (C5)
- Gate lodge Luruper Chaussee** (side gate) 12a (E3)
- Gas service 13a+b (C3)
- Vacuum laboratory 14 (C4)
- CSSB 15 (D3)
- MKK / Power station 16 (C3)
- Heating plant 17 (C3)
- Site service yard 18,18a (D3)
- Carpenters' building 19 (D3)
- Synchrotron building 20 (C3)
- Power-House DESY 20c (C3)
- LUX 22 (C3)
- Laboratory of the Universities of Hamburg and Lübeck** 22a (C3)
- REGAE 23 (C3)
- LINAC II 24 (D2)
- PIA tunnel 24a (D3)
- FS experimental hall 25 (C2)
- Office and laboratory building EMBL** 25a (C2)
- FS office and laboratory building 1 25b (D2)
- Detector Assembly Facility (DAF) 25c (C2)
- FS office and laboratory building 4 25d (C2)
- FS office and laboratory building 5+2 25e,f (D2)
- Detector Assembly Facility (DAF) / Experimental hall I 25e,f (C3)
- DESY testbeam / Experimental hall II 27 (C3)
- Testing area 27a (C2)
- Experimental hall III 28,28a (C2)
- FLASH tunnel 428 (C1/2)
- FLASH experimental hall „Albert Einstein“ 28c (C1)
- FLASH experimental hall „Kai Siegbahn“ 28k (C1)
- FLASH2 undulator building 28i (C1)
- FLASH laser hut 28g (C1)
- Water treatment plant 29a (C2)
- Accelerator control room (BKR) / SINBAD 30 (C2)
- Supplying hall 30a (C2)
- Accelerator operation building 30b (C3)
- ARGUS detector 30e (C4)
- Accelerator components building 31a (C2)
- Guest house 2 32 (C5)
- Kindergarten 32c (C5)
- Guest house 3 33 (C5)
- Training area 34 (B3)
- School lab physik.begreifen 34a (B3)
- Safety group / SAVE 35 (C3)

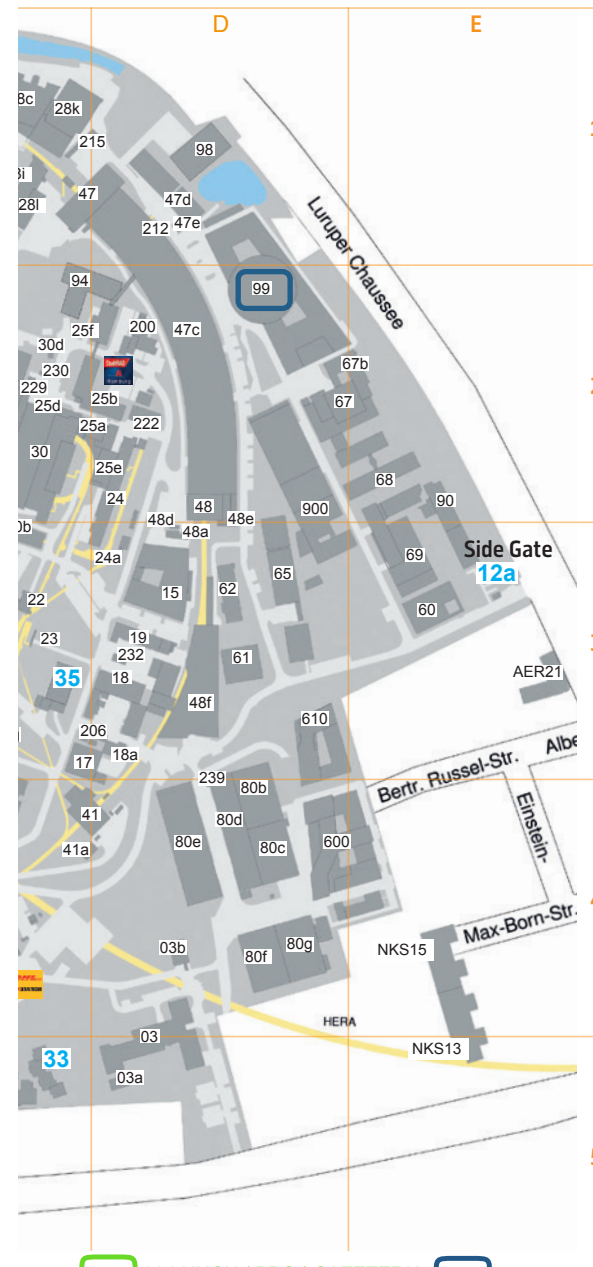


Building	Floor	Room
01	First floor	021
01e	Ground floor	528
02b	Basement	011b
03	Third floor	323
05	Ground floor	005
07	Third floor	309
09a	First floor	106
10	First floor	116
11	Basement	006
12	Ground floor	003
15	First floor	259
NKS15	Forth floor	007
25b	Ground floor	029
25c	Ground floor	004

Building	Floor	Room
25f	Ground floor	063
28c	Ground floor	025a
30	Second floor	223b
30b	First floor	165b
34	Ground floor	006
46g	Ground floor	016
47c	First floor	L112a
48f	Basement	014
50	Seventh floor	733
55	Ground floor	007
72	Ground floor	005
99	Ground floor	017
99	First floor	008a
99	Second floor	008a

05 LECTURE HALL

SITE PLAN



- (C3) 35 Communication engineering
- (B2) 36 Preparation hall / Experimental hall V
- (C4) 41, 41a PETRA halls SO
- (B4) 42, 42a-c PETRA halls S
- (A4) 43, 43a-b PETRA halls SW
- (A2) 44 PETRA hall W
- (A1) 45, 45a-c PETRA halls NW
- (B/C1) 46a-c PETRA halls N
- (C1) 46g PETRA III experimental hall „Paul P. Ewald“
- (C/D1) 47 PETRA halls NO
- (D1-2) 47c PETRA III experimental hall „Max von Laue“
- (D1) 47d PETRA III cooling plant
- (D2) 48, 48e PETRA halls O / EMBL
- (D3) 48f PETRA III experimental hall „Ada Yonah“
- (C1) 49, 49a Office and laboratory building
- (B2) 50 HERA hall W
- (B2) 54 Refrigeration technology hall (Cryogenic control room)
- (B2) 55 Magnet measurement hall
- (B2) 55a M office building
- 60-69 University Hamburg**
- (E3) 60 Univ. school lab Light & Schools
- (D3) 61 Auditorium (university)
- (D3) 62 Institute for experimental physics
- (D3) 65 Workshop
- (D2) 67 SALOME
- (D/E2) 67-68 Institute for experimental physics
- (E3) 69 Institute for laser physics
- (C2) 70 Module test hall CMTB
- (B1) 71 XTL mock-up
- (B1) 72 AMTF hall
- (D4) 80b-g Storage buildings
- (E2) **90 Centre for optical quantum technologies (Z00)**
- (C/D2) **94 CXNS, HEREDN, CAU Photon Science User Office**
- (D1) **98 Start-up Labs Bahrenfeld**
- (D2) **99 CFEL**
- (D2) 200 Innovation Village
- (D2) 222 FS office building
- (D/E4) **600 CHYN**
- (D3) **610 HARBOR**
- (B2) 700 European XFEL injector entrance
- (A2) 702 European XFEL tunnel entrance
- (A2) 703 European XFEL modulator hall
- (D2/3) **900 Max Planck Institute (MPSD)**
- Off-site buildings:**
- 51 HERA hall N/ALPS II
- 52 HERA hall O
- 53 HERA hall S
- (E3) AER21 Project management DESY (PT DESY)
- (E5) NKS13 EU project office, administration
- (E4) NKS15 Finance department V3

Parking on the DESY premises is at your own risk. All city traffic regulations are valid and a speed limit of 30 km/h is allowed. Upon leaving the DESY premises random spot checks will be made at both gates. Please halt at the red traffic signal or the horn signal for inspection.

09 LUNCH / BBQ | CAFETERIA 99 POSTER SESSION CFEL-Foyer

## ORGANISERS | COMMITTEE

## LOCAL ORGANISERS

<b>Jan Baumbach</b>	University of Hamburg
<b>Daniel Buchberger</b>	University of Hamburg
<b>Christina Saak</b>	University of Hamburg
<b>Eda Seibitz</b>	University of Hamburg
<b>Nina Wenke</b>	University of Hamburg

## PROGRAMME COMMITTEE

<b>Michael Altenbuchinger</b>	UMG Göttingen
<b>Jan Baumbach</b>	University of Hamburg
<b>Tim Beißbarth</b>	UMG Göttingen
<b>David Blumenthal</b>	FAU Erlangen
<b>Sebastian Böcker</b>	FSU Jena
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<b>Tim Conrad</b>	FU Berlin
<b>Thilo Figge</b>	FSU Jena
<b>Caroline Friedel</b>	LMU München
<b>Anne-Christin Hauschild</b>	UMG Göttingen
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<b>Gunnar Klau</b>	University Düsseldorf
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<b>Manja Marz</b>	FSU Jena
<b>Josch Pauling</b>	TU München
<b>Sven Rahmann</b>	University of Saarbrücken
<b>Matthias Rarey</b>	University of Hamburg
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<b>Richard Röttger</b>	SDU, Odense/DK
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<b>Michael Schroeder</b>	TU Dresden
<b>Marcel Schulz</b>	Goethe University Frankfurt
<b>Julia Schulze-Hentrich</b>	University of Tübingen
<b>Stefan Schuster</b>	FSU Jena
<b>Johannes Soeding</b>	University of Göttingen
<b>Andrew Torda</b>	University of Hamburg
<b>Dirk Walther</b>	MPI Potsdam
<b>Ralf Zimmer</b>	LMU München
<b>Olga Zolotareva</b>	University of Hamburg

## SUPPORTERS

We thank our Supporters:



Institute for Computational Systems Biology  
Hamburg/D



German Network for Bioinformatics  
Infrastructure – de.NBI  
Bielefeld/D



Fachgruppe Bioinformatik



International Society for  
Computational Biology – ISCB  
Leesburg, VA/USA



Universität Hamburg  
DER FORSCHUNG | DER LEHRE | DER BILDUNG

Universität Hamburg  
Hamburg/D



Deutsches Elektronen-Synchrotron DESY  
Hamburg/D



Deutsche Forschungsgemeinschaft  
(DFG, German Research Foundation)  
Bonn/D



Gesellschaft für Biochemie  
und Molekularbiologie e.V.  
Frankfurt am Main/D



Syte – Strategy Institute  
for Digital Health  
Hamburg/D

## PROGRAMME OVERVIEW

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	Monday 11 September	Tuesday 12 September	Wednesday 13 September	Thursday 14 September
09:00	<b>WORKSHOPS</b>  WS2 WS3 WS5 WS6 WS7 WS8 WS9	Registration	<b>KEYNOTE 2</b> Joseph Loscalzo	<b>KEYNOTE 3</b> Sebastian Böcker
09:45		<b>OPENING</b>		
09:50		<b>KEYNOTE 1</b> Nataša Pržulj	<b>SESSION III</b>	Coffee Break
10:00				Coffee Break
10:30				<b>SESSION VI</b>
10:50		Coffee Break		
11:15		<b>SESSION I</b>	<b>SESSION IV</b>	<b>CLOSING + BEST POSTER</b>
11:45				
12:00				
12:15	Lunch Break			
12:55	End of GCB 2023			
13:00	<b>WORKSHOPS</b>  WS1 WS4 WS6 WS7 WS9	Lunch Break	Lunch Break	
13:20		<b>SESSION II</b>	<b>SESSION V</b>	
14:20				Coffee Break
15:20		<b>FaBI prize lecture</b>		
15:45				
16:00	Coffee Break			
16:25	<b>JUNIOR KEYNOTE 1</b> Olga Tsoy	<b>FaBI- Assembly</b>	<b>JUNIOR KEYNOTE 1</b> Nadine Töpfer	
16:30				
17:00	<b>POSTER SESSION</b>			
17:30		End of Day 2		
18:00		<b>PC DINNER</b>		
19:00				
19:30	<b>BBQ-DINNER</b>			
23:00		End of Day 1		

## WORKSHOPS | TUTORIALS

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(with registration only)

<b>Monday, 11 September 2023</b>		<b>09:00 – 12:00</b>
<b>WS2</b>	<b>How to analyze spatial transcriptomics data (visium 10x) with R and Python</b>	
Room:	Organizers: Sonja Hänzelmann; Fabian Hausmann; Robin Khatri (Universität Hamburg)	
4064 / 4 <sup>th</sup> floor		
<b>WS3</b>	<b>Standardizing and harmonizing NGS analysis workflows</b>	
Room:	Organizers: Dr. Florian Heyl (German Cancer Research Center, Workflow Coordinator for GHGA); Dr. Kübra Narci (German Cancer Research Center); Dr. Christian Mertes (Technical University of Munich); Dr. Julia Philipp (European Molecular Biology Laboratory, Training Coordinator for GHGA)	
1083 / 1 <sup>st</sup> floor		
<b>WS5</b>	<b>Federated Ensemble Learning for Biomedical Data</b>	
Room:	Organizers: Prof. Dr. Anne-Christin Hauschild; Hryhorii Chereda; Youngjun Park; Maryam Moradpour (University Medical Center Göttingen)	
1076 / 1 <sup>st</sup> floor		
<b>WS6</b>	<b>Bioinformatics education - starting at 10 am</b>	
Room:	Organizers: Jan Grau (MLU Halle); Stefan Kurtz (ZBH Hamburg); Kay Nieselt (University Tübingen); Sven Rahmann (Universität des Saarlandes); Ralf Zimmer (LMU München)	
3114 / 3 <sup>rd</sup> floor		
<b>WS7</b>	<b>Constrained-based modelling in Python applied to plant systems</b>	
Room:	Organizers: Stefano Camborda; Tiago Machado; Nadine Töpfer (University of Cologne)	
1012 / 1 <sup>st</sup> floor		
<b>WS8</b>	<b>Build your own interactive, online network-based drug repurposing application using DrugSt.One</b>	
Room:	Organizers: Michael Hartung; Andreas Maier (University of Hamburg)	
1006 / 1 <sup>st</sup> floor		
<b>WS9</b>	<b>FeatureCloud: privacy-aware federated learning in biomedicine</b>	
Room:	Organizers: Mohammad Bakhtiari, Mohammad Mahdi Kazemi, Julian Klemm, Niklas Probul	
3066 / 3 <sup>rd</sup> floor		
12:00 – 13:00	Lunch-Break	
		<b>13:00 – 16:00</b>
<b>WS1</b>	<b>1001 reasons for a Data Management Plan</b>	
Room:	Organizers: Helena Schnitzer (ELIXIR Germany); Daniel Wibberg (Forschungszentrum Jülich)	
3062 / 3 <sup>rd</sup> floor		
<b>WS4</b>	<b>How to interpret multi-omics single-cell and spatial transcriptomics data (Visium, 10x, MERFISH) with R and Python (Advanced level)</b>	
Room:	Organizers: Tore Bleckwehl; Rafael Kramann; Sikander Hayat (Institute of Experimental medicine and systems Biology, Uniklinik Aachen)	
4064 / 4 <sup>th</sup> floor		
<b>WS6</b>	<b>Bioinformatics education</b>	
Room:	Organizers: Jan Grau (MLU Halle); Stefan Kurtz (ZBH Hamburg); Kay Nieselt (University Tübingen); Sven Rahmann (Universität des Saarlandes); Ralf Zimmer (LMU München)	
3114 / 3 <sup>rd</sup> floor		
<b>WS7</b>	<b>Constrained-based modelling in Python applied to plant systems</b>	
Room:	Organizers: Stefano Camborda; Tiago Machado; Nadine Töpfer (University of Cologne)	
1012 / 1 <sup>st</sup> floor		
<b>WS9</b>	<b>FeatureCloud: privacy-aware federated learning in biomedicine</b>	
Room:	Organizers: Mohammad Bakhtiari, Mohammad Mahdi Kazemi, Julian Klemm, Niklas Probul	
3066 / 3 <sup>rd</sup> floor		

Details available at <https://gcb2023.de/Workshops.html>

## LECTURE PROGRAMME

Tuesday, 12 September 2023

09:00 Registration

Room: SPEICHERING 05 LECTURE HALL

09:45 **OPENING**J. Baumbach<sup>1</sup> <sup>1</sup>Universität Hamburg/DChair: J. Baumbach<sup>1</sup>; <sup>1</sup>Universität Hamburg/D09:50 **KEYNOTE I**

**Omics Data Fusion for Understanding Molecular Complexity Enabling Precision Medicine**  
 N. Przulj<sup>1</sup>; <sup>1</sup> Catalan Institution for Research and Advanced Studies (ICREA); Barcelona  
 Supercomputing Center; University College London, Barcelona/E

10:50 Coffee-Break

**SESSION I**Chair: C. Dieterich<sup>1</sup> <sup>1</sup>University Hospital Heidelberg/D11:15 **The continuation of the de.NBI/ELIXIR Germany network and its activities in research data management training**D. Wibberg<sup>1</sup>; H. Schnitzer<sup>1</sup>; A. Tauch<sup>1</sup>; <sup>1</sup> Forschungszentrum Jülich GmbH - Außenstelle  
Universität Bielefeld/D11:40 **Stability of feature selection utilizing Graph Convolutional Neural Network and Layer-wise Relevance Propagation**H. Chereda<sup>1</sup>; A. Leha<sup>1</sup>; T. Beißbarth<sup>1</sup>; T. Beißbarth<sup>2</sup>; <sup>1</sup> University Medical Center  
Göttingen/D; <sup>2</sup> University of Göttingen/D12:05 **Improved reconstruction of transcripts and coding sequences from RNA-seq data**J. Grau<sup>1</sup>; J. Keilwagen<sup>2</sup>; <sup>1</sup> Martin Luther University Halle-Wittenberg, Halle/D; <sup>2</sup> Julius Kühn-  
Institut, Quedlinburg/D12:30 **Multiple-omics based metabolic modelling reveals effects of drug-induced liver toxicity**Z. Soons<sup>1</sup>; H. Cordes<sup>1</sup>; L. Kuepfer<sup>1</sup>; <sup>1</sup> Uniklinik RWTH Aachen/D12:55 **A disease network-based deep learning approach for characterizing melanoma**X. Lai<sup>1</sup>; J. Vera<sup>2</sup>; <sup>1</sup> Tampere University, Tampere/FIN; <sup>2</sup> Universitätsklinikum Erlangen and  
Friedrich-Alexander-Universität Erlangen-Nürnberg, Erlangen/D

13:20 Lunch-Break

Room: SPEICHERING 09 KANTINE / CAFETERIA

## LECTURE PROGRAMME

Tuesday, 12 September 2023

Room: SPEICHERING 05 LECTURE HALL

**SESSION II**Chair: C. Friedel<sup>1</sup> <sup>1</sup>Ludwig-Maximilians-Universität München (LMU), München/D14:20 **When False Positives Hit are the Norm: Uncovering True Positives from False Positives at the Example of RNA Virus Detection in the Human Genome**M. Ritsch<sup>1</sup>; M. Marz<sup>1</sup>; <sup>1</sup> Friedrich Schiller University Jena/D14:45 **permGWAS: Efficient Permutation-based Genome-wide Association Studies for Normal and Skewed Phenotypic Distributions**M. John<sup>1</sup>; M. Ankenbrand<sup>2</sup>; C. Artmann<sup>2</sup>; J. Freudenthal<sup>2</sup>; A. Korte<sup>2</sup>; D. Grimm<sup>1</sup>; <sup>1</sup> TUM  
Campus Straubing for Biotechnology and Sustainability, Weihenstephan-Triesdorf  
University of Applied Science, Straubing/D; <sup>2</sup> University of Würzburg/D15:10 **Correcting 4sU induced quantification bias in nucleotide conversion RNA-seq data**K. Berg<sup>1</sup>; <sup>1</sup> Julius-Maximilians-Universität Würzburg/D15:35 **Xengsort2: Ultrafast accurate xenograft sorting**J. Zentgraf<sup>1</sup>; S. Rahmann<sup>1</sup>; <sup>1</sup> Saarland University, Saarbrücken/D

16:00 Coffee-Break

Chair: M. L. Elkjær<sup>1</sup> <sup>1</sup>Universität Hamburg/D16:30 **JUNIOR KEYNOTE I**17:30 **Towards the systems biology of alternative splicing**O. Tsoy<sup>1</sup>; <sup>1</sup> Universität Hamburg, Hamburg/D17:30 **POSTER SESSION**

Room: CFEL-Foyer

19:30 **BBQ Dinner with DJ**

Room: SPEICHERING 09 KANTINE / CAFETERIA

23:00 End of day one

## LECTURE PROGRAMME

## Wednesday, 13 September 2023

Room: SPEICHERING 05 LECTURE HALL

Chair: S. Böcker<sup>1</sup> Friedrich Schiller Universität Jena/D

- 09:00 **KEYNOTE II**  
**Network Medicine and Bioinformatics: An Alliance in Search of Pathobiological Mechanism and Drug Discovery**  
 J. Loscalzo<sup>1</sup>; <sup>1</sup> Harvard Medical School, Boston/D

## SESSION III

Chair: S. Böcker<sup>1</sup> Friedrich Schiller Universität Jena, Jena/D

- 10:00 **Machine Learning to optimize personalized treatment recommendations**  
 S. Schrod<sup>1</sup>; M. Altenbuchinger<sup>1</sup>; <sup>1</sup> University Medical Center Göttingen/D
- 10:25 **Cracking the black box of deep sequence-based protein-protein interaction prediction**  
 J. Bernett<sup>1</sup>; D. Blumenthal<sup>2</sup>; M. List<sup>1</sup>; <sup>1</sup> Technical University of Munich, Freising/D; <sup>2</sup> Friedrich-Alexander-Universität Erlangen-Nürnberg (FAU) and Universitätsklinikum Erlangen/D
- 10:50 Coffee-Break

## SESSION IV

Chair: D. Heider<sup>1</sup> Philipps-Universität Marburg/D

- 11:15 **UnPaSt: Identification of differentially expressed biclusters for unsupervised patient stratification**  
 O. Zolotareva<sup>1</sup>; M. Hartung<sup>1</sup>; A. Maier<sup>1</sup>; F. Delgado-Chaves<sup>1</sup>; O. Isaeva<sup>2</sup>; F. Patroni<sup>3</sup>; K. Kaufmann<sup>1</sup>; D. He<sup>4</sup>; A. Savchik<sup>5</sup>; Z. Chervontseva<sup>1</sup>; A. Abisheva<sup>6</sup>; E. Zotova<sup>6</sup>; N. Probul<sup>1</sup>; O. Tsoy<sup>1</sup>; D. Blumenthal<sup>7</sup>; M. Ester<sup>8</sup>; J. Baumbach<sup>1</sup>; <sup>1</sup> University of Hamburg, Hamburg/D; <sup>2</sup> The Netherlands Cancer Institute, Amsterdam/NL; <sup>3</sup> University of Campinas, Campinas/BR; <sup>4</sup> University of British Columbia, Vancouver/CDN; <sup>5</sup> ACMetric, Amsterdam/NL; <sup>6</sup> Altius Institute for Biomedical Sciences, Seattle/USA; <sup>7</sup> Friedrich-Alexander-Universität Erlangen-Nürnberg, Erlangen/D; <sup>8</sup> Simon Fraser University, Burnaby/CDN
- 11:40 **Using large-scale structural annotation for the construction of conditional gene-gene interaction networks**  
 A. Gress<sup>1</sup>; O. Kalinina<sup>1</sup>; H. Nguyen<sup>2</sup>; O. Tsoy<sup>2</sup>; J. Baumbach<sup>2</sup>; <sup>1</sup> Helmholtz Institute for Pharmaceutical Research Saarland (HIPS), Saarbrücken/D; <sup>2</sup> Institute for Computational Systems Biology, Hamburg/D
- 12:05 **Heterogeneous domain adaptation for cross-species transfer learning without gene homology**  
 Y. Park<sup>1</sup>; N. Muttray<sup>2</sup>; A. Hauschild<sup>1</sup>; <sup>1</sup> University Medical Center Göttingen/D; <sup>2</sup> Georg-August-Universität Göttingen/D
- 12:30 **Graph-Theoretical Prediction of Biological Modules on the Level of Single Proteins up to Large Protein Complexes**  
 F. Gisdon<sup>1</sup>; M. Zunker<sup>1</sup>; J. Wolf<sup>1</sup>; J. Ackermann<sup>1</sup>; I. Koch<sup>1</sup>; <sup>1</sup> Goethe University Frankfurt am Main/D
- 12:55 **ODNA: Identification of Organellar DNA by Machine Learning**  
 R. Martin<sup>1</sup>; M. Nguyen<sup>1</sup>; N. Lowack<sup>1</sup>; D. Heider<sup>1</sup>; <sup>1</sup> Philipps University of Marburg/D
- 13:20 Lunch-Break

Room: SPEICHERING 09 KANTINE / CAFETERIA

## LECTURE PROGRAMME

## Wednesday, 13 September 2023

Room: SPEICHERING 05 LECTURE HALL

## SESSION V

Chair: D. Walther<sup>1</sup> Max Planck Institute of Molecular Plant Physiology, Potsdam-Golm/D

- 14:20 **Assessing the impact of alternative splicing on the functional diversification of a proteome**  
 I. Ebersberger<sup>1</sup>; J. Dosch<sup>1</sup>; C. Bluemel<sup>1</sup>; <sup>1</sup> Goethe University, Frankfurt, Frankfurt/D
- 14:45 **Morphology-based Molecular Classification of Spinal Cord Ependymomas Using Deep Neural Networks**  
 Y. Schumann<sup>1</sup>; M. Dottermusch<sup>2</sup>; L. Schweizer<sup>3</sup>; M. Krech<sup>4</sup>; U. Schüller<sup>2</sup>; J. Neumann<sup>2</sup>; P. Neumann<sup>1</sup>; <sup>1</sup> Helmut-Schmidt-Universität/Universität der Bundeswehr Hamburg, Hamburg/D; <sup>2</sup> University Medical Center Hamburg-Eppendorf (UKE), Hamburg/D; <sup>3</sup> University Medical Center Frankfurt, Frankfurt/D; <sup>4</sup> Charité Berlin, Berlin/D

- 15:10 Coffee-Break

## FABI SESSION

Chair: I. Koch<sup>1</sup>; <sup>1</sup> Goethe University Frankfurt am Main/D

- 15:45 **Lecture of FaBi Dissertation Prize Winner**  
**Mutual Hazard Networks: Markov Chain models of cancer progression**  
 R. Schill<sup>1</sup>; <sup>1</sup> Universität Regensburg/D
- 16:05 **FaBI assembly**

Chair: K. Newaz<sup>1</sup>; <sup>1</sup> Universität Hamburg/D

- 17:00 **JUNIOR KEYNOTE II**  
**Metabolic flux modelling as a useful tool for predicting crop improvement strategies**  
 N. Töpfer<sup>1</sup>; <sup>1</sup> University of Cologne, Köln/D
- 18:00 End of day two
- 19:00 **Programme Committee Dinner**

Thursday, 14 September 2023

Room: SPEICHERING 05 LECTURE HALL

Chair: J. Schulze-Hentrich<sup>1</sup> Saarland University, Saarbrücken/D

09:00 **KEYNOTE III**  
**Untargeted metabolomics: Turning tandem mass spectra into metabolite structures**  
 S. Böcker<sup>2</sup>; <sup>1</sup>Friedrich Schiller Universität Jena/D

10:00 Coffee-Break

**SESSION VI**Chair: J. Schulze-Hentrich<sup>1</sup> Saarland University, Saarbrücken/D

10:30 **Fully differentiable methods for RNA sequence design**  
 M. Matthies<sup>1</sup>; A. Torda<sup>1</sup>; <sup>1</sup> University of Hamburg/D

10:55 **grandR: a comprehensive package for nucleotide conversion RNA-seq data analysis**  
 T. Rummel<sup>1</sup>; L. Sakellaridi<sup>1</sup>; F. Erhard<sup>2</sup>; <sup>1</sup> Julius-Maximilians-Universität Würzburg/D;  
<sup>2</sup> Universität Regensburg/D

11:20 **Scaling up Marker Discovery from Whole Genome Sequences**  
 B. Vieira Mourato<sup>1</sup>; F. Klötzl<sup>2</sup>; B. Haubold<sup>1</sup>; <sup>1</sup> Max-Planck-Institute for Evolutionary Biology,  
 Ploen/D; <sup>2</sup> Illumina, Ltd., Cambridge/UK

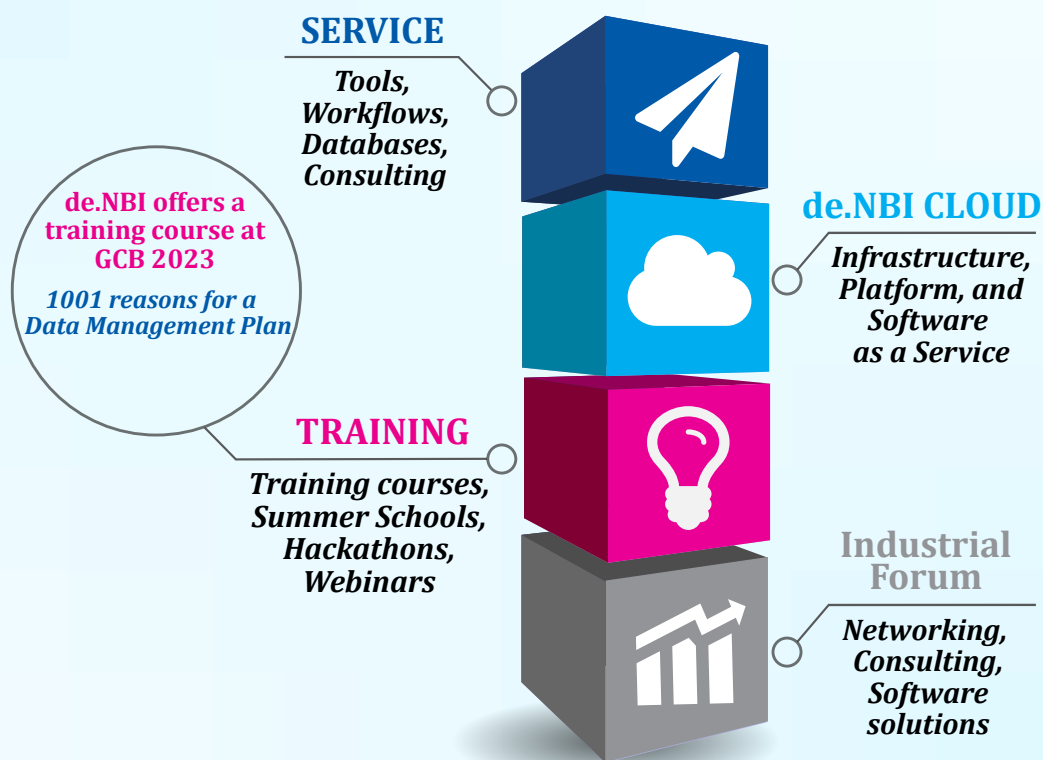
11:45 **CLOSING & BEST POSTER**  
 Chair: J. Baumbach<sup>1</sup>; <sup>1</sup>Universität Hamburg/D

12:15 Farewell Coffee

13:00 End of GCB 2023

## THE GERMAN NETWORK FOR BIOINFORMATICS INFRASTRUCTURE

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## POSTER PROGRAMME

- P01 **A network medicine approach for identifying diagnostic and prognostic biomarkers and exploring drug repurposing in human cancer**  
X. Lai<sup>1</sup>; J. Vera<sup>2</sup>; <sup>1</sup> BioMediTech, Faculty of Medicine and Health Technology, Tampere University, Tampere, Finland, Erlangen/D; <sup>2</sup> Laboratory of Systems Tumor Immunology, Department of Dermatology, Universitätsklinikum Erlangen and Friedrich-Alexander-Universität Erlangen- Nürnberg, Erlangen, Germany, Erlangen/D
- P02 **Untangling the Knot: Machine Learning Uncovers Knotted Patterns in Protein Structures**  
E. Klimentová<sup>1</sup>; <sup>1</sup> CEITEC MU, Brno/CZ
- P03 **Accessible and scalable pipelines for fast and easy (foodborne) pathogens detection and tracking**  
E. Nasr<sup>1</sup>; A. Henger<sup>2</sup>; T. Schindler<sup>3</sup>; B. Grüning<sup>1</sup>; B. Batut<sup>1</sup>; <sup>1</sup> Albert-Ludwigs-Universität Freiburg, Freiburg im Breisgau/D; <sup>2</sup> Biolytix AG, Witterswil/CH; <sup>3</sup> Amplytico gmbh, Sissach/CH
- P04 **ENQUIRE Reconstructs and Expands Gene and MeSH Networks from Literature, by Querying Unexpectedly Interrelated Entities**  
L. Musella<sup>1</sup>; <sup>1</sup> Friedrich-Alexander University (FAU) Erlangen-Nürnberg and Universitätsklinikum Erlangen, Erlangen/D
- P05 **An M for an A: Using Bioinformatics to characterize DNA methyltransferase specificities through the utilization of MALDI-TOF and sequencing methodologies.**  
J. Otto<sup>1</sup>; N. Ueberschaar<sup>1</sup>; V. Wesp<sup>1</sup>; G. Pohnert<sup>1</sup>; M. Bauer<sup>2</sup>; A. Busch<sup>1</sup>; <sup>1</sup> Uni Jena/D; <sup>2</sup> University Hospital Jena/D
- P06 **Towards reliable prediction of significant changes in microbial communities based on time series data**  
A. Brüggemann<sup>1</sup>; <sup>1</sup> Universität Duisburg Essen, Essen/D
- P07 **Interpretable deep learning models for elucidating the complex cis-regulatory code of model plant species**  
F. Peleke<sup>1</sup>; S. Zumkeller<sup>2</sup>; J. Symanski<sup>3</sup>; <sup>1</sup> Leibniz-Institut für Pflanzengenetik und Kulturpflanzenforschung (IPK), Gatersleben/D; <sup>2</sup> Institute of Bio- and Geosciences, IBG-4: Plant Sciences, Forschungszentrum Jülich, Jülich/D; <sup>3</sup> Leibniz Institute of Plant Genetics and Crop Plant Research (IPK), Gatersleben/D
- P08 **Microbiome data analysis using the Galaxy platform**  
P. Zierep<sup>1</sup>; B. Batut<sup>1</sup>; E. Nasr<sup>1</sup>; B. Grüning<sup>1</sup>; <sup>1</sup> Albert-Ludwigs-Universität Freiburg/D
- P09 **Network-based analysis of heterogeneous patient-matched brain and extracranial melanoma metastases pairs reveals three homogeneous subgroups**  
K. Grützmann<sup>1</sup>; T. Kraft<sup>1</sup>; M. Meinhardt<sup>2</sup>; D. Westphal<sup>2</sup>; M. Seifert<sup>1</sup>; <sup>1</sup> Technische Universität Dresden/D; <sup>2</sup> University Hospital Dresden/D
- P10 **Interactive visualization and exploratory data analysis of variant call matrices with DivBrowse**  
P. König<sup>1</sup>; S. Beier<sup>2</sup>; M. Mascher<sup>1</sup>; N. Stein<sup>1</sup>; M. Lange<sup>1</sup>; U. Scholz<sup>1</sup>; <sup>1</sup> Leibniz Institute of Plant Genetics and Crop Plant Research (IPK), Seeland/D; <sup>2</sup> Forschungszentrum Jülich GmbH, Jülich/D

## POSTER PROGRAMME

- P11 **Which collagen types can crosslink with each other?**  
V. Wesp<sup>1</sup>; L. Scholz<sup>1</sup>; S. Schuster<sup>1</sup>; H. Stark<sup>1</sup>; <sup>1</sup> Friedrich-Schiller-University Jena/D
- P12 **Inverse folding based pre-training for the reliable identification of intrinsic transcription terminators**  
V. Brandenburg<sup>1</sup>; F. Narberhaus<sup>1</sup>; A. Mosig<sup>1</sup>; <sup>1</sup> Ruhr-University Bochum/D
- P13 **Combining data analysis strategies to identify gene targets for the optimisation of production cell lines**  
M. Rattay<sup>1</sup>; S. Pijaud<sup>1</sup>; A. Antonakoudis<sup>2</sup>; P. Jonsson<sup>3</sup>; O. Cloarec<sup>4</sup>; A. Richelle<sup>5</sup>; <sup>1</sup> Sartorius Stedim Cellca GmbH, Ulm/D; <sup>2</sup> Sartorius Stedim UK Ltd., Epsom/UK; <sup>3</sup> Sartorius Stedim Data Analytics AB, Umea/S; <sup>4</sup> Sartorius Stedim France S.A.S, Aubagne/F; <sup>5</sup> Sartorius Stedim Belgium S.A., Brussels/B
- P14 **MANTRA: Metabolic-Network Analysis to Identify Changes in Reaction Activity**  
N. Köhler<sup>1</sup>; V. Würf<sup>1</sup>; J. Pauling<sup>1</sup>; <sup>1</sup> Technical University of Munich, Freising/D
- P15 **Synechocystis sp. PCC 6803 photosynthesis under different light colours - in silico analysis**  
T. Pfennig<sup>1</sup>; E. Kullmann<sup>1</sup>; G. Bernát<sup>2</sup>; J. Červený<sup>3</sup>; O. Ebenhöf<sup>4</sup>; T. Závřel<sup>3</sup>; A. Matuszyńska<sup>1</sup>; <sup>1</sup> RWTH Aachen University, Aachen/D; <sup>2</sup> Centre for Ecological Research, Tihany/H; <sup>3</sup> Czech Academy of Sciences, Brno/CZ; <sup>4</sup> Heinrich Heine University Düsseldorf/D
- P16 **Motif mining with deep learning tools is accelerating identification, annotation and inference of gene regulatory networks in plants**  
S. Zumkeller<sup>1</sup>; F. Peleke<sup>2</sup>; J. Engelhorn<sup>3</sup>; T. Hartwig<sup>3</sup>; J. Szymański<sup>2</sup>; <sup>1</sup> Forschungszentrum Jülich, Jülich/D; <sup>2</sup> Leibniz Institute of Plant Genetics and Crop Plant Research (IPK), OT Gatersleben/D; <sup>3</sup> Max-Planck-Institut für Pflanzenzüchtungsforschung, Köln/D
- P17 **RNAIntels: A machine learning-based tool for the identification of coding and noncoding small RNAs in human RNA-seq data**  
O. Sarumi<sup>1</sup>; D. Heider<sup>1</sup>; R. Martin<sup>1</sup>; <sup>1</sup> Philipps University of Marburg, Marburg/D
- P18 **Deciphering key regulatory networks and drug repurposing candidates through scRNAseq data analysis using SCANet**  
M. Oubounyt<sup>1</sup>; <sup>1</sup> University of Hamburg, Hamburg/D
- P19 **ChimericFragments: A visual approach to the analysis of global RNA-RNA interaction networks**  
M. Siemers<sup>1</sup>; A. Lippegaus<sup>1</sup>; K. Papenfort<sup>1</sup>; <sup>1</sup> Friedrich-Schiller-University Jena/D
- P20 **Is BLAST a thing of the past?**  
M. Schroeder<sup>1</sup>; <sup>1</sup> TU Dresden/D
- P21 **Searching for orthologs in un-annotated genome assemblies with fDOG-Assembly**  
H. Muelbauer<sup>1</sup>; M. Bálint<sup>2</sup>; I. Ebersberger<sup>1</sup>; <sup>1</sup> Goethe University, Frankfurt am Main/D; <sup>2</sup> Senckenberg Biodiversity and Climate Research Centre, Frankfurt am Main/D

## POSTER PROGRAMME

- P22 **Unraveling the complexity of the gut microbiota in liver cirrhosis**  
K. Tsenova<sup>1</sup>; J. Ackermann<sup>2</sup>; M. Vehreschild<sup>3</sup>; I. Koch<sup>2</sup>; <sup>1</sup> Goethe University, Frankfurt, Frankfurt am Main /D; <sup>2</sup> Goethe University, Frankfurt, Frankfurt am Main/D; <sup>3</sup> University Hospital Frankfurt, Frankfurt am Main/D
- P23 **Plant growth and survival as a real-time strategy game**  
D. Koch<sup>1</sup>; S. Camborda<sup>2</sup>; N. Töpfer<sup>2</sup>; J. Szymański<sup>1</sup>; <sup>1</sup> Leibniz Institute of Plant Genetics and Crop Plant Research, Seeland/D; <sup>2</sup> University of Cologne, CEPLAS, Cologne/D
- P24 **DataSAIL: Data Splitting Against Information Leakage**  
R. Joeres<sup>1</sup>; A. Gress<sup>1</sup>; A. Tolkmitt<sup>1</sup>; I. Senatorov<sup>1</sup>; O. Kalinina<sup>1</sup>; <sup>1</sup> HZI/HIPS, Saarbruecken/D
- P26 **Missing data imputation leads to wrong statistical interference in metabolomics data analysis**  
M. Burdukiewicz<sup>2</sup>; <sup>1</sup> Medical University of Białystok, Białystok/PL
- P27 **Analysis of expression patterns with fuzzy concepts as FlowSets**  
M. Joppich<sup>1</sup>; F. Offensperger<sup>1</sup>; R. Zimmer<sup>1</sup>; <sup>1</sup> Ludwig-Maximilians-Universität München/D
- P28 **Mining structured biomedical resources to systematically identify disease signatures from single-cell data**  
S. Hayat<sup>1</sup>; M. Joppich<sup>2</sup>; R. Kramann<sup>1</sup>; <sup>1</sup> Uniklinik RWTH Aachen/D; <sup>2</sup> Ludwig-Maximilians-Universität München/D
- P29 **Standardizing and harmonizing NGS analysis workflows in the German Human Genome-Phenome Archive (GHGA) – A national secure infrastructure for omics data**  
K. Narci<sup>1</sup>; <sup>1</sup> German Cancer Research Institute (DKFZ), Heidelberg/D
- P30 **Onkopos: A Decision Support Framework for Evidence- Based Interpretation of Biomarkers in Cancer Research and Precision Medicine**  
N. Kurz<sup>1</sup>; K. Kornrumpf<sup>1</sup>; T. Tucholski<sup>1</sup>; V. Gnass<sup>1</sup>; K. Drogenik<sup>1</sup>; T. Beissbarth<sup>1</sup>; J. Dönitz<sup>1</sup>; <sup>1</sup> University Medical Center Göttingen/D
- P31 **An M for an A: Using Bioinformatics to characterize DNA methyltransferase specificities through the utilization of HPLC-HESI-MS and sequencing methodologies**  
A. Busch<sup>1</sup>; <sup>1</sup> Uni Jena/TME, Jena/D
- P32 **Inference of metabolic properties and transcriptional programmes across altered adipocyte/immune cell ratios**  
V. Zouboulis<sup>1</sup>; H. Ulrich<sup>1</sup>; C. Kilian<sup>1</sup>; L. Adlung<sup>1</sup>; <sup>1</sup> University Medical Center Hamburg-Eppendorf (UKE), Hamburg/D
- P33 **Holomics: an R Shiny application for the holistic integration and analysis of multiple omics data**  
K. Munk<sup>1</sup>; G. Brader<sup>1</sup>; E. Molin<sup>1</sup>; <sup>1</sup> AIT Austrian Institute of Technology, Tulln/A

## POSTER PROGRAMME

- P34 **Understanding Tomato Heat Response: A large-scale Transcriptomic Meta-Analysis**  
D. Psaroudakis<sup>1</sup>; A. Khayer<sup>1</sup>; L. Aiyesa<sup>1</sup>; A. Tissier<sup>2</sup>; L. Yunlong<sup>3</sup>; P. Wigge<sup>3</sup>; A. Israeli<sup>4</sup>; N. Teboul<sup>4</sup>; J. Szymanski<sup>1</sup>; <sup>1</sup> IPK Gatersleben, Gatersleben/D; <sup>2</sup> IPB Halle, Halle/D; <sup>3</sup> IGZ Großbeeren, Großbeeren/D; <sup>4</sup> HUJI Jerusalem, Jerusalem/IL
- P35 **Detection of genome rearrangements responsible for microbial phenotype switching**  
O. Bochkareva<sup>1</sup>; <sup>1</sup> University of Vienna, Vienna/A
- P36 **Consideration of spatial constraints improves prediction of photosynthetic metabolism**  
T. Machado<sup>1</sup>; N. Töpfer<sup>1</sup>; <sup>1</sup> University of Cologne, Köln/D
- P37 **Nanopore sequencing: A guidance and most common pitfalls stepping into Nanopore Sequencing**  
D. Meyer<sup>1</sup>; D. Wollny<sup>1</sup>; M. Marz<sup>1</sup>; <sup>1</sup> Friedrich-Schiller-Universität Jena/D
- P38 **The evolution of the de.NBI / ELIXIR-DE training platform in 2023**  
D. Wibberg<sup>1</sup>; N. Lübke<sup>1</sup>; H. Schnitzer<sup>1</sup>; <sup>1</sup> Forschungszentrum Jülich GmbH - Außenstelle Universität Bielefeld, Bielefeld/D
- P39 **The ELIXIR Research Data Management (RDM) Trainer Network - Developing training and sharing knowledge, best practices, and standards**  
H. Schnitzer<sup>1</sup>; X. Pérez Sitjà<sup>2</sup>; N. Fatima<sup>3</sup>; R. Andrews<sup>4</sup>; N. Lübke<sup>1</sup>; K. Poterlowicz<sup>2</sup>; D. Wibberg<sup>1</sup>; <sup>1</sup> Forschungszentrum Jülich GmbH, Bielefeld/D; <sup>2</sup> University of Bradford, Bradford/UK; <sup>3</sup> University of Oslo, Oslo/N; <sup>4</sup> Cardiff University, Cardiff/UK
- P40 **From genes to clinically actionable hypotheses**  
A. Maier<sup>1</sup>; M. Hartung<sup>1</sup>; M. List<sup>2</sup>; O. Zolotareva<sup>1</sup>; J. Baumbach<sup>1</sup>; <sup>1</sup> University of Hamburg, Hamburg/D; <sup>2</sup> Technical University Munich, Munich/D
- P41 **Interpretable deep learning models for elucidating the complex cis-regulatory code of model plant species**  
F. Peleke<sup>1</sup>; S. Zumkeller<sup>2</sup>; J. Szymanski<sup>1</sup>; <sup>1</sup> Leibniz-Institut für Pflanzengenetik und Kulturpflanzenforschung (IPK), Gatersleben/D; <sup>2</sup> Institute of Bio- and Geosciences, IBG-4: Plant Sciences, Forschungszentrum Jülich/D
- P42 **NeDRex – an integrative and interactive network medicine platform for drug repurposing**  
A. Maier<sup>1</sup>; S. Sadegh<sup>1</sup>; J. Skelton<sup>1</sup>; J. Baumbach<sup>1</sup>; <sup>1</sup> University of Hamburg, Hamburg/D
- P43 **In silico characterization of Plasmodium PfMYST complex and identification of novel antimalarial compounds against its catalytic HAT protein PfMYST**  
J. Khurana<sup>1</sup>; A. Gupta<sup>1</sup>; Shiv Nadar Institution of Eminence, Gautam Buddha Nagar, Greater Noida, Uttar Pradesh/IND
- P44 **Interrogating intra-cellular and inter-patient heterogeneity of tumor cells in Glioblastoma PDOXs upon treatment by using longitudinal scRNA-seq data**  
B. Nosirov<sup>1</sup>; Y. Yabo<sup>1</sup>; A. Oudin<sup>1</sup>; K. Grzyb<sup>2</sup>; T. Kaoma<sup>1</sup>; A. Skupin<sup>2</sup>; S. Niclou<sup>2</sup>; S. Nazarov<sup>1</sup>; A. Golebiewska<sup>1</sup>; <sup>1</sup> Luxembourg Institute of Health, Strassen/L; <sup>2</sup> University of Luxembourg, Belval/L

## POSTER PROGRAMME

- P45 **Virtual screening of cyclooxygenase inhibitors from *Tinospora cordifolia* using the machine learning tool**  
A. Karlapudi<sup>1</sup>; <sup>1</sup> Vignan's Foundation for science Technology and Research, Vadlamudi, Guntur/D
- 
- P46 **Unveiling Novel Therapeutic Strategies for Lymphatic Filariasis: A Pan-Proteomic Exploration and Inhibitor Design Paradigm**  
R. Nalamolu<sup>1</sup>; A. Mathe<sup>2</sup>; S. Katari<sup>2</sup>; <sup>1</sup> Vignan's Foundation for science Technology and Research, Guntur, Andhra Pradesh/IND; <sup>2</sup> Vignan's Foundation for science Technology and Research, Guntur/IND
- 
- P47 **Computational Analysis of Bone-resident Mesenchymal Stromal Cells Identifies Transcriptional Cell State Shift During Ageing**  
M. Leer<sup>1</sup>; G. Soultoukis<sup>1</sup>; T. Schulz<sup>1</sup>  
<sup>1</sup> German Institute of Human Nutrition Potsdam-Rehbruecke (DIFE), Nuthetal/D
- 
- P48 **Molecular docking of *legionella pneumophila* in human RAB8A type protein and human NK1 protein fragments (peptides) against BRAC1 protein**  
N. Jahan<sup>1</sup>; <sup>1</sup> Jahangirnagar university, Dhaka/BD
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- P49 **Identifying Phylum Specific Adaptions to Nutrient Level Modulation Using Metagenome Assembled Genomes from European Freshwaters**  
M. Shah<sup>1</sup>; T. Bornemann<sup>1</sup>; J. Nuy<sup>1</sup>; A. Probst<sup>1</sup>; M. Hahn<sup>2</sup>; D. Beisser<sup>3</sup>; J. Boenigk<sup>1</sup>  
<sup>1</sup> University of Duisburg-Essen, Essen/D; <sup>2</sup> University of Innsbruck, Innsbruck/A; <sup>3</sup> Westphalian University of Applied Sciences, Recklinghausen/D
- 
- P50 **Identification of genome-wide expression differences between patient-matched intra- and extracranial melanoma metastasis pairs using Hidden Markov Models**  
T. Kraft<sup>1</sup>; K. Grützmann<sup>1</sup>; M. Meinhardt<sup>2</sup>; F. Meier<sup>2</sup>; D. Westphal<sup>2</sup>; M. Seifert<sup>1</sup>;  
<sup>1</sup> TU Dresden, Dresden/D; <sup>2</sup> University Hospital Dresden, Dresden/D
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- P51 **Gaining a deeper understanding of acute-on-chronic liver failure by analyzing the JAK-STAT pathway in hepatocytes using ODE and Petri net models**  
M. Keßler<sup>1</sup>; J. Ackermann<sup>1</sup>; S. Henninger<sup>1</sup>; L. Klemt<sup>1</sup>; C. Welsch<sup>1</sup>; H. Mühl<sup>1</sup>; I. Koch<sup>1</sup>;  
<sup>1</sup> Goethe-Universität Frankfurt am Main, Frankfurt am Main/D
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- P52 **Calculate polygenic score from matrix factorization**  
V. Dang<sup>1</sup>; S. Rahmann<sup>1</sup>; <sup>1</sup> Saarland University, Saarbrücken/D
- 
- P53 **Employing machine learning on large scale perturbation screens for SARS-CoV-2 host factors identifies PRI-724 interfering  $\beta$ -catenin/CBP interaction as a new antiviral**  
M. Kelch<sup>1</sup>; A. Vera-Guapi<sup>1</sup>; T. Beder<sup>2</sup>; M. Oswald<sup>3</sup>; A. Hiemisch<sup>3</sup>; N. Beil<sup>4</sup>; P. Wajda<sup>4</sup>; S. Ciesek<sup>1</sup>; H. Erfle<sup>4</sup>; T. Toptan-Grabmair<sup>1</sup>; R. Koenig<sup>3</sup>; <sup>1</sup> Goethe University Frankfurt am Main/D; <sup>2</sup> University Hospital Schleswig-Holstein, Kiel/D; <sup>4</sup> Jena University Hospital, Jena/D; <sup>4</sup> Heidelberg University, Heidelberg/D

## POSTER PROGRAMME

- P54 **Using graph topology and transcriptome data of Neuroblastoma for the prediction of Ganglioside GD2 across tumor entities**  
A. Ustjanzew<sup>1</sup>; R. Sandhoff<sup>2</sup>; C. Paret<sup>3</sup>; <sup>1</sup> University Medical Center of the Johannes Gutenberg-University Mainz, Mainz/D; <sup>2</sup> Lipid Pathobiochemistry, German Cancer Research Center, Heidelberg/D; <sup>3</sup> University Medical Center of the Johannes Gutenberg-University Mainz, Mainz/D
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- P55 **Natural products from reconstructed bacterial genomes of the Middle and Upper Paleolithic**  
A. Ibrahim<sup>1</sup>; <sup>1</sup> Leibniz Institute for Natural Product Research and Infection Biology, Jena/D
- 
- P56 **Dual Annealing: A Promising Novel Global Optimization Method in the Systems Biology and Epidemiology Modelling**  
Y. Xiang<sup>1</sup>; S. Gubian<sup>1</sup>; F. Calvino-Martin<sup>1</sup>; <sup>1</sup> Philip Morris Products S.A., Neuchatel/CH
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- P57 **Systematic evaluation of differential splicing tools for single-cell RNA-sequencing**  
T. Duez<sup>1</sup>; O. Tsoy<sup>2</sup>; <sup>1</sup> Institute for Computational Systems Biology, Elmshorn/D; <sup>2</sup> Institute for Computational Systems Biology, Hamburg/D
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- P58 **dsLassoCov: a federated Lasso approach incorporating covariate control**  
H. Cao<sup>1</sup>; A. Anguita<sup>2</sup>; X. Basagaña<sup>3</sup>; E. Schwarz<sup>4</sup>; <sup>1</sup> Department of Theoretical Neuroscience, Central Institute of Mental Health, Medical Faculty, Heidelberg University, Germany, Mannheim/D; <sup>2</sup> ISGlobal, Barcelona, Spain; Universitat Pompeu Fabra (UPF), Barcelona, Spain; CIBER Epidemiologia y Salud Pública, Madrid, Spain, Barcelona/E; <sup>3</sup> ISGlobal, Barcelona, Spain; Universitat Pompeu Fabra (UPF), Barcelona, Spain; CIBER Epidemiologia y Salud Pública, Madrid, Spain., Barcelona/E; <sup>4</sup> Department of Psychiatry and Psychotherapy, Central Institute of Mental Health, Medical Faculty, Heidelberg University, Mannheim/D
- 
- P59 **Binding motifs are highly conserved in related transcription factors in plants**  
S. Zenker<sup>1</sup>; D. Wulf<sup>1</sup>; A. Bräutigam<sup>1</sup>; <sup>1</sup> Bielefeld University, Bielefeld/D
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- P60 **Promiscuity in drug discovery on the verge of the structural revolution**  
S. Bolz<sup>1</sup>; M. Schroeder<sup>1</sup>; <sup>1</sup> Technische Universität Dresden, Dresden/D
- 
- P61 **CLARUS: An Interactive Explainable AI Platform for Manual Counterfactuals in Graph Neural Networks**  
J. Beinecke<sup>1</sup>; A. Saranti<sup>2</sup>; A. Angerschmid<sup>2</sup>; B. Pfeifer<sup>3</sup>; V. Klemt<sup>4</sup>; A. Holzinger<sup>2</sup>; A. Hauschild<sup>1</sup>; <sup>1</sup> University Medical Center Göttingen (UMG), Göttingen/D; <sup>2</sup> University of Natural Resources and Life Sciences Vienna, Vienna/A; <sup>3</sup> Medical University Graz, Graz/A; <sup>4</sup> Philipps University Marburg, Marburg/D
- 
- P62 **Repurposing of approved drugs as candidates for the treatment of kala-azar: a computational study on Rab5a and PTR1 from *Leishmania donovani* as targets**  
B. Arsić<sup>1</sup>; J. Janjić<sup>2</sup>; J. Miličević<sup>3</sup>; S. Glišić<sup>3</sup>; <sup>1</sup> Department of Chemistry, Faculty of Sciences and Mathematics, University of Niš, Niš/SRB; <sup>2</sup> Faculty of Biology, University of Belgrade, Belgrade/SRB; <sup>3</sup> Laboratory for Bioinformatics and Computational Chemistry, Vinča Institute of Nuclear Sciences, University of Belgrade, Belgrade/SRB

## POSTER PROGRAMME

- P63 **FRED – A tool to generate FAIR metadata for omics experiments**  
J. Walter<sup>1</sup>; M. Looso<sup>1</sup>; C. Kuenne<sup>1</sup>; <sup>1</sup> Max Planck Institute for Heart and Lung Research, Bad Nauheim/D
- P64 **FACT: Federated Adversarial Cross Training**  
S. Schrod<sup>1</sup>; J. Lippl<sup>1</sup>; A. Schäfer<sup>2</sup>; M. Altenbuchinger<sup>1</sup>; <sup>1</sup> University Medical Center Göttingen (UMG), Göttingen/D; <sup>2</sup> Universität Regensburg, Regensburg/D
- P65 **Unraveling the Influence of Organic and Inorganic Model Aerosols on Lung Surfactant Membrane**  
D. Mohammad-Aghaie<sup>1</sup>; S. Boroomand<sup>1</sup>; F. Keshavarz<sup>2</sup>; <sup>1</sup> Shiraz University of Technology, Shiraz/IR; <sup>2</sup> Lappeenranta-Lahti University of Technology (LUT), Lappeenranta/FIN
- P66 **Systematic Evaluation of Normalization Approaches on Tandem Mass Tag and Label-Free Protein Quantification Data**  
L. Arend<sup>1</sup>; J. Pauling<sup>2</sup>; J. Baumbach<sup>1</sup>; T. Laske<sup>1</sup>; <sup>1</sup> University of Hamburg, Hamburg/D; <sup>2</sup> Technical University of Munich, Freising/D
- P67 **Superior Protein Thermophilicity Prediction With Protein Language Model Embeddings**  
F. Haselbeck<sup>1</sup>; M. John<sup>1</sup>; D. Grimm<sup>1</sup>; <sup>1</sup> TUM Campus Straubing for Biotechnology and Sustainability, Weihenstephan-Triesdorf University of Applied Science, Straubing/D
- P68 **BCU repository: the cloud based web frontend to access and explore omics datasets**  
N. Knoppik<sup>1</sup>; P. Goymann<sup>1</sup>; J. Walter<sup>1</sup>; D. Spothelfer<sup>1</sup>; C. Künne<sup>1</sup>; M. Looso<sup>1</sup>; <sup>1</sup> Max Planck Institute for Heart and Lung Research, Bad Nauheim/D
- P69 **NucleoDetective: Predicting nucleosome positions using single-cell ATAC-seq data**  
M. Hobein<sup>1</sup>; M. Bentsen<sup>1</sup>; C. Kuenne<sup>1</sup>; M. Looso<sup>1</sup>; <sup>1</sup> Max Planck Institute for Heart and Lung Research, Bad Nauheim/D
- P70 **Magnipore: Detecting Single Nucleotide Changes in ONT Data of SARS-CoV-2**  
J. Spangenberg<sup>1</sup>; <sup>1</sup> Friedrich Schiller Universität Jena, Jena/D
- P71 **Building a robust workflow for reproducible metabolic network curation**  
S. Camborda La Cruz<sup>1</sup>; N. Töpfer<sup>2</sup>; <sup>1</sup> University of Cologne, Köln/D; <sup>2</sup> University of Cologne, CEPLAS, Köln/D
- P72 **Analysis of large-scale gene expression datasets in *Synechocystis* sp. PCC 6803 using gene regulatory networks**  
F. Matten<sup>1</sup>; B. Frommer<sup>1</sup>; A. Bräutigam<sup>1</sup>; <sup>1</sup> Bielefeld University, Bielefeld/D
- P73 **A computational approach to identify genetic directional dependencies**  
V. Heger<sup>1</sup>; R. Çetin<sup>2</sup>; M. Kaulich<sup>2</sup>; M. Looso<sup>1</sup>; <sup>1</sup> Max Planck Institute for Heart and Lung Research, Bad Nauheim/D; <sup>2</sup> Goethe University Frankfurt am Main, Frankfurt am Main/D
- P74 **Human leukocyte antigen (HLA) typing of a broad panel of cancer patient-derived xenograft (PDX) models enables personalized, preclinical immune-oncology studies**  
T. Conrad<sup>1</sup>; M. Stecklum<sup>1</sup>; A. Wulf-Goldenberg<sup>1</sup>; M. Becker<sup>1</sup>; M. Dahlmann<sup>1</sup>; S. Rhein<sup>1</sup>; K. Klinghammer<sup>2</sup>; J. Hoffmann<sup>1</sup>; <sup>1</sup> EPO Berlin-Buch GmbH, Berlin/D; <sup>2</sup> Charité University Medicine, Berlin/D

## POSTER PROGRAMME

- P75 **Single cell ATAC-seq Pipeline**  
J. Detleffsen<sup>1</sup>; M. Bentsen<sup>1</sup>; M. Looso<sup>1</sup>; <sup>1</sup> Max Planck Institute for Heart and Lung Research, Bad Nauheim/D
- P76 **sORFDB – A database for sORFs, small proteins, and small protein groups in bacteria**  
J. Hahnfeld<sup>1</sup>; A. Goesmann<sup>1</sup>; O. Schwengers<sup>1</sup>; <sup>1</sup> Justus Liebig University, Giessen/D
- P77 **Predictions of DNA mechanical properties at a genomic scale reveal potentially new functional roles of DNA flexibility**  
G. Back<sup>1</sup>; D. Walther<sup>1</sup>; <sup>1</sup> Max Planck Institute of Molecular Plant Physiology, Potsdam-Golm/D
- P78 **Comparative analysis of Illumina and Nanopore amplicon sequences of eukaryotic communities from sediment samples**  
D. Bludau<sup>1</sup>; <sup>1</sup> Universität Duisburg Essen, Essen/D
- P79 **Timeshifting computation to reduce the carbon emissions of software**  
A. Hartebrod<sup>1</sup>; J. Matschinske<sup>2</sup>; D. Blumenthal<sup>3</sup>; <sup>1</sup> Friedrich-Alexander-Universität Erlangen-Nürnberg (FAU), Erlangen/D; <sup>2</sup> Bitspark GmbH, Nuernberg, Nuremberg/D; <sup>3</sup> Friedrich-Alexander-Universität Erlangen-Nürnberg (FAU), Erlangen/D
- P80 **Decoding the Hidden Secrets of SNP Data: Revealing Ancestral Origins, Genomic Predictions, and Polygenic Risk Score**  
J. Schwarzerová<sup>1</sup>; M. Hurta<sup>1</sup>; W. Weckwerth<sup>2</sup>; D. Walther<sup>3</sup>; <sup>1</sup> Brno University of Technology, Brno/CZ; <sup>2</sup> University of Vienna, Vienna/A; <sup>3</sup> Max-Planck-Institute of Molecular Plant Physiology, Potsdam/D
- P81 **Analysis of the mutual impact and importance of SNPs with random forest approaches**  
L. Voges<sup>1</sup>; S. Seifert<sup>1</sup>; <sup>1</sup> Universität Hamburg (UHH), Hamburg/D
- P82 **Uncovering uncharacterized binding of transcription factors from ATAC-seq footprinting data**  
H. Schultheis<sup>1</sup>; M. Bentsen<sup>1</sup>; V. Heger<sup>1</sup>; M. Looso<sup>1</sup>; <sup>1</sup> Max Planck Institute for Heart and Lung Research, Bad Nauheim/D
- P83 **A Metatranscriptomic Approach to Study the Effect of Multiple Stressors on the Microbial Community Involved in CPOM Degradation in Freshwater Habitats**  
A. Deep<sup>1</sup>; <sup>1</sup> University of Duisburg-Essen, essen/D
- P84 **multicrspr2: A Versatile R Package for High-Throughput CRISPR-Cas gRNA Design with focus on gRNA pairs**  
R. Wiegandt<sup>1</sup>; M. Looso<sup>1</sup>; <sup>1</sup> Max Planck Institute for Heart and Lung Research, Bad Nauheim/D
- P85 **Incorporating RNA 3D motifs into RNA secondary structure prediction**  
M. Sebeke<sup>1</sup>; B. Voß<sup>2</sup>; <sup>1</sup> University of Stuttgart, Stuttgart /D; <sup>2</sup> University of Stuttgart, Stuttgart/D
- P86 **Effects of balanced and concordant complexes on the evolution of yeast metabolic networks**  
A. Küken<sup>1</sup>; D. Langary<sup>1</sup>; Z. Nikolski<sup>1</sup>; <sup>1</sup> Universität Potsdam, Potsdam/D

## POSTER PROGRAMME

- P87 **Proteomic Meta-Study Harmonization, Mechanotyping and Drug Repurposing Candidate Prediction with ProHarMeD**  
K. Adamowicz<sup>1</sup>; L. Arend<sup>1</sup>; A. Maier<sup>1</sup>; J. Schmidt<sup>2</sup>; B. Küster<sup>3</sup>; O. Tsoy<sup>1</sup>; O. Zolotareva<sup>1</sup>; J. Baumbach<sup>1</sup>; T. Laske<sup>1</sup>; <sup>1</sup> University of Hamburg, Hamburg/D; <sup>2</sup> Fraunhofer Institute for Cell Therapy and Immunology IZI, Leipzig/D; <sup>3</sup> Technical University of Munich, München/D
- P88 **Multi-omics translational research – from human stem cell model to data to mechanistic insights**  
A. Hoffrichter<sup>1</sup>; A. Rossetti<sup>1</sup>; R. Wilkens<sup>1</sup>; A. Jabali<sup>1</sup>; J. Ladewig<sup>1</sup>; P. Koch<sup>1</sup>; <sup>1</sup> Department of Translational Brain Research, Central Institute of Mental Health (ZI), University of Heidelberg/Medical Faculty Mannheim, Mannheim/D
- P89 **HOGVAX: Exploiting Epitope Overlaps to Maximize Population Coverage in Vaccine Design**  
S. Schulte<sup>1</sup>; A. Dilthey<sup>2</sup>; G. Klau<sup>1</sup>; <sup>1</sup> Heinrich Heine University Düsseldorf, Düsseldorf/D; <sup>2</sup> University Clinic Düsseldorf, Düsseldorf/D
- P90 **Research data management on genetic resources of *Marchantia polymorpha* ecotype 'BoGa' using the Annotated Research Context**  
B. Frommer<sup>1</sup>; W. Halpape<sup>1</sup>; A. Busch<sup>2</sup>; S. Zachgo<sup>2</sup>; A. Bräutigam<sup>1</sup>; <sup>1</sup> Bielefeld University, Bielefeld/D; <sup>2</sup> University of Osnabrück, Osnabrück/D
- P91 **Unraveling the RNA Interactome through Identifier-Based RNA Duplex Detection**  
C. Adelman<sup>1</sup>; C. Schaal<sup>1</sup>; C. Sylvester<sup>1</sup>; B. Voß<sup>1</sup>; <sup>1</sup> University of Stuttgart, Stuttgart/D
- P92 **Comparative Analysis of Fine-Tuned Data Center Models and Federated Learning for Multi-Center Breast Cancer Subtype Prediction**  
T. Nguyen<sup>1</sup>; A. Hauschild<sup>2</sup>; <sup>1</sup> University of Göttingen - Georg-August-Universität Göttingen, Göttingen/D; <sup>2</sup> University Medical Center Göttingen (UMG), Göttingen/D
- P93 **Modeling bacterial growth in the human colon using ordinary differential equations**  
A. Otto<sup>1</sup>; J. Ackermann<sup>1</sup>; I. Koch<sup>1</sup>; <sup>1</sup> Goethe University Frankfurt, Frankfurt am Main/D
- P94 **Discovering chromatin states using a flexible distribution hidden Markov model with duration modeling**  
J. Schmitz<sup>1</sup>; N. Aggarwal<sup>1</sup>; L. Laufer<sup>1</sup>; J. Walter<sup>1</sup>; A. Salhab<sup>1</sup>; S. Rahmann<sup>1</sup>; <sup>1</sup> Saarland University, Saarbrücken/D
- P95 **A Toolbox for Biological Sequence Data Conversion: The Coordinate Converter Service (CCS)**  
K. Kornumpf<sup>1</sup>; T. Tucholski<sup>1</sup>; K. Drogenik<sup>1</sup>; N. Kurz<sup>2</sup>; J. Dönitz<sup>1</sup>; T. Beißbarth<sup>1</sup>; <sup>1</sup> University Medical Center Göttingen (UMG), Göttingen/D
- P96 **Classification of 3D FDG-PET Scans for Alzheimer's Disease Detection**  
L. Bente<sup>1</sup>; L. Himstedt<sup>1</sup>; T. Kacprowski<sup>1</sup>; <sup>1</sup> TU Braunschweig, Braunschweig/D
- P97 **responseR: Summary Measures Simplify the Analysis of Repeated Measures Data**  
G. Grabert<sup>1</sup>; <sup>1</sup> Technical University of Braunschweig, Braunschweig/D
- P98 **PyCoMo: a python package for community metabolic model creation and analysis**  
M. Predl<sup>1</sup>; M. Mießkes<sup>1</sup>; J. Zanghellini<sup>1</sup>; T. Rattei<sup>1</sup>; <sup>1</sup> UniWien, Vienna/A
- P99 **Small molecule machine learning: All models are wrong, some may not even be useful**  
F. Kretschmer<sup>1</sup>; J. Seipp<sup>2</sup>; M. Ludwig<sup>1</sup>; G. Klau<sup>2</sup>; S. Böcker<sup>1</sup>; <sup>1</sup> Friedrich Schiller University Jena, Jena/D; <sup>2</sup> Heinrich Heine University Düsseldorf, Düsseldorf/D

## POSTER PROGRAMME

- P100 **Gene Regulatory interActive Network Difference Explorer (GRANDE)**  
N. Meyerhöfer<sup>1</sup>; D. Blumenthal<sup>1</sup>; A. Hartebrodt<sup>1</sup>; <sup>1</sup> Friedrich-Alexander-Universität Erlangen-Nürnberg (FAU), Erlangen/D
- P101 **CatInfer- A Deep Learning model for classification of enzymes and localization of catalytic sites using XAI**  
J. Kiederle<sup>1</sup>; D. Blumenthal<sup>1</sup>; S. Lindner<sup>2</sup>; <sup>1</sup> Friedrich-Alexander-Universität Erlangen-Nürnberg (FAU), Erlangen/D; <sup>2</sup> Heidelberg University, Heidelberg/D
- P102 **Phosphoproteomics workflow to decipher the mechanisms behind CXCR7-mediated platelet inhibition**  
Ö. Osmanoglu<sup>1</sup>; J. Balkenhol<sup>1</sup>; S. Lorocho<sup>2</sup>; J. Katzer<sup>3</sup>; K. Dipali<sup>3</sup>; A. Sickmann<sup>3</sup>; T. Dandekar<sup>1</sup>; M. Chatterjee<sup>4</sup>; <sup>1</sup> Julius-Maximilians-Universität Würzburg, Würzburg/D; <sup>2</sup> Ruhr University Bochum, Bochum/D; <sup>3</sup> Leibniz-Institut für Analytische Wissenschaften - ISAS, Dortmund/D; <sup>4</sup> University Hospital Tübingen, Tübingen/D
- P103 **Feature Reduction Improves Drug Response Prediction**  
F. Firoozbakh<sup>1</sup>; B. Yousefi<sup>2</sup>; O. Tsoy<sup>1</sup>; J. Baumbach<sup>1</sup>; B. Schwikowski<sup>2</sup>; <sup>1</sup> Universität Hamburg, Hamburg/D; <sup>2</sup> Institut Pasteur, Paris/F
- P104 **Resolving chimeric tandem mass spectra to investigate molecular structures in dissolved organic matter**  
W. Tang<sup>1</sup>; A. Ivanova<sup>2</sup>; K. Dührkop<sup>1</sup>; S. Schröter<sup>2</sup>; C. Simon<sup>3</sup>; G. Gleixner<sup>2</sup>; S. Böcker<sup>1</sup>; <sup>1</sup> Friedrich Schiller University Jena, Jena/D; <sup>2</sup> Max Planck Institute for Biogeochemistry, Jena/D; <sup>3</sup> Helmholtz-Centre for Environmental Research, Leipzig/D
- P105 **Interactive Visualization and Analysis of Lipidomics Data**  
T. Olzhabaev<sup>1</sup>; L. Müller<sup>2</sup>; D. Krause<sup>2</sup>; D. Schwudke<sup>2</sup>; A. Torda<sup>1</sup>; <sup>1</sup> Universität Hamburg, Hamburg/D; <sup>2</sup> Bioanalytical Chemistry, Research Center Borstel, Leibniz Lung Center, Borstel/D
- P106 **Exploring Interaction Patterns of DNA and RNA using PLIP**  
K. Linnemann<sup>1</sup>; M. Adasme<sup>1</sup>; S. Bolz<sup>1</sup>; F. Kaiser<sup>2</sup>; S. Salentin<sup>1</sup>; V. Haupt<sup>2</sup>; M. Schroeder<sup>1</sup>; <sup>1</sup> Technische Universität Dresden, Dresden/D; <sup>2</sup> PharmAI GmbH, Dresden/D
- P107 **Intronic Polyadenylation Isoforms: A Novel Path For Therapy**  
R. Barbieri<sup>1</sup>; G. Blahetek<sup>1</sup>; S. Vorlova<sup>1</sup>; F. Erhard<sup>2</sup>; A. Zernecke<sup>1</sup>; <sup>1</sup> Uniklinikum Würzburg, Würzburg/D; <sup>2</sup> University of Würzburg, Würzburg/D
- P108 **AGING: An Advanced Bioinformatic Approach for Comprehensive Longevity Research**  
S. Crouch<sup>1</sup>; A. Caliskan<sup>1</sup>; E. Bencurova<sup>1</sup>; M. Scherrer<sup>1</sup>; T. Breitenbach<sup>1</sup>; T. Dandekar<sup>1</sup>; <sup>1</sup> Julius-Maximilians-Universität, Würzburg/D
- P109 **Modelling carbon dioxide harvesting in plants**  
S. Saha<sup>1</sup>; O. Osmanoglu<sup>1</sup>; E. Özer<sup>1</sup>; J. Müller<sup>2</sup>; E. Bencurova<sup>1</sup>; T. Dandekar<sup>1</sup>; <sup>1</sup> University of Würzburg, Würzburg/D; <sup>2</sup> Julius-Maximilians-Universität Würzburg, Rauhenebrach, Germany, Würzburg/D
- P110 **Annotating small molecules from massive affinity selection libraries**  
N. Haupt<sup>1</sup>; E. van der Nol<sup>2</sup>; M. Hoffmann<sup>3</sup>; M. Ludwig<sup>1</sup>; M. Engler<sup>3</sup>; K. Dührkop<sup>1</sup>; S. Pomplun<sup>2</sup>; S. Böcker<sup>1</sup>; <sup>1</sup> Friedrich Schiller Universität Jena, Jena/D; <sup>2</sup> Leiden University, Leiden/NL; <sup>3</sup> Bright Giant GmbH, Jena/D

POSTER PROGRAMME

- P111 **Transcriptional Regulator Identification Using Prize-Collecting Steiner Trees**  
G. Galindez<sup>2</sup>; B. Lopez<sup>2</sup>; D. Blumenthal<sup>3</sup>; T. Kacprowski<sup>4</sup>; <sup>1</sup> Technical University of Braunschweig, Braunschweig/D; <sup>2</sup> University of the Philippines Manila, Manila/RP; <sup>3</sup> Friedrich-Alexander-Universität Erlangen-Nürnberg (FAU), Erlangen/D; <sup>4</sup> Technische Universität Braunschweig and Hannover Medical School, Braunschweig/D
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- P112 **Online bias-aware disease module mining with ROBUST-Web**  
S. Sarkar<sup>1</sup>; M. Lucchetta<sup>2</sup>; A. Maier<sup>3</sup>; M. Abdrabbou<sup>4</sup>; J. Baumbach<sup>3</sup>; M. List<sup>5</sup>; M. Schaefer<sup>2</sup>; D. Blumenthal<sup>4</sup>; <sup>1</sup> Friedrich-Alexander University (FAU) Erlangen-Nürnberg and Universitätsklinikum Erlangen, Erlangen/D; <sup>2</sup> IEO European Institute of Oncology IRCCS, Milan/I; <sup>3</sup> University of Hamburg, Hamburg/D; <sup>4</sup> Friedrich-Alexander-Universität Erlangen-Nürnberg (FAU) and Universitätsklinikum Erlangen, Erlangen/D; <sup>5</sup> Technical University of Munich, Freising/D
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- P113 **PetriAgents – Combining Petri Net-based Simulations of Metabolisms with Agent-Based Modeling**  
M. Kirchner<sup>1</sup>; J. Ackermann<sup>1</sup>; I. Koch<sup>1</sup>; I. Đikić<sup>1</sup>; <sup>1</sup> Goethe University Frankfurt, Frankfurt/D
- 
- P114 **Explainable Graph Convolutional Networks vs. Gradient Boosting for Identifying Therapy Stage Based on Metabolomic Profiles in HCV Patients**  
D. Dehncke<sup>1</sup>; G. Grabert<sup>1</sup>; L. Kalix<sup>1</sup>; J. Tauwald<sup>2</sup>; A. Kraft<sup>2</sup>; M. Cornberg<sup>2</sup>; T. More<sup>3</sup>; K. Hiller<sup>3</sup>; A. Dietrich<sup>4</sup>; M. List<sup>4</sup>; T. Kacprowski<sup>1</sup>; <sup>1</sup> Technische Universität Braunschweig and Hannover Medical School, Braunschweig/D; <sup>2</sup> Hannover Medical School (MHH), Hannover/D; <sup>3</sup> TU Braunschweig, Braunschweig/D; <sup>4</sup> Technical University of Munich, München/D
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- P115 **Assessing CNV Detection Algorithms for Ultra-Low-Coverage Whole-Genome Sequencing Data across Lung Cancer Types**  
L. Kalson<sup>1</sup>; M. Fediuk<sup>2</sup>; J. Lindenmann<sup>2</sup>; K. Kashofer<sup>1</sup>; P. Jost<sup>3</sup>; L. Brcic<sup>1</sup>; S. Vosberg<sup>3</sup>; <sup>1</sup> Diagnostic and Research Institute for Pathology, Medical University of Graz, Graz/A; <sup>2</sup> Division of Thoracic Surgery and Hyperbaric Surgery, Department of Surgery, Medical University of Graz, Graz/A; <sup>3</sup> Clinical Division of Oncology, Department of Internal Medicine, Medical University of Graz, Graz/A
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- P116 **Exploring Evolution in a Changing Climate: Gamified Scientific Communication through Simulation**  
L. Kalix<sup>1</sup>; L. Bente<sup>1</sup>; T. Kacprowski<sup>1</sup>; <sup>1</sup> TU Braunschweig, Braunschweig/D
- 
- P117 **Detection of alternative splicing: deep sequencing or deep learning**  
L. Hackl<sup>1</sup>; O. Tsoy<sup>1</sup>; J. Baumbach<sup>1</sup>; <sup>1</sup> Universität Hamburg, Hamburg/D
- 
- P118 **DRaCOoN: Advanced Differential Regulation Analysis for Large-scale Biological Networks**  
F. Delgado-Chaves<sup>1</sup>; F. Spurny<sup>1</sup>; O. Zolotareva<sup>1</sup>; J. Baumbach<sup>1</sup>; <sup>1</sup> Institute for Computational Systems Biology, Hamburg/D
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- P119 **Multi-omics analysis of the effect of drought and heat stress on seed germination in Hordeum vulgare**  
A. Sahu<sup>1</sup>; <sup>1</sup> Leibniz-Institut für Pflanzengenetik und Kulturpflanzenforschung (IPK), Gatersleben/D
- 
- P120 **VirJenDB: the virus genome database from Jena**  
N. Cassman<sup>1</sup>; S. Saghaei<sup>1</sup>; H. Ziraksaz<sup>1</sup>; M. Marz<sup>1</sup>; <sup>1</sup> Friedrich Schiller Universität Jena/D

POSTER PROGRAMME

- P121 **Analysis of single cell data with the nf-core workflow scrnaseq**  
F. Heyl<sup>1</sup>; <sup>1</sup> German Cancer Research Institute (DKFZ), Heidelberg/D
- 
- P122 **Investigating the role of Arabidopsis HISTONE DEACETYLASE 14 in chloroplasts**  
F. Kotnik<sup>1</sup>; C. Markiton<sup>1</sup>; J. Eirich<sup>1</sup>; I. Finkemeier<sup>1</sup>; <sup>1</sup> University Münster, Münster/D
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- P123 **SWGTS - A Platform for Stream-Based Host DNA Depletion**  
P. Spohr<sup>1</sup>; M. Ried<sup>1</sup>; L. Kühle<sup>1</sup>; A. Diltthey<sup>2</sup>; <sup>1</sup> Heinrich Heine University Düsseldorf, Düsseldorf/D; <sup>2</sup> University Hospital Düsseldorf, Düsseldorf/D
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- P124 **Decoding micro and alternative peptides through CRISPR-mediated functional profiling**  
S. Talyan<sup>1</sup>; <sup>1</sup> Max Planck Institute for Heart and Lung Research, Bad Nauheim/D
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- P125 **Characterization of amplification bias in prokaryotic single-cell transcriptomics**  
J. Münch<sup>1</sup>; M. Sobol<sup>2</sup>; A. Kaster<sup>2</sup>; B. Brors<sup>1</sup>; <sup>1</sup> German Cancer Research Center (DKFZ), Heidelberg/D; <sup>2</sup> Karlsruhe Institute of Technology, Karlsruhe/D
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- P126 **A knowledge-graph based approach to connect nutrition and disease on a molecular level**  
V. Würf<sup>1</sup>; L. Falk<sup>1</sup>; N. Köhler<sup>1</sup>; J. Pauling<sup>1</sup>; <sup>1</sup> Technical University of Munich, Freising/D
- 
- P127 **Mining Ribo-Seq Data from the Sequence Read Archive**  
K. Maidhof<sup>1</sup>; F. Erhard<sup>2</sup>; <sup>1</sup> Julius-Maximilians-Universität Würzburg, Würzburg/D; <sup>2</sup> Universität Regensburg, Regensburg/D
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- P128 **OM2DNA: Fast and Robust Processing of Optical Mapping Data by Encoding Label Information Into Artificial DNA Sequences**  
L. Kühle<sup>1</sup>; J. Köster<sup>2</sup>; G. Klau<sup>1</sup>; <sup>1</sup> Heinrich Heine University Düsseldorf, Düsseldorf/D; <sup>2</sup> University of Duisburg-Essen, Essen/D
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- P129 **Investigation of transposon mediated gene silencing in the evolutionary context of algal vitamin B12 dependency**  
A. Holzer<sup>1</sup>; P. Mehrshahi<sup>2</sup>; S. Strobbe<sup>3</sup>; J. Verstraete<sup>3</sup>; D. Salmon<sup>4</sup>; F. Bunbury<sup>2</sup>; L. Heughebaert<sup>3</sup>; S. Newsad<sup>2</sup>; A. Sayer<sup>2</sup>; L. Archer<sup>2</sup>; N. Smirnov<sup>4</sup>; C. Stove<sup>3</sup>; D. Van Der Straeten<sup>3</sup>; A. Smith<sup>2</sup>; <sup>1</sup> Saarland University, Saarbrücken/D; <sup>2</sup> University of Cambridge, Cambridge/UK; <sup>3</sup> Ghent University, Ghent/B; <sup>4</sup> University of Exeter, Exeter/UK
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- P130 **Modelling Non-local information processing of the cortex**  
J. Balkenhol<sup>1</sup>; <sup>1</sup> Uni Würzburg, Würzburg/D
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- P131 **Towards the integration of phenotypic and molecular signatures into a prodromal marker for Parkinson's disease**  
T. Hentrich<sup>1</sup>; E. Schenk<sup>2</sup>; M. Kobor<sup>3</sup>; O. Rieß<sup>2</sup>; J. Schulze-Hentrich<sup>1</sup>; <sup>1</sup> Saarland University, Saarbrücken/D; <sup>2</sup> University of Tübingen, Tübingen/D; <sup>3</sup> University of British Columbia, Vancouver/CDN
- 
- P132 **The Proteomes That Feed The World**  
C. Saylan<sup>1</sup>; S. Hein<sup>1</sup>; G. Tsiklauri<sup>1</sup>; Q. Abbas<sup>1</sup>; J. Pan<sup>1</sup>; A. Soleymaniyani<sup>1</sup>; M. Picciani<sup>1</sup>; G. Haljiti<sup>1</sup>; E. Aydin<sup>1</sup>; V. Ramirez<sup>1</sup>; G. Giordano<sup>1</sup>; P. Andrade Galan<sup>1</sup>; L. Würstl<sup>1</sup>; S. Urzinger<sup>1</sup>; A. Piller<sup>1</sup>; P. Röhrl<sup>1</sup>; S. Brajkovic<sup>1</sup>; C. Dawid<sup>1</sup>; S. Wilhelm<sup>1</sup>; C. Schwechheimer<sup>1</sup>; C. Schön<sup>1</sup>; V. Avramova<sup>1</sup>; J. Pauling<sup>1</sup>; C. Ludwig<sup>1</sup>; D. Frischmann<sup>1</sup>; M. Wilhelm<sup>1</sup>; C. Gutjahr<sup>1</sup>; R. Hückelhoven<sup>1</sup>; B. Poppenberger<sup>1</sup>; B. Kuster<sup>1</sup>; <sup>1</sup> Technical University of Munich, Freising/D
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- P133 **Studying protein 3D structures using network science**  
K. Newaz<sup>1</sup>; <sup>1</sup> University of Hamburg, Hamburg/D

## POSTER PROGRAMME

## NOTES

- P134 **Graph Based Strategies to Finding CRISPR Arrays in Metagenomic Data**  
F. Talibli<sup>1</sup>; B. Voß<sup>1</sup>; <sup>1</sup> University of Stuttgart, Stuttgart/D
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- P135 **ScyNet: Visualizing interactions in communities with metabolic models**  
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- P136 **Facilitating Diagnostic Marker Development from Whole Genomes through the Identification of Taxonomic Neighborhoods**  
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- P137 **Comprehensive and Rapid Profiling of TCR Repertoires: Unraveling the Immune Response and Tracking Dynamic Changes**  
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- P138 **Single-Cell Omics Strategies Shedding Light on Intronic Variants and Mis-Splicing in Primary PDAC**  
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- P139 **Privacy-Preserving Federated Differential Protein Expression Analysis with FedProt**  
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- P140 **Privacy-Aware Microbiome Profiling for Colorectal Cancer Detection using Federated Learning**  
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