



# Survival Guide



GCB 2015

German Conference on Bioinformatics 2015

University Alliance Ruhr, Dortmund, September 27-30, 2015

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A big Thank You to everyone who made GCB 2015 possible!

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# Program

Sunday, 27th September 2015			
10:00 - 11:00	Registration, coffee		
11:00 - 13:00	Tutorials		
Lunch Break			
14:00 - 15:40	Tutorials		
Coffee Break			
16:00 - 17:30	Tutorials		
17:30 - 19:00	Welcome reception		

	Monday, 28th September 2015		
8:00 - 9:00	Registration, coffee, poster set-up		
	Session Chair: Sven Rahmann		
9:00 - 9:30	Opening: Winfried Schulze, Matthias Rarey		
9:30 - 10:20	Invited Talk: Arndt von Haeseler Modelling Coverage in RNA Sequencing		
	Coffee Break		
	Session Chair: Knut Reinert		
11:00 - 11:20	Nico Pfeifer Statistical Learning in Computational Biology		
11:20 - 11:40	Salome Horsch, Dominik Kopczynski, Jörg Ingo Baumbach, Jörg Rahnenführer and Sven Rahmann From raw ion mobility measurements to disease classification: a comparison of analysis processes		
11:40 - 12:00	Ivo Grosse, Jan Grau and Jens Keilwagen Computing and Visualizing Precision-Recall Curves and Receiver Operating Characteristic Curves for Soft-labeled and Hard-labeled Data		
12:00 - 12:20	Maike Ahrens, Michael Turewicz, Katrin Marcus, Helmut E. Meyer, Caroline May, Martin Eisenacher and Jörg Rahnenführer  FSOL - a workflow for the detection of patient subgroups and affected molecular features in high-throughput omics data		
12:20 - 12:40	Heiko Giese, Joerg Ackermann, Ulrich Brandt, Ilka Wittig and Ina Koch Cluster analysis and visualization techniques for large datasets in complexome pro- filing		
	Lunch Break		
	Session Chair: Martin Eisenacher		
14:00 - 14:40	Invited Talk: Eric Rivals  LoRDEC: a tool for correcting errors in long sequencing reads		
14:40 - 15:00	Nina Hesse, Christopher Schröder and Sven Rahmann An Optimization Approach to Detect Differentially Methylated Regions from Whole Genome Bisulfite Sequencing Data		

15:00 - 15:20	Benedikt Zacher, Rafael Campos-Martin, Julien Gagneur and Achim Tresch Integrative analysis of Epigenomics Data using hidden Markov Models in the R package STAN
	Coffee Break
	Session Chair: Sebastian Böcker
16:00 - 16:20	Tobias Marschall Algorithms for Computational Genomics
16:20 - 16:40	Stefanie König, Lars Romoth, Lizzy Gerischer and Mario Stanke Simultaneous Gene Finding in Multiple Genomes
16:40 - 17:00	Chris-Andre Leimeister, Marcus Boden, Sebastian Lindner, Sebastian Horwege and Burkhard Morgenstern Fast alignment-free sequence comparison using spaced-word frequencies
17:00 - 17:30	Poster flash presentations
17:30 - 19:00	Poster session

	Tuesday, 29th September 2015
8:00 - 9:00	Registration, coffee, view posters
	Session Chair: Tobias Marschall
0.00 0.40	Invited Talk: Veli Mäkinen
9:00 - 9:40	From sequence analysis to graph analysis
9:40 - 10:00	Caroline C. Friedel
9.40 - 10.00	Virus-Host Transcriptomics
10:00 - 10:20	Anna Feldmann and Nico Pfeifer
10.00 - 10.20	From Predicting to Analyzing HIV-1 Resistance to Broadly Neutralizing Antibodies
	Mathieu Clément-Ziza, Francesc Marsellach, Sandra Codlin, Manos Papadakis, Su
	sanne Reinhardt, Maria Rodriguez-Lopez, Stuart Martin, Samuel Marguerat, Alexan
10:20 - 10:40	der Schmidt, Eunhye Lee, Christopher Workman, Jürg Bähler and Andreas Beyer
	Natural genetic variation impacts expression levels of coding, non-coding and anti-
	sense transcripts in fission yeast
	Coffee Break
	Session Chair: Jörg Rahnenführer
11:20 - 11:40	Christopher Schröder and Sven Rahmann
11:20 - 11:40	Efficient Duplicate Rate Estimation from Subsamples of Sequencing Libraries
11:40 - 12:00	Manuel Landesfeind, Robin Martinjak, Heiner Klingenberg and Peter Meinicke
11:40 - 12:00	Ultra-fast functional classification of short reads using UProC with Pfam and KEGG
12:00 - 12:20	Thomas Bellitto, Tobias Marschall, Alexander Schoenhuth and Gunnar W. Klau
12:00 - 12:20	Next Generation Cluster Editing
12:20 - 12:40	Markus Fleischauer and Sebastian Böcker
12.20 - 12.40	Collecting reliable clades using the Greedy Strict Consensus Merger
12:40 - 13:00	Julia Catherine Engelmann, Claus Hellerbrand and Rainer Spang
12.40 - 15.00	Causal modelling of stroma-cancer cell communication
	Lunch Break
	Session Chair: Axel Mosig
14.00 14.40	Invited Talk: Andrew Smith
14:00 - 14:40	ELIXIR Europe: the European life science infrastructure for biological data

# 14:40 - 15:20 Fachgruppe Bioinformatik (FaBI)

## Coffee Break

16:00 - 21:00 Social Event in Bochum

Wednesday, 30th September 2015				
8:00 - 9:00	Registration, coffee, remove posters			
	Session Chair: Ina Koch			
9:00 - 9:40	Invited Talk: Roland Schwarz			
9.00 - 9.40	Intra-tumour heterogeneity and genomic rearrangements in human malignancies			
9:40 - 10:00	Annalisa Marsico			
9.40 - 10.00	Statistical models of non-coding RNA-mediated gene regulation			
10:00 - 10:20	Jan Grau, Ivo Grosse, Stefan Posch and Jens Keilwagen			
10:00 - 10:20	Motif clustering with implications for transcription factor interactions			
10:20 - 10:40	Jan Grau and Jens Keilwagen			
10.20 - 10.40	Varying levels of complexity in transcription factor binding motifs			
	Coffee Break			
	Session Chair: Caroline C. Friedel			
	Johannes Kirchmair			
11:20 - 11:40	Development and application of computational methods for lead identification and			
	optimization			
	Stefan Bietz and Matthias Rarey			
11:40 - 12:00	Integrating Sequence and Structure Information for Efficient Retrieval and Align-			
	ment of Flexible Protein Binding Sites			
12:00 - 12:20	Dagmar Waltemath			
12.00 - 12.20	SEMS: Improving the management of simulation studies in computational biology			
12:20 - 12:40	Stefan Schuster, Daniel Boley, Philip Möller and Christoph Kaleta			
12:20 - 12:40	A minimal model for explaining the higher ATP production in the Warburg effect			
12:40 - 13:00	Best Poster Award, Closing			

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Structure prediction of GPCRs using piecewise homologs and application to the human CCR5 chemokine receptor: validation through agonist and antagonist docking  Karthik Arumugam, Andy Chevigne, Carole Devaux and Jean-Claude Schmit	2
The Roles of Post-translational Modifications in the Context of Protein Interaction Networks  Guangyou Duan and Dirk Walther	
Structural determinants of metabolite-protein binding events  Paula Korkuc and Dirk Walther	4
Solving the Differential Peak Calling Problem  Manuel Allhoff	5
Prediction of interaction-dependent enzyme activity in the trisporic acid pheromone system by modelling of in silico mutants  Sabrina Ellenberger, Stefan Schuster and Johannes Wöstemeyer	6
Pathway Analysis of a Herbicide Resistant Grass  Norma J. Wendel and Antje Krause	
Identifying Sequences by k-Mer Analysis of Amino Acids in a Custom-Built Database  Silvio Weging and Andreas Gogol-Döring	8
SHIVA - A web application for drug resistance testing in HIV  Mona Riemenschneider, Thomas Hummel, Ursula Neumann and Dominik Heider	9
GNATY: A tools library for faster variant calling and coverage analysis  Beat Wolf, Pierre Kuonen and Thomas Dandekar	0
Robust Signature Selection from High-Throughput Genomic Data Sangkyun Lee, Joerg Rahnenfuehrer, Michel Lang, Katleen De Preter, Pieter Mestdagh, Jan Koster, Rogier Versteeg, Raymond L. Stallings, Luigi Varesio, Shahab Asgharzadeh, Johannes H. Schulte, Kathrin Fielitz, Melanie Schwermer, Katharina Morik and Alexander Schramm	.1
Functional Analysis of Metabolic Networks using Sparse Group Lasso  Satya Swarup Samal, Andreas Weber and Holger Froehlich	2
Eosinophil Detector - A new approach for recognizing Eosinophiles within label-free CARS images Thomas Temme, Daniel Niedieker, Dennis Petersen, Erik Freier, Klaus Gerwert and Axel Mosig 1	.3
Discovering Associations between Patient Phenotypes and Gene Functions  Lara Urban, Christian W. Remmele, Roland F Schwarz, Pietro Lio, Marcus Dittrich and Tobias  Müller	.4
Mobile elements present a challenge in the analysis of Bacteroides vulgatus mpk  Sina Beier, Anna Lange, Daniel H. Huson, Ingo B. Autenrieth and Julia-Stefanie Frick	.5
N-gram analysis of amyloid data Michal Burdukiewicz, Piotr Sobczyk, Pawel Mackiewicz and Malgorzata Kotulska	6
Generation of artificial count data for the simulation of feature subsets in NGS or proteomics experiments  Jochen Kruppa, Frank Kramer, Tim Beissbarth and Klaus Jung	.7
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A Generic Approach to Antigen Design Based on Minimising Sequence Distances  Jan T Kim, Tom Peacock and Munir Iqbal	20
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AnnoTALE - Identification, Annotation and Classification of Transcription Activator-Like Effectors  Annett Erkes, Jan Grau, Maik Reschke, Jana Streubel, Richard D. Morgan, Geoffrey G. Wilson, Ralf  Koebnik and Jens Boch
Polar Plots for Visualizing the Effects of Different Treatments on Gene Regulation  Yvonne Poeschl and Andreas Gogol-Döring
Motif independent recognition of microRNA precursor sequences  Thorsten Schmidt and Thilo Wilts
APP is a functional regulator at the presynaptic active zone Martin Wegner, Melanie La $\beta$ ek, Jens Weingarten, Walter Volknandt, Ina Koch and Jörg Ackermann 25
Assessing the genetic code optimality using multiobjective optimization approach  Malgorzata Wnętrzak, Paweł Błażej and Paweł Mackiewicz
TRAPLINE: An Integrated Galaxy Pipeline for RNAseq Data Processing, Evaluation and Prediction Markus Wolfien, Ulf Schmitz, Robert David and Olaf Wolkenhauer
Can we predict environmental conditions from NGS biological observations?  Irina Maria Curuia, Daniel Hoffmann, Jens Boenigk and Manfred Jensen
Bioinformatics Analysis of Alternative Splicing in the human-pathogenic fungus Candida glabrata Patricia Sieber, Reinhard Guthke, Stefan Schuster and Jörg Linde
De-novo transcriptome assembly and the reconstruction of alternatively spliced isoforms  Lasse Feldhahn, Francois Buscot, Vsevolod Makeev, Mika Tarkka and Ivo Grosse
Graph-based analysis of CD30+ cell distributions in Hodgkin Lymphoma  Hendrik Schäfer, Tim Schäfer, Joerg Ackermann, Sylvia Hartmann, Claudia Döring, Martin-Leo  Hansmann and Ina Koch
Bioinformatics Analysis of Heterogeneous Data Reveals Characteristic Mutational Landscapes of Neuroblastoma Relapses  Corinna Ernst, Johannes Köster, Daniela Beisser, Christopher Schröder, Marc Schulte, Alexander Schramm and Sven Rahmann
Rapid Phylogeny Reconstruction with Support Values Fabian Klötzl and Bernhard Haubold
Prediction of Heterosis in Brassica napus by Modeling with a Gene Regulatory Network  Christian Rockmann, Philipp Franke and Heike Pospisil
Cancer Specific Copy Number Variations Stefanie Marczok, Birgit Bortz and Heike Pospisil
Prioritizing cancer driver genes with ContrastRank Rui Tian, Malay K. Basu and Emidio Capriotti
Recent development of the phylogenetic tree editor TreeGraph 2  Ben C Stöver, Sarah Wiechers and Kai F Müller
How good is Flux Balance Analysis? A comparison with nonlinear simulations of a simplified whole-cell model
Hugo Dourado and Martin J. Lercher
Evaluation of LOH detection approaches on whole-genome and exome sequencing data of 30 retinoblastoma patients  Corinna Ernst, Christopher Schröder, Petra Temming and Sven Rahmann
Markov-Chain Monte-Carlo Sampling of Metabolite Concentrations to Identify Thermodynamically Feasible Reaction Directionalities for Flux Balance Analysis  Ulrich Wittelsbürger, Katrin Schrankel and Martin J. Lercher
Metabolic modelling reveals evolution of complex phenotypes through successions of adaptive steps  Tin Yau Pang and Martin Lercher
Unifying open chromatin assays using supervised learning for transcription factor prediction Florian Schmidt, Jonas Fischer, Karl J. Nordstroem, Nina Gasparoni, Gilles Gasparoni, Kathrin Kattler, Nico Pfeifer, Joern Walter and Marcel H. Schulz

dinopy: Efficient DNA Input and Output with Cython  Henning Timm and Till Hartmann
CompGSA: A Comparability Approach using Gene Set Analysis and Trimmed Linear Regression Yang Xiang and Florian Martin
Image processing algorithms for online monitoring of cell density in Pichia pastoris cultivations by In situ Microscopy
Daniel Marquard, Anton Enders, Gustavo Roth, Patrick Lindner and Thomas Scheper
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Bertram Vogel, Sebastian Böcker, Manja Marz, Annegret Wilde and Franziska Hufsky
Mining for common reactivity patterns of human autoantibodies against endogenous protein targets using clustered autoantibody reactivities
Hans-Dieter Zucht, Daniel Chamrad, Anna Telaar, Martin Gamer, Stefan Vordenbäumen, Peter Schulz-Knappe, Matthias Schneider and Petra Budde
Prediction of Specific Transcription Factor Binding Sites from DNase-seq data using Hidden Markov Model
Michael Rauer, Mathieu Clément-Ziza, Achim Tresch and Uwe Ohler
$\label{lem:conditional} \begin{tabular}{l} Inferring Directional Genetic Interactions from Mutli-Parametric Combinatorial Perturbation Screens \\ Bernd Fischer$
Dynamic updates of reference improve NGS read mapping  Karel Břinda, Valentina Boeva and Gregory Kucherov
Ultra-fast phylo-functional classification of metatranscriptomic reads  Heiner Klingenberg and Peter Meinicke
Experimentally-based simulation and quantification of transcriptomic high-throughput sequencing Steffi Kästner, Christian W. Remmele, Marcus Dittrich and Tobias Müller
An Information Theoretic View on Gene Expression Analysis  Sibylle Hess and Katharina Morik
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MeTavGen: a Taverna-based pipeline for the analysis of shotgun metagenomic data Giorgio Gonnella, Laura Glau and Stefan Kurtz
Newtonian dynamics in the space of phylogenetic trees  Björn Hansen and Andrew E. Torda
Circular permutations: detecting evolutionarily related protein pairs based on structural alignments  Martin Mosisch and Andrew E. Torda

## **Conference Information**

#### Venue

The conference site is located at **Seminarraumgebäude I** (SRG I) at Friedrich-Wöhler-Weg 6 on the North Campus (Campus Nord) of TU Dortmund (see map).

#### Registration desk and conference office

Registration is open from 8:00 h (Sunday: 10:00 h). The registration desk and conference office is in the foyer of SRG I and open throughout the conference.

### **Speakers**

Thank you for giving a talk! Please either bring your own laptop and practice switching or copy your PDF to the conference laptop in the break before your session or earlier. The conference laptop will not support PowerPoint, only PDF.

#### Arriving on time with local transportation

When you register, we will provide you with a VRR zone-B ticket valid from Sunday till Wednesday. This ticket allows you to use local public transportation in Dortmund. You will be using it (mainly with S1 from Dortmund main station) to come to the university, please plan your timing accordingly to arrive on time for the first talk. The ticket is also required to go to the social event on Tuesday. We cannot hand out replacements.

#### **Morning Coffee**

Coffee, tea, water and small snacks will be provided in the morning, but please be sure to get a real breakfast in your hotel or on the way. (You will walk past the Mensa building when you arrive with the S-Bahn S1, where you can buy breakfast.)

#### Lunch

We will provide coffee, tea, water and small snacks during coffee breaks, but full lunch is not included in the conference fee.

You can have lunch at the Mensa (canteen), where a variety of food, including vegetarian and vegan options, is provided. Students can show their student ID and the GCB badge to purchase their meal at student prices.

There are other options as well (see the map for locations):

**E** Mensa: First floor, best value for students.

Restaurant Calla: Same floor as the Mensa, nice restaurant with a seasonal kitchen.

Galerie: Ground floor, Cafeteria with snacks and burgers.

Vital: Underground floor, natural and healthy foods.

- F Food Fakultät: Fresh pasta and pizza (also vegan, vegetarian), but limited space.
- **G** BistroTec: Four different menus and a vegetarian menu each day.
- **H** PizzaTec: Great variety of freshly made pizzas.
- I ISM: Nearest place to get some food, e. g. sandwiches.
- **J** Biskotto: Small bistro-like restaurant with a limited choice of food. You should be there before 12:30 or some food may not be available.

#### Cash points

Public cash points can be found at E (Volksbank) and F (Sparkasse) on the map.

#### Internet access

If your university participates in *eduroam*, you have access to the corresponding wireless network. Additionally, we provide you with guest accounts for our local WLAN. Personalized logins are provided at the conference office upon request. Please remember that you have come for the talks and scientific interaction.

#### Meeting room

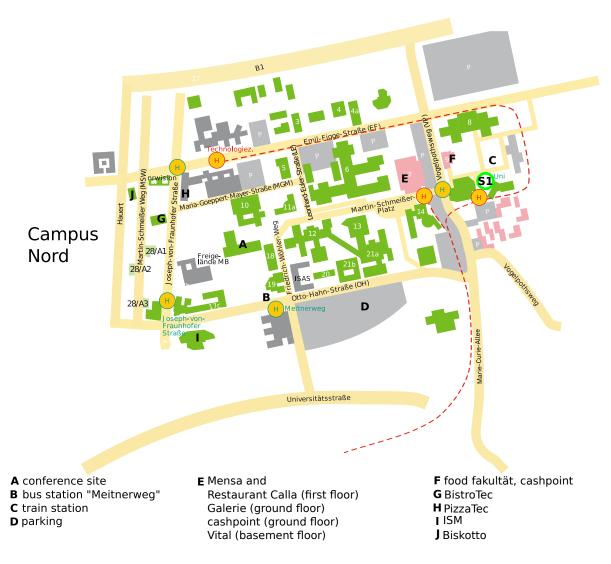
From Monday to Wednesday, room 2.009 (second floor) can be used as meeting room and for discussions in small groups.

#### Restrooms

Please use the restrooms on the ground floor of SRG (especially on Sunday).

#### **Smoking**

Smoking is not allowed in any university building. Please use the designated smoking area just outside of the seminar room building.



## **Getting Around (Travel Information)**

The venue of the conference is the seminar room building "Seminarraumge-bäude I (SRG I)" at Friedrich-Wöhler-Weg 6 on North Campus. The registration is located in the entrance hall of SRG I.



#### Arrival on Sunday afternoon

Warning! On Sunday between 17:30 and 19:15, there is a football match in the stadium (BVB vs. Darmstadt). As the university parking lot is a Park&Ride location for the stadium, the streets, trains, as well as the parking lots will be crowded after 16:00. If you arrive for the welcome reception, expect delays! The best option is to take the S-Bahn (S1) from Dortmund main station and walk to the seminar room building. There are almost no buses on Sunday.

#### Arrival by car

If you arrive from the highway (Autobahn) A45, take exit "DO-Eichlinghofen". If you come from the B1 (A40), take exit "DO-Dorstfeld/Universität". A parking lot near the conference site is at "Otto-Hahn-Straße" close to the Max Planck Institute (MPI) and marked as **D** on the campus map. For navigation, you may want to use Otto-Hahn-Str. 11 in 44227 Dortmund as your destination, which will take you to the MPI. The seminar room building is on the other side, a distance away from the street.

#### Arrival by train

Dortmund Hbf (main station) is served by main trains, including the Intercity-Express (ICE) network. Most hotels in the city center are just a few walking minutes away from the main station. If you want to come directly to the conference, change to the S-Bahn S1 at Dortmund Hbf. The third stop is "Dortmund Universität"; see below for details and more options.

#### **Public transport**

You will receive a public transportation ticket for the duration of the conference. Please fill in your name to validate the ticket. Please note the timetables provided in this guide. You can also get timetable information at http://efa.vrr.de.

**To university** We recommend to take the train S1 from "Dortmund HBF" to "Dortmund Universität". You can also take the subway U42 from "Reinoldikirche" or "Stadtgarten" in the city center (some hotels are also close to "Kreuzstraße") in the direction to Hombruch, exit "An der Palmweide" and change to a bus. The buses are (be careful to take the bus in the correct direction):

- 445 towards Otto-Hahn-Straße, get off at "Meitnerweg"
- 462 towards Huckarde/Marten/Uni, get off at "Meitnerweg"
- 447 towards Revierpark/Uni/Bandelstraße, get off at "DO-Universität S" (10 minutes walk)

Guideposts will direct you to the conference site.

**To the city / hotels** You can take the train S1 from "Dortmund Universität" to "Dortmund HBF". Please note that after 19:00 and on Sunday, the train only runs every half-hour.

If you want to have dinner directly after the conference (or lunch on Wednesday), you might consider taking the bus and subway to the city, as some of the restaurants and bars are located at "Kreuzstraße". The buses towards the U-Bahn are (except Sunday!):

• 445 at "Meitnerweg" (towards An der Palmweide/Renninghausen), departs each 20 minutes at 09, 29, 49 until 19:29,

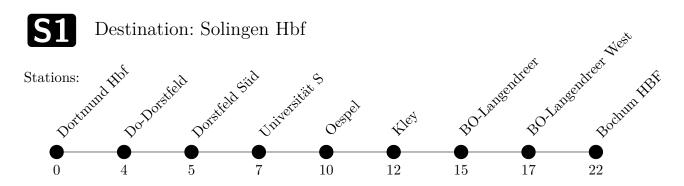
- 462 at "Meitnerweg" (towards An der Palmweide), departs each 20 minutes at 17, 37, 57 until 20:17,
- 447 at "DO-Universität", each 20 minutes at 02, 22, 42 until 20:02, then every half-hour at 34, 04. (Sunday: Every half-hour at 24, 54.)

Get off at "An der Palmweide" and take the subway U42 towards "Grevel".

#### Taxi

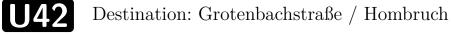
You can order a taxi by calling +49 (231) 14 44 44, or ask at the conference office.

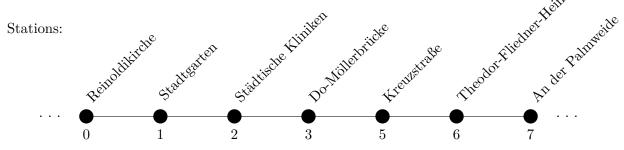
#### **Timetables**



Dortmund Hbf $\rightarrow$ Dortmund Universitat				
Monday-Friday Satu		Saturd	ay, Sunday	
Hour	Minute	Hour	Minute	
	13 33 53	$00 \! - \! 05$		
19 – 23	23 53	06 - 23	$23 \ 53$	

Dortmund Universität $\rightarrow$ Dortmund Hbf				
Monday–Friday Sa		Saturd	Saturday, Sunday	
Hour	Minute	Hour	Minute	
	19 39 59	01 - 05		
19–00	29 59	06-23	29 59	





Reinoldikirche $\rightarrow$ An der Palmweide			
Monday–Friday S			y
Hour	Minute		Minute
04 – 19	06 16 26 36 46 56	07 - 08	19 49
20 - 23	04 19 34 49	09-23	04 19 34 49

An der Palmweide $\rightarrow$ Reinoldikirche						
Monday-Friday		Sunday				
	Minute		Minute			
	06 16 26 36 46 56	07 - 08	19 49			
20 - 23	04 19 34 49	09-23	04 19 34 49			

#### Social Event and Conference Dinner

On Tuesday evening, we will visit the *Bergbaumuseum* in Bochum and have our conference dinner there. The address is "Am Bergbaumuseum 28, 44791 Bochum" (QR code).



From the museum's website: The Deutsches Bergbau-Museum Bochum (DBM) offers extensive insights into the worldwide mining of all mineral resources from prehistoric times to the present day. Exhibitions above ground and a faithfully reconstructed visitor mine underground offer visitors an insight into the world of mining. As an added attraction, the headframe provides a fantastic view of Bochum and the Ruhr.

#### Getting there and back

**TU Dortmund to Bergbaumuseum** After the Tuesday afternoon coffee break, we will split into two groups and take the train to Bochum. We will take the S-Bahn S1 to "Bochum HBF", and there the subway U35 (direction "Herne") to "Bochum Deutsches Bergbau-Museum".

The first group takes the train at 16:00, and therefore departs from the conference building by **15:40** at the latest. The second group takes the train at 16:20, and departs by **16:00**. Please remember to bring the VRR zone B ticket that we gave you during registration. If you forget it, you have to buy your own train ticket!

Bergbaumuseum to Dortmund city (via Bermuda3eck) After the conference dinner, the subway U35 departs every 15 minutes to Bochum HBF. There, you can take regional trains

- RE11 (every hour at 26, platform 5 until 22:26),
- RE1 towards "Hamm" (every hour at 04, platform 5 until 1:04),
- S1 (slow, every half-hour at 14, 44, platform 8). The last train departs at 1:44!

On the other hand, you can spend the evening in Bochum's Bermuda3eck in walking distance from the main station; see below.

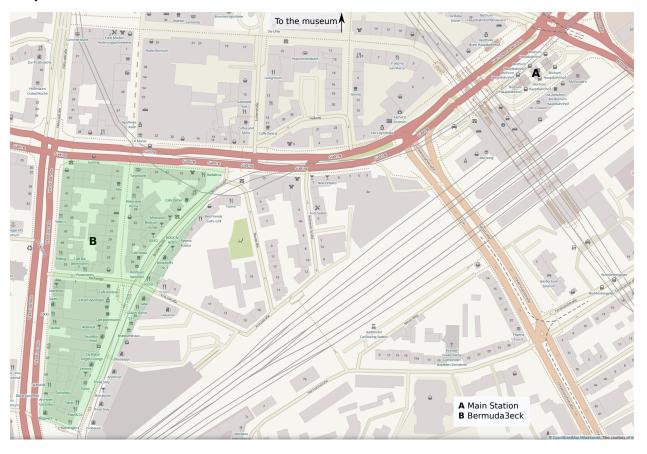
#### Social Event Alternative (Bochum Stadtpark)

If you have visited the Bergbaumuseum before and are looking for an alternative you can take a walk through the city park near the museum. The city park is designed in the style of English landscape gardens. You can spend some additional time at the cafe and the zoo located within the park. The park entrance is located at "Am Alten Stadtpark, Bochum". To get there, we recommend to get to the Bergbaumuseum along with the other attendees. When you arrive at the museum just go down the street. At the end of the street, turn left and take the first street to your right.

## In the evening

The conference dinner ends roughly at 21:00. Bochum is famous for the "Bermuda3eck", a triangle of three streets crowded with pubs and bars. The Bermuda3eck is close to the main station (see the map).

# Map of Bochum Hbf and Bermuda3eck



#### After Work in Dortmund

Some pubs and restaurants within the inner city of Dortmund are listed below. (The selection is not to be understood as a direct recommendation by the organizers.)

#### **Pubs**

A Atlantico - Weißenburgerstraße 35–37

Peanuts are always for free here. Mexican food, burger and cocktails.

**B Bam Boomerang** - Kuckelke 20

Australian Pub and Grill: Burger, kangaroo filet and emu tagliatelle in a big Australian sports bar filled with wooden tables and mural paintings. Happy Hour: 18–20h for beer and 20–24h for cocktails.

C Cu-bar - Kampstraße 41

Snacks and cocktails.

**D** Domicil - Hansastr. 7–11

One of the oldest Jazz clubs placed in an old cinema. Monday Night Session (Jazz Jam Session) begins at 20h.

E Rock Cafe - Reinoldistraße 21

Happy Hour: Astra & Mexikaner 21–23h

F Klubhaus 1249 - Kleppingstrasse 37

Sports bar with burgers and some Karaoke.

#### Restaurants

**G Kyoto** - Rosental 9

Japanese-European fusion cuisine.

**H** Fatto in casa - Liebigstraße 47

Italian restaurant with home-made pasta.

I Pfefferkorn - 2x: Hoher Wall 38, Am Markt 6

Traditional steakhouses.

J Kitchen-Club - Saarlandstraße 102

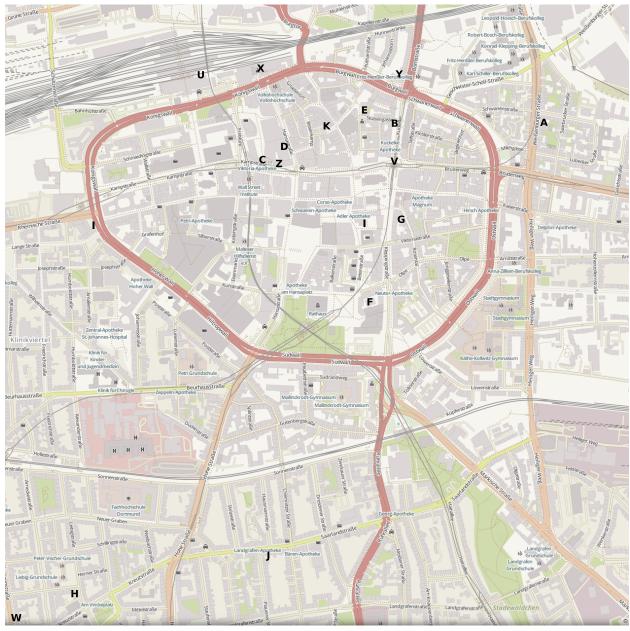
Modern cross-over food and vegetarian dishes.

**K** Kartoffellord - Gerberstr. 1

Since 1988 only vegetarian and vegan food (rather a snack bar than a restaurant).

After Work in Dortmund 17

# Map of Pubs, Restaurants and Hotels in Dortmund



U main stationV subway station "Reinoldikirche"W subway station "Kreuzstraße"

X Hotel NH Dortmund Y Hotel Esplanade Z Mercure Hotel

# Notes

