GCB 2013

German Conference on Bioinformatics
10 - 13 September 2013

Conference Program

Welcome

Dear GCB 2013 Attendee,

On behalf of the GCB 2013 organization committee, it is our great pleasure to welcome you in Göttingen, a city with an extraordinary research tradition. In the first half of the 20th century, Göttingen was the city most often mentioned in combination with the Nobel Prize. This period is therefore called the "Göttinger Nobelpreiswunder". More than forty Nobel laureates worked or lived in Göttingen, and thirteen of them have been awarded the Nobel Prize for the very research conducted during their time in Göttingen.

In association with this tradition, we invited the Nobel laureate Erwin Neher (Max-Planck-Institute for Biophysical Chemistry, Göttingen, Germany) to speak at the GCB 2013. In addition to this talk, inspiring keynotes will be given by leading scientists: Eugene Myers (Max-Planck-Institute of Molecular Cell Biology and Genetics, Dresden, Germany), Terry Speed (Walter and Eliza Hall Institute of Medical Research, Melbourne, Australia), Andreas Dress (Max-Planck-Institut für Mathematik in den Naturwissenschaften, Leipzig, Germany) and Sarah Teichmann (Wellcome Trust Sanger Institute, and European Bioinformatics Institute, Cambridge, UK).

Special interests will be addressed in four satellite workshops, which are part of the conference program: Statistical Methods in Bioinformatics, Computational Methods for Metagenomics and Meta-Omics, Alignment-Free Sequence Comparison, and Methods for Integrated Analysis of Multi-Level Datasets.

We are grateful to the GCB 2013 program committee who, out of 45 submitted manuskripts, selected 24 highlight and twelve regular papers to be presented during the conference. In addition, more than 90 poster abstracts were accepted and will be presented. We are very grateful to the authors of the submitted papers and poster abstracts, to the speakers and to all participants. The most important ingredients to the success of a conference are scientific contributions and discussions.

Furthermore, it is our pleasure to thank for all the voluntary contributions of the diverse bioinformatics groups from the University of Göttingen, the Max-Planck-Institute for Biophysical Chemistry, and the University Medical Center Göttingen. In particular, we thank Anne-Kathrin Schultz who did most of the organization work for the conference. We also thank our cooperation partners, the German Society for Chemical Engineering and Biotechnology (DECHEMA), the Society for Biochemistry and Molecular Biology (GBM) and the Special Interest Group on Informatics in Biology of the German Society of Computer Science (GI). Our special thanks go to the sponsors who supported the conference financially.

We wish you a nice meeting, and hope you will get new insights and be inspired.

Thank you for joining us in Göttingen!
The GCB 2013 organization committee

Photos: Britta Leinemann

GCB 2013 Organization

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Burkhard Morgenstern
Edgar Wingender

Organization Committee

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PD Dr. Martin Kollmar
Prof. Dr. Burkhard Morgenstern
Prof. Dr. Stephan Waack
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Mario Stanke
Jens Stoye
Martin Vingron
Arndt Von Haeseler
Stephan Waack
Thomas Werner
Ralf Zimmer

General Information

Registration Desk & Information

Opening hours:

- Tuesday, 09:00 – 15:00, Göttingen North Campus, Foyer Faculty of Physics
- Tuesday, 19:00 – 21:00, Welcome Reception, Old Town Hall ("Altes Rathaus")
- Wednesday-Thursday, 8:00 – 17:00, Göttingen North Campus, Foyer Faculty of Physics
- Friday, 8:00 – 13:00, Göttingen North Campus, Foyer Faculty of Physics

> **Phone number**
> (Tue - Fri)
> 0551-39-13884

Conference Proceedings

The conference proceedings will be published via Open Access Series in Informatics of Schloss Dagstuhl. Highlight papers, poster abstracts and proceedings are available online via the conference website (*http://www.gcb2013.de/proceedings*).

Internet access

WLAN is accessible through eduroam. If you have no access to eduroam, login and password will be provided at registration.

Lunch

Lunch will be provided at "Nordmensa", a canteen at North Campus. Lunch vouchers (Wed - Fri) are available upon registration.

Coffee Breaks

Coffee and snacks will be provided in the foyer. Coffee breaks are supported by KWS.

Speaker presentation upload

Presentations can be uploaded in the break prior to your talk in the speaker preparation room (HS4).

Poster session

The poster session will take place on Wednesday, 11th September.

- Even numbers: 15:00 – 16:30
- Odd numbers: 16:30 – 18:00

The poster price is sponsored by KWS.

Social Events

- ***Welcome Reception***
  Tuesday, 19:00 – 21:00, Old Town Hall (Altes Rathaus, Markt 9)
  Prof. Dr. Ulrike Beisiegel, President of the University of Göttingen, is pleased
  to welcome the conference participants. Enjoy finger food and drinks.
- ***Conference Dinner*** *(ticketed event - ticket required for entry)*
  Wednesday, 19:00, Bullerjahn, Cellar of Old Town Hall (Ratskeller, Markt 9)
  Supported by Bullerjahn
- ***Guided Walks*** *(ticketed event - ticket required for participation)*
  Thursday, 17:30 – 19:00, Meeting point: Inside Old Town Hall (Altes Rathaus, Markt 9)
 Sponsored by MoBiTec

For further information, please contact the Information Desk.

Satellite Workshops

Four satellite workshops will take place on 10 September 2013 on Göttingen's North Campus.

- HS1, Faculty of Physics
  Statistical Methods in Bioinformatics
- HS2, Faculty of Physics
  Computational Methods for Metagenomics and Meta-Omics
- HS3, Faculty of Physics
  Alignment-Free Sequence Comparison
- HS4, Faculty of Physics
  Methods for Integrated Analysis of Multi-Level Datasets

Conference Venue
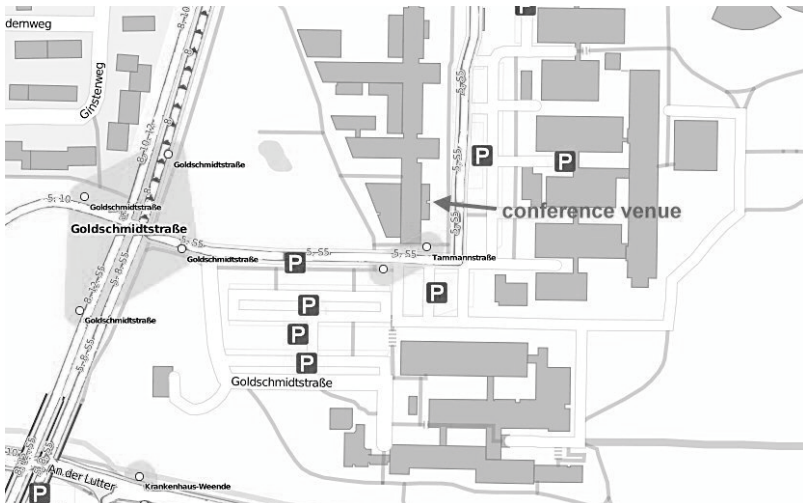
From city centre take bus no. 5 (direction Nikolausberg) or no. 8 (direction Weende/Ost) and get off at bus stop Tammannstraße or Goldschmidtstraße, respectively. From train station take bus no. 8 (see above) or no. 12 (direction Holtenser Berg) and get off at bus stop Goldschmidt-straße or take bus no. 51 (direction Faßberg) and get off at bus stop Tammannstraße.

Tickets can be bought in the bus, but only in cash. You can either buy a single ticket or a "Vi-ererkarte" which can be used for 4 rides (or persons). Day tickets, group tickets or weekly season tickets can also be bought in the bus.

(Taxi: Puk Minicar GmbH Tel. 0551 - 484848; Taxi-Zentrale Tel. 0551 - 69300)

Sightseeing

Gänseliesel – the most kissed girl in the world

Göttingen is a lovely, historic city coined by its university and students. The Gänseliesel (goose girl) figure on the fountain at the market square in front of the Old Town Hall is the landmark of Göttingen. It is also the scene of the university's most prominent tradition: Every newly graduated gives the Gänseliesel a kiss, wearing a self-made graduation hat.

Walk around the history city centre

Walking through the historic city centre, you will come across eight churches and many half-timbered houses dating from 14th to the 18th century. In one of those churches, Paulinerkirche (St. Paul's Church), you will find part of the Göttingen State and University Library. A rampart surrounds the historic city centre. The path on the top of the wall will take to wonderful corners and places such as Göttingen's main theatre, the "Bismarck house" (in which he was banned due to illegal duelling) and a wonderful mill now being used as a student dorm. The Lichtenberghaus house where Georg Christoph Lichtenberg (1742-1799) lived and was teaching is in the corner of the Gotmar- and Prinzenstraße. His audience included Carl Friedrich Gauss and Alexander von Humboldt. In his living rooms he welcomed numerous guests like Gotthold Ephraium Lessing, Johann Wolfgang von Goethe and Johann Kaspar Lavater. Schrödersches Haus (1549) near St. Jacobi church and Junkernschänke (1446 build, 1547-49 rebuild) belong to the most beautiful frame houses of Göttingen. The Aula am Wilhelmsplatz (Great Hall, 1835-37) was spent by Wilhelm IV for the 100. anniversary of the Georgia-Augusta (Göttingen University). The gable wall created by Ernst von Bandel illustrates the four faculties of that time: Theology, Law, Medicine and Philosophy.

The historical botanical garden – a place to dwell

Founded in 1736 by Albrecht von Haller, the historical botanical garden is one of the oldest academies of the university. Located near the wall, the garden is the most beautiful park in the city centre.

Cultural establishments

Göttingen has two professional theatres, the Deutsches Theater Göttingen and the Junges Theater. In addition, there is Theater im OP Göttingen (ThOP), which mostly presents student productions. Göttingen also has an orchestra, the symphonic orchestra Lower Saxony (GSO). The Städtisches Museum (city museum) shows the history of Göttingen, which was first mentioned in a document in 953 AD as the village Gutingi. Another museum, the university's Ethnographic Collection includes an internationally significant South Seas exhibition (Cook/Forster collection).

Historical observatory

The Göttingen Observatory was established in 1816. His first director was the famous mathematician and physical scientist Carl Friedrich Gauss, who was appointed Professor of Astronomy in 1807. He lived and researched here until his death in 1855.

Photos: Britta Leinemann

Keynote Speakers

Sarah Teichmann

Wellcome Trust Sanger Institute, and European Bioinformatics Institute, Cambridge, UK
Gene expression genomics in T cells

Wednesday, 11 September 2013, 9:05

Andreas Dress

Max-Planck-Institut für Mathematik in den Naturwissenschaften, Leipzig, Germany
Predicting the Past: Two recent applications of phylogenetic-network construction regarding the evolution of the HOX-gene cluster and the placental mammals

Wednesday, 11 September 2013, 14:15

Erwin Neher

Max-Planck-Institute for Biophysical Chemistry, Göttingen, Germany
Blind source separation applied to multiply labeled fluorescence images

Thursday, 12 September 2013, 9:00

Gene Myers

Max-Planck-Institute of Molecular Cell Biology and Genetics, Dresden, Germany
Light-Based Systems Biology

Thursday, 12 September 2013, 13:45

Terry Speed

Walter and Eliza Hall Institute of Medical Research, Melbourne, Australia
Normalization of RNA-Seq Data: Are the ERCC Spike-In Controls Reliable?

Friday, 13 September 2013, 9:00

Conference Schedule

Tuesday, 10 September 2013

Satellite Workshops (Faculty of Physics, Göttingen's North Campus)

13:15- 17:15	Workshop 1 (Tim Beißbarth; room HS1) Statistical Methods in Bioinformatics
13:30 - 17:30	Workshop 2 (Peter Meinicke, Thomas Lingner; room HS2) Computational Methods for Metagenomics and Meta-Omics
10:00 - 16:00	Workshop 3 (Burkhard Morgenstern, Susana Vinga; room HS3) Alignment-Free Sequence Comparison
14:00 - 18:00	Workshop 4 (Edgar Wingender; room HS4) Methods for Integrated Analysis of Multi-Level Datasets

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19:00 -   **Welcome Reception**
21:00   Old Town Hall (Markt 9, 37073 Göttingen)

19:30   **Welcome**
          Prof. Dr. Ulrike Beisiegel, President of the University of Göttingen

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Wednesday, 11 September 2013

Main conference takes place at Faculty of Physics, lecture hall HS1

R *… Regular Paper*   **H** *… Highlight Paper*

8:00   Registration opens, poster mounting

9:00   **Opening**
          Burkhard Morgenstern

9:05   **KEYNOTE**
          Gene expression genomics in T cells
          Sarah Teichmann (Wellcome Trust Sanger Institute, and European Bioinformatics Institute, Cambridge, UK)

9:50   *GEDEVO: An Evolutionary Graph Edit Distance Algorithm for Biological Network Alignment* (R)
          Rashid Ibragimov, Maximilian Malek, Jiong Guo and Jan Baumbach

10:15	*PanCake: A Data Structure for Pangenomes* (R) Corinna Ernst and Sven Rahmann

10:40	Coffee break

11:10	*Continuous rapid expansion of the mutually exclusive spliced exome in Drosophila species* (H) Klas Hatje and Martin Kollmar
11:35	*Avoiding Ambiguity and Assessing Uniqueness in Minisatellite Alignment* (R) Benedikt Löwes and Robert Giegerich
12:00	*GenomeTools: a comprehensive software library for efficient processing of structured genome annotations* (H) Gordon Gremme, Sascha Steinbiss and Stefan Kurtz
12:25	*Aligning Flowgrams to DNA Sequences* (R) Marcel Martin and Sven Rahmann

12:50	Lunch break

14:15	**KEYNOTE** *Predicting the Past: Two recent applications of phylogenetic-network construction regarding the evolution of the HOX-gene cluster and the placental mammals* Andreas Dress (Max-Planck-Institut für Mathematik in den Naturwissenschaften, Leipzig, Germany)

15:00	15:00 - 16:30	Poster Session Even numbers	15:00	GI board meeting (Room SR1, A1.101, 1st floor)
	16:15 - 16:45 Coffee Break			
	16:30 - 18:00	Poster Session Odd numbers	16:00	DECHEMA board meeting (Room SR1, A1.101, 1st floor)
19:00	**Social event**: Conference Dinner at the restaurant Bullerjahn (only with ticket)			

Thursday, 12 September 2013

9:00	**KEYNOTE** *Blind source separation applied to multiply labeled fluorescence images* Erwin Neher (Max-Planck-Institute for Biophysical Chemistry, Göttingen, Germany)

9:45   *Utilization of ordinal response structures in classification with high-dimensional expression data* (R)
Andreas Leha, Klaus Jung and Tim Beißbarth

10:10   *Versatile prioritization of candidate disease genes or other molecules with NetworkPrioritizer* (H)
Tim Kacprowski, Nadezhda T. Doncheva and Mario Albrecht

10:35   Coffee break

11:00   *Exploiting structural information for target assessment* (H)
Andrea Volkamer and Matthias Rarey

11:25   *Efficient Interpretation of Tandem Mass Tags in Top-Down Proteomics* (R)
Anna Katharina Hildebrandt, Ernst Althaus, Hans-Peter Lenhof, Chien-Wen Hung, Andreas Tholey and Andreas Hildebrandt

11:50   *On the estimation of metabolic profiles in metagenomics* (R)
Kathrin Petra Aßhauer and Peter Meinicke

12:15   Lunch break

13:45   **KEYNOTE**
Light-Based Systems Biology
Gene Myers (Max-Planck-Institute of Molecular Cell Biology and Genetics, Dresden, Germany)

14:30   *On Weighting Schemes for Gene Order Analysis* (R)
Matthias Bernt, Nicolas Wieseke and Martin Middendorf

14:55   *Alignment-free sequence comparison with spaced k-mers* (R)
Marcus Boden, Martin Schöneich, Sebastian Horwege, Sebastian Lindner, Chris Leimeister and Burkhard Morgenstern

15:20   *Dinucleotide distance histograms for fast detection of rRNA in metatranscriptomic sequences* (R)
Heiner Klingenberg, Robin Martinjak, Frank Oliver Glöckner, Rolf Daniel, Thomas Lingner and Peter Meinicke

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15:45   Coffee break

16:00   GBM board meeting (Room SR1, A1.101, 1st floor)

17:30   **Social event**: Guided walks through Göttingen's center (only with ticket)

19:30   Program Committee Dinner at the Kartoffelhaus (by invitation only)

Friday, 13 September 2013

9:00   **KEYNOTE**
Normalization of RNA-Seq Data: Are the ERCC Spike-In Controls Reliable?
Terry Speed (Walter and Eliza Hall Institute of Medical Research, Melbourne, Australia)

9:45   *Reconstructing Consensus Bayesian Network Structures with Application to Learning Molecular Interaction Networks* (R)
Holger Fröhlich and Gunnar W. Klau

10:10   *Application of a Novel Triclustering Method (δ-TRIMAX) to Mine 3D Gene Expression Data of Breast Cancer Cells* (H)
Anirban Bhar, Martin Haubrock, Anirban Mukhopadhyay and Edgar Wingender

10:35   *Paving the Way for Automated Clinical Breath Analysis and Biomarker Detection* (H)
Anne-Christin Hauschild, Jörg Ingo Baumbach and Jan Baumbach

11:00   Coffee break

11:30   *TALEs of virulence and biotechnology* (H)
Jan Grau, Annett Wolf, Maik Reschke, Ulla Bonas, Stefan Posch and Jens Boch

11:55   *Learning Gene Network Structure from Time Laps Cell Imaging in RNAi Knock-Downs* (H)
Henrik Failmezger, Paurush Praveen, Achim Tresch and Holger Fröhlich

12:20   *Extended Sunflower Hidden Markov Models for the recognition of homotypic cis-regulatory modules* (R)
Ioana M. Lemnian, Ralf Eggeling and Ivo Grosse

12:45   Closing Remarks, Award of Best Poster Prize

Posters

P 01   SubtiWiki - more than just a Wiki
Raphael Michna and Jörg Stülke

P 02   Wondolin: A Web Service for Protein Sequence Comparison
André Ahrens and Martin Kollmar

P 03   WaggaWagga: a Web Service to Compare and Visualize Coiled-Coil Predictions, and to Assess the Oligomerisation State of Coiled-Coils
Dominic Simm, Klas Hatje and Martin Kollmar

P 04   OPTIMAS-DW: Integrating Different Maize -Omics Information into a Data Warehouse
Christian Colmsee, Tobias Czauderna, Anja Hartmann, Martin Mascher, Jinbo Chen, Matthias Lange, Falk Schreiber and Uwe Scholz

P 05   Definitions and nomenclatures for alternative splicing events
Martin Pohl and Stefan Schuster

P 06   EndoNet: An information resource about the intercellular signaling network
Jürgen Dönitz and Edgar Wingender

P 07   BRENDA in 2013: integrated strains, kinetic data, improved disease classification
Sandra Placzek and Dietmar Schomburg

P 08   Combining ontology design and flexible data management in biomedical sciences.
Timm Fitschen, Alexander Schlemmer, Daniel Hornung, Philip Bittihn, Johannes Schröder-Schetelig, Ulrich Parlitz and Stefan Luther

P 09   Comparison Of Platforms To Integrate Transcriptome Data From Different Sources
Sarah N. Mapelli, Bjoern Schumacher, Ankit Arora and Karsten R. Heidtke

P 10   Resource-Constrained Analysis of Ion Mobility Spectra with the Raspberry Pi
Elias Kuthe, Alexey Egorov, Alexander König, Marcel Köppen, Henning Kühn, Suzana Mitkovska, Marianna D'Addario, Dominik Kopczynski and Sven Rahmann

P 11   rBiopaxParser: A new package to parse, modify and merge BioPAX-Ontologies within R
Frank Kramer, Michaela Bayerlova, Annalen Bleckmann and Tim Beissbarth

P 12   MarVis-Graph for integrative analysis of metabolic reaction chains in non--targeted experiments
Manuel Landesfeind, Alexander Kaever, Kirstin Feussner, Ivo Feussner and Peter Meinicke

P 13   The MarVis-Suite: Integrative and explorative analysis of Metabolomics and Transcriptomics data
Alexander Kaever, Manuel Landesfeind, Kirstin Feussner, Ivo Feussner and Peter Meinicke

P 14   FractalQC: A Bioconductor Package for Quality Control of RNA-Seq Coverage Patterns by Means of the Fractal Dimension
Stefanie Tauber and Arndt von Haeseler

P 15 Quantum Coupled Mutation Finder: Predicting functionally or structurally important sites in proteins using quantum Jensen-Shannon divergence and CUDA programming
Mehmet Gültas, Martin Haubrock, Edgar Wingender and Stephan Waack

P 16 EnzymeDetector: Enhancements in 2013 for high throughput applications
Marcus Ulbrich and Dietmar Schomburg

P 17 BAM A tool for basic analysis of microarray data
Marc Bonin, Florian Heyl, Irene Ziska, Lydia Ickler, Denise Sinning, Jekaterina Kokatjuhha and Thomas Häupl

P 18 DeNovoGUI: an open-source graphical user interface for de novo sequencing of tandem mass spectra
Thilo Muth, Lisa Weilnböck, Erdmann Rapp, Christian Huber, Lennart Martens, Marc Vaudel and Harald Barsnes

P 19 mascR: Efficient NGS fragment-size estimation
Orr Shomroni and Stefan Bonn

P 20 New Network Analysis Tools Beyond Hairballs
Tim Kacprowski, Nadezhda T. Doncheva and Mario Albrecht

P 21 Identification of allele-specific expression and RNA editing sites in paired NGS data by ACCUSA2
Michael Piechotta and Christoph Dieterich

P 22 Dynamics of Two-Photon Two-Color Transitions in Flurophores Excited by Femtosecond Laser Pulses
Oleg Vasyutinskii, Karl-Heinz Gericke, Peter Shternin, Andrey Smolin, Sebastian Herbrich and Stefan Denicke

P 23 BiSQuID: Bisulfite Sequencing Quantification and Identification
Cassandra Falckenhayn, Guenter Raddatz and Frank Lyko

P 24 Detection and monitoring of excited biomolecules by means of holographic technique
Irina Semenova, Oleg Vasyutinskii and Alexandra Moskovtseva

P 25 A spherical model of alveolar macrophages using computerized graphical techniques
Dominic Swarat, Martin Wiemann and Hans-Gerd Lipinski

P 26 Computing metabolic costs of amino acid and protein production in *Escherichia coli*
Christoph Kaleta, Sascha Schäuble, Ursula Rinas and Stefan Schuster

P 27 The HGT Calculator: targeted detection of horizontal gene transfer from prokaryotes to protozoa in small data sets
Sabrina Ellenberger, Stefan Schuster and Johannes Wöstemeyer

P 28 Linking Phenotypes and Genomic Regions: the Forward Genomics Approach
Xavier Prudent and Michael Hiller

P 29 Automated combined analysis of DNA methylation and transcription profiles in different immune cells
Marc Bonin, Lorette Weidel, Stephan Flemming, Andreas Grützkau, Biljana Smiljanovic, Till Sörensen, Stephan Günther and Thomas Häupl

P 30   Automated Classification of Cell Populations with Multi-channel Flow Cytom-
        etry Data - Using Sparse Grids Classifying A Sparsely Populated Data Space
        Manuel Nietert, Steve Wagner, Annalen Bleckmann, Klaus Jung, Dorit Arlt and Tim Beissbarth

P 31   Spatial distribution of cells in Hodgkin Lymphoma
        Hendrik Schäfer, Tim Schäfer, Joerg Ackermann, Norbert Dichter, Claudia Döring, Sylvia Hart-
        mann, Martin-Leo Hansmann and Ina Koch

P 32   Sequence based analysis of plant myosins
        Stefanie Mühlhausen and Martin Kollmar

P 33   Transcriptome analysis of the model organism *Tribolium castaneum*
        Sarah Behrens, Robert Peuß, Barbara Milutionivic, Hendrik Eggert, Daniela Esser, Philip Rosen-
        stiel, Erich Bornberg-Bauer and Joachim Kurtz

P 34   Analysis of Wt1 ChIP Seq data from mouse glomeruli
        Stefan Pietsch, Christoph Englert and Lihua Dong

P 35   Newtonian dynamics in the space of phylogenetic trees
        Björn Hansen and Andrew E. Torda

P 36   Design of new inhibitors for HIV-Integrase: Implications of structure based
        drug design by Molecular Modeling approach
        Jitendra Kumar Gupta, Nandhini K P, Annie Cynthia B, T. Gopala Krishnan and Asif Naqvi

P 37   Elucidating soil microbial communities in agricultural soils
        Yudai Suzuki, Kazunari Yokoyama, Naomi Sakuramoto and Y-H Taguchi

P 38   A Novel Approach for Determining Spatial Colocalization of Proteins Inside
        Ceramide-rich Domains
        Christian Imhäuser, Heike Gulbins, Erich Gulbins and Hans-Gerd Lipinski

P 39   Structure modeling of proteins for the biosynthesis of sex pheromones in
        zygomycetous fungi
        Sabrina Ellenberger and Johannes Wöstemeyer

P 40   Functional and metabolic characterization of plant peroxisomal proteomes
        Ana Tzvetkova, Sigrun Reumann, Peter Meinicke and Thomas Lingner

P 41   Different expression of classical Hodgkin lymphoma and primary mediastinal
        B-cell lymphoma
        Denis Dalic, Ina Koch, Martin-Leo Hansmann and Claudia Döring

P 42   Statistical analysis of Hodgkin lymphoma based on tissue image data
        Jennifer Scheidel, Tim Schäfer, Hendrik Schäfer, Jörg Ackermann, Claudia Döring, Sylvia Hart-
        mann, Martin-Leo Hansmann and Ina Koch

P 43   Analysis of RNA-seq data for identifying flowering time regulators in vernal-
        ized and non-vernalized rapeseed
        Claus Weinholdt, Nazgol Emrani, Ioana Lemnian, Nicole Jedrusik, Carlos Molina, Christian
        Jung and Ivo Grosse

P 44   Towards an optimal transcriptome assembly of the Naked Mole Rat
        Martin Bens, Karol Szafranski and Matthias Platzer

P 45   Distinction of Type 2 diabetes using PCA, miRNA as features
        Shodai Katsukawa and Y-H. Taguchi

P 46   Multiple Protein Alignment using Domain Information
        Layal Al Ait and Burkhard Morgenstern

P 80 An efficient approach to generate chemical substructures for MS/MS peak assignments in MetFrag
Christoph Ruttkies and Steffen Neumann

P 81 Gamification of gene prediction
Klas Hatje, Dominic Simm and Martin Kollmar

P 82 Identification of gene co-expression networks associated with different cellular and immunological states
Marc Bonin, Jekaterina Kokatjuhha, Stephan Flemming, Biljana Smiljanovic, Andreas Grützkau, Till Sörensen and Thomas Häupl

P 83 Combining features for protein interface prediction
Torsten Wierschin, Keyu Wang, Stephan Waack and Mario Stanke

P 84 Circular permutations: detecting evolutionary related protein pairs based on structure analysis
Martin Mosisch, Thomas Margraf and Andrew Torda

P 85 A scalable method for the correction of homopolymer errors
Giorgio Gonnella and Stefan Kurtz

P 86 Multiple genome comparison based on overlap regions of pairwise local alignments
Katharina Jahn, Henner Sudek and Jens Stoye

P 87 Enrichment Analysis for Hierarchical Clusters
Jan T Kim, Karen Staines, John Young, Zenon Minta, Krzysztof Smietanka, Devanand Balkissoon, Raul Ruiz-Hernandez and Colin Butter

P 88 A general approach for discriminative de-novo motif discovery from high-throughput data
Jan Grau, Stefan Posch, Ivo Grosse and Jens Keilwagen

P 89 Novel Visualization Approach Integrating Network and Structure Analysis of Proteins
Nadezhda T. Doncheva, John H. Morris, Eric F. Pettersen, Conrad C. Huang, Karsten Klein, Francisco S. Domingues, Thomas E. Ferrin and Mario Albrecht

P 90 Protein Subcellular Location Prediction Using Principal Component Analysis
Daichi Nogami, Yuichi Nakano and Yoshihiro Taguchi

P 91 Analyzing taxon and pathway coverage profiles with applications to metatranscriptomics
Daniela Beisser and Sven Rahmann

P 92 Bringing together only what belongs together: Characterizing and distinguishing protein structure families using distances based on contact map overlap
Inken Wohlers, Gunnar W. Klau and Rumen Andonov