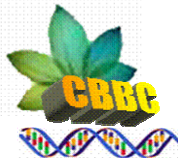




# First Tunisian-German Meeting on Bioinformatics



*Caribbean World Hotel\*\*\*\**

*Borj-Cédria*



**(8-10 September 2006)**

Organized by the Center of Biotechnology (Technopark of Borj-Cédria, Tunisia) & AIPlanta, Institute for Plant Research (RLP AgroScience GmbH, Germany)

under the auspices of the

**Tunisian Ministry of Scientific Research, Technology and Competency Development**

## Objective:

This meeting will favour direct contact and exchange between Tunisian and German scientists and is intended to establish bilateral networks and initiate specific projects on bioinformatics and genomics

## Topics:

- Bioinformatics and structural genomics
- Bioinformatics and functional genomics
- Bioinformatics and comparative genomics
- Bioinformatics and systems biology

**Abstract submission:**

**Deadline** for oral and poster presentation: 30 June 2006

**Registration fees:**

**Students:** 150 dinars **Full fees:** 200 dinars

**Language:**

English

**Payment:**

Amicale de la Technopole de Borj-Cédria,  
Banque Nationale Agricole, Agence de Soliman;

**RIB: 03404002010100260974 (TN59)**

### German Coordinator

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### Tunisian Coordinator

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**Friday September 8<sup>th</sup>, 2006:**

- 08<sup>30</sup>-10<sup>30</sup>: *Registration and opening ceremony*
- 10<sup>30</sup>-10<sup>45</sup>: *Coffee break*
- 10<sup>45</sup>-11<sup>00</sup>: Malek Kochleff, **Research in Tunisia: main objectives and focus**
- 11<sup>00</sup>-11<sup>30</sup>: N.N., **Status and perspectives of FP7 (Quality of Food / Life Sciences)**

**Session I: *General introduction to bioinformatics***

- 11<sup>30</sup>-12<sup>15</sup>: Mohamed BEN AHMED, **Knowledge and discovery from bioinformatic databases**
- 12<sup>15</sup>-13<sup>00</sup>: Ralf HERWIG, **From genes to pathways: resources, tools and methods for systems biology**
- 13<sup>00</sup>-14<sup>30</sup>: *Lunch*

**Session II: *Bioinformatics and structural genomics***

- 14<sup>30</sup>-15<sup>15</sup>: Andrew TORDA, **Protein structure predictions, comparisons based on optimisation, empiricism and optimism**
- 15<sup>15</sup>-15<sup>35</sup>: Sonia ABDELHAK, **The human genome: impact in the biomedical domain**
- 15<sup>35</sup>-16<sup>05</sup>: Jürgen SÜHNEL, **New insights into protein structure by structural bioinformatics approaches**
- 16<sup>05</sup>-16<sup>35</sup>: Birgit KERSTEN, **GABI-primary database service: Collection, administration and analysis of plant data**
- 16<sup>30</sup>-17<sup>00</sup>: *Coffee break*
- 17<sup>00</sup>-17<sup>20</sup>: Nabil MILED, **Structural modelling of proteins**
- 17<sup>20</sup>-18<sup>40</sup>: Ikram GUIZANI, **Comparative genome and function analysis for the identification and/or characterization of Leishmania targets for intervention and control**
- 17<sup>40</sup>-18<sup>00</sup>: Ahmed FOURATI, **Combining multiple models for Prokaryotic promoter prediction**
- 18<sup>00</sup>-18<sup>30</sup>: Ekaterina SHELEST, **Conserved regulatory patterns and extrapolation in promoter modelling**
- 18<sup>30</sup>-19<sup>00</sup>: Helmut BLÖCKER, **Mobile phones, pattern recognition and „conserved evolution“**
- 19<sup>00</sup>-19<sup>30</sup>: Kouji NAKAMUARA, **Eubacteria : Structural and functional analysis of small non-coding RNA**
- 20<sup>30</sup>- o.e: *Dinner*

**Saturday September 9<sup>th</sup>, 2006:**

**Session III:      *Bioinformatics and functional genomics***

- 08<sup>30</sup>-09<sup>15</sup>:      Dirk WALTHER, **The regulatory code in the genome of *Arabidopsis thaliana***
- 09<sup>15</sup>-09<sup>45</sup>:      Kenneth W. BERENDZEN, **Plant functional genomics: promotor analyses**
- 09<sup>45</sup>-10<sup>15</sup>:      Stefan POSCH, **Prediction of transcription factor binding sites using variable order Markov models and Bayesian networks**
- 10<sup>15</sup>-10<sup>40</sup>:      *Coffee break*
- 10<sup>40</sup>-11<sup>00</sup>:      Mohsen HANANA, **VVNHX1 structural analysis: bioinformatic approach**
- 11<sup>00</sup>-11<sup>20</sup>:      Walid HAMADA, **The use of bioinformatics to dissect the interaction of *Nicotiana* sp. and the pathogen *Phytophthora infestans***
- 11<sup>20</sup>-11<sup>40</sup>:      Sami FATTOUCH, **Bioinformatics in structure-based biotechnology: automated docking for the comparison of polyphenol oxidase kinetics**
- 11<sup>40</sup>-12<sup>00</sup>:      Balkiss BOUHAOUALA, **Molecular modelling for prediction of structure-function relationships**
- 12<sup>00</sup>-12<sup>30</sup>:      Ivo GROSSE, **Computational mapping of crop plant ESTs**
- 12<sup>30</sup>-12<sup>50</sup>:      Mourad ELLOUMI, **Algorithms for processing biological sequences**
- 12<sup>50</sup>-14<sup>30</sup>:      *Lunch*

**Session IV:      *Bioinformatics and comparative genomics***

- 14<sup>30</sup>-15<sup>15</sup>:      Ahmed REBAI, **Rice genome annotation: study of protein families involved in stress tolerance**
- 15<sup>15</sup>-15<sup>35</sup>:      Khaddouja BENJENFA, **Multiple alignment methods for protein sequencing**
- 15<sup>35</sup>-16<sup>05</sup>:      Roland KRAUSE, **Comparative genomics of (plant-) pathogenic bacteria**
- 16<sup>05</sup>-16<sup>35</sup>:      Mohamed M. Ibrahim ABOUELHODA, **A software system for comparative genomics**
- 16<sup>35</sup>-17<sup>00</sup>:      *Coffee break*
- 17<sup>00</sup>-17<sup>20</sup>:      Helmi MARDASSI, **Comparative genomics of PE\_PGRS genes of *Mycobacterium tuberculosis* provides new insights into the evolutionary scenario of the tubercle bacillus**
- 17<sup>20</sup>-17<sup>50</sup>:      Remy BRUGGMANN, **Uneven chromosome contraction and expansion in the maize genome**

**Session V:      *Poster Session***

- 17<sup>50</sup>-19<sup>50</sup>:      **Poster & Discussion**
- 20<sup>30</sup>:              *Dinner show*

**Sunday September 10<sup>th</sup>, 2006:**

**Session VI: *Bioinformatics and systems biology***

- 08<sup>30</sup>-09<sup>15</sup>: Joachim SELBIG, **Integrative analysis of complex biological profile data**
- 09<sup>15</sup>-10<sup>00</sup>: Alia BELKAHLA, **Modelling of the macrophage response to Leishmania infection**
- 10<sup>00</sup>-10<sup>30</sup>: *Coffee break*
- 10<sup>30</sup>-10<sup>50</sup>: Hanene MASMOUDI, **Implicit networks: an alternative to Bayesian networks for modelling signal transduction pathways**
- 10<sup>50</sup>-11<sup>10</sup>: Inès HAMDİ, **Modelling and study of biological interactions**
- 11<sup>10</sup>-11<sup>40</sup>: Ralf HOFESTÄDT, **Integrative bioinformatics - metabolic pathway prediction**
- 11<sup>40</sup>-12<sup>10</sup>: Falk SCHREIBER, **Analysis and visualisation of high-throughput data in the context of relevant networks**
- 12<sup>10</sup>-12<sup>40</sup>: Alexander KEL, **How promoters help to find drug targets**
- 12<sup>40</sup>-13<sup>10</sup>: Wolfram WECKWERTH, **Bioinformatic and biophysical concepts for the processing and interpretation of metabolite- und protein profiling**
- 13<sup>10</sup>-14<sup>30</sup>: *Lunch*

**Session VII: *Closing session and round tables***

- 14<sup>30</sup>-15<sup>15</sup>: Helmut DIETRICH, **Support programs for bilateral cooperation**
- 15<sup>15</sup>-15<sup>45</sup>: *Coffee break*
- 15<sup>45</sup>-18<sup>00</sup>: Conclusions, general recommendations and possible bilateral collaborations
- 20<sup>30</sup>: *Dinner*

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**Local Organising Committee:**

Manef Abderrabba (TBC), Abdelwahed Ghorbel (CBBC), Abdelaziz Mougou (IRESA), Houcine Khattali (IRA), Ezzedine Triki (TST), Hamadi Ayadi (CBS), Bisma Hentati (ISBS), Ridha Mrabet (INSTM), Khira Maaroufi (ISBM), Abdeladhim Ben Abdeladhim (IPT), Samir Ben Ahmed (INSAT), Hedi Zarrouk (INRAP), Hassen Maaref (IMIM), Balkiss Bouhaouala (FST), Fatma Ben Abdallah (CNUDST), Khaddouja Boujenfa (ISG), Ines Hamdi (ENSI), Mounir Bezzarga (TBC), Walid Berri (CBBC), Walid Dridi (CBBC).

**Local Scientific Committee:**

Abdelwahed Ghorbel (CBBC), Balkiss Bouhaouala (FST), Khaddouja Boujenfa (ISG), Ahmed Rebaï (CBS), Alia Ben Kahla (IPT), Ahmed Mliki (CBBC), Inès Hamdi (ENSI), Med Elarbi Aouani (CBBC), Chedly Abdelly (CBBC), Moktar Zarrouk (CBBC), Med. Elyes Kchouk (CBBC), Ali Ferchichi (IRA), Néjib Marzouki (INSAT), Youssef Trifa (INAT); Sonia Abdelhak (IPT); Amel Gaïed (FST).

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Ministry of Scientific Research Technology and Competency Development-Tunisia  
Center of Biotechnology of Borj Cedria - Tunisia  
AIPianta Institute for Plant Research - Germany  
DFG - German Research Foundation  
Chambre de Commerce Tunisa - Allemande  
Tunesisch-Deutsche Freundschaft

## First Tunisian-German Meeting on Bioinformatics 2006 – Final program

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### Invited Speakers - Tunisia:

**Sonia ABDELHAK**, Institut Pasteur de Tunis: The human genome: impact in the biomedical domain

**Alia BELKAHLA**, Institut Pasteur de Tunis: Modelling of the macrophage response to Leishmania infection

**Mohamed BEN AHMED**, Ecole Nationale des Sciences Informatiques: Knowledge and discovery from bioinformatic databases

**Khaddouja BENJENFA**, Institut Supérieur de Gestion: Multiple alignment methods for protein sequencing

**Balkiss BOUHAOUALA**, Faculté de Médecine de Tunis-Université de Tunis El Manar: Molecular modelling for prediction of structure-function relationships

**Mourad ELLOUMI**, Faculté des Sciences Economiques et de Gestion de Tunis: Algorithms for processing biological sequences

**Sami FATTOUCH**, Institut National Supérieur des Applications Technologiques: Bioinformatics in structure-based biotechnology: automated docking for the comparison of polyphenol oxidase kinetics

**Ahmed FOURATI**, Bioinformatics Department, Centre of Biotechnology of Sfax: Combining multiple models for Prokaryotic promoter prediction

**Ikram GUIZANI**, Institut Pasteur de Tunis: Comparative genome and function analysis for the identification and/or characterization of Leishmania targets for intervention and control

**Walid HAMADA**, National Agronomic Institute of Tunisia. Tunis: The use of bioinformatics to dissect the interaction of Nicotiana sp. and the pathogen Phytophthora infestans

**Inès HAMDJ**, Ecole Nationale des Sciences Informatiques: Modelling and study of biological interactions

**Mohsen HANANA**, Centre de Biotechnologie de Borj-Cédria: VVNHX1 structural analysis: bioinformatic approach

**Helmi MARDASSI**, Institut Pasteur de Tunis: Comparative genomics of PE\_PGRS genes of Mycobacterium tuberculosis provides new insights into the evolutionary scenario of the tubercle bacillus

**Hanene MASMOUDI**, Centre de Biotechnologie de Sfax: Implicit networks: an alternative to Bayesian networks for modelling signal transduction pathways

**Nabil MILED**, Ecole Nationale d'Ingénieurs de Sfax: Structural modelling of proteins

**Kouji NAKAMUARA**, University of Tsukuba Japan: Eubacteria : Structural and functional analysis of Small non-coding RNA

**Ahmed REBAI**, Centre de Biotechnologie de Sfax: Rice genome annotation: study of protein families involved in stress tolerance

**Mdme. Belkhouja**, Délégation de la Commission Européenne en Tunisie: Status and perspectives of FP7 (Quality of Food / Life Sciences)

**Malek Kochleff**, Ministry of Scientific Research, Technology and Competency Development: Research in Tunisia: main objectives and focus

## First Tunisian-German Meeting on Bioinformatics 2006 – Final program

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### Invited Speakers - Germany:

**Abouelhoda Mohamed M. M. IBRAHIM**, Faculty for Informatics, University of Ulm: A software system for comparative genomics

**Kenneth W. BERENDZEN**, ZMBP - Centre for Plant Molecular Biology, University of Tübingen: Plant functional genomics: promotor analyses

**Helmut BLÖCKER**, HZI - Helmholtz Centre for Infection Research - Department of Genome Analysis, Braunschweig: Mobile phones, pattern recognition and „conserved evolution“

**Remy BRUGGMANN**, Munich Information Center for Protein Sequences, Institute for Bioinformatics: Uneven chromosome contraction and expansion in the Maize genome

**Ivo GROSSE**, BIC-GH Bioinformatics Centre Gatersleben - Halle: Computational mapping of crop plant ESTs

**Ralf HERWIG**, Max-Planck-Institute for Molecular Genetics, Berlin: From genes to pathways: resources, tools and methods for systems biology

**Ralf HOFESTÄDT**, Institute for Bioinformatics, Technical University of Bielefeld: Integrative bioinformatics - metabolic pathway prediction

**Alexander KEL**, BIOBASE GmbH, Bioinformatics Research: How promoters help to find drug targets

**Birgit KERSTEN**, RZPD German Resource Centre for Genome Research GmbH Berlin: GABI-primary database service: Collection, administration and analysis of plant data

**Roland KRAUSE**, Max-Planck-Institute of Infection Biology, Berlin: Comparative genomics of (plant-) pathogenic bacteria

**Stefan POSCH**, Martin-Luther-University Halle-Wittenberg, Institute of Computer Science: Prediction of transcription factor binding sites using variable order Markov models and Bayesian networks

**Falk SCHREIBER**, IPK Gatersleben - Molecular Genetics: Analysis and visualisation of high-throughput data in the context of relevant networks

**Joachim SELBIG**, Institute of Biochemistry and Biology, University of Potsdam: Integrative analysis of complex biological profile data

**Ekaterina SHELEST**, Universität Göttingen, Department of Bioinformatics, Center of Informatics, Statistics and Epidemiology, UKG: Conserved regulatory patterns and extrapolation in promoter modeling

**Jürgen SÜHNEL**, Leibniz Institute for Age Research - Fritz Lipmann Institute (FLI): New insights into protein structure by structural bioinformatics approaches

**Andrew TORDA**, University of Hamburg, Centre for Bioinformatics: Protein structure predictions, comparisons based on optimisation, empiricism and optimism

**Dirk WALTHER**, Max-Planck-Institute for Molecular Plant Physiology, Golm: The regulatory code in the genome of *Arabidopsis thaliana*

**Wolfram WECKWERTH**, Max-Planck-Institute for Molecular Plant Physiology, Golm: Bioinformatic and biophysical concepts for the processing and interpretation of metabolite- und protein profiling

**Helmut DIETRICH**, German Academic Exchange Service, Lectorate Université La Manouba: Support programs for individual and bilateral research cooperation