

Newsletter

INBIOMEDvision

In This Issue

- 1 Interview with Dr. Søren Brunak
- 2 Members Update
- 3 INBIOMEDvision News
- 5 BMI News Roundup
- 5 Upcoming Events

Interview with Dr. Søren Brunak

Center for Biological Sequence Analysis, Department of Systems Biology, DTU

Professor Søren Brunak from the Technical University of Denmark and the University of Copenhagen has recently published the article "Using electronic patient records to discover disease correlations and stratify patient cohorts" in the open-access Journal PLoS Computational Biology. This study demonstrates how text mining extracts clinically relevant terms from psychiatric patient records and how mapping these to disease codes in the International Classification of Disease ontology (ICD10) helped construct phenotypic profiles for each patient. These profiles were used both to identify correlations between diseases and to cluster patients into groups with highly similar clinical features.



→ The study identified a large number of diseases and symptoms which co-occur much more than expected when compared to the individual frequencies of the diseases. Give us your opinion about the reuse of clinical records in basic biomedical research. Could text mining speed up the transfer of new discovery in clinical practice and which barriers do you think should be overcome to ensure that these translational studies help patients to get a more personalized treatment?

Most of the records are kept inside the hospitals and are mainly used for gathering cohorts for specific diseases based on manual read. They are not being used in research or in a context for computational analysis. If clinical records were used to look for patterns across many records, doctors and so on, they would be a potential source for discoveries that could be used for research.

Another very important aspect is that the records that we have, for example in Scandinavia, going many years back, are based on disease codes, terminologies and classifications which have been taken manually.

The classification work can be improved by doing text mining and actually feeding those mined terms into the record. By improving the quality of the registries by text mining of patient records we could find a lot of information through computational research, increasing the statistical significance of many findings. We see that we can find ten times more codes than has been assigned, then of course we create more opportunities for finding multi-code correlations.

"In exploiting the individual genome variation we have a long way to go before it would be trivial to link the genome to the phenotype"

→ Do you find differences between Europe or US in this aspect?

Clinical records is a difficult area to be an expert in because rules and practices are different all over the world. There might be a state or a hospital or county where things are different but my general feeling is that in the USA they have problems with availability; that is, making records available for research outside hospitals. They can do things inside hospitals, and this is where the USA is stronger than Europe, but moving the records to research environments outside the hospitals, I think that in Europe we are in a better position. Although in Europe there are differences between countries; there are some countries where using hospital records for research would be out of the question. It is difficult to say where the situation is better, but my feeling is that if we can analyze the data in the university settings also we are better off in Europe.

→ Your recently published study also discovers a possible genetic cause behind the disease by investigating gene overlaps in protein interaction networks already linked to the individual diseases. Within the biomedical research field, only few areas have undergone such exponential growth in recent decades as Systems Biology has done. Could you comment briefly about what is been accomplished



and what remains to be done in System Biology focusing particularly in developments that could be applied in human diseases and therapies?

I guess the main systems medicine challenge is to use human variation data to improve disease gene finding and patient stratification and classification. This is an area, of course, where we have very little experience because we haven't got millions of genetic sequences of individuals yet, and we are not really sure of how to undertake an integrated analysis of a complete human genome in a clinical context. It is work in progress.

In exploiting the individual genome variation we have a long way to go before it would be trivial to link the genome to the phenotype. The statement summarised in one paper published in Genome Medicine: "The \$1,000 genome, the \$100,000 analysis?" is likely to be true, since analyzing individual genomes in detail is not straightforward and will cost a lot of money.



The GWAS, Genome-Wide Association Studies, have generated a lot of information, but they did not immediately link genetic variation to the phenotype as much as expected, but systems biology approaches may be a way of repairing this fact. It seems that human genome variation maps more to networks than to individual genes and mapping human variation data to networks, instead of analysing gene by gene, should be the way forward to find part of the missing links.

→ The kind of studies that you have carried out have led to the view that a new predictive, preventive, and personalised medicine, is emerging. Ten years from now, do you think we will see a really dramatic transformation in how health care is delivered using these translational informatics technologies?

Ten years is a good estimate for putting a lot of this into general clinical practice, any shorter period of time would not be realistic because of the many unsolved problems there still are. There are a lot of approvals by the FDA that need to take place before a lot of this information can be used for decision making, but still a lot will happen in ten years. I believe that politicians cannot even imagine how much pressure will be created by people when they come with their own DNA sequence requesting their treatment taking their genome sequence into account.

→ By Victoria Lopez Alonso (ISCIII)

INBIOMEDvision Members Update

New members have been engaged to the membership

Alejandro Pazos
Universidade da Coruña

Alfonso Valencia
Spanish National Cancer Research Centre CNIO

Anthony Brookes
University of Leicester

Antoine Geissbuhler
Geneva University Hospitals

Arthur Thomas
Proteus Associates, UK

Bruno G. Loos
ACTA (Academic Centre for Dentistry Amsterdam), University of Amsterdam, VU University Amsterdam

Charles Auffray
CNRS Institute of Biological Sciences

Christian Ohmann
Universitätsklinikum Düsseldorf, Heinrich-Heine-Universität

Dipak Kalra
CHIME - University College London

Fernando Martín Sanchez
Health Informatics Melbourne Medical School

Francesca Incardona
EuResist Network

George Mihalas
European Federation for Medical Informatics; Victor Babes University of Medicine and Pharmacy

Georges De Moor
University of Ghent; CUSTODIX

Gerhard Ecker
University of Vienna

Giorgos Potamias
Institute of Computer Science (ICS), Foundation for Research & Technology Hellas

Gustavo Deco
Pompeu Fabra University

Jana Zvárová
Institute of Computer Science, Academy of Sciences of Czech Republic, EuroMISE Centre

José Luis Oliveira
University of Aveiro

José Manuel Gómez- Pérez
Intelligent Software Components (iSOCO) S.A.

Lucciano Milanese
Institute for Biomedical Technologies CNR, Italy

Martin Dugas
University of Münster

Montserrat Robles
Universidad Politécnica de Valencia

Niels Rossing
Rossing Consultancy

Norbert Graf
Saarland University, University Medical Centre

Nuria Lopez-Bigas
Pompeu Fabra University

Patrick Ruch
HEG/University of Applied Sciences, Geneva

Peter Ghazal
University of Edinburgh

Reinhold Haux
Peter L. Reichertz Institute for Medical Informatics, University of Braunschweig, Institute of Technology and Hannover Medical School

Riccardo Bellazzi
University of Pavia

Sabine Koch
Karolinska Institutet

Scott Boyer
AstraZeneca R&D

INBIOMEDvision Project News

Think Tank on Re-use of Clinical Information for Research. June 24, 2011. London.

INBIOMEDvision organises three main Think Tank sessions, seeking the involvement of participants from different and multidisciplinary scientific communities. The purpose of these sessions is to focus in detail on the state of Biomedical Informatics and to identify opportunities for future collaborative work. The first of these events was held on 24 June 2011 at University College London (UCL) under the auspices of the INBIOMEDvision Project Consortium.



This event, organised by **Dr. Nour Shublaq**, brought together scientists and health care experts with a view to improving approaches to managing health and personal welfare through innovations in scientific research and information technology.

Next Think Tanks

Genotype-Phenotype resources. October 5, 2011. Brussels

Translational Systems biology and Bioinformatics. October 17, 2011. Barcelona

The Think Tank meeting, co-chaired by **Prof. Peter Coveney** and **Prof. Dr. Norbert Graf**, with 27 selected key stakeholders was held on the "Re-use of Clinical Information for Research" and the prerequisite IT considerations for Medical Informatics. As organizers said: "This is key to the future implementation of predictive, preventive and personalised (3P) medicine in healthcare, the medicine of the 21st century that is fast becoming a reality. The aim was to have a small meeting enabling an open discussion between key players capable of shaping this reality".

More information about the Think Tank can be found at: http://www.inbiomedvision.eu/PDF/Thinktank2_website.pdf

INBIOMEDvision Workshop at MIE 2011.

The XXIII International Conference of the European Federation for Medical Informatics was held on 28-31 August in Oslo (Norway) attracting more than 650 participants. It is the main scientific event in medical, biomedical, and health informatics, annually held in Europe.



The INBIOMEDvision project held a successful workshop at MIE2011 on 31 August, 2011, where European experts presented new advances on Biomedical Informatics and the challenges bound with this discipline. The workshop was fully aligned with one of the main objectives of INBIOMEDvision: the dissemination of the Biomedical Informatics concepts, knowledge and resources, and the consolidation of a multidisciplinary community of researchers, by means of congregating and promoting interaction between scientists from a wide range of related fields.

In addition, the workshop showed examples of computational methods and tools that connect biological systems described at the molecular level with the clinical physiopathology and the extension of the electronic healthcare record concept in order to incorporate new information types, such as these resulting from "omics" technologies which contribute to the further development of personalized medicine. Workshop's speakers—representatives of the different partners of the project, presented their point of view about Biomedical Informatics, taking in account different perspectives. The speakers and titles of their presentations:

- **Prof. Ferran Sanz** from Universitat Pompeu Fabra (Spain): "Integrative Biomedical Informatics: general concepts and particular examples in the pharmaceutical field"
- **Prof. Søren Brunak** from Danish Technical University (Denmark): "Extracting information from electronic patient records"
- **Dr. Victoria López-Alonso** from Instituto de Salud Carlos III (Spain): "Translational Bioinformatics: infectious diseases as a case study"

For more information about this event, please visit: <http://www.inbiomedvision.eu/PDF%5CWorkshopMIE.pdf>

Within its dissemination activities, the INBIOMEDvision project:

- ✓ *Communicates and disseminates findings and results to external groups and professionals*
- ✓ *Spreads the knowledge generated to relevant target groups, such as scientists, technologists, healthcare professionals, authorities, industry and citizens in Europe but also all over the world*
- ✓ *Fosters the strengthening of the European scientific community in the area*



INBIOMEDvision Training Challenge2012: Call for students applications now open

The *Training Challenge* is a training format originally promoted by the Network of Excellence INFOBIOMED (<http://www.infobiomed.org/>) in which two teams of students from several European countries, with widely varying but complementary backgrounds relevant to Biomedical Informatics, participate. Each team works during one week on the basis of a single case study related to a specific research problem related to Biomedical Informatics.



The INBIOMEDvision 2012 Training Challenge will be held in a relatively isolated location which allows teams to work intensely with the continuous guidance of experts-tutors. At the end of the Training Challenge, teams present their work in front of a jury. The Training Challenge is a truly innovative training format which takes into account the multidisciplinary nature involved in INBIOMEDvision and promotes cross-talk between disciplines in order to advance towards a more personalised healthcare.

Next Issue of the Newsletter

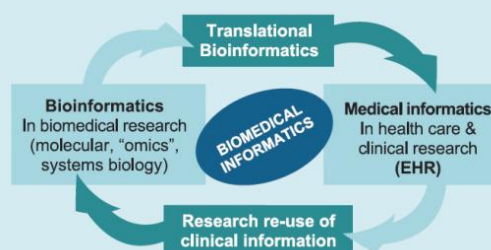
Work Package focus (WP4):

The INBIOMEDvision Training Challenge

For more and application form, please visit www.inbiomedvision.eu.

ISMB-ECCB 2011

On the 18-19 July 2011, in Vienna, INBIOMEDvision members participated in the ISMB-ECCB 2011, the 19th Annual International Conference on Intelligent Systems for Molecular Biology (<https://www.iscb.org/ismbeccb2011>) which is the major meeting of the International Society for Computational Biology. ISMB/ECCB brings together scientists from computer science, molecular biology, mathematics, statistics and related fields. Building on past successes, the Vienna conference was designed to cater to variety of disciplines within the bioinformatics/computational biology community.

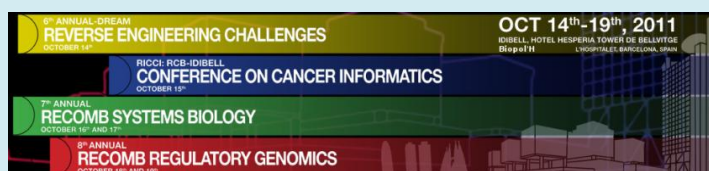


During the conference's poster session, the main project objectives and activities were presented to a broader audience by Dr. **Miguel Ángel Mayer**, from UPF (Universitat Pompeu Fabra).

More information about this event can be found at: <http://www.iscb.org/ismbeccb2011>

RECOMB DREAM 2011

On 14-19 October, 2011, in Barcelona, the 6th Annual DREAM on Reverse Engineering Challenges, the 7th Annual RECOMB Satellite on Systems Biology, and the 8th Annual RECOMB Satellite on Regulatory Genomics



will be jointly held. INBIOMEDvision acts as co-organizer and sponsor of this event and organises a special Think Tank session on Translational Systems Biology and Bioinformatics on the 17 Oct within the RECOMB Systems Biology.

The main objective of the INBIOMEDvision consortium here is to strengthen the Biomedical Informatics community by addressing issues of common concern that affect European research groups, such as research infrastructures, resources, training and dissemination, with an emphasis on interdisciplinary and new trends.

I-Health 2011

I-Health 2011 will take place from 3 to 4 October 2011 in Brussels, bringing together health, science and information technology groups. INBIOMEDvision is one of the sponsors and co-organizers of this forum for discussion and dissemination. Interdisciplinary aspects -- like how informatics can deliver new research data and knowledge to patients, doctors, and other healthcare stakeholders -- will open the workshop to a wider community of biomedical and computer scientists. The workshop programme can be downloaded [here](#).



BMI News Round-Up

- ✓ Five Member States give safeguarding biological information the green light: An EU-funded pan-European initiative to operate a sustainable infrastructure for managing and safeguarding biological information in Europe. [More...](#)
- ✓ The AMIA 2011 Annual Symposium will take place in Washington DC on 22-26 October, 2011. [More...](#)
- ✓ Health 2.0 Europe will be held on 27-28 October 2011, in Berlin (Germany): over 35 speakers already confirmed. [More...](#)
- ✓ The Virtual Physiological Human Network of Excellence will hold the second of the series of VPH Conferences on 18–20 September 2012. [More...](#)
- ✓ Call for Papers: 2012 World of Health IT & eHealth Week 2012. [More...](#)
- ✓ VPH/Physiome in IEEE Transactions on Medical Imaging: Special Issue on Medical Imaging in Computational Physiology (January 2013). [More...](#)
- ✓ More Studies Assessing Quality Improvement Using Electronic Health Records. [More...](#)



Upcoming Events

The calendar of upcoming events of the project includes project activities, consortium meetings and scientific events.

- I-Health Conference, Brussels** 3 - 4 October
- Think Tank Genotype-phenotype resources, Brussels** 5 October
- RECOMB::DREAM 2011, Barcelona** 14 - 19 October
- Think Tank Translational Systems Biology and Bioinformatics, Barcelona** 17 October
- 3rd Consortium Meeting, Barcelona** 18 October
- 4th Consortium Meeting, Madrid** 16 December

October 2011						
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31						

- Project ID Card -

- **Objective:** Virtual Physiological Human (ICT-2009.5.3)
- **Grant Agreement n° 270107**
- **EU contribution:** 998.000 euro
- **Duration:** 1 February 2011 - 31 January 2013 (24 months)
- **Funding scheme:** Coordination and support actions
- **Project management and coordination:**
 - Ferran Sanz (UPF), Scientific Co-ordination
 - Carlos Díaz (FIMIM), Project Management
- **Core partners:**
 - Søren Brunak (DTU)
 - Johan van der Lei (EMC)
 - Victor Maojo (UPM)
 - Victoria López Alonso (ISCIII)
 - Peter Coveney (UCL)

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November 2011						
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December 2011						
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