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1 Introduction

1.1 Purpose of this document

This report covers the organisation and participation by the INBIOMEDvision project in various scientific events, during the first 10-month period of the project (01/02/2011 - 30/11/2011). One major scientific event was co-organised by INBIOMEDvision, and another one sponsored, in October 2011. In addition, three Think tanks sessions were organised in June and October respectively, and various other contributions were made at national and international scientific events.

1.2 Project overview

INBIOMEDvision aims to monitor and promote the field of Biomedical Informatics (Sanz et al. 2011). Biomedical Informatics (BMI) is “the application of the science of information as data-plus-meaning, to problems of biomedical interest” (Bernstam et al., 2009). INBIOMEDvision is a European-wide initiative intended to monitor the evolution of the Biomedical Informatics field, and address its scientific challenges by means of collaborative efforts performed by a broad group of experts with complementary perspectives on the field. In order for the Biomedical Informatics field to evolve, it is necessary to disseminate relevant knowledge to a wide community of scientists, clinicians, authorities, industry and citizens throughout Europe and beyond, as well as encourage and actively forge networking in the community.

A key goal of INBIOMEDvision is to organise and deliver dissemination activities which address a wide scientific audience (the “stakeholders”), targeting researchers, clinicians, and R&D industrialists in various fields such as Biomedical Informatics, Medical Informatics, Bioinformatics, Systems Biology, Medical Imaging, Public Health Informatics, and Neuroinformatics, in addition to the community of the Virtual Physiological Human (Fenner et al. 2008). The types of dissemination activities include publications in scientific journals as well as organisation of and participation in relevant scientific events, which contribute to fostering collaborations among these different stakeholders.

In addition to engaging leading European and international experts in these scientific events, the INBIOMEDvision Consortium asked some of its Members1 to actively participate.

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1 To get the involvement of a wider scope of European Experts from relevant institutions, the Project has invited a group of experts from various fields related to BMI to become INBIOMEDvision Members and to participate in the Project activities, such as think tanks and scientific events.
2 Organisation of scientific events

2.1 Think Tank sessions

Three invitation-only Think Tanks were organised in June and October 2011, on the “Re-use of Clinical Information in Research” (24th of June, London), “Genotype-Phenotype Resources” (5th of October, Brussels), and “Translational Systems Biology and Bioinformatics” (17th of October, Barcelona). The Think Tanks were followed by the preparation of consensus-view strategic reports aimed at the European Commission as well as the wider scientific community.

2.1.1 Think Tank on Re-use of Clinical Information in Research

This Think Tank, convened at UCL, was held jointly with a Clinical Workshop on the Implementation of Preventive, Predictive and Personalised Medicine. The Think Tank represented five hours of intensive discussions between 27 invited experts (5 of whom were INBIOMEDvision Members). These experts were drawn up from a wide range of backgrounds, including clinicians, physicians, engineers, medical scientists, IT directors within hospitals, industry representatives, and scientists active on translational research projects. It consisted of two sessions, IT considerations of Medical Informatics, and Exploiting Medical Data in Research. Areas covered in the sessions included data, IT security, information governance, and legal issues with regard to clinical data.

The first Think Tank report (deliverable D4.1, published online at www.inbiomedvision.eu) stated that a "digital vision" and agenda are needed within Europe, to cover the next five years and beyond. EU member states are urged to commit significant resources to this effort, and to adopt clear and fully aligned legal positions to allow the optimum re-use of data in research and to support clinical decision-making. This would substantially facilitate the digital revolution in healthcare provision that is urgently required. It is important to involve Internet-savvy "expert patients" and their families not only in their own treatment, but to actively contribute to basic biomedical research into their conditions.

2.1.2 Think Tank on Genotype-Phenotype Resources

This Think Tank, convened at Thon Hotel Brussels City Centre, Belgium was held following the I-Health 2011 Workshop (described in section 2.2). The Think Tank represented 4.5 hours of intensive discussions between 17 invited experts (6 of whom were INBIOMEDvision Members). These experts were drawn up from a wide range of backgrounds, including bioinformaticians, geneticists, engineers, pharma representatives, modellers, and scientists active on genotype-to-phenotype research projects. The Think Tank consisted of two sessions, State-of-the-art on Genotype-Phenotype Data Integration, and Challenges and Opportunities for a Better Set-up and Exploitation of Genotype-Phenotype Information Sources. Areas covered in the sessions included genotype and phenotype data, ontology and standardisation, data and text mining, genotype-phenotype integration, genotype-phenotype resources for clinical research exploitation, and future gene sequencing opportunities.
The second Think Tank report (in preparation) addresses prospects for the development and application of genotype-phenotype resources and considers these to be very promising. Establishing clear relationships (correlations) between increasing amounts of genotypic information available from clinical studies (e.g. as provided by genome wide association studies (GWAS)), and similarly of phenotype information at the population level, is still largely impossible today. Also, assuming that the genotype controls the phenotype in all cases is unlikely to be correct. Indeed there are rather general grounds for thinking that, making any trivial correlations will always be fraught with difficulty. This can also assist in “stratification” – instead of rejecting so many drugs, it could be that several existing ones will work well for sets of patients on genetic grounds.

### 2.1.3 Think Tank on Translational Systems Biology and Bioinformatics

This Think Tank, convened at the Hospital de Llobregat, Spain was held following the RECOMB::DREAM 2011 Conference (described in section 4.1). The Think Tank represented 2.5 hours of intensive discussions between 23 invited experts (1 of whom was an INBIOMEDvision Member). These experts were drawn up from a wide range of backgrounds, including bioinformaticians, geneticists, engineers, modellers, system biologists, medical doctors, and scientists active on translational medicine research projects. The Think Tank consisted of two sessions, Application of Systems Biology to Medicine, and Reliability, Reproducibility and Verification of Computational Models. In each session, two key statements were given, which were later followed by a discussion. Key statements were given by Prof. Andrea Califano (Columbia University, USA), Prof. David Selwood (University College London, UK), Dr. Gustavo Stolovitzky (IBM Computational Biology Center, USA), and Prof. Dr. Jaap Heringa (Free University, The Netherlands).

The third Think Tank report (in preparation) sees potential in sub-cellular (or molecular) systems biology approaches to biomedicine, as compared to conventional methods of drug design. Despite these approaches being at an infant state, and a vast amount of research remains to be done, they may be able to assist in more personalised approaches to drug treatment, for example in the use of multi-target therapy, for finding genotype association to risk of disease and drug response. For translational systems biology to make a major impact, the whole system of data access (including access to medical records) needs to be transformed into one based on more openness and sharing of information between hospitals, academia and industry. Various societal structures currently impede this development. Regulatory and funding agencies must be involved to overcome these obstacles.
2.2 I-Health 2011

2.2.1 Overview

I-Health 2011 ([http://www.gen2phen.org/i-health2011/](http://www.gen2phen.org/i-health2011/)), took place on 3-4 October in Brussels, and was concerned with the “full integration of research and healthcare by IT innovations” (Figure 2). This was a two-day workshop with 59 invited delegates convened at the Thon Hotel Brussels City Centre in Belgium.


The main organiser GEN2PHEN is a large-scale international project funded by the European Commission under Framework Programme 7, with one of its principle aims to unify human and model organism genetic variation databases in order to directly link Genotype-to-Phenotype data, and from that into other biomedical knowledge sources.

UKIERI aims to enhance educational links between India and the UK.

![Figure 1 I-Health 2011 sponsors](http://www.gen2phen.org/i-health2011/)

The organising committee was composed of:

**Prof. Anthony J. Brookes**, Chair in Genomics and Bioinformatics and Director of the ‘NUCLEUS’ Genomics Services Facility at the University of Leicester, scientific co-ordinator of the GEN2PHEN project, Science Advisor to FP7 IP "European Sequencing & Genotyping Infrastructure, Member of the International Steering Committee of P3G, Member of ORCID (Open Researcher & Contributor ID) Technical Working Group, Editor for Genomic Medicine (HUGO Journal) & Chair of its Publications Committee, Communicating Editor for Human Mutation, Founding Board member of the Human Variome Project (HVP), Co-Founder and Board Member of the Human Genome Variation Society, Chair of the founding member of the Human Variome Project, Communicating Editor for the journal Human Mutation, innovator and lead organiser of the annual 'Human Genome Variation' international meeting series, and
creator of the GWAS Central database of genetic association studies. Member of INBIOMEDvision.

Prof. Ferran Sanz, professor of biostatistics and biomedical informatics at University Pompeu Fabra (UPF) of Barcelona, director of the Research Unit on Biomedical Informatics (GRIB) of the IMIM and UPF, and vice-rector for Scientific Policy of UPF. Coordinator of INBIOMEDvision.

Dr. Debasis Dash, heads the Functional Genomics Unit, G.N. Ramachandran Knowledge Centre for Genome Informatics, Institute of Genomics and Integrative Biology, New Delhi, India.

Scientific Committee members were:

Prof. Søren Brunak, professor and director of the Center for Biological Sequence Analysis of Denmark Technical University, Partner of INBIOMEDvision.

Prof. Norbert Graf, medical director of the Department for Pediatric Hematology and Oncology at University Hospital of Saarland, and Chairman of the SIOP 2001/GPOH Trial on Nephroblastoma, dean for student affairs at the Faculty of Medicine of University of Saarland, Member of INBIOMEDvision. Member of INBIOMEDvision.

Prof. Heinz U. Lemke, professor of Computer Science (Computer Graphics and Computer Assisted Medicine) at the Technical University Berlin, deputy editor of Academic Radiology, Editor-in-Chief of the International Journal of Computer Assisted Radiology and Surgery (CARS), visiting professor and senior advisor of Research Strategies for the Innovation Center of Computer Assisted Surgery at University of Leipzig, Germany, research professor of Radiology at University of Southern California, USA.

2.2.2 Event Summary

During I-Health 2011, health, science and information technology groups were brought together to address the question of how informatics can deliver new research data and knowledge to patients, doctors, and other healthcare stakeholders, particularly in the emerging era of personalised medicine. This is important so as to bridge between traditional research bioinformatics and current activities in the realm of e-Health.

The workshop speakers explored the gaps in current Information and Communication Technologies (ICT) that lie at the heart of the I-Health challenge, discussing with the attendees possible solutions. It was agreed that research and healthcare informatics cannot be ‘stretched’ to form a continuum, but instead a radically new scientific and technological discipline is needed to link the two and move towards optimising personal, patient and community health. Such a system would intelligently locate, distill, and repurpose all the key biomedical knowledge and models, framed ultimately in the specific context of group or individual level clinical decision support (a form of ‘health avatar’ for each patient), and then place this at the fingertips of doctors, patients, the public and many other stakeholders, in a real-time and multi-lingual format that they can use. It would simultaneously facilitate research use of extensive clinical data, probably accessed from electronic healthcare records using various privacy protecting interrogation technologies.
Figure 2 The integration of research and healthcare ICT is needed and will bring many benefits. This connection is generally assumed to be achievable by extending each of these areas of ICT in a merged effort termed BioMedical informatics, but this may not be sufficient (http://www.gen2phen.org/i-health2011).

2.2.3 Summary of Key Statements

Monday October 3rd

Introduction and Welcome

The day began with an introduction and welcome by Anthony Brookes (Leicester), who explained GEN2PHEN’s goals of integrating bioinformatics and medical ICT by further understanding Electronic Health Records (EHRs), diagnostics and decision-making, modelling and statistics, and data integration/semantics.

Session 1: Research and healthcare data: what is available?

Andrew Devereau (National Genetics Reference Laboratories, Manchester, UK) stated what research and healthcare data are most easily available today, the most prominent of which are related to the mainly conventional bioinformatics data. Devereau discussed the standardisation, sharing, quality and consent issues of such data, establishing the challenges we can expect in the future as it is made increasingly available for research and clinical decision-making.

Session 2: Identifying new and improved capabilities

Norbert Graf (University of Saarland) led the second session, addressing how I-Health should develop. He warned that there is a value conflict between a patient’s personal interest and the society’s collective interest. A frequent conflict arises with connecting patient’s privacy (data confidentiality) and data access. Graf noted that the cost of interpreting -omics data will soon be more than the cost of generating the data itself. This is known as the “$1000 genome, $100,000
analysis” problem (Mardis, 2010). Graf also asserted that there is a need for approaches based on systems biology to continue to be developed, towards an increasingly complete understanding of biology, health, and disease, and computational models thereof (such as promoted by the Virtual Physiological Human initiative).

Session 3: Information required for translational research

Hans Lehrach (Max Planck Institute for Molecular Genetics) held the third session of the day on Information required for translational research, where he discussed the various levels required to achieve this, both molecular/cellular/tissue/organ/man/population and environmental.

Session 4: Information required for personalised healthcare

Mihaela Ulieru (IMPACT Institute for the Digital Economy) stated in this session that the information required for personalised healthcare is not purely based on “holistic” community based guidelines, but has a specific relevance to the individual. She suggested that research today is much more aligned with the future directions of personalised medicine, rather than contemporary healthcare needs, which are still at a regressive stage. Ulieru discussed the challenges that exist to make enormous amounts of data available to the scientific community. She asserted that we should shift the focus from diseases to wellness.

The session closed with statements by Allan Hanbury (PRIP) and Erkki Leego (IT Head of the Biobank, Estonia). Hanbury stated that we should develop new tools to provide access to interesting new research, while Leego discussed the state of personalised medicine in Estonia.

Tuesday October 4th

Session 5: Standards required for bridging bioinformatics and e-Health

Søren Brunak (Denmark Technical University) opened this session by discussing the immense cost of analysing genomic data, even if the cost of reading genomes was brought down to less than $1000. He noted that standards are needed to facilitate the integration of bioinformatics, systems biology and medical informatics.

Peter Robinson (Institute for Medical Genetics, Charite Universitätsmedizin Berlin) then covered e-Health for Genomic Medicine, access to data for research, and the need for portals to integrate and present data coherently. Robinson addressed the need for semantically marked up EHRs for improved searching and analysis. He noted that EHRs are tools for studying co-morbidity and other clinical parameters and can be used to identify patients for studies.

This was followed by a presentation from Denise Downs (NHS Department of Health Informatics Directorate, UK). Downs stated that in the UK, EHR will be based on a common terminology, that of SNOMED CT (which stands for Systematized Nomenclature of Medicine Clinical Terms, http://www.connectingforhealth.nhs.uk/systemsandservices/data/uktc/). She noted that clinicians prefer to use their own shortcuts and they do not yet see the benefit of doing the extra work of using a common terminology, especially when having to enter data while seeing patients (i.e. in a limited amount of time). She stated that the NHS plans to support back-mapping of past patients’ records in several surgeries from the standard World Health Organisation ICD 10 (International Classification of diseases) to SNOMED CT.
The session closed with a statement by Mauno Vihinen (Institute of Medical Technology), who described the need for effective ontology and exchange format standards, such as Vario and Vario-ML now being developed.

Session 6: Various types of modelling in personalised medicine

Heinz U. Lemke (Technical University Berlin) opened the sixth session by commenting on systems biology in research; one claim by this community is that they will develop multi-scale multi-level models, thereby integrate systems biology. He noted that in healthcare, modelling takes place in a doctor’s head. Lemke’s view is to adopt a middle way approach: i.e. to use computers but build from clinical knowledge. He noted that modelling is one of the overall components to achieve personalised medicine, but the full view requires use of graph-theoretic approaches in which modelling is only one element.

The session closed with a statement by Peter Coveney (University College London), who suggested we need to understand the correlations between the multi-levels, rather than assume the genome unlocks everything about personalised medicine.

Corrado Priami (COSBI, Italy) and Henning Müller (University of Applied Sciences, Switzerland) rounded out this session with perspectives from their own salient areas of work, namely algorithmic modelling/simulation, and complex information retrieval/visualization respectively.

Session 7: Security/access technologies

The seventh session was held by Simona Rossi (Experimental Therapeutics and Cancer Genetics, Swiss Institute of Bioinformatics) who discussed the EU FP7 p-medicine project http://www.p-medicine.eu, and issues of identity management in virtual organisations, authentication and usability, privacy protection for e-Health applications, privacy-enhancing techniques in medicine, as well as good clinical practice and security.

Session 8: Funding and sustainability issues

The eighth and final session followed on with Debasis Dash (Institute of Genomics & Integrative Biology) discussing sustainable development of I-Health, meeting needs of the present without compromising capabilities of the future. He noted that, from a research point of view, it has to be translational, affordable and with a dimension that promotes networking. On funding, Debasis proposed the creation of global scale interdisciplinary networks. He asserted that there should be a focus on short-term value creation for physicians and patients.

Next Steps

Anthony Brookes discussed with the delegates the importance of the I-Health Challenge. There was an agreement that he would lead the write up of a technical report, with contributions from the delegates.
3 Participation in scientific events

3.1 MIE 2011

**Workshop** INBIOMEDvision: Promoting and Monitoring Biomedical Informatics in Europe
Ferran Sanz, Søren Brunak, and Victoria Lopez-Alonso

The workshop held at MIE 2011 was fully aligned with one of the main objectives of INBIOMEDvision, dissemination of the Biomedical Informatics knowledge and resources, and the consolidation of a Biomedical Informatics community of researchers, by congregating and promoting interaction between scientists from a wide range of related fields.

The workshop consisted of three presentations, summarised below

**Speaker 1: Ferran Sanz.** IMIM-Hospital del Mar, Pompeu Fabra University. General introduction on INBIOMEDvision concepts and activities.

A Biomedical informatics approach for bridging gaps between Bioinformatics and Medical informatics was presented to build on fostering Translational Bioinformatics (from Bioinformatics to health care and clinical research), and reuse of clinical information (e.g. electronic health records) in biomedical research. Biomedical Informatics was thus defined to deal with the integrative management and synergic exploitation of the wide and inter-related scope of information that is generated and needed in healthcare settings, biomedical research institutions and health-related industry. Example from the field of pharmacovigilance (EU-ADR project, http://www.alert-project.org/) was presented, and current biomedical Informatics challenges highlighted.

**Speaker 2: Søren Brunak.** Center for Biological Sequence Analysis. Dept. of Systems Biology, Technical University of Denmark. Perspectives in Medical Informatics in the interface to genomics and systems biology.

Electronic patient records remain a rather unexplored, but potentially rich data source for discovering correlations between diseases. The presentation described a general approach for gathering phenotypic descriptions of patients from medical records in a systematic and non-cohort dependent manner. By extracting phenotype information from the free-text in such records this work demonstrates that we can extend the information contained in the structured record data, and use it for producing fine-grained patient stratification and disease co-occurrence statistics. The approach uses a dictionary based on the International Classification of Disease ontology and is therefore in principle language independent. As a use case it was

**Speaker 3: Victoria López-Alonso. Carlos III Institute of Health (ISCIII), Madrid. Bioinformatics challenges in a personalised medicine pipeline.**

The presentation gave an overview on personalised medicine. Currently Translational bioinformatics uses computational tools for the analysis of large biological databases and intends to fully comprehend disease mechanisms by not only understanding the genetics and the proteomics but also by associating them with the clinical data. Specific Bioinformatics challenges for personalized medicine were identified: i) processing large-scale genomic data, ii) interpretation of functional effect of genomic variation, iii) integration of systems data, and iv) translation into medical practice.

### 3.2 ISMB/ECCB 2011

**Poster** INBIOMEDvision: Promoting and Monitoring Biomedical Informatics in Europe

Miguel Ángel Mayer on behalf of the INBIOMEDvision Consortium

The annual international conference on Intelligent Systems for Molecular Biology (ISMB) is the major meeting of the International Society for Computational Biology (ISCB).

The poster presented the project’s main goals and operational objectives:
INBIO MEDvision participation to the conference was a success taking into account the good turnout and the large number of scientific activities carried out.

The importance of an integrative approach in helping to bridge the gaps between the different scientific areas and activities carried out by the project were presented to researchers from a wide range of disciplines as ISMB/ECCB 2011 brought together scientists from molecular biology, biology, medicine, computer science, mathematics, and statistics fields.
3.3 Enabling Systems Biology Conference

Enabling Systems Biology Conference
University College London, UK. April 11th – 14th, 2011

Poster INBIOMEDvision: Promoting and Monitoring Biomedical Informatics in Europe

Nour Shublaq on behalf of the INBIOMEDvision Consortium

This conference gathered the current expertise in data integration and systems biology approaches to tackle four domains of research: cell cycle, cellular signalling, metabolism and stem cells.

A workshop was also planned to allow participants to practice various bioinformatics tools aimed at analysing and integrating biological data.

Figure 4 INBIOMEDvision poster at Enabling Systems Biology Conference
In addition to these international events, the INBIOMEDvision project was presented by Nour Shublaq at the EBI “Foundations for Biomedical Data and Model Interoperability” Workshop, an event organised by the European Bioinformatics Institute in Hinxton, Cambridgeshire (March 28th-29th, 2011), as well as the Virtual Physiological Human Toolkit Meeting (March 29th-30th, 2011). It was also featured in the COMBIOMED "IV International Symposium of Biomedical Informatics in Europe" in A Coruña, Spain (June 6th, 2011), and at the Welcome Trust “Applied Bioinformatics and Public Health Microbiology 2011” Scientific Conference, an event organised by the Welcome Trust in the Welcome Trust Genome Campus, in Hinxton, Cambridgeshire (June 1st-3rd, 2011) and at the Ibero-NBIC Network annual meeting in Aveiro, (October 10th-11th, 2011) by Guillermo López Campos.

4 Sponsorship

4.1 RECOMB::DREAM 2011

RECOMB::DREAM 2011 (http://recomb-dream2011.org/index.php/recomb2011/recombdream2011/index.html) was a six-day conference held on 14-19 October at the Hesperia Tower, Bellvitge, Barcelona. It brought together computational and experimental scientists in the areas of regulatory genomics and systems biology, to discuss current research directions, latest findings, and establish new collaborations towards a systems-level understanding of gene regulation, with particular emphasis on cancer.

The conference combined the 6th Annual DREAM on Reverse Engineering Challenges (14 October), the 7th Annual RECOMB Satellite on Systems Biology (16-17 October), the 8th Annual RECOMB Satellite on Regulatory Genomics (18-19 October), and the IDIBELL Conference on Cancer Informatics (RICCI) (15 October) (Figure 5).

Figure 5 Four meetings within RECOMB::DREAM 2011
There were 101 oral presentations of which 23 were keynote, and 60 poster presentations. The conference partnered with Genome Research and the Journal of Computational Biology to review 33 full-length papers that were presented as oral presentations at the conference. The third Think Tank (Translational Systems Biology and Bioinformatics) was organised in the framework of the RECOMB Systems Biology meeting, where INBIOMEDvision sponsored participation of Keynote speakers at the Think Tank session on the 17th October. Altogether RECOMB::DREAM 2011 was sponsored by 18 organisations.

The total number of people who registered for the conference this year was 224, with 177 registering for RECOMB Regulatory Genomics, 193 for RECOMB Systems Biology, 114 for DREAM, and 151 for RICCI.

Organisers

Manel Esteller, director of the Cancer Epigenetics and Biology Programme, IDIBELL, leader of the Cancer Epigenetics Group, professor of Genetics in the School of Medicine of University of Barcelona, and research professor at the Catalan Institution for Research and Advanced Studies (ICREA)

Gabriel Capellá, IDIBELL scientific director and director of the Hereditary Cancer Programme of ICO and IDIBELL

Roderic Guigó, coordinator for the Bioinformatics and Genomics Program of the Center for Genomic Regulation, Barcelona

Núria López-Bigas, head of Biomedical Genomics laboratory of GRIB (IMIM-UPF), University Pompeu Fabra

Miguel Angel Pujana, group Leader at Catalan ICO, IDIBELL

Chairs

The four sub-conferences of RECOMB::DREAM 2011 were each chaired by a distinguished scientist as specified below.

RECOMB Systems Biology Chair: Andrea Califano, professor of systems biology in Biomedical Informatics and the Institute for Cancer Genetics, chief of the Division of Biomedical Informatics, director of the Columbia Initiative in Systems Biology, director of the Center for Multiscale Analysis of Genomic Networks, associate director for Bioinformatics, Herbert Irving Comprehensive Cancer Center

RECOMB Regulatory Genomics Chair: Manolis Kellis, associate professor of Computer Science at MIT, director of the MIT Computational Biology Group of the Broad Institute of MIT and Harvard

RICCI Chair: Miguel Angel Pujana, group leader at Catalan Institute of Oncology, IDIBELL
DREAM Chair: Gustavo Stolovitzky, manager, IBM Functional Genomics and Systems Biology Group, IBM Research

Summary of Key Talks

6th Annual DREAM Reverse Engineering Challenges

Ewan Birney, European Bioinformatics Institute, Wellcome Trust Genome Campus, Cambridge, UK. ENCODE: “Understanding our genome”.

Edda Klipp, Humboldt-Universitat zu Berlin. “Cellular stress response on different levels: Zooming in and out in networks”.

RICCI: RCB-IDIBELL Conference on Cancer Informatics

Raymond Cho, Department of Dermatology, University of California, San Francisco, USA. “Temporal dissection of tumorigenesis in primary cancers”.


Núria López-Bigas, Research Unit on Biomedical Informatics, Department of Experimental and Health Sciences, University Pompeu Fabra, Barcelona, Spain. “Integration and data-mining of multidimensional oncogenic data”.

Franziska Michor, Department of Biostatistics and Computational Biology, Dana-Farber Cancer Institute, Harvard School of Public Health, Boston, USA. “Evolution of the cancer genome”.

Dana Pe’er, Department of Biological Sciences, Center for Computational Biology and Bioinformatics, Columbia University, New York, USA. “On the road to personalized therapy, a systems approach”.

Julio Sáez-Rodríguez, European Bioinformatics Institute, Welcome Trust Genome Campus, Cambridge, UK. “Comparative logical models of signalling networks in normal and transformed hepatocytes”.

Gustavo Stolovitzky, IBM Computational Biology Center, Yorktown Heights, USA. “Quantitative modeling of the terminal differentiation of B cells and mechanisms of lymphomagenesis”.

Alfonso Valencia, Structural Bioinformatics Group, Spanish National Cancer Research Centre, Madrid, Spain. “Bioinformatics in personalized cancer medicine”.

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7th Annual RECOMB Systems Biology

Scott Armstrong, Division of Hematology/Oncology, Children’s Hospital of Boston. Harvard Stem Cell Institute, Harvard Medical School, USA. “Gene expression and epigenetic programs in leukemia stem cell development”.

Barry Honig, Department of Biochemistry and Molecular Biophysics. Center for Computational Biology and Bioinformatics. Howard Hughes Medical Institute, Columbia University, New York, USA. “Structure-based prediction of protein-protein interactions on a genome-wide scale”.

Manolis Kellis, Computer Science and Artificial Intelligence Laboratory, Massachusetts Institute of Technology, The Broad Institute, Cambridge, USA. “Epigenomic views of complex disease associations reveal thousands of causal SNPs”.

Rune Linding, Center for Biological Sequence Analysis, Technical University of Denmark, Denmark. “Modelling of cancer kinome network”.

Sylvia Plevritis, Department of Radiology, Stanford University, Stanford, USA. “Inferring biological progression from high dimensional data”.

Luis Serrano, Systems Biology Research Unit, European Molecular Biology Laboratory, Center for Genomic Regulation, Barcelona, Spain. “A quantitative systems biology study on a model bacterium”.

Dennis Vitkup, Center for Computational Biology and Bioinformatics, Department of Biomedical Informatics, Columbia University, New York, USA. “Systems biology of autism and schizophrenia”.

8th Annual RECOMB Regulatory Genomics

Martha L. Bulyk, Brigham & Women’s Hospital, Harvard-MIT Division of Health Sciences and Technology, Harvard Medical School, Boston, USA. “Transcription factors and DNA regulatory elements”.

Andrea Califano, Center for Computational Biology & Bioinformatics, Department of Biomedical Informatics. Columbia University, New York, USA. “MicroRNA-mediated regulation accounts for missing genetic variability in cancer”.

Eileen Furlong, Genome Biology Unit, European Molecular Biology Laboratory, Heidelberg, Germany. “Making global predictions of cis-regulatory activity”.

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Jonathan Pritchard, Department of Human Genetics, Howard Hughes Medical Institute, University of Chicago, Chicago, USA. “Variation in chromatin accessibility is a key determinant of heritable variation in gene expression”.

Alexander Stark, Institute of Molecular Pathology, Vienna, Austria. “Regulatory genomics in Drosophila”.

Gary Stormo, Washington University School of Medicine, St. Louis, USA. “Predicting DNA-binding specificity from protein sequence”.

5 Future Plans

Co-organisation of I-Health 2011 and sponsorship of RECOMB::DREAM 2011 allowed interactions with various other communities such as GEN2PHEN, UKIERI, RECOMB and DREAM teams, and acted as a platform to open dialogue and engage in discussions with a view to evolve the field of Biomedical Informatics, through creation and dissemination of knowledge and increased networking between scientists in related fields.

As agreed during the I-Health 2011 workshop, a database was produced for the community containing the details of experts working in the "I-Health" field. It is hoped that this interdisciplinary network can be used as a robust starting point for finding collaborations and funding. During the workshop, several delegates independently suggested the name for this network hence the creation of "I4Health" http://www.i4health.eu and its mailing list mailing-list@i4health.eu, where "I4" represents the Integration and Interpretation of Information for Individualised Healthcare.

For RECOMB::DREAM 2011, there is a possibility to publish selected papers from the event (e.g. in theme issues of the Philosophical Transactions of the Royal Society A’s journal or Journal of the Royal Society Interface Focus), and to invite writers of particularly highly rated contributions to submit full papers for inclusion in the journal.
REFERENCES

- Elaine R. Mardis, “The $1,000 genome, the $100,000 analysis?”, Genome Medicine, 2(84), (2010)