

INFOBIOMED

NEWSLETTER

N.4 DECEMBER 2005



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**BIOMEDICAL INFORMATICS
TO SUPPORT INDIVIDUALISED HEALTHCARE**

PORT INDIVIDUALISED HEALTHCARE

SUMMARY

NEWS

Genomic commonality between tuberculosis and leprosy: study
Setting the standard for computer models of life
TCGA - The Cancer Genome Atlas Pilot Launched
Scientists Close In On Genes Responsible For Parkinson's Disease
EU consortium Polygene
Cancer Scientists Lobby for Human Epigenome Project

PG. 2

pg. 2
pg. 2
pg. 3
pg. 4
pg. 4
pg. 5

INFOBIOMED PROFILES

The Danish HNPCC-register
FORTH

PG. 6

pg. 6
pg. 7

RESOURCES

The DrugBank database
Inside DNA
GFINDER New modules

PG. 8

pg. 8
pg. 8
pg. 9

EVENTS

PG. 10

BMI INITIATIVES IN EUROPE

PG. 11

NEWS

Genomic commonality between tuberculosis and leprosy: study

<http://www.hinduonnet.com/thehindu/thscrip/print.pl?file=2005121314400100.htm&date=2005/12/13/&prd=th&>

Source: The Hindu 13/12/05

The Department of Immunology in Madurai Kamaraj University (MKU) is studying the human genetic predisposition for tuberculosis and leprosy. This Department developed an immunogenetic study that reveals the existence of genes involved both in tuberculosis and leprosy.

Rm. Pitchappan, Professor and Head of the Department of Immunology-MKU said in an interview to *the Hindu* that the first phase of the study is nearly to finish, and it will continue with micro-array technology. He also said, "Once we understand the genes, it becomes easier to develop drugs and launch an effective diagnostic methodology" and mentioned that the results till now point towards genomic commonality between TB and leprosy.

This study will provide a better understanding of tuberculosis, and may lead an early diagnosis and prognosis of the disease.

Dr. Pitchappan and his collaborators include in their study the whole genome scan of 250 leprosy families from Kumbakonam and Erode.

In order to advance in the research they will include the micro-array technology in such a way that 20,000 human genes can be studied simultaneously.

Developed in parallel, Hospital St. Louis University of Paris also carried out a tuberculosis specific study, for which the Indian Council for Medical Research (ICMR) provided a part of the funds.

The cost of the genetic study of 300 patients from Madurai from blood and sputum tests using state-of-art technology supposes a cost of 400 US Dollars for each patient.

Meanwhile, the University Grants Commission and Centre for Potential in Genomic Sciences, MKU, is collaborating with the Department of Immunology that is now hosting a workshop (from Dec. 5 to 16) on "micro-array".

Setting the standard for computer models of life

<http://www.bioinformaticsforumuk.net/?nav=newsitem.tem/IJE9BR51>

Source: UK Bioinformatics Forum. EMBL-EBI Press Release. 08/12/05

Nature Biotechnology published in December 6th the proposal from 14 different organizations around the world, including the EMBL-European Bioinformatics Institute, that described a new quality standard for biochemical models: MIRIAM (for Minimum information requested in the annotation of biochemical models) that would facilitate researches the use of computer models of biochemical processes and thus providing them with a better understanding of life at the molecular and cellular level.

Many biology researches concentrate their efforts in cataloguing all the molecular and even atomic components of the living things to be able to create computational models that can reproduce or simulate living processes in order to built more complex combining models that would explain faithfully the global function of biological systems, including cells, organs, organisms or ecological niches. These approaches have many applications like the optimization of the treatments and also many diseases would be simulated.

"The computational systems biology community has made enormous progress in improving access to models," explains the EMBL-EBI's Nicolas Le Novère, lead author of the paper. "We've begun to share programming languages for encoding them (e.g. systems biology markup language, www.sbml.org) and to build public repositories so we can share them (e.g. www.ebi.ac.uk/biomodels). The current challenge is quality control: systems biologists won't use publicly available models if they can't search them properly, or if a model's reuse is hampered by a tiny mistake in the way that it's encoded. MIRIAM is an attempt to address these issues."

MIRIAM is divided in to parts: the first one checks the match of the model to its description, in other

words, its provenance (who created it, whether it's been modified, and a stable link to its full description). The second one is a set of schemes that links the components of the model to relevant bioinformatics resources in a such way that facilitates the search of models on the basis of their components, to contact the creators of the model if they need more information, and to track the history of a model if it has been modified.

The four major repositories for models: BioModels Database, Cell MLModel Repository, DOQCS and SigPath are actually working in the process of making the models in their repositories MIRIAM compliant. "By adopting MIRIAM as a voluntary code of conduct, we will be able to provide our users with a reasonable level of quality assurance, so they'll be able to get on with the business of generating and testing new hypotheses instead of recoding someone else's old hypothesis," continues Le Novère. "We also hope that journal editors will adopt MIRIAM as a quality control measure for papers that describe models.

This approach has worked very well for other fields - for example the microarray community, by enabling authors, publishers and data providers to work together to improve access to meaningful biological information."

TCGA - The Cancer Genome Atlas Pilot Launched

<http://www.bio-itworld.com/newsitems/-2005/dec2005/12-13-05-news-tcga?page:int=-1>

Source: Bio-IT World.com 19/12/05

The National Cancer Institute (NCI) and the National Human Genome Research Institute (NHGRI) announced in December 13th the launch of a three-year, \$100-million pilot program for the Human Cancer Genome Project (HCGP).

The researches have completed the genome sequence catalogues of more than 300 organisms: the Human Genome Project (HGP) finished 30 months ago and it also includes first drafts of the dogs and chimpanzees done this year.

Although the complete inventory of human genes does not provide itself a huge advance in the

understanding of molecular biology of cancer, many senior U.S. researches have publicly positioned launching a more ambitious cancer genome project derives from the medical necessity since there exists a high mortality associated with the cancer in USA.

Eric Lander, Broad Institute director, Harold Varmus, NIH director and others have promoted in this year the survey of 250 genome samples from each of 250 tumour types, producing a comprehensive catalogue of cancer-causing mutations. This way, the HCGP will last for 9 years and will cost \$1.3 billion becoming the most ambitious project in the study of mutations associated with cancer.

Francis Collins, NHGRI director, communicated in the National Press Club in Washington the creation of the project called "The Cancer Genome Atlas" (TCGA) that would provide a complete inventory of the genetic aberrations in cancer. Collins said that the unique collaboration between the NCI and the NHGRI would "*go beyond and behind the frontlines to create the first list of genomic insurgents that lead to cancer*". He also said that this audacious project would unite the "*powerful resources and experience of the [NCI], with the genome attitude of the [NHGRI]... Together, we've committed to investing \$100 million over the next three years to construct a powerful network of researchers, technology and resources to tackle the cancer problem like never before*".

Andrew Von Eschenbach, director of the NCI, said that the *TCGA pilot project would help make cancer a chronic manageable condition. "Mapping the cancer genome will be ... an important step in the understanding of the genetic component of the cancer process and the genetic susceptibility of people who are threatened by cancer"*.

The data generated by this project will be deposited in the public domain and they will be managed by the NIH Center for Bioinformatics and the NCI's cancer Biomedical Informatics Grid (caBIG). Much of the funding will go towards identifying better technologies and to encourage the small business community through SBIR programs.

In the next months the first tumor for this study will be selected, though it is necessary to delimit the limits that this project will reach.

Not all the investigators agree with this idea of the HCGP, Steve Elledge and Greg Hannon believe that the goal set will not be met and will take money away from more fruitful research. However other important researchers such as Harold Varmus, Nobel Prize laureate, and Bruce Stillman, director of Cold Spring Harbor Laboratory, support the project since they believe that it will bring about a better description of the genetic damage that is behind human cancers.

Collins is aware of the high cost of TCGA and he said that the cost of expanding the project from 2-3 tumors to 50 or more will be based on the experience of the next three years.

NIH Director Elias Zerhouni believes that these types of initiatives bring about opportunities for researchers.

Scientists Close In On Genes Responsible For Parkinson's Disease

Source: Bio.com – News & Features. 12/19/05

http://www.bio.com/newsfeatures/newsfeatures_research.jhtml?cid=15600017

Scientists from the Imperial College of London, UK and the University of Liege, Belgium, have recently published in Neurogenetics their study on Parkinson's disease, which involved the analysis of brains from 15 recently deceased patients and 8 controls. The researches employed microarray technology to examine for the first time, all human genes (25, 000) in these brains. The analysis revealed that people with Parkinson's had abnormal regulation of 570 genes when compared to those in controls'.

The work consisted in establishing the transcriptional expression profile of two of the main parts of the brain which are affected by neurodegeneration in Parkinson, the medial and lateral substantia nigra and the superior frontal cortex. In the for-

mer, which is the area of the brain most affected by this disease, researchers ruled out 15,000 genes that were not active in this area from having any role in this disease.

According to the Bio.com News Dr Linda Moran from Imperial College London and one of the authors of the paper pointed out that they had shown that there are a large number of genes associated with Parkinson's disease and that the application of this knowledge might aid in the search of a therapies for these patients.

Another author, Dawn Duke, MS, also from Imperial College London said: "*In addition to identifying those genes linked with the development of Parkinson's, this research has also shown that many of these genes were especially active in Parkinson's brains. By limiting the activity of these genes, we may be able to control or even stop the development of Parkinson's*".

EU consortium POLYGENE led by Iceland genomics corporation receives a 3m grant from the 6th framework programme to study inherited risk of breast and prostate cancer

http://www.huginonline.com/plsql/try/pressreleases.queryview?P_IDENTIFIER=1026484&p_la=5&p_web=5

The Icelandic cancer project instrumental in EU cancer discovery effort

Iceland Genomics Corporation ("IGC") announced December 19, 2005, that POLYGENE an EU consortium including IGC, Bioinformatics ApS of Denmark, the Department of Statistics at the University of Oxford, UK, and the Radboud University Nijmegen Medical Center of the Netherlands, has been awarded with 3 million Euros from the European Union 6th Framework Programme "to study the inherited risk of breast and prostate cancer". The project will not only include the study of the genetic causes but it will also "evaluate the combined effects of multiple

genes on differences in responses to therapy and disease outcome” of these two common cancers affecting women and men in Europe, breast and prostate cancer, respectively.

Cancer Scientists Lobby for Human Epigenome Project

<http://www.bio-itworld.com/newsitems/-2005/dec2005/12-15-05-news-epigenome>

Source: bio-IT World.com 15/12/05

A genome-wide project be launched to explore the large amount of chemical modifications to the genome or the epigenetic changes that affect the activity of specific genes and also they could be associated with genetic diseases like cancer.

The establishment of the international Human Epigenome Project, supported by 40 cancer experts in the field of epigenetics from the United States, Europe, and Japan, as well as representatives from Affymetrix, NimbleGen Systems, Orion Genomics, and Epigenomics AG in Germany, is published in December issue of journal Cancer Research. The proposal results from a June workshop held in Virginia and sponsored by the American Association for Cancer Research (AACR).

Since a lot of advances in technology have been arisen in science, many researches assert that “such an effort [the HEP] should be launched as soon as it is feasible” so that the role of epigenetics in the cause of cancer can be fully established.”

Andrew Feinberg of Johns Hopkins University said there has been “a groundswell of opinion from the community at large [for HEP], but nobody has decided at the upper levels that this is something they want to get behind.” He organized last November a workshop in order to clarify the most useful areas to invest in and he said that ideally, he and his colleagues would like to strive for “a 1-base resolution of DNA methylation and a comprehensive analysis of chromatin” and the more

specific studies of which the competition among industry would take charge.

Many others opinions support this project like Frank Rauscher, III, editor-in-chief of Cancer Research that said “It is time to create a concerted international effort to unlock the epigenomic information stored in our genome and use it for the benefit of human health” or Peter A. Jones, AACR president and director of the Norris Comprehensive Cancer Center at the University of Southern California who also said “A coordinated, large-scale Human Epigenomic Project would pave the way for unforeseen breakthroughs in understanding normal and disease states.”

There are a lot of epigenetic modifications of DNA that influence on gene activity like acetylation, phosphorylation etc., but the methylation (addition of a methyl chemical group in DNA that produces a signal to genes to switch off) is the best understood. Recently there have been developed technologies to study these epigenetics changes including ChIP/chip methodology, in which intact chromosomal DNA is analyzed on DNA microarrays.

The epigenetic modifications change on having be compared between tissues fabrics or between cells so workshop participants agreed that many samples should be examined using a “scanning” approach to investigate the effects of epigenetic changes on gene expression.

INFOBIOMED PROFILES

The Danish HNPCC-register



The register is a public national central database including epidemiological and genomic information on all Danish HNPCC-families since 1991, with the purpose to improve the prognosis for people with hereditary colon cancer by identifying the high-risk family-members and establish screening. The HNPCC-register is a non-profit organisation physically placed in the Surgical Gastroenterology Department in the Hvidovre Hospital - Hovedstadens Sygehusfællesskab (responsible authority).

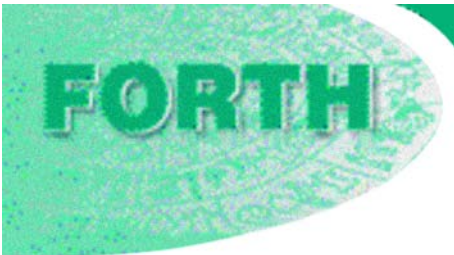
Hvidovre Hospital is a university hospital with 725 beds and 3.500 employees. The Surgical Gastroenterology Department plays an important role in the region as one of the largest centers treating colorectal diseases. Several national clinical quality databases are managed in the department where science and research on especially treatment of sporadic and hereditary colorectal cancer for long time has been in order of priority. The amount of genomic information has exploded during the last 10 years and many new genes have been identified and associated with different diseases. However, the exact disease-causing mutation in the individual family often is not known. Diagnosis of an increased risk of disease for the individual patient, therefore, often has to be based on the family pedigree and clinical judgment. Decisions have to be taken based on clinical information from many family members.

The Register identifies HNPCC-families and recommends screening, as do the genetic departments in Denmark and all the data are collected in the HNPCC-database in order to standardize the

screening program established in the individual family regardless of different geographically settlement of single family members. Centralization of data in a register, with access to information on relevant data for health professionals dealing with the individual patient, has the advantage of preventing double examinations and diagnostic delay. Collection of all the screening-results also gives the opportunity to evaluate and adjust the programmes with respect to the outcome in families with different type of hereditary predisposition for colorectal cancer. One of the main goals of the register is to provide the health professionals with this information in an annual report and based hereon recommend guidelines. Besides the national co-operation on treatment and research with different departments involved in HNPCC-treatment in Denmark, the register has also since the establishment been an active member of the International Society for hereditary gastrointestinal tumours (www.insight-group.org) where international guidelines and collaborative studies are performed.

The data collected is today sent in a paper version to the HNPCC-register and here typed into the HNPCC-database. In the INFOBIOMED project the Danish register is used as a model for electronic exchange of epidemiological and molecular-genetic data on this high-risk group, between treating departments and the central database. The aim of this pilot is to obtain knowledge useful for the planning and organization of screening in families with a high-risk of developing CRC and generate tools useful and generic enough also to be implemented in other countries and for other oncogenetic diseases.

FORTH



<http://www.ics.forth.gr/>

The **Foundation for Research and Technology - Hellas (FORTH)** is one of the largest research centres of Greece, with well organised facilities and a highly qualified staff. It is a private non profit research organization that operates under the supervision of the Greek Ministry of Development.

The Institute of Computer Science, (ICS), since its establishment in 1983, is a pioneering contributor towards the deployment and adoption of Information Society Technologies in Greece and plays a leading role in worldwide efforts towards the development of an Information Society accessible and acceptable by all citizens. The ICS-FORTH group involved in INFOBIOMED is the **Biomedical Informatics (BMI) Laboratory**.

The Laboratory was founded in 1985 by Professor Stelios Orphanoudakis (1948 -2005) who led the laboratory until March 2005. From the start the laboratory was named "Center for Medical Informatics & Health Telematics Applications". In subsequent changes and expansions it was renamed into "eHealth Laboratory" and most recently into "Biomedical Informatics Laboratory". From the start the direction of its research and development (R&D) activities were very carefully selected, so that they would always be at the forefront of health informatics and eHealth research.

Today the laboratory has two main research directions, which are (a) biomedical informatics in support of individualized medicine and (b) ambient intelligence eHealth environments.

Biomedical Informatics, focusing on various computational aspects of biomedical informatics, such as (a) ontology based integration and analysis of genetic and medical information for health applications; (b) Grid-based approaches to demanding molecular-biomedical applications; (c) analysis, simulation and modeling of complex biomedical processes, and (d) design and development of novel and prototypical DM/KDD methods, techniques, algorithms, tools and systems.

Ambient Intelligent eHealth environments, focusing on the development of new, innovative ambient intelligence service platforms for automatic, context sensitive offering and contracting of eHealth and mobile Health (mHealth) services across heterogeneous networks as well as on supporting mobility among users by integrating them with seamlessly accessible ubiquitous intelligent surroundings that support self-configuring devices using semantic agents and tools for ambient awareness and decision support.

The Biomedical Informatics Laboratory is involved in the following research activities:

- :: eHealth
- :: Data Mining and Knowledge Discovery for Databases
- :: Bio-imaging
- :: Bioinformatics

The R&D activities of the BMI Laboratory focus on the development of innovative computer methods and tools in the area of medical informatics, ehealth, m-Health, medical imaging and bioinformatics. Research in machine learning and data mining is an additional important activity of the eHealth Laboratory. These techniques facilitate knowledge discovery in medical databases. More specifically, systems for inductive learning from examples have been developed to support the diagnostic and therapeutic decision-making processes. In addition, constraint satisfaction methods are exploited towards more flexible learning operations and systems.

RESOURCES

The DrugBank database

DrugBank



Source:

<http://redpoll.pharmacy.ualberta.ca/drugbank/index.html> and *Nucleic Acids Res.* 2006 1;34

There is a new resource for in-silico drug discovery and exploitation called "DrugBank Database". It is a Bioinformatics and chemoinformatics resource that provides complete information arisen from the combination of drug data (chemical, pharmacological and pharmaceutical data) information and drug target (sequence, structure and pathway involved) information. The users of DrugBank can obtain information of "nearly 4100 drug entries including >700 FDA-approved small molecule drugs, 110 FDA-approved biotech (protein/peptide) drugs, >100 nutraceuticals and >3200 experimental drugs. Additionally, more than 15,000 protein (i.e. drug target) sequences are linked to these drug entries". This resource can be queried in several ways depending on the data we want to retrieve some examples are the simple text query (general text queries), the easy-to-use relational query search or the query for a BlastP sequence searches of the sequences contained in the database.

(see article Wishart DS et al., DrugBank: a comprehensive resource for in silico drug discovery and exploration. *Nucleic Acids Res.* 2006 1;34 and the website for more detail).

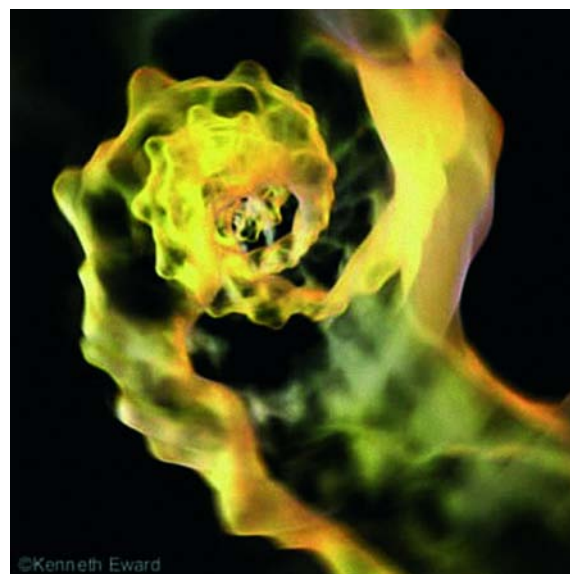
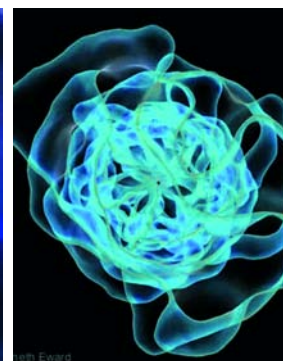
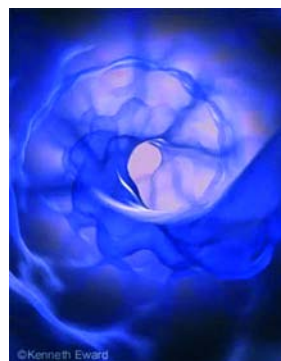
Inside DNA

<http://www.genomenewsnetwork.org/articles/2004/10/15/insidedna.php>

The artist Kenneth Eward has developed a new form of visualization of DNA strands by making digital images using 3-D animation software, Photoshop, and molecular modeling software.

These finally create an image of the ADN as if you were inside the molecule. The idea came to him from the request of the National Geographical magazine about genetics and the cosmos. In this work named Nautilus Eward he wanted to accentuate the fluid and organic representation of the ADN and emphasize its spiral structure. His inspiration and images are based on the first works in X-ray crystallography done by Rosalind Franklin and Maurice Wilkins.

In 2003 he completed a web exhibit creating more of his DNA images, several of these images can be seen in the biografx webpage <http://www.biografx.com/index.html>. Eward was honored in the 2004 Science and Engineering Visualization Challenge sponsored by Science magazine and the National Science Foundation".



GFINDER New modules

Source: Masseroli M, Galati O, Manzotti M, Gibert K, Pinciroli F. Inherited disorder phenotypes: controlled annotation and statistical analysis for knowledge mining from gene lists. *BMC Bioinformatics*. 2005 Dec 1; Suppl 4:S18.

To better understand disease processes in inherited diseases it is important to not only analyse the associated phenotype but also to understand the gene interactions, it is through the analyses of these factors that we can then apply the acquired knowledge to the clinic. It is for this purpose that the developers of Genome Function Integrated Discoverer (GFINDER) have added new modules to the system. In the article the authors describe GFINDER as a *“Web system previously developed to dynamically aggregate functional annotations of user uploaded gene lists and allows performing their statistical analysis and mining”*. The new additions allow *“annotating large numbers of user classified biomolecular sequence identifiers with morbidity and clinical information, classifying them according to genetic disease phenotypes and their locations of occurrence, and statistically analyzing the obtained classifications”*. As a conclusion the authors describe the new GFINDER as a system that supports *“phenotype analyses of inherited diseases and biomolecular functional evaluations, GFINDER facilitates a genomic approach to the understanding of fundamental biological processes and complex cellular mechanisms underlying patho-physiological phenotypes”*. The system is open to registered and non registered users.

<http://www.bioinformatics.polimi.it/GFINDER/>

Source: Attimonelli M, Accetturo M, Santamaria M, Lascaro D, Scioscia G, Pappada G, Russo L, Zanchetta L, Tommaseo-Ponzetta M. HmtDB is a Human Mitochondrial Genomic Resource Based on Variability Studies Supporting Population Genetics and Biomedical Research. *BMC Bioinformatics*. 2005 Dec 1;6 Suppl 4:S4

The Human mitochondrial DataBase (HmtDB) consists of a database of Human Mitochondrial Genomes annotated with population and variability data. It provides a human mitochondrial resource aimed at supporting population genetics and mitochondrial disease studies based on site-specific nucleotide and aminoacid variability estimation. HmtDB can be freely accessed at <http://www.hmdb.uniba.it>. HmtDB's contains 1255 human mitochondrial genomes derived from public databases (GenBank and MitoKor).

The genomes have been stored and analysed as a whole dataset and grouped in continent-specific subsets (AF: Africa, AM: America, AS: Asia, EU: Europe, OC: Oceania).

It's main purposes are to collect, integrate and provide a public human mitochondrial genomes data in order to predict new haplogroups or and/or modifying existing classifications.

<http://www.hmdb.uniba.it/hmdb/>

EVENTS

InfoTechPharma® 2006

March 13 - 16, 2006 - Novotel London West,
United Kingdom
<http://www.abc-lifesci.com/novotel/2006/-it2006/premailer/it2006pre.asp?mainp>

Drug Discovery Technology™ Europe 2006

March 13 - 16, 2006 - Novotel London West,
United Kingdom
<http://www.abc-lifesci.com/novotel/2006/ddt-2006/main/ddt2006.asp?page=overview>

Genomes to Systems Conferences

March 22 - 24, 2006 - Manchester, United
Kingdom
<http://www.genomestosystems.org/>

Med-e-Tel 2006

April 5 - 7, 2006 - Luxexpo, Luxembourg
<http://www.medetel.lu/index.php>

CSIT 2006: The 4th International Multiconference on Computer Science and Information Technology

April 5 - 7, 2006 - Amman, Jordan
<http://csit2006.asu.edu.jo/>

EFMI Special Topic Conferences (STC): Integrating Biomedical Information: "From e- Cell to e-Patient"

April 6 - 8, 2006 - Timisoara, Romania
<http://medinfo.umft.ro/stc2006/>

BIOS 06: 1st International Workshop on Bioinformatics and Security

April 20 - 22, 2006 - Vienna, Austria
<http://www.ares-conf.org/?q=bios>

IST-Africa 2006 Conference and Exhibition

May 3 - 5, 2006 - Pretoria, South Africa
<http://www.ist-africa.org/Conference2006/>

Training Course in Biomedical Ontology

May 21 - 24, 2006 - Saarbrücken, Germany
<http://ontology.buffalo.edu/06/os2/index.html>

SFTeHIN: Society for Telemedicine and eHealth in Nigeria

June 19 - 21, 2006 - Abuja, Nigeria
<http://www.sftehin.org/>

CBMS 2006: 19th IEEE International Symposium on Computer-Based Medical Systems

June 22 - 23, 2006 - Salt Lake City, Utah, United
States
<http://cbms2006.ece.byu.edu/>

IPMU 2006: Information Processing and Management of Uncertainty in Knowledge- Based Systems

July 2 - 7, 2006 - Paris, France
<http://ipmu2006.lip6.fr/index.php>

DILS 2006 - 3rd International Workshop on Data Integration for the Life Sciences

July 20 - 27, 2006 - Hinxton, United Kingdom
<http://www.informatik.hu-berlin.de/dils2006/>

11th International Congress on Human Genetics

August 6 - 10, 2006 - Brisbane, Australia
<http://www.ichg2006.com/>

ECCB 06: 5th European Conference on Computational Biology

September 10 - 13, 2006 - Eilat, Israel
<http://www.eccb06.org/>

BioDigital 2006

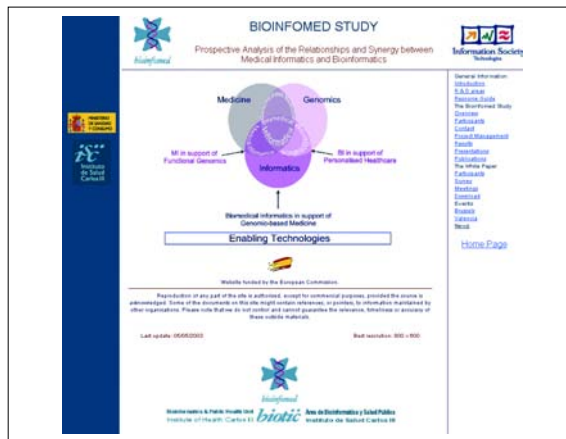
October 11 - 13, 2006 - Freiburg, Germany
<http://www.messe-freiburg.de/?src=kq1025poe>

BMI INITIATIVES IN EUROPE



SYMBIOmatics: this project (<https://www.symbio-matic.org>), funded by the European Commission within its FP6 Programme by the ICT for Health unit in the Directorate General Information Society, is another example of the consolidation of the BMI in Europe. After the Bioinfomed project (<https://bioinfomed.iscii.es>), the EBI proposes to corroborate and to improve the expectations of this new discipline with the consolidation in these two years of the research agenda proposed in the White Paper "Synergy between Medical Informatics and Bioinformatics: Facilitating Genomic Medicine for Future Healthcare" and to search for new areas.

This effort headed by Graham Cameron from the EBI, relies on the participation of nine associates for the year 2006:



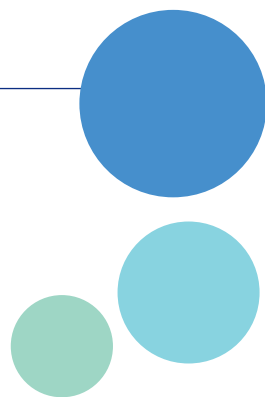
| | | |
|--------------------------------|---|----|
| Graham Cameron | European Bioinformatics Institute, EMBL | UK |
| Dominic Clark | Scientific Generics Ltd | UK |
| Fernando Martin-Sanchez | Institute of Health "Carlos III" | ES |
| Eva Del Hoyo Barbolla | The Ministry of Education and Science | ES |
| Ioannis G. Tollis | Foundation for Research and Technology Hellas | GR |
| Francesco Beltrame | University of Genoa | IT |
| Luciano Milanesi | Institute of Biomedical Technologies | IT |
| Johan Van der Lei | Erasmus Medical Center | NL |
| Jean-Louis Coatrieux | INSERM | FR |

The dynamics of work will consist on carrying out an internet survey where questions related to 31 lines of work will serve as base to obtain information through the insights of the experts who take part in the survey. These lines arise from an internal preliminary survey sent to a limited group of experts to determine the main lines. At the same time, an important data mining effort will be carried out to gather literature on the synergy between the BI and MI. One of the main innovations of the project is the study the ethical and

legal aspects specific to this new discipline since the area of the survey includes the Biomedical Industry, IT Industry, Clinical and the Basic research. "The project will document the state-of-the-art in biomedical informatics in Europe and identify areas of new opportunity".

The results of the work will be reflected in a White Paper, an update of the one produced in the Bioinfomed project. It will be officially presented in an Open meeting, in July 2006.

BIOMEDICAL INFORMATICS
TO SUPPORT INDIVIDUALISED HEALTHCARE



BIOMEDICAL INFORMATICS TO SUPP

<http://www.infobiomed.org>

