

INFOBIOMED

NEWSLETTER

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BIOMEDICAL INFORMATICS
TO SUPPORT INDIVIDUALISED HEALTHCARE

PORT INDIVIDUALISED HEALTHCARE

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NEWS

NYU ALGORITHM ENHANCES ABILITY TO DETECT CANCER GENES

Source:

<http://bio.com/realm/research.jhtml?realmId=3&cid=19100044>

A recent article published by bio.com news described the work carried out by researchers at New York University's Courant Institute of Mathematical Sciences. The work by Iuliana Ionita, Raoul-Sam Daruwala, and Bud Mishra focused on the development of an algorithm to detect cancer genes and has been published in an article in the July issue of the American Journal of Human Genetics.

These scientists developed an algorithm that can help detect tumour suppressor genes. They used gene-chips to scan patient genomes and compare them to control genomes. They were able to detect variations in the genomes where chromosomal segments have been gained or lost. These findings could point towards the location of tumour suppressor genes implicated in cancer. The algorithm provided an automated method to scan all data obtained from these gene-chips to map tumour suppressor genes by using a multi-point statistical function by providing information of possible important segments deleted in the DNA and calculating the possibility detecting a tumour suppressor gene implicated in the disease.

They initially tested their theory in silico by using different simulated artificial data sets to see how well the algorithm detected the right genes by adversely modifying parameters. Then with the encouraging results obtained, the researchers decided to test the algorithm in available patient data to detect genes already mentioned in the literature as being tumour suppressor genes. In this test run they were able to detect not only the genes already known but they also found other genes that were statically significant but that they were not described in literature.

It is thought that, as the development and use of technologies and of statistical algorithms improve,

they can be applied to solve many important issues such as finding biomarkers, drug discovery, disease diagnosis or identifying the most appropriate treatment for each patient in a more efficient and cost effective manner.

"The members of the NYU group (the authors, Dr. Salvatore Paxia and Dr. Thomas Anantharaman) are in the process of creating a simpler user interface for their software, providing interoperability across many different chip technologies, and finally, making it publicly available in order to facilitate its free and wide-spread usage".

FREE ACCESS TO WORLD-CLASS BIOLOGICAL DATABASES FOR EUROPEAN SCIENCE THANKS TO FELICS Biological databases to get infrastructure

Source: EMBL press release

<http://www.embl.org/aboutus/news/press/2006/03may06/index.html>

Funded by the European Union under the EU's Sixth Framework Platform's Research Infrastructures action, a unique computational infrastructure project to support biological research has gotten underway. The project, which is funded with 16.7 million, was launched by the European Bioinformatics Institute, the Swiss Institute for Bioinformatics, the University of Cologne and the European Patent Office. The name of the project is "Free European Life-science Information and Computational Services", FELICS, and its main objective is to provide researchers with unrestricted access to several major international biological databases.

According to the EMBL press release, FELICS is conservatively estimated to receive 10 million hits daily within the next five years. The project is coordinated by the EBI, "Europe's largest curator and disseminator of biological information". The services will include many of the EBI's databases together. Thanks to the support of their respective organizations, it will also provide access to the data included in BRENDA, the University of Cologne enzyme database that is currently under licensing constraints and it will collaborate on the CheBI, a database of chemical entities of biological interest. The inclusion of the European Patent

Office ensures support to access the information contained in patent literature. The project aims to meet the growing need of a centralised public information resource that *“provides global services for basic and applied biomolecular and biomedical research”*.

WORLD COMMUNITY GRID SETS UP A PROJECT TO "HELP DEFEAT CANCER"

Source: CIBERP@ÍS EL PAÍS 27-07-2006 and the World Community Grid webpage <http://www.worldcommunitygrid.org>

IBM has joined efforts with researchers in several USA universities to develop a project that uses the computing power of the virtual computer to investigate cancer. This is the third initiative that uses the potential of the Grid and they have called it “help defeat cancer”. The other two are “Fight-AIDS@Home Project” and “the Human Proteome Folding” - which is in its second phase.

The main aim of “Help Defeat Cancer project” is to advance in the knowledge of cancer mechanism for improving treatment and therapy in cancer patients. This project uses the computational power offered by World Community Grid, the world’s biggest public computing grid. It will allow researchers the simultaneous and fast analysis of many cancer tissue microarrays. It will analyse large numbers of microarrays of cancer tissues simultaneously as well as to carry out some short term experiments.

The World Community Grid uses the computer power of many computers put together using the idle periods of these PCs around the world. Therefore it is possible to split the work into little pieces that are done simultaneously reducing the research time sensibly. Robert Foran, Professor of Pathology & Laboratory Medicine and Radiology, Robert Wood Johnson Medical School explained that the World Community Grid is able to analyse in one hour the same number of samples that a regular computer would do in 130 years.

For more information you can access the World Community Grid webpage at <http://www.worldcommunitygrid.org>

JOINT CENTER FOR MOLECULAR MODELING ESTABLISHED BY BURNHAM INSTITUTE FOR MEDICAL RESEARCH & UC SAN DIEGO

Source: Genetic News 24 July 2006 <http://www.medicalnewstoday.com/medical-news.php?newsid=47845>

A group of scientists of the Burnham Institute for Medical Research and UCSD's Computer Science and Engineering department in California, USA led by Adam Godzik make the consortium known as the Joint Center for Molecular Modelling whose main objective is to design tools that will accelerate the interpretation and potential use of the information obtained in the Human Genome Project.

The available budget for the project is \$2.1 million over the next three years. Researchers will collaborate in designing tools that will improve in the prediction of three-dimensional protein structure from the raw genetic code. The idea that Dr. Godzik and his co-principal investigators Drs. Pavel Pevzner, Yuzhen Ye and Piotr Cieplak have is to use *“the structures of proteins that have already been solved to develop novel ways to extract rules and trends of how structures change and evolve”*.

The tools developed in this project will be made available to researchers worldwide through open source databases and it is thought that they will help in the design of new “smarter” drugs in the future.

BRITISH GOV'T OFFICIALLY LAUNCHES UK BIOBANK PROJECT; DATA GATHERING TO TAKE FOUR YEARS

Source: Genomeweb news, August 23, 2006

British health officials have given the go ahead to the UK Biobank project. It is a voluntary program that aims to gather DNA samples and lifestyle information from more than half a million Britons between the ages of 40 and 69. All the data

obtained will be included in a database accessible to researchers to investigate the genetic and environmental causes of diseases and their connections.

The Medical Research Council, the Wellcome Trust, the Scottish Executive, and the Northwest Regional Development Agency have funded this project that will start in the next few months with a recruitment phase. It will include 35 centers in England, Scotland and Wales that will be open for six months at a time to recruit the participants and collect the data. It is thought that the first phase of the project may last about three to four years.

In March a pilot program took place in the south Manchester area. The Biobank invited 3000 residents to spend an hour in an assessment center in the region where they were asked questions about their lifestyle, they provided blood and urine samples for their analysis and they also granted permission the UK Biobank to carry out a health follow up during many years ahead. The results of this pilot were encouraging and gave the final push to the project.

The founders said in a statement to the Genomeweb news that the *“UK Biobank has the potential, in ways that are not currently available elsewhere, to support a wide range of research, particularly investigations into complex interactions of various exposures, including genetic and lifestyle factors in the pathways to disease and health”*.

GTB: GLOBAL TRIAL BANK (AMIA)

Source: <http://www.amia.org/gtb/>

The American Medical Informatics Association (AMIA, www.amia.org) has developed an international registry, supporting critical data standards, called the Global Trial Bank (GTB). GTB is a non-profit, available free and peer reviewed resource for knowledge management in biomedicine. In order to promote biomedical discovery GTB offers a computable repository of clinical trial information sufficiently detailed to support evidence-based decisions, practice and policy making (e.g., systematic reviews) and it includes study design,

study execution and summary and individual participant-level results. It also interested in activities related with the dissemination, understanding, synthesis, and translation of clinical trials to improve human health.

Clinicians, medical researches, medical informatics experts, patients and general public could benefit from obtaining clinical trial information available through the GTB.

The GTB is briefly characterized as follows:

- It contains the sufficient detail and information for improving science research.
- It has got computable information.
- It is integrated peer review.
- It promotes transparency, interoperation, and open access.

(further details can be found in <http://www.global-trialbank.org>)

One of the mayor challenges for the GTB is to provide a new approach to the publishing of all clinical research results in a computable form. It uses the controlled medical vocabulary SNOMED for coding the data fields ensuring the reproducibility.

HOW WELL DO HAPMAP SNPS CAPTURE THE UNTYPED SNPs?

Source: <http://www.biomedcentral.com/1471-2164/7/238>

The main aim of the International HapMap Project is to provide a catalogue of human genetic variation in four different populations (USA with European ancestry, Chinese, Nigerian and Japanese) to identify the common patterns in DNA sequence variation and the correlation between them.

In a recent article published in BMC Genomics on 19 September 2006 the authors, Tantoso, Yang and Li, show that the HapMap SNPs (single nucleotide polymorphisms) data are not enough to capture most of the variation and untyped SNPs in

the human genes. In their work they used SNPs identified by National Institute of Environmental Health Science (NIEHS SNPs) obtained by resequencing. They first checked that the data from the HapMap project was transferable to the NIEHS and then they studied the how well the SNPs in HapMap can capture untyped SNPs in the NIEHS. They saw that even though HapMap found most SNPs in some genes it did not perform well in most genes failing to capture the untyped variants.

The conclusion of this article is the probable need of resequencing the missing regions to cover more SNPs or variants to obtain tagSNPs that can represent all the variants in the selected genes for association studies.

A TOP-LEVEL ONTOLOGY OF FUNCTIONS AND ITS APPLICATION IN THE OPEN BIOMEDICAL ONTOLOGIES.

Source:

http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?cmd=Retrieve&db=PubMed&dopt=Abstract&list_uids=16873523

There is a great amount of information gathered from the knowledge obtained from functions of cells, cell components and gene products.

The department of Computer Science of the University of Leipzig and the Max Planck Institute for Evolutionary Anthropology have developed projects related with the application of ontologies in biomedicine, like the 'Ontology of Functions', dedicated to finding the function of genes and their products. They investigate novel top-level ontologies and the core of ontological models of functions, and see how they can be applied to biomedical ontologies. There is a need to formalize the available biological knowledge stored in many sources to then be able to integrate this information in order to make biologically and biomedical meaningful discoveries. Ontologies allow the process of linking biomedical knowledge by providing a common vocabulary and structuring the knowledge in a way that permits large scale analy-

sis of the data related with biological functions. The researches are also investigating other applications like facilitation of ontology interoperability and automated reasoning, developing tools for community creation and editing of biomedical ontologies and establishing criteria for the assessment of quality of biomedical ontologies.

The Ontology of Functions software and related information is available in the following webpage: <http://onto.eva.mpg.de/>.

"CONNECTIVITY MAP" BETWEEN GENES, DRUGS AND DISEASES

Source: El médico Interactivo (30/2-10-2006)
http://www.elmedicointeractivo.com/noticias_ext.php?idreg=12825

"El medico Interactivo" outlined in its October 30th edition the study carried out by researchers at the "Broad Institute" of The Institute of Technology of Massachusetts and Harvard's university in Cambridge (USA) published in "Science" in the September 29th issue. It consisted in the development of a new tool used to find connections among small molecules that share a mechanism of action, chemicals and physiological processes, and diseases and drugs. This "Connectivity Map" is a collection of gene-expression profiles from cultured human cells treated with bioactive small molecules, together with pattern-matching software to mine these data. The main aim of this catalogue is to discover new possible effects of drugs and the development of new therapies.

Using such a resource, a researcher studying a drug candidate, a gene, or a disease state could compare its signature to the database to discover unexpected connections. To validate the "Connectivity Map" the researches studied obesity induced by the diet, Alzheimer's disease and a form of leukaemia resistant to drugs.

There is a Web-based tool (www.broad.mit.edu/cmapp) available. It allows researchers to perform their own Connectivity Map analyses with user defined signatures in real time.

NATIONAL INSTITUTES OF HEALTH TO MAP GENOMIC CHANGES OF LUNG, BRAIN, AND OVARIAN CANCERS

Source: NIH news September 13th
<http://www.nih.gov/news/pr/sep2006/nci-13.htm>

The National Cancer Institute (NCI) and the National Human Genome Research Institute (NHGRI) have announced through the National Institutes of Health (NIH) news that the first stage of The Cancer Genome Atlas (TCGA) pilot will include three different types of cancer, lung, brain (glioblastoma) and ovarian cancer (<http://cancergenome.nih.gov>).

These specific cancer diseases were selected because of their high prevalence and associated mortality in USA, and because the TCGA's disposes of broad biospecimen collections of these diseases that meet the scientific, technical and ethical requirements. The criteria considered to include the samples are detailed at <http://cancergenome.nih.gov/media/qanda.asp>.

The different cancer biospecimens, lung cancer, brain cancer (glioblastoma) and ovarian cancer will be supplied by the Lung Cancer Tissue Bank of the Cancer and Leukemia Group B (CALGB) clinical trials group, the MD Anderson Cancer Center in Houston, Texas and the Gynecologic Oncology Group tissue bank at the Children's Hospital of the Ohio State University in Columbus, Ohio, respectively.

The NCI and NHGRI have selected the International Genomics Consortium, part of the Translational Genomics Research Institute, of Phoenix, Arizona to manage TCGA's BCR and all the processes between groups.

The TCGA project began in December 2005 and will last three years. It is an integrated collaboration between Biospecimen Core Resource (BCR), Cancer Genome Characterization Centers, Genome Sequencing Centers, and a Principal Bioinformatics Resource. The project began by identifying the biospecimens that will be used. The

selection of the three cancer types to be studied by TCGA signals the scientific start according to NIH Director Elias A. Zerhouni, M.D.

The Centers included in the project will analyse the samples by high throughput genomic techniques in the following months. The main aim is to establish a publicly available database with the support of the NCI's cancer Biomedical Informatics Grid™ (caBIG™) and the National Library of Medicine's National Center for Biotechnology Information (NCBI). This resource will store all the generated knowledge to facilitate scientific research by making a comprehensive "atlas" of molecular processes involved in the development of these cancers that will help in their diagnostics, therapeutics and prevention, which represents one more step towards personalized medicine.

"The Cancer Genome Atlas will use cutting-edge technologies and knowledge from the Human Genome Project and other genomic studies to assess the range of genomic changes that cause the uncontrolled cell growth that characterizes cancer," explained National Human Genome Research Institute Director Francis S. Collins, M.D., Ph.D. "TCGA will analyse hundreds of tumour specimens with multiple technologies, including the comparison of genome sequences from the cancers with the normal DNA sequence derived from the same patients, in order to identify changes that are specifically associated with cancer."

RESOURCES

MAPPING THE PROTEIN WORLD

Source: http://bio.com/newsfeatures/newsfeatures_research.jhtml;jsessionid=IQ52IFILHB-MVJR3FQLMCFEWHUWBNSIV0?cid=19900108

Nowadays, the advances in computational tools for molecular modelling and graphics crystallographic studies play a major role in current efforts towards protein structure determination, although the protein model constructing of the tertiary structure from experimental data remains complex, time-consuming and requires experts intervention.

Recently bio.com has published the announced of the grant of more than 800,000 US Dollars that the U.S. National Institutes of Health (NIH) gave to Victor Lamzin at the Hamburg Outstation of the European Molecular Biology Laboratory (EMBL) and Anastassis Perrakis at the Netherlands Cancer Institute (NKI) in Amsterdam for developing ARP/wARP. This award will last four years.

ARP/wARP is a package for automated protein model building and structure refinement. It is based on a unified approach to the structure solution process by combining electron density interpretation (for more information see <http://www.embl-hamburg.de/ARP/>). Lamzin said that this software was widely used in scientific researches and the main aim of the new efforts was to facilitate and improve the automated generation of structural models.

Perrakis added that ARP/wARP also be employed in the study of new drugs against human diseases like cancer, infections, etc. He finally concluded his interview saying that "ARP/wARP needs to meet a two fold challenge: firstly, it needs to be able to work with structural information at lower resolution, within the range of 3.0 to 3.5 Ångstroms, and secondly, the models produced have to be complete and validated. The new NIH grant will help us to approach these aims. In the future researchers will be able to focus on structure analysis rather than just building the structure and, who knows, by combining ARP/wARP with new cell imaging techniques we might be able to model the molecules of a complete cell," Perrakis concludes.

SCIENTISTS DEVELOP ENDEAVOUR - A COMPUTER PROGRAM FOR IDENTIFYING DISEASE GENES

Source: <http://bio.com/realm/research.jhtml?realmId=3&cid=19100032> and the VIB, Flanders Interuniversity Institute of Biotechnology, Press release 8th May 2006

The VIB, Flanders Interuniversity Institute of Biotechnology made public a press release announcing the development and characterization of a new gene prioritization free software tool: ENDEAVOUR (accessible through www.esat.kuleuven.ac.be/endeavour or www.bits.vib.be/endeavour) developed by ESAT-SCD (Engineering Sciences) and the Flanders Interuniversity Institute for Biotechnology (VIB) connected to the Catholic University of Leuven.

ENDEAVOR is a bioinformatics framework able to compare and integrate all available gene characteristics using algorithms and statistical methods in order to classify unknown candidate "test" genes involved in human diseases and biological processes according to their similarity with known "training genes". To validate this software the researchers tested a candidate gene involved in DiGeorge syndrome.

This research was published in the journal of Nature Biotechnology (Gene prioritization through genomic data fusion; Aerts et al., Nature Biotechnology, 2006), and more information can be found in www.esat.kuleuven.ac.be/endeavour or www.bits.vib.be/endeavour.

SNP FUNCTION PORTAL: A WEB DATABASE FOR EXPLORING THE FUNCTION IMPLICATION OF SNP ALLELES

Source:

http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?cmd=Retrieve&db=PubMed&dopt=Abstract&list_uids=16873516

Bioinformatics journal published last June the article titled "SNP Function Portal: a web database for exploring the function implication of SNP alleles" that describes the SNP Function Portal (available through <http://brainarray.mbni.med.umich.edu/Brainarray/Database/SearchSNP/snpfunc.aspx>).

It is a free bioinformatics resource that facilitates the understanding of functional implications of SNP alleles identified in genome-wide association studies incorporating functional annotation data from diverse data sources and analysis methods to promote the generation of testable hypothesis.

The SNP Function Portal can help researchers' work facilitating SNP function exploration since it includes SNP functional annotations and explores the potential functional implications of different types of genetics markers through HapMap Phase II search function. It also identifies the biological implication and relationship of genetic markers and genes. Further efforts will be made towards including haplotypes in protein domain analysis.

Availability:

<http://brainarray.mbni.med.umich.edu/Brainarray/Database/SearchSNP/snpfunc.aspx>.

UK VERSION OF PUBMED CENTRAL LAUNCHED

Source:

http://www.wellcome.ac.uk/doc_WTX032990.html and <http://www.e-health-insider.com/news/-item.cfm?ID=2040>

The Wellcome Trust as one of the nine members of major UK biomedical research funders announced in a press release that they have awarded the contract to develop and manage the UK version of PubMed Central (UKPMC) to a partnership between the British Library, The University of Manchester and the European Bioinformatics Institute (EBI). The design is based on the US National Library of Medicine's (NLM) PubMed Central (PMC).

The UKPMC Implementation Group is in charge of setting up and supporting the service, developing the author submissions processes, marketing the resource to the research community, and integrating the knowledge in biomedical domain, etc. This service will be launched next January 2007.

The press release included the words of Professor Stephen Oliver, of the University of Manchester's Faculty of Life Sciences. He said: "*There has been an explosive growth in both the number of biomedical publications and the size of their accompanying data sets; UKPMC will become a major tool to allow both the research community and the public to access and analyse this information*".

The main objective of this initiative is to create a stable, permanent, and free access to digital archive of the full-text, peer-reviewed research publications (and datasets) in the medical and life sciences. It also provides links to other online databases resources.

It is expected to be a platform that offers new services not only for the UK but for all the European biomedical research community as Richard Boulderstone, Director of e-Strategy and Programmes at the British Library said.

INFOTBIOMED PROFILES

INFORMA



INFORMA is a service company in the medical-scientific field, at the cutting edge in providing hi-tech solutions.

Our history

Informa (www.informacro.info) was created in Rome in 1992. In the early days it built a reputation in clinical research for its know-how on data management and statistical analysis in clinical studies; shortly afterwards, by creating a Medical Division, it became a **Contract Research Organization** for fully-fledged management of research project during their whole lifecycle.

From the very beginning Informa had a strong drive for technology and innovation: it has been one of the first companies to offer scientific and information services online, and has kept on developing this strategy, which has led to today's commitment to **Research and Development**.

Today

The Informa organisation counts more than 50 people employed in the company's headquarters in Rome and in the recently opened centre in South Italy (Pisticci, Basilicata). The organisation is also supported by a nationwide network of around 20 clinical monitors.

With the new centre in Pisticci Informa gave stronger impulse to its activity in **Education and training**: ECM on-site and remote activities, **e-learning**, wide scope training programs for spe-

cialistic fields (high specialisation schools, with internationally reputed lecturers), and as **Site Management Organisation**.

Informa technical-scientific structure has a wide experience in pharmaceutical research and marketing. It belongs to a group (1-GIANT) of companies specialised in software programs, I&C technologies and in Registration Authority services for e-signature. It has long-term cooperation agreements with institutions like Parco Biomedico S. Raffaele, IHG, PhaseForward.

Our clients

Our projects are designed for Pharmaceutical companies, -both as clients and sponsors for third party projects -, for research groups of any size, for research institutions, for medical associations. Informa has cooperated with more than 40 pharmaceutical companies, including all the most relevant.

What we do

Informa's business can be summarised in the following fields:

- Clinical Pharmacological research (phases II-IV) in all steps of project development
- Non pharmacological clinical research (Observational studies) for project management
- Ecm/Training
- Hi- tech applications for the health sector (Technology integration, Mobile and wireless, Research projects).

Mobile devices

In the last two years, also thanks to the Palmplanet project (co-funded by Glaxo Wellcome), Informa has become **one of the major Italian companies in the field of mobile application for healthcare**. Palmplanet raises from the good results of the Palmhospital project, which was started in 2000 to provide the "Ospedali Riuniti di Bergamo" (a major hospital institution in North Italy) with a palm-based system for prescription

and dispensing. The system is now adopted by other 14 hospitals in Italy.

Since then Informa realised several projects based on palm devices for epidemiological trials involving globally around 5000 doctors (GP and specialists).

- Informa is leader in the Italian market for palm based systems for hospital medical management (PalmPlanet project and Mobi-Dev project).
- It is leader in the Italian market for palm based systems for epidemiological studies (META project with 2750 GPs and specialists involved, Synapsi with 1000 specialists, OPS with 1000 specialists).
- It designs, implements and manages electronic clinical studies with its proprietary E-Trial product or with Inform product (FDA compliant) in partnership with PhaseForward (UK subsidiary of a USA company).
- It has leaded important epidemiological studies organised by Intranet, like ICONA (more then 3500 patients observed and registered in a wide database accessible via Internet).
- It provides **palm based medical content** (Esculapius project).

Training and e-learning

Informa is involved in the design and realisation of ECM courses (courses approved and certified by the Italian Minister of Health to give permanent training to healthcare providers), both residential and at distance. In particular the new site of Pisticci is active to organise, implement and host specialistic training programs.

Among these we can cite the:

ECM course on Genotype-Response issue - Organised together with University of Siena, with the support of GlaxoSmithKline.

Master in vaccine science: Organised together with University of Basilicata - The first year of the residential course starting on May 2003.

Informa has developed its **proprietary e-learning platform**, which is the base for the **E-learning platform** provided to the III University of Roma (2004).

Web collaborative working environment

Informa has also acquired expertise in **designing**

and realizing web platforms which are full-fledged groupware web applications providing support to project management and facilitating information sharing among involved users.

Informa has now its **proprietary collaborative working environments**, aiming at optimised management of distributed messages and documents in order to improve and to fasten information and communication flows within workgroups, include features such as:

- Access regulated at different permission levels;
- Messaging section where users can read and post messages - possibly with attachments - organised according to definable discussion items. All messages are permanently stored in an accompanying database and can be retrieved at any moment, possibly using a multi-option search functionality;
- Repository for project official documents and deliverables, which can be uploaded exclusively by the webmaster under request of the project coordination team. This section of the working area is used to maintain a single centralised archive of all the information relative to and/or produced during the project;
- Series of advanced tools providing the opportunity of writing online project reports as well as project deliverables.

Their flexible structure make these platforms appropriate working tools both for extended and organized groups and for limited number of users.

Research projects

Informa has an R&D unit with the mission to design and coordinate research projects in line with the company activities. The R&D unit has consolidated experience both in National and European co-financed research.

HIV Resistance:

Informa has a long term experience in providing specific services for infectious diseases dept. and HIV cohort studies (e.d. ICONA initiative, one of the world most important Cohort of Antiretroviral Naïve Patients). From 2002 it participates to the HIVARCA initiative managing the DB and with a

research framework agreement with University of Siena and III University of Roma on the study of HIV response to treatment based on Viral genotypes (the study saw a contribution from Glaxo-SmithKline).

Informa and its subsidiary Arakne participated in various EU projects:

- **TESEMED** Telematics applications in community pharmacies for responsible self-medication (funded by the EU Telematics Applications Programme and by the EU INCO-DC Programme: INFOPHARMA project).
- **CIPRESS** - Complex Information Patterns Retrieval with a Parallel Distributed Processing Knowledge Engine (EP 26313, funded by the EU Esprit Programme).
- **Mobi-Dev: Mobile devices for healthcare applications** (IST-2000-26402, funded by the EU 5th Framework Programme) - www.mobi-dev.arakne.it Arakne was project scientific coordinator - Informa was partner. Mobi-Dev came to its end successfully in 2003. It has been chosen among the projects presented in the e-Health inter-ministerial conference 2003. Mobi-Dev working in the hospital has been filmed and showed by the European TV channel.

■ **MEMO:** Medical Mobile devices: cluster of EU funded projects. (IST-2001-35027, funded by the EU 5th Framework Programme) - www.med-mobile.org

■ **MobiDis:** Telemedicina tramite telefonia mobile (FIRB project, funded by MIUR-CNR), in which it is studying a mobile interface for electronic clinical trials management. www.prorec.it/mobidis/intro.htm

■ **SecurePhone:** Secure contracts signed by mobile Phone (IST-2002-506883 funded by the EU 6th Framework Programme) www.secure-phone.info - Informa was Project Scientific Coordinator.

Informa is presently involved in

■ **EuResist:** Integration of viral genomics with clinical data to predict response to anti-HIV treat-

ment (IST-2004-027173) www.EuResist.org - Informa is Project Coordinator.

■ **Infobiomed** Network of Excellence – eHealth (IST-2002-507585 funded by the EU 6th Framework Programme). <http://www.infobiomed.net>.

■ **FIRB PalmHIV** - A model of integrated care based on the use of mobile devices for patients (FIRB project, funded by MIUR-CNR) <http://palmhiv.informadoc.net/>.

■ **ULSYS:** Multi Monitoring Medical Chip for Homecare Applications (COOP-CT-2004-508739 funded by the EU 6th Framework Programme). <http://ulsys.europarama.it>

■ **IATPAD** Improvement of access to treatment for people with alcohol- and drug-related problems (IATPAD Improvement of access to treatment for people with alcohol- and drug-related problems (PH 3.1.3-2005 n. 2005322 funded by Public Health EU Program).

Within the Mobi-Dev project Informa organised the first **International Symposium on Mobile Devices for Healthcare** (Villa Mondragone, Frascati, 8, 9 May 2003).

UEDIN – GTI



Introduction to the Scottish Centre for Genomic Technology and Informatics (GTI)

GTI is a centre for post-genomic research located within the University of Edinburgh Medical School, Edinburgh, Scotland. The goal of the centre is to

integrate post-genomic science with medicine in order to develop innovative new methods for the diagnosis and treatment of human diseases.

GTI is conducting research programmes in the following areas:

1. Pathway Biology

This is aimed at developing a computational framework for understanding complex molecular interactions in the human body and exploring new methods for understanding their role in health and disease. These efforts are focussed on the development of graphical, notational systems for representing biological pathways and the synthesis of models for subsequent mathematical translation and utilisation in simulation-based studies.

This work is underpinned by the centres' ability to measure multiple biomarkers through biochips or other parallel measurement technologies.

The GTI's Pathway Biology research programme has adopted an integrated approach to understanding immune regulation and in particular the role of interferon in regulating host responses to infection, cardiovascular disease and *oncology*.

Research in this area typically combines three research activities - systematic literature mining, transcriptional profiling and network analysis - to build a consensus which aids in our understanding of the hundreds of molecular interactions involved in the body's interferon-regulated immune response.

Such a consensus provides a mechanism for storing and communicating a large volume of previously fragmented information and provides a basis for further analysis and research.

2. Biochip Medicine

This program of work is focussed on translating pathway research into clinical healthcare applications using advanced biochip techniques to measure molecular interactions.

Research projects are concerned with the development and optimisation of biochip platforms for clinical research and monitoring. This includes the development of new protein arrays and advanced nucleic acid detection techniques and technologies for molecular biosensing.

Our ultimate aim is to translate our pathway research findings into clinical practice by developing smart biochip systems for monitoring multiple biomarkers.

GTI's research capabilities include:

- Transcriptional profiling using Affymetrix, Agilent and GE platforms
- The fabrication of custom microarrays including cDNA, oligonucleotide, proteins and cells
- Whole-genome siRNA screening
- Yeast 2 hybrid screening
- Statistical design and analysis of multi-parameter experiments
- Development and maintenance of MIAME-compliant database and LIMS systems

Through local research partners, we can also access facilities for:

- Silicon microarray technology and cleanroom fabrication
- Proteomic identification and mass spectroscopy.

GTI employs a collaborative, multidisciplinary style of research based on integrated teams working on common research goals. Studies typically cross traditional boundaries and combine science and technology, blue-sky and applied research, academia and business.

To achieve these aims, GTI personnel have been recruited from a wide variety of areas including: biology, medicine, chemistry, engineering, physics, computer science and business.

EVENTS

International Workshop Integrative Bioinformatics

September 4 - 6, 2006 - Harpenden, Hertfordshire, United Kingdom
<http://www.rothamsted.bbsrc.ac.uk/bab/conf/ibiof/>

Genomic Perspectives to Host Pathogen Interactions

September 7 - 10, 2006 - New York, United States
<http://meetings.cshl.edu/meetings/pathuk06.shtml>

ECCB 06: 5th European Conference on Computational Biology

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

GridWorld 2006

September 11 - 14, 2006 - Washington, DC, United States
<http://www.gridworld.com/live/42/>

HGV2006: 8th International Meeting on Human Genome Variation and Complex Genome Analysis

September 14 - 16, 2006 - Hong Kong, China
<http://hgv2006.nci.nih.gov/home.cfm?CFID=1282172&CFTOKEN=55061950>

14th Annual International Meeting on Microbial Genomics

September 24 - 28, 2006 - Lake Arrowhead, CA, United States
<http://www.mimg.ucla.edu/arrowhead2006/>

SMCM '06: The 1st Semantic Mining conference on SNOMED CT

October 1 - 3, 2006 - Copenhagen, Denmark
<http://www.hiwww.org/smcs2006/>

Third INFOBIOMED Training Challenge

October 2 - 6, 2006 - Edinburgh, United Kingdom
http://www.infobiomed.net/paginas_en/training_challenge_information_frame_third.htm

BioDigital 2006

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

CONSCI06: International Conference Converging Sciences 2006

October 16 - 17, 2006 - Trento, Italy
<http://www.msr-unitn.unitn.it/events/consci06.php>

CMSB06: International Conference on Computational Methods in Systems Biology

October 18 - 19, 2006 - Trento, Italy
<http://www.msr-unitn.unitn.it/events/cmsb06.php>

Nuclear Receptors: Bench to Bedside

November 1 - 5, 2006 - New York, United States
<http://meetings.cshl.edu/meetings/nrd06.shtml>

KR-MED 2006: Biomedical Ontology in Action

November 8, 2006 - Baltimore, Maryland, United States
<http://www.imbi.uni-freiburg.de/medinf/kr-med-2006/index.html>

AMIA 2006 - Biomedical and Health Informatics

November 11 - 15, 2006 - Washington, DC, United States
<http://www.amia.org/meetings/f06/>

Pharmacogenomics

November 15 - 18, 2006 - New York, United States
<http://meetings.cshl.edu/meetings/pharm06.shtml>

e-Science 2006: 2nd IEEE International Conference on e-Science and Grid Computing

December 4 - 6, 2006 - Amsterdam, Netherlands
<http://www.escience-meeting.org/eScience2006/index.html>

ISBMDA 2006: 7th International Symposium on Biological and Medical Data Analysis

December 7 - 8, 2006 - Thessaloniki, Greece
<http://isbmda06.med.auth.gr/>

ICICT 2006: Fourth International Conference on Information and Communication Technology

December 10 - 12, 2006 - Cairo, Egypt
<http://www.icict.gov.eg/ICICT-2006/ICICT2006.html>

BMI INITIATIVES IN EUROPE

BIOPATTERN

Driving the Future of Individualised Healthcare

<http://www.biopattern.org/>

BIOPATTERN is a groundbreaking project that integrates key elements of European research to underpin eHealth. The Grand Vision is to develop a pan-European, intelligent analysis of a citizen's bioprofile; to make the analysis of this bioprofile remotely accessible to patients and clinicians; and to exploit bioprofile to combat major diseases such as cancer and brain diseases.

Objectives of the project

Today, the ability to produce vast amounts of bio-data has vastly outstripped our ability to sensibly make use of the data for decision making. Producers of novel biosensors and probes assume that the knowledge infrastructure exists to support new sensing technologies, but this assumption is false. Even the existence of technologies such as the Grid is of limited usefulness unless intelligent algorithms and supporting infrastructure exist to take advantage of such technologies. Modern medicine already generates vast amounts of data which require considerable expertise and time to analyse, interpret and use. Genomic-based research and the drive towards personalised healthcare are providing new information about the root causes of diseases and how they might develop and treated, but will generate more data and exacerbate the situation. New computational intelligence techniques for bio-data analysis are needed to fully exploit information from the vast amounts of data generated from various sources (e.g. clinical, bio-sensors, genomics, proteomics, laboratory, electrophysiology and imaging). Hitherto, research activities in this area were fragmented and uncoordinated in Europe.

Much of the work was carried out in isolation in many centres, with outcomes of excellent work often inaccessible. Valuable research resources were wasted 're-inventing the wheel' (e.g. developing 'new techniques' and collecting 'new cases' which may already exist).

Project

A key objective of BIOPATTERN is to address the problem of fragmentation in this key area by bringing together key researchers to create a critical mass of specialists to promote the development of computational intelligence methods underpinning e-Healthcare. The idea is to move away from local solutions to local problems and towards European wide solutions to European problems.

The main objectives are:

- Integration - to tackle and reduce fragmentation of existing research capacities in this area
- Virtual Research Institute - to create a new research community
- New opportunities - to identify how bioprofile could be exploited for healthcare, such as disease prevention, diagnosis and treatment
- Roadmap - to identify gaps in knowledge, key challenges and to initiate joint activities to address them
- Standards - To identify technical and ethical issues on which guidelines and standards should be based with regard to the acquisition, transmission and analysis of a bioprofile
- Societal challenges - To contribute to finding solutions to some of the demanding societal challenges in healthcare.

BIOPATTERN is a Network of Excellence (NoE) project within the ICT for Health. It integrates key elements of European research to enable Europe to become a world leader in eHealth. The Grand Vision is to develop a pan-European, coherent and intelligent analysis of a citizen's bioprofile; to make the analysis of this bioprofile remotely accessible to patients and clinicians; and to exploit bioprofile to combat major diseases such as cancer and brain diseases.

A biopattern is the basic information (pattern) that provides clues about underlying clinical evidence for diagnosis and treatment of diseases. Typically, it is derived from specific data types, e.g. genomics information and vital biosignals such as the EEG.

A bioprofile is a personal 'fingerprint' that fuses together a person's current and past medical history, biopatterns and prognosis. It combines data, analysis and predications of possible susceptibility to diseases.

BIOPATTERN proposes to provide novel computational intelligent techniques for biopattern analysis and a pan-European integrated, intelligent analysis of an individual's bioprofile. Information from distributed databases will be made available, securely, over the Internet and bioprofiles analysed using on-line algorithms, libraries and processing facilities.

BIOPATTERN integrates the research efforts of 30 institutions across Europe to tackle and reduce fragmentation in the new field of biopattern and bioprofile analysis. It brings together leading researchers in medical informatics and bioinformatics from academia, the healthcare sector and industry in a new way, harnessing expertise and information to put Europe at the forefront of eHealth.

BIOPATTERN aims to identify how bioprofile could be exploited for individualised healthcare such as disease prevention, diagnosis and treatment. Its ultimate goal is to become a Virtual Research Institute recognised as a world-leading scientific resource.

The Grand Vision of the project is long term and there are many challenges to it, including technological as well as ethical, security and operability. The special interest areas of Cancer and Brain Diseases form the focus of activities. The Network is set up to address these challenges through the core Joint Programme of Activities by mobilising resources from 40 centres across Europe and integrating and co-ordinating research efforts into the following generic themes:

- Data Acquisition
- Analysis
- Evaluation and Benchmarking
- E-Delivery
- Dissemination and exploitation
- Management

The Grand Vision of the project is long term, however short term goals will be achieved by the end of 2007. These include identifying how the bioprofile could be exploited for individualised healthcare such as disease prevention, diagnosis and treatment, and creating the basis for a Virtual Research Institute recognised as a world leading scientific resource.

Expected results and impact of BIOPATTERN include the following:

- Identifying how bioprofile could be exploited for healthcare, such as disease prevention, diagnosis and treatment on an individual basis. This is in line with the trend in modern medicine towards individualisation of healthcare and should lead to significant improvement in the quality of healthcare.
- Integration of the research expertise of 30 partners. This would reduce fragmentation of existing research capacities in this area and strengthen European excellence in this field.
- Creation of a new research community. BIOPATTERN will provide a dynamic platform for academics, healthcare professionals and industrialists to network in the area of biomedical informatics (medical informatics + bioinformatics) to advance knowledge in biopattern and bioprofile analysis to underpin new generation of eHealth systems.
- Contribution to finding solutions to some of the demanding societal challenges. The initial target clinical areas are cancer and brain diseases.
- Contribution to the development of new standards and guidelines in areas such as acquisition of bio-data, bio-data representation, evaluation and benchmarking techniques and interfaces for biomedical informatics web services and tools.
- Identification of technical, ethical and legal issues and principles on which guidelines and standards should be structured and based with regard to the acquisition, transmission and analysis of a bioprofile.
- Development of commercially exploitable prototype eServices to support early clinical diagnosis and care of subjects at risk of major diseases such as cancer (e.g. breast and ovarian) and dementia and brain injury early in life.
- Spreading excellence within and beyond the partners. BIOPATTERN will regularly organise workshops, training events and conferences to spread excellence and to raise public awareness.

Using and disseminating knowledge widely and providing SMEs access to new knowledge to increase innovation and competitiveness and by making resources (techniques, software tools, data, reports, best practice etc) accessible to the academic, scientific and industrial communities.

INFOBIOMED PILOT

GENOMICS AND MICROBIOLOGY (PILOT 6.2)

Work undertaken as part of the Infobiomed WP6.2 pilot project is focussed on:

- The development and integration of novel BMI strategies for the analysis, characterisation and representation of virus-host pathway interactions with an emphasis on the interface between pathogen and Interferon signalling networks.
- Methods for the integration of data from laboratory and BMI studies with clinical data to facilitate personalised medicine.

This study focuses on 2 viruses of clinical significance: Cytomegalovirus (CMV) and Hepatitis C virus (HCV). Strategies, methods and approaches for dissecting interactions with host interferon signalling pathways are being developed which will underpin a clinical analysis of host responses to interferon therapy. When combined, these activities will provide a 'global' perspective on how the pathogen and patient interact with each other.

Specific activities in this pilot include:

1. A pilot clinical study designed to investigate early markers for therapeutic success in type 1 Hepatitis C infected patients. This is a collaborative project with Professor Peter Hayes and Dr Norma McAvoyn of the Wellcome Trust Clinical Research Facility in Edinburgh. The study will involve a whole genome microarray expression analysis of samples from patients prior to and at a range of times after the onset of peg-interferon therapy. On completion of this study, data will be analysed in the context of the pathway biology projects in this work-package and the extensive clinical data collected relating to the patient cohort.

2. The application of the software framework 'PIANA' to the further characterisation of host interferon signalling pathways and host-pathogen protein interactions. PIANA is a tool developed in IMIM/ UPF which aggregates publicly available protein interaction information and combines this with a prediction algorithm and graph-drawing capability. This is the first application of this software to a system-wide host and pathogen analysis and the project has focussed on the development of sensitivity/ specificity analysis metrics for PIANA, the expansion of 'canonical' interferon pathways and the prediction of new host-

pathogen protein interactions. New leads from this project have included the identification of a CMV gene of unknown function which may modulate the host interferon response. Laboratory work is underway to confirm this prediction.

3. The computational prediction of virus/ host microRNA sequences and their targets in the interferon pathway. This will reveal how small non-coding RNAs can alter host and/ or pathogen protein production in the infected cell and may yield new targets for therapeutic intervention. To-date, novel cytomegalovirus microRNA's have been identified by computational prediction, laboratory studies are underway to confirm their existence and a parallel computational analysis has been initiated to investigate the implications of these molecules on host cell signalling pathways. When the above projects are integrated with other WP6.2 pathway data modelling and notational development activities, it is hoped they will provide a foundation for the future evolution of Pathway Biology-related Biomedical Informatics.

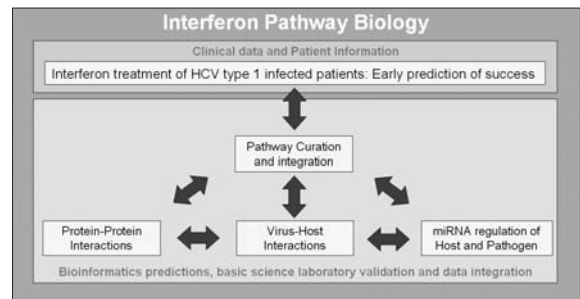


Figure 1. Schematic overview of WP6.2 project structure

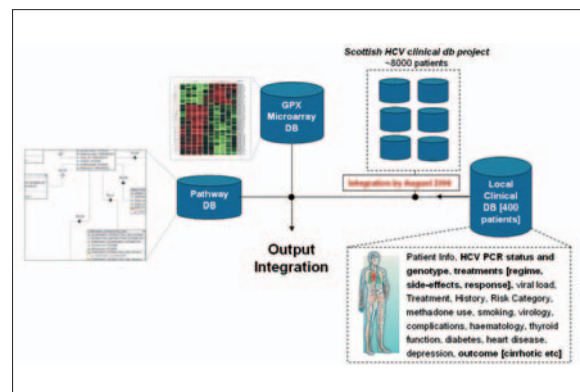
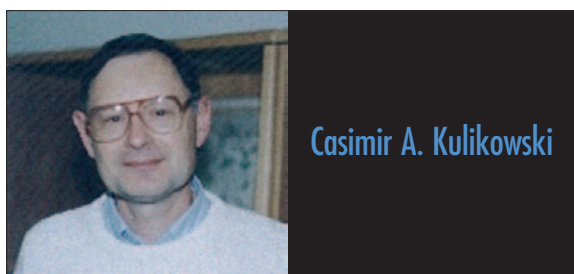


Figure 2. Schematic overview of pathway, microarray and clinical resources to be integrated as part of WP6.2

INTERVIEW

INTERVIEW WITH SCIENTIFIC ADVISORY BOARD MEMBERS

Picture



Bio-sketch

Casimir A. Kulikowski, PhD is Board of Governors Professor of Computer Science at Rutgers University. He is a member of the Institute of Medicine of the National Academy of Sciences (IOM-NAS) of the United States, a Founding Fellow of the American Academy of Medical Informatics (ACMI) and the American Association of Artificial Intelligence (AAAI), and a Fellow of the American Association for the Advancement of Science (AAAS) and the Institute of Electrical and Electronic Engineers (IEEE), and of the American Institute for Medical and Biological Engineering (AIMBE).

Professor Kulikowski received a Bachelor of Engineering in 1965 (Honors in Electrical Engineering), and a Master of Science degree in Engineering and Applied Science in 1966, both from Yale University. He received his PhD from the University of Hawaii in 1970 on the topic of pattern recognition methods for medical diagnosis under the supervision of Professor Satoshi Watanabe.

Questions:

■ *Brief description of the place where you work and the main research topics in which you are involved.*

Professor Kulikowski has worked at the Department of Computer Science at Rutgers University in New Brunswick New Jersey since 1970, carrying out a wide range of research on biomedical informatics involving collaborations nationally and internationally. With long-time collaborator Sholom Weiss, he co-

developed the first medical consultation system based on causal network models of disease (CAS-NET), the first compiled ruled-based expert system (EXPERT), which served as the basis for a large number of academic and commercial first generation expert systems and the first expert system on a chip incorporated in a medical instrument (the Helena Labs' scanning densitometer for protein serum electrophoresis). Later he worked on problems in biomedical imaging (model-based multi-model learning) and bioinformatics (AUTOASSIGN, which carries out automatic assignment of residues to spin systems in multimodal protein NMR interpretation). Professor Kulikowski headed the Rutgers Research Resource on AI in Medicine from 1984 to 1992. He served as Chair of the Computer Science Department at Rutgers University from 1984 to 1990, and was Director of the Laboratory for Computer Science Research from 1985 to 1996. He was chair of the National Library of Medicine's Biomedical Library Research Committee from 1997 to 1999.

Major areas of research are artificial intelligence, biomedical informatics, geophysical prediction, and the societal impact of computers, especially from biomedical technologies. In AI, concentration is on expert problem solving and knowledge representation, pattern recognition, clustering, visual reasoning and image interpretation. In medical informatics he works on models for clinical guidelines, on methods of medical decision support, biomedical imaging and predictive data mining. In bioinformatics I am working on pattern recognition and clustering methods for genomics and proteomics. In geophysics he is collaborating on hydrocarbon prospecting in basement rock formations. On societal impact, he is investigating the effects of computer technology on medical practice, biomedical research, and how it has affected the history of technology.

At present Professor Kulikowski is on the Editorial Board of *Methods of Information in Medicine*, is Co-Editor of the *Yearbook of Medical Informatics* of the International Medical Informatics Association, Associate Editor of the *Artificial Intelligence in Medicine Journal*, and is on the Program Committee of the American Association of Medical Informatics (AMIA) 2006 Meeting. He was Co-Chairman of the Program Committee of the triennial World Congress of Medical Informatics held in San Francisco in 2004. He has served on several scientific advisory committees and panels in the US (NAS-NRC 2001-2005, NIH

Director's Roadmap Advisory 2003-04, National Library of Medicine Long Term Planning Committee 2005-06), and Europe (EC-BIOINFOMED 2004-06). He has given invited keynote lectures in Europe, China, Japan, Taiwan, South America, Australia and the US on topics ranging from biomedical informatics to visual reasoning in artificial intelligence, and the societal impact of biomedical computing and IT more generally.

■ *What do you understand by Biomedical Informatics?*

Biomedical informatics involves the fundamental information representation and processing methods involved in biomedical research and the practice of health care, from the most basic biological mechanisms of disease at the molecular level to their clinical and public health impact worldwide. As a discipline it is uniquely able to investigate how both computational and human models of information interact in their impact on health care through the practice of medicine, nursing, and increasingly patients' own preventive care. Biomedical informatics works on all models of information in biomedical science that increase our understanding of, and ability to manage human health and disease in the individual and in groups or populations within an increasingly interconnected global environment.

■ *Which new relevant developments have you seen lately in the field of Biomedical Informatics, particularly in Europe?*

Europe has built on its strengths in many large-scale medical informatics demonstration projects and ongoing hospital and clinical systems to address how a new informatics will have to emerge to handle the great burdens on the health systems that will come from an aging population, coupled with the opportunities from ubiquitous highly distributed and pervasive computing. There are many groups engaged in creative technologies for patients in the home and outside of traditional tertiary care hospital settings. Likewise there is an emphasis on the socio-technical interactions that come from the complex effects of introducing technologies into existing health care systems, and the resulting needs for developing methods of testing and evaluation of systems in their organizational contexts. These are important thrusts that will help biomedical informatics extend beyond the overly technological focus so prevalent in the past,

and rigorously consider the factors needed to design effective, and human-centered health care systems.

■ *In your opinion, which are the new trends and future challenges for Biomedical Informatics?*

Challenges can be most easily grouped into several major categories depending on whether they are at the fundamental level of research in informatics itself, or applied to elucidating and supporting basic biological science, clinical science, clinical practice, or epidemiology/public health. Fundamental informatics issues include:

a) Developing foundational models of information processing and control from the molecular to the cellular to the tissue and systems levels, going beyond current static ontological frameworks, to capture the dynamics of bio-informational systems as they play out in genotype-phenotype relationships, understood in their developmental and evolutionary contexts;

b) Developing informatics models that increase the symbiosis between human perceptual and cognitive capabilities and those we have been able to increasingly emulate in "intelligent machines and systems". Biomedicine lends itself uniquely in studying how symbiotic capabilities with strong informatics components can help prevent negative health outcomes and extend our life-spans. Vast networks of distributed information provide complementary memories, sharable structures of information, and dramatically faster speeds of processing unmatched by individual humans, yet are strangely inept compared to the flexibilities of human ingenuity. The challenge for informatics is to discover how to take best advantage of complementarities as computational systems are designed to evolve to provide us better health-related insights and care.

c) Developing social models of systems organization that will work with human models of organization and health care provision, education, and improvement to help us in our design for future active health-enabling systems, rather than merely health-support ones as we have now.

More specific technical trends and challenges for informatics could be listed as:

a) Moving from IT-centered to human-centered design of information systems;

- b) Integration and scale-up of systems to handle a much larger number of health care interactions, not only with patients, but with health consumers who wish to prevent adverse future impacts on health.
- c) Investigate how visual and graphical components of human and machine reasoning can be more effectively understood from a bioscience and mathematical perspective to provide a foundation for our informatics theories.
- d) Integrate genomic and proteomic information in the clinical record and deal with the privacy and confidentiality issues involved.
- e) Understand better how patient's attitudes towards risk and uncertainty affect strategies of treatment and long term management
- f) Learn how to evaluate health technology as it is introduced prospectively into health care settings.
- g) Understand the broader regional, national, and global implications of pervasive information in an age of rapid transmission of health hazards – develop strategies for management and international coordination.

■ *Could you briefly compare the current situation Biomedical Informatics in Europe vs USA; Which are the strengths and weaknesses of each?*

Fundamental biomedical informatics models for research have been strong on both sides of the Atlantic. Traditionally, in Europe, biomedical informatics has benefited from a much stronger infrastructure of government-supported clinical care, which has led to major experiments and systems for structuring information with computerized health records and decision support within health care processes and organizations. In the USA, fragmentation of health care, especially in its funding and insurance mechanisms, has resulted in fewer large-scale informatics systems, but instead in many innovative, successful local and a few regional solutions to clinical problems. These trends continue, even though there is more convergence as Europe (except for Britain) finds it harder to afford health care systems, and the USA is inching towards more standardization of health information systems, while continuing fragmentation in administration. So, primary differences today seem to stem more

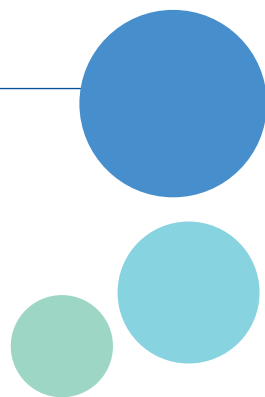
from underlying scientific and technological cultures affecting the biomedical informatics fields. In universities, the USA has always promoted entrepreneurial activities by its faculties, driven by strong competition for both government and private funds, increasingly encouraged to work in large cross-institutional groups, collaboratories, or consortia. European academic researchers have become more entrepreneurial in recent years in competing for EC and national funds by building coalitions of researchers also. The question in both Europe and the USA is whether such groups or coalitions will indeed deliver research and technology which is "more than the sum of the parts", rather than simply being a convenient administrative device for funding agencies to more easily manage research and promote diversity and inclusion across institutions, regions, and nations which, however desirable socially, may or may not improve the science, technology and health care outcomes!

For industrial groups in biomedical informatics, Europe has benefited from more stable long term research support of specialized instrument and systems – oriented research and development. The USA has typically been more short-term in its approach, but has also had significant technological innovation, which, however, has not generally translated into widespread general hospital and clinical improvements, which usually lag years, if not decades behind in their IT infrastructure from the trend setters in major research institutions.

The above is all changing as increasing expectations from informatics methods and the supporting IT puts pressure on informaticians to analyze the complex mix of technology and human organizations that together determine whether the informatics methods improve or detract from health care outcomes in the longer term. This is now reflected in an emphasis on all kinds of standardization initiatives, from the conceptual, with knowledge ontologies, to the practical, with standards for systems and their implementations and applications.

But, basic research on bioinformatics still finds elusive an underlying theory of informatics for health which is dynamic and can help us understand the evolutionary changes that occur with the introduction of all new technologies, and how they affect our ways of thinking and acting about health, disease, and the roles of human care givers that are essential to making any technology effective.

BIOMEDICAL INFORMATICS TO SUPPORT INDIVIDUALISED HEALTHCARE



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