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THE BIOLOGICAL CONTINUUM

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BACKGROUND

The 15th February 2001 was an important date in the history of medicine. This was the date of the publication, in Nature, of the paper that reported the initial sequencing of the Human Genome. In practical terms, it is possible to argue that this date represents the dawn of the 'New Medicine' ie molecular based medicine. From now on there will be a rapidly developing trend away from data poor to data rich healthcare systems; and a move away from treating clinical evident disease to diagnosis and treatment based on an understanding of disease mechanisms (down to the proteomic and genomic levels). Both of these trends will have a profound effect upon the way in which medicine in practiced.

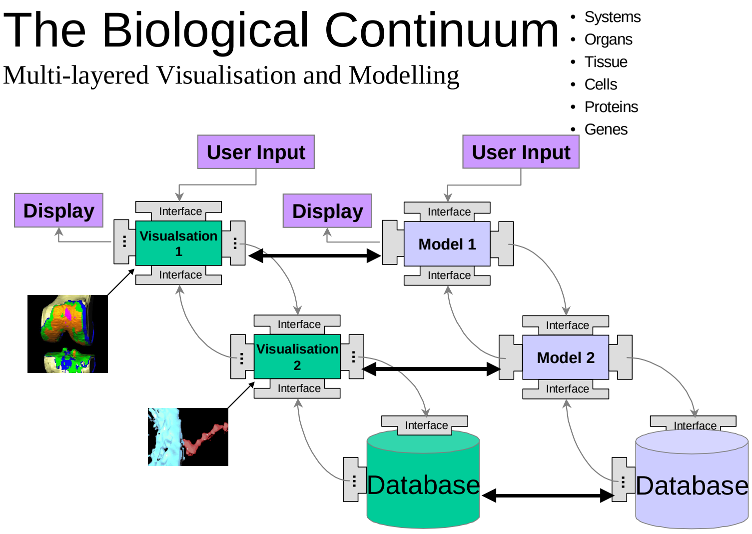
In a lecture in 2002 Dr Francis Collins- Director of the NIH Human Genome Project – said that "Sequencing the genome would not have been possible without major input from information and communication technology". In the exhibit we broaden this statement to show how engineering and physical science will play an ever increasing, important role in the future of medicine. We argue that central to the development of the 'New Medicine' is the concept of the Biological Continuum ie the hierarchy of the human organism comprising:

- Systems
- Organs
- Tissue
- Cells
- Proteins
- Genes

Medicine today is often practiced at one or two of these levels, ie there is generally no vertically integrated approach. This is set to radically change. We focus on a number of areas including imaging and visualisation; structural biology; gene and protein sequencing; as well as the specific contribution of technology (eg web-based clinical information systems –CISs; picture archiving and communication systems – PACS; and advanced database designs). The ability to image at all of these levels will become central to the practice of medicine.

ABOUT THE RESEARCH

In order to incorporate the concept of the biological continuum into that of a computer-based system, which can operate across the entire range from physiological to genes, it was necessary to develop schema for such a system. This is illustrated in Figure1. Referring to the figure, it is important to understand that the architecture comprises three levels: Level 1, user input and display; Level 2, visualisation and modelling; and Level 3, databases. For the purposes of the



diagram, only two of the six layers of the biological continuum have been illustrated; hence, in reality, Level 2 would comprise layers for systems, organs, tissue, cells, proteins and genes. There is now a range of imaging techniques which are being used in basic medical science. These methods range from well known clinical imaging techniques such as MR and PET (which can operate at the whole body level) to cryo electron microscopy (used for imaging molecules and protein machine,

Figure 1 The architecture for a computer based system to incorporate data from the Biological Continuum

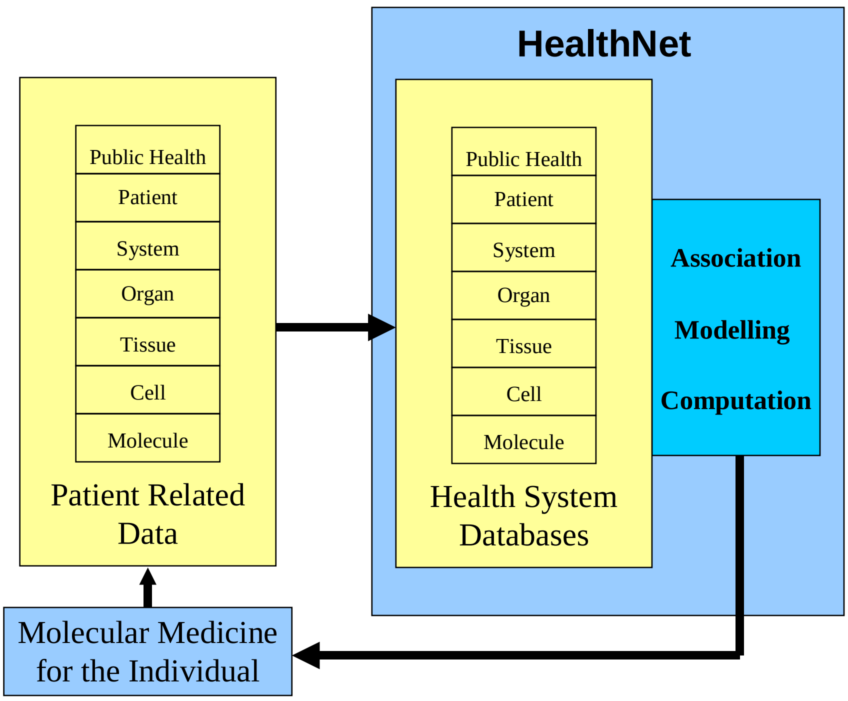
cells etc) to atomic force microscopy (AFM) at the molecular level. It is likely that many of these techniques will be introduced into clinical medicine over the next few years (covering a broad range of specialties). From and imaging and visualisation standpoint, the acquisition of data using these and other techniques varies according

to the technology. However, once the data have been acquired, their manipulation, in terms of 2D images and the creation of 3D models (rendering), uses virtually the same approach for all the methods. Hence, the schema illustrated in Figure1 is based on common software at all the levels.

The further development of clinical information systems (CISs), including PACS, is likely to be based on the architecture shown in Figure1. This will provide clinicians with the ability to move seamlessly through the different levels of the biological continuum. In addition, CISs are now being developed which not only cover the various levels of the biological continuum from an imaging standpoint, but also incorporate modelling techniques (for example**,** physiological systems and systems biology models**;** as well as, for example, 3 dimensional models of proteins**)**. The use of models to compare predicted results with actual results will, we believe, be an important feature of future CISs. Hence, in the future it will be possible to extend diagnosis from the traditional approach using signs and symptoms right through to studying genetic and proteomic abnormalities (ie the molecular basis of disease for the individual patient). For this to become reality, it is necessary to develop fast sequencing techniques for genes and proteins, as well as modelling techniques based in structural biology, in order to understand their structure and function.

Another important feature of this new type of CIS will be the ability of clinicians to get universal access to all of a patient's data in real-time (ie at multiple locations). There are four key technology components which make these objectives achievable: (i) the price and power of PCs; (ii) the availability and use of industry standard hardware and operating systems; (iii) the use of comprehensive international standards (ie DICOM, HL7 and XML); and (iv) the ability to provide fully web-based (ie Internet Protocol based) CISs, including PACS. This means that the new architecture for CISs (including PACS) will be based on a model which comprises system architecture using internet protocol (IP) technology and standard telecommunications technology. Specifically, the architecture is likely to be based on a four-layer model. This comprises, at its base layer, advance database technology. The next layer is an application layer. Above this is a communication layer. The top layer of the system comprises the web browser.

In summary, more advanced CISs are likely to be based on the architecture illustrated in Figure1. The concept of the biological continuum means that clinicians and healthcare systems will use a much broader range of data and information. The scope of the future CIS is illustrated in Figure2. Referring to the figure, it can be seen that in addition to data and information from across the biological continuum, public health data are included. All of this information will be incorporated into a universal health database, HealthNet [our term], which may be for a region, a country or European wide.



deltaDOT CTO Dr John Hassard with Imperial College London’s Rector, Sir Richard Sykes at the Royal Society, July 2004