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EDITORIAL

- by Georgios Stamatakos, Research Professor, ICCS NTUA, CHIC Coordinator –

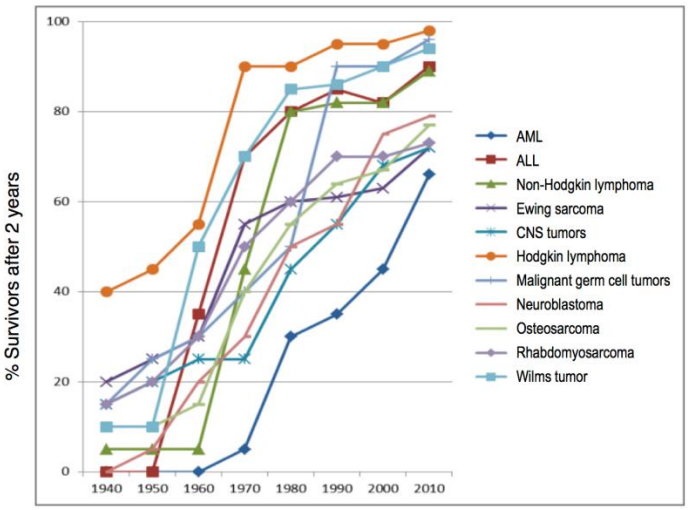
Following the successful completion of the second year of the CHIC project implementation, the CHIC consortium is looking forward to demonstrating a comprehensive workflow exploiting major scientific and technological advances of the project. The main demonstrator scenario to be presented during the next annual review meeting refers to the design and the technologically supported semi-automatic implementation of a hypermodel (composite model) to help a clinician in selecting the optimal treatment scheme and schedule for a given lung cancer patient. The end user will be able to reuse hypomodels (component models) simulating several crucial tumour behaviour

mechanisms manifested at various spatiotemporal scales which have already developed by different modelling groups located in both Europe and the United States. The representative hypermodel to be created will be compared with real multiscale pseudonymized clinical data provided by Professor Rainer Bohle, University of Saarland, Germany. In this issue several CHIC partners and research groups present their activities, offering a flavour of both the CHIC project and the consortium. The special guests are Professor Emeritus David Ingram, University College London, specializing in biomedical informatics and a Member of the External Advisory Committee of CHIC and Professor Norbert Graf, Director of the Pediatric Oncology and Hematology Clinic, University of Saarland, Germany. Norbert is the leader of two workpackages dealing with the user needs and requirements as well as the crucial issue of clinical validation of hypermodels. I hope you will find this newsletter both informative and enjoyable.

The future of in-silico oncology in the clinical context

- by Norbert Graf, Pediatric Oncologist from Saarland University, Germany -

Paediatric Oncology has been one of the success stories in medicine over the last 40 years. Cure rates of cancer in childhood dramatically increased from nearly zero to now around 80% for all children with cancer in the Western World. Nevertheless we are facing the problem that we are not able to cure every child. It seems that we are approaching a threshold that cannot be surpassed by common medical knowledge and practice. The main reason for the success story in the past was the enrolment of over 90% of children with cancer in prospective, multicentre and randomized clinical trials. This is in big contrast to adult oncology, where only 5% are enrolled in clinical trials.



Increase of survival in pediatric oncology for different cancer types

Due to the results of the clinical trials today we can classify patients in different treatment groups according to their individual risk factors. This allows less treatment for those patients with good prognosis and spares them acute long-term side effects, and more aggressive treatment for those patients with poor prognosis. But even in doing so we do not understand why some patients relapse and die. To overcome this situation new approaches in clinical research and medical care are needed.

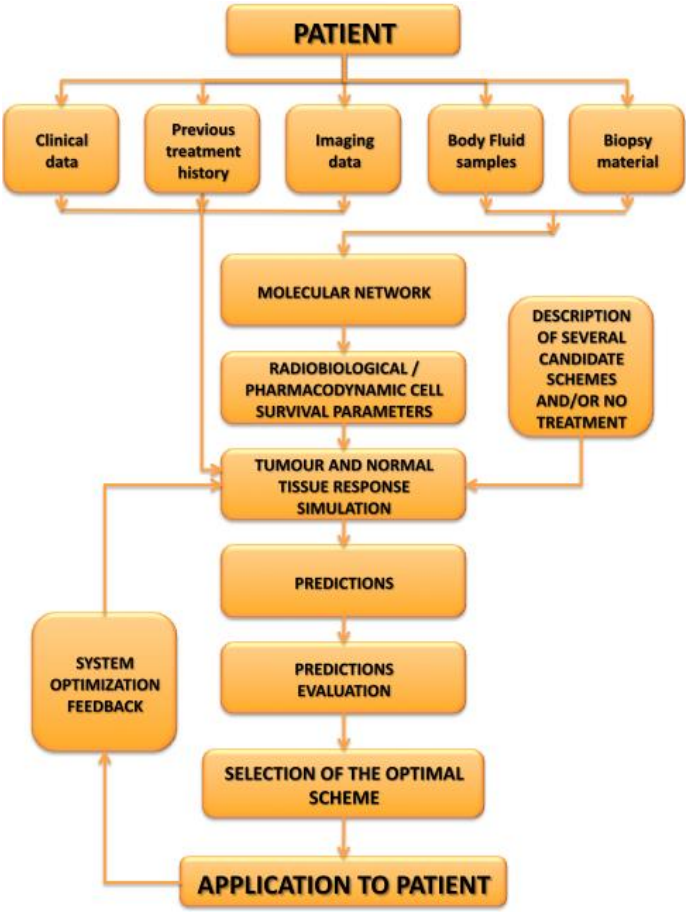
Medicine is undergoing a revolution that is transforming the nature of healthcare from reactive to preventive and to a personalized predictive treatment[1]. The changes are catalysed by a new systems approach to disease that has triggered the emergence of personalized medicine — a medicine that focuses on the integrated diagnosis, treatment and prevention of disease in individual patients. Immense progress in IT-technology, computer-science and molecular biology facilitates such a new approach. Information arising from post-genomic

[1] http://www.cra.org/ccc/initiatives

research and combined genetic and clinical trials on one hand, and advances from high-performance computing and informatics on the other, are rapidly providing the medical and scientific community with an enormous opportunity to improve prognosis of patients with cancer by individualizing treatment and going towards personalized medicine. Multi-level data collection within clinico-genomic trials and interdisciplinary analysis by clinicians, molecular biologists and others involved in life science is mandatory to further improve the outcome of cancer patients. It is essential to merge the research results of biomolecular findings, imaging studies, scientific literature and clinical data from patients and to enable users to easily join, analyse and share even great amounts of data.

This development has motivated the concept of the Virtual Physiological Human (VPH) that seeks to develop a scientific methodological and technological framework within which it will be possible to construct models of the human body as a single complex dynamic system. While research in VPH is going on, resulting disease models simulators have not reached an acceptable level of maturity to be used in clinical routine. Especially in cancer this is a highly demanding endeavour. A sound multiscale and multidimensional modelling of the *natural phenomenon* of cancer is a *sine qua non* prerequisite for a clinically exploitable understanding of the disease as already emphasized during the 1st Transatlantic Workshop on Multiscale Cancer Modelling, jointly funded by EC (ICT) and the National Cancer Institute in US (NCI) (Brussels 2008)[2].

Based on the latest advancements in the field, clinically driven complex multiscale cancer models can produce rather realistic spatio-temporal simulations of concrete clinical interventions such as radio-chemotherapy applied to individual patients. Clinical data processing procedures and computer technologies play an important role in this context. Following clinical adaptation and validation within the framework of clinico-genomic trials, models are expected to enhance individualized treatment optimization.

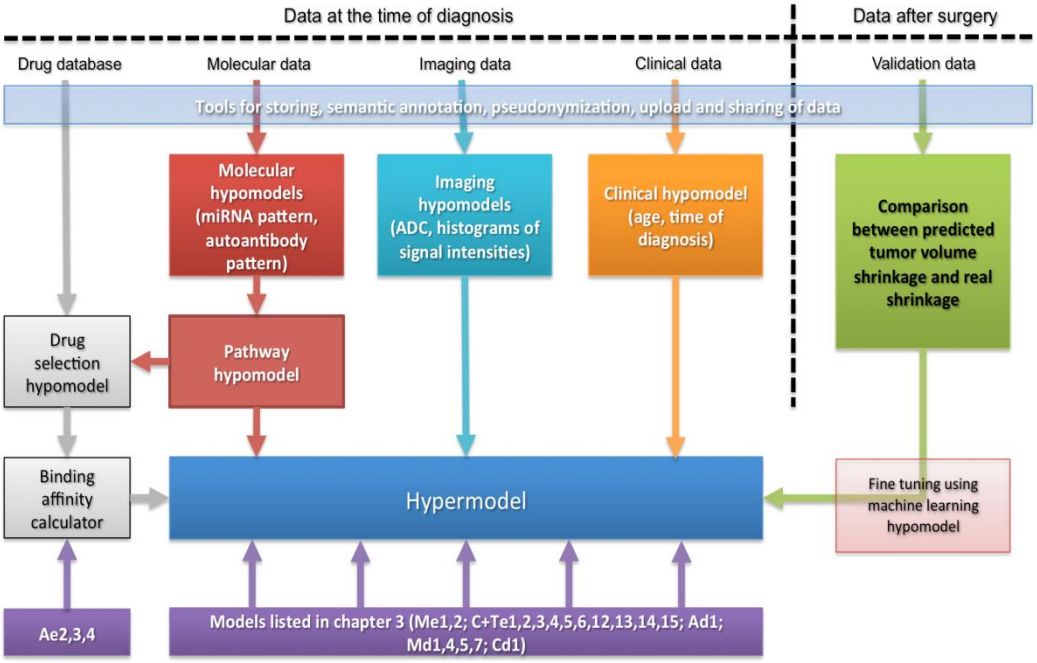


The latter constitutes the long-term goal of the emergent scientific, technological and medical discipline of in-silico oncology. Treatment optimization is to be achieved through experimentation in-silico i.e. on the computer. Moreover, provision of insight into tumour dynamics and optimization of clinical trial design and interpretation constitute short- and mid-term goals of this important VPH domain.

The Oncosimulator, an in-silico model or tool, is at the same time a concept of multilevel integrative cancer biology, a complex algorithmic construct, a

[2] http://ec.europa.eu/information_society/events/ict_bio/2008/docs/2008 11cancer-model-wkshp-report.pdf

biomedical engineering system and eventually in the future a clinical tool which primarily aims at supporting the clinician in the process of optimizing cancer treatment in the patient individualized context through conducting experiments in-silico. Additionally it is a platform for simulating, investigating, better understanding and exploring the natural phenomenon of cancer, supporting the design and interpretation of clinic-genomic trials and finally training doctors, researchers and interested patients alike[3,4,5].



A synoptic outline of the clinical utilization of a specific version of the Oncosimulator, as envisaged to take place following an eventually successful completion of its clinical adaptation, optimization and validation process is provided in the form of steps.

From a clinical perspective it is important to know that the oncosimulator depends on the usage of heterogeneous reliable data. To support the development of the oncosimulator, an IT framework needs to be in place that will handle these data and make it accessible by the oncosimulator within a legal framework. Initial questions to be answered by the oncosimulator should be easy and possible to validate.

The clinician is always the person who will perform the validation and judge if the prediction of the oncosimulator is correct or not. A feedback loop from the result of the validation will fine-tune the Oncosimulator. Machine learning processes support the ooptimazation of the Oncosimulator. Figure 3 shows a schematic overview of the data needed by the oncosimulator as it will be developed as a hypermodel in the CHIC project for nephroblastoma, the most common kidney cancer in childhood. The question that will be answered is if preoperative chemotherapy will shrink the tumor volume.

Today the Oncosimulator can be compared with the weather forecast 20 years ago. It can be awaited that further improvements will result in an Oncosimulator that will give precise answers on how a given tumor in an individual patient will respond to which kind of treatment. At that time and after validation and certification of the Oncosimulator it can be used in clinical care as a decision support service, allowing testing a treatment for a cancer patient just before applying the treatment to the patient. This might also spare animal experiments if the scientific community will

[3] Stamatakos, G. S. and Uzunoglu, N. 2006b. Computer simulation of tumour response to therapy. In S. Nagl Ed. Cancer Bioinformatics: from therapy design to treatment. John Wiley & Sons Ltd, Chichester,UK. pp.109-125

[4] Stamatakos G.S., D.D. Dionysiou, N.M. Graf, N.A. Sofra, C. Desmedt, A. Hoppe, N. Uzunoglu and M. Tsiknakis. 2007a. The Oncosimulator: a multilevel, clinically oriented simulation system of tumor growth and organism response to therapeutic schemes. Towards the clinical evaluation of in silico oncology. Proc 29th Annual Intern Conf IEEE EMBS. Cite Internationale, Lyon, France Aug 23-26. SuB07.1: 6628-6631

[5] Graf, N., A. Hoppe , E. Georgiadi, R. Belleman, C. Desmedt, D. Dionysiou, M. Erdt , J. Jacques, E. Kolokotroni, A. Lunzer, M. Tsiknakis and G. Stamatakos. 2009. "In silico oncology" for clinical decision making in the context of nephroblastoma. Klin Paediatr 221: 141-149

accept the oncosimulator. To reach all these goals medical doctors need to learn the possibilities of these new technologies and curricula of medical schools need to be changed to teach also IT-technologies and the advantage of tools and models. Therefore dissemination activities of the achievements of the CHIC projects are of utmost importance and will be carried out in an unprecedented way.

Prof. Dr. Norbert Graf is Professor of Paediatrics and Director of the Clinic for Paediatric Oncology and Haematology and a member of the Faculty of Medicine of Saarland University and currently the dean for study affairs. He is the chairman of the Renal Tumour Study Group of the International Society of Paediatric Oncology (SIOP-RTSG) and the Principal Investigator of the current Trial for Childhood Renal Tumours within SIOP. He is an Associate Member of COG (Children's Oncology Group, North America) and closely cooperating with the COG Renal Tumor Study Group. Prof. Graf has more than 25 years of experience in running clinical trials. He is a member in many national and international scientific societies. As the coordinator of p-medicine, an EU funded large integrated project, he tries to pave the way to personalized medicine. He is also a member of the board of the VPH-Institute and further ongoing EU funded research projects (EURECA, CHIC, MyHealthAvatar, iManageCancer).

Some personal reflections on the CHIC project

- by David Ingram, Emeritus Professor of Health Informatics at University College London and member of the External Advisory Board of CHIC –

David Ingram pictured almost, but not quite, at the Clooney wedding taking place nearby

In the best traditions of the CHIC and p-medicine genre of projects, my request for some reading to help me prepare for the recent Advisory Board meetings in Ghent led to an intensive day-long reading session of some 500 pages of reports, newsletters and deliverables that were emailed to my inbox, by return! As a reviewer of the earlier ACGT project, my colleague Olle Bjork was wont to announce the huge page count of reading that the panel had undertaken, ahead of the formal meetings! Last week, the CHIC document describing the progress with implementation and testing of interesting new multiscale models, sent by Georgios Stamatakos (coordinator of CHIC), was a great read and showed how far the project has progressed since I last attended at Luton in the UK.

It took me back to my dominant academic research stream, thirty years ago, which focussed on mathematical modelling of the human cardiorespiratory system and its application in teaching medical students and trainee anaesthetists. We installed mass-spectrometry equipment close to the ICU, to record the state of the art, then, of data about management of the acute respiratory disorders affecting the patients, and the capability to match our models to these dynamic situations, as artificial ventilator and oxygen settings, as well as acid-base balance corrections, were invoked to seek to stabilise them, while they recovered.

A number of key themes emerged which chime with the progress of CHIC.

1. The models themselves depended on the critical insights and abilities of clinical research colleagues, to form and guide the creation of valid simulations of the underlying systems, in health and disease. These were often less than elegant to the physicist and mathematician in me, but they conveyed a level of realism and meaning that it was hard to achieve with more traditional mathematics of non-linear differential equations.

2. Matching the models to the data we collected was a tough challenge - finding the best strategy for optimising this fit took several years to work through.
3. Likewise learning about the synergy achievable between what could be achieved in data collection and the related model formulation and parameterisation, was an iterative process that went through many cycles.

I had gone through a similarly enlightening experience in my earlier doctoral research project, matching models of cardiovascular system dynamics to data from patients being treated after suffering heart attacks, to see what could be learned, non-invasively, about the diminution and recovery of cardiac pump performance. Collecting 10 days of continuous data on a small cohort of ICU patients proved a nigh-on impossible operational challenge for the clinical team supporting me. In subsequent years, as I progressed from Lecturer to first UK Professor of Medical Informatics, a somewhat odd and smiled at badge in those days, I went through similar learning in other areas of clinical physiology model identification, working with some of the top physiologists and physicians of that era. What came out of it were models that travelled the world, published as an experiment by Oxford University Press, finding their way into the curricula and research programmes of hundreds of medical schools and research institutes. But in the end we could not achieve a good enough balance of achievable data collection and useful model formulation. After two decades of exciting development, the models became technologically obsolete and lost their pioneering scientific champions in London and at McMaster University in Canada. So there was a loss of staying power and a resulting failure to sustain the promise.

By contrast, I reflect on a success story – probably the most outstanding success thus far in computer decision support in medicine – notable as much for the fact that it is seldom mentioned as such, for its founding contribution to this domain. It worked, and works, so well that it is largely invisible! In today's speak, I refer to *in silico* radiotherapy treatment planning. My career spanned the earliest pioneering work of those that conducted experimental studies of absorption of radiation by tissue, and derived mathematical models that could be manipulated in the computer to predict the effect of combining different beam angles and durations of the cobalt and linear accelerator radiotherapy treatment machines. Thereby, the models provide an interactive means to support efforts to concentrate dose to the tumour, and minimise impact on local healthy and vulnerable tissue. This transformed what had hitherto been a rather laborious desk-based paper exercise, laying measured beam profile transparencies onto a map of the patient cross-section being treated, and, working by eye and with experience, arriving at a good plan. The computerised methods survived and evolved, in large part because they met a need and fitted the capabilities of the service and work force of the time. They were published openly and could be taken up into new commercial products and services of the radiotherapy equipment suppliers, and could be validated and checked in experiments with tissue equivalent materials and *in vivo*, using well-established physical measurements of dose. The modelling was thus anchored in both relevant and achievable measurements, and a clinical treatment and physics support service that was conducive to developing and optimising, and then accrediting and supervising, the safety of the method.

In my early work, the mismatch between achievable measurement and the mathematical modelling of the clinical physiology systems could not be bridged. What had made an impact worldwide as an educational resource did not make a transition into clinical practice. CHIC appears poised at this moment of truth in its own evolution. Can the already impressive and persuasive models of tumour growth and treatment move from plausible verification to real-life validation in larger experimental cohorts of patients, and demonstrate an added value that is in some sense worth the price, in health care delivery and outcome terms. It is a long journey, with potential to lead to transforming outcomes for health care as well as in basic science, and that will be a fascinating progression to observe. The project has some hugely capable and devoted champions. It's a great pleasure and privilege to be a close observer and friend of this journey.

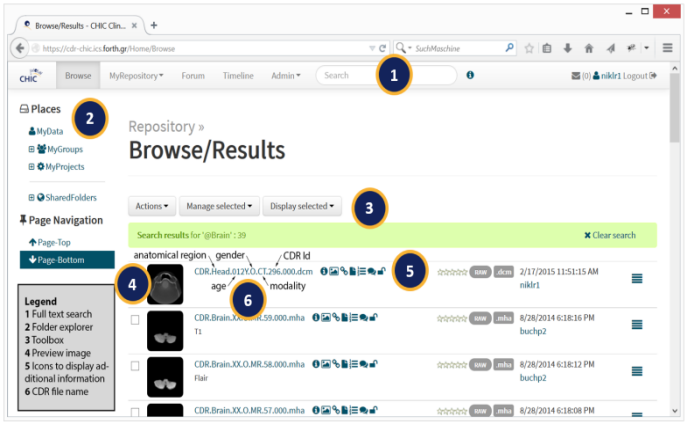
David Ingram studied Physics at Oxford University and then worked for some years in the medical engineering industry and hospital medical physics. His subsequent doctoral research at UCL in London, focused on the clinical application of mathematical models of physiological systems, in close partnership with McMaster University in Canada. He moved on to a lectureship in the Department of Medicine at St Bartholomew's Medical College London, where he became the first UK Professor of Medical Informatics in 1989, and from 1995-2010 he led the development of health informatics at UCL. He has been active in numerous, large scale research projects of the EU and UK Research Councils, starting with the EU GEHR project in 1991-1994. This laid the foundations for the freely available openEHR specifications for electronic health records, now implemented in a rapidly growing number of commercial products, national programmes and research projects, throughout the world. His retirement interests include continuing professional roles as President and Chairman of the Board of Governors of the openEHR Foundation and as a Trustee of the OpenEyes project, which is building open source electronic records for ophthalmology. Nine grandchildren, and a shared passion with his wife Bozena, for Ballroom, Latin, Salsa and Argentine Tango dance, keep life full of fun.

SPECIAL FOCUS: THE CHIC TOOLS AND SERVICES

The CHIC Clinical Data Repository

- by Philippe Büchler, Michael Kistler, Roman Niklaus
University of Bern, Switzerland –

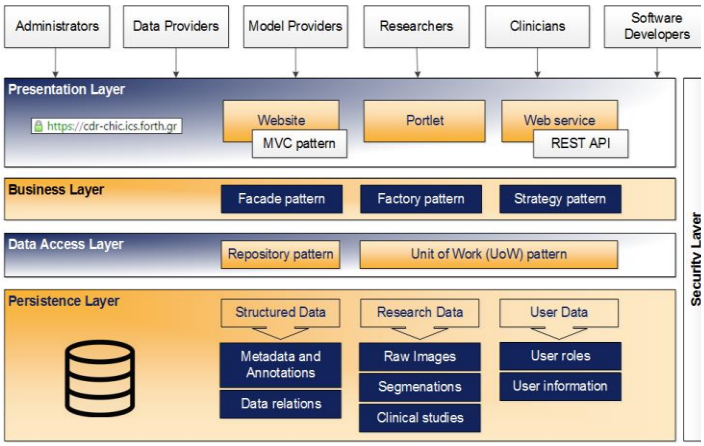
Accessibility of a large quantity of reliable data is key for the development and validation of any predictive model. In the medical field, the need of modeling teams to access data conflicts with the ethico-legal constraints that protect the patient. The role of the Clinical Data Repository is to provide the CHIC modelers with clinical data in a way that conforms to legal requirements and that fulfills data protection principles. In addition, the data repository provides mechanisms for data annotation to ensure that a high level of data quality can be maintained and to allow for easy identification and retrieval of the stored information.



Web-based user interface to visualize the content of the Clinical Data Repository and organize the data within personal work spaces.

The development of the clinical data repository was initiated in 2010 with a focus on collecting large amount of medical images to study bone morphological variability [1]. Within CHIC, the system has been adapted to permanently host all the clinical data produced or collected during the project. It embraces a pseudo-anonymisation approach to protect patient's privacy: Similarly to a cryptographic hash function, a unique pseudonym is generated for every patient by a trusted third party (for CHIC, Custodix NV in Belgium), so that no

identifying information can be obtained from the database without explicit authorization. This one-way concept can be applied to the general data upload workflow in CHIC. Additionally, authentication and authorization mechanisms are in place to control and restrict access to any clinical data stored in the database.



The multi-layer architecture of the Clinical Data Repository

As various types of data are required to build multi-scale disease models, clinicians in CHIC will provide medical images, histological photographs, genomic data or clinical data. Storing this diverse data requires a flexible system. For this reason, the CHIC Clinical Data Repository was built around the concept of "data objects" which can be any type of image file, processed data or clinical data. This approach provides flexibility in terms of data formats supported by the system, data organization, and data collaboration. The design is intended to have the capacity to provide the same basic functionality as a PACS (Picture Archiving and Communication System), but it is more flexible and can integrate additional research data, such as labeled images or any other clinical data.

The system will extract metadata associated with each clinical dataset and store this information to enable efficient search. Additional semantic annotation will allow data retrieval through advanced concept-based queries against domain ontologies.

Users can access the full content of the Clinical data Repository through a web portal [2]. Through this interface, users may also create personal workspaces where they can use virtual folders to organize available datasets and to store query results. A RESTful API [3] has been implemented for direct programmatic access to the database.

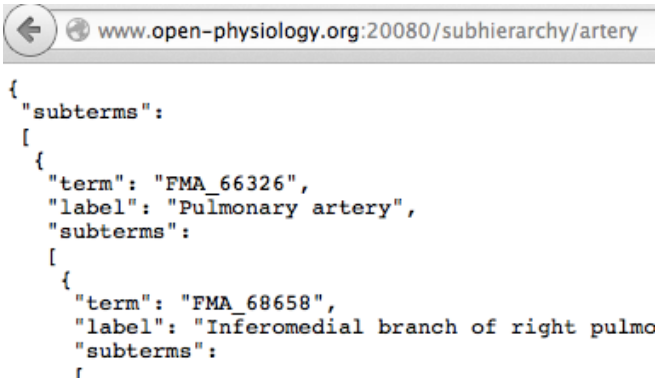
We encourage you to visit our demonstration prototype following the links below, and we look forward to receive your feedback.

[1] http://www.jmir.org/2013/11/e245
[2] https://cdr-dev-chic.ics.forth.gr
[3]https://cdr-dev-chic.ics.forth.gr/api/help

Usage of Semantic Metadata within CHIC

- by Bernard de Bono and Samuel Alexander, University College London, UK –

Imagine you've got a stack of a dozen X-ray images. On each one, the technicians wrote key information by hand. "Left lung," says one, in jagged cursive. Another says, "This image was taken 3/4/97". (Is that April 3rd or March 4th, you groan.) You're gonna have to go through every one of these and make what you can of it. Soon they'll be taking X-rays of you, to diagnose your chronic stress breakdown!



Fortunately that nightmare is past. We live now in the age of semantic metadata, where X-rays are annotated with unambiguous subject-verb-object style triples in a triplestore, from a standardised vocabulary (or ontology—see Figure). Image processing should be focused on finding tumours, not on decrypting handwriting!

One of the key advantages of semantic metadata is interoperability. What that means is the data can be shared between different computer programs, without tons of ad hoc, error-prone special case translation efforts. If you're writing a program to run mathematical models, the last thing you want to do is churn out 10,000 lines of code to deal with subtle distinctions between the different names of the different arteries and veins and nerves.

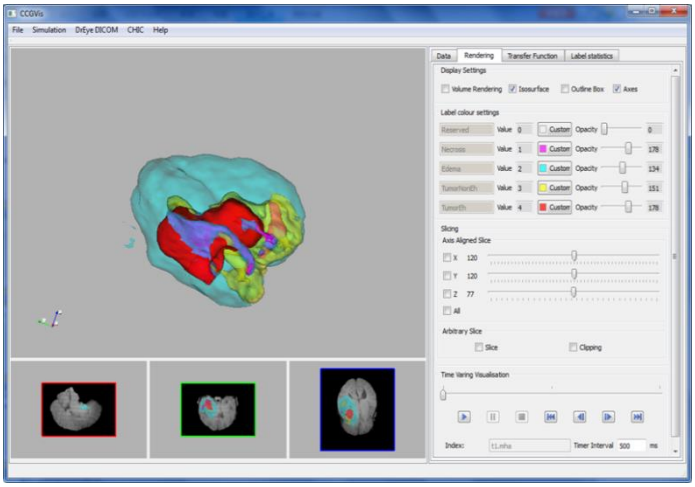
UCL has prepared RICORDO, a suite of semantic metadata APIs for usage within CHIC. There's the OWLKB API, which makes complex ontological expression as easy as writing a noun-phrase in English. There's the RDFStore template system, which allows experts to create a template one time, so that end-users can perform a needed search infinitely many times, without having to know the tricky languages normally used to query triplestores. And there's the Local Ontology Lookup Service, or LOLS, which allows blazing fast lookups against standard ontologies, so that, to the end-user, it seems like your program has all that medical vocabulary built-in.

So tell your technicians to put down those markers. There's no more need to jot notes down on X-rays. Instead, let's transcribe things in a standardised store of annotations, just bursting with programmatic analysis potential.

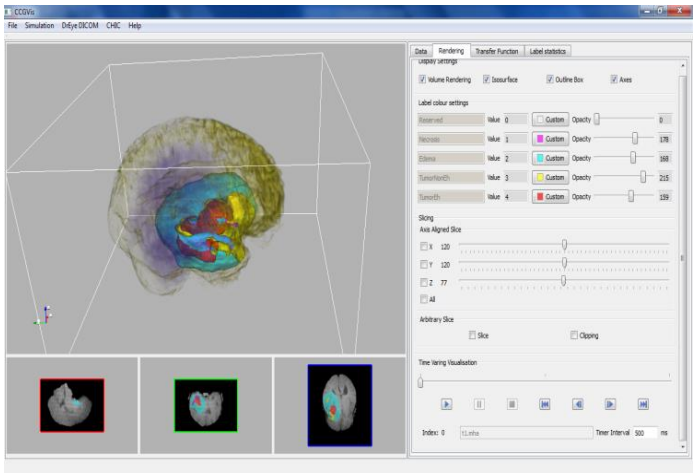
A Story of CCGVis

- by Feng Dong and Youbing Zhao, University of Bedfordshire, UK –

Time-dependent simulations and time-varying data are commonly used in clinical applications and research. CHIC supports the creation of multiscale cancer hyper-models. The state-of-the-art in silico technologies allow advanced modelling of many cancer growing processes in response to different treatment regimes both in the spatial and temporal domains. This results in a significant amount of time-varying data, which are dynamic in nature and the ability to visualize the time-varying phenomena is of great important for clinicians and medical researchers to allow for correct interpretation and analysis, provoking insights and communicating those insights to others. Studying these dynamic aspects of the biological processes is critical to the advances of in silico simulation, as well as to clinical decisions in clinical practices. An increasingly challenging problem that the clinicians and medical researchers must face is how to effectively explore and understand these resulting time-varying volume data that is large in space, time and variable domain.



As part of the integrated image processing and visualization platform Dr Eye, CCGVis is a suite that provides relevant clinicians and medical researchers a means to interactively view and analyse the growth of the tumour as well as the predicted responses to clinical treatments. It enables the users to seek insight of the process and outcomes of the tumour simulation by examining the tumour size, shape, position and composition at different time points in a highly interactive manner. Slice views with highlighted tumour segmentation are useful to position the tumours in 3D space. 3D surface and volume rendering of the segmented tumour in the temporal domain are provided in order to display the shape of the tumours and their locations in the body.



GET TO KNOW US!

As a large scale European collaborative project with a transatlantic arm, CHIC consists of a very diverse consortium of experts in cancer research. In each of the 4 annual CHIC newsletters, we introduce you to individual members of our consortium, their institution, research and tasks in the CHIC project.

The Institute of Surgical Technology and Biomechanics (ISTB), University of Bern, Switzerland

The Institute for Surgical Technology and Biomechanics (ISTB, www.istb.unibe.ch) from the University of Bern was established in 2003 .The institute stands in the tradition of Maurice E. Müller, one of the pioneers of modern orthopedic surgery, who is known not only for his many innovations related to devices and instruments for joint replacement and fracture treatment, but also for his vision that only a close collaboration between surgeons, scientists, engineers, and industrialists will enable sustainable progress in the field. To date the ISTB hosts five research groups in various fields of basic and applied research for the prevention, diagnosis and treatment of disease, working from the cell level to organ systems.

Premises of the ISTB at the University of Bern

The mission of the multidisciplinary team of the ISTB is to advance human understanding, health, and quality of life. The focus is on developing solutions that address particular clinical problems or unmet clinical needs. It supports this effort through internationally recognized research, discovery, and invention in the area of biomedical engineering, as well as through translation of research results from the lab to the clinic, transfer of scientific discoveries and biomedical technology through industrial collaborations and an international post-graduate biomedical engineering education program.

Prof. Mauricio Reyes leads the Medical Image Analysis group at the ISTB, which aims at developing mathematical models, algorithms, and computational tools to leverage the use of medical image information in the clinical scenario. The role of medical imaging is pivotal in today's medical practice and has shown to play a great role in the development of new solutions for the treatment of patients. In the last years, the Medical Image

Analysis group has developed new approaches to effectively use the vast amount of available imaging information for the treatment of brain tumors, as well as other diseases of the central nervous system. As result of this research, translation into the clinics has been performed through dedicated software tools, which are now being used in different areas, such as neurosurgery, neuroradiology, and radiotherapy. As an example, the software tool BraTumIA (Brain Tumor Image Analysis) has been clinically evaluated and made available to the scientific community. Since its release, BraTumIA has been downloaded in more than 45 countries and over 150 different institutions. The dissemination of the tool has allowed us to foster improvements as well as to promote the visions of the CHIC project. In this regard, the CHIC project is for the Medical Image Analysis group an important niche of developmental improvement, rich clinical feedback and dissemination platform.

The ISTB team at the University of Bern

The Computational Bioengineering Group lead by Prof. Philippe Büchler tackles challenges in basic and applied medical research using modern computational simulation tools. Rather than focusing on the computational methods themselves, we are concerned with their appropriate application for the resolution of practical and fundamental clinical questions. Based on the expertise in modeling soft and hard tissues, biomechanical simulations have been developed to estimate the mechanical stress in the healthy and pathological tissue around cancerous tissue. This information is used to drive the geometric evolution of a growing tumor Combined with models of tumour biology, the resulting multi-scale model will be used in oncosimulators for tumor types where the morphometric information plays a major role in treatment and surgical planning.

CINECA Supercomputing Centre

CINECA, established in 1969, is a non-profit consortium of 70 Italian Universities, 4 Italian Research Institution and the Ministry of Education, University and Research (MIUR). CINECA is the largest Italian supercomputing centre, and one of the most important world-wide with an HPC environment equipped with cutting-edge technology and highly-qualified personnel which cooperates with researchers in the use of the HPC infrastructure, in both the academic and industrial fields.

CINECA headquarters

CINECA's mission is to enable the Italian and European research community to accelerate the scientific discovery using HPC resources in a profitable way, exploiting the newest technological advances in HPC, data management, storage systems, tools, services and expertise at large. With more seven hundred employees, it operates in the

technological transfer sector through high performance scientific computing, the management and development of networks and web based services, and the development of complex information systems for treating large amounts of data. It develops advanced Information Technology applications and services, acting like a trait-d'union between the academic world, the sphere of pure research and the world of industry and Public Administration.

The SCAI Department in CINECA has a long experience in cooperating with the researchers in parallelising, enabling and scaling-up their applications in different computational disciplines, covering condensed matter physics, astrophysics, geophysics, chemistry, earth sciences, engineering, CFD, mathematics, life sciences and bioinformatics, but also "non-traditional" ones, such as biomedicine, archaeology and data-analytics. CINECA has strong relationship with its own stakeholders and collaborates with the scientific communities to enable and develop new applications and tools to better address the challenges of the high-end HPC systems.

CINECA Supercomputing Centre

CINECA represents Italy in many European Union projects, participating in numerous activities relative to the promotion, development and diffusion of the most advanced information technologies.

On mandate of the MIUR Ministry, CINECA represents Italy in PRACE, the Partnership for Advanced Computing in Europe (www.prace-ri.eu), a persistent pan-European Research Infrastructure (RI) providing leading HPC resources to enable world-class science and engineering for academia and industry in Europe. CINECA is one of the four PRACE Tier-0 Hosting Centers. Since June 2014, Sanzio Bassini, director of Supercomputing, Application and Innovation Department (SCAI) in CINECA, is the chair of the PRACE Council.

CINECA is one of the founding members of the European Technology Platform for HPC (ETP4HPC), an industry led forum providing a framework for stakeholders, to define research priorities and action plans on a number of technological areas where achieving EU growth, competitiveness and sustainability requires major research and technological advances in the medium to long term period. Moreover CINECA SCAI is the Italian representative in the pan-European EUDAT Collaborative Data e-Infrastructure and core partner in Human Brain Project, the EU flagship project facing the big challenge of understanding the human brain.

CINECA has several years of experience in EU projects since FP3: PRACE Series PP, 1IP, 2IP, and PRACE-3IP (www.prace-ri.eu); European Exascale Software Initiative EESI and EESI2 (www.eesi-project.eu); in HPC-Europa 2 CINECA was the Coordinator (www.hpc-europa.eu); European Data Infrastructure EUDAT (www.eudat.eu); Flag Ship Human Brain Project HBP (www.humanbrainproject.eu), VPH-Share: Virtual Physiological Human: Sharing for Healthcare - A Research Environment (www.vph-share.eu).

The CHIC Summer School 2015

September 7-9, 2015

Register now!

The CHIC Summer School 2015 addresses early-stage researchers, modellers, clinicians, medical students, engineers, IT specialists and others who wish to exchange ideas and learn more about the fairly recent discipline of *in silico* oncology. The Summer School is part of a whole series of workshops dedicated to IT-aided and personalized computational medicine and follows the 6th International Advanced Research Workshop on In Silico Oncology and Cancer Investigation (IARWISOCI) which was held in Athens in 2014.

The CHIC Summer School 2015 will cover a range of topics, from (hyper) modelling of tumors and diseases in general to IT-related topics such as semantics, tools, services and interoperability. Moreover, a full day of the workshop will be dedicated to the advances in *in silico* oncology in the clinical context. The goal of the CHIC Summer School is to foster exchange, ideas and further research and, ultimately, to increase the skills and knowledge required to understand the complexity of the fascinating, innovative discipline of *in silico* medicine.

The venue of this year's workshop is the renowned Leibniz Center for Informatics at Schloss Dagstuhl in Germany which offers state-of-the-art facilities for a successful workshop.

The CHIC project is very well embedded in the VPH and computational oncology community with several consortium partners in other projects, such as VPH-Share, MyHealthAvatar, Dr Therapat and the recently started project iManageCancer. Members of these consortia are very welcome to participate in the CHIC Summer School. The workshop is, however, open to all interested parties.

Further information about the workshop, registration/ paper submission, the venue and the workshop programme are available at http://chic-vph.eu/summer-school/

Registration can be directly accessed via http://chic-vph.eu/summer-school/registration/

Your contact for the event:

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Local organizer of the Summer School

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Please visit us at **www.chic-vph.eu**

Subscription

Stay up to date and sign up for our bi-monthly CHIC e-mail newsletters!

http://chic-vph.eu/newsletter/

The bi-monthly newsletter includes the latest news from the CHIC project and the wider VPH-community as well as up to date information on conferences and workshops in the field of computational medicine.

Disclaimer

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The CHIC consortium is not responsible and may not be held accountable for any loss suffered as a result of reliance upon the content of this newsletter.

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