ACGT is a European Commission co-funded project supported by grant FP6-IST-026996.

NEWSLETTER

ACGT on Cancer

Advancing Clinico Genomic Trials

EDITORIAL

Welcome to this second edition of the ACGT Newsletter!

The recognition that clinico-genomic trials are part of the critical path has turned the spotlight on this aspect of drug development which for ACGT means that a very important opportunity exists to make an impact in an area of significant unmet needs.

Some of these needs especially in the area of trials that target child populations are addressed by the development of a European register of clinical trials in children. As reported in the Clinical Trials News section, the goal of these initiatives is treatment optimization and ultimately better therapies in Paediatrics. Still, this is only one aspect of the broader task of supporting clinico-genomic trials and ACGT is looking to create a host of tools that can be integrated in an easy to use environment. In the Grid News section we report on the latest features of Gridge Resource Management, an open source meta-scheduling system which allows developers to build and deploy resource management systems for large scale distributed computing infrastructures.

There is also some exciting news in terms of ACGT software deliverables. In the products section, the team at Fraunhofer presents the latest on GridR, an ACGT-grid enabled version of the well known

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Newsletter Edition
Volume 2 . Spring 2008
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statistical analysis package R. In the data protection area, we consider the question of whether patients want feedback of data from clinico-genomic research. The question of individual donor feedback (IDF) is certainly complex and the group at Hannover University will be analysing their findings in this and future editions.

The feature article of this edition discusses many of the challenges and requirements in the emerging field of Molecular Medicine and shows how many of these will eventually be served by the solutions methodologies and data exchange standards adopted by ACGT.

ACGT is certainly progressing and what better proof than a growing 'ACGT member family'? EORTC (the European Organization Cancer) is our newest member and will be joining the consortium in order to contribute its experience in clinical trials needs and in the design of effective supporting infrastructures.

We hope that you will find this second issue of the ACGT newsletter interesting and look forward to welcoming you too as an active member of the growing ACGT community!

Clinical Trials News

Latest developments in the world of clinical trials in cancer

It is by now recognized by all that clinical trials play a fundamental role in establishing new treatments for all kinds of diseases. For example, in Cancer, clinico-genomic trials as proposed by ACGT are critical in providing new insights on the molecular biology of the disease, leading to more personalized medicine with higher cure rates and fewer side effects. For child populations clinico-genomic trials help promote evidence based use of drugs, given that a lot of drugs used in children today are off-label.

In recognition of the importance of clinico-genomic trials the European Community has decided to support the development of a European register of clinical trials in children as part of its Fifth Framework Programme, Thematic Programme «Quality of Life» (contract QLG4-CT-2002-01054), in 2002. The project "The European register of clinical trials on medicines for children - Drug Evaluation in Children" (DEC-net), is coordinated by the Laboratory of Mother and Child Health of the «Mario Negri» Institute for Pharmacological Research in Milan and currently involves members from four countries: France, Italy, Spain, and the United Kingdom. It is unique in that it is the first population oriented clinical trial register.

The DEC-net register (www.dec-net.org) which was activated on July 1st 2004 is freely available to anyone interested in accessing information on paediatric drug therapy clinical trials. The register was set up by four groups (Italy, UK, France, Spain). A recent publication (Chiara Pandolfini et al.: The DEC-net European register of paediatric drug therapy trials: contents and context. Eur J Clin Pharmacol (2008) 64:611–617) updates the results for the years 2004 to 2006 of the registry.

Altogether only 257 trial re-

cords were analysed (86 from Italy, 84 from UK, 56 from France and 31 from Spain). Included are multinational and also single-centre trials. 46 different countries are listed as participating in the multinational trials. Those appearing most commonly, aside from the project's member countries, were Germany (in 36 trials), Belgium (28), Sweden (19), the Netherlands (19) and Switzerland (17). Only 39 % of these trials were funded by Industry. Charities and Universities still play an important source of funding (13 %, 12 %). Interestingly the majority of the trials was experimental (79%), and most were in phase III (48%) and in phase IV (30%). A majority of the trials was randomised (62%). The most commonly represented diseases, based on ICD9 group, were neoplasms (14%).

A total of 429 drugs were involved in the trials. The treatment regimens in cancer are much more complicated and only the drug class was entered. The most frequent ATC class (anatomical main group) represented was "antineoplastic and immunomodulating agents" (157 drugs), with 26% trials involving 1 drugs in this class. The most common ATC subclasses (therapeutic subgroups) were antineoplastic (117 drugs; 15% trials) and immunosuppressive agents (30; 10%) showing the importance of clinical trials in childhood cancer.

What becomes obvious according to this study is that the creation of the European Medicines Agency's (EMEA) EudraCT database is potentially one of the most important steps in regulating clinical trials. According to the latest Paediatric Regulations information on paediatric clinical trials will have to be entered in this European database while results of clinical trials will also have to be published and made available to the public. In the end the expectation is that this process will ultimately lead to better therapies and treatment optimization in Paediatrics.

News:

The International SIOP Renal Tumour Study Group (SIOP-RTSG) held a meeting in Milan in April 2008. The Group decided on a new structure and elected Prof. Dr. Norbert Graf from Homburg/Germany as their chairman and Prof. Dr. Kathy Pritchard-Jones from London/UK as their Vice-Chairman. One topic of the meeting was dealing with possible questions that should be asked in an upcoming clinico-genomic trial for Wilm's Tumour. It was stated that a common IT infrastructure for SIOP-RTSG is mandatory. In the upcoming SIOP meeting in Berlin ACGT will hold a workshop to demonstrate the Grid infrastructure and present the advantages of ACGT and ObTiMA for SIOP-RTSG and other study groups within SIOP.

Products and Services

News on the latest products or services in our area of interest

GridR

GridR is an analysis tool based on the statistical environment R (http://www.r-project.org/).

GridR supports the use of the collection of methodologies available as R packages, in a grid environment. Within the ACGT project the aim of GridR is to provide a powerful framework for the analysis of clinico-genomic trials involving large amount of data (e.g. multilevel data from microarray-based clinical trials).

The R environment provides a broad range of state-of the-art statistical, graphical techniques and advanced data mining methods including comprehensive packages for linear and non-linear modelling, cluster analysis, prediction, hypothesis tests, resampling, survival analysis and time-series analysis. It is easily extensible and has turned out to be the de facto standard for statistical research and many applied statistics projects, especially in the biomedical field. The associated project BioConductor addresses the needs of the biomedical and biostatisticians community for genomic data-analysis oriented R packages. Numerous methods available as R/BioConductor packages that were considered experimental a few years ago are now accepted as standard in the analysis of high throughput genomic data.

In May 2008, a first beta version of the GridR R package will be published by ACGT and offered as open source. The package contains functions and libraries that allow the user to access and make use of a distributed environment in a transparent way from a client side R environment. Based on the technology of call-backs, active bindings and paring of error code, the package will provide the functionality of remote function execution in distributed environments. More specifically, different modes for the submission and execution of the computation will be supported in order to allow the user to work with different environments. For example, computations will be able to be submitted via SSH or via web services and executed directly on a remote machine, on a condor cluster or be forwarded to a GT4 machine. The functionality of using parameter sweeps when executing functions remotely will also be provided.

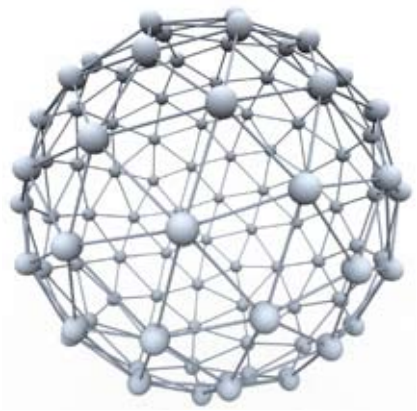
The availability of GridR will be of great use to clinicians and clinical-data analysts interested in computationally heavy data-mining, such as re-sampling techniques, full cross-validation of classifiers or meta-analyses.

With the GridR R package in its current version users can perform computations in distributed environments of different architectures from their local R environment in a nearly transparent way.

Grid News

Latest developments in the world of computer grid research

New features of Gridge Resource Management System for ACGT



An important component of the ACGT Grid infrastructure is the Gridge Resource Management System (GRMS). GRMS is an open source meta-scheduling system, which allows developers to build and deploy resource management systems for large scale distributed computing infrastructures. GRMS is based on dynamic resource selection, mapping, advanced scheduling technologies and feedback control architecture in order to deal with dynamic Grid environments and resource management challenges such as load-balancing among clusters, remote job control or file staging support.

Therefore, the main goal of the GRMS is to manage the whole process of remote job submission to various batch queuing systems, clusters or resources. It has been designed as an independent core component for resource management processes which can take advantage of various low-level Core Services and existing technologies. GRMS can be considered as a robust system which provides abstraction of the complex grid infrastructure as well as a toolbox which helps to adapt to distributing computing environments.

One of the primary goals of ACGT is the support of standards in all possible grid-related areas. A good example of such a standard is JSDL which will be used for describing 'jobs' for GRMS.

JSDL (Job Submission Description Language) is an extensible XML specification developed by the Global Grid Forum for the description of the structure of the tasks that can be submitted to local scheduling and queuing systems.

JSDL describes the submission aspects of a job, and does not attempt to describe the state of running or historic jobs. Instead, JSDL includes descriptions of properties such as:

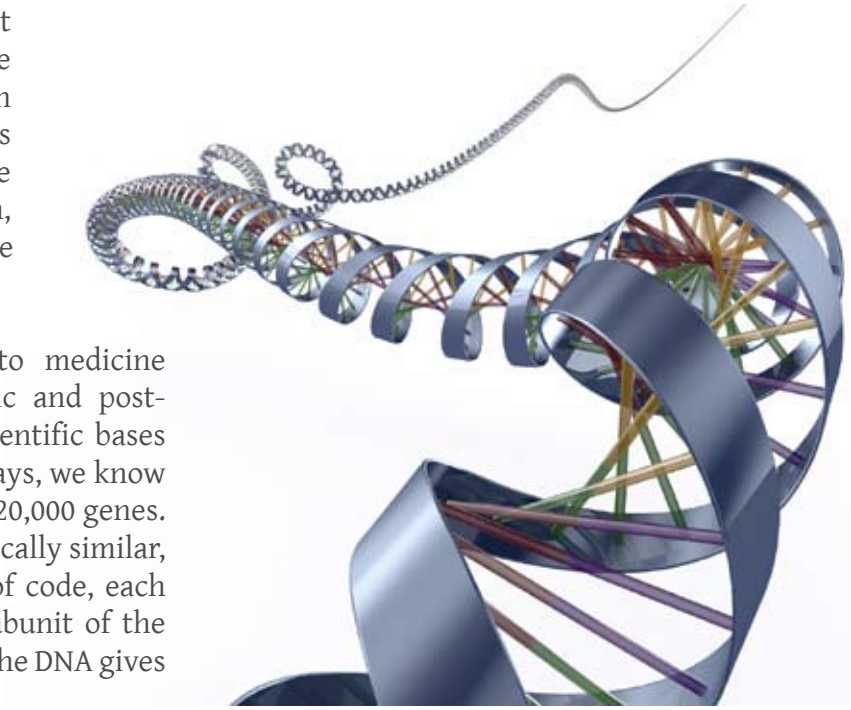
- Job name description
- Resource requirements that computers must meet in order to be eligible for scheduling, such as total RAM available, total swap available, CPU clock speed, number of CPUs, Operating System, etc.
- Execution limits, such as the maximum amount of CPU time, wall clock time, or memory that can be consumed.
- File staging, or the transferring of files before or after execution.
- Command to execute, including its command-line arguments, environment variables to define, stdin/stdout/stderr redirection, etc.

In the case of GRMS, JSDL can be used as an alternative to a specialized language describing jobs for GRMS. Even though JSDL is less powerful, it has been adopted by ACGT in order to support groups of users that are already familiar with well known standards that are being used in other environments. This choice also simplifies the cooperation with already existing client applications providing grid submission capabilities.

Feature Article

Challenges in post genomic molecular medicine and clinical trials

Medical doctors have long known that people differ in susceptibility to disease and response to medicines. But, with little understanding on what causes these differences and little guidance on how to best account for them, treatments have been optimised for the many, not for the few.



However, this classical approach to medicine has been changing, and the genomic and post-genomic "revolution" is providing scientific bases for individualising treatments. Nowadays, we know that human DNA codes for more than 20,000 genes. Each person's overall 'blueprint' is basically similar, made up of about 3 billion "letters" of code, each letter corresponding to a chemical subunit of the DNA molecule. But subtle variation in the DNA gives humans their individual identities.

Beyond physical appearance, genes determine the distinct and complex way our bodies interact and respond to the environment. The chemistry and biology taking place in our bodies at various levels (what we can call the "molecular signatures" of individuals) sometimes predispose people to particular diseases, and it can affect the way a person responds to therapies. These concepts form the basis of a relatively new scientific field called Molecular Medicine (MM). MM's final aim is to be able to "personalise" medical treatments by using genomic (gene), proteomic (proteins) and eventually metabolomic (biochemical reactions) information to understand how a patient would react to a therapy and select the correct therapy for him or her. Already, there are applications of MM. For example, for breast cancers variants of a gene linked to it can be the index of susceptibility to developing or surviving the disease, whereas the production of a particular protein signals that it might be controlled with the drug Herceptin. In this vein, several molecular signatures have been developed to predict prognosis and drug response in the context of breast cancer (reviewed in [1]).

Two pillars of MM are embedded in the name itself of this research field: medical science and molecular biology. All those interested in MM know its popular and effective motto: «From the bench to the bedside», however only a small fraction of them ask themselves: «How is the knowledge moved from the former to the latter?". And this is by no means a minor question.

Although there exist some real practical examples where this is really happening [1], there remain

difficulties in bridging the gap between the two. However, we argue here that this process could be immensely helped by a greater understanding and deployment of a third, and equally important, pillar: Computational Biosciences. In this term are included topics such as Medical Computer Science, Bio-informatics, Systems Biology and literature mining that together will contribute to organizing, understanding, standardizing and translating the knowledge accumulated in the laboratories to the clinic.

Some readers who have a purely-experimental view of the cell might be amazed to read that one of the main pillars of the medicine of the future is based on numbers, equations and inter-connecting computers. In fact, in traditional medicine the qualitative and «classical laboratory» data (e.g. jaundice, high level of transaminases, tiredness) of a single patient enables the physician to find out the correct diagnosis thinking of differential diagnosis and performing further examinations and parameters. Based on the heterogeneity and mass of information the implementation of complex molecular findings in the diagnostic and treatment process can not be realized without the help of computational bioscience and mechanisms to make the MM efficiently useful for the treatment of the patient.

On the contrary, the data from current MM are inherently complex, heterogeneous and often produced in different laboratories from the one the patient is treated at. There is a lack of ways and networks to transfer, organize, integrate and then decipher this data; however, it is exactly the complexity of this data that sometimes allows a deeper understanding of the chemistry and biology occurring in our bodies.

The new challenges posed by MM can only be properly addressed by large collaborative efforts where researchers from many disciplines, from geneticists and clinical specialists, to computer scientists and engineers, share knowledge and work together. Based on the fact that researchers of different disciplines work together in a combined approach with sensitive data and, even sometimes indirect, treatment of humans, attention has to be turned to the ethical and legal guidelines and standards to protect the patients. Observance of ethical and legal issues in MM is mandatory regarding the rapidly increasing developments.

One engineering challenge is developing better systems to rapidly assess a patient's genetic profile; another is collecting and managing massive amounts of data on individual patients; and yet another is the need to create less expensive and efficient diagnostic devices.

In addition, improved drug development and system biology methods are necessary to find effective and safe drugs that can exploit the new knowledge on the differences between individuals. New technologies are needed for delivering personalized drugs quickly and efficiently to the site in the body where the disease is localized. For instance, research is being carried out to engineer nanoparticles that are capable of intelligently delivering a drug to its target in the body.

Information and Communications technology is playing an increasingly critical role in health and life sciences due to the profound expansion in the scope of research projects and clinical needs in the post-

genomic age. Robust data management and analysis systems are becoming essential enablers of MM. Many efforts are underway to develop standards and technologies to promote large-scale integration of publicly-available resources systems and databases. Predicted benefits include an enhanced ability to conduct meta-analyses, an increase in the usable lifespan of data, a funding agency-wide reduction in the total cost of IT infrastructure, and an increased opportunity for the development of third party software tools.

We think that, many of these cogent issues might find a preliminary tentative framework in the ACGT project [2]. In fact, ACGT focuses its research and development efforts in defining a framework for clinical-genomic trials where properly collected data stored in a unique user friendly and easily accessible virtual database (masking different geographically distributed archives), will be amenable to parallel net-based bio-informatics and sophisticated computation bio-statistics (based on the GRID framework) Once this data has been collected, analyzed and validated, it will be possible to build mathematical models, which describe, in a unified way both the molecular (e.g. the metabolomics) and the macroscopic (e.g. the pathological tissue growth) components. Realistic multi-scale models, such as the Oncosimulator, with easy-to-use software systems will help the oncologists in their work. These support tools will be used both, in research work, and in the future, in practical clinical work, not only to better understand the mechanisms of action of drugs and scheduling, but also in designing new clinico-genomic trials.

The key point of the ACGT project is that it proposes a robust general framework where new specific tools can be «simply» inserted. This point is of interest since new and robust biology-oriented mathematical algorithms are being produced in the research community.

Moreover, patients safety, data protection and strict clinical evaluation of each developed software that is related directly/ or indirectly to treatment of patients is essential. The aim of ACGT is to realize an interactive community of specialists that provide an end-user friendly and easy to use platform used for all disciplines.

However, on this specific point we have an important final remark: we do not want by any means to say that the oncologist of the future will have to be a computer scientist. Simply, she/he will have to work more closely with the computer scientist community and to be more familiar with computational tools. Note that this already happens to some extent in various fields of medicine. For example, a cardiologist must be familiar with the physics of the heart and must be able to use physical devices such as ECG; a radio-oncologist must have elementary knowledge of radiation physics and she/he must be able to discuss a radiotherapy computed dose plan with physicists.

«Patients safety, data protection and strict clinical evaluation of each developed software that is related directly/ or indirectly to treatment of patients is essential. The aim of ACGT is to realize an interactive community of specialists that provide an end-user friendly and easy to use platform used for all disciplines»

References:

[1] Sotiriou C and Piccart M. Taking gene-expression profiling to the clinic: when will molecular signatures become relevant to patient care? Nat Rev Cancer. 2007 ; 7:545-553

[2] M. Tsiknakis et. Al. «Developing a European Grid infrastructure for cancer Research: vision, architecture and services», E-Cancermedical sciences (2007)

Community View

Invited contributions from non-ACGT members of the wider research community

The case for expanding the ACGT family

Any large undertaking such as ACGT that aims to develop an infrastructure to support a wide range of target users, must constantly seek input from these users to ensure that it addresses true rather than imagined needs and that the solutions it puts together fit in well with current practices and deliver true value.

To date the guiding role of end user has been assumed by 2 partner organizations active in clinical trials and 2 biology research institutes, both groups representing the major target users of ACGT. Acquiring patient data and thoroughly testing standards and IT systems in use however is a demanding task that can only benefit from the involvement of as many end users as possible. With this in mind the European Organization for Research and Treatment of Cancer (EORTC) has been invited and will be actively joining ACGT in the next few months.

Created in 1962, EORTC is a not-for-profit international cancer research organization under Belgian Law. EORTC's mission is to improve the standard of cancer treatment in Europe through the development of new drugs and to test more effective therapeutic strategies, using drugs which are already commercially available, surgery or radiotherapy. EORTC has the aim to facilitate the passage of experimental discoveries into state-of-the-art treatment by keeping to a minimum the time lapse between the discovery of new anti-cancer agents and the implementation of their therapeutic benefit for patients with cancer. EORTC research takes place in a network of over 300 participating institutions located in 32 countries. More than 2,000 clinicians are collaborating on a voluntary basis in 15 Disease/ Treatment Oriented Groups. In addition more than 5,000 cancer patients are entered into EORTC multidisciplinary trials each year. EORTC is the cooperative cancer clinical research group that detains the biggest publication record worldwide.

The activities of EORTC are peer reviewed by the US National Cancer Institute and the EORTC Drugs Master File is registered with the US Food and Drug Agency. EORTC Headquarters are a unique facility in Europe located in Brussels that provide scientific, legal, logistic and administrative support to EORTC clinical and translational research activities (protocol development, data management, statistical analysis, new drugs development, translational research, virtual biobanking, quality of life, regulatory and ethical affairs management, Pharmacovigilance and Quality Assurance). All EORTC protocols are written and conducted in accordance with international standards for ethics: the declaration of Helsinki, Good Clinical Practice guidelines approved by the International Conference on Harmonization.

EORTC is the sole European Institution with such a strong representation across patients' and clinicians'communities. Its role within ACGT will be to:

- Define potential new clinico-genomic scenarios to be fitted within the ACGT model.

• Practically assess the ACGT security architecture and evaluate the tools for data (pseudo) anonymization.

• Contribute to the ACGT model validation activities by providing practical examples from the EORTC clinical trials. Specifically, EORTC will provide a range of Case Report Forms from past trials executed by EORTC to be used for further developing the ACGT Master Ontology on Cancer and for validating its completeness.

EVENTS

Information on upcoming events of interest

UICC World Cancer Congress, August 2008 Geneva

ACGT will be participating at the next UICC World Cancer Congress planned August 27th to 31st in Geneva. ACGT will be present with its own stand during the whole duration of the event.

The event which brings together world leaders in cancer control will be attended this year by more than 3000 delegates from 125 countries including researchers, clinicians, nurses, management administrators, government and public health officials, health journalists and of course patients. ACGT staffers will be presenting results to date, looking to attract new end users and ultimately seeking new collaborations.

40th Annual SIOP Meeting

The SIOP (International Society of Paediatric Oncology) Annual Meetings are the most significant scientific and educational events for paediatric oncology worldwide. Physicians of all disciplines co-operating in the research and treatment of childhood cancer, but also scientists, psychologists, nurses, parents and former patients will meet and discuss novel developments at the 40th Annual Meeting in Berlin from the 1st to the 6th of October 2008.

During this occasion, ACGT will have a half-day workshop on the 2nd of October presenting an infrastructure to facilitate the building and running of clinico-genomic trials in accordance with all European legal and ethical regulations. Different software demonstrations, scientific presentations and open discussions will highlight the infrastructure of ACGT for a better and more personalized medicine in Oncology including Paediatric Oncology, as shown in Nephroblastoma.

Data Protection

The latest thinking on legal, ethical and data security issues surrounding clinical trials

Do patients want feedback of data from clinico-genomic research?

ACGT-Poster presentation at the international conference "Genomics & Society"

In clinico-genomic cancer trials tumor tissue is analyzed to identify genetic components which are involved in cancer development, reaction to treatment and prognosis. Though genetic factors may influence these processes, they do not cause them in the narrow sense of the term. Therefore, the clinical relevance of research findings is difficult to evaluate – and so are the ethical and social implications regarding the feedback of such findings to patients.

At least in the European context it is indisputable that everyone has the right to make inquiries about personal data which have been collected about him or her. Due to legal provisions, investigators are obliged to disclose such data on request. This is especially applicable if a research process yields information that helps to avoid sickness or adverse drug reactions. But what is about information on genetic polymorphisms and gene expression whose clinical significance has not been fully established yet? Should such information that has only the potential to be clinically relevant be returned to patients? And if yes, should researchers actively approach patients to return study findings that might be or become relevant for him or her?

According to ethical guidelines and legal regulations from Europe and the United States, there exists no obligation for such an individual donor feedback (IDF). In addition, empirical data on patients' perspectives and expectations towards IDF and data protection are rare and mainly limited to the US-health care system. To illuminate what patients in clinico-genomic

and clinical trials on cancer want and think about IDF, we are conducting two surveys in the context of ACGT. One survey is a cross-national study on breast cancer patients in several European countries (Germany, Belgium, Greece, and Great Britain) and a Germany-wide survey on parents of children with malignant diseases.

The poster presentation "Disclosure and confidentiality in clinico-genomic research: Patients' attitudes and perspectives towards Individual Donor Feedback" presented at the international conference "Genomics & Society" (17th/18th April 2008, Amsterdam) discussed central aspects that might affect patients' attitudes and perspectives on IDF: the probabilistic character of genetic information and the pleiotropic nature of genes (what to feed back?); the potential impact of genetic information on family relationships and reproduction (to whom to feed back?); the potential impact on lives and interests of other family members (who feeds back?); and the increasingly prevalence of genetic research in common disorders such as cancer (how to organize feedback?).

The poster presentation convinced by its content and design: it was awarded two prizes. The first one was the one of the audience, and the second award was given to it by the scientific jury composed of acknowledged scholars from different disciplines.

Life in ACGT

ISCG 2008

The International Symposium on Grid Computing (ISGC) 2008 was held in Taipei, Taiwan from 7 to 11 April 2008. Organized by ASGC since 2002, ISGC is stepping into the 7th year of this grand event. ISGC is one of the most significant annual international events in the Asia Pacific region that brings together scientists and engineers to exchange ideas and to present on challenges, solutions and future development issues in the field of Grid Computing.vv

ACGT was represented by our partner Poznan Supercomputing Center. Juliusz Pukacki presented the Grid aspects of ACGT in the «Biomedicine and Life Sciences» session. The presentation included a general overview of ACGT goals, and the role of Grid technologies in cancer research.

ACGT Technical meeting, Milan

In February we had a nice and fruitful general consortium meeting in Milan, Italy, organized by our partner European Institute of Oncology (IEO). We thank our hosts IEO, the food (of course!) was excellent and to top it all up, ACGT members were introduced to our new guest star (the ACGT Magnetic piggy)!

EBCC-6, Berlin, April 15-16

In the recent European Breast Cancer Conference (EBCC-6) ACGT organized the workshop "Advancing Clinico Genomic Trials on cancer: open grid services for improving medical knowledge discovery". Attended by over 50 delegates from both industry and academia the workshop presented the rationale of the ACGT initiative together with latest results both on the clinical and technical aspects of the project.

ACGT PEOPLE

Christine Desmedt

Christine Desmedt received her bio-engineer degree in Cells and Genes Biotechnology from the Catholic University of Leuven, Belgium, in 2000. Since then she is working at the Jules Bordet Institute, an autonomous comprehensive cancer centre devoted entirely to the fight against cancer. For two years she worked as a clinical monitor for the Breast European Adjuvant Studies Group (Br.E.A.S.T), co-coordinating the monitoring activities of external groups for the conduct of breast cancer trials. In 2002, she joined the Functional Genomics & Translational Research Unit of the Bordet Institute, where she is currently coordinating different research programs. In 2004 she earned a master in bio-medical sciences at the Free University of Brussels and her work is supported by a grant from the "Fonds National de la Recherche Scientifique".

Her current research projects, conducted in collaboration with different international institutions, involve the identification and validation of prognostic and predictive markers in breast cancer, as well as a better characterization of breast cancer development and metastasis.

Dr. Stefan Rüping

Dr. Stefan Rüping is the leader of the Integrated Data Mining group at Fraunhofer IAIS. He studied Computer Science at the University of Dortmund and worked as research assistant at the artificial intelligence chair at the University of Dortmund in the DFG Collaborative Research Center on Complexity Reduction in Multivariate Data (SFB 475), where he also finished his PhD thesis on Learning Interpretable Models in 2006.

His research interests are on the combination of statistical and machine learning algorithms, novel learning tasks, and on the interpretability and adaptability of machine learning models. He co-organized a workshop on Learning with Multiple Views at the International Conference on Machine Learning ICML'05. He served as a member of the program committee of several international conferences, e.g. the European Conference on Machine Learning (ECML) 2005-2008. His project experience includes leading the technical management committee of the EU integrated project ACGT, work package leadership in several other EU projects, and management of a wide range of commercial projects.

JOIN ACGT

Membership in ACGT is open to all. Here are some benefits you enjoy as an ACGT member:

- Access to all member resources
- Support in solving problems in the areas of interest of ACGT
- Direct contact with ACGT experts in a variety of fields including clinical trials, cancer research, advanced software development, Grid implementations, legal, ethical and data security issues and much more
- Ability to contribute to the ACGT infrastructure and receive support for it.

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