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Editorial



In June 2000, scientists announced that they had completed deciphering the draft human genome sequence. Society as a whole expected a lot from this breakthrough, even a revolution in diagnosing, preventing and treating human diseases.

Ten years later, while great progress has been made thanks to this achievement, the genome sequence has also revealed that life is far more complex than expected. What can we do to help our life sciences researchers? As bioinformaticians, we strive to assist them in their research by facilitating and optimising their data extraction and analysis, and,

more importantly, providing the means to extract pertinent information from their research results. This is essential for a better understanding of biological systems. Bioinformatics is, and will undoubtedly remain, an essential ally in this quest.

Since its creation, SIB together with our research and service groups have been committed to providing outstanding software and carefully annotated databases, as well as research support and infrastructure to the life sciences research community. Swiss-Prot, which remains a worldwide central protein knowledgebase, is a good example. Since we announced two years ago – as SIB celebrated its 10th anniversary – the completion of the annotation of the entire set of human proteins, SIB is taking a new step with the development of neXtProt, a knowledge platform totally devoted to human proteins. With a first version planned to be available in the autumn, we expect neXtProt to further help biomedical researchers in making sense of the complex universe of biological processes that take place in the human body.

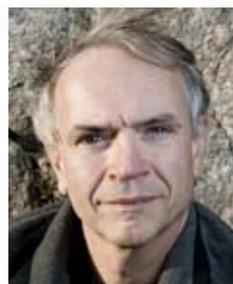
We hope you enjoy reading this new issue of *Swiss Bioinformatics*, in which we highlight a few of SIB's activities. You will also notice that SIB just welcomed two new groups, and that our international collaborations are being reinforced, showing that we are determined to unite the talents needed to face all the challenges ahead.

Hope you have a great summer!

Ron Appel, Executive Director

News in brief

Otto Naegeli Prize 2010 awarded to Amos Bairoch



"I consider this prize as an encouragement for our new endeavour. With CALIPHO, we aim to help biomedical researchers in their quest to uncover the role and function of human proteins in health and disease."

At the end of April, Professor Amos Bairoch was awarded the Otto Naegeli Prize 2010. This award acknowledges his exceptional contribution to the field of protein sequence analysis and, more particularly, to the development of resources that have been put at the disposal of the scientific community, such as Swiss-Prot. This protein knowledgebase remains, since its creation in 1986, a central and essential resource for life sciences researchers around the world.

As a pioneer of Bioinformatics, Amos Bairoch is also a co-founder of SIB Swiss Institute of Bioinformatics, which was created in 1998.

In 2009, Amos Bairoch launched a new project and a corresponding SIB group called CALIPHO, which stands for Computer and Laboratory Investigation of Proteins of Human Origin.

This year's prize was awarded jointly to Ruedi Aebersold, Professor of Molecular Systems Biology (Federal Institute of Technology Zurich and University of Zurich).

The Otto Naegeli Prize for the promotion of medical research, awarded every two years, is one of Switzerland's most prestigious awards.

SIB Awards 2010

On 25 June, during the eighth [BC]² Computational Biology Conference in Basel, SIB Swiss Institute of Bioinformatics announced the two winners of the SIB Awards 2010.



SIB Young Bioinformatician Award 2010

The winner of the SIB Young Bioinformatician Award is Aitana Morton de Lachapelle, 27, a PhD student in the Computational Biology Group led by Professor Sven Bergmann at the Department of Medical Genetics of the University of Lausanne, which she joined after graduating in Physics from EPFL (Swiss Federal Institute of Technology in Lausanne). Her PhD thesis, currently underway, investigates how robust pattern formation can be achieved during development.

The Young Bioinformatician Award is given yearly by SIB. It recognises a graduate student or young researcher who has carried out a research project centred on the in silico analysis of biological sequences, structures and processes. The award is given competitively by a jury of experts and comes with a cash prize of CHF 10,000.

SIB Best Graduate Paper Award 2010

The winner of the 2010 SIB Best Graduate Paper Award is Rajesh Ramaswamy, 27, a PhD student in the MOSAIC Group of Professor Ivo Sbalzarini at ETH Zurich (Swiss Federal Institute of Technology in Zurich). The title of his paper is "A new class of highly efficient exact stochastic simulation algorithms for chemical reaction networks".

The Best Graduate Paper Award is given yearly by SIB. It recognises outstanding contributions to the fields of bioinformatics and computational biology made by young researchers who have not yet completed their PhD. The award is given competitively by a jury of experts and carries a cash prize of CHF 5,000.

Most-cited Swiss paper in the world

"SWISS-MODEL: An automated protein homology-modeling server", written by Torsten Schwede, Jürgen Kopp, Nicolas Guex and Manuel Peitsch, has become the most-cited Swiss paper in worldwide scientific literature for the past 10 years.

<http://sciencewatch.com/dr/cou/2010/10janALLPAPRS/>

New Group Leaders

1st July, our Institute welcomed two new Group Leaders, whose nominations were ratified by SIB's Foundation Council:

Professor Henrik Kaessmann, from the Center for Integrative Genomics at the University of Lausanne, joined SIB as a new Group Leader. Dr. Peter Kunszt, SyBIT project manager at SystemsX.ch joined as an Affiliate Group Leader.

Research

Wasp Sting for Pest Control



Wasps are best known for the pain of their sting. Yet there are some that can be beneficial, such as the parasitic wasps *Nasonia*, whose venom can kill agricultural pests. *Nasonia* are unusual in that they act like "smart bombs" by killing off only certain kinds of insects. Consequently, *Nasonia* would be preferable to certain chemical pesticides, which are frequently non-specific and harmful to the environment, including humans.

To harness such features, the molecular nature of *Nasonia* venom needs to be unravelled along with the processes involved in selecting their targets. As part of an international project involving the sequencing of three parasitoid *Nasonia* wasp species, Professor Evgeny Zdobnov of the University of Geneva Medical School and the SIB Swiss Institute of Bioinformatics compared the genomes of *Nasonia* and other organisms. The results were published in January in the Science journal.

The comparison revealed that almost 7,000 *Nasonia* genes have recognisable counterparts in humans, many of which are not found in the current standard model for genetic studies – the fruit fly – thus making *Nasonia* a better representative of insects. These characteristics, along with the wasps' venom and their biology of selective killing, could be useful for pest control and medicine as well as provide important insights into evolution and genetics.

For further reading: Werren JH, Nasonia Genome Working Group. Functional and evolutionary insights from the genomes of three parasitoid Nasonia species Science 2010,327(5963),343-348.

Decoding the genome to speed up drug production

Fifty years ago scientists discovered the genetic code in a groundbreaking discovery. Biologists found the key to how nature reads an organism's genome to produce proteins, which are necessary for its development and survival. Nevertheless, deciphering the genome has proved to be a very complex task and knowledge of the underlying syntax and grammar is still in its infancy.

Recently, Professor Yves Barral from the Biology Department at ETH Zurich, along with computer scientists Dr. Gina Cannarozzi and Professor Gaston Gonnet from the Computer Science Department of ETH Zurich and the SIB Swiss Institute of Bioinformatics, published results relating how nature uses "synonyms" to speed up or slow down the reading of a gene and hence the expression of its proteins.

Indeed, the rate of expression of a protein is essential; in the event of poisoning, for instance, an organism must react swiftly. What is more, with this knowledge, genetic engineers have now a new tool to regulate the production of therapeutic agents such as insulin.

For further reading: Cannarozzi G, Schraudolph N, Faty M, von Rohr P, Friberg M, Roth AC, Gonnet P, Gonnet G and Barral Y. A role for codon in translation dynamics. Cell 2010;141(2),355-367.

Internal collaboration

300 members in unison!

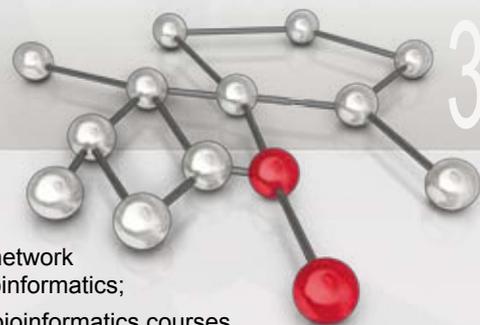


On the 1st and 2nd of February this year, 300 SIB members met in Montreux during the "SIB Days", our Institute's annual internal meeting. This event brings our members together to get to know each other better and to further their collaboration. Members had the opportunity to enjoy presentations of some of the Group Leaders' projects and they took part in workshops on themes such as biology and evolution, probability and statistics, and structure-based drug development. These workshops offer a great opportunity to discuss projects involving the whole institute, such as the development and evolution of the SIB Web presence. The "Web Team" in charge of this project was able to take concerted actions regarding the design, Web services and interoperability of our Websites.



Every year the program also includes a social event, which is a time to relax, share ideas and deepen relationships.

This year 300 SIB members literally drummed together during one hour under the direction of Doug Manuel, the energetic leader of SEWA Beats. This musical session – called "Do you speak Djembe?" – emphasises the need to listen to each other and to beat each Djembe drum in precise unison. It is the same in life and in our daily activities: SIB focuses on collaborative projects to provide outstanding support to the life sciences research community.



International collaborations

Relations reinforced with the Weizmann Institute of Science (WIS)

At the end of 2009, SIB and WIS signed a memorandum of understanding to strengthen collaboration between both organisations. The Weizmann Institute of Science is located in Rehovot, Israel and is one of the top-ranking multi-disciplinary research institutions in the world.

The aim of this relationship is to work together in the fields of bioinformatics research, support and education, which will, among other things, lead to joint projects with scientists from both institutes, the sharing of expertise and the exchange of students and teaching material.

A scientific meeting between both organisations is planned for the beginning of next year in Israel. This symposium will allow a thorough presentation of both organisations and an exchange between scientists to identify projects where collaboration is possible.

Formalised collaboration with the Netherlands Bioinformatics Centre (NBIC)

SIB and the Netherlands Bioinformatics Centre (NBIC) have signed a memorandum of understanding to formalise their existing relations. NBIC is a collaborative institute of the bioinformatics groups in the Netherlands. These groups perform cutting-edge research, develop novel tools and support platforms, create an e-science infrastructure and educate the next generation of bioinformaticians.

In 2008, when our Institute celebrated its 10th anniversary, a delegation of SIB scientists visited NBIC in Amsterdam. The first contacts between both organisations were then established and topics for future collaboration identified. Joint work is now underway in the field of proteomics, among others.

The memorandum of understanding signed in May of this year formalises this relationship between both organisations and underlines their intention to foster joint projects in research and to unite forces in the international bioinformatics field, where relevant.

Education is another field where the two bodies work together. Two years ago, NBIC and SIB agreed to encourage student exchange and to link their educational programmes.

This year we will be organising our first joint SIB/NBIC Summer School from 2 to 6 August in Amsterdam. This annual high-level event brings together teachers and students from international organisations to cover current topics in bioinformatics. This year's theme will address "Quantitative imaging and modelling of biological processes".

<http://www.isb-sib.ch/education/sib-phd-training-network/phd-summer-school-2010.html>

Education and outreach

It is essential to train the next generation of bioinformaticians to maintain the exceptional quality of bioinformatics in Switzerland. Education is thus one of the missions of the SIB. In general, the SIB members:

- Help to coordinate under-graduate education related to bioinformatics and to deliver most of the bioinformatics courses within Swiss Universities and Federal Institutes of Technology;
- Promote bioinformatics at all educational levels from high school to undergraduate and graduate degrees;

- Maintain a training network of PhD students in bioinformatics;
- Provide professional bioinformatics courses, workshops and consulting for life scientists;
- Collaborate with international institutions, such as the Netherlands Bioinformatics Centre (NBIC), to organise common educational activities and to link bioinformatics in Europe.

The SIB PhD Training Network currently counts 43 students working in the five cities where SIB is present: Basel, Bern, Geneva, Lausanne and Zurich. The objectives of this network are twofold: to offer graduate students in bioinformatics a set of cutting-edge courses that provide both the theoretical and the practical knowledge necessary for a successful PhD research project in bioinformatics; and to foster the emergence of a network of PhD students and promote the exchange of ideas, as well as mobility of the students between participating institutions. Some of the past activities that illustrate these objectives are:

- The international Summer School on "Determinism, Stochasticity and Robustness in Biological Processes" held in August 2009 in Lugano;
- The one-week course on "Computational Methods for Proteomics Data Analysis" organised in December 2009 in Geneva;
- The workshop organised in September 2009 which combined the presentation of Allan Drummond (FAS Center for Systems Biology, Harvard) and the interactive sessions in which the students could present their work and share ideas with their peers.

PhD students are also encouraged to participate as much as possible in the social/scientific life of the SIB as they have many opportunities to interact with their peers as well as with all the other SIB members throughout their studies. In the future we will also organise laboratory rotations in which the PhD students can expand their knowledge by participating in the research activities of multiple SIB groups.



Yannick Wurm, recently graduated with a PhD in bioinformatics:

"At first, the SIB PhD courses and other students' research topics seemed light years away from the subject of my PhD. But, in many cases, I took home knowledge, tools and concepts that have ultimately made me a more balanced and productive computational biologist. Furthermore, courses and workshops connected me with competent people that I continue to contact regularly to obtain technical and theoretical advice. In some cases these exchanges even led to fruitful collaborations. Finally, sharing experiences with the other PhD students from around Switzerland brought me new colleagues and also some close friends."

Chromosome Walk in Divonne-Les-Bains

The travelling exhibition "Chromosome Walk" crossed the border and settled in Divonne-Les-Bains, France from 1st May to 30 June 2010. Chromosome Walk was created in 2008 for the 10th anniversary of the SIB. Divonne marked the final halt for this exhibition made of 23 modules describing the minute worlds of chromosomes, genes and proteins and the ever-growing one of bioinformatics.

Link with the industry

Focus on GeneBio

Geneva Bioinformatics (GeneBio) SA is a leading bioinformatics company providing the life science community with world-class solutions that accompany the industry's paradigm shift from information stacking to knowledge generation. The company was created in 1997 in parallel with its strategic partner, SIB. GeneBio provides the market with a suite of software platforms and knowledge bases targeted at small molecules screening and protein research.

Since its creation, GeneBio has evolved from its original and ongoing mandate as the commercial arm of the SIB to become a truly global multifaceted bioinformatics company offering the life sciences community a spectrum of original solutions. "With the increasing quantity of data generated by the industry, the life sciences community needs more than ever to bridge the gap between information gathering and knowledge generation," says Nasri Nahas, GeneBio's CEO. GeneBio is currently focusing on analysing small molecules by mass spectrometry as well as protein-centric knowledge management and organisation. The company's headquarters are in Geneva and, since 2004, it has also been operating a Japanese branch in Tokyo.



What's the SIB-GeneBio partnership like today?

13 years later, GeneBio still remains an important link between SIB and the industry. The partnership was recently strengthened through NextProt, a resource in development within Professor Amos Bairoch's group, CALIPHO, and which is expected to become a comprehensive knowledge resource on human proteins. This project was started in 2009 with the support of CTI-KTI.

SmileMS: example of a success story

SmileMS was developed in collaboration with major institutions such as SIB and the Department of Genetics and Laboratory Medicine of the Geneva University Hospital. MS stands for Mass Spectrometry, which is a powerful analytical technique used to screen and identify a wide range of chemical compounds. MS is used routinely in many laboratories in fields such as Laboratory Medicine, Forensic Toxicology, Doping Control, Food Testing, and Metabolomics research. SmileMS is a software platform, which permits identification of small molecules for both fast routine analysis and in-depth research.

The University Centre of Legal Medicine of Lausanne-Geneva (CURML-UTCF), and more precisely its Forensic Toxicology and Chemistry Unit, sees in this software an outstanding opportunity. Dr. Marc Augsburger, Operational Manager of this unit, says: "Further fine-tuning of SmileMS in relation to our research and our routine analysis will positively benefit users in the domain of forensic toxicology." That is why GeneBio and CMURL/UTCF announced in May their collaboration to develop further the SmileMS software platform for large-scale forensic toxicology studies.

A study now underway and based on saliva collected from about 1,000 randomly-selected drivers already shows that SmileMS is capable of identifying a number of illicit substances with a high level of certainty.

What is bioinformatics?

Over the past 30 years new biological research techniques, combined with developments in information technology, have increased both the amount and complexity of biological data. That is why scientists must often apply information technology to biological problems – a science called bioinformatics.

Life scientists use bioinformatics to store, process and analyse large amounts of data – advancing their knowledge and understanding of biological processes. This, in turn, can lead to scientific breakthroughs that enhance our quality of life – for example, in designing better medical treatments or improving crop yields.

About SIB www.isb-sib.ch

The SIB Swiss Institute of Bioinformatics is an academic not-for-profit foundation federating bioinformatics activities throughout Switzerland. Its two-fold mission is to provide world-class core bioinformatics resources to the life sciences research community at both the national and international levels in key fields such as genomics, proteomics and systems biology, as well as to lead and coordinate the field of bioinformatics in Switzerland.

It has a long-standing tradition of producing state-of-the-art software for the life sciences research community, as well as carefully-annotated databases. The SIB includes 29 world-class research and service groups, which gather 400 researchers, in the fields of proteomics, transcriptomics, genomics, systems biology, structural bioinformatics, evolutionary bioinformatics, modelling, imaging, biophysics and population genetics in Basel, Bern, Geneva, Lausanne and Zurich. SIB expertise is widely appreciated and its infrastructure and bioinformatics resources are used by life sciences researchers worldwide.

Institutional members:

Swiss Federal Institute of Technology Lausanne (EPFL)
 Swiss Federal Institute of Technology Zurich (ETHZ)
 University of Basel
 University of Bern
 University of Geneva
 University of Lausanne
 University of Zurich
 Ludwig Institute for Cancer Research (LICR)
 Friedrich Miescher Institute for Biomedical Research (FMI)
 Geneva Bioinformatics (GeneBio) S.A.
 Hewlett Packard

A full list of SIB research projects can be found at:
www.isb-sib.ch/research/projects.html



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