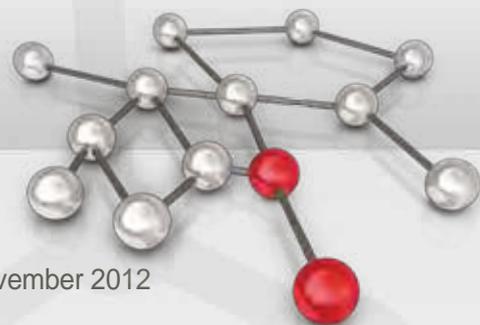




Swiss Institute of
Bioinformatics

SWISS BIOINFORMATICS

A newsletter published by SIB Swiss Institute of Bioinformatics



Editorial



Bioinformatics is indispensable to life science research as reflected by the growth of its community. No research project in the life sciences can be carried out today without the help of bioinformatics databases, tools or expertise. This explains why our institute gained eight new groups over the past year and has now more than 550 members; it also explains the number of chairs for bioinformatics that are regularly created in the Swiss Universities.

This collective awareness reaches far beyond the Swiss borders. ECCB, the European Conference on Computational Biology, is a perfect barometer for the high interest and activity in this field. Organized by SIB

and the Biozentrum of the University of Basel, this year's edition was held in Basel from 9 to 12 September and was really exceptional, not only in terms of programme content but also in terms of attendance: there were 1,200 participants as opposed to the 600 initially expected! During the four intensive conference days, experts and researchers exchanged views on the latest trends and developments.

Given the daunting amount of data researchers will have to handle in the coming years and the urgency that exists to find solutions to tackle the grand challenges our societies are facing - such as healthcare for an ageing population, food security, energy diversification and environmental protection - bioinformatics is not a fashion phenomenon, but truly a discipline which must be given the attention and space it deserves. A provider of precious support to research, bioinformatics now requires support in return. The funds available for the development and maintenance of bioinformatics resources will not be sufficient to meet the fast growing need for specialized and well-trained people, as well as methodologies and infrastructure.

Well aware of the necessity to train next generation bioinformaticians, SIB has been providing a variety of courses, workshops and seminars to help it keep up to date with the latest trends and tools. Today, with the support of generous partners, SIB is going a step further by launching its Fellowship programme which will give a selection of the best students from around the world the opportunity to carry out their PhD research in one of its 38 research and service groups located across Switzerland. The call for applications is now open and the programme will start in 2013. SIB has high hopes for this programme and its future development.

Ron Appel, Executive Director

● November 2012

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News in brief



Passing of Peter Malama

On 22 September, Peter Malama, National Councillor and President of the SIB Foundation Council passed away. The Swiss scientific community and SIB lost a faithful friend and will miss his unflinching support to scientific research and progress.

Chromosomewalk.ch

The French version of SIB's new virtual exhibition has been online since July 2012 and has already proved to be very successful. The English version will be available in December thus allowing a wider audience to become acquainted with the fabulous world of chromosomes and their genes.

www.chromosomewalk.ch

SIB signed the MoU to establish GOBLE

In July, SIB signed the Memorandum of Understanding for the creation of a Global Organisation for Bioinformatics Learning, Education and Training. GOBLET is meant to become an umbrella organization based on criteria of training and pedagogical excellence. The objective is to coordinate worldwide bioinformatics training initiatives, organize international events, raise funds to support activities and to establish a joint web-based portal for training information and tools.

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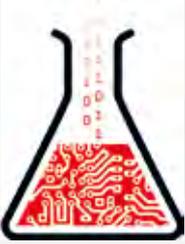
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NEWS



Education and outreach

SIB Fellowship programme



One of SIB's missions is to train the next generation of bioinformaticians. This is all the more important with life scientists generating massive amounts of data thus creating the need for more and more specialized well-trained bioinformaticians to analyse, visualize and interpret them. SIB already provides courses, workshops and seminars, and wishes to go a step further with the implementation of its

Fellowship programme starting in 2013. Supported by the Swiss government exclusively for the development of bioinformatics core resources, our institute managed to raise funds to attract the best students from around the world who would like to embrace a career in bioinformatics. The deadline for application submission is 15 November 2012. www.isb-sib.ch/fellowship.html

SIB Open House



SIB opens its doors to young scientists who are considering a career in bioinformatics. During the next SIB Days – our institute's annual internal meeting – on 28 and 29 January 2013, ten selected applicants will have the opportunity to participate in the event: a great opportunity for them to meet potential employers and learn about job opportunities among the creators of UniProt, SWISS-MODEL, the ExPASy portal, and many other Swiss bioinformatics tools and resources.

This opportunity is open to Bachelors, Masters, PhD students or postdocs interested in Bioinformatics. The application deadline is 10 November 2011. www.isb-sib.ch/education/openhouse.html

Report on ECCB'12

The 11th Conference on Computational Biology took place in Basel from 9 to 12 September. Organized by SIB and the Biozentrum in Basel, the conference was a tremendous success in terms of programme and attendance. Over one thousand participants from around the world came to listen to keynote speakers such as Aaron Ciechanover - Nobel Laureate in Chemistry (2004) – Gene Myers, Søren Brunak and Barry Honig.



Highlights

Interview with keynote speaker Gene Myers

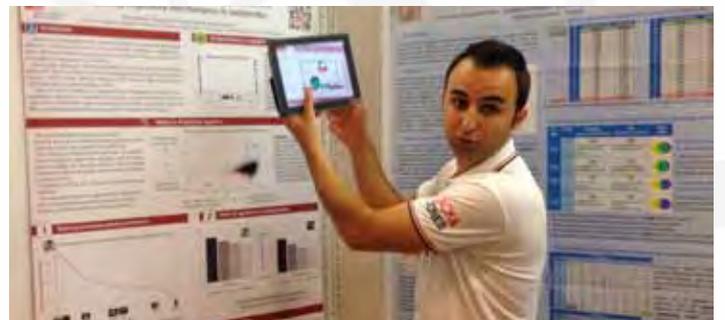
One of the keynote speakers at this year's ECCB held in Basel, Gene Myers is particularly well known for the development of BLAST in the 1990s, the sequence alignment tool which continues to be used worldwide today. After a few years at Celera Genomics where he was involved in sequencing the human genome, the computer scientist is currently based at the Max Planck Institute in Dresden where his team extracts and analyses information from images obtained by microscopy.

Gene Myers witnessed the very beginnings of computer science and sequencing, and always seems to have had a capacity to foresee what could make a difference. "Back then I had no particular interest in biology" he confesses. "I loved the technical side of things and was asked to apply my know-how to DNA sequences. So I did". After BLAST, his career in sequencing continued with Celera Genomics and the human genome, followed by those of the mouse and the Drosophila.

"I came to a point where I was in need of a new challenge", Myers confides. And, in 2002, he developed an interest in an emerging field: image and labelling techniques. "Changing directions can be very difficult", he states. "I was a leader in my field and, from one day to the next, became a novice. It takes a pinch of humility. Changing is also risky; it may not work out. And funding aspects can be a burden." In this respect, Myers regrets the current narrow-mindedness where funds depend on the experience a scientist has acquired in a given field, instead of the scientist's merit as an investigator.

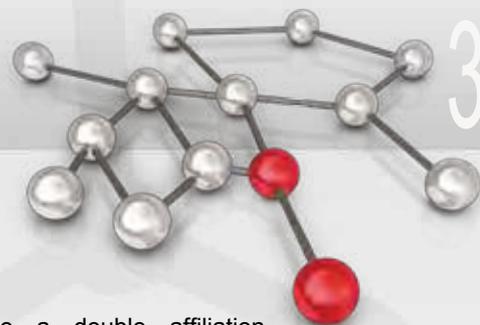
"Over the years, I have developed a real interest in biology and how a cell works", he continues. Nowadays, it is possible to label about 40,000 gene products and Myers is looking for ways to explore this at the 250 nanometer scale! Is he thinking of applications? "All I want to do is have a look inside a cell and understand what is going on", he explains. "It is a very complex story". This said, Myers believes that imaging techniques will become the norm of investigation because they will reveal more about what is going on at the sub-molecular level than any other current approach. Is he a visionary? "Perhaps I see things other people don't", he says. "However, all I would like now is to inspire the upcoming generation".

1st and 2nd Poster Prize for SIB Members



About 500 posters were presented during the conference. The first prize went to Adem Bilican, Anamaria Necseulea and Henrik Kaessmann, from SIB and the Center for Integrative Genomics (UNIL) for their innovative poster "The evolution of alternative splicing patterns and splicing regulatory mechanisms in vertebrates", which included a 3D application. They definitely paved the way for a new generation of posters!

Second Prize went to Barbara Piasecka, Pawel Lichocki and Marc Robinson-Rechavi, from SIB and UNIL for their poster entitled "Modular approach uncovers different developmental patterns of evolution on different molecular levels".



Happy Birthday UniProt!

UniProt celebrates its 10th anniversary. For the occasion, about 150 scientists from all over the world attended the “Bioinformatics Research Infrastructure for the Life Sciences: The First 10 Years of UniProt” workshop at the ECCB’12 conference in Basel on 8 September 2012.



Some quotes:

“A wonderful example of successful collaboration between different countries and different people”.

Rolf Apweiler, EBI

“Many thanks to UniProt which provides us with this fundamental and essential functional information”.

Minoru Kanehisa, Kyoto University, Japan

“UniProt is really a wonderful resource: available, responsive, a place for a mutual share of information”.

Judith Blake, Mouse Genome Informatics, USA

Twelve renowned speakers described their work and how they make use of the UniProt databases in different research fields such as protein-protein interaction, protein modelling, proteomics, genome analysis and genome annotation. In addition, 20 posters highlighted how protein databases are underpinning the life sciences. The workshop was really successful and reached its goal by showing how many tools and resources are relying on UniProt.

UniProt is a collaboration between SIB, the European Bioinformatics Institute (EBI) and Protein Information Resource (PIR). In the three institutes, 100 people are involved in different tasks, such as database curation, software development and support. The mission of UniProt is to provide the scientific community with a comprehensive, high-quality and freely accessible resource of protein sequence and functional information.

Research

e-bioinformatician: a precious bridge

Life science researchers generate a growing quantity of data on a constant basis and the pace will only accelerate in the coming years. It is therefore crucial for them not only to know how to store their data in the most efficient way but also to run fast and pertinent analyses of their results. When in need of advice and guidance, life science researchers have had the possibility of contacting SIB whose bioinformatics core facilities provide informatics and statistical support. However, given the growing requests of laboratories to hire full-time bioinformaticians for deeper integration into their laboratories and projects, SIB introduced a new concept: embedded bioinformaticians, also known as “e-bioinformaticians”.

What exactly is an e-bioinformatician ?

e-bioinformaticians have a double affiliation and form a sort of bridge between SIB and external research projects. First, they are part of an SIB group and, second, they can be temporarily assigned to specific research projects or laboratories according to needs.

e-bioinformaticians dedicate all or part of their time to research group projects at the partner institution while working with an SIB group in the context of one or more of these research projects. He or she then reports to the research group leader for the biological/experimental aspects, and to the SIB group leader for the bioinformatics and computational aspects.

Such a model has already been successfully implemented and about 30 e-bioinformaticians are currently spread across research groups at the Universities of Basel, Bern, Lausanne, Geneva, and at EPFL and CHUV.

David Gatfield, Center for Integrative Genomics, University of Lausanne

The moment David Gatfield received the grant to launch his own research group, he knew that his projects would require strong bioinformatics support. “To begin with, I thought this could be done on a collaborative basis with groups that had the computational expertise I needed”, says the researcher. But he soon realized that the amount of data the group was generating would become problematic and just end up creating a bottleneck for most projects. It took a further year to raise the money needed for an embedded bioinformatician and to find a suitable candidate – a former geneticist cum computationalist, Bulak Arpat.

“The collaboration has proved to be well beyond my expectations”, enthuses Gatfield. Barely four months after joining the group, Arpat’s computational competences helped several projects make major leaps, namely those which involved high-throughput sequencing data. Gatfield expresses delight at how the time between sequencing, data analysis and the elaboration of novel hypotheses for the lab is continuously decreasing. He also explains that a bioinformatician so close at hand makes communication far more spontaneous and uninhibited. “Arpat started off as an experimental biologist which is an asset”, says Gatfield. “His analytical and quantitative approaches will help to make great contributions to the experimental part of our projects”.

Bulak Arpat, embedded bioinformatician

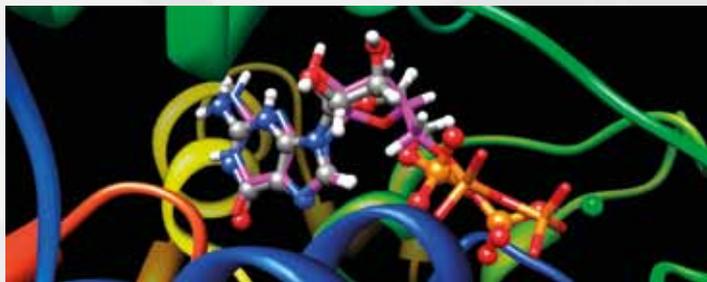
Bulak Arpat is using his computational skills within David Gatfield’s research group in the Center for Integrative Genomics at the University of Lausanne. Trained as a biologist and geneticist, with a strong background in wet lab research, the young scientist likes being on the bridge between the life sciences and computation, where he is able to share views with both worlds. “I consider being able to communicate with biologists and computationalists, a strength”, says Bulak. He also enjoys being immersed in a specialized field of research as it gives him the opportunity to become far more acquainted with a given subject.

Although Bulak has only been in Gatfield’s group for a short time, the collaboration has already proved fruitful. He enjoys the contacts he has with scientists from all fields and the exchanges that occur on different collaborative projects. In particular, he appreciates the interactions he has with experimentalists, which are useful for discussing experimental setups, analysis and interpretation. Naturally, the scientist collaborates with traditional bioinformaticians and statisticians with whom he hones the technical aspects. “Collaborations are so close”, says Bulak, “that my knowledge of non-bioinformatics issues is also expanding, which is great”.

Success Story

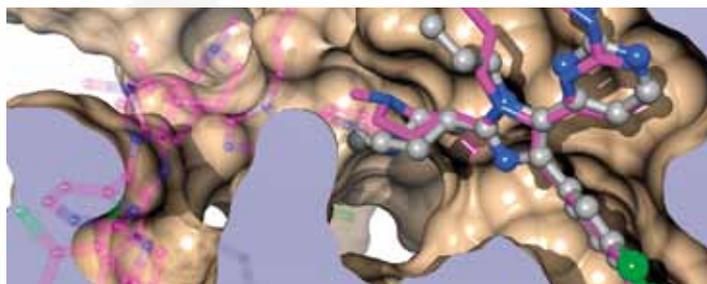
SwissDock: A successful development for drug design

Olivier Michielin and his team from SIB's Molecular Modelling Group in Lausanne develop molecular modelling tools – namely EADock which has proved to be particularly useful in designing drugs to fight cancer. Though barely two years old, SwissDock – EADock's web interface – is now used by scientists worldwide.



"I enjoy the field of 3D modelling because it's a way of bridging the basic fields of science such as chemistry and physics with the life sciences – in particular the medical sciences", explains Olivier Michielin. He and his team – Aurélien Grosdidier, Vincent Zoete and Ute Röhrig – are developing a docking tool known as EADock, to design small molecule inhibitors. The group's interest in cancer started at the very beginning of Michielin's research. "However, it is only within the past ten years that the field of bioinformatics and research in oncogenic mechanisms drew closer", he underlines.

For five years now, the team has been working on the inhibition of a key enzyme which is able to mask tumours from the immune system. "In this respect, EADock – with important know-how on the part of Ute Röhrig and Vincent Zoete – has proved to be pretty successful", says Michielin. The group managed to design molecules that inhibit this particular target at nanomolar concentrations. "These compounds have been validated in mouse models, and we hope to begin clinical trials at CHUV within the next two years".



To make EADock accessible to the scientific community, the team is also developing a web service called SwissDock. The idea is to make drug design easily accessible to as many scientists as possible – in particular biologists. The group gets very satisfactory feedback from external researchers and collaborators, which helps to continuously improve EADock and SwissDock.

In the past 12 months, SwissDock has received 23,000 visits and accumulated 138,900 page views, for a total of 6,000 jobs! Most visitors come from Europe and India, followed by the USA. "It has only been online for two years, and is now regularly cited in scientific publications for drug design applications", continues Michielin. "An excellent result given the time it takes to complete a drug design project and then have it published!".

"We are particularly happy with the kind of researchers who use SwissDock – namely biologists (60%). Scientists can leave messages regarding their results or experiments, and we have received hundreds of encouraging comments on the quality and the user-friendly interface of SwissDock. Which is, of course, very satisfying and encouraging for future developments".

What is bioinformatics?

Over the past 30 years, new biological research techniques, along with developments in information technology, have increased both the amount and complexity of biological data. This 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 to advance their knowledge and understanding of biological processes. This, in turn, can lead to scientific breakthroughs that enhance our quality of life in fields such as designing better medical treatments or improving crop yields.

About SIB www.isb-sib.ch

SIB Swiss Institute of Bioinformatics is an academic not-for-profit foundation, recognized of public utility, which federates bioinformatics activities throughout Switzerland. Its two-fold mission is to provide world-class core bioinformatics resources to the life science 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 science research community, as well as carefully-annotated databases. SIB includes 38 world-class research and service groups that bring together over than 550 researchers in the fields of proteomics, transcriptomics, genomics, systems biology, structural bioinformatics, evolutionary bioinformatics, modelling, imaging, biophysics and population genetics in Basel, Bern, Fribourg, Geneva, Lausanne, Lugano and Zurich. SIB expertise is widely appreciated and its infrastructure and bioinformatics resources are used by life science researchers worldwide.

Institutional members:

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 Swiss Federal Institute of Technology Zurich (ETHZ)
 University of Basel
 University of Bern
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 Ludwig Institute for Cancer Research (LICR)
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A full list of SIB research projects can be found at:
www.isb-sib.ch/research/projects.



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Quartier Sorge
 Bâtiment Génopode
 CH-1015 Lausanne
 Switzerland
 t +41 21 692 40 50
 f +41 21 692 40 55
www.isb-sib.ch

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