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SyBIT – Systems Biology IT, and more



The almost complete SyBIT team at its first retreat in February, in central Switzerland (Rigi Kaltbad). Photo: Peter Kunszt

Peter Kunszt, SyBIT Project Leader
Everyone knows about the Large Hadron Collider at CERN and about the very large amounts of data that are being produced by the huge detectors 100m below ground in Geneva. For the high energy physics community it has taken several years to build the dedicated world-wide computing infrastructure to assure that they are able to deal with their immense amount of data. The project, called Worldwide LHC Computing Grid WLCG is a large international collaborative effort, involving almost every physics data center in the world.

The needle in the haystack

On a national scale, SystemsX.ch needs to address the same problem, with a similar amount of data. In many ways the problem is more complicated in biology than in high energy physics. At CERN there are only four instruments producing very similar, well-understood data, at SystemsX.ch we have many different kinds of instruments, including new experimental ones, producing very different, often not yet well-understood data. A large part of SystemsX.ch research goes into

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Biology: an in silico discipline?

Ralph Schlapbach, Functional Genomics Center Zurich

Not quite, but not far from wrong either. Sequencing the human genome was possible using technologies that, from today's viewpoint, were not very complex, of low throughput, largely manual, almost mechanical. Their latest high-tech counterparts run massively parallel protocols in an automated fashion, largely independent of human intervention, and they produce highly complex data in huge quantities and within a short time. The respective output poses an enormous challenge for data management, processing, and analysis, not to speak of interpretation. This is equally true for many other technologies and methods applied in life science research. High throughput imaging is used alongside quantitative mass spectrometry; large-scale functional screens are combined with metabolic read-outs; every combination of molecular and functional data is thinkable and eventually feasible.

Only by combining the biological knowledge with data processing and analysis expertise of the information sciences can we deal

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SyBIT
SystemsX.ch
Biology IT

the analysis of the data being produced in the laboratories, trying to understand the underlying biology. While in physics the data is mostly being scanned for rare events – the needle in the haystack problem – in biology people look for patterns, and apply many different statistical tools to analyze complex workflows.

Comprehensive service

The SyBIT project was created with similar goals in mind as the WLCG, to support the researchers in the production, validation, analysis, and publication of their data. Of course, such support existed before SystemsX.ch created SyBIT, just not dedicated to Systems Biology on a national scale. SyBIT is not a new and separate organization, but a national project joining all groups where local IT and bioinformatics support has already been implemented to a large degree (see box on

SyBIT facts). On a national scale, the Swiss Institute of Bioinformatics (SIB) already acts as an overarching coordinating entity, with which SyBIT is integrated as an affiliated partner group.

SyBIT builds on knowledge and expertise already available at the partner sites. Through SyBIT, researchers can share experience and knowledge in order to address the distributed nature of SystemsX.ch RTD projects. One of the most important aspects of SyBIT is to assure that this information exchange works, and that the individual groups do not need to duplicate the same tools and infrastructure across Switzerland. SyBIT places its personnel directly inside the relevant teams of the local partners, so they can really work closely with the SystemsX.ch researchers they are supporting.

Meeting specific needs

To ensure that the tools SyBIT develops and supports are of immediate benefit to the researchers, SyBIT projects are always set up as a joint project between the local SyBIT team and the local researchers. The

scientists lead these projects; they are in the driving seat when it comes to defining the requirements and evaluating the results of the project. In the first year of SyBIT, we deliberately created only short-term projects (3-6 months), in order to focus on the most urgent needs and to assess the overall requirements. We also needed to find out where additional personnel was necessary. This approach proved to be highly successful. By the end of 2009 we completed several projects, and have placed over 10 new people at various partner institutions.

Promising experiences

The initial projects also helped us understand how to be efficient in reusing experience and tooling across Switzerland. We quickly realized, for example, that it makes a lot of sense to group our user communities into technology domains. At the 2009 All-SystemsX.ch-Day in Bern we held SyBIT sessions dedicated to proteomics, genomics, screening, and modeling technologies to see whether people are interested in similar tools and standards. With the exception of modeling,

the result was that people indeed implement very similar things all across SystemsX.ch and that there is a lot of potential for cooperation. Since then we have started a few community projects where we hope to have a larger impact, producing tools that are interesting for more than just one SystemsX.ch lab (see section on SyBIT Tools).

Important partner

However, SyBIT is not only about tool development and support. SyBIT also assists in the planning and the coordination of necessary hardware infrastructure. SyBIT provides collaboration services to SystemsX.ch, like mailing lists, wiki pages, and public websites. Last but not least, SyBIT initiated the collaboration with ZORA, the University of Zurich's Open Repository and Archive, where all SystemsX.ch publications can be deposited according to Open Access standards.

In summary, SyBIT is more than the SystemsX.ch IT backbone; it is an important enabler and preserver of SystemsX.ch science.

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SyBIT Facts

SyBIT is the only project initiated by SystemsX.ch. Unlike classical research projects which get SystemsX.ch funding, SyBIT is a support project. Its funding is 6.9m CHF for the period of 2009-2011, which is used mostly for personnel placed inside the partner institutions, but also for infrastructure that supports SystemsX.ch projects.

The current SyBIT collaborators (in alphabetical order):

- Bioinformatics and Biostatistics Core Facility – EPF Lausanne
- Biozentrum – University of Basel and SIB
- Center for Information Science and Databases – ETH Zurich's D-BSSE department in Basel
- Friedrich Miescher Institute in Basel
- Functional Genomics Center Zurich – University of Zurich and ETH Zurich
- Institute of Molecular Systems Biology – ETH Zurich
- Light Microscopy Center – ETH Zurich

- Vital-IT – Swiss Institute of Bioinformatics in Lausanne

This list may grow in the future, as SystemsX.ch will involve more and more institutions.

The SyBIT project management is located together with the SystemsX.ch management office in Zurich. Both the project manager Peter Kunszt and his deputy Ela Hunt regularly visit the various SyBIT project sites in Basel, Lausanne and Zurich.

The SyBIT team, which includes all people working on SyBIT projects and supporting the SystemsX.ch researchers, consists of over 20 people. Not all are funded or co-funded by SyBIT; some are paid either by our partner institutions or through other SystemsX.ch projects. The team meets every 3-4 months to discuss technical issues and the most recent developments.

See also <https://wiki.systemsx.ch/display/sybit>

SYSTEMSX.CH NEWS

New Interdisciplinary Pilot Projects (IPP) and Bridge to Industry Projects (BIP) approved

The Scientific Executive Board (SEB) of SystemsX.ch has come to a decision regarding the seven IPP proposals submitted in January 2010. The following IPP project listed below has been approved and will be funded for a year.

- «Multidimensional genome organization: correlating 5C and SIM» from Susan Gasser (FMI) and Andrzej Stasiak (Unil)

Additionally, one Bridge to Industry project (BIP), submitted on February 1, has been approved. This project is a collaboration between Bernd Wollscheid (ETHZ) and Agilent Technologies and will run for one year. It is called:

- «Development and Application of CHIP-LC-MS Technology for Systems Biology Research»

A decision from the Swiss National Science Foundation on the 21 IPhDs submitted in January is expected by July 2010.

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SyBIT Tools

With SyBIT we follow a toolbox approach for the support of software in SystemsX.ch. We are supporting a set of tools in this toolbox – whether they are open source or commercial – if there is sufficient demand for them from the SystemsX.ch community. However, we try to keep as few redundant tools in the toolbox as possible, with the possibility to phase out tools that can be replaced with better ones, where «better» not only means better usage but also better support and better manageability.

Two examples of tools we want to mention here are a data management framework to track and annotate raw data (openBIS), and a framework to analyze screening data automatically (iBRAIN). Both tools were written before SyBIT started.

OpenBIS is being developed at the ETH's Center for Information and Science Databases CISD in Basel. As a result of SyBIT projects, it is now deployed and in daily use by several SystemsX.ch partner institutions to manage their data, and more laboratories are interested in testing and using it. SyBIT also contributes to the development

of openBIS at CISD; adapting it to the various needs of SystemsX.ch. OpenBIS is highly configurable and extensible, and therefore reusable in many contexts. Currently it is used in screening, proteomics, genomics and metabolomics, and has also attracted interest from the imaging community.

iBRAIN tool was written by Berend Snijder, a PhD student in Prof. Lucas Pelkmans' laboratory at ETH Zurich. Several other institutions are interested in this tool, which is in daily use by almost everyone in the Pelkmans laboratory. However, as often happens with tools written by the scientists themselves, iBRAIN is very specific to the environment inside this particular laboratory, and cannot be easily installed at another institution.

In addition, Snijder is now at the end of his PhD, and when he leaves, there will be nobody left to maintain the system. SyBIT is now working to create a version that is both portable and maintainable, and can be extended to support automation of any new analysis in the future. SyBIT involves several laboratories directly in this development. All of those in-

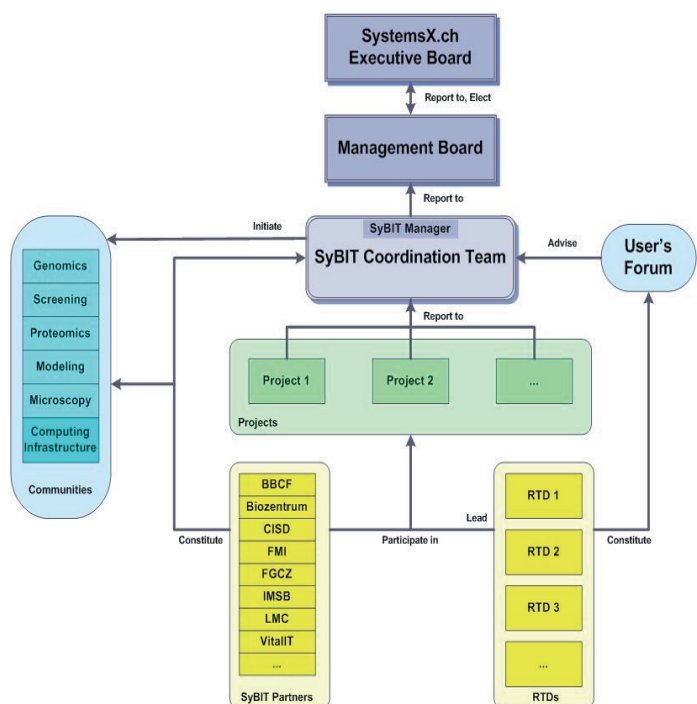
terested are interested in using iBRAIN.

The SyBIT toolbox is dynamic and aims to meet the needs of the new researchers and their new research. We are open to take up and support new tools, or to start contributing to existing ones, especially if they are

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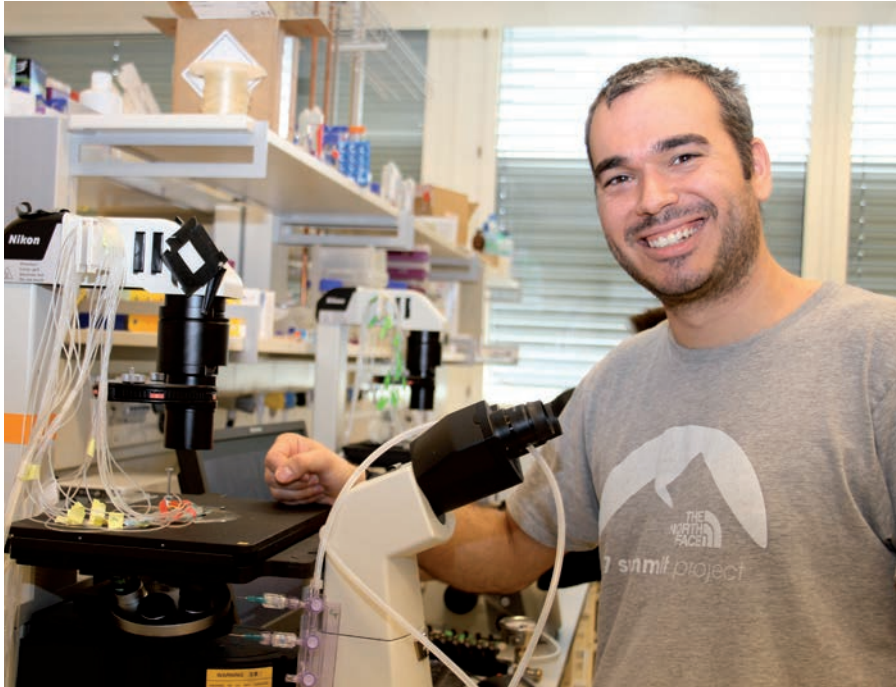
Biology: an in silico discipline?

with the vast amount of information and identify the underlying mechanisms and the key regulating factors of our biological systems. While biology will never become a pure in silico discipline, its complexity will only be understood via the integration of multiple molecular and functional levels by computational methods.



The SyBIT Project Structure. The SyBIT collaborators and SystemsX.ch RTD projects form the SyBIT project teams, led by the scientific groups. The coordination team is composed of the local collaboration site managers and the SyBIT project manager. The communities and users forum are additional vehicles to assure SyBIT is optimally integrated with the researchers and can address the most relevant topics. Graph: Peter Kunszt

At «Dynamix» everything is in flow thanks to new technologies



Sebastian Maerkl, head of the RTD-Project «Dynamix».

Photo: msc

science whose progress strongly depends on technological innovations. The ever more complex questions presuppose the proportionate innovation», says the scientist.

However, the Dynamix team is not waiting for appropriate technology to become available – they developed it themselves. «We've succeeded in making a tool that makes it possible for us to do a range of parallel measurements on the cell», says Maerkl.

Hi-tech under the microscope

The hi-tech instrument, known as the «microfluidic device», looks remarkably unspectacular. A little bigger than a postage stamp, it's made of a transparent synthetic material and contains an inner field of geometrically ordered lines. «These linear structures are the core of our development. They enable us to control the flow of a medium», says Maerkl, centering a plate under the microscope. Indeed, only with this magnification does the complexity of the structure become apparent. A host of small chambers stand in rank and file next to, above and below one another. «To start the experiment these chambers are smeared with a layer of yeast cells. The micro-organisms then live in them under controlled conditions». They are provided with constant nutrition by a medium that flows through the chambers.

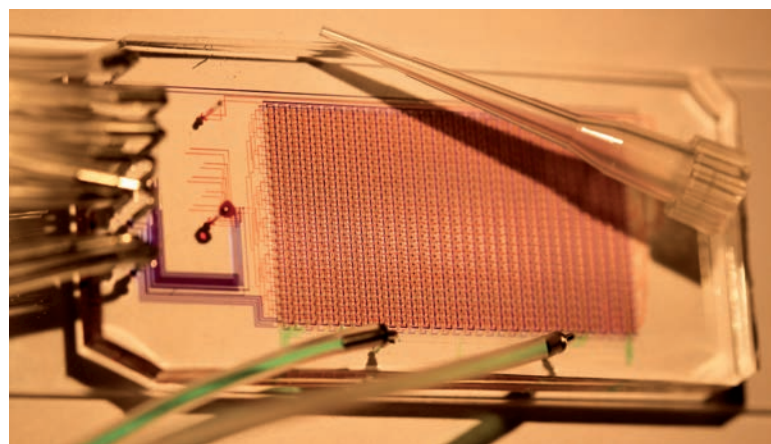
As soon as the cells are fed, their metabolism kicks in and they begin to repro-

Matthias Scholer
Something anyone who has ever made bread knows is that you can't do it without yeast. As soon as these micro-organisms come into contact with sugar and water, they are brought to life. They start by dismantling the sugar and proceed to reproduce. At a first glance, a commonplace procedure but one that is only possible thanks to a complex collaboration of various cell factors, especially proteins.

Researchers working on the RTD Project «Dynamix» are concentrating on precisely the genesis and function of these proteins. Head of project Sebastian Maerkl from EPF Lausanne explains why his team decided on yeast as the trial object. «This organism has already been the focus of a great deal of research and we were able to base our work on a large amount of already available data. What's more the number of genes and proteins in yeast is manageable and results can be applied to other organisms, like human cells.»

No research without innovation

Above all Maerkl and his team are interested in the dynamics of proteins and measuring them quantitatively. «Among other things we'd like to know how much protein is produced in a cell and at what point in time, and when and how these proteins interact among themselves». The knowledge gained from the ensuing data will be used to develop computer models that can simulate the function of an organism. However, there is still a long way to go. «Biology is a



The «Microfluidic Device» with its ingenious chamber arrangement.

Photo: Maerkl

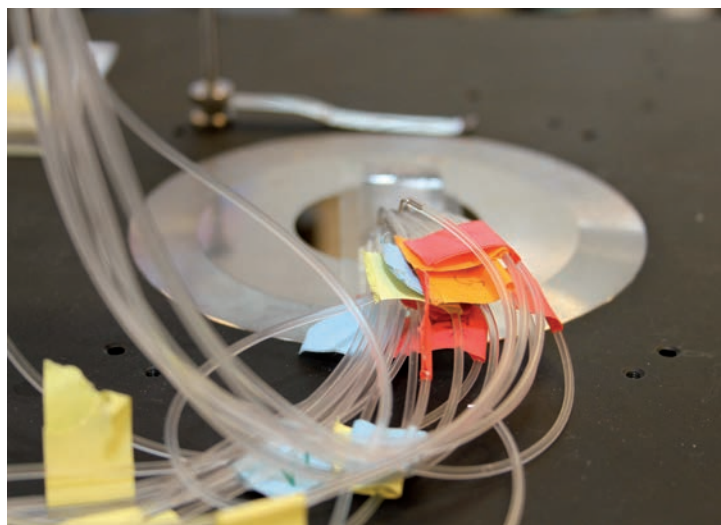
duce. They migrate upwards in the chamber and once they reach the edge they are rinsed out by the medium. In this way, a constant population of cells establishes itself in each «incubator».

These conditions allow the team to examine, in detail, the life cycles of each individual yeast cell. «Thanks to the chamber arrangement we can run complex biological experiments in parallel. And rapidly and precisely into the bargain», is how Maerkl sums up the advantages of the method.

Measuring protein activity

For the main part, the DynamiX team uses the plates in two areas of research: on the one hand, to carry out quantitative measurements of the protein and, on the other, to examine the interactions of the protein among themselves and with the DNA.

In order to obtain the necessary data, the researchers allocate yeast cells that have been loaded with a fluorescent marker to each chamber. This marking allows them to optically follow the development of the protein over a defined



Complex experiments thanks to High-Tech

Photo: msc

period of time. «For the duration of a second we record, on film, each and every chamber. So, in a quarter of an hour we can record the activity in each chamber. We can repeat this procedure any number of times and in the end we have obtained enough film to investigate and measure the dynamics of the proteins», explains Maerkl.

It is not only the protein activity under normal conditions that interests the biologists, however. They also carry out a targeted stressing of the cells. For instance, by adding a stressor agent to the medium, which damages the genet-

ic substance of the trial cells. Interestingly, this activates specific proteins in the cell to repair the damaged DNA. These repair jobs are extraordinarily complex and one stage of the process triggers or initiates the next. «We learn a lot of new facts from such trials about the function of the individual proteins», adds Maerkl.

Looking into the future

But what advantage can be gained in the long run from knowledge

about the dynamics of proteins? «Trial arrangements already exist to analyse the reaction of pathogens to the deactivation of specific genes. Subsequently, we can observe whether and how the reaction patterns of the proteins change when antibiotics are added», says Maerkl, referring to a possible interface with human medical research. So perhaps further down the line certain medical diseases and disorders can be treated more efficiently and more effectively thanks to yeast research. Perhaps something to ponder on next time while we're kneading the bread dough.

DynamiX is teamwork

The RTD project «DynamiX» includes five project heads, each with a different area of responsibility:

Davis Shore

- The transcriptional regulation of the ribosomal biogenesis
- The regulation of cell growth

Jacques Rougemont

- Bioinformatics and biostatistics

Michael Unser

- Development of imaging techniques
- Processing biomedical recordings

Felix Naef

- Computer-based modeling of cell-cycle regulation and its temporal sequence

Sebastian Maerkl

- Development of «microfluid techniques»
- Systems Biology

«DynamiX – Yeast Protein Network Dynamics» at a glance



DynamiX
Yeast Protein
Network Dynamics

Principal Investigator	Sebastian Maerkl
Involved research groups	Prof. Sebastian Maerkl, EPF Lausanne; Prof. Michael Unser, EPFL; Prof. Davis Shore, University of Geneva; Prof. Felix Naef, EPFL; Dr. JacquesRougemont, EPFL
Number of research groups	5
Researchers : Administration	12 : 0
Biologists : Non-biologists	7 : 5
Total budget (2008-2011)	4'790'000, thereof 2'296'000 CHF from SystemsX.ch

Discovery of a new genetic sub-code

Scientists at ETH Zurich and the Swiss Institute of Bioinformatics (SIB) have succeeded in identifying a new genetic sub-code. This determines the rate at which cells make proteins.

The newly discovered sub-code also provides insight into the cellular processes at the molecular

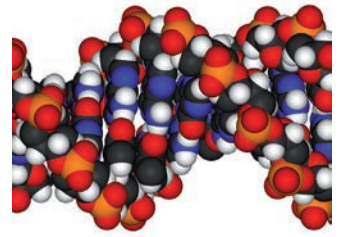
level, such as the functionality of ribosomes. Initial results indicate that the ribosomes recycle their own components, the so-called tRNA, to optimize the speed of protein synthesis.

Owing to the fact that many therapeutic reagents, such as insulin, for instance, are produced in host organism

like bacteria and yeast, the new sub-code might also be used in therapeutic measures.

The knowledge of the sub-code could now help to change the DNA information in order to improve the synthesis of the host cell.

The study was published on 16th April in the magazine «Cell».



A sub-code in the DNA enables scientists to know which genes are turned-on quickly and which are best expressed slowly. (Credit: ETH Zurich)

How plants put themselves in a good light

Whether the sky is blue or grey, the sun pale or glaring, plants can photosynthesize and thus produce energy under widely varying light conditions. But how does this assimilation actually work in changing spectra? Two Swiss research teams have come a good deal closer to answering this key question.



Photo: Christian Fankhauser

Together with colleagues, Michel Goldschmidt-Clermont and Jean-David Rochaix examined the light concentration through the antenna complex LHCII. In collaboration with researchers from the University of Linköping (Sweden), the NCCR Plant Survival team succeeded in identifying the enzyme PPH1, which is responsible for the adaptation of the photosynthesis process to changing light conditions. This mechanism can be likened to two motors (photosystems I and II), that are linked via a «conveyor belt» – in this case a transport chain composed of electrons. The results of

the research now reveal that the PPH1 enzyme ensures the best possible adaptation of the plant to changing light conditions by maintaining a balance between the two photosystems.

In a parallel experiment, Christian Fankhauser from the University of Lausanne succeeded in showing the importance of the PKS2 protein with regard to the positioning and flattening of the leaves. Comparable to solar panel adjustment, the plant can optimize the angle of its leaves' position to the sun. The researchers in Lausanne have now been able to show that the PKS2 protein plays a

pivotal role.

Both discoveries concern fundamental research on the simple model plant «Arabidopsis» and aim to explain the mechanism plants use to adapt to light conditions. The understanding of this process may one day mean that plants that deliver a higher yield can be cultivated under adverse environmental conditions and may also one day be applied in agriculture.

Michel Goldschmidt-Clermont research was published at the end of February in the highly-regarded «Proceedings of the National Academy of Sciences» (PNAS); Christian Fankhauser's results can be found in the journal «Plant Physiology».

Plunging the depths

Microscopes play a major role when it comes to finding answers to biological questions. Over the 400 years since its invention this instrument has continued to be further developed and refined. Despite all the technological advancements, however, the depths which can be glanced with a microscope remain a restraining factor. This is because light is strongly scattered by dense tissue and cannot reach the coveted depths.

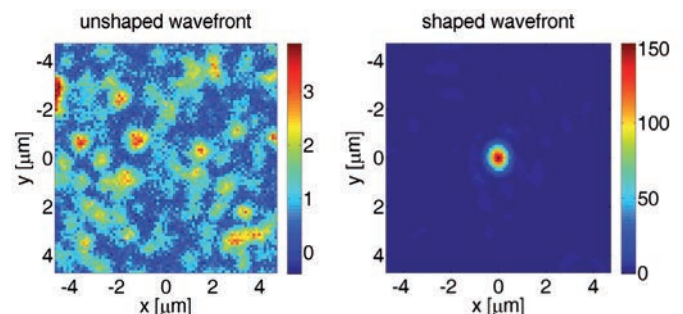
Scientists involved in the RTD-Project «WingX» have

now succeeded in developing a technique that makes it possible to overcome this optical limitation with the fluorescent microscope. The light emitted from the microscope is no longer bundled to a single point but the focal point constantly swings to-and-fro.

The level of reflected light is measured for each position. This enables the depiction of the hitherto hidden structures in thick tissue – and what's more with an optical resolution.

msc

More at: www.systemsx.ch/mediareleases



The two pictures above illustrate the principle of the microscope. Usually, when laser light is passed through a turbid sample, only a disordered, low intensity set of spots is obtained, which prohibits any form of imaging. After adjusting the illumination to the scattering in the sample, a single, sharp high intensity focus is obtained. In the microscope, this focus is scanned across a sample to excite fluorescent structures.

Dancing laser points

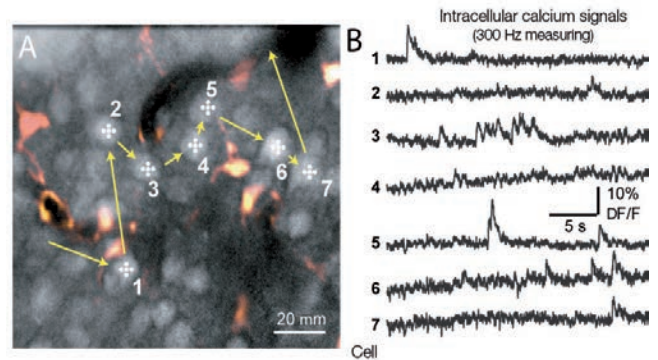
Mango or banana? Left or right? Fight or flee? In everyday life we constantly take decisions, sometimes well-considered, sometimes un-thinkingly. The processes that run in our brain is the focus of scientists working on the SystemsX.ch RTD-Project «Neurochoice». What these scientists are investigating is how neuronal networks portray certain stimuli, how these impulses are processed and how, in the end, the results influence our behavior, as for instance when we make decisions.

An important method used here is the so-called «two-photon-microscopy». This allows researchers to make the activity of individual nerve cells in the brain instantaneously visible. The laser beams scan the neurons onto a raster and the fluorescence is measured

at each point. The more active a cell proves itself to be, the higher the fluorescence. In this way the scientists obtain an image of the activity of all examined nerve cells.

Up until now this type of investigation has been carried out using mechanical laser reflectors whose inertia restricted the imaging to a few hertz (1-30Hz). Within the framework of the Neurochoice Project, Fritjof Helmchen and his group of researchers have now succeeded in developing the «two-photon» microscopy technique with which neuronal activity of mice can be observed with a high temporal resolution.

The new method, called «laser-scanning», employs two «acousto-optic» crystals. With the help of these the position of the laser beam can



(A) An image of the population of neurons (grey) and glia cells (red) in the cortex of a mouse: before examination the neurones were dyed with a calcium sensitive dye that changes its fluorescence when the cell is active. The new examination method scans small point rasters on each individual cell, one after the other, at speeds of up to 1 kHz. (B) The calcium fluorescence signals of the tagged neurones from (A) spread out over time: in all, in this measuring process 55 neurones were measured in this process (of which only seven are shown here) at a repeat rate of 300 Hz.

be changed, at will, within a few millionths of a second.

This means that it is possible to make the laser beam jump from cell to cell while rapidly carrying out the fluorescence measurements (cf. fig. A). And with this method the research group can actually capture the activities of a host of neu-

rons within a network with a temporal resolution of many hundreds up to one kilohertz (cf. example fig. B). In future, this new high-speed scanning technique will enable a more detailed and more comprehensive examination of the neuronal networks of the brain.

More at: www.systemsx.ch/mediareleases

Tracking down cancer

In Switzerland around 30,000 are diagnosed or living with cancer and every year 15,000 people die of the malignant disease. However, in many cases the disease can be successfully treated or even cured. The important factor is time: the sooner a cancer is discovered, the greater the healing chances. And it is here that the commercial idea of the firm «ProteoMediX» enters the fray.

Precise testing methods

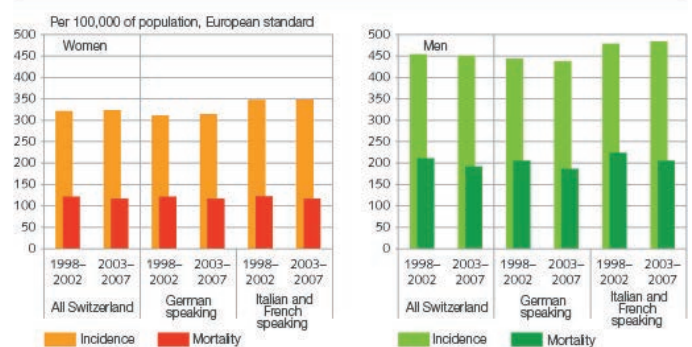
The young company, the result of an application-oriented research collaboration between professors from ETH Zurich with colleagues from the University Hospitals of Zurich and St. Gallen, has developed an innovative method for the early detection of cancer. In future, using this method it should be pos-

sible to find specific proteins in the blood on the basis of which scientists can say, with very high accuracy, whether a patient has cancer or not. Testing procedures until now are often inaccurate and this leads to many patients being confronted with false positive results. This does not only mean unnecessary psychological stress for the person concerned; often, they then have to undergo painful biopsies, to verify the results. Proteomedix aims to remedy the situation with the blood test it has developed. The first product from this start-up firm, an early detection test for prostate cancer, is to be marketed.

Wide support

The private initiative «venture kick» is supporting ProteoMediX, and, together

Incidence¹ and mortality according to language region: total cancers²



¹ Estimate of incidence for 2003-2006 period

² Incidence excluding non-melanotic skin cancer

Source: BFS, TU, NICER, KKR

© BFS

Cancer in Switzerland

Cancer is the second most common cause of death in Switzerland. The number of new cases and deaths is rising owing to an ageing population. However, the rate of cancer cases standardized according to age remains unchanged and death rates are falling slowly. Source: BFS

with Mirasense, a further ETH spin-off, granting them a start capital of CHF 130,000 as well as entrepreneurial know-how for the first nine months. Moreover, notable experts such as Professor Thomas Cueny, President of the Swiss Cancer League, Professor Ruedi Aeber-

sold, a pioneer in proteomics technology and Professor Wilhelm Krek, cancer biologist specialist, are also supporting the ETH spin-off. The goal is to transfer the results from the fundamental research into clinical application.

More at: www.proteomedix.ch

Honours for two **protein research** pioneers



Ruedi Aebersold

The Otto Naegeli Prize for the advancement of medical research is endowed with CHF 200,000 and is one of Switzerland's most prestigious scientific awards. The prize, which is awarded every other year, goes this year to Professor Ruedi Aebersold (ETH Zurich and the University of Zurich) and Professor Amos Bairoch (University of Geneva and SIB, the Swiss Institute of Bioinformatics).

Ruedi Aebersold receives the award for his work in the field of proteomics. Among other things, the scientist developed a series of analytical methods and computer models that identify proteins and measure their abundance. The results of this work have led to a new understanding of biochemical processes. The knowledge thereby gained is likely to be used in the development of new diagnostic tools for cancer and metabolic disorders.

Amos Bairoch receives the award for outstanding work in the field of protein sequence analysis and particularly for the development of numerous resources, such as databases and websites, which he made available to the scientific community in a simple and comprehensive-

ly accessible way.

An article about SystemsX.ch RTD-project «PhosphoNetX» (lead by Ruedi Aebersold) appeared in the X-Letter no. 19

Amos Bairoch, founder of the protein data base «Swiss-Prot» was portrayed in the X-Letter no. 18. msc

Both newsletters can be downloaded from: www.systemsx.ch/x-letter



Amos Bairoch

NEWS

Meeting-up of microbiologists in Paris

From 22nd to 24th March microbiologists with an affinity to Systems Biology met up at a conference in Paris entitled the «Systems Biology of Microorganisms». Innovations were presented during the event, especially those in the fields of models development and data integration, and subsequently discussed. Among numerous speakers there were also many Systems biologists from Switzerland. The

meeting, organized by two EU-syndicates, was the first of its kind and is expected to take place in future every other year. msc

More at: www.systemsmicrobiology.org

PhD Student Retreat

The SystemsX.ch retreat for PhD students will take place this year on 30th September/1st October in the idyllic setting of Murten. Organized by SystemsX.ch this event will allow participants to touch base with their academic peers and gain an

overview and exchange experience about what's happening in current research. Over the two-day event, PhD's will be able present their own work with a poster or a short presentation. Moreover, there will also be opportunities to discuss Systems biology issues with the two top-class invited guest speakers, Professor Wolfram Weckwerth and Professor Jörg Stelling. Registration deadline for the meeting is 30th June 2010. msc

More at: www.systemsx.ch/events

Conferences and Events

June 24-25, 2010	8th [BC]2 Basel Computational Biology Conference	Basel, Switzerland
August 16-20, 2010	Systems Biology of Development	Ascona, Switzerland
August 17-24, 2010	SystemsX.ch Summer Course in Computational Biology	Split, Croatia
September 14-15, 2010	7th annual RNAi & miRNA Europe	Dublin, Ireland
September 30-Oct 1, 2010	SystemsX.ch PhD Student Retreat	Murten, Switzerland
October 10-15, 2010	International Conference on Systems Biology	Edinburgh, UK
November 1-2, 2010	All-SystemsX.ch-Day 2010	Geneva, Switzerland

Glossary of SystemsX.ch

Research, Technology and Development Project (RTD project): SystemsX.ch's flagship project, multi-year duration.

Interdisciplinary Pilot Project (IPP): Research involving risks. One-year duration.

Interdisciplinary Doctorate (IPhD): Duration of 3 to 4 years.

Board of Directors (BoD):

SystemsX.ch's highest steering body composed of the presidents, rectors and directors of all participating institutions.

Scientific Executive Board (SEB):

Operative committee composed of scientists from the participating institutions.



SystemsX.ch

The Swiss Initiative in Systems Biology

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