

# X-Letter

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## SYBIT

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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-

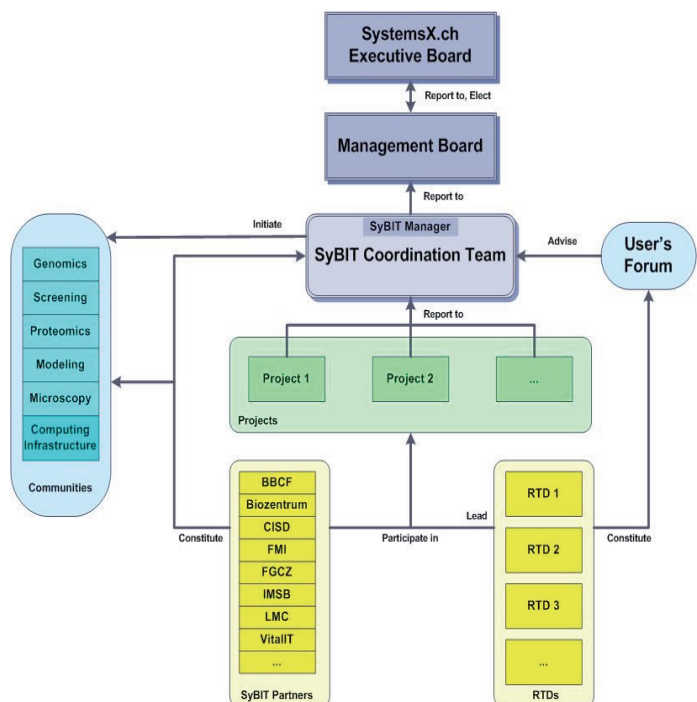
terested are interested in using iBRAIN.

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