

The national bioinformatics infrastructure

www.scilifelab.se/platforms/bioinformatics/

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Bioinformatics Long-term Support (a.k.a.WABI)

Enabler for Life Sciences

The Bioinformatics platform

SciLifeLab

National
Genomics
Infrastructure

Joakim Lundeberg
Ann-Christine Syvänen
Ulf Gyllensten

Bioinformatics

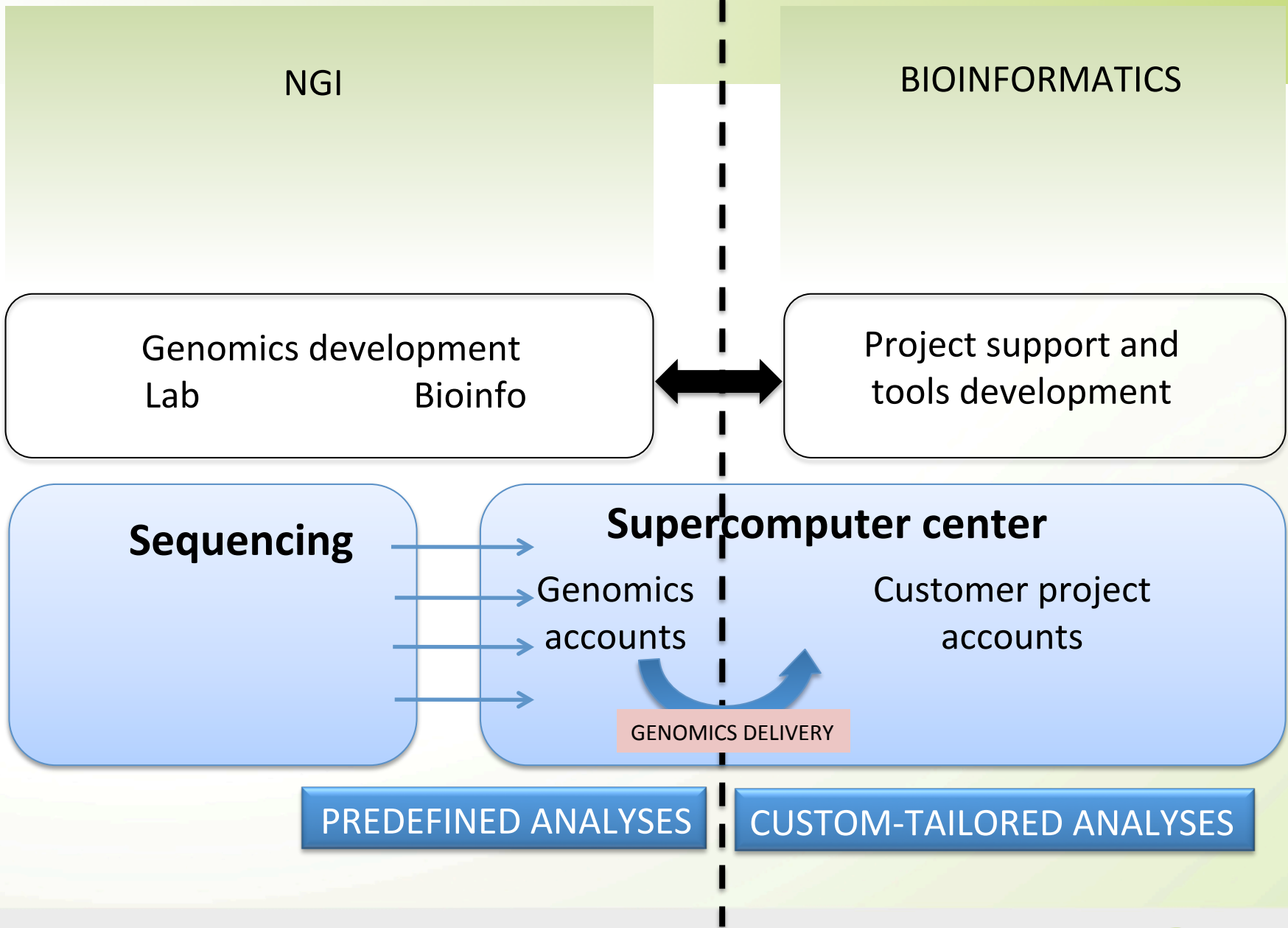
Bengt Persson

Clinical
Diagnostics

...

Ongoing merge of
BILS, WABI and more;
complete 2016.

National, distributed



Deliverables 2014

Consultancy and Training

- Continuing providing advanced bioinformatics support to projects nation-wide and maintaining (old) and building (new) domain-specific competence
- Expand into new competence areas (e.g. Integrative bioinformatics / Big Data)
- Genome annotation platform used in at least 3 new projects
- Delivering success stories within our supported research projects
- Drop-in bioinformatics consultancy at SciLifeLab
- Provide advanced training in 10+ courses nation-wide

Infrastructure

- Provision of a repository of good/useful scripts
- Secure system for compute and storage *Mosler*
- Production system for SciLifeLab platforms, providing redundant HPC resources w/ high availability
- User-friendly interface towards UPPNEX compute resources
- Prototype system for cloud computing in bioinformatics

International

- Integration of the Human Protein Atlas (HPA) into ELIXIR as Swedish node contribution
- Hosting the European ELIXIR Heads-of-Nodes meeting in May

Organisational

- Integrate all activities as a National Bioinformatics Infrastructure; Regular platform meetings
- Coordination meetings with genomics platforms

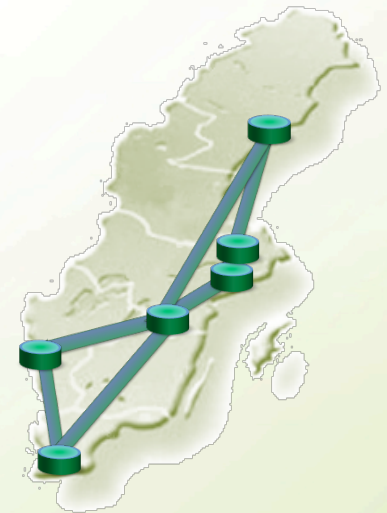
Bioinformatics Platform provides custom-tailored analyses

- Study design consultation (free)
support@bils.se
- Short-term support (≤ 80 h; free; first come first serve)
- Medium-term support (> 80 h; user fee; first come first serve)
<http://bils.se/resources/supportform/index.php>

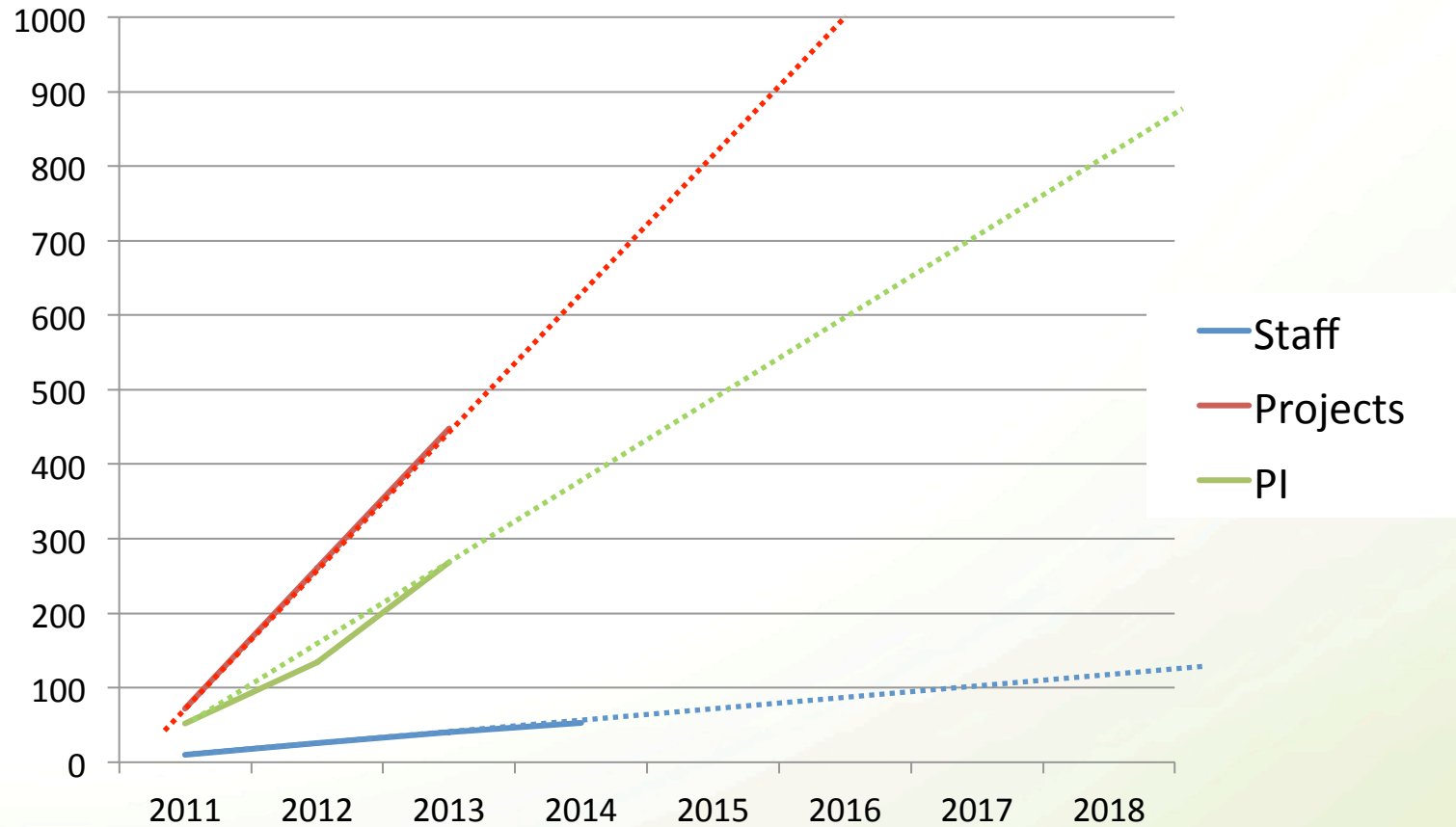
- Long-term support (500h; free: scientific evaluation)
<http://www.scilifelab.se/facilities/wabi/>

Next deadline for applications Feb 27!

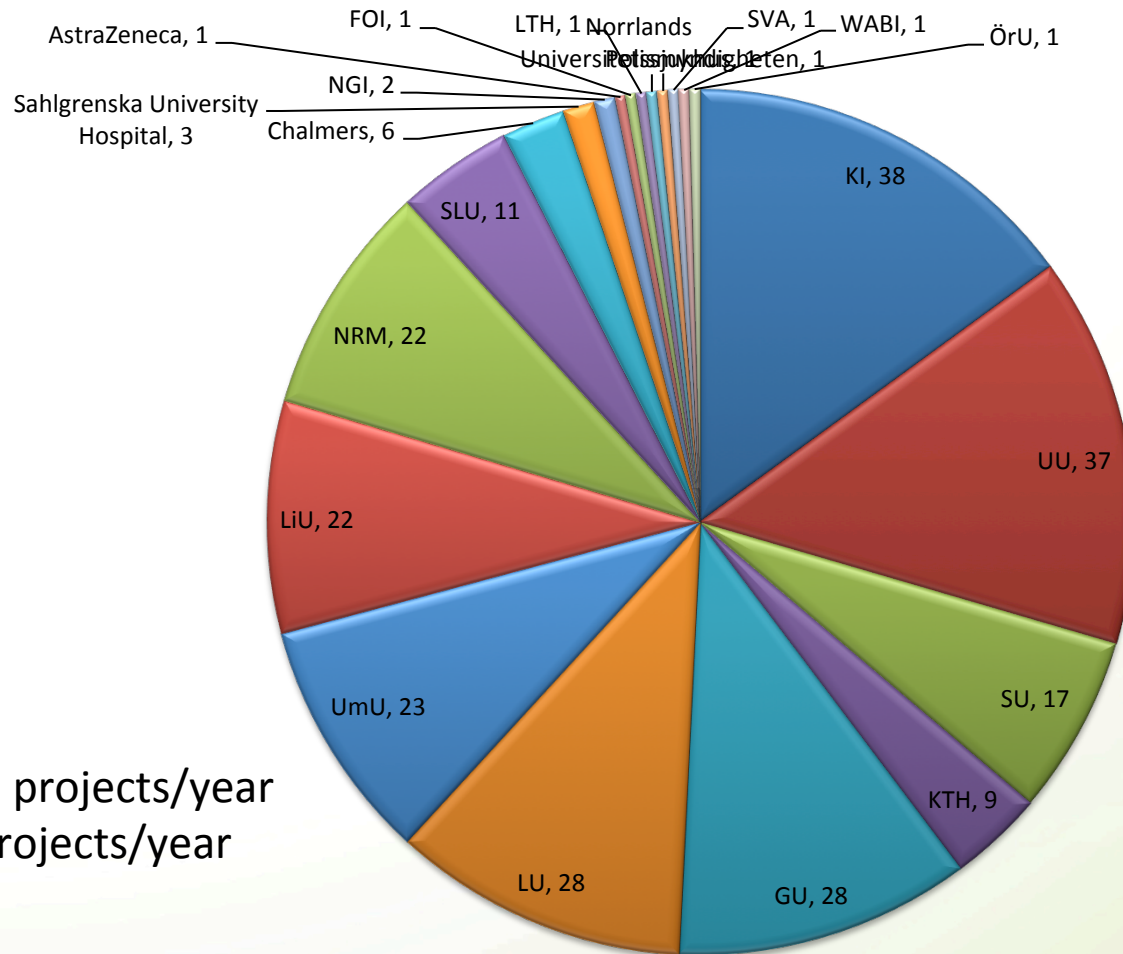
- Compute and storage (free; majority of hardware and system administration belongs to SNIC)
<http://www.uppmax.uu.se/>



Growth (Numbers from BILS)



Distribution of PIs in projects in 2013



~400 short-term projects/year
~20 long-term projects/year

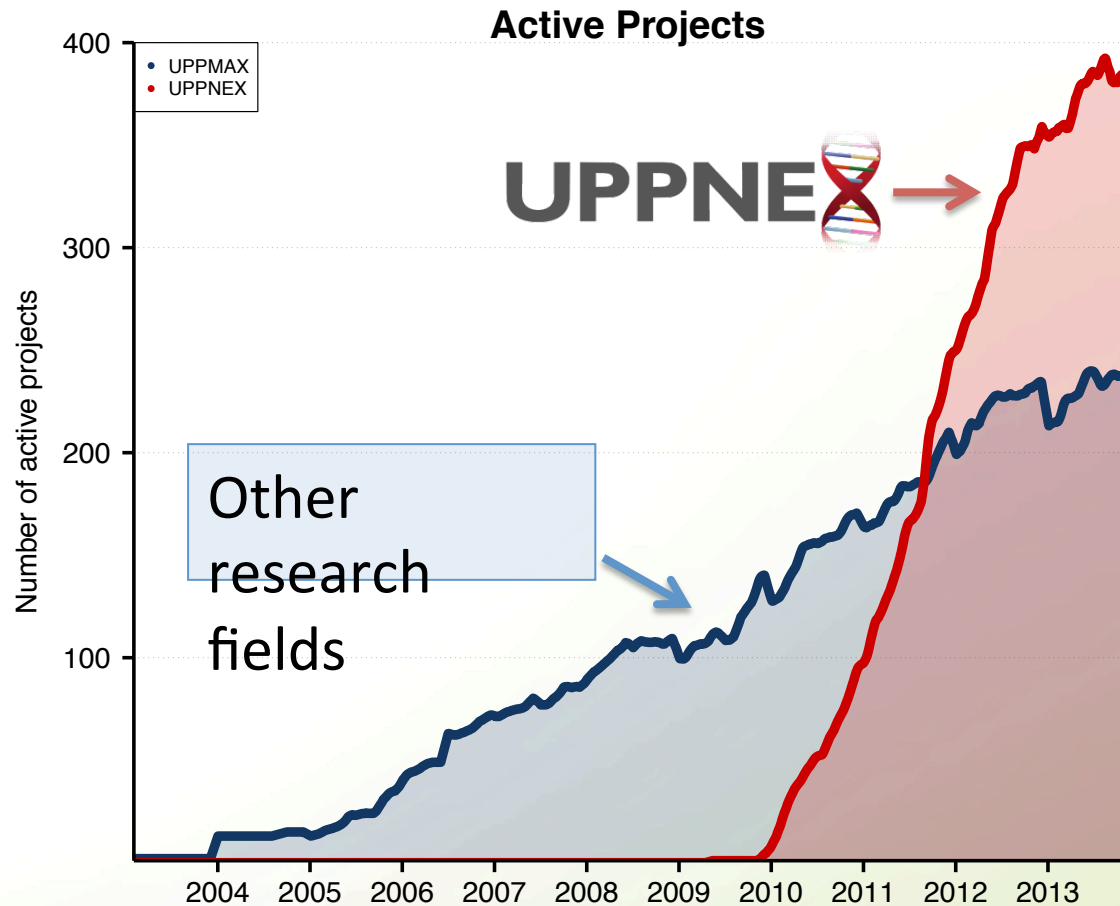
2014: Over 450 active projects from all over Sweden



Large sequencing projects use UPPNEX



Integrated in Swedish e-Science infrastructure



2014: Over 450 active projects from all over Sweden

Short-term Support and Infrastructure

BILS – Bioinformatics Infrastructure for Life Sciences

www.scilifelab.se/facilities/bils/

- BILS is a distributed national research infrastructure supported by the Swedish Research Council (VR)

- Nodes at each of the 6 large universities
- Coordination with other bioinformatics activities
- Training activities, annual symposium/user meeting

- BILS provides

- Support/Consultancy (“human eCloud” for life sciences) 80 hours for free, additional hours for a subsidised fee
- Databases and software tools
- Computing and storage in collaboration with SNIC

- BILS coordinates the Swedish node in the European infrastructure for biological information ELIXIR

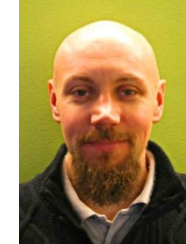
- Annual budget ~3.5 MEUR (2014)
 - ~2.2 MEUR from Swedish Research Council

Director



Bengt Persson

Technical coordinator



Mikael Borg

Proteomics coordinator



Fredrik Levander

Genomics coordinators



Magnus Alm-Rosenblad



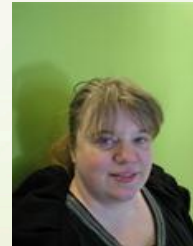
Henrik Lantz

Syst. development coordinator



Jonas Hagberg

Training coordinator



Sara Light

Long-term Support

Wallenberg Advanced Bioinformatics Infrastructure

www.scilifelab.se/facilities/wabi/

Tailored solutions – high impact

Applied bioinformatics: 500h free support/project

- Variant analyses in health and disease
- Transcriptomics
- Novel genomes
- Metagenomics

Directors



Siv Andersson

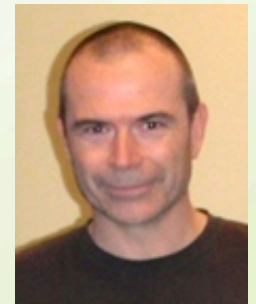


Gunnar von Heijne

Managers



Björn Nystedt



Thomas Svensson

Swedens strongest unit for analyses of large-scale genomic data (13 FTE, increasing)

National committee reviews and selects projects based on scientific quality

The BILS genome annotation and assembly platform

Annotation is a complex, time-consuming process

Producing an annotation for a vertebrate genome can take months

Requires both experience and computational infrastructure

Which data do I combine in what ways to achieve optimal results?

What pipelines are available and how do I set them up?

What computational resources are required?

Do I have the capability to develop custom solutions if my data requires it?

Is using my grant money to train someone a good long-term investment for me?

Teaching

www.scilifelab.se/education/courses/

2015-04-07 - 2015-04-09, Course | Uppsala
[RNA-seq, 1 hp](#)

2015-04-27 - 2015-04-28, Course | Uppsala
[Introduction to Genome Annotation, 1 hp](#)

2015-05-18 - 2015-05-23, Course | Uppsala
[Perl Programming with Application to Bioinformatics, 2 hp](#)

The Swedish Bioinformatics Advisory Program

A new teaching model, where PhD students get a senior bioinformatician as a personal advisor during 2 years of their PhD.

Three grand meetings per year with all the students, and their advisors and PhD supervisors, to aid networking and knowledge transfer.

First call late 2014:

>50 applicants for 15 places

Next call late 2015

www.scilifelab.se/education/mentorship/the-swedish-bioinformatics-advisory-program/