

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

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Ann-Christine Syvänen
Ulf Gyllensten

Bioinformatics

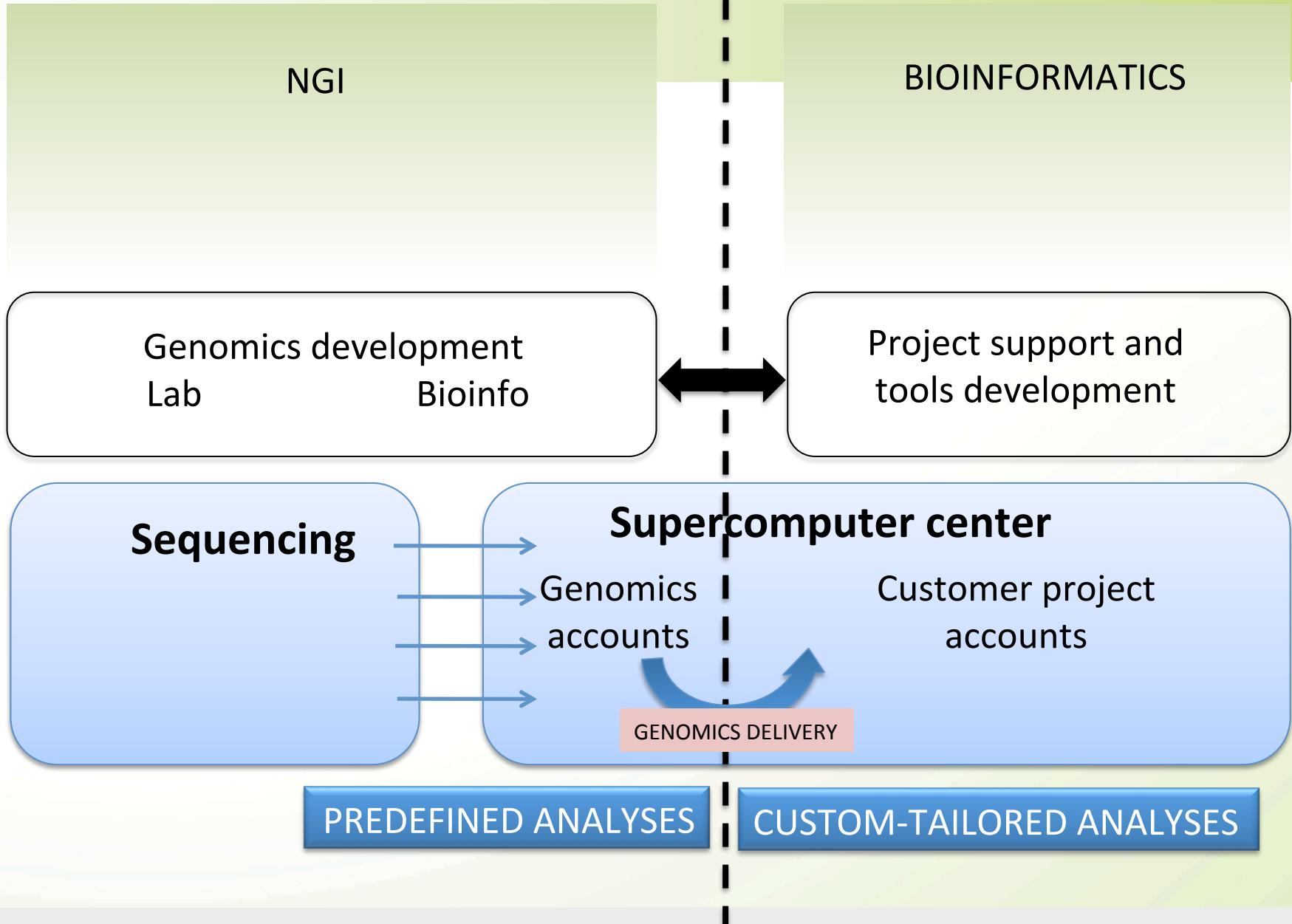
Bengt Persson

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

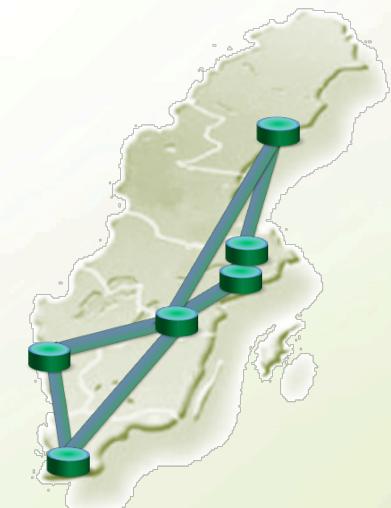
- Integrate all activities as a National Bioinformatics Infrastructure; Regular platform meetings
- Coordination meetings with genomics platforms

Bioinformatics Platform provides custom-tailored analyses

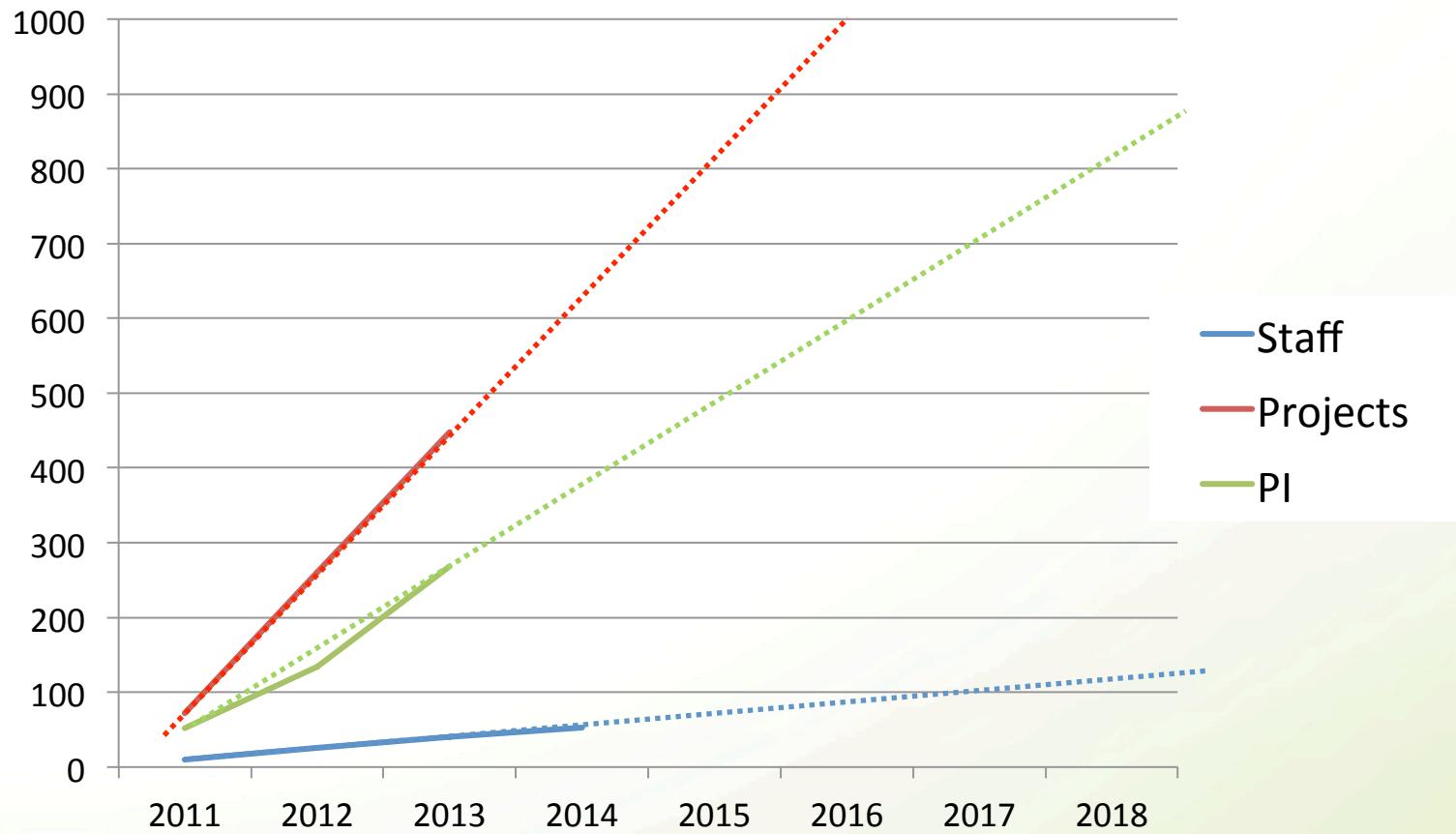
- Study design consultation (free)
support@bils.se
- Short-term support ($\leq 80h$; free; first come first serve)
- Medium-term support ($>80h$; user fee; first come first serve)
<http://bils.se/resources/supportform/index.php>
- Long-term support (500h; free: scientific evaluation)
<http://www.scilifelab.se/facilities/wabi/>

Next deadline for applications Feb 27!

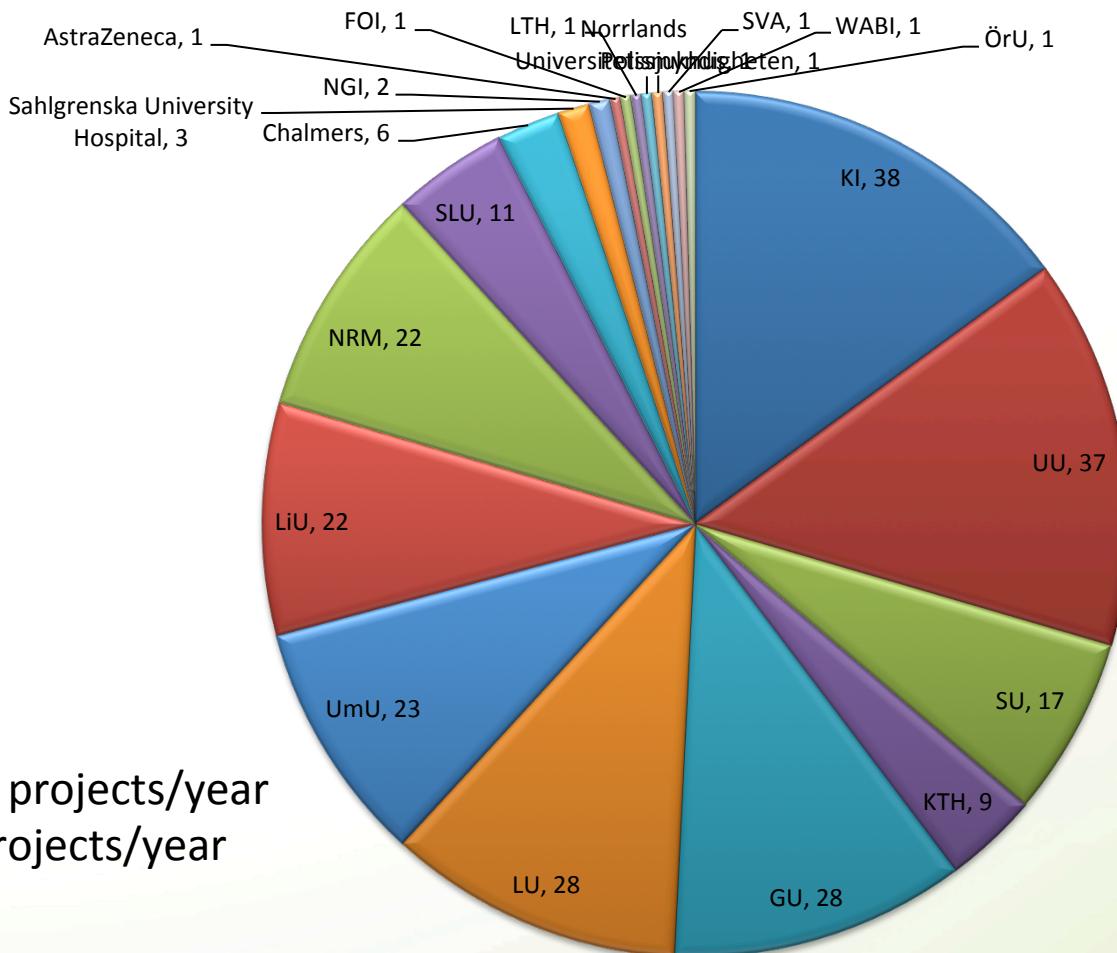
- Compute and storage (free; majority of hardware and system administration belongs to SNIC)
<http://www.uppmax.uu.se/>



Growth (Numbers from BILS)



Distribution of PIs in projects in 2013



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

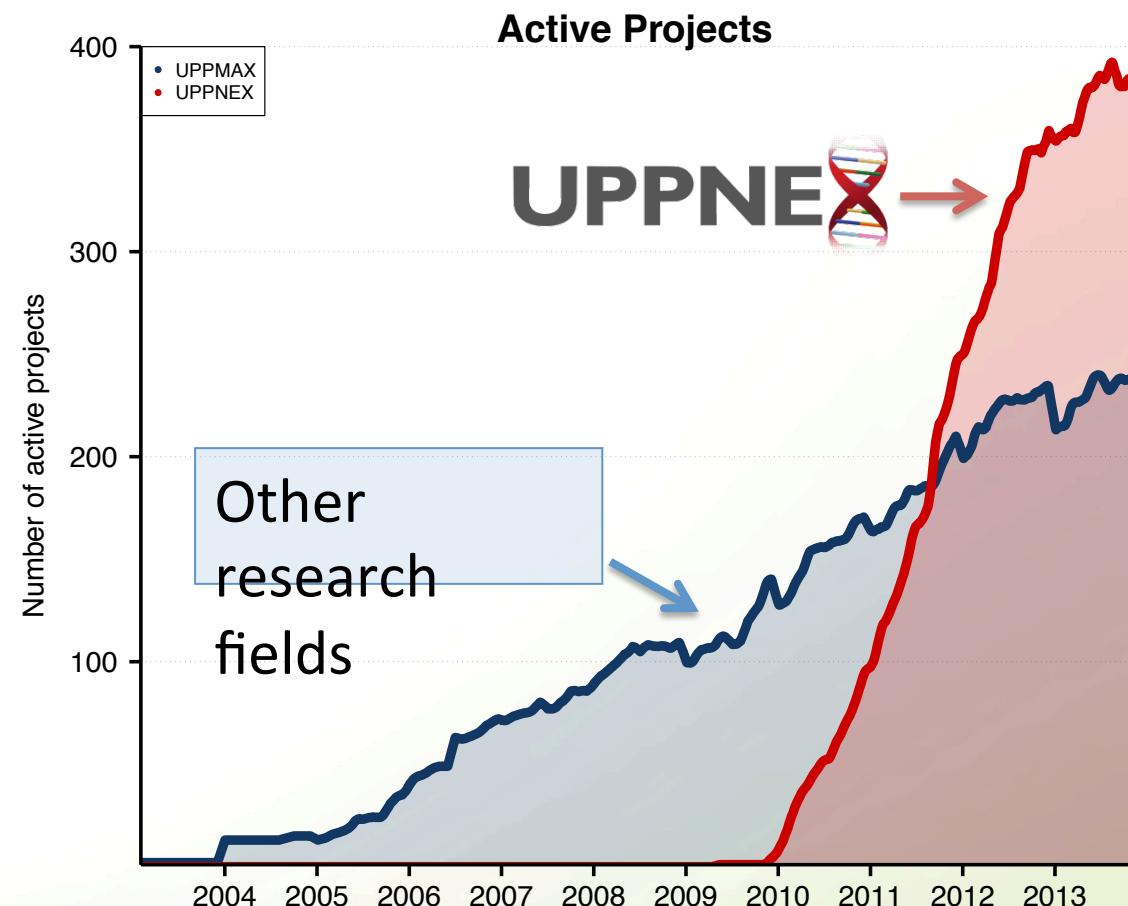
2014: Over 450 active projects from all over Sweden



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* *Training
coordinator*



Jonas
Hagberg



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

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

National committee reviews and selects projects based on scientific quality

Directors



Siv Andersson Gunnar von Heijne

Managers



Björn Nystedt Thomas Svensson

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/