

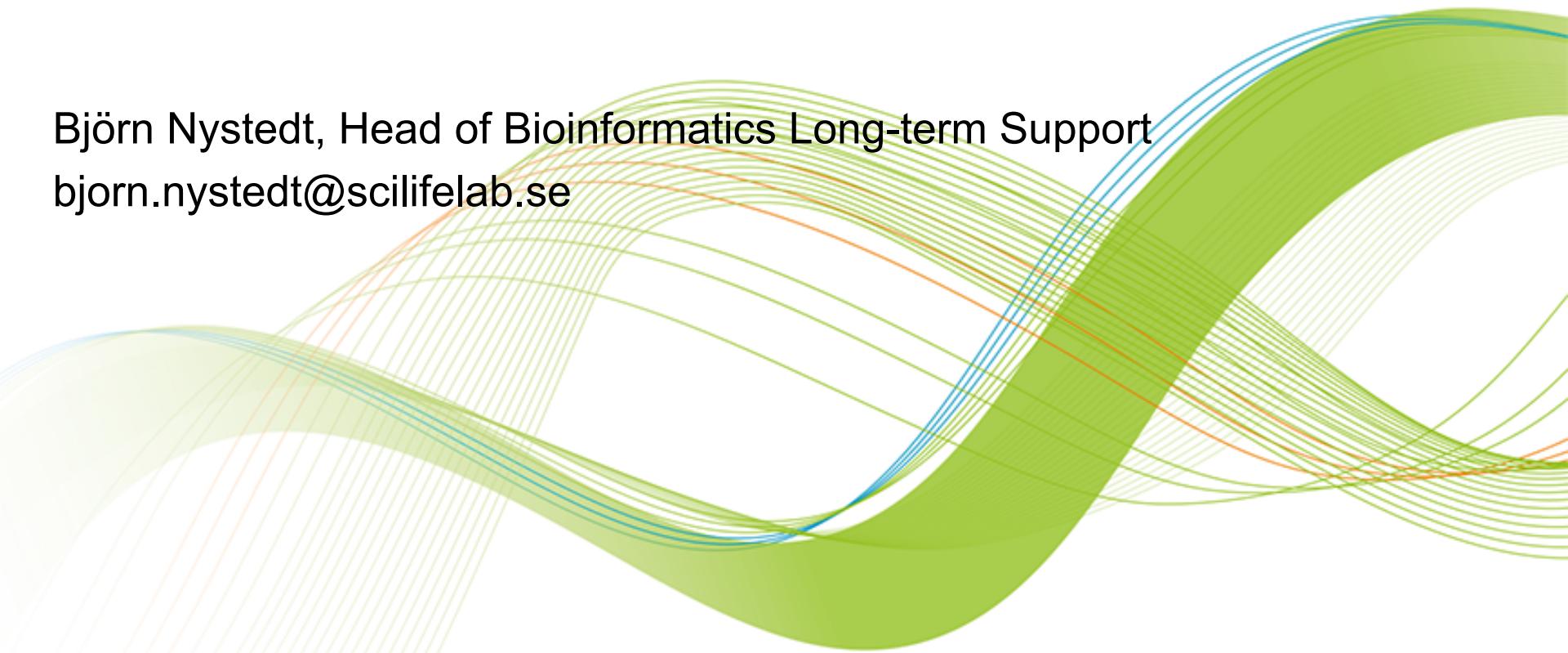


The National Bioinformatics Infrastructure Sweden (NBIS)

www.scilifelab.se/platforms/bioinformatics/

Björn Nystedt, Head of Bioinformatics Long-term Support

bjorn.nystedt@scilifelab.se



SciLifeLab

National service

The Swiss army knife for Swedish Life Science researchers

Local scientific center



Director: Olli Kallioniemi

Co-director: Lena Claesson-Welsh

Vision:

To be an internationally leading center that develops, uses and provides access to advanced technologies for molecular biosciences with focus on health and environment.

2010: Strategic research initiative

2013: National resource

2015: New management/chairman

SciLifeLab provides state-of-the art services



- **NGI (One of the largest sequencing centers in Europe)**
X-Ten, HiSeq, MiSeq, PacBio, IonTorrent, MinIon, Optical mapping
- **Clinical Diagnostics**
Sequencing and other omics for new clinical applications
- **Bioinformatics**
Approaching >70 FTE for custom-tailored project support, methods and systems development, data publishing, training
- **Functional Genomics**
Single-cell transcriptomics, genomics, and proteomics
- ...

National facilities

Affinity Proteomics

Biobank Profiling
Cell Profiling
Fluorescence Tissue Profiling
Mass Cytometry
PLA Proteomics
Protein and Peptide Arrays
Tissue Profiling

Bioimaging

Advanced Light Microscopy
Fluorescence Correlation Spectroscopy

Bioinformatics

Bioinformatics Compute and Storage (UPPNEX)
Bioinformatics Long-term Support (WABI)
Bioinformatics Short-term Support and Infrastructure (BILS)

Chemical Biology Consortium Sweden

Laboratories for Chemical Biology Umeå (LCBU)
The Laboratories for Chemical Biology at Karolinska Institutet (LCBK)
Uppsala Drug Optimization and Pharmaceutical Profiling (UDOPP)

Clinical Diagnostics

Clinical Biomarkers
Clinical Genomics
Clinical Sequencing

Drug Discovery and Development

ADME (Absorption Distribution, Metabolism Excretion) of Therapeutics (UDOPP)
Biochemical and Cellular Screening
Biophysical Screening and Characterization
Human Antibody Therapeutics
In Vitro and Systems Pharmacology
Medicinal Chemistry – Hit2Lead
Medicinal Chemistry – Lead Identification
Protein Expression and Characterization

Functional Genomics

Eukaryotic Single Cell Genomics
Karolinska High Throughput Center (KHTC)
Microbial Single Cell Genomics
Single Cell Proteomics

National Genomics Infrastructure

NGI Stockholm (Genomics Applications)
NGI Stockholm (Genomics Production)
NGI Uppsala (SNP&SEQ Technology Platform)
NGI Uppsala (Uppsala Genome Center)

Structural Biology

Protein Science Facility

SciLifeLab platforms

SciLifeLab national service

National
Genomics
Infrastructure

Clinical
Diagnostics

Functional
Genomics

National
Bioinformatics
Infrastructure
Sweden

Bengt Persson



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

VR

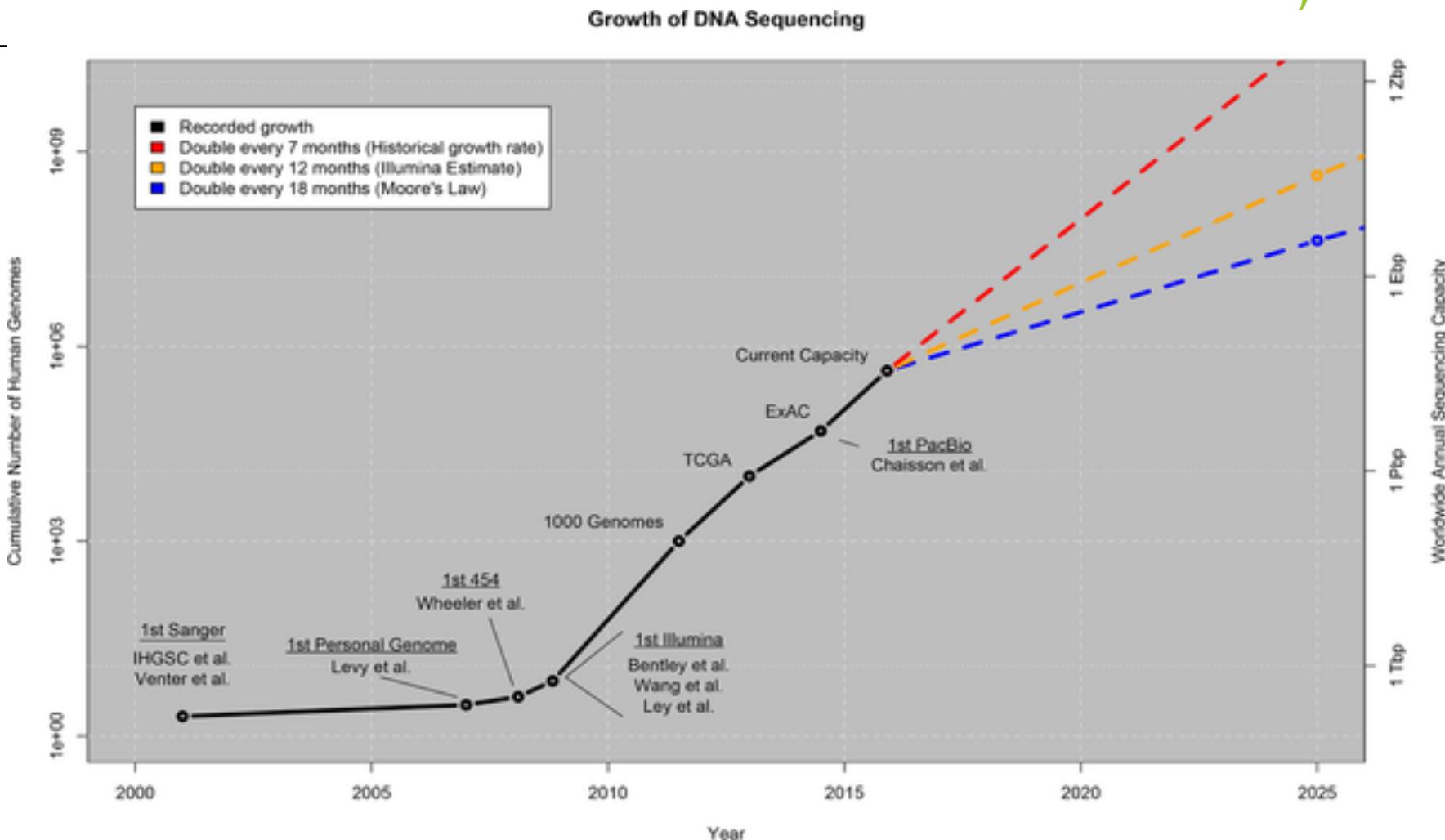
SNIC



Computer
resources
free for
Swedish
researchers

Why do we invest in a bioinformatics infrastructure?

Fig 1. Growth of DNA sequencing.



Stephens ZD, Lee SY, Faghri F, Campbell RH, Zhai C, et al. (2015) Big Data: Astronomical or Genomical?. *PLoS Biol* 13(7): e1002195. doi:10.1371/journal.pbio.1002195

<http://127.0.0.1:8081/plosbiology/article?id=info:doi/10.1371/journal.pbio.1002195>

Table 1. Four domains of Big Data in 2025.

Data Phase	Astronomy	Twitter	YouTube	Genomics
Acquisition	25 zetta-bytes/year	0.5–15 billion tweets/year	500–900 million hours/year	1 zetta-bases/year
Storage	1 EB/year	1–17 PB/year	1–2 EB/year	2–40 EB/year
Analysis	In situ data reduction	Topic and sentiment mining	Limited requirements	Heterogeneous data and analysis
	Real-time processing	Metadata analysis		Variant calling, ~2 trillion central processing unit (CPU) hours
	Massive volumes			All-pairs genome alignments, ~10,000 trillion CPU hours
Distribution	Dedicated lines from antennae to server (600 TB/s)	Small units of distribution	Major component of modern user's bandwidth (10 MB/s)	Many small (10 MB/s) and fewer massive (10 TB/s) data movement

doi:10.1371/journal.pbio.1002195.t001

Stephens ZD, Lee SY, Faghri F, Campbell RH, Zhai C, et al. (2015) Big Data: Astronomical or Genomical?. PLoS Biol 13(7): e1002195. doi:10.1371/journal.pbio.1002195

<http://127.0.0.1:8081/plosbiology/article?id=info:doi/10.1371/journal.pbio.1002195>

Bioinformatics know-how as infrastructure

The screenshot shows the header of the Nature website with the title "nature International weekly journal of science". Below the header, the URL "http://www.nature.com/news/core-services-reward-bioinformaticians-1.17251" is visible. The main content area features a headline "Core services: Reward bioinformaticians" and a sub-headline "Jeffrey Chang". The date "08 April 2015" is listed below the author's name. The text of the article begins with "Biological data will continue to pile up unless those who analyse it are recognized as creative collaborators in need of career paths, says Jeffrey Chang." At the bottom of the page, there are links for "PDF" and "Rights & Permissions".

"The scientific community has failed to craft attractive career paths for those who do the analyses it increasingly requires. Institutions and funding bodies must carve out a viable place for bioinformaticians who focus on collaborations, and reward them for their abilities to navigate the myriad demands of multidisciplinary projects."

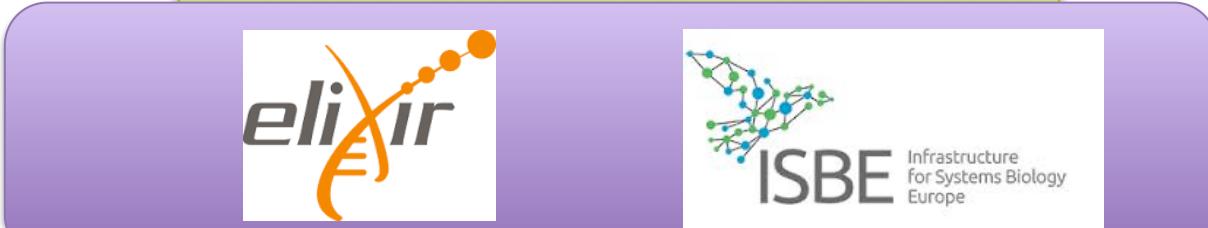
<http://www.nature.com/news/core-services-reward-bioinformaticians-1.17251>

**HEALTH
AND AGING**

**ENVIRONMENT
AND ECOLOGY**

**EVOLUTION AND
ORIGIN OF LIFE**

Support, tools and training



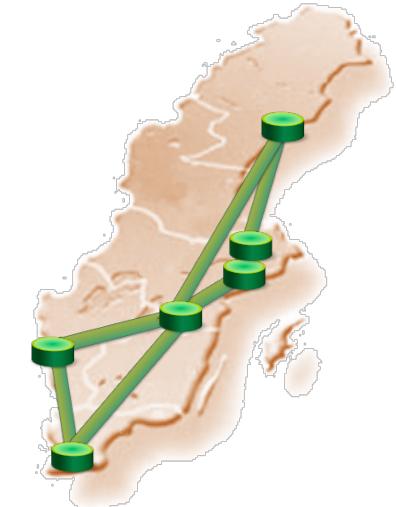


Custom-tailored support

New contact routes later 2016, stay tuned at
www.scilifelab.se/platforms/bioinformatics/

- Study design consultation (free)
support@bils.se
+ drop-in sessions every week @ all 6 sites
- Short-term support (≤ 40 h, free)
<http://bils.se/resources/supportform/index.php>
- Medium-term support (+ 40 h, user fee)
<http://bils.se/resources/supportform/index.php>
- Long-term support (500h, free, scientific evaluation)
<http://www.scilifelab.se/facilities/wabi/>

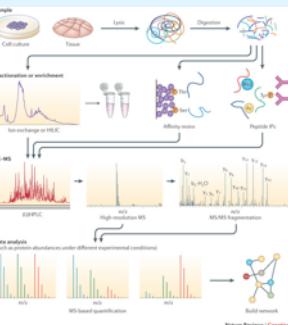
Next deadline for applications Feb 12!



Short-term support



Genomics

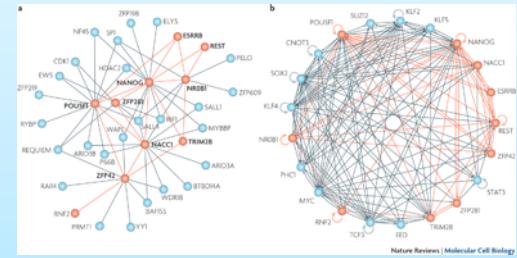


Proteomics

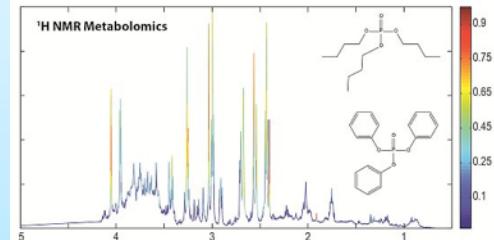


Biostatistics

Support decisions
every 2nd week



Systems biology



Metabolomics

Bioinformatics Long-term Support

Wallenberg Advanced Bioinformatics Infrastructure

www.scilifelab.se/facilities/wabi/



70% of funding

Tailored solutions – high impact

Applied bioinformatics: 500h free support/project

- Variant analyses
- Transcriptomics
- Single-cell analyses
- Epigenetics
- Metagenomics

Sweden's strongest unit for analyses of large-scale genomic data (24 FTE)

National committee reviews and selects projects based on scientific quality

Basic science!



Directors



Siv Andersson

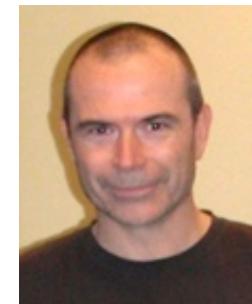


Gunnar von Heijne

Managers



Björn Nystedt



Thomas Svensson

Bioinformatics Long-term Support



Johan
Reimegård



Åsa
Björklund



Pär
Engström



Jakub
Orzechowski
Westholm



Estelle
Proux-Wéra



Markus
Ringnér



Sanela
Kjellqvist



Björn
Nystedt



Diana
Ekman



Páll
Ólason



Anna
Johansson



Marcel
Martin



Malin
Larsson



Allison
Churcher



Alvaro
Martinez Barrio



Per
Unneberg



Leif
Väremo



Nikolay
Oskolkov



Lena
Hansson



Sergiu
Netoaea



Mikael
Huss



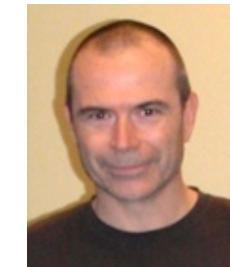
Bengt
Sennblad



Rasmus
Ågren



Stefania
Giacomello



Thomas
Svensson

Application procedure

- Open to all research groups in Sweden
- Applications 3 times every year (accept 5-10 projects per call)
- Requires hands-on involvement from the research group



National committee

- 500h effective time over ~6-18 calendar months
- Co-authors according to normal contribution criteria
- Staff 100% support (not driving own research)

www.scilifelab.se/facilities/wabi/

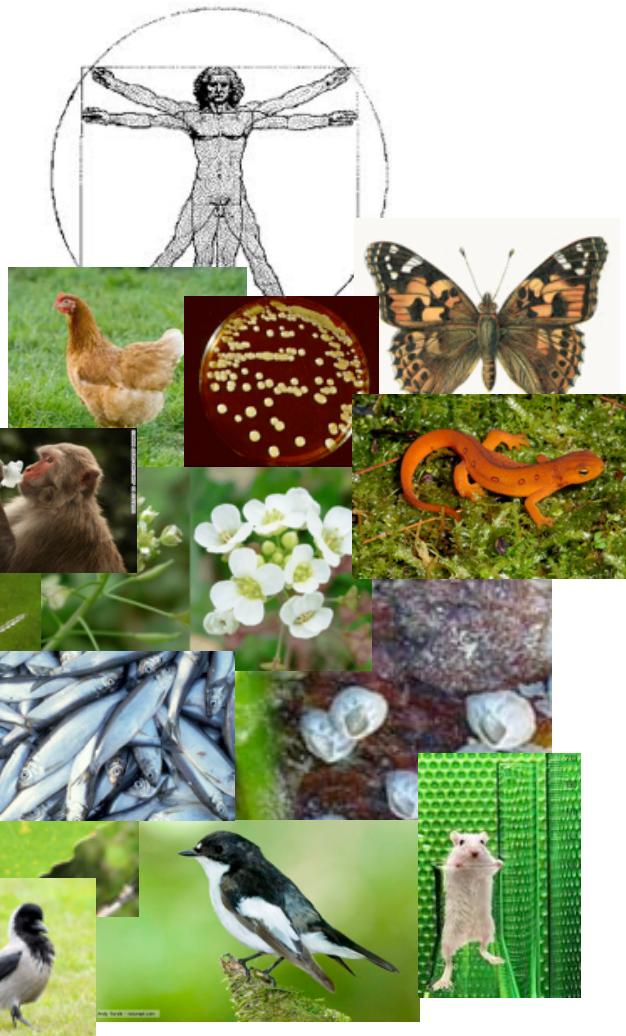
New!

Opening for a few projects in integrative omics as of Feb 12

Custom-tailored support

“Routinely unique”

Difficult to foresee/automate



Human health and disease (13)

- 5 Variant analyses (cohort, family, cell fate)
- 3 Epigenetics
- 2 RNA, method
- 1 Differential gene expression
- 1 Lipidomics
- 1 Integrative

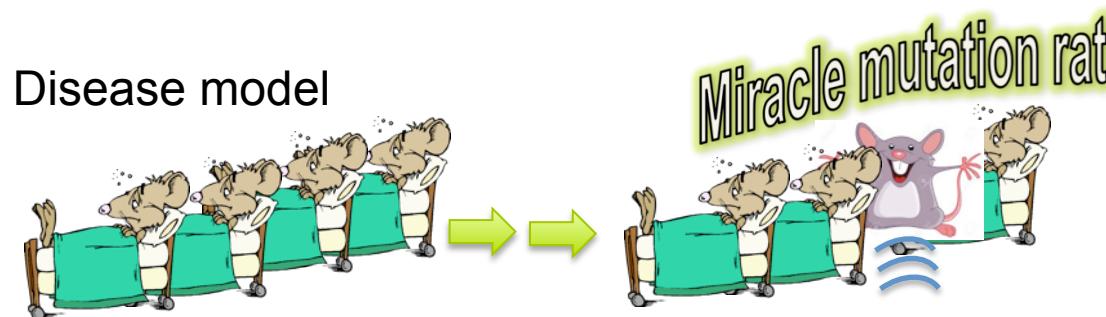
(Medical) animal models (10)

- 4 single-cell RNA
- 2 Differential gene expression
- 2 Targeted
- 1 ChipSeq
- 1 miRNA

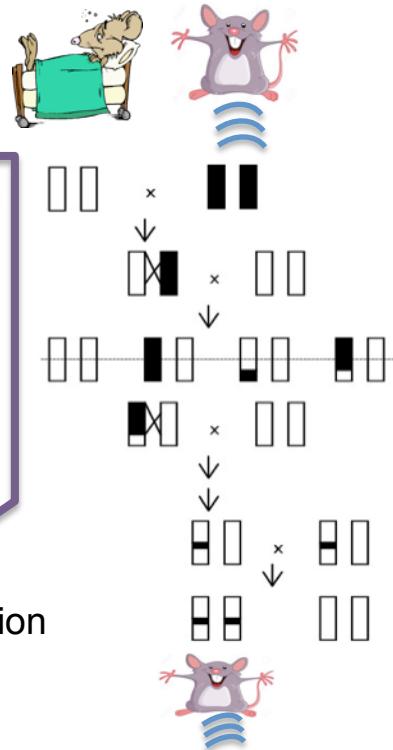
Ecology/Evolution (8)

- 3 Population genomics
- 2 De novo genome assembly/analyses
- 2 Phylogenomics/genome evolution
- 1 Epigenetics

Miracle mutation in rat model



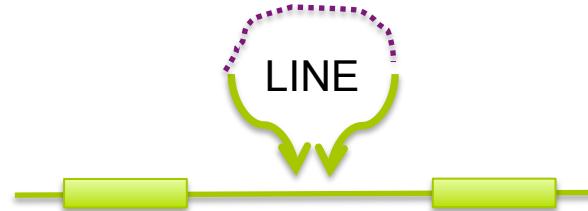
Old and slow



New and fast

Global DNA and RNA sequencing

- 1 differentially expressed gene in region. But no SNPs.
- Manual inspection and local assembly of genomic reads.

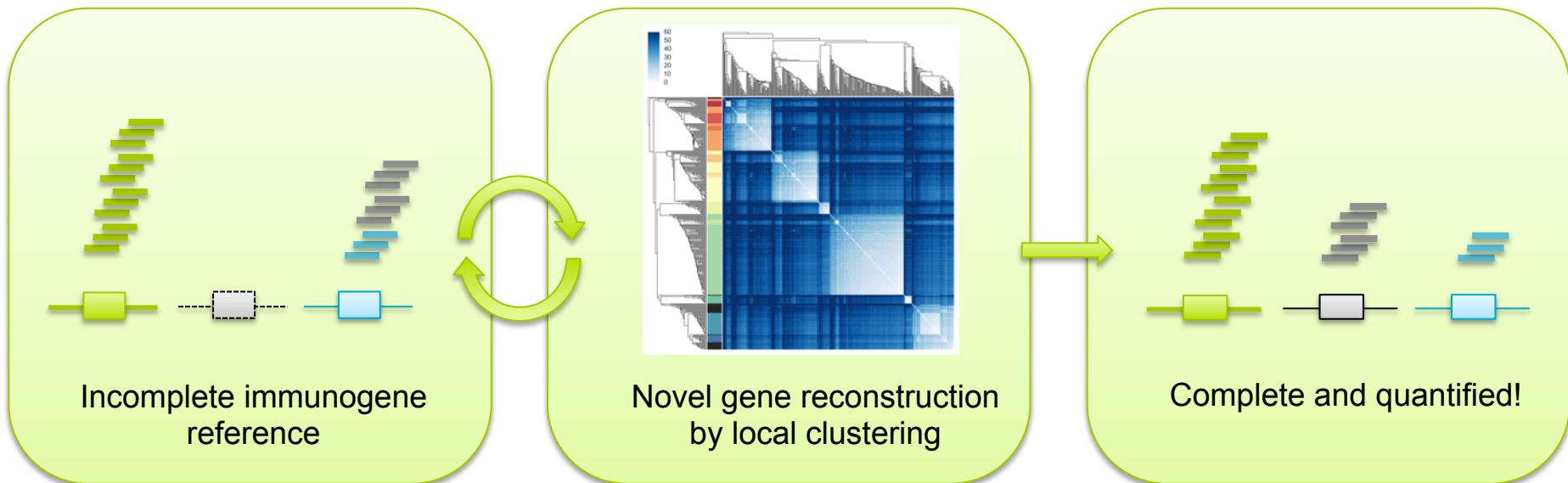
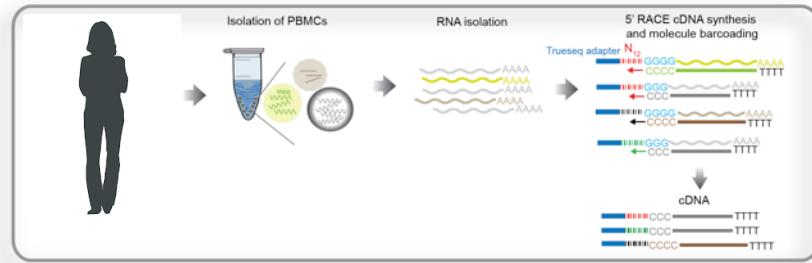


Complete protection
by intronic LINE in
unknown gene!





IgY-Pipe: Immunorepertoire profiling



- Automatic V/D/J gene profiling
- Novel gene discovery works extremely well!
- Single-read tracing
- Any species (any region)
- Open Source release end of January 2016

Gunilla Karlsson Hedestam
Infection immunology



Speciation in action

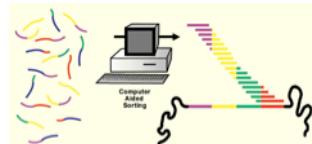


Henrik Lantz



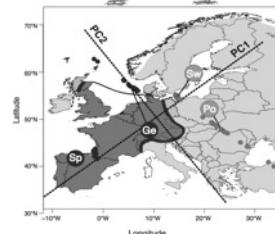
SciLifeLab
Per Unneberg

Genome assembly and annotation



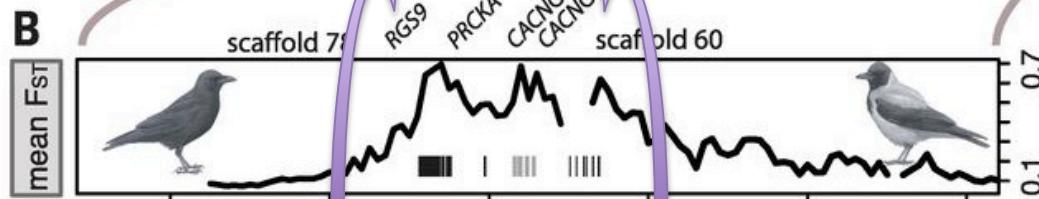
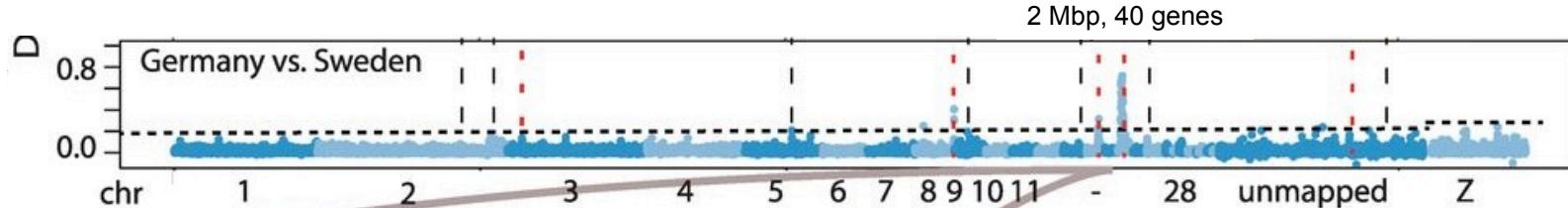
1.2 Gbp

21,000 genes



2+2 populations per species
60 individuals, 12X

Population contrasts



"Mating preferences and sexual selection alone can cause phenotypic and genotypic differentiation"

Affects visual perception

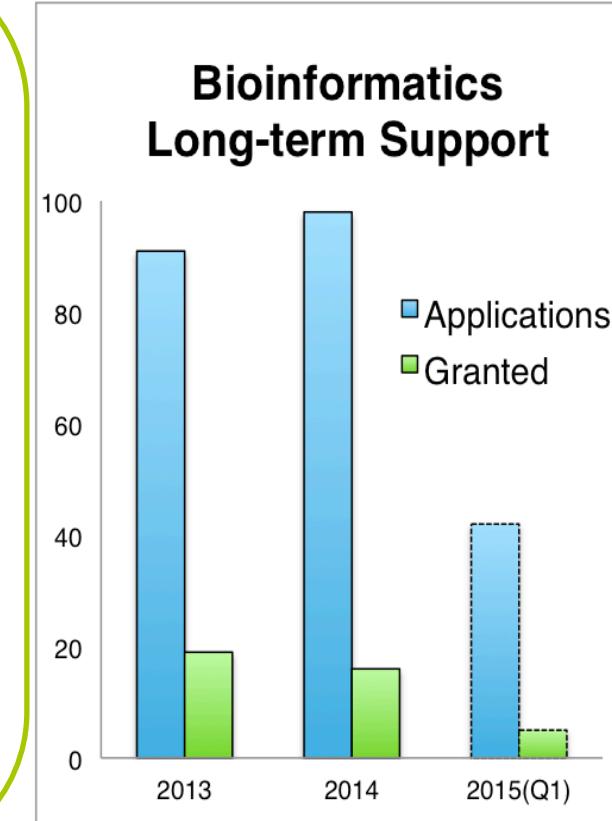
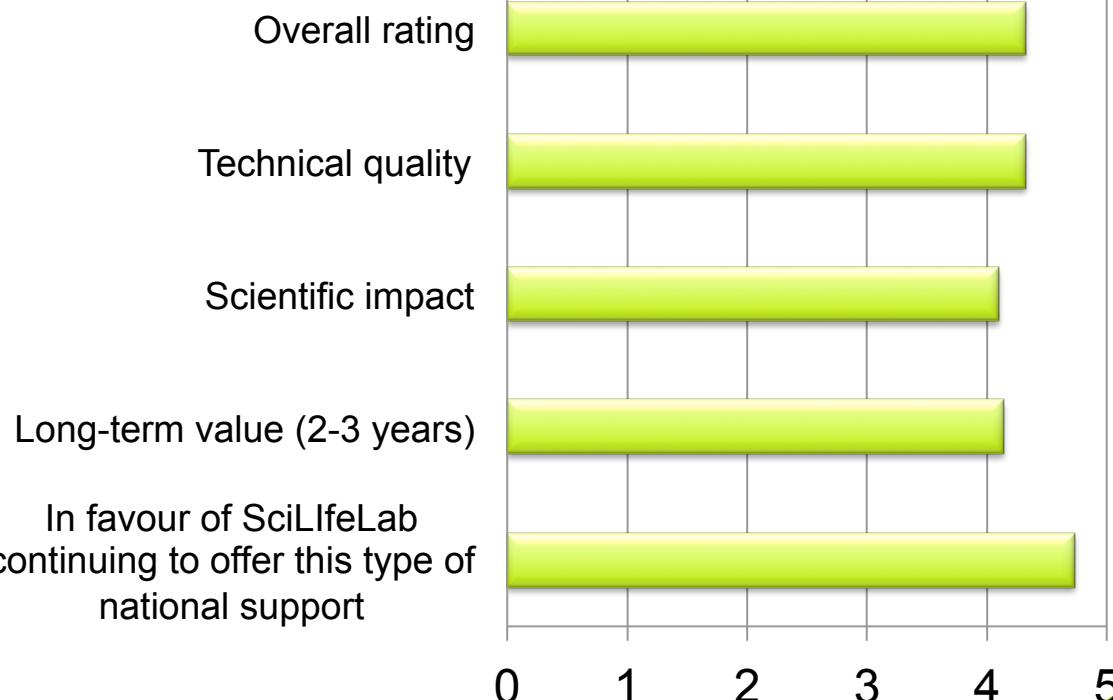
Transcription factor *MITF*
Melanogenesis pathway

Jochen Wolf
Evolutionary biology
Poelstra et al. (2014)
Science 344:1410-1414



Happy users, high demand

User evaluation April 2015





- Immuno gene repertoire profiling
- hg38-compatible GATK
- Haloplex variant calling pipeline
- ChIP-Seq pipeline
- Genomic phasing tool (long reads)
- Single-cell transcriptomics QC pipeline

- Snakemake workflow management system
- WGS structural variation pipeline
- WGS somatic variant calling pipeline
- ...

High performance computing for sensitive personal data



From Personal Data Act to Publication



"We have had a sense of full security in using the Mosler system when doing research with sensitive personal information"



Tove Fall
Epidemiology



Genome assembly and annotation



- 10 - 20 projects per year
- Highly specialized staff and robust pipelines
- Tight user interaction
- Numerous manual and semi-manual QC steps
- Supports ENA submission
- Editable user interface

Cost effective with high quality!



SciLifeLab Bioinformatics Courses

Course	Date	Participants	Evaluation score (max 5)
Introduction to bioinformatics using NGS data	April 2013	24	4.6
	Nov 2013	24	4.3
	March 2014	24	4.5
	April 2014	24	3.8
	Sept 2014	24	4.1
	Nov 2014	24	4.3
Perl programming for biological sciences	May 2013	20	4.4
	Oct 2014	20	4.4
Genome Assembly	Nov 2013	20	4.7
	Nov 2014	20	4.5
	Oct 2014	20	4.1
Human Genetic Variation	June 2013	15	4.4
	Sept 2013	20	3.9
	June 2013	15	4.5
RNAseq	Sept 2013	20	4.1
	June 2013	15	4.2
	Oct 2014	20	4.3
	June 2014	20	4.1
RNAseq and proteomics	Nov 2014	20	4.1
Metagenomics	Nov 2014	20	4.2
TOTAL 2013 + 2014		394	4.3

The Swedish Bioinformatics Advisory Program

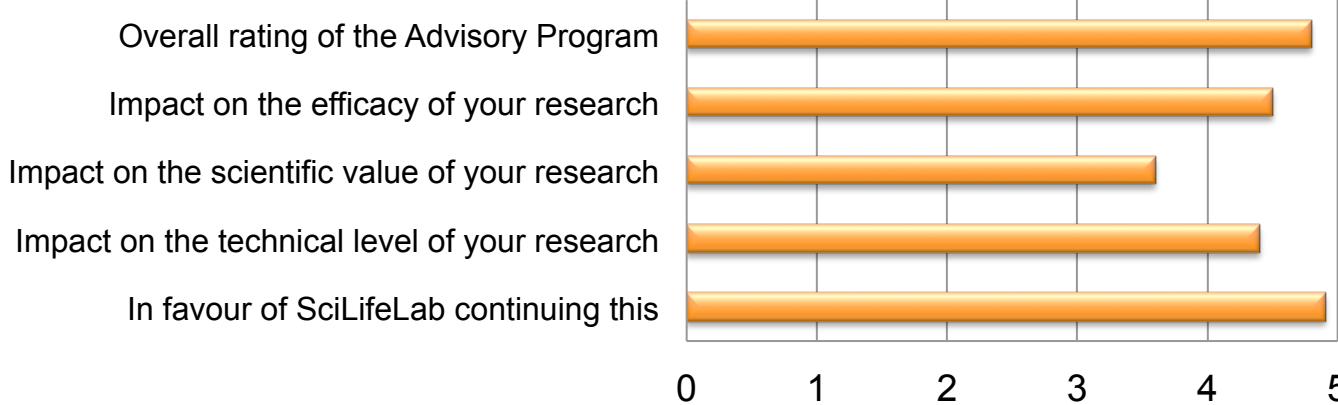
PhD students get a senior bioinformatician as a personal advisor during 2 years of their PhD. Monthly project meetings + two grand meetings per year to aid networking and knowledge transfer.

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

Currently 27 PhD student enrolled

The Swedish Bioinformatics Advisory Program

Student evaluation, June 2015



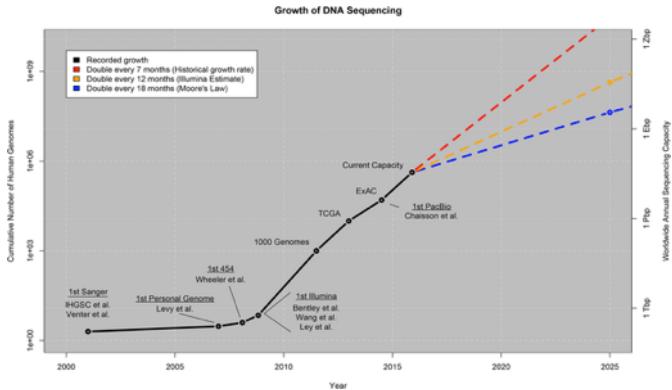
Looking ahead



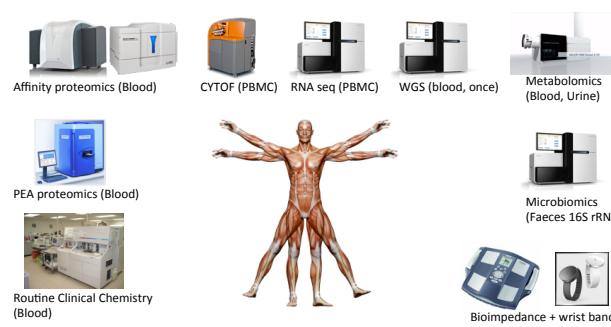
The future is bright ☺

..and integrated!
..and unbalanced!

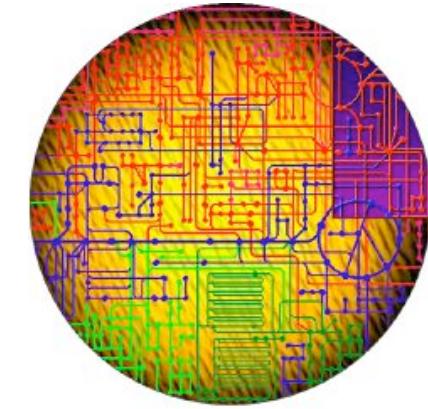
SciLifeLab



Volume



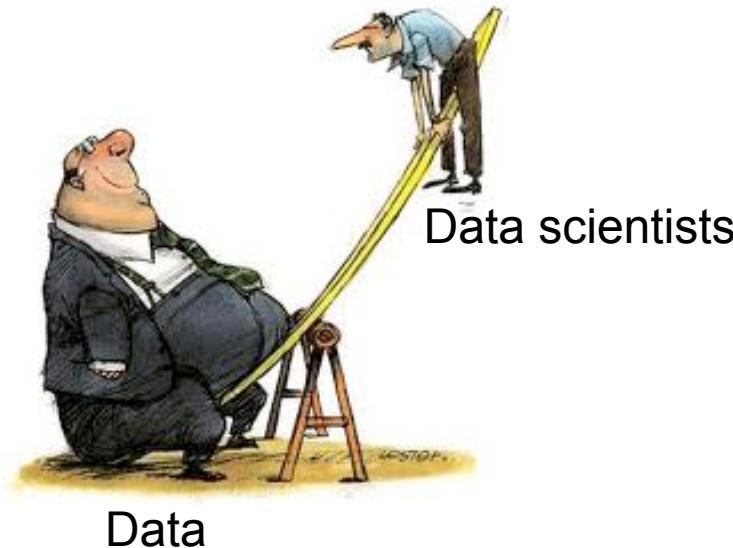
Integration



Systems/processes

Strategic positioning

- Tools development
- Data management
- Integrative omics
- Systems Biology
- Medical genomics



Mikael Huss
BigData/Integrative bioinformatics



We're here for you!



Acknowledgements

SciLifeLab



Stockholm University
Uppsala University
Karolinska Institutet
The Royal Institute of Technology
Chalmers University of Technology
The University of Gothenburg
Linköpings University
Lund University
Umeå University
The Swedish Agricultural University