



# SciLifeLab Bioinformatics Platform

National Bioinformatics Infrastructure Sweden (NBIS)

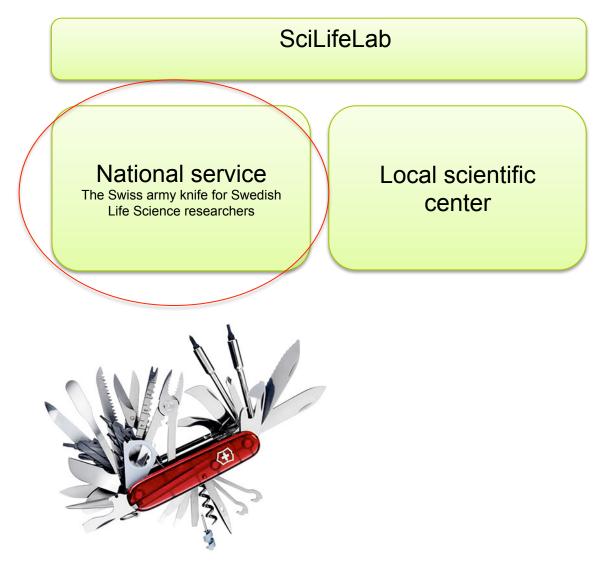
Björn Nystedt www.nbis.se

*Uppsala* 13.03.2017

**RNA** course

# SciLifeLab







Director: Olli Kallioniemi Co-director: Lena Claesson-Welsh

#### Vision:

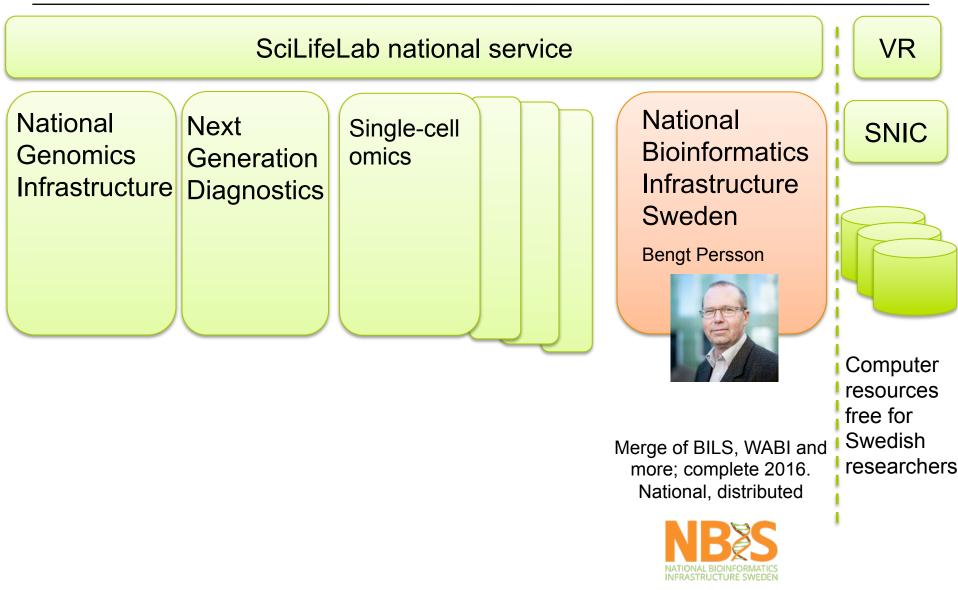
To be an internationally leading center that develops, uses and provides access to advanced technologies for molecular biosciences with focus on health and environment.

2010: Strategic research initiative2013: National resource2015: New management/chairman

## www.scilifelab.se

# SciLifeLab platforms









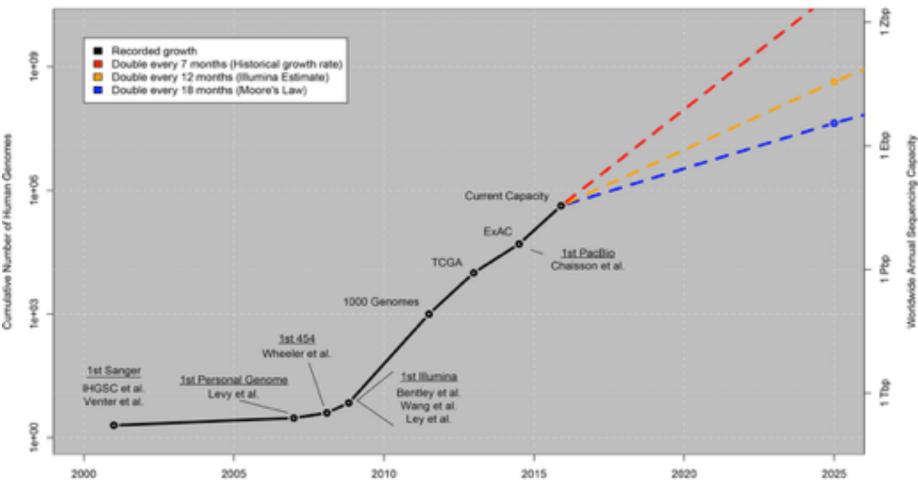
**Bioinformatics as infrastructure** 



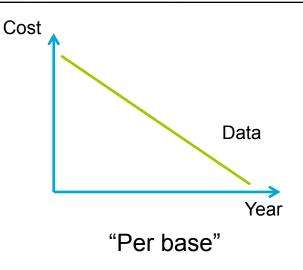
## **Data growth**

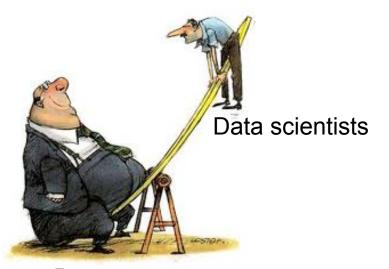








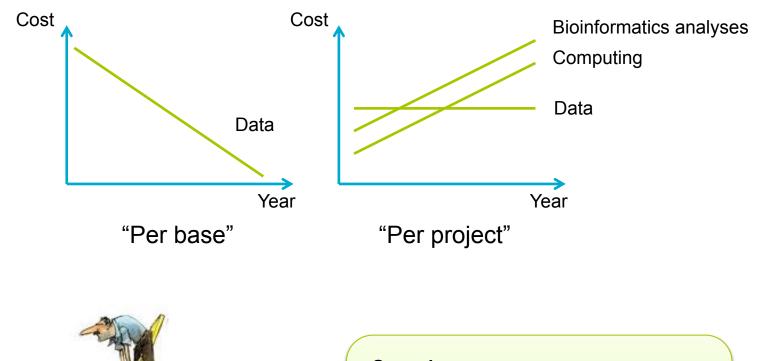


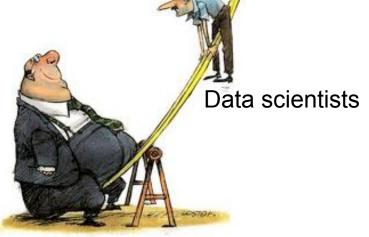


#### Our role

We want to help the Swedish Life Science community to **build knowledge** in large-scale data analysis, and to make bioinformatics **easily accessible** for all.

## NBES Production is cheap, analysis is not SciLifeLab





#### **Our role**

We want to help the Swedish Life Science community to **build knowledge** in large-scale data analysis, and to make bioinformatics **easily accessible** for all.





**NBIS** activities

# SciLifeLab

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# Support, tools and training







# 4 facilities, ~60 FTEs

- Support and Infrastructure
   Wide competence in bioinformatics, Assembly/Annotation, SysDev
- Long-term support (WABI)
   Large collaborative projects selected by scientific ranking
- Systems biology
   Network analyses and Integrative bioinformatics
- Compute and storage Computational and storage resources for bioinformatics, especially next-generation sequencing





**NBIS** 

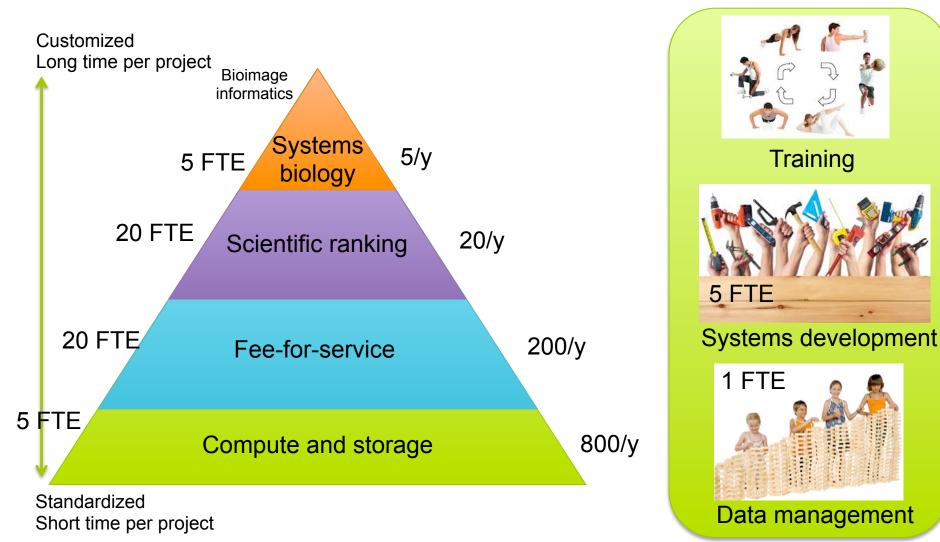


Training

Data management

5 FTE

1 FTE

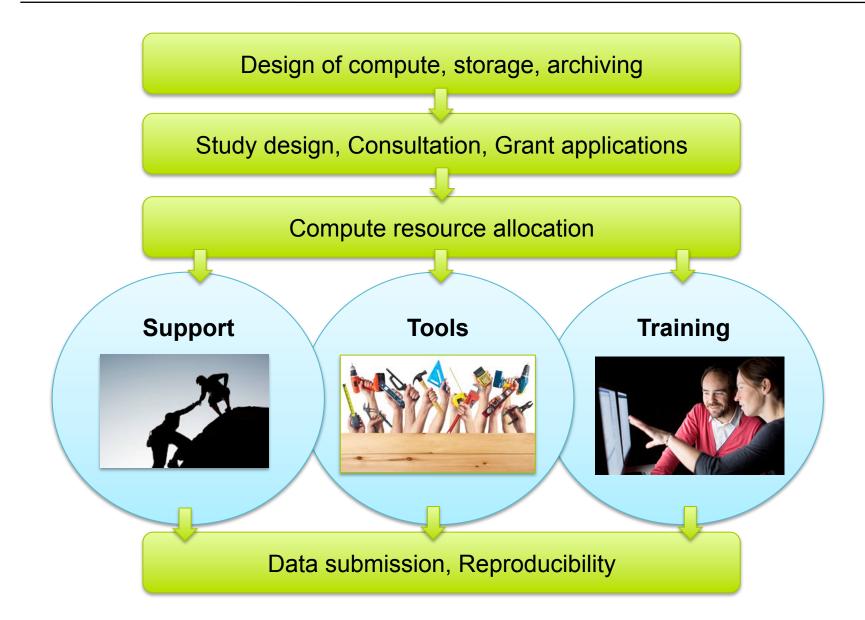


Custom-tailored support





## **User benefits**









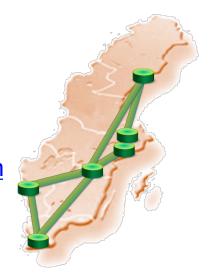


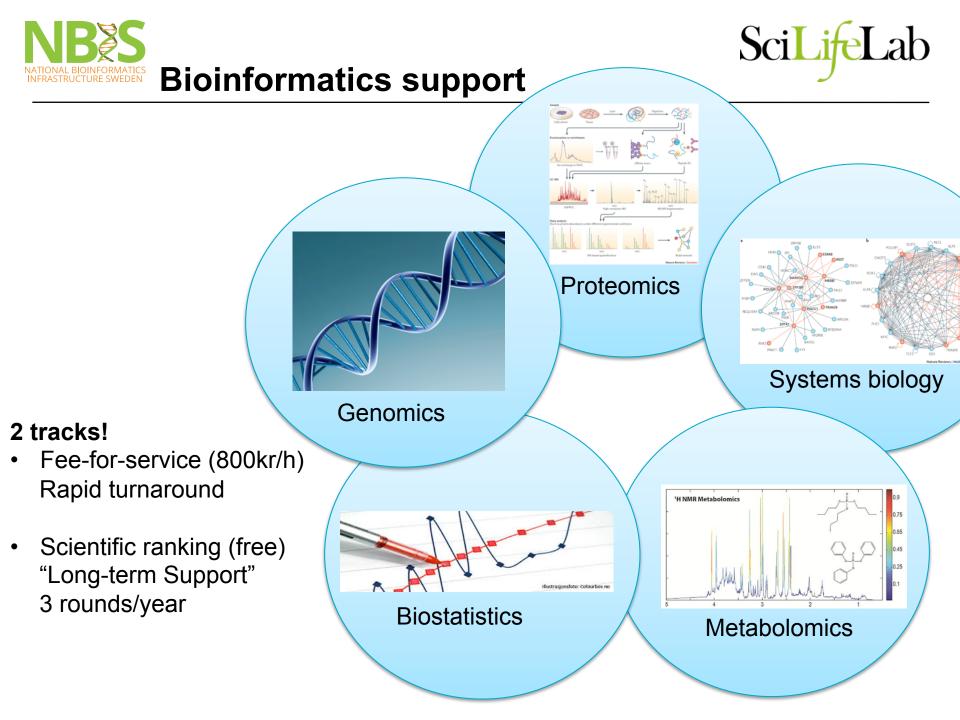


## **Custom-tailored support**

www.scilifelab.se/platforms/bioinformatics/ www.nbis.se

- Study design consultation (free) <u>www.nbis.se/support/supportform/index.php</u> + drop-in sessions every week @ 6 sites
- Short- and Medium-term support (User fee 800 kr/h) <u>www.nbis.se/support/supportform/index.php</u>
- Long-term support and systems biology (500h, free, scientific evaluation) <u>www.nbis.se/support/supportform/index.php?form=longterm</u>

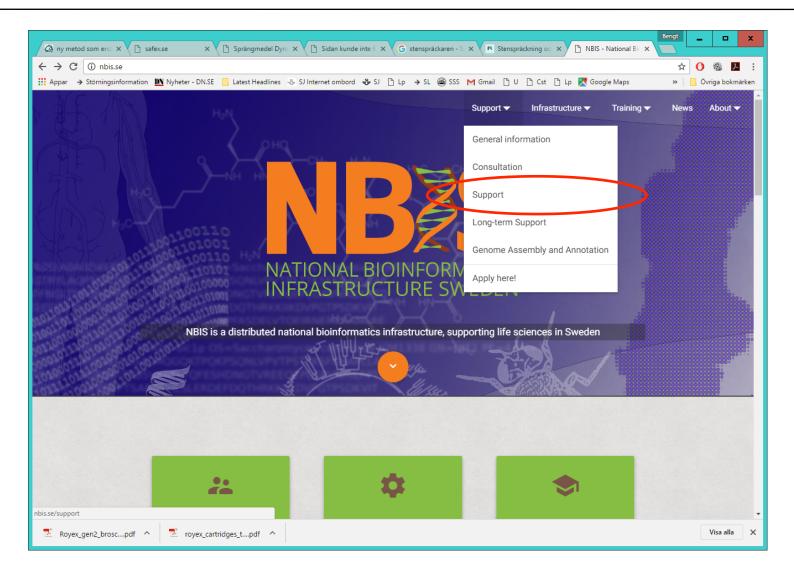






# How to get support nbis.se

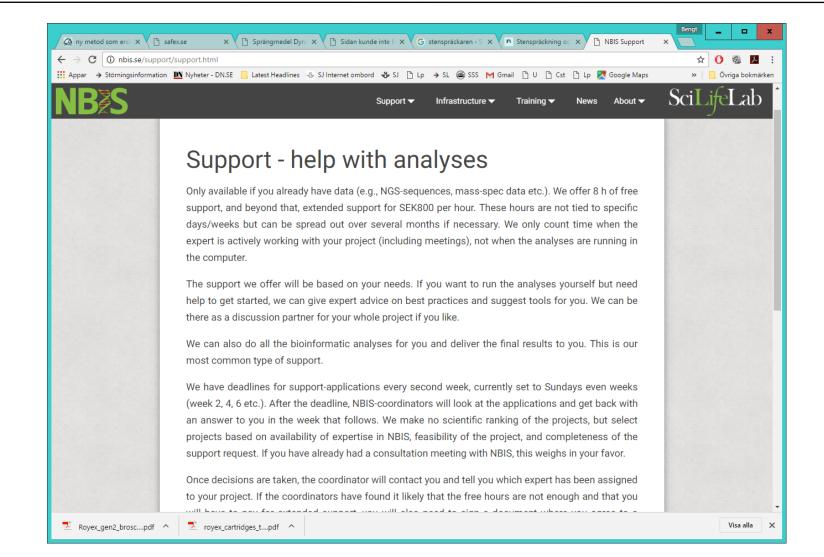






# **Support information**







# Support form

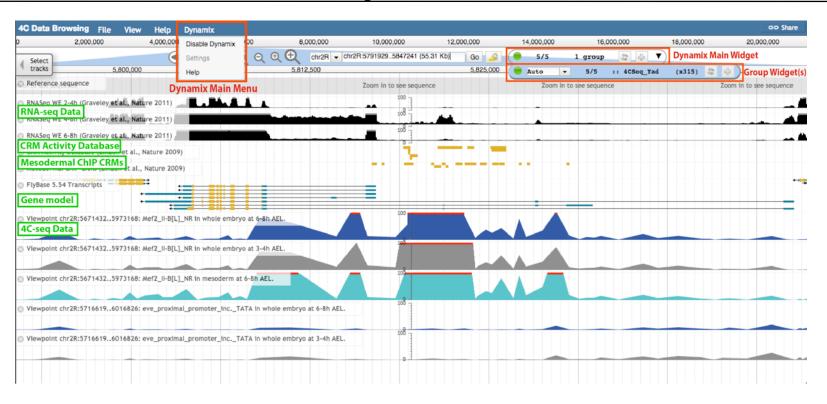


NBZS				Support 🗸	Infrastructure 🔻	Training 👻	News	Events	About 👻	SciLifeLat
	CONS	ULTATION	SUPPORT		LONG-TERM	SUPPORT				
NBIS offers	s bioinformatic	s consultations as a free service	e.							
Click here	for further info	rmation about the NBIS consulta	ation service.							
Support re-	equests are revi	ewed every second week, please	e allow for up to three weeks before yo	ou hear back fro	om us.					
By applying	g for NBIS Supp	port you also agree to our <mark>user</mark> a	agreement.							
- NBIS Co Name	onsultation Rec	quest Form								
		Your name								
e-mail		Your e-mail address								
Ы		Name of Principal Investigator								
Pi e-mail	I	PI e-mail address								
Research	h organization	Chalmers					•			
Funding		ALF					•			
Project T	Title	Please include descriptive keyword	ds.							
Subject		NGS					•			
Descripti	ion	Brief project description.								
Starting t	time	ASAP								





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!





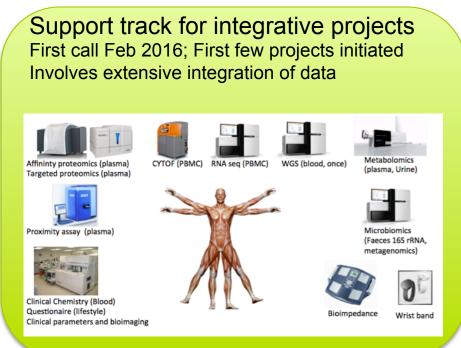
# **BigData/Integrative omics**

## 4 FTE, joint effort by Long-term Support and Systems Biology

Projects apply in the regular Long-term Support calls

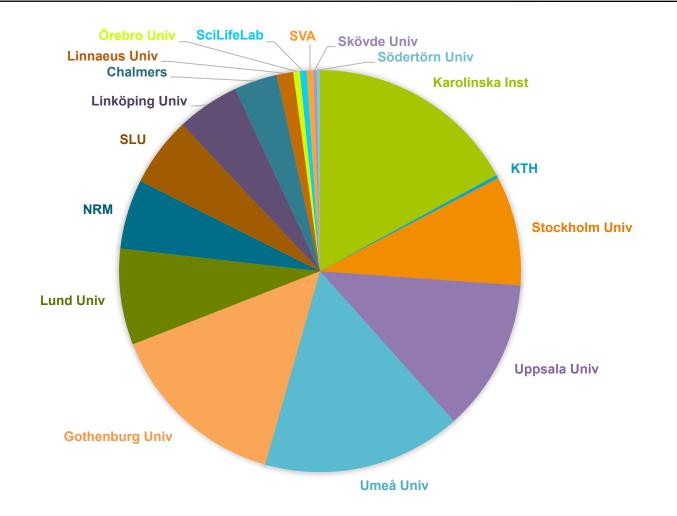
## Combine data from SciLifeLab platforms

- Building tools and resources for handling very large and/or complex biological data sets
- Typically performed in the context of longer support projects
- State-of-the-art analytical methods for integrating multi-modal biological data sets, eg
  - Machine learning/deep learning
  - Graph-based models
  - Genome-scale metabolic models





# Geographical Distribution of Projects 2015



SciLifeLab





# **Tools and infrastructure**



#### https://docs.google.com/spreadsheets/d/1PrehKn2eb0ymfaFtCfvbLrOSKtpTL3qLcWZ2YwoXOIU/edit#gid=0

## Compute and storage of sensitive data

- Local EGA
- ePouta integration pilot
- microMosler
- Pouta Blueprints
- web-servers with EGI cloud vo.NBIS.se

## WGS tools and resources

- SweGen 1000 genomes
- WGS somatic variant calling WF
- WGS structural variation WF

## Software maintenance

- MrBayes
- Structure prediction web services

## Assembly and annotation

- Falcon on Milou
- ENA submission help

## Other tools and resources

- Human Metabolic Atlas (HMA)
- Haloplex variant calling pipeline
- WhatsHap: Genomic phasing
- IgDiscover: Immunorepertoire

	NBIS SYSDEV BETS BC			ert kn	owledg		ization date: 2016-09-02 ive data integration, advanc	ced train	ing, e	fficien	t data i	oublication a
We fund Rank	data and analysis methods. NOW have done the experimenting, we have learned, and we're read ed, plans are clear and we an predid with resanable confiden Bet/Project	y to bui	ld it for the w	orld. It is	fully	We'n	NEXT experimenting with different ways to identified so we can build the right thi Bet/Project	create vali	ue with	an oppo	rtunity	We believe ti we're investig
1	Local EGA	x	NJ?	?	6?	1	Tools and guides collection		PE	?	<1	Impute GW
2	SweFreq	x	Adam A	NJ	<1	2						Permutatio
3	ePouta integration pilot	x	Antti P	JH?	1	3						Developme
4	microMosler		NJ?	JH	1?	4						Improve bi
5	WGS structural variation WF		BN	PO	1	5						Single-cell
6	Falcon on milou		HL	JB	<1	6						Chip-seq p
7	Pouta Blueprints		OS	JH	2							CWL for N
8	web-servers with EGI cloud vo.NBIS.se		MB	NS	2							OpenCB
9	Human Metabolic Atlas (HMA)		TS	LH	1-6							Local Ense
10	SSC HPC2N region dynamic resource allocation		MB	NS	2							NBIS Tools
11	Database for SciLife/AZ proj	x	BPn?	JV?	4?							IgDiscover
	Ongoing dev projects not resourced by the dev tea											
	WGS somatic variant calling WF		BN	(SJ)	0							_
	Haloplex variant calling pipeline		PE	ML	0							
	WhatsHap: Genomic phasing tool		PE	MM	0							_

### Open prioritization and background descriptions

Tools and development projects needs to be much more visible! Work in progress...

# SweGen: 1000 Swedish genomes

#### SweGen Variant Frequency Database

- 950 twin registry + 50 Northern Sweden
- Deep coverage WGS (30X)
- ExAC browser interface
- Data Beacon
- Full SNP frequency table download



1<sup>st</sup> release October 2016!

#### Variant: 22:46615880 T / C

Allele Count 7 / 2000 UCSC 22-466158 ClinVar Click to see	80-T-C 🗗 arch for variant in Clinvar 🖓	Sit	te Quality Me	trics			
Annotations This variant falls on 7 transcripts in 1 ger missense	nes: intron			equencie <sup>• Allele</sup> <sub>Number</sub>	S Number of Homozygotes	♦ Allele Frequency	
PPARA     Transcripts -	• PPARA - ENST00000434345	SweGen Total	7	2000 2000	0	0.0035	-
non coding transprint over							
non coding transcript exon     PPARA - ENST00000493286      Note: This list may not include additional trans	cripts in the same gene that the variant does not overlap						
PPARA - ENST00000493286  Note: This list may not include additional trans  Read Data	vs reads that went into calling this variant.						Funding: SciLifeLab Sequencing: NGI Variant calling: NGI
PPARA - ENST00000493286  Mote: This list may not include additional trans  Read Data  This interactive IGV.js visualization show							Sequencing: NGI
PPARA - ENST00000493286  Mote: This list may not include additional trans  Read Data  This interactive IGV.js visualization show	is reads that went into calling this variant.				(hide labels)	= +	Sequencing: NGI Variant calling: NGI



# SciLifeLab







# **Outreach & Training**

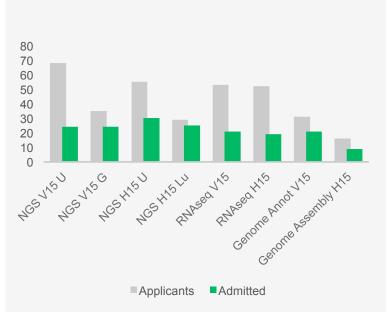


- Bioinformatics Drop-In
  - Weekly at all sites initial consultations
- 20-odd courses every year
  - Introduction to Bioinformatics using NGS
  - Introduction to Linux
  - Perl programming
  - Introduction to genome annotation
  - Introduction to multivariate analysis
  - RNA-seq
  - Advanced workshop on NGS data analysis
  - Advanced functional genomics
  - Advanced bioinformatics
- Additional local activities
- Bioinformatics Advisory programme
  - Mentorship in bioinformatics

From spring 2017, we plan to double our training efforts to match the increased demands from the scientific community

www.scilifelab.se/education/courses/ www.nbis.se/training/events.html

Gender balance: 54% female / 46% male



Courses 2015



## 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/

2

3

5

4

Recent call (2017/2018): 111 applicants for 15 places (!)

# The Swedish Bioinformatics Advisory Program Program Program Student evaluation, June 2015 Overall rating of the Advisory Program Impact on the efficacy of your research Impact on the scientific value of your Impact on the technical level of your Impact on the technical level of your In favour of SciLifeLab continuing this Impact on the technical level of your

0





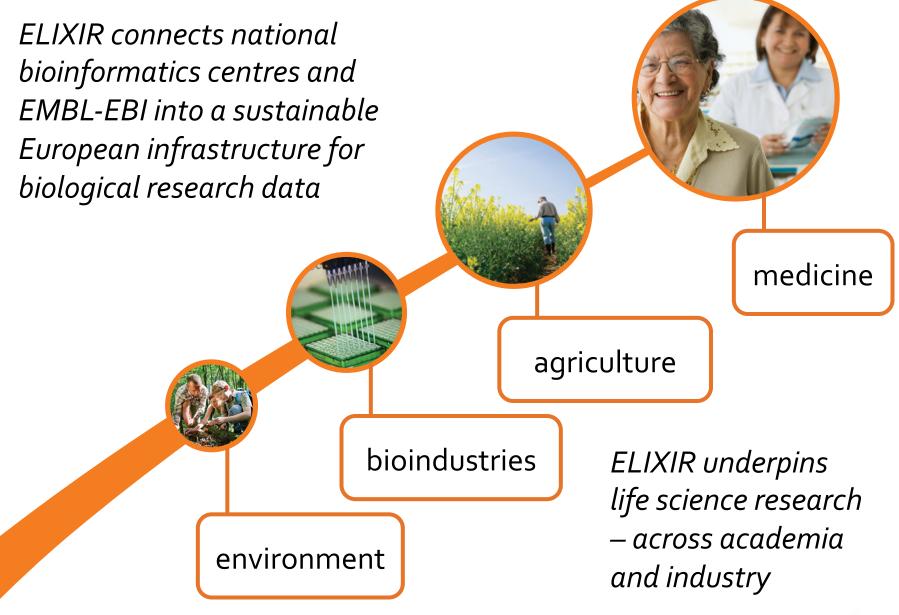


Elixir

# Why ELIXIR?

- Creating a robust infrastructure for biological information is a bigger task than any individual organisation or nation can take on alone
- These are issues of such complexity that no single institution or country can tackle alone
- Biology has by far the largest research community:
  - ~3 million life science researchers in Europe
  - >7 million web hits a day at EMBL-EBI alone









## We're here for you! nbis.se



