

# The Bioinformatics Core Facility in Oslo

Staff:



Core facility leader Eivind Hovig

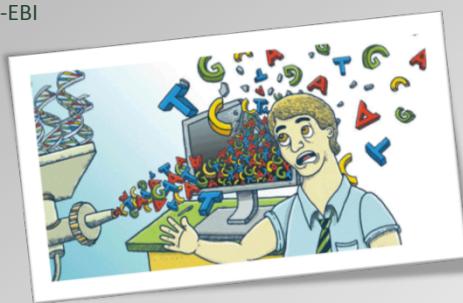


[http://core.rr-research.no/  
bioinformatics](http://core.rr-research.no/bioinformatics)



## The biological data explosion

The greatest challenge facing the molecular biology community today is to make sense of the wealth of data that has been produced by the genome sequencing projects – EMBL-EBI



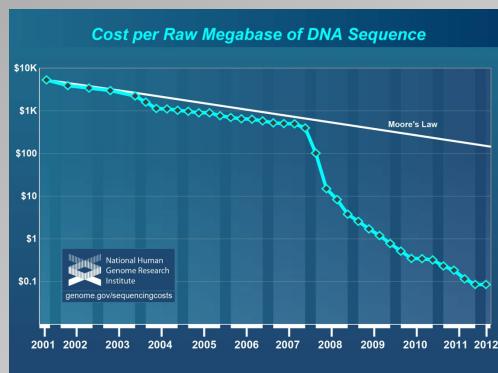
Bioinformatics algorithms and computing power are the main bottlenecks for analyzing huge amount of data generated by the current technologies (Gálvez *et al.*, *Bioinformatics* **26**, 683 (2010)).



[http://core.rr-research.no/  
bioinformatics](http://core.rr-research.no/bioinformatics)



## The biological data explosion



<http://www.genome.gov/sequencingcosts>

- Storage and processor capacity roughly double every two years (Moore's Law)
- New biological data is at present doubling every five months – rate is increasing
- New sequencing machines produce billions of bases per experiment
- Both users and informatics infrastructure have trouble adapting

- Very *real* and *serious* challenge for molecular biology, in Norway and elsewhere



[http://core.rr-research.no/  
bioinformatics](http://core.rr-research.no/bioinformatics)



BIOINFORMATICS CORE FACILITY



## The advantages of having a bioinformatics core facility

- Providing infrastructure
- Broad, stable and increased competence
- Cost efficient for large-scale projects
- Help for projects of all sizes
- Increase probability of a grant award
- We can guide you to the correct people



[http://core.rr-research.no/  
bioinformatics](http://core.rr-research.no/bioinformatics)



BIOINFORMATICS CORE FACILITY



# Who are we?

**Tromsø:** Nils Peder Willassen

**Trondheim:** Finn Drabløs

**Bergen:** Inge Jonassen

**Oslo:** Eivind Hovig

**Ås:** Dag Inge Våge

**Part of ELIXIR Norway – The National Technology Platform for Bioinformatics**

**elixir NORWAY**

<http://core.rr-research.no/bioinformatics>

**BCF BIOINFORMATICS CORE FACILITY**

## ELIXIR Norway

- Builds on the infrastructure and expertise built up by the FUGE bioinformatics platform (Funded by Research Council of Norway 2003-2012)
- Elixir Norway funded by the RC for the period 2013-2017 (2015)
- National centre with nodes in Bergen, Oslo, Ås, Trondheim, and Tromsø
- Offers *state of the art* research based infrastructure and services to Norwegian users in academia, industry, and government
  - Build and offer an e-infrastructure for users within molecular life science
  - Work tightly with other technology platforms
  - Provide *state of the art* bioinformatics support
  - Ensure that Norwegian data are stored in standardized formats – supporting re-use of data
  - Work with the generic e-infrastructure providers to make their resources available towards bioinformatics
- Headed by Professor Inge Jonassen, Bergen

**elixir NORWAY**

<http://core.rr-research.no/bioinformatics>

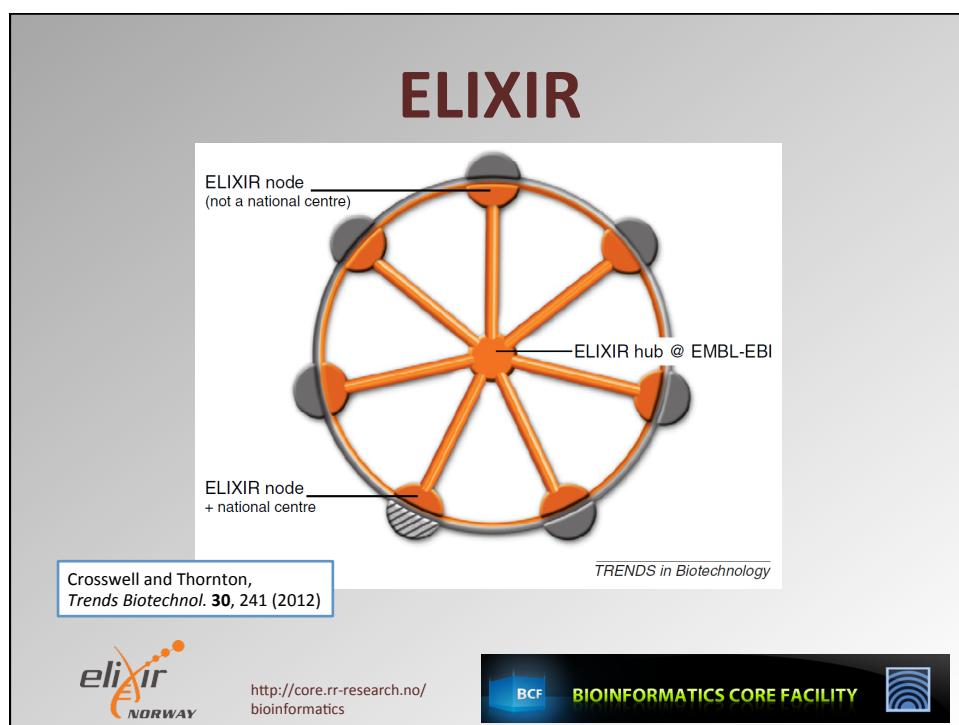
**BCF BIOINFORMATICS CORE FACILITY**

# ELIXIR

- *The purpose of ELIXIR is to construct and operate a sustainable infrastructure for biological information in Europe to support life science research and its translation to medicine and the environment, the bio-industries and society*
- Challenges for life scientists in Norway and all European countries
  - maintain open access to biological data to enhance competitiveness and innovation (free access to databases)
  - manage the data deluge
  - integrate the data to reduce fragmentation of effort and research
  - exploit new types of data
- These challenges are too vast for any single institution or country, and must therefore be managed by joining forces at European and global levels



[http://core.rr-research.no/  
bioinformatics](http://core.rr-research.no/bioinformatics)



## The Bioinformatics Core Facility in Oslo is a part of ELIXIR Norway

**ELIXIR node (not a national centre)**  
ELIXIR hub @ EMBL-EBI  
TRENDS in Biotechnology

**ELIXIR node + national centre**

Tromsø: Nils Peder Willlassen  
Trondheim: Finn Drabløs  
Bergen: Inge Jonassen  
Oslo: Eivind Hovig  
Ås: Dag Inge Våge

We are funded by

- RCN – ELIXIR Norway
- Helse Sør-Øst
- User fees (*Large projects only*)

**HELSE SØR-ØST**

**Forskningsrådet**

**elixir NORWAY**

[http://core.rr-research.no/  
bioinformatics](http://core.rr-research.no/bioinformatics)

**BCF BIOINFORMATICS CORE FACILITY**

## Who are we in Oslo?

	Vegard Nygaard – Microarray and sequence data analysis		Eivind Hovig – manager		Merete Molton Worren – High-throughput sequencing analysis
	Morten Johansen – Programming, scripting, web servers		Ståle Nygård – Statistical genomics <b>Oslo and National Helpdesk manager</b>		Daniel Vodák – HTS analysis
	Marit Holden, Norsk Regnesentral – Statistical genomics		Jon K. Lærdahl – Protein structure analysis		Torbjørn Rognes – sequence analysis
	Clara-Cecilie Günther, Norsk Regnesentral – Statistical genomics		Sveinung Gundersen – Hyperbrowser		

Roughly 6 man-years of bioinformatics expertise

**elixir NORWAY**

[http://core.rr-research.no/  
bioinformatics](http://core.rr-research.no/bioinformatics)

**BCF BIOINFORMATICS CORE FACILITY**

## What do we do?

- Providing Service and Support
- Access to Computing Facilities
- Access to Storage
- Organize and Contribute to Courses
- Organize and Contribute to Conferences and Workshops



[http://core.rr-research.no/  
bioinformatics](http://core.rr-research.no/bioinformatics)

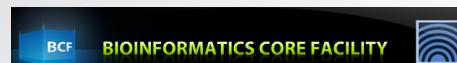


## What is a bioinformatician?

- An intimate knowledge of UNIX-based operating systems
- Fluent in scripting languages such as Perl or Python
- Understanding programming languages such as C++/C / Java, and ability to develop software encapsulating new analysis methods
- Knowledge of network-based data storage
- Understanding of relational databases and database architecture



[http://core.rr-research.no/  
bioinformatics](http://core.rr-research.no/bioinformatics)



## What is a bioinformatician?

- Skills in statistical analysis
- Understanding of experimental design
- Knowledge of mathematical modeling
- *And of course, we have a general knowledge of molecular biology and genomics*



[http://core.rr-research.no/  
bioinformatics](http://core.rr-research.no/bioinformatics)



## What can a bioinformatician do for you?

- Provide the computational/statistical analysis of data derived from your biological/medical experiments
  - *It is always better to be involved early in the project, before the experiments have been performed*
    - Contribute to planning and experimental setup
    - Not: Here are the results/data, tell us what they mean...!
- Our knowledge and experience makes us well equipped to seek out and test novel bioinformatics software and analysis pipelines
- We can do the programming/scripting for you if you wish to do the main part of the analysis yourself



[http://core.rr-research.no/  
bioinformatics](http://core.rr-research.no/bioinformatics)



## Bioinformatics Core Facility Helpdesk

- High quality **research based** bioinformatics support
- Part of the National ELIXIR Norway helpdesk
- Headed by Ståle Nygård in Oslo
- Common point of access: [contact@bioinfo.no](mailto:contact@bioinfo.no)
- Or contact the experts directly – see our webpages
- Have supported 100s of life science research projects the last decade
  - FUGE (2003-12) and Helse Sør-Øst funding
- Now expertise from the FUGE period supplemented with new ELIXIR personnel
  - ELIXIR (2013-17) and Helse Sør-Øst funding



[http://core.rr-research.no/  
bioinformatics](http://core.rr-research.no/bioinformatics)



BIOINFORMATICS CORE FACILITY



## Bioinformatics Core Facility Helpdesk

- Common point of access: [contact@bioinfo.no](mailto:contact@bioinfo.no)
- Or contact the experts directly – see our web pages
- Services within all major areas in bioinformatics analysis, e.g.
  - Sequence analysis
  - Analysis of High-throughput sequencing data
  - Protein structure analysis
  - Analysis of DNA variation
  - Genetic linkage studies
  - Microarrays
  - General gene association studies
  - Statistical genomics
  - Database construction and access
  - Web services

– Arranging courses and  
workshops

Located both at the Norwegian  
Radium Hospital, Montebello,  
and at the top floor of Ole-  
Johan Dahls hus, the new  
Informatics building at UiO

Close collaboration with other Core Facilities, e.g. Genomics  
Core Facility (GCF, Radium Hospital) and the Oslo Genotyping  
Core Facility



[http://core.rr-research.no/  
bioinformatics](http://core.rr-research.no/bioinformatics)



BIOINFORMATICS CORE FACILITY



# Services we provide - examples



[http://core.rr-research.no/  
bioinformatics](http://core.rr-research.no/bioinformatics)

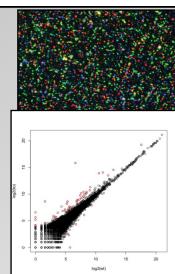


BIOINFORMATICS CORE FACILITY



## Services we provide

- **Analysis of high-throughput sequencing data**
  - RNA-seq: expression analysis
  - ChIP-seq: finding protein-DNA interactions
  - Genome sequencing: finding SNPs, indels, structural variants
  - Bisulfite: DNA methylation
  - small-RNA-seq: Detecting novel noncoding RNAs, expression
  - Metagenomics: Calculating operational taxonomic units (OTUs), creating phylogenetic trees, assigning species



[http://core.rr-research.no/  
bioinformatics](http://core.rr-research.no/bioinformatics)

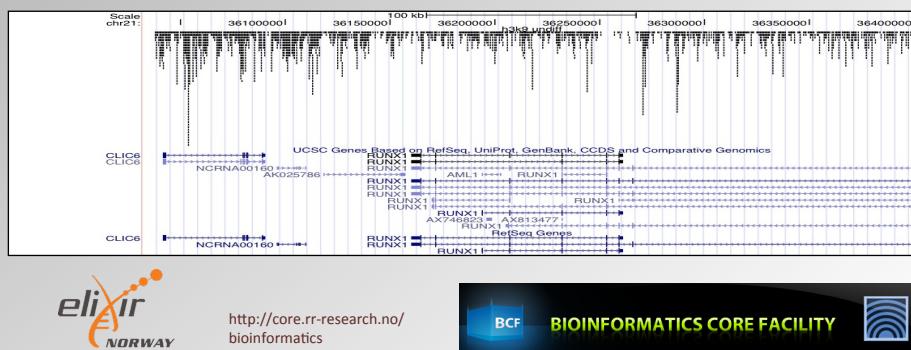


BIOINFORMATICS CORE FACILITY



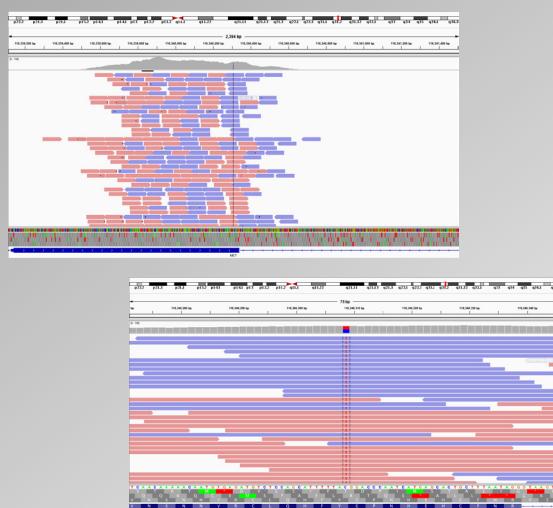
## Services we provide

- I want to visualize my data, and see where on the reference genome the (high-throughput) sequencing reads can be aligned
- I want to see which genes are affected, and how
- I want as much as possible out of my data



## Services we provide - examples

- Discovery of germline/somatic variants
- Detection of structural aberrations
- Variant annotation

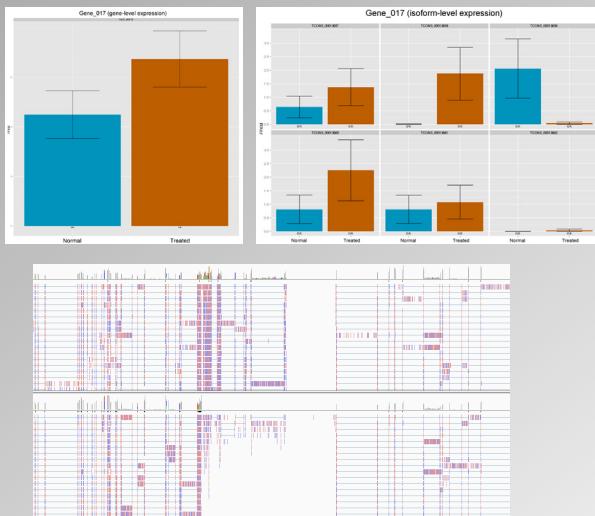


[http://core.rr-research.no/  
bioinformatics](http://core.rr-research.no/bioinformatics)

BCF BIOINFORMATICS CORE FACILITY



## Services we provide - examples

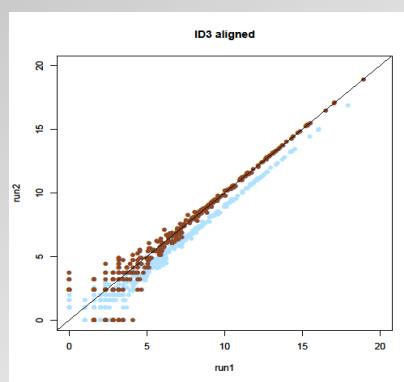


- Differential gene/transcript expression analysis
- Discovery of differential splicing
- Identification of novel transcripts

**elixir NORWAY** <http://core.rr-research.no/bioinformatics> **BCF BIOINFORMATICS CORE FACILITY**

## Services we provide - examples

- Finding miRNAs expressed in colorectal cancer cells
- Testing the effects of different normalization methods on the data
- Checking for differential expression between groups

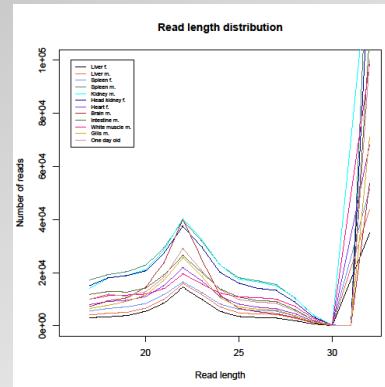


PLoS ONE 8, e66165 (2013)

**elixir NORWAY** <http://core.rr-research.no/bioinformatics> **BCF BIOINFORMATICS CORE FACILITY**

## Services we provide - examples

- Detecting miRNAs in the Atlantic salmon
- Novel and known expressed miRNAs
- Differential expression analysis between different tissues, and between individuals infected with ISA and healthy controls



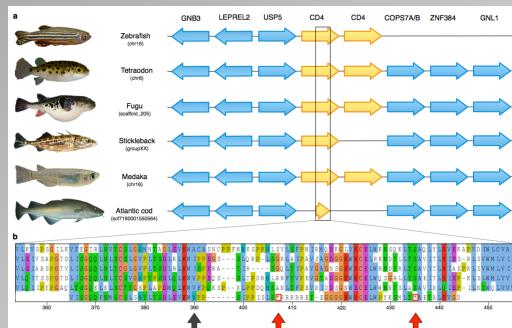
BMC Genomics 14, 482 (2013)



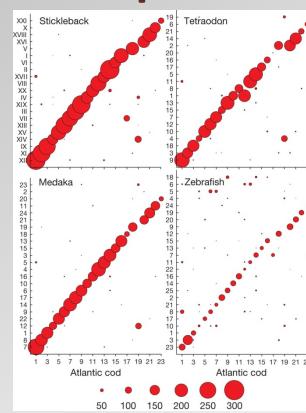
[http://core.rr-research.no/  
bioinformatics](http://core.rr-research.no/bioinformatics)



## Services we provide - examples



- Annotation and analysis of the recently assembled cod genome
  - Cross-species comparison and analysis of data
  - Using sequence alignment tools and annotation databases to identify syntenic regions across species
  - Using synteny information to infer reliability of missing genes/regions in newly mapped genomes



Nature 477, 207 (2011)



[http://core.rr-research.no/  
bioinformatics](http://core.rr-research.no/bioinformatics)



## Services we provide – The Genomic HyperBrowser

- If you have a genomic track, we can analyse it!
  - Research based service
  - Genome-scale analysis made robust and easy
  - Analyze your own data, and get custom-developed methodology and tools
  - Comes with >100 000 genomic tracks, 76 analyses, 42 tools
  - From quick analysis to robust statistical testing, in simple web interface



UP  
MP  
US  
MS  
F

Track 1 → Track 2 →

**Data**

Analysis

Results

Null hypothesis

Track 1 (UP): Preserve all  
Track 2 (US): Preserve segment lengths, Resemble positions

Statistical test

Monte Carlo   Exact

Global results

P-value  
Test statistic  
Mean of null dist. (...)

Local results

P-value  
(or test statistic)  
Mean of null dist.  
Base  
Masted away  
Genome pos.



[http://core.rr-research.no/  
bioinformatics](http://core.rr-research.no/bioinformatics)

**BCF** BIOINFORMATICS CORE FACILITY



## The Genomic HyperBrowser

- Start in your internet browser
  - A public, web-based interface allows sophisticated genome analysis by simple point-and-click
- If you have questions, just ask
  - If you need input, we can assist you directly from where you left off
- If you need even more
  - We have a team of programmers and statisticians that can develop novel software and methodology

*Nucleic Acids Res* 41, W133 (2013)



[http://core.rr-research.no/  
bioinformatics](http://core.rr-research.no/bioinformatics)

**BCF** BIOINFORMATICS CORE FACILITY



## The Genomic HyperBrowser - examples

- Regulation by C-myb transcription factor
  - Predict binding based on motifs and ENCODE data
- Promoters with methylation pattern
  - Statistical evaluation of association with CpG islands
- Pathology of multiple sclerosis
  - Determine involved cell types from ENCODE data
- Map environment to genome *PLoS One* 7, e32281 (2012)
- Vitamin D association to disease through receptor *Hum Mol Genet* 21, 3575 (2012)

[http://core.rr-research.no/  
bioinformatics](http://core.rr-research.no/bioinformatics)

*Hum Mol Genet* 21, 3575 (2012)



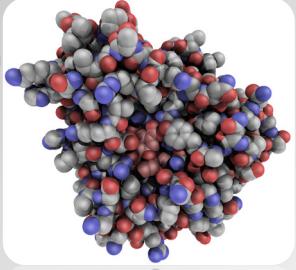
## Services we provide

- Analysis of gene sets
  - Gene-set enrichment analysis
  - Finding statistically overrepresented GO-terms and pathways
  - Finding related genes based on literature
  - Grouping together correlated genes
  - Mapping gene-lists to pathways

Untitled			
ENSG00000219466	ENST000000985362	16	86115027
ENSG00000219463	ENST000000511252	16	86320833
ENSG00000219462	ENST000000511253	16	87320833
ENSG00000219461	ENST000000511254	16	87320834
ENSG00000219460	ENST000000511255	16	87320835
ENSG00000219459	ENST000000511256	16	87320836
ENSG00000219454	ENST000000493879	16	88799303
ENSG00000219453	ENST000000493879	16	88799304
ENSG00000219452	ENST000000493879	16	88799305
ENSG00000219451	ENST000000493879	16	88799306
ENSG00000219450	ENST000000511269	16	88949688
ENSG00000219449	ENST000000432274	16	89334612
ENSG00000219448	ENST000000432274	16	89334613
ENSG00000219447	ENST000000432274	16	89334614
ENSG00000219446	ENST000000511268	16	89334615
ENSG00000219445	ENST000000511269	16	89334616
ENSG00000219444	ENST000000511270	16	89334617
ENSG00000219443	ENST000000493878	16	89549405
ENSG00000219442	ENST000000493878	16	89549406
ENSG00000219441	ENST000000493878	16	89549407
ENSG00000219440	ENST000000493878	16	89549408
ENSG00000219439	ENST000000493878	16	89549409
ENSG00000219438	ENST000000493878	16	89549410
ENSG00000219437	ENST000000493878	16	89549411
ENSG00000219436	ENST000000493878	16	89549412
ENSG00000219435	ENST000000493878	16	89549413
ENSG00000219434	ENST000000493878	16	89549414
ENSG00000219433	ENST000000493878	16	89549415
ENSG00000219432	ENST000000493878	16	89549416
ENSG00000219431	ENST000000493878	16	89549417
ENSG00000219430	ENST000000493878	16	89549418
ENSG00000219429	ENST000000493878	16	89549419
ENSG00000219428	ENST000000493878	16	89549420
ENSG00000219427	ENST000000493878	16	89549421
ENSG00000219426	ENST000000493878	16	89549422
ENSG00000219425	ENST000000493878	16	89549423
ENSG00000219424	ENST000000493878	16	89549424
ENSG00000219423	ENST000000493878	16	89549425
ENSG00000219422	ENST000000493878	16	89549426
ENSG00000219421	ENST000000493878	16	89549427
ENSG00000219420	ENST000000493878	16	89549428
ENSG00000219419	ENST000000493878	16	89549429
ENSG00000219418	ENST000000493878	16	89549430
ENSG00000219417	ENST000000493878	16	89549431
ENSG00000219416	ENST000000493878	16	89549432
ENSG00000219415	ENST000000493878	16	89549433
ENSG00000219414	ENST000000493878	16	89549434
ENSG00000219413	ENST000000493878	16	89549435
ENSG00000219412	ENST000000493878	16	89549436
ENSG00000219411	ENST000000493878	16	89549437
ENSG00000219410	ENST000000493878	16	89549438
ENSG00000219409	ENST000000493878	16	89549439
ENSG00000219408	ENST000000493878	16	89549440
ENSG00000219407	ENST000000493878	16	89549441
ENSG00000219406	ENST000000493878	16	89549442
ENSG00000219405	ENST000000493878	16	89549443
ENSG00000219404	ENST000000493878	16	89549444
ENSG00000219403	ENST000000493878	16	89549445
ENSG00000219402	ENST000000493878	16	89549446
ENSG00000219401	ENST000000493878	16	89549447
ENSG00000219400	ENST000000493878	16	89549448
ENSG00000219409	ENST000000493878	16	89549449
ENSG00000219408	ENST000000493878	16	89549450
ENSG00000219407	ENST000000493878	16	89549451
ENSG00000219406	ENST000000493878	16	89549452
ENSG00000219405	ENST000000493878	16	89549453
ENSG00000219404	ENST000000493878	16	89549454
ENSG00000219403	ENST000000493878	16	89549455
ENSG00000219402	ENST000000493878	16	89549456
ENSG00000219401	ENST000000493878	16	89549457
ENSG00000219400	ENST000000493878	16	89549458
ENSG00000219409	ENST000000493878	16	89549459
ENSG00000219408	ENST000000493878	16	89549460
ENSG00000219407	ENST000000493878	16	89549461
ENSG00000219406	ENST000000493878	16	89549462
ENSG00000219405	ENST000000493878	16	89549463
ENSG00000219404	ENST000000493878	16	89549464
ENSG00000219403	ENST000000493878	16	89549465
ENSG00000219402	ENST000000493878	16	89549466
ENSG00000219401	ENST000000493878	16	89549467
ENSG00000219400	ENST000000493878	16	89549468
ENSG00000219409	ENST000000493878	16	89549469
ENSG00000219408	ENST000000493878	16	89549470
ENSG00000219407	ENST000000493878	16	89549471
ENSG00000219406	ENST000000493878	16	89549472
ENSG00000219405	ENST000000493878	16	89549473
ENSG00000219404	ENST000000493878	16	89549474
ENSG00000219403	ENST000000493878	16	89549475
ENSG00000219402	ENST000000493878	16	89549476
ENSG00000219401	ENST000000493878	16	89549477
ENSG00000219400	ENST000000493878	16	89549478
ENSG00000219409	ENST000000493878	16	89549479
ENSG00000219408	ENST000000493878	16	89549480
ENSG00000219407	ENST000000493878	16	89549481
ENSG00000219406	ENST000000493878	16	89549482
ENSG00000219405	ENST000000493878	16	89549483
ENSG00000219404	ENST000000493878	16	89549484
ENSG00000219403	ENST000000493878	16	89549485
ENSG00000219402	ENST000000493878	16	89549486
ENSG00000219401	ENST000000493878	16	89549487
ENSG00000219400	ENST000000493878	16	89549488
ENSG00000219409	ENST000000493878	16	89549489
ENSG00000219408	ENST000000493878	16	89549490
ENSG00000219407	ENST000000493878	16	89549491
ENSG00000219406	ENST000000493878	16	89549492
ENSG00000219405	ENST000000493878	16	89549493
ENSG00000219404	ENST000000493878	16	89549494
ENSG00000219403	ENST000000493878	16	89549495
ENSG00000219402	ENST000000493878	16	89549496
ENSG00000219401	ENST000000493878	16	89549497
ENSG00000219400	ENST000000493878	16	89549498
ENSG00000219409	ENST000000493878	16	89549499
ENSG00000219408	ENST000000493878	16	89549500
ENSG00000219407	ENST000000493878	16	89549501
ENSG00000219406	ENST000000493878	16	89549502
ENSG00000219405	ENST000000493878	16	89549503
ENSG00000219404	ENST000000493878	16	89549504
ENSG00000219403	ENST000000493878	16	89549505
ENSG00000219402	ENST000000493878	16	89549506
ENSG00000219401	ENST000000493878	16	89549507
ENSG00000219400	ENST000000493878	16	89549508
ENSG00000219409	ENST000000493878	16	89549509
ENSG00000219408	ENST000000493878	16	89549510
ENSG00000219407	ENST000000493878	16	89549511
ENSG00000219406	ENST000000493878	16	89549512
ENSG00000219405	ENST000000493878	16	89549513
ENSG00000219404	ENST000000493878	16	89549514
ENSG00000219403	ENST000000493878	16	89549515
ENSG00000219402	ENST000000493878	16	89549516
ENSG00000219401	ENST000000493878	16	89549517
ENSG00000219400	ENST000000493878	16	89549518
ENSG00000219409	ENST000000493878	16	89549519
ENSG00000219408	ENST000000493878	16	89549520
ENSG00000219407	ENST000000493878	16	89549521
ENSG00000219406	ENST000000493878	16	89549522
ENSG00000219405	ENST000000493878	16	89549523
ENSG00000219404	ENST000000493878	16	89549524
ENSG00000219403	ENST000000493878	16	89549525
ENSG00000219402	ENST000000493878	16	89549526
ENSG00000219401	ENST000000493878	16	89549527
ENSG00000219400	ENST000000493878	16	89549528
ENSG00000219409	ENST000000493878	16	89549529
ENSG00000219408	ENST000000493878	16	89549530
ENSG00000219407	ENST000000493878	16	89549531
ENSG00000219406	ENST000000493878	16	89549532
ENSG00000219405	ENST000000493878	16	89549533
ENSG00000219404	ENST000000493878	16	89549534
ENSG00000219403	ENST000000493878	16	89549535
ENSG00000219402	ENST000000493878	16	89549536
ENSG00000219401	ENST000000493878	16	89549537
ENSG00000219400	ENST000000493878	16	89549538
ENSG00000219409	ENST000000493878	16	89549539
ENSG00000219408	ENST000000493878	16	89549540
ENSG00000219407	ENST000000493878	16	89549541
ENSG00000219406	ENST000000493878	16	89549542
ENSG00000219405	ENST000000493878	16	89549543
ENSG00000219404	ENST000000493878	16	89549544
ENSG00000219403	ENST000000493878	16	89549545
ENSG00000219402	ENST000000493878	16	89549546
ENSG00000219401	ENST000000493878	16	89549547
ENSG00000219400	ENST000000493878	16	89549548
ENSG00000219409	ENST000000493878	16	89549549
ENSG00000219408	ENST000000493878	16	89549550
ENSG00000219407	ENST000000493878	16	89549551
ENSG00000219406	ENST000000493878	16	89549552
ENSG00000219405	ENST000000493878	16	89549553
ENSG00000219404	ENST000000493878	16	89549554
ENSG00000219403	ENST0000		

## Services we provide

- Protein structure/sequence/function analysis
  - Investigate splice variants, possible posttranslational modifications, signal peptides, a localization signals by using state of the art bioinformatics tools
  - Identify protein domains, disordered regions and prediction of secondary structure
  - If possible, build 3D models
  - Identify orthologs from other species
  - Phylogeny
  - Identify functionally important domains/segments/ residues
  - Predict effects of mutations or suggest residues for site-directed mutagenesis




1	2	3	4	5	6	7	8	9
Variable	Average	Conserved						

**elixir NORWAY**

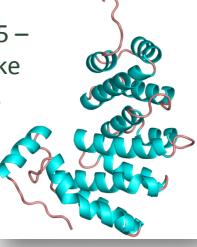
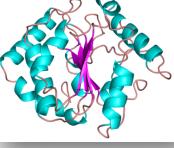
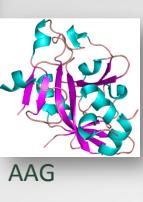
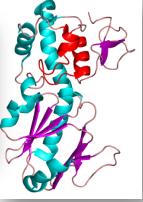
[http://core.rr-research.no/  
bioinformatics](http://core.rr-research.no/bioinformatics)

**BCF BIOINFORMATICS CORE FACILITY**

## Services we provide - examples

- Discovered a new, 5th structural superfamily of DNA glycosylase repair enzymes
- Modelled the 3D structure – homology modelling
- Located active site and suggested residues for site-directed mutagenesis
- Experimental follow-up

*Nucleic Acids Res.* **35**, 2451 (2007)

**elixir NORWAY**

[http://core.rr-research.no/  
bioinformatics](http://core.rr-research.no/bioinformatics)

**BCF BIOINFORMATICS CORE FACILITY**

## Services we provide - examples

**A**

**B**

**C**

	80	R	155	V	180	P	215	P	270	G	
Human	R	GYWSCL	86	-	PGIANS	C	156	LPAV	GAA	181	LA
Mouse	Q	GYWSCL	85	-	PGIANS	C	155	LPAV	GAT	180	RA
Dog	R	GYWSCL	86	-	PGIANS	C	156	LPAV	GAA	181	AL
Bovine	R	GYWSCL	86	-	PGIANS	C	156	LPAV	GAA	181	AL
Opossum	H	GYWPCL	86	-	PGIANTC	C	156	LPSV	VAA	181	AL
Lizard	L	YHTGCF	83	-	SNETCS	C	157	IPSL	LA	182	AL
Frog	F	GHICM	89	-	TESNC	C	164	IPSL	LA	189	AL
Medaka	L	SESSCL	84	-	NRTI	CCS	182	LPAV	LLI	207	AL

- Generated 3D model of human bile acid receptor TGR5 (a G-protein coupled receptor)
- Predicted effect of mutations/ SNPs
- Experimental follow-up

*PLOS One* 5: e12403 (2010)

[http://core.rr-research.no/  
bioinformatics](http://core.rr-research.no/bioinformatics)

BCF BIOINFORMATICS CORE FACILITY

## Services we provide - examples

**Adenylyl cyclase**   **cAMP-gated ion channels**

*Pidoux & Taskén, J. Mol. Endocrinol* 44, 271 (2010) (not our work!)

**Evolution/phylogeny of PKA catalytic subunits  $\alpha$ ,  $\beta$ , and  $\gamma$**

K. Søberg, T. Jahnsen, T. Rognes, B.S. Skålhegg & J.K. Lærdahl, *Plos ONE* 8, e60935 (2013)

**A**

**B**

**C**

[http://core.rr-research.no/  
bioinformatics](http://core.rr-research.no/bioinformatics)

BCF BIOINFORMATICS CORE FACILITY

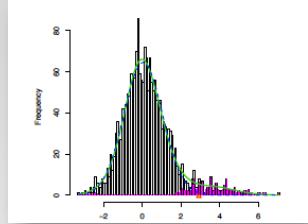
## Services we provide

- Statistical genomics
  - Experimental design
  - Pattern discovery
  - Clustering
  - Multivariate regression
  - Hierarchical inference
  - Multiple testing
  - Event history analysis
    - Survival analysis
  - Other types of analysis upon request





$$\hat{y} = a + b_1x_1 + b_2x_2 + b_3x_3 + \dots + b_nx_n$$





[http://core.rr-research.no/  
bioinformatics](http://core.rr-research.no/bioinformatics)

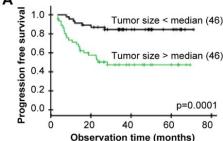


**BCF** BIOINFORMATICS CORE FACILITY



## Services we provide - examples

**A**



Tumor size < median (46)

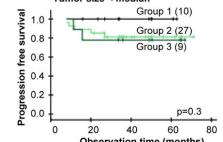
Tumor size > median (46)

p=0.0001

Observation time (months)

**B**



Tumor size < median

Group 1 (10)

Group 2 (27)

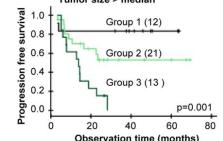
Group 3 (9)

p=0.3

Observation time (months)

**C**



Tumor size > median

Group 1 (12)

Group 2 (21)

Group 3 (13)

p=0.001

Observation time (months)

- Integrative analysis of gene dosage, expression and ontology (GO) data
- Identified driver genes in the carcinogenesis and chemoradioresistance of cervical cancer
- Found overrepresented biological processes including apoptosis and metabolism

*PLoS Genet.* 5, e1000719 (2009)



[http://core.rr-research.no/  
bioinformatics](http://core.rr-research.no/bioinformatics)



**BCF** BIOINFORMATICS CORE FACILITY



## Services we provide - examples

- Genome-wide gene expression analysis of bone biopsies from patients with postmenopausal osteoporosis and healthy controls, adjusting for age and BMI
- Found 256 transcripts confirmed for disease

*J Bone Miner. Res.* **26**, 1793 (2011)

<http://core.rr-research.no/bioinformatics>

## Services we provide

- DNA and protein microarray analysis
  - Design of experiment
  - Image analysis
  - Copy number analysis
  - Genotyping analysis
  - Differential analysis
  - Classification and clustering
  - Survival analysis
  - Meta analysis
  - Quality control
  - Public repository submission

<http://core.rr-research.no/bioinformatics>

## Services we provide

- **Database and web services**
  - Database access
  - Provide access to local copies of selected databases
  - Provide snapshot access to patient data in defined formats
- **Web services**
  - Provide access to local web services
  - Maintain pointers to useful other web services
- **Scripting and software services**
  - Support on scripting/programming
  - Support on use of Linux/Unix tools
  - Help with setup of required software and web-interfaces



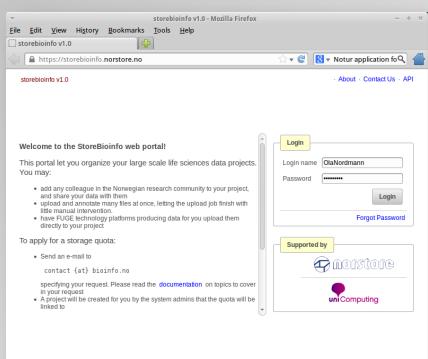
[http://core.rr-research.no/  
bioinformatics](http://core.rr-research.no/bioinformatics)



## Services we provide

- Facilitating use of computational resources together with USIT
  - CPU: <http://uio.no/hpc/abel>
  - Disk: <https://storebioinfo.norstore.no>







[http://core.rr-research.no/  
bioinformatics](http://core.rr-research.no/bioinformatics)



# Services we provide - examples

End of section



[http://core.rr-research.no/  
bioinformatics](http://core.rr-research.no/bioinformatics)



## Helpdesk – How it works

- Users contact us through e-mail or in person
- Simple services (“less than 3 days work”) offered free of charge to Norwegian academic/government users
- ***Always free to ask questions***
- Larger projects may require user fees or some form of collaborative research, depending on prior agreement. Any user fees will be based on a non-profit model and should be considered reasonable
- It is recommended to ***think about bioinformatics funding already in the planning stages of your research*** as this is an important and resource intensive step



[http://core.rr-research.no/  
bioinformatics](http://core.rr-research.no/bioinformatics)



## Bioinformatics Core Facility and ELIXIR Norway Helpdesk

**Our job is to help you with your bioinformatics  
needs. Please use us!**



[http://core.rr-research.no/  
bioinformatics](http://core.rr-research.no/bioinformatics)



## Bioinformatics Core Facility and ELIXIR Norway Helpdesk

**After this course: Don't go home to your lab  
and try to do everything yourself!**

**COLLABORATE!!**



[http://core.rr-research.no/  
bioinformatics](http://core.rr-research.no/bioinformatics)



## ELIXIR Norway Trondheim node – Integrated with the Bioinformatics Core Facility

- Located in the Laboratory Centre of St Olavs Hospital and NTNU
- Focus on biomedical research, gene regulation and large scale genomics
- Helpdesk services by Bioinformatics Core Facility (BioCore, funded by NTNU)
- Close collaboration with Genomics Core Facility (GCF)



Finn Drabløs  
Professor  
Leader ELIXIR-NTNU



Morten Rye  
Researcher  
ELIXIR-NTNU



Kjetil Klepper  
Staff Engineer  
ELIXIR-NTNU



Pål Sætrom  
Professor  
Head BioCore



Jostein Johansen  
Senior Engineer  
Manager BioCore



<http://www.motiflab.org>

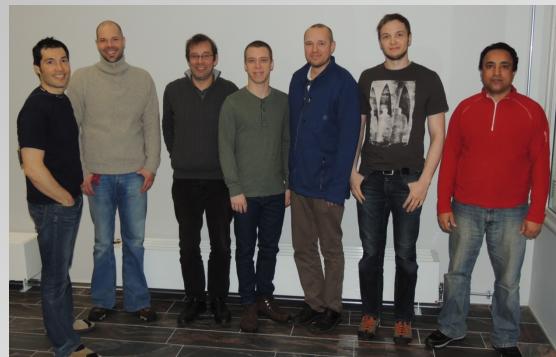


NTNU – Trondheim  
Norwegian University of  
Science and Technology

HELSE MIDT-NORGE

## ELIXIR Norway Tromsø node - SYSBIO

- Located both at the Science Park and NT faculty, UiT
- Collaboration between Dept. of Chemistry and Dept. of Informatics, UiT
- Focus on marine genomics/metagenomics
- Contact persons;  
Erik Hjerde (Help desk)  
Nils Peder Willlassen (Head)



From left to right: Erik Hjerde, Tim Kalkhe, Nils Peder Willlassen, Edvard Pedersen, Peik Haugen, Espen Robertsen and Said Ahmed. Lars Ailo Bongo not present



ELIXIR Norway - Tromsø

## ELIXIR.NO Ås node.

- Located at Centre for Integrative Genetics (CIGENE), Norwegian University of Life Sciences (UMB).
- CIGENE has established pipelines for handling large-scale sequencing data, with focus on *de novo* assembly (e.g. the Atlantic salmon genome) and development of DNA - markers (SNPs). The research is aimed at bridging the gap between genotype and phenotype in production biology species.
- The primary contribution to ELIXIR Norway will be to make fish genomic resources and tools available to the national and international research community.
- Node manager: Dag Inge Våge



ELIXIR Norway - Ås



## ELIXIR.NO Bergen node – the Computational Biology Unit

- The University of Bergen coordinates the ELIXIR Norway project and the (aspiring) Norwegian ELIXIR Node
- Bioinformatics at UiB organised in CBU – Computational Biology Unit – including research groups and a service group
- ELIXIR Norway personnel includes programmers, service scientists
- Close coupling with LiceBase within Sea Lice Research Centre (SFI)
- Collaboration with Norwegian Genomics Consortium (NGC), PROBE (proteomics), Department of public health (biobanks)
- Project leader: Inge Jonassen



ELIXIR Norway - Bergen



# Thank you!



[contact@bioinfo.no](mailto:contact@bioinfo.no)



<http://core.rr-research.no/>  
bioinformatics

