NeLS workshop

Dept of Informatics, UiO

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

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Agenda

- About ELIXIR Norway (short intro)
- About NeLS/Galaxy/Storebioinfo (short intro)
- Hands-on session
  - NeLS (file upload etc)
  - Galaxy (analysis)
    - Single tool
    - RNA-seq pipeline

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Bioinformatics underpins life-science research

1 Genomes contain genes

2 Genes are transcribed

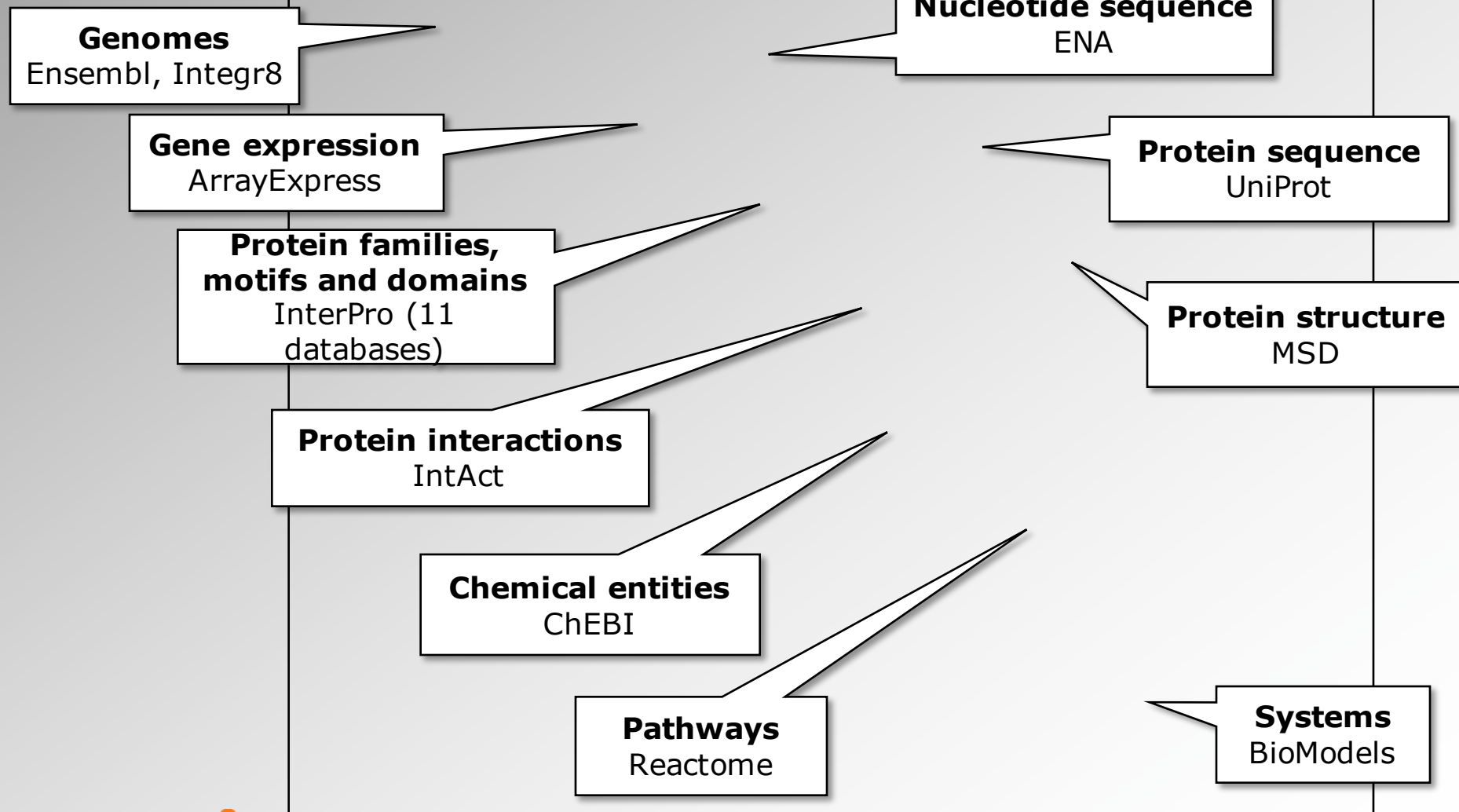**3** Transcripts translate to protein sequences

4 Proteins form three-dimensional structures

5 Proteins interact with each other and with small molecules to form pathways

6 Pathways combine to build systems

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Bioinformatics underpins life-science research

Genomes
Ensembl, Integr8

Nucleotide sequence
ENA

Gene expression
ArrayExpress

Protein sequence
UniProt

Protein families, motifs and domains
InterPro (11 databases)

Protein structure
MSD

Protein interactions
IntAct

Chemical entities
ChEBI

Pathways
Reactome

Systems
BioModels

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ELIXIR - Hub and node model

- ELIXIR – A distributed European infrastructure for life-science information

- ELIXIR Nodes builds on national strengths and priorities

- ELIXIR Nodes build local bioinformatics capacity throughout Europe

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ELIXIR

ELIXIR Hub:

Hinxton, UK

ELIXIR members:

Czech republic	Portugal
Estonia	Sweden
Denmark	Switzerland
Finland	UK
Israel	EMBL-EBI
Netherlands	France
Norway	Spain
Italy	
Belgium	

ELIXIR observers:

Greece
Slovenia
Ireland

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- ~3 million life science researchers in Europe
- >9 million web hits a day at EMBL-EBI alone
- 1 million unique users per year

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ELIXIR Norway

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HELSE ••••• SØR-ØST

Forskningsrådet

elixir NORWAY

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Inst. for cancer research, OUH

Eivind Hovig
Scientific leader

Ståle Nygård
Service leader

Vegard Nygaard
Microarray and sequence data analysis

Morten Johansen
Programming, scripting, web servers

Sumana Kalyanasundaram
HTS analysis, general "omics"

Oleg Agafonov
HTS, systems biology

Norwegian computing center

Marit Holden, Statistical genomics

Clara-Cecilie Günther
Statistical genomics

Biomedical research group, UiO

Jon K. Lærdahl
Protein structure analysis

Torbjørn Rognes
Sequence analysis

Hildur Sif Thorarensen
Programming

Sveinung Gundersen
Hyperbrowser

Antonio Mora
Gene regulation

Abdulrahman Azab
Computation

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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

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 Willassen (Head)

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

ELIXIR Norway - Tromsø

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 publich health (biobanks)

- Project leader: Inge Jonassen

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ELIXIR Norway - Bergen

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

Services we provide

- High throughput sequencing data analysis:
    - DNA sequencing
    - RNA-Seq
    - miRNA-Seq
    - ChIP-Seq
- Microarray data analysis
- Proteomic data analysis
- Protein structure analysis
- Statistical genomics
- Functional genomics
- General bioinformatics
- Facilitating use of computational resources together with USIT
    - CPU: http://uio.no/hpc/abel
    - Disk: https://storebioinfo.norstore.no
    - TSD (Tjeneste for Sensitive Data)

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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 (750 NOK per hour) 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

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Bioinformatics Core Facility and ELIXIR Norway Helpdesk contact@bioinfo.no

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