

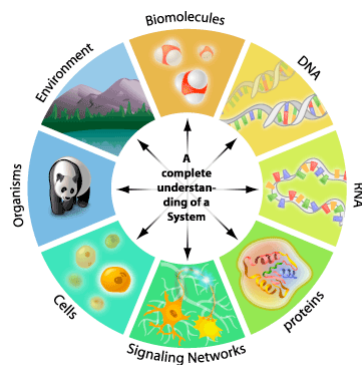
Toward a bioinformatics Centre of Excellence

Inge Jonassen
Institutt for Informatikk
& CBU, BCCS



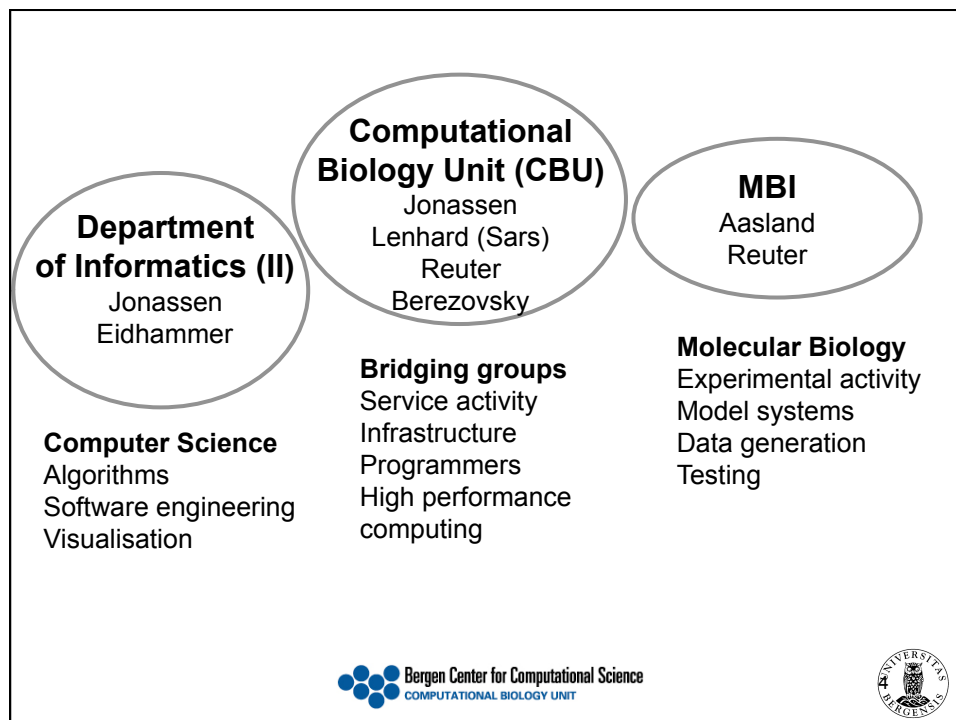
Bioinformatics, computational biology

- Development and use of computational methods for storing, analysing, and understanding (molecular) biological data



Background – activity at UiB

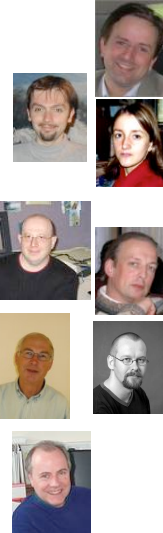
- Bioinformatics established at II from 1990
- Gradual build-up during 90s
- Close links to MBI, Sars, and others
- Initiative to establish Computational Biology Unit 2001
 - Coinciding with birth of FUGE program
- CBU has grown since 2002
- CoE status stated as goal from 2002



Bioinformatics groups

- Inge Jonassen (CBU/II) – Genomics, protein structure
- Boris Lenhard (CBU/Sars) – Transcription, regulation
- Nathalie Reuter (CBU/MBI) – Molecular dynamics
- Igor Berezovsky (CBU) – Protein evolution and function
- Service group (CBU) – FUGE service
- Pål Puntervoll (CBU/MBI) - eSysBio
- Rein Aasland (MBI/CBU) – Chromatin, motifs
- Ingvar Eidhammer (II) – Proteomics
- Willie Taylor (CBU/II – NIMR) 20% - Protein bioinformatics

In total 30-40 persons



Externally funded projects include

- Gas and Biotechnology (II, Bio, MBI, TIGR) ~ 98-
- FUGE 2002-2012
 - CBU – Bioinformatics platform (35M+12M from NFR)
 - NMC – Microarray platform
 - Genofisk platform
 - Other projects (>3PhDs)
- eVita (eSysBio) – with Parallab (BCCS) – 18M
- Boris Lenhard YFF (10M) and BFS (8+8M)
- Nathalie Reuter BFS (7.2+7.2M)
- EU: InterPro, DESPRAD, Angiotargeting, Embrace, EUtracc,...
- Strong support from UiB, faculty, II, MBI



FUGE platform positively reviewed

"Midterm" evaluation report:

"The project is very well led and well organized"

"In the Nordic countries, the [...] platform is the only one of its kind"

"the platform has delivered more service to users than its [...] obligations"

"... the platform has an excellent track record



nature genetics

På HØYDEN
Nettavis for Universitetet i Bergen - onsdag 3. mai 2006

Har funnet geneses på-knapper
Hvordan genene våre reguleres og kommer til uttrykk, er mer komplisert enn man hittil har trodd. Nå må modellene forandres og lærebøkene skrives om.
Les mer...

Genome-wide analysis of mammalian promoter architecture and evolution

PLoS GENETICS

2,21, Albin Sandelin^{1,3,21}, **Boris Lenhard^{1,3,20,21}**, **Shintaro Katayama¹**, Kazuro Shimizu^{1,20}, Colin A M Semple^{1,4}, Martin S Taylor^{1,5}, **Pär G Engström³**, Martin C Frith^{1,6}, Forrest⁶, Wynand B Alkema³, Sin Lam Tan⁷, Charles Plessy², Rimantas Kodzius^{1,2}, Li^{1,6,8}, Takeya Kasukawa^{1,9}, Shiro Fukuda¹, Mutsumi Kanamori-Katayama¹, Yayoi Kita^{1,9}, Chikatoshi Kai¹, Mari Nakamura¹, Hideaki Konno¹, Kenji Nakano^{1,9}, Tabar^{3,20}, Peter Arner¹⁰, Alessandra Chesi¹¹, Stefano Gustincich¹¹, Francesca Persico¹¹, Sean M Grimmond⁶, Christine A Wells¹⁹, Valerio Orlando¹³, Claes Wahlestedt^{3,20}, Matthias Harbers¹⁵, Jun Kawai^{1,2}, Vladimir B Bajic^{1,7,16}, David A Hume^{1,6,21} & Shizaki^{1,2,17,18}

The Genome Network
Project/FANTOM3 Collection



PRIDE Converter: making proteomics data-sharing easy

Harald Barsnes¹, Juan Antonio Vizcaino²,
Ingvar Eidhammer¹ & Lennart Martens²

¹Department of Informatics, University of
Bergen, Norway; ²EMBL Outstation, European
Bioinformatics Institute (EBI), Wellcome Trust
Genome Campus, Hinxton, Cambridge, UK.
e-mail: lennart.martens@ebi.ac.uk



Accurate determination of
microbial diversity from
454 pyrosequencing data

Christopher Quince¹, Anders Lanzén²,
Thomas P Curtis³, Russell J Davenport³, Neil Hall⁴,
Ian M Head³, L Fiona Read³ & William T Sloan¹



ITRAQ based proteomic profiling reveals increased metabolic activity and cellular
crosstalk in angiogenic compared to invasive Glioblastoma phenotype

Authors:

Uros Rajcevic¹, Kjell Petersen², Jacob C. Knol³, Maarten Loos⁴, Sébastien Bougnaud¹, Oleg
Klychnikov¹, Ka Wan Li¹, Thang V. Pham¹, Jian Wang¹, Hrvoje Miletic⁵, Zhao Peng⁶, Rolf
Bjerkvig^{1,5}, Connie R. Jimenez⁷ and Simone P. Niclou¹

Computational prediction of the binding site
of proteinase 3 to the plasma membrane

Eric Hajjar,^{1,2} Maja Mihajlovic,³ Véronique Witko-Sarsat,⁴ Themis Lazaridis,³
and Nathalie Reuter^{1,5}



Bergen Center for Computational Science
COMPUTATIONAL BIOLOGY UNIT



Three developing areas

- **New sequencing technology**
 - New opportunities and challenges
 - On-going efforts in de-novo sequencing, metagenomics, chip-seq, RNA-seq, etc
 - Applied for NFR e-Infrastructure SEQ (April 22, 2009)
- **Data integration and systems biology**
 - eVita project eSysbio
 - Grid technologies, standardized data types, ...
 - Elixir **ESFRI-project** (European Bioinformatics Infrastructure)
 - FUGE service platform(s)
- **Computational & model-driven biology**



Bergen Center for Computational Science
COMPUTATIONAL BIOLOGY UNIT



Strengthening bioinformatics activity at UiB

- Gives **competitive advantage** in functional genomics, systems biology, translational medicine, e-science,...
- FUGE platform & projects as well as eVita, BFS, YFF gives high activity
 - **Needs to be based on strong bioinformatics research activity**
- Need for UiB to support research and to **secure longterm competence** through
 - **CBU groups** including recruitment positions
 - New **professorships**
 - New **engineer position(s)**
 - Balance between permanent UiB staff and dynamic groups
- **Complement CoE with Norwegian Elixir (ESFRI) node**
- Unified activity with **critical mass** at/around CBU