

## MINUTES

### ELIXIR.NO meeting with Marine Genomics groups in Norway

Gardermoen, June 18, 2013, 10:00-15:00

23 participants (list enclosed)

The meeting started with presentations from the ELIXIR.NO leader group. Inge Jonassen (UiB) gave an introduction to the ELIXIR infrastructure, including Norwegian e-infrastructure for Life Science (NeLS). Dag Inge Våge (UMB) gave a presentation on fish genomics, including briefly the salmon genome sequencing project (ICSASG) and the Aqua Genome project. Nils Peder Willassen (UiT) gave a presentation on marine metagenomics, in particular the META-pipe pipeline, and how metagenomics is a basis for collaboration with EBI (on an ELIXIR pilot project on metagenomics) and EMBRC, the European Marine Biological Resource Centre.

Next Kjetill Jacobsen and Lex Nederbragt (UiO) gave a presentation of the Aqua Genome project, which involves sequencing of 1000 genomes of cod and salmon. The project aims at identifying genetic variation underlying both adaptive and production related traits, and also includes epigenetics on temperature-dependent muscle development. The presentation highlighted important challenges in sequencing, as for example short tandem repeats and polymorphic (heterozygous) regions. Although these can potentially be handled using sequencing technologies with very long reads (PacBio), this introduces additional challenges, and improved assembly approaches are needed.

Steinar Bergseth (NFR) gave an overview of relevant funding sources for genome-oriented marine research. This focused on Biotek2021, INFRA programme funding, and Horizon2020. For infrastructure funding also the indirect funding (fee paid by users of services) is essential. The Horizon2020 presentation included JPI Oceans, ERA-NET MarineBiotech and European Institute of Innovation and Technology (EIT).

This was followed by short (5 minutes) presentations by the groups / laboratories / institutions present at the meeting (see enclosed list of participants). The topics mentioned include most of the possible research areas of marine genomics, but some topics were highlighted as being of special importance.

- Data storage; some projects will generate large data sets, and there is a need for storage of project data, as well as submitting data to international repositories (often needed for publication). Need for standards and for policies on data sharing and publication.
- Collaboration on bioinformatics; bioinformaticians is a limited resource compared to the needs.
- Basic help on getting started; some groups have limited experience with genomic methods using high throughput sequencing.
- Integration and visualization of data; genomic data sets are large and complex, and it may be difficult to find the novel or important information, must be able to filter out noise.
- Two-way flow of tools; some groups already have their own bioinformatics activity and may be able to provide useful tools to ELIXIR.NO / NeLS.

- Grey boxes for standard problems; there is a need for processing tools for standard problems that most researchers can use, but the boxes must not be completely black to the user, the user must have some basic understanding of function.
- Training of people with molecular biology background; many of these lack competence in bioinformatics, but have to use such tools in new projects.
- Outreach and information; important that researchers are aware of ELIXIR and ELIXIR.NO and what can be provided.
- NFR pointed at the need for a meeting place for developing new large projects. ELIXIR.NO is important for efficient use of resources, but commitment from user groups (here the marine sector) is needed.

Then there was discussion on a few key topics.

*What are the bioinformatics needs in the Norwegian marine community? Needs not covered by the existing (medicine oriented) efforts.*

- Infrastructure must be close to the actual problems, as both generic and specialized tools are needed, depending on the project, and bioinformaticians must therefore be close to the data. Challenges are changing fast (due to technology development). More hands are needed!
- Large projects have demands for storage and compute capacity close to the storage
- Standards for data publication are needed, in particular for metagenomics data. There is ongoing work, e.g. at EBI.
- How to do transcriptomics on non-model organisms (i.e. where good reference genome is missing).
- How to combine different sequencing technologies in the same project.
- What can be learned from biomedical projects, in particular human re-sequencing projects?
- Annotation of data, connecting different information sources.
- Training courses!

*How do we best coordinate nationally? Need for meeting series/forum.*

- ELIXIR.NO needs to demonstrate what can be done, for example by giving presentations. May also try to mix marine and biomedicine for this. Can the Norwegian Bioinformatics Forum (NBF) meetings be used?
- Also a need for narrower thematic meetings.

*Information exchange. Standards, what data types. Policy for data release.*

- NFR pointed out that there is a political focus on data handling, and that in this context ELIXIR is not just an option for data handling, it is the infrastructure that has to be used.
- But then more resources are needed ...

The meeting was closed at 15:00.

Participants:

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