

Megx.net – a web portal for marine ecological genomics

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Today, more than 25 complete genomes of marine prokaryotic organisms are available in the public databases. This number is going to increase dramatically since the Moore Foundation (www.moore.org) will release around 90 genome sequences of marine origin soon. Furthermore, large-scale metagenomic studies focus on marine habitats, revealing a plethora of new genes and a high prokaryotic diversity (e.g. the Sargasso Sea project).

These sequencing efforts lead to the emergence of “marine ecological genomics”, defined as the application of genomic sciences to understanding the structure and function of marine ecosystems. The exponentially growing genomic data source represents a huge potential to gain more insights into marine ecosystems by exploring possible correlations between the genetic potential and the corresponding habitat for prokaryotic key-organisms.

Therefore specialised bioinformatic platforms are needed to systematically acquire, store, analyse and visualise this deluge of sequence data in the ecological context.

We present **Megx.net**, a web data portal especially designed for marine ecological genomics and metagenomics.

Megx.net includes:

- 1)** Fast and interactive **Genome browsing** of marine organisms.
- 2)** **Precomputed analyses** of environmentally relevant gene families and new group specific genes.
- 3)** A tool for the classification of metagenomic fragments based on oligonucleotides signatures.
- 4)** The “**Genomes Mapserver**”: a Geographic Information System (GIS) to store and systematically analyse (meta-) genomic data in correlation with ecological information.

These integrative databases and webserver is intended to support researchers to generate a better understanding of the functioning of marine ecosystems.

Visit us at <http://www.megx.net>