

Mini Workshop 2

Handling large genomic datasets

Conveners

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Workshop description

Sequencing algal genomes has provided a step change in our understanding as to how these globally significant organisms have evolved and adapted to the marine system. Genomes of micro- and macroalgae have been sequenced, and there are many more to come as current algal genomes only represent a minor fraction of extant algal diversity. As many algal lineages have an entangled evolutionary history and are therefore complex genomes of sometimes significant size, it is instrumental to use the most appropriate sequencing technology and genome assemblers to resolve the level of ploidy, haplotype heterozygosity and long-range contiguity. Our workshop will address the application of different sequencing technologies in the context of the complexity of algal genomes and transcriptomes from bench to bioinformatics. In addition to introducing the latest sequencing technologies including their applications and challenges, invited speakers will present case studies for the analysis of complex algal genomes and transcriptomes. A podium discussion at the end of the workshop with active participation of the audience will help to address issues of interest concerning genomic datasets from any algae.

Invited speakers:

Dr. Uwe John, Alfred-Wegner Institute, Bremerhaven, Germany

Prof. Gernot Gloeckner, University of Cologne, Germany

Dr. Gareth Pearson, Centre of Marine Sciences (CCMAR), Universidade do Algarve, Portugal

Prof. Hwan Su Yoon, Sungkyunkwan University, Korea to quantify the redox reactions of the photosynthetic electron transport chain in algae
