

Curriculum vitae for Niels Larsen

Born in Aarhus, Denmark, 1953. Danish citizenship. Address: Skt. Lucas Kirkeplads 8, 8000 Aarhus C, Denmark. E-mail: niels@genomics.dk.

Education and Employments

- 1973-78: Bachelors degree of Biology at University of Aarhus.
- 1979-83: Travel and extra-curricular activities.
- 1984-87: Candidate of Science (Cand. scient.) from Professor Roger A. Garrett's laboratory, Institute of Chemistry, Aarhus University. The thesis "Automated phylogenetic and structural analysis of RNA" exposed the first long-range contacts within rRNA.
- 1987-90: PhD of Science (Lic. scient.) from Professor Jens Nyborg's laboratory of protein crystallography, Institute of Chemistry, Aarhus University. Improved comparative methods were created and used on a wider range of RNA molecules, resulting in structure models that have been verified experimentally.
- 1991-93: Developed ribosome databases and services at Department of Microbiology, University of Illinois, Urbana, U.S.A. in collaboration with Professor Carl Woese (discoverer of the Archaea), funded by a two-year grant from the Danish Natural Sciences Research Council.
- 1991-95: Post-doctoral position in the laboratory of Professor Carl Woese.
- 1995-98: Visiting Assistant Professor at Center for Microbial Ecology at Michigan State University. Further analyses services were developed to assist microbe detection and classification.
- 1998-02: Software development leader at Integrated Genomics Inc, Chicago, U.S.A. Responsibilities included customer relations and development of web-based user interfaces for the company's genome integration platform (the most comprehensive then in existence.)
- 2003-04: Associate Professor at Bioinformatics Research Center, Aarhus University, Denmark.
- 2005: Initiated Danish Genome Institute, a consulting firm (<http://genomics.dk>). Part-time employment at University of Chicago.
- 2006-: Part-time employment at Institute of Molecular Biology, Aarhus University. Web-based clients are being developed to provide overviews of non-coding RNAs, high-throughput sequence data, and expression experiments.

Experience and Training

Since 1984 I have created tools for comparative RNA analysis, general sequence analysis, tree analysis, database curation/searches, image analysis, secondary structure model building, genomic assembly and large-scale genome integration analysis. Between 1998 and 2002 my roles were production programming, management, customer service and courses. Since 2005, the "BION" package has been developed into a freely available analysis platform. It integrates select public packages, automates certain common tasks and contains partial viewer support for future genomes and high-throughput data.

Publications

I have written or contributed to 58 publications in peer-reviewed journals. H- and G-indices are 30 and 81 respectively, as calculated by the scHolar index (<http://interaction.lille.inria.fr>). I have been invited speaker within Denmark and at many scientific meetings abroad.

Biology interests

Presentation and navigation of molecular biology and molecular medicine data can be made much simpler and more scalable, so users will not drown in unwanted detail. I have ideas for better RNA structure prediction and other areas in need of improvement, and are generally interested in the future and all new technologies that benefit the public. Current focus is on improving microbiome analysis methods.