Aarhus Genome Center - *i*SEQ lunch seminar series on Precision Medicine

Thursday 13 September 2018 at 12.00 – 13.15

Andrew G. Clark
Professor of Population Genetics, Cornell University, USA.

Talk:
Polymorphism and Divergence of Heterochromatin

Abstract:
Densely compacted, gene-poor heterochromatic regions of genomes have received relatively scant attention by evolutionary genomicists, in part because of the challenge of assembling these regions of the genome. Using a simple kmer-based approach on raw sequence reads, we have been able to draw inferences about many aspects of both the diversity and evolutionary turnover of heterochromatic sequences. This includes quantitative assessment of mutation rates (both copy number and sequence) based on mutation-accumulation experiments in Daphnia, Chlamydomonas, flies and mice. PacBio and other long-read technologies are also yielding insights about heterochromatin evolution, especially at euchromatin-heterochromatin boundaries. Several studies have shown that the total amount of heterochromatin in a genome impacts chromatin state genome-wide, and we have shown that the composition of the heterochromatin also has target-specific impacts on gene expression. These trans-acting impacts of heterochromatin can potentially have considerable adaptive consequences for the species, imposing relatively strong selection on this component of the genome formerly dismissed as junk. A comprehensive model of the way that mutational processes are balanced by selection acting on functional attributes of heterochromatin still eludes us, but progress in identification of key components of such a model has been accelerating.

Biosketch:
Andy is the Jacob Gould Schurman Professor of Population Genetics in the Department of Molecular Biology and Genetics and a Nancy and Peter Meinig Family Investigator. He received a B.S. in Biology and Applied Mathematics at Brown University in 1976, and a Ph.D. in Population Genetics at Stanford University in 1980. He did postdoctoral work at Arizona State University and the University of Aarhus, Denmark, and a sabbatical at the University of California at Davis. Prior to joining the Cornell faculty in 2002, he was a professor in the Department of Biology at Penn State University.

Dr. Clark's research focuses on the genetic basis of adaptive variation in natural populations, with emphasis on quantitative modeling of phenotypes as networks of interacting genes. Dr. Clark has been active in

genomics research and has been a frequent consultant with Celera Genomics since April 1999. He was elected Fellow of the American Association for the Advancement of Science in 1994, and serves on review panels for the NIH, NSF, and the Max Planck Society. In May of 2012, Dr. Clark was elected to the National Academy of Science.

Dr. Clark has been working on methods for statistical inference of population genetic attributes of population samples since obtaining his PhD at Stanford in 1980. He has published more than 360 peer-reviewed papers in the field of population genetics, and is co-author with Dan Hartl of Principles of Population Genetics. His work is split between efforts in human and Drosophila empirical population genetics, with an emphasis on computationally challenging statistical methods, and on theoretical population genetics, including large simulation studies. He has contributed to the inference of haplotype phase from population genetic samples, to inference of natural selection from genome-wide data, and to inference of past demography from sample genotype data. Many projects have a common theme of relating variation and genotypic and phenotypic levels, which integrates understanding of gene regulatory networks and modern genome-wide approaches to quantitative genetics.

Venue:

Merete Barker Auditory, The Lakeside Theatres, Aarhus University, Bartholins Allé 3, 8000 Aarhus C.

Refreshments:

Sandwiches will be served right before the talk, at 12 o'clock, and the talk starts at 12.15.
Therefore, please email Anne Hedemand (anne@biomed.au.dk) no later than 11 September 2018, if you would like to participate.