

Software tools for genome analysis: The development of software for epigenome research using Bisulfite sequencing

A new PhD project from Health, Aarhus University, presents software tools for genome analysis. The project was carried out by Shengjie Gao, a bioinformatician also associate to BGI, China, who is defending his dissertation on 14 December 2016.

Bisulfite sequencing is a widely used method to investigate the role of DNA methylation in regulating gene expression and cellular difference. Massive amount of genome sequencing data is generated by this method, which poses significant challenges for advanced methods and tools that require domain specific knowledge. In this dissertation, Shengjie Gao proposes novel methods for methylation analysis using bisulfite genomic sequencing. The design and implementation of the corresponding softwares is also presented, which makes it possible to handle and analyse massive amount of bisulfite sequencing data to identify mutations and integrated vira. The softwares are available open source and the evaluations show that they are highly efficient and scale well on high-performance computing platforms. The defence is open to the university public, which take place at 13:00 on December 14, 2016 in the Lecture Theatre 1241-211 ("Læsesalen" in the Bartholin Building), Aarhus University, 8000 Aarhus C. The title of the dissertation is "The development of software for epigenome research using bisulfite sequencing". For more information, please contact PhD student Shengjie Gao at +45 71290195.