



Seminar Series in Statistics and Data Science

08.12.2020, 14:15 @ Erling Sverdrups plass, Niels H. Abels hus, 8th floor
@ Zoom (ID: 664 6837 7366, Passcode: 138017)

William R. P. Denault: Detecting differentially methylated regions using a fast wavelet-based approach to functional association analysis

Abstract: We present here a computational shortcut to improve a powerful wavelet-based method by Shim and Stephens (2015) called WaveQTL that was originally designed to identify DNase I hypersensitivity quantitative trait loci (dsQTL). WaveQTL relies on permutations to evaluate the significance of an association. To boost computational speed, we applied a recent method by Zhou and Guan (2017) for calculating the distribution of Bayes factors, which allowed the significance of an association to be estimated by simulations rather than permutations. We called this simulation-based approach “fast functional wavelet” (FFW), and tested it on a publicly available DNA methylation (DNAm) dataset on colorectal cancer. Our simulations confirmed a substantial gain in computational speed compared to the permutation-based approach in WaveQTL. Furthermore, we show that FFW controls the type I error satisfactorily and has good power for detecting differentially methylated regions. Our approach has broad utility and can be applied to detect associations between different types of functions and phenotypes.



William R. P. Denault

Norwegian Institute of Public Health

William R. P. Denault is a Ph.D. candidate at the University of Bergen, his work focuses on apply wavelet-based approaches for loci identification in genome-wide genotype data. William has an M.Sc in Statistics from the University of Strasbourg (FRA).

Next seminar

This is the last seminar of the year . . .
... so long and thanks for all the fish

Contact Information

Riccardo De Bin – debin@math.uio.no
Riccardo Parviero – riccarpa@math.uio.no