ΟΙΚΟΝΟΜΙΚΟ ΠΑΝΕΠΙΣΤΗΜΙΟ ΑΘΗΝΩΝ
ATHENS UNIVERSITY OF ECONOMICS AND BUSINESS

ΣΧΟΛΗ ΕΠΙΣΤΗΜΩΝ & ΤΕΧΝΟΛΟΓΙΑΣ ΤΗΣ ΠΛΗΡΟΦΟΡΙΑΣ
SCHOOL OF INFORMATION SCIENCES & TECHNOLOGY

ΤΜΗΜΑ ΣΤΑΤΙΣΤΙΚΗΣ
DEPARTMENT OF STATISTICS

ΚΥΚΛΟΣ ΣΕΜΙΝΑΡΙΩΝ ΣΤΑΤΙΣΤΙΚΗΣ ΟΚΤΩΒΡΙΟΣ – ΔΕΚΕΜΒΡΙΟΣ 2014

Brunilda Balliu
Department of Medical Statistics
Leiden University Medical Centre

A Retrospective Likelihood Approach for Efficient Integration of Multiple Omics Factors in Case-Control Association Studies

ΤΕΤΑΡΤΗ 22/10/2014
15:00 – 16:00

ΑΙΘΟΥΣΑ 607, 6ος ΟΡΟΦΟΣ,
ΚΤΙΡΙΟ ΜΕΤΑΠΤΥΧΙΑΚΩΝ ΣΠΟΥΔΩΝ
(ΕΥΕΛΠΙΔΩΝ & ΛΕΥΚΑΔΟΣ)

ΠΕΡΙΛΗΨΗ (ΣΤΑ ΑΓΓΛΙΚΑ)

Integrative omics, the joint analysis of outcome and multiple types of omics data, such as genomics, epigenomics and transcriptomics data, constitute a promising approach for powerful and biologically relevant association studies. These studies often employ a case-control design, and often include non-omics covariates, such as age and gender, that may modify the underlying omics risk factors. An open question is how to best integrate multiple omics and non-omics information to maximize statistical power in case-control studies that ascertain individuals based on the phenotype. Recent works on integrative omics have used prospective approaches, modeling case-control status conditional on omics and non-omics risk factors. Compared to univariate approaches, jointly analyzing multiple risk factors with a prospective approach increases power in non-ascertained cohorts. However, these prospective approaches often lose power in case-control studies. In this article, we propose a novel statistical method for integrating multiple omics and non-omics factors in case-control association studies. Our method is based on a retrospective likelihood function that models the joint distribution of omics and non-omics factors conditional on case-control status. The new method provides accurate control of Type I error rate and has increased efficiency over prospective approaches in both simulated and real data.

AUEB STATISTICS SEMINAR SERIES OCTOBER– DECEMBER 2014

Brunilda Balliu
Department of Medical Statistics,
Leiden University Medical Centre

A Retrospective Likelihood Approach for Efficient Integration of Multiple Omics Factors in Case-Control Association Studies

Wednesday 22/10/2014
15:00 – 16:00

ROOM 607, 6th FLOOR,
POSTGRADUATE STUDIES BUILDING
(EVELPIDON & LEFKADOS)

ABSTRACT

Integrative omics, the joint analysis of outcome and multiple types of omics data, such as genomics, epigenomics and transcriptomics data, constitute a promising approach for powerful and biologically relevant association studies. These studies often employ a case-control design, and often include non-omics covariates, such as age and gender, that may modify the underlying omics risk factors. An open question is how to best integrate multiple omics and non-omics information to maximize statistical power in case-control studies that ascertain individuals based on the phenotype. Recent works on integrative omics have used prospective approaches, modeling case-control status conditional on omics and non-omics risk factors. Compared to univariate approaches, jointly analyzing multiple risk factors with a prospective approach increases power in non-ascertained cohorts. However, these prospective approaches often lose power in case-control studies. In this article, we propose a novel statistical method for integrating multiple omics and non-omics factors in case-control association studies. Our method is based on a retrospective likelihood function that models the joint distribution of omics and non-omics factors conditional on case-control status. The new method provides accurate control of Type I error rate and has increased efficiency over prospective approaches in both simulated and real data.