Luca Tardella

Dipartimento di Scienze Statistiche – Sapienza Universita di Roma (Italy)

A novel Bayesian mixture of Poisson estimation for expressed sequence tag sampling

ΤΕΤΑΡΤΗ 27/1/2016
13:00

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

ΠΕΡΙΛΗΨΗ

Expressed sequence tag (EST) clustering is a process that identifies and assembles ESTs which correspond to the same gene. A cDNA library can be sampled and the number of tags observed from each distinct gene are often summarized in terms of a gene cluster profile $(n_1, ... ,n_j, ... n_T)$ where n_j represents the number of genes that had j ESTs in the sample. This profile has been used for gene capture prediction and overlap estimation in EST sequencing based on the appropriate modelling of the so-called frequency of frequencies (Susko, E. and Roger, A.J., 2004; Wang et al. 2005). We focus on the estimation of the unobserved expressed genes and we propose a novel moment-based flexible Bayesian approach comparing the new estimator with those already available and we discuss computational and inferential challenges.

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Wednesday 27/1/2016
15:00 – 17:00

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

ABSTRACT

Expressed sequence tag (EST) clustering is a process that identifies and assembles ESTs which correspond to the same gene. A cDNA library can be sampled and the number of tags observed from each distinct gene are often summarized in terms of a gene cluster profile $(n_1, ... ,n_j, ... n_T)$ where n_j represents the number of genes that had j ESTs in the sample. This profile has been used for gene capture prediction and overlap estimation in EST sequencing based on the appropriate modelling of the so-called frequency of frequencies (Susko, E. and Roger, A.J., 2004; Wang et al. 2005). We focus on the estimation of the unobserved expressed genes and we propose a novel moment-based flexible Bayesian approach comparing the new estimator with those already available and we discuss computational and inferential challenges.