

Σεμινάριο Διαχείρισης και Επεξεργασίας Πληροφοριών

Τμήμα Πληροφορικής, Οικονομικό Πανεπιστήμιο Αθηνών

Τίτλος ομιλίας: "Auxiliary Counting Variables for Optimal Decoding in Hidden Markov Models with Applications to Cancer Genomics"

Ομιλητής: Μιχάλης Τίτσιας (Τμήμα Πληροφορικής, ΟΠΑ)

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Ωρα: 13:00-14:00

Αίθουσα: Α41 (πτέρυγα Αντωνιάδου, κεντρικά κτίρια ΟΠΑ Πατησίων, 4ος όροφος)

Περίληψη:

Hidden Markov Models (HMMs) are one of the most popular methods for sequence analysis in statistics and signal processing including genetics and genomics where they have found widespread use. However, posterior summaries of dependencies found from modelling are poorly developed. Motivated by applications in cancer genomics we present new computational algorithms that can reveal interesting structure in the data. In particular we present a linear time method for deriving the most probable hidden state sequence conditional on a user defined number of state-transitions, possibly of a particular type. This provides optimal K-segment partitioning of the data. The methods, while developed for applications in cancer genomics, are generic and importantly can be applied retrospectively to HMMs already fitted to data.

Λίγα λόγια για τον ομιλητή:

Michalis Titsias received a Diploma in Informatics from the University of Ioannina, Greece, in 1999, an MSc degree also from the University of Ioannina, in 2001, and a PhD degree from the School of Informatics, University of Edinburgh, in 2005. From October 2007 to July 2011, he worked as a research associate in the machine learning and optimization research group at the School of Computer Science of the University of Manchester, while from November 2011 to September 2012 he worked as a postdoctoral research scientist in statistical cancer genomics at the Wellcome Trust Centre for Human Genetics and the Department of Statistics at the University of Oxford. Starting from 2012, he is a Lecturer in the Department of Informatics of the Athens University of Economics and Business. His research interests include applied Bayesian statistics, machine learning, bioinformatics and statistical cancer genomics.

Σας προσκαλούμε να παρακολουθήσετε την ομιλία. Η αίθουσα Α41 βρίσκεται στο ίδιο κτίριο και όροφο με το Εργαστήριο Επεξεργασίας Πληροφοριών (βλ. http://nlp.cs.aueb.gr/contact_gr.html), αλλά *δεξιά* βγαίνοντας από τους ανελκυστήρες. Περισσότερες πληροφορίες για το σεμινάριο θα βρείτε στη διεύθυνση: <http://sdep.cs.aueb.gr/>