# BioSys/BioISI Research Seminar

**Construction of robust human gene coexpression networks based on transcriptomic analysis and mapping of gene evolutionary age and functional modules.**

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Human genome-wide expression data from a large set of normal-healthy tissues is used to build a confident human gene co-expression network avoiding both pathological and technical noise. We combine several computational strategies to achieve robust normalization, expression signal and correlation calculations with estimation of the statistical accuracy and coverage of the data. The human gene co-expression network built maps the links and proximity between genes based in their transcriptomic profiles and allows the identification of many biological modules, as well as the recognition of "housekeeping" and "tissue-enriched" genes. We also present a combined analysis of the global human gene expression profiling with human protein time-scale ancestry mapping that allow us to reveal 8 evolutionary major steps, considered as "evolutionary hallmarks" of the human genes. In this way, we are also able of presenting the estimated age of the human genes placing them in a functionally enriched gene network.

**Date: 27 May 2016 – 11h00**

Faculdade de Ciências da UL, Lisboa (Portugal), Building C8 – room 8.2.39