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Co-expression analyses of RNA-seq data in practice with the R/Bioconductor package coseq

vendredi 22 juin 2018 16:15 (45 minutes)

In this talk, I will present some of the features of the R/Bioconductor package coseq, which provides a straight-forward wrapper to identify groups of co-expressed genes from RNA sequencing data using Poisson mixture models (Rau et al., 2015), Gaussian mixture models (Rau et al., 2017), or the K-means algorithm (Godichon-Baggioni et al., 2018) in conjunction with appropriately chosen data transformations. In particular, I will focus on our efforts to facilitate use of coseq within standard RNA-seq analysis pipelines. I will also highlight some successful recent biological applications of coseq at INRA in a variety of organisms, including the chicken (Endale Ahanda et al., 2014), tomato (Sauvage et al., 2017), and a parasite of the honeybee (Mondet et al., 2018). Finally, I will briefly discuss some of our recent efforts to integratively make use of multiple data views (i.e., biological levels of molecular information) to identify biologically relevant and interpretable clusters from multi-omics data.

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