

# Abstract

## English

Cell differentiation is often regulated by some key players (transcription factors) activating specific genes being mainly responsible for the formation of the respective phenotype. Public available gene expression data on early myogenesis and prediction of regulatory sequences (potential transcription factor binding sites) were used to gain insights into the regulatory process of muscle cell development. Several methods based on different mathematical background were applied to integrate this two types of data: over representation analysis of transcription factor binding sites of co-expressed genes, binding association with sorted expression (BASE) and network component analysis (NCA). A combined strategy for these three methods applied on the same underlying data led to already known transcription factors like MyoD and the MEF family playing a key role in myogenesis. Some transcription factors were identified previously not associated with the myogenesis process.

**Keywords:** Myogenesis, gene expression, transcriptional regulation, network component analysis, binding association with sorted expression.