



## Using the *attract* method to identify core pathways in juvenile idiopathic arthritis

J.S. Li<sup>1</sup>, X.L. Gao<sup>2</sup>, Y.R. Liu<sup>3</sup> and Y. Dong<sup>4</sup>

<sup>1</sup>Department of Rheumatology and Immunology, Binzhou People's Hospital, Binzhou, Shandong Province, China

<sup>2</sup>Department of Endocrinology, Binzhou People's Hospital, Binzhou, Shandong Province, China

<sup>3</sup>Department of Central Sterile Supply, Binzhou People's Hospital, Binzhou, Shandong Province, China

<sup>4</sup>Pathogenic Biology and Immunology Laboratory, Basic Medical College, Mudanjiang Medical University, Mudanjiang, Heilongjiang Province, China

Corresponding author: Y. Dong

E-mail: dongyanmudanjiang@163.com

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**ABSTRACT.** The aim of this study was to identify core pathways associated with juvenile idiopathic arthritis (JIA) using the *attract* method. Kyoto Encyclopedia of Genes and Genomes pathways were determined using the GSEA-ANOVA method, based on the gene expression data of JIA. Syn-expression groups within core attractor pathways were identified by hierarchical clustering. Correlated sets of genes exhibiting highly similar profiles to the syn-expression groups were identified and each correlated set was subjected to a gene ontology functional enrichment analysis to discover potentially shared biological themes. Based on a false-discovery rate < 0.05, we identified 11 significant pathways were identified as potential attractors. Flag genes

or uninformative genes were removed and 5 discriminative pathways: the proteasome, ribosome, protein export, spliceosome, and Parkinson's disease pathways were identified. A final set of syn-expression groups with a consistent trend of relative expression of pathway-related genes was obtained; that is, the proteasome, ribosome, protein export, spliceosome, and Parkinson's disease pathways were composed of 2, 2, 1, 2, and 3 clusters, respectively. Genes in each correlated set shared common roles, and changes at the pathway level were more likely to be real. In light of these, the *attract* method was able to on expand important context to find distinguishing expression patterns within pathways. This paper predicted that the functional themes involved in protein synthesis (such as proteasome, ribosome, spliceosome) were closely related to the progression of JIA, which might contribute to the detection of therapy target for JIA.

**Key words:** Juvenile idiopathic arthritis; *Attract*; Syn-expression group; Gene ontology