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Prioritization of pathologies based on the analysis of gene networks of various macrophage phenotypes using ANDSystem

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Motivation and Aim: Macrophages (immune system cells) are the central control element of immune responses [1]. Depending on the stimulus received, the plasticity of the macrophage response leads it to a pro-inflammatory phenotype (M1) or to one of the anti-inflammatory phenotypes of the M2 group, which promote wound healing and tissue regeneration [2]. In publications, there are observations about the relationship of M1 or M2 macrophages phenotypes with certain pathologies, or the relationship of the outcome of the disease with a certain macrophages phenotype. Understanding of the molecular genetic processes that ensure the plasticity of the macrophages can make it possible to control their functions.

Methods and Algorithms: Automatic analysis of a large amount of scientific data (published articles and factual databases information) was carried out by using of the ANDSystem system, which contains the ANDVisio program for visualization and analysis of gene networks [3]. ANDSystem software tools was also used to search for associated biological processes and pathologies, and their further prioritization. Cluster analysis of biological processes and pathologies ontologies was carried out by using the MCL method [4], with using Wang's measure of semantic similarity of biological processes [5].

Results: We have reconstructed the gene networks of five macrophage phenotypes (M1, M2a, M2b, M2c, M2d). The gene networks were based on groups of genes and proteins, the expression of which is significantly increased in the studied macrophage phenotypes according to published experimental data. Relationships between objects are reconstructed based on automatic analysis of texts and database contents. The search for associations of gene networks of M1, M2a, M2b, M2c, M2d macrophages with biological processes and their subsequent prioritization was carried out, the most significant ones for each macrophage phenotype were identified. The next step was to identify pathologies associated with different macrophage phenotypes using the built-in ANDSystem tools and prioritize them with the identification of the most typical macrophages for each phenotype.

Conclusion: The identified biological processes and pathologies that are specific for different macrophage phenotypes can complete the understanding of the causes and consequences of the experimentally shown facts of their relationships.

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