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The Classification of the Gene Expression Profiles in Brain Tumour

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High heterogeneity and multiplicity of glioma development pathways require the discovery of new molecular markers and identification of new targets for effective therapies that are directed against the unique molecular aberrations within a patient's tumour. Identification of gene-expression signatures, which represent characteristic expression patterns of groups of genes that are associated with specific tumour traits, favours this problem. Data clusterization of 20 genes was performed by self-organized Kohonen's map (SOM) [1]. As a result, we've obtained a trained map, on which gene expression profiles corresponding to different kinds of tumour (glioblastomas, anaplastic astrocytomas, diffuse astrocytomas, pilocytic astrocytomas) and normal brain were grouped in different regions. The most pronounced were regions corresponding to normal tissue and the WHO grade I tumour (pilocytic astrocytoma).

[1] T. Kohonen, *Self-Organizing Maps*, Springer, Berlin, Heidelberg, 1995.