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Application of self-organizing maps
to description of relationship
between amino acid composition of proteins
and ecological properties of microorganisms

We have tested usefulness of Self-Organizing Maps (SOM) in classification of proteins coming from different prokaryotic taxa. The final neural network was carefully selected based on three criteria: Bayesian Information Criterion, topological error, and spatial autocorrelation. The carried out analyses showed a clear relationship between amino acid composition of proteins and the environment in which live the studied species. Interesting differences were observed in the composition of domain and non-domain regions as well as proteins classified to various functional groups. The obtained results indicate that SOM can be successfully applied in analyses of huge sequence data sets.