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Modern Methods of Intelligent Multidimensional Data Analysis in Smart Agro Tasks: From Classical Clustering to Hierarchical MST-Taxonomy of Crop Stress Tolerance

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Abstract: The article presents an analytical review of the development of graph-theoretic algorithms and their application in digital agriculture (Smart Agriculture). The evolution of methods from classical clustering (K-Means) to algorithms for the decomposition of Minimum Spanning Trees (MST) is considered. Based on the analysis of global research, a scientific gap in existing approaches related to the static nature of threshold graph division criteria is substantiated. The concept of Eshankulov's hybrid algorithm is proposed, which utilizes a dynamic recursive recalculation of local subtree metrics to construct a multi-class taxonomy of crop stress tolerance under soil and environmental stress conditions.
Keywords: Smart Agriculture, agrobioinformatics, Minimum Spanning Tree, Zahn's algorithm, Eshankulov's algorithm, dynamic threshold, recursive decomposition, soil salinity.

Introduction and Relevance of the Topic

The modern stage of development of the agricultural sector of the Republic of Uzbekistan requires the active implementation of 'Smart Agriculture' technologies. One of the key tasks of agrobioinformatics is the automatic classification and zoning of monitored field plots based on their degree of stress tolerance to soil salinity and moisture deficit. The solution to this problem is complicated by the high dimensionality, non-linearity, and mutual overlap of agro-ecological factors, which renders classical data grouping methods ineffective.

Evolution of MST Theory: Founding Scholars and Classical Algorithms

At the heart of intelligent data analysis using graph theory lie fundamental mathematical works on the optimization of discrete structures. Historically, the first solution to the problem of constructing a Minimum Spanning Tree (MST) was Otakar Borůvka's algorithm [1], originally developed to optimize the electrical grid of Moravia. The further development of topological search is tightly linked to the works of V. Jarník [2] and R. Prim [3], who proposed the canonical algorithm for the sequential search for shortest connections, as well as J. Kruskal [4], who implemented the 'greedy' method of sorting graph edges by their weights (distances). In modern cybernetics and computer science, the Prim-Jarník algorithm serves as a reliable mathematical foundation for constructing a primary connected graph from multidimensional matrices of agro-ecological characteristics.

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Transition to Taxonomy: Zahn's Algorithm

The first conceptual transition from transport logistics problems to pattern recognition and data taxonomy was accomplished by Charles Zahn in 1971 [5]. Zahn introduced a method for the decomposition (cutting) of an MST graph by automatically removing "inconsistent edges".

However, Zahn's algorithm relies on a global static threshold criterion: an edge is recognized as critical if its weight significantly exceeds the mean value (μ) of the weights of neighboring edges across the entire graph. Global experience in applying this approach has demonstrated that under complex, overlapping environmental factors (such as the simultaneous influence of soil salinity, nitrogen NPK fertilizer doses, and moisture), Zahn's static threshold leads to the loss of fine internal data structures, causing flat graph splitting and the degradation of the algorithm's adaptive capabilities.

Modern Global Experience in MST Application within Smart Agriculture

An analysis of recent Scopus-indexed literature shows a steady growth of interest in graph structures within agronomy. For instance, an Indo-Chinese research group (Kumar, Singh, Zhang) actively utilizes MST for processing satellite imagery of vegetation indices (NDVI) and field zoning [9]. However, in their workflows, MST is applied only at the preliminary visualization stage, while the final data separation is delegated to the K-Means algorithm. K-Means groups data into coarse geometric hyperspheres and entirely ignores the hierarchical relationships between soil parameters and crop yield quality.

European schools of bioinformatics apply traditional hierarchical clustering to analyze the genetic diversity of crops (cotton, wheat) under salt stress [10,11]. Nevertheless, existing algorithms (AGNES, DIANA) face extremely high computational complexity when scaling data matrices and do not allow flexible real-time adjustment of threshold parameters.

Identification of the Scientific Gap and Justification of Eshankulov's Algorithm Novelty

An analysis of existing global works—from classical algorithms of Borůvka, Prim, and Kruskal to modern modifications of Zahn's method in agroecology—shows that in all known architectures of MST graph decomposition, the threshold division criteria remain static or locally restricted.

To overcome this limitation, the authors developed Eshankulov's Hybrid Algorithm. Its key distinction is the abandonment of rigid constants and the introduction of a mechanism for dynamic recursive graph decomposition with continuous recalculation of local statistical metrics of subtrees (μ_{sub}, σ_{sub}, N_{sub}) bat each iteration step:

$$\lambda^{(t)} = \mu_{sub}(t) + k \cdot \sigma_{sub}(t) \cdot \log_{10}(N_{sub}^{(t)})$$

Such a mathematical solution allows the algorithm to automatically adapt to the changing density of the graph. As the tree splits, the scaling parameter N_sub monotonically decreases, which completely eliminates the need for 'manual tuning' of numbers. This guarantees the stable identification of hidden, overlapping groups of objects—specifically, fine sub-classes of high crop stress tolerance (the 4th and 5th taxonomy blocks), which remain entirely inaccessible to classical methods [6,7,8].

Conclusion

The conducted analytical review proves the scientific validity and global novelty of the proposed Eshankulov hybrid algorithm. Transferring the mathematical core of the system from the biomedical field into the sphere of agrobioinformatics makes it possible to efficiently solve fundamental

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classification tasks of multidimensional ecological data, providing rigorous automation and protecting the results from expert subjectivity.

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