Implementasi *Hierarchical Clustering* dalam *DNA Barcoding* untuk Menentukan Taksonomi Tumbuhan

SKRIPSI

Diajukan untuk Memenuhi sebagian dari
Syarat Memperoleh Gelar Sarjana Komputer
Program Studi Ilmu Komputer

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PROGRAM STUDI ILMU KOMPUTER
FAKULTAS PENDIDIKAN MATEMATIKA DAN ILMU PENGETAHUAN ALAM
UNIVERSITAS PENDIDIKAN INDONESIA
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Implementasi *Hierarchical Clustering* dalam *DNA Barcoding* untuk Menentukan Taksonomi Tumbuhan

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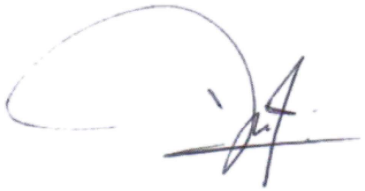
DISETUJUI DAN DISAHKAN OLEH PEMBIMBING:
Pembimbing I,



Prof. Dr. Lala Septem Riza, M.T.

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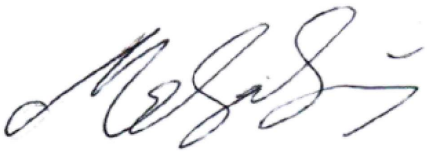
Pembimbing II,



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PERNYATAAN

Dengan ini penulis menyatakan bahwa skripsi dengan judul "Implementasi *Hierarchical Clustering* dalam *DNA Barcoding* untuk Menentukan Taksonomi Tumbuhan" ini beserta seluruh isinya adalah benar-benar karya penulis sendiri. Penulis tidak melakukan penjiplakan atau pengutipan dengan cara-cara yang tidak sesuai dengan etika ilmu yang berlaku dalam masyarakat keilmuan. Atas pernyataan ini, penulis siap menanggung risiko/sanksi apabila di kemudian hari ditemukan adanya pelanggaran etika keilmuan atau ada klaim dari pihak lain terhadap keaslian karya penulis ini.

Bandung, Agustus 2023

Yang Membuat Pernyataan,

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Implementasi *Hierarchical Clustering* dalam *DNA Barcoding* untuk Menentukan Taksonomi Tumbuhan

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ABSTRAK

Pendekatan *DNA Barcoding* telah digunakan secara luas dalam taksonomi dan filogenetik. Perbedaan dalam urutan DNA tertentu dapat membedakan dan membantu mengklasifikasikan organisme ke dalam taksa. Hal ini telah digunakan dalam kasus-kasus perselisihan taksonomi dimana pendekatan morfologi saja tidak cukup. Penelitian ini bertujuan untuk memanfaatkan *hierarchical clustering*, sebuah metode *unsupervised machine learning*, untuk menentukan dan menyelesaikan sengketa dalam taksonomi famili tumbuhan. Studi kasus *Leguminosae* secara historis ada yang mengklasifikasikan ke dalam tiga famili (*Fabaceae, Caesalpiniaceae, dan Mimosaceae*) tetapi ada juga yang mengklasifikasikan ke dalam satu famili (*Leguminosae*). Penelitian ini dibagi menjadi beberapa tahap, yaitu: (i) *data collection*, (ii) *data preprocessing*, (iii) *finding the best distance method*, and (iv) *determining disputed family*. Data yang digunakan dalam penelitian ini dikumpulkan dari beberapa sumber, termasuk *National Center for Biotechnology Information* (NCBI), jurnal, dan website. Data untuk validasi metode dikumpulkan dari NCBI dan digunakan untuk menentukan *distance method* terbaik untuk membedakan famili atau genera. Data untuk studi kasus pada kelompok *Leguminosae* dikumpulkan dari Berbagai jurnal dan *website*. Percobaan bertujuan untuk mendapatkan *distance method* terbaik yang kemudian digunakan untuk menentukan famili yang disengketakan. Ditemukan bahwa studi kasus *Leguminosae* harus dikelompokkan ke dalam satu famili berdasarkan penelitian ini.

Kata Kunci: *DNA Barcoding, Unsupervised Learning,* Bioinformatika*, Hierarchical Clustering, Machine Learning, Taxonomy, R Programming Language*

Hierarchical Clustering Implementation in DNA Barcoding for Determining Plant Taxonomy

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ABSTRACT

The DNA barcoding approach has been used extensively in taxonomy and phylogenetics. The differences in certain DNA sequences are able to differentiate and help classify organisms into taxa. This tool has been used in cases of taxonomic disputes where morphology by itself is insufficient. This research aimed to utilize hierarchical clustering, an unsupervised machine learning method, to determine and resolve disputes in plant family taxonomy. We take a case study of Leguminosae that historically some classify into three families (Fabaceae, Caesalpiniaceae, and Mimosaceae) but others classify into one family (Leguminosae). This study is divided into several phases, which are: (i) data collection, (ii) data preprocessing, (iii) finding the best distance method, and (iv) determining disputed family. The data used in this study are collected from several sources, including National Center for Biotechnology Information (NCBI), journals, and websites. The data for validation of the methods were collected from NCBI and used to determine the best distance method for differentiating families or genera. The data for the case study in the Leguminosae group was collected from journals and a website. The experiment aimed to identify the best distance method, which was then used to determine the disputed family. It was found that the Leguminosae case study should be grouped into one family based on this research.

Keywords: DNA Barcoding, Unsupervised Learning, Bioinformatics, Hierarchical Clustering, Machine Learning, Taxonomy, R Programming Language

KATA PENGANTAR

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Penyusunan skripsi ini diajukan untuk memenuhi dan melengkapi salah satu syarat untuk penyusunan skripsi yang merupakan syarat untuk mendapatkan gelar sarjana komputer atas jenjang studi S1 pada Program Studi Ilmu Komputer Fakultas Pendidikan Matematika dan Ilmu Pengetahuan Alam Universitas Pendidikan Indonesia.

Penulis menyadari bahwa dalam penyusunan skripsi ini masih terdapat banyak kekurangan dan keterbatasan yang perlu disempurnakan. Oleh karena itu, penulis sangat mengharapkan saran maupun kritik yang membangun agar tidak terjadi kesalahan yang sama di kemudian hari dan dapat meningkatkan kualitas ke tahap lebih baik.

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