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Beyond Species: Enhancing Botanical Data Integrity Using Similarity Metrics in Authorship Attribution

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Abstract Representing data extracted from text as Knowledge Graphs (KG) significantly enhances information analysis. In criminal investigations of financial fraud and money laundering, graphs provide essential visualizations for understanding relationships between investigated entities. However, due to the increasing volume of data, manually preparing these structures has become an arduous and costly task. Recent advances in Artificial Intelligence and the availability of open-access Large Language Models (LLMs) offer a viable alternative for automated graph construction from unstructured data. Nevertheless, the limited context window of open-source LLMs poses a challenge when processing large documents, necessitating text segmentation before the data is processed by the model. This paper proposes *OpenPDFGraph*, a framework that integrates open-access LLMs, PDF documents, open CNPJ databases, and segmentation libraries from the LangChain ecosystem, combined with prompt engineering techniques. The study evaluates the LLM's performance in identifying entities and relationships across different segmentation strategies. The results indicate that text segmentation significantly improves graph construction performance, with effectiveness varying according to the specific library utilized.

Keywords: Botanical Databases, Text Similarity, International Code of Nomenclature

1 Introduction

This paper is an extended version of the work originally presented at the 39th Brazilian Symposium on Databases (SBBD 2024), titled "Optimizing Botanical Data Integrity: A Comparative Study of Text Similarity Methods", by Rios *et al.*, 2024]. The current version expands the original content, including new datasets (*Sargassaceae* and *Agaricaceae*), additional evaluations, a broader analysis of text similarity functions, and refined methodological explanations.

Taxonomy in biology seeks to name and organize biological diversity, allowing universal communication by assigning scientific names. This practice, initiated by Carl Linnaeus in the 18th century, relies on an extensive community of researchers who update taxon names and describe new species. With the rapid growth in the number of new species described annually and the expansion of herbaria globally, effective data management strategies in botanical databases have become crucial. The International Code of Nomenclature for algae, fungi, and plants (ICN) sets precise rules for indicating authorship in botanical nomenclature to ensure clarity, consistency, and traceability. Basically, these rules define the differentiation between the original authors who first described a species and those who later may reclassify the same species into a different genus, and this nomenclature is then used in scientific papers that describe the botanical species.

The need to accurately represent authorship, which indicates who first described a species and any subsequent revisions or reclassifications, complicates data entry and retrieval in botanical databases. Issues of synonymy, where multiple names exist for a single taxonomic entity due to historical revisions or taxonomic differences, further complicate database integrity. These challenges demand sophisticated similarity algorithms capable of recognizing and reconciling nuanced differences to ensure the consistency and reliability of botanical databases. Text similarity measurement algorithms play a fundamental role in identifying duplicate or erroneously cataloged records.

To some of these challenges, similarity algorithms of text similarity measurement can be applied. A text similarity measurement is a text mining approach to measure the similarity between two snippets and can consider both accounts for the semantic similarity between texts and shared semantic properties of two words Wang and Dong (2020). It plays a fundamental role in this process, providing methods for identifying duplicate or erroneously cataloged records that suggest that two strings might represent the same real-world object. Algorithms such as Levenshtein, Jaccard, Jaro-Winkler, Metaphone, N-grams, Smith-Waterman, and Fingerprinting have been widely explored in the literature for their effectiveness in detecting similarities between text strings, even in the presence of spelling errors, orthographic variations, or standard abbreviations in botanical records, according to Christen and Christen (2012) and Navarro (2001). Some studies have demonstrated the applicability of these algorithms in various biological contexts, emphasizing the importance of specific adaptations to increase their effectiveness in specialized databases (García *et al.* (2015) and Smith *et al.* (1981)). For example, the analysis of botanical collections of the *Begoniaceae* family reveals unique challenges related to nomenclature and specific temporal references of authors, requiring fine-tuning of the algorithms and similarity thresholds to accurately identify duplicates.

This study investigates the challenges posed by the ”Authors” attribute in deduplicating data within botanical databases. Our research evaluates various similarity algorithms and thresholds to address these deduplication challenges, aiming to enhance the integrity and accuracy of biological databases. We conducted an empirical evaluation of different similarity functions to identify the most effective approach for handling potential duplicates, imprecise data, and misspellings. The results show improvements in data deduplication and standardization efforts, highlighting the effectiveness of tailored similarity algorithms in managing botanical information. However, the specific challenges presented by the databases in this study remain unsolved, indicating the need for further research and differentiating our work from related studies.

This article is organized as follows: Section 1 provides an introduction to the study, outlining the research problem and objectives. Section 2 discusses ICN rules for authorship data structure. Section 3 reviews related works. Section 4 describes the methodology, divided into Overview, Preprocessing, Similarity Function, and Threshold Choice. Section 5 covers the experimental evaluation, including Datasets, Evaluation Metrics, and Results. Section 6 discusses the results and their implications. Section 8 concludes the article, summarizing the main findings and suggesting avenues for future research. Section 9 acknowledges contributions, followed by the Bibliography.

2 ICN rules to Authorship

The International Code of Nomenclature for algae, fungi, and plants (ICN) mandates precise rules for indicating authorship in botanical nomenclature, aimed at ensuring clarity, consistency, and traceability of scientific names’ origins. The ICN’s chapter VI, about citation, emphasize the rules of authorship citation, which, while crucial for maintaining nomenclatural accuracy, introduce unique challenges for botanical databases. The need to accurately represent the author’s role, indicating who first described a species and any subsequent revisions or reclassifications, complicates data entry and retrieval. Additionally, the issue of synonymy, where multiple names may exist for a single taxonomic entity due to historical revisions or differences in taxonomic opinion, further complicates the database integrity. This complexity demands sophisticated similarity algorithms capable of recognizing and reconciling such nuanced differences, presenting a significant challenge in ensuring the consistency and reliability of botanical databases.

According to Turland *et al.* (2018), these challenges underscore the importance of developing and implementing deduplication strategies that can navigate the intricacies of botanical nomenclature, taking into account the specific rules of authorship and synonymy as outlined by the ICN, to enhance the accuracy and utility of digitized biological data. However, the integration and analysis of these vast datasets face significant challenges due to duplicate or inaccurate information, especially in botanical databases, where accuracy in species identification is crucial for taxonomic, ecological, and conservation research. Efficient deduplication of these data becomes essential to ensure the reliability of information and facilitate subsequent analyses.

In ICN, there are specific codes such as ”ex” and ”&”, along with rules for authors in parentheses and authors without parentheses and/or abbreviation of author names. These rules distinguish between the original publication of a name by an author and subsequent reclassifications. This system introduces a temporal logic to the description of a species. In the botanical databases used in this work, there are examples such as ”(Brade ex L.B.Sm & R.C.SM.) E.L. Jacques & Mamede”, ”Mart ex DC.”, ”(C.DC.) L.B.Sm. & B.C.Schub.”, and ”(Klotzsch) A.DC.”. These nuances present significant deduplication and similarity challenges for data analysis.

The example of authorship shown in the Figure 1 illustrates some of the ICN authorship rules.

The ICN establishes intricate rules governing the attribution of scientific names. Authors listed outside the parentheses are those who originally published the name of the species, reflecting the original description and naming. When authors are mentioned within parentheses, it indicates that the species was originally described under a different genus and later reclassified into a new genus, with the names inside the parentheses being the original describers and the name(s) outside the parentheses being those who performed the reclassification.

Central to these rules is the differentiation between the original authors who first described a species and those who later may reclassify the same species into a different genus. Authors whose names appear outside parentheses (”E.L. Jacques and Mamede” in Figure1) are credited with the initial description and naming of the species, they are labeled as ”pioneiros” or ”validadores”. Conversely, when names are enclosed in parentheses, it signifies that the species was initially described under a different genus and has since been reclassified, with the parenthesized names belonging to the original describers and the names outside the parentheses to the reclassifiers, or ”revisores”. This nuanced approach not only maintains the historical integrity of species classification but also introduces a layer of complexity in the management and analysis of botanical data.

Moreover, large botanical databases exhibit a variety in the format of authorship records. In some databases, in addition to the abbreviation of author names, the authors are separated by semicolons, whereas, in other instances, they are separated by commas, ”and”, ”et”, and a pipe, as in ”J.A. Jarenkow | C.F.N. Widholzer”. Additionally, two scenarios pose challenges in the preprocessing and organization of the database: 1) when multiple authors are involved, the first name is written, and the remainder is represented as ”*et al.*”, commonly used in references; and 2) when authors are part of a group, and the group’s name is written, such as ”Taxonomy field 2017/green group”.

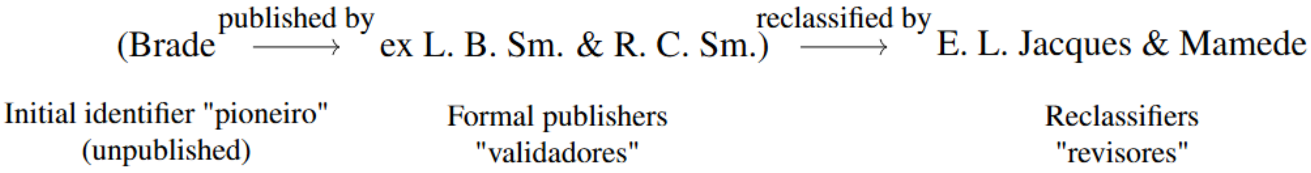


Figure 1. Authorship schema showing roles of different contributors as per ICN.

3 Related Works

This section reviews pivotal studies that leverage text similarity algorithms to address these challenges, demonstrating how they enhance data integrity and reliability in botanical databases.

Several studies focus on hybrid models and specific techniques for deduplication tasks. Gyawali *et al.* (2020) present a hybrid model combining locality-sensitive hashing (LSH) and word embeddings to identify near and exact duplicates in scholarly documents, achieving a macro F1-score of 0.90. This method is beneficial for botanical databases where precise handling of minor variations in taxonomic descriptions and author names is required.

Additionally, Liu *et al.* (2013) propose a ranking-based author disambiguation method called RankMatch, which combines string similarity and heterogeneous meta-path analysis to improve precision in large bibliographic datasets. Although not specific to botanical data, the robustness of this approach in noisy and heterogeneous contexts offers valuable insights for enhancing entity matching in biological databases with incomplete or inconsistent author entries.

Another group of studies provides comprehensive overviews and classifications of text similarity methods. Gomaa and Fahmy (2013) offer a survey categorizing text similarity methods into string-based, corpus-based, and knowledge-based approaches, highlighting their strengths and weaknesses. This survey aids in selecting effective algorithms for botanical data management, with methods such as Jaccard, Levenshtein, Jaro-Winkler, and N-grams being directly applicable to improving data deduplication and standardization efforts. Complementing this, Silva *et al.* (2019) discuss various text similarity measurement techniques and provide a classification system, offering insights into text distance and representation methods that refine algorithms used for deduplicating botanical data.

Some studies emphasize the importance of context and semantic understanding in text similarity measures. Prakoso *et al.* (2021) focus on methods for measuring similarity in short texts, crucial for managing concise botanical descriptions and author names. Their review classifies these methods into string-based, corpus-based, knowledge-based, and hybrid-based categories, supporting the refinement of text similarity algorithms for more accurate deduplication of botanical data.

Ferreira *et al.* (2012) provide a taxonomy and survey of automatic author name disambiguation methods, distinguishing between grouping and assignment-based approaches. Their insights are especially relevant for botanical databases, where disambiguating ambiguous author entries is critical for accurate species records. The discussion of similarity functions and clustering techniques contributes to understanding how to structure effective deduplication pipelines.

Additionally, tools designed for data quality and validation play a significant role in improving botanical database management. Silva *et al.* (2021) present a tool for validating and importing data into herbarium databases, addressing similar data quality issues as this study. The tool's implementation of filters and validations to check taxonomic and geographic data accuracy aligns with our goal of improving database integrity through rigorous data preprocessing and similarity checks.

Moreover, Levin and Heuser (2010) investigate the integration of social network analysis with syntactic similarity functions for author name disambiguation in digital libraries. Their findings demonstrate that relational data, such as co-authorship networks, can substantially improve the accuracy of entity resolution tasks. This perspective reinforces the potential of incorporating structural metadata when refining similarity-based matching in botanical datasets.

These studies provide a foundation for applying text similarity and matching algorithms in botanical databases, highlighting the broader implications for ensuring data accuracy and reliability. By improving data deduplication and standardization, these methodologies significantly enhance the integrity and utility of botanical information systems. Our research situates itself within this context, empirically evaluating various similarity functions to identify the most effective approaches for handling potential duplicates, imprecise data, and misspellings, thereby facilitating accurate botanical research. Nonetheless, the challenge posed by the specific databases used in this study remains unresolved, indicating an area where further work is needed and differentiating our study within the field of biological database management.

4 Author's Name Similarity Method

In the outlined methodology, as shown in the Figure 2, an initial data cleansing step is executed by discarding variables from the dataset that are comprised of 90% or more missing values. This is followed by the standardization of data types, with date columns converted to integers and all other columns to strings, which facilitates uniform data handling. A ”Missing Category” is then introduced to systematically categorize any data that remains unaccounted for, ensuring comprehensive dataset integrity.

Subsequently, the approach involves filtering '&' and 'et al.' in the author variable to apply similarity functions. Authors are categorized based on text location, considering ICN's rules. Nine different similarity functions are then applied to quantify the likeness between author names, and a customized threshold is established to determine the criteria

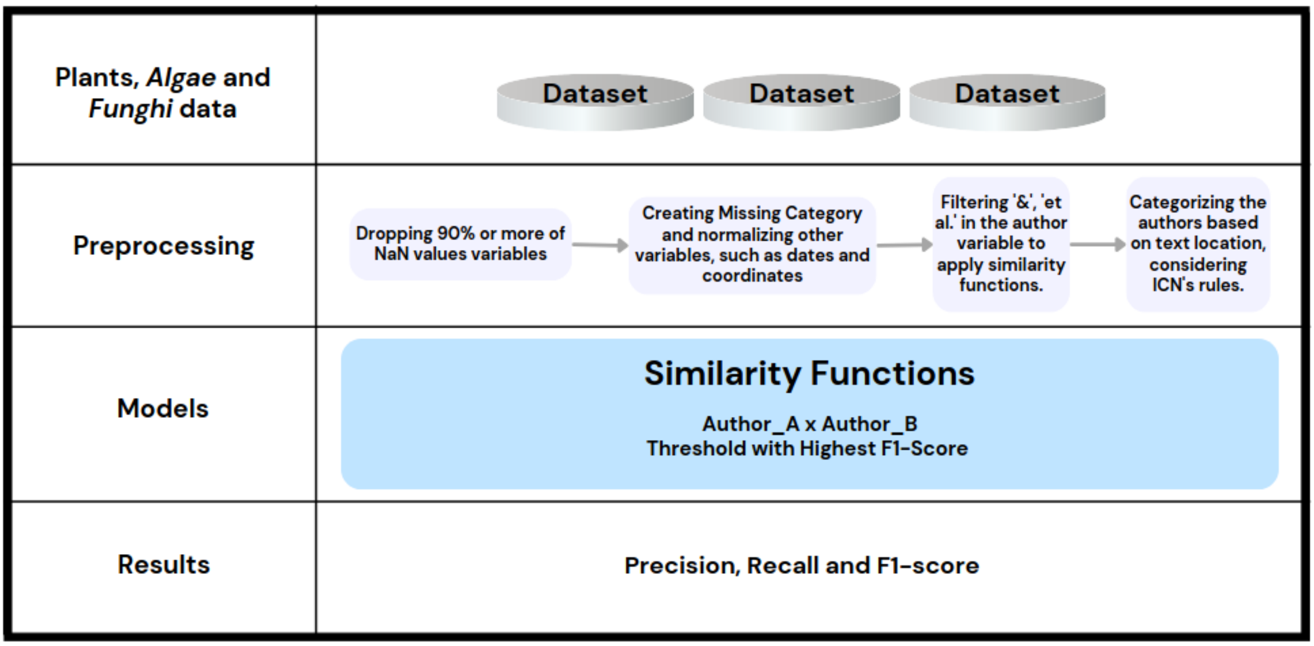

Plants, *Algae* and *Funghi* data
Dataset
Dataset
Dataset
Preprocessing
Dropping 90% or more of NaN values variables
Creating Missing Category and normalizing other variables, such as dates and coordinates
Filtering '&', 'et al.' in the author variable to apply similarity functions.
Categorizing the authors based on text location, considering ICN's rules.
Models
Similarity Functions
Author_A x Author_B
Threshold with Highest F1-Score
Results
Precision, Recall and F1-score

Figure 2. Methodology Overview

for author name grouping by setting the threshold with the highest F1-Score. The final step employs evaluation metrics to assess the efficacy of the data processing techniques.

4.1 Preprocessing

The preprocessing step aims to ensure the integrity and usability of the data for further analysis. In this work, preprocessing involves cleaning the dataset and using a recursive function to flag the authors. Variables exhibiting more than 90% NaN (Not a Number) values were systematically removed from the dataset, as their high levels of missing data would likely contribute little to meaningful analysis and could introduce bias or inaccuracies in the study's findings.

A ”missing value category” was additionally created to normalize other variables, such as dates and coordinates. This approach streamlined the dataset by focusing on variables that offer unique insights and contribute significantly to the biological data's diversity and specificity, ensuring a cleaner, more manageable dataset optimized for subsequent data analysis stages. Authors were categorized based on text location, as shown in Fig. 1, considering ICN's rules, and specific author name, as ”Collector Unspecified” or ”Taxononomia de grupo 2017/grupo verde” patterns, which don't specify the authors, were filtered and standardized to ensure consistency for applying similarity functions.

4.2 Threshold Choice

The selection of thresholds for similarity algorithms is a crucial aspect of text analysis. Thresholds define whether two entities are considered similar, thereby directly impacting the algorithm's sensitivity (recall) and specificity (precision). The optimal threshold is task-dependent, influenced by the characteristics of the dataset and the desired balance between false positives and false negatives. As discussed by Manning (2008), empirical validation plays a key role in tuning thresholds in information retrieval contexts.

In this work, threshold values were chosen based on empirical analysis. The algorithm's performance was evaluated across a range of thresholds, from 0.1 to 1.0 in increments of 0.05. This experimental approach allowed us to observe the variations in results and to identify the threshold that maximized overall performance.

The evaluation relied on precision, recall, and the F1-score to assess each configuration. Although the F1-score was the primary metric used to select the best threshold—since it balances precision and recall—reporting all three metrics ensured a more comprehensive performance analysis. In the event of a tie in F1-score across multiple thresholds, the lowest threshold among them was chosen. This strategy favors higher recall in borderline cases, aligning with our goal of minimizing false negatives when possible. To promote reproducibility and enable comparison across different applications, a structured and standardized threshold selection process was adopted. This involved defining a customized thresholding procedure and consistently applying it across all experiments.

5 Experimental evaluation

The main objective of the experiments is to evaluate different similarity functions to identify the most effective approach for handling potential duplicates for indicating authorship in botanical nomenclature as dictated by the ICN.

5.1 Setup

The experimental setup was conducted using a Lenovo Ideapad 310-15ISK notebook, equipped with an Intel Core i5-6200U processor, 8GB of RAM, a 1TB HDD, running Windows 10. The computational tasks were executed on Google

Colab, an online platform that provides access to cloud-based computing resources, allowing for the execution of Python code in a Jupyter Notebook environment. The Python libraries utilized in the experiment included ‘pandas‘ for data manipulation, ‘os‘ for operating system interactions, ‘google.colab.drive‘ for managing Google Drive connections, ‘random‘ for generating random numbers, ‘re‘ for regular expression operations, ‘seaborn‘ and ‘matplotlib.pyplot‘ for data visualization, and ‘itertools.combinations‘ for generating combinations of data elements. Notably, only two similarity functions relied on external libraries: Metaphone, utilizing the ‘metaphone‘ function, and N-grams, using the NLTK library. All other similarity functions were implemented from scratch.

5.2 The Datasets

SpeciesLink[1] is a digital platform that consolidates botanical data from various herbaria and collections across Brazil, enhancing research and conservation of Brazilian flora. It offers access to detailed records, including images, taxonomic classifications, and geographic distributions. By integrating data from multiple sources, SPLINK facilitates scientific study and promotes the visibility of Brazil’s botanical diversity to a global audience. It integrates data from various herbaria within Brazil, offering access to a wealth of information including specimen images, taxonomic classifications, geographic locations of collections, collector details, and collection dates. For this study, two botanical families, an algae family and a funghi family were used from SPLINK: *Begoniaceae*, *Bignoniaceae*, *Sargassaceae*, and *Agaricaceae*, respectively.

The data for *Begoniaceae* comprises approximately 16,900 collections, while the data for *Bignoniaceae* comprises approximately 34,900 collections. In the *Begoniaceae* dataset from SPLINK, 25% of the dataset contained variables with 90% or more NaN values, while in the *Bignoniaceae* dataset, 47.70% of the data had 90% or more NaN values. *Agaricaceae* dataset from SpeciesLink had 1356 collections with 33.6% of variables with more than 90% NaN values and *Sargassaceae* dataset from SpeciesLink, with 2280 collections and 27.27% variables with more than 90% NaN values

Brazil’s botanical data ecosystem is further enriched by the REFLORA database. REFLORA[2] is a robust initiative aimed at digitizing and disseminating historical and contemporary botanical data pertinent to Brazil’s flora. It hosts a comprehensive repository of specimens gathered from both national and international herbaria. This project plays a critical role in the recovery and digital archiving of Brazilian plant specimens, originally housed overseas. The database offers access to high-quality digital images of specimens, enhanced metadata, and vital taxonomic information. REFLORA’s platform is instrumental in supporting research by providing a centralized resource that aids in the identification and study of plant species, promoting the conservation of Brazil’s unique botanical heritage.

From REFLORA, two datasets were used: *Begoniaceae* and *Sargassaceae* families. The *Begoniaceae* dataset from REFLORA comprises approximately 1,900 collections, with 25% of the dataset containing variables with 90% or more NaN values. The *Sargassaceae* dataset from REFLORA provided 1070 collections with 25% of variables with more than 90% NaN values. The *Agaricaceae* dataset was not included in REFLORA analysis due to its very smaller size of only 63 collections and lack of deduplication issues related to the author variable.

Table 1. Top Scientific Name Authors by Frequency above 100

#	Name	Frequency
0	Willd.	1334
1	A.DC.	1085
2	Raddi	1035
3	Schrank	930
4	(Klotzsch) A.DC.	857
5	Brade	854
6	Vell.	795
7	Irmsch.	653
8	Dryand.	355
9	Link	339
10	A. DC.	309
11	Thunb.	250
12	Schott	174
13	Schott ex A.DC.	167

The International Code of Nomenclature (ICN) prescribes specific author name formatting conventions such as the use of ”ex” and ”&” to clarify authorship contributions (Table 1). The ”ex” notation is used when an author, ”validadores”, formally publishes a species name that was originally proposed by another, ”pioneiros”, often unpublished, author, thereby recognizing the contribution of both parties. The ampersand (”&”) is employed to link multiple authors who jointly published the name of a species. These rules can be applied either jointly or individually. The presence of parentheses, ”ex”, ”&”, or any other delimiter are not conditioned upon each other. This makes the process of identifying duplicates, or even text similarity, unique for this variable in this type of database. These conventions, while facilitating a more precise attribution of authorship, pose significant challenges in data deduplication efforts within botanical databases, particularly when aligning records from diverse sources.

5.3 The Ground Truth

The ground truth was established based on the 114 unique author values identified within the *Begoniaceae* speciesLink’s dataset, 48 unique author values in *Begoniaceae* REFLORA’s dataset, and 151 unique values in *Bignoniaceae* speciesLink’s dataset. This involved a manual process where, for each group of similar names, a single correct value was chosen to represent all variants. For instance, variations such as ’A. DC’ (1 dot), ’A. DC.’(2 dots), ’A.D.C.’(3 dots), and ’A.DC.’ (no space between letters) were consolidated under a singular, correct equivalent, ’A. DC’. This decision was predicated on the understanding that the aforementioned variants were not distinct entities but rather the result of typographical inconsistencies. By selecting one correct value for

[1] http://www.splink.org.br/

[2] http://www.reflora.jbrj.gov.br/

each set of similar names, the ground truth effectively rectifies these errors, serving as a critical reference for data cleaning and normalization efforts. This approach ensures that the dataset is both accurate and reliable, facilitating more precise analyses and interpretations.

Additionally, the data analysis executed during the ground truth creation revealed other challenges in the authors' list of unique values. Names such as 'Aitch.', 'Downs', 'Klotz.', 'Meisn.', and 'Moric.' do not appear as authors, reviewers, or validators in the publications describing the species. They are referenced to the International Plant Names Index (IPNI) website (https://www.ipni.org/), probably referencing plant names and indicating potential recording errors in the datasets. The value 'Hort. Berol.' was found as the author name, but is actually a botanical garden and museum in Berlin, not an author. The authors 'G.' and 'L. B.' appear in the database after processing but were absent before preprocessing, suggesting that the authors' names were separated during database preprocessing, highlighting the challenge of finding preprocessing solutions that do not result in such issues.

Lastly, two authors were mistakenly recorded under the same abbreviation 'Gomes da Silva': Ary Gomes da Silva, whom the abbreviation is 'Gomes da Silva', and is the "pioneiro" for the species *Begonia mamedeana*, and Sandra Jules Gomes da Silva, whom the abbreviation is 'S. J. Gomes da Silva', and is the "pioneiro" for species such as *Begonia salesopolensis* and *Begonia jureiensis*. However, some records incorrectly use the same abbreviation for both, an error since even authors sharing a surname should have distinct abbreviations to accurately reflect their individual contributions. After these steps, to create the ground truth, we applied the similarity functions to identify the possibilities of two values representing the same real object among the unique values for authors names.

5.4 Similarity Functions

The following algorithms were incorporated into the methodology:

1. Jaccard Similarity: The Jaccard similarity measure assesses similarity and diversity between sets by comparing the intersection of items to the union of items. It finds application in scenarios where the presence or absence of features is more pertinent than their frequency, particularly in evaluating similarity between botanical species in databases.
2. Levenshtein Distance: The Levenshtein distance, or edit distance, quantifies dissimilarity between two strings by calculating the minimum number of operations needed for transformation. It encompasses insertions, deletions, or substitutions of single characters, proving valuable for rectifying typographical errors and accommodating minor variations in names.
3. Jaro-Winkler Similarity for Names: The Jaro-Winkler similarity algorithm specializes in comparing strings, particularly names, highlighting common prefixes. It assigns higher similarity scores to strings with similar beginnings, thus improving matching and correction of name variations.
4. Metaphone or Double Metaphone: Metaphone or Double Metaphone are phonetic algorithms encoding names based on pronunciation, facilitating comparison of names with similar sounds. These algorithms handle cases where variations in spelling result in similar or identical pronunciations.
   The algorithm works by processing a word to remove non-alphabetic characters and then removes vowels except when the word begins with a vowel. The remaining consonants are processed according to specific rules that consider the pronunciation characteristics of English consonants and their typical combinations in English words. Double Metaphone creates two phonetic codes per word: a primary code for general comparisons and a secondary code used when the primary code might not uniquely identify a word.
5. N-grams: N-grams involve breaking names into sequences of contiguous letters or sounds of length 'n', capturing similarities in names by considering overlapping subsequences. It enhances the matching process by identifying structural similarities in names.
6. Smith-Waterman Similarity: The Smith-Waterman similarity algorithm, a local sequence alignment method prevalent in bioinformatics, identifies and corrects local similarities in names, accounting for sub-sequence variations.
   First, a scoring matrix is created. The dimensions of the matrix depend on the lengths of the two sequences to be compared. Each cell in the matrix represents a potential alignment between elements of the two sequences. Additionally, each cell is initially set to zero, and the algorithm also decides on penalty scores for gaps (insertions or deletions) and mismatched characters. The matrix is then filled in based on a set of scoring rules:

   The optimal local alignment ends in the cell with the highest score in the matrix. This score represents the highest scoring local alignment between the two sequences. Starting from the highest scoring cell, the algorithm traces back through the matrix to reconstruct the alignment. The trace-back follows the path of choices (diagonal, up, or left) that led to the highest score in each cell, stopping when it hits a cell with a score of zero, which signifies the start of the aligned region in the matrix. The trace-back reveals the best local alignment, showing which parts of each sequence align with each other.
7. Fingerprinting Algorithm: The Fingerprinting algorithm generates unique fingerprints for names, aiding in efficient comparison and identification of similarities. It employs binary vectors, known as molecular fingerprints, quantifying similarity using the Tanimoto coefficient, which evaluates overlap between binary vectors.

   Additionally, the union of the fingerprints is calculated by counting all bits set to '1' in either vector. The Tanimoto coefficient is then computed as the ratio of the intersection to the union. A result of 1 signifies perfect similarity, showing that the fingerprints are identical, while a score of 0 indicates no similarity, with no features in common.

The use of these diverse algorithms aimed to comprehensively address the intricacies of variations in the representation of author's names in the biological databases.

5.5 Evaluation Metrics

To measure the effectiveness of our approach, we have used the classical metrics of evaluation: accuracy, precision, recall, and F1-measure Baeza-Yates and Ribeiro-Neto (2008). These evaluation metrics play vital roles in assessing the performance of author name deduplication algorithms. Ensuring accuracy and reliability in deduplication within botanical databases, especially concerning author names following ICN rules, is crucial for maintaining scientific record integrity.

Precision measures the proportion of accurately identified duplicates among all instances classified as duplicates, indicating the true positives rate. High precision is imperative to minimize false positives, particularly in botanical databases where merging distinct author names could result in significant information loss. Recall evaluates the algorithm's capability to detect all true duplicates within the dataset. In botanical databases, high recall ensures the correct identification of all variations of an author's name, conforming to ICN rules, belonging to the same individual, notwithstanding challenges posed by diverse name formats and potential typographical errors.

The F1 score offers a harmonic mean of precision and recall, presenting a single metric that balances both the accuracy and completeness of the deduplication process. Given the equal importance of minimizing false positives (to prevent incorrect merges) and false negatives (to ensure comprehensive deduplication), the F1 score serves as a critical indicator of overall algorithm efficacy.

$$Precision = \frac{TP}{TP + FP} \tag{1}$$

$$Recall = \frac{TP}{TP + FN} \tag{2}$$

These metrics are based on the definitions by Yacouby and Axman.[3]

6 Results

Figures 5 presents the results of comparing the text similarity methods using the three botanical datasets: SPLINK for *Bignoniaceae*, SPLINK for Begoniaceae, and REFLORA for *Begoniaceae*. It shows results for precision, recall, and F1-score for each method across all three datasets: a) *Bignoniaceae* - SPLINK, b) *Begoniaceae* - SPLINK, and c) *Begoniaceae* - REFLORA.

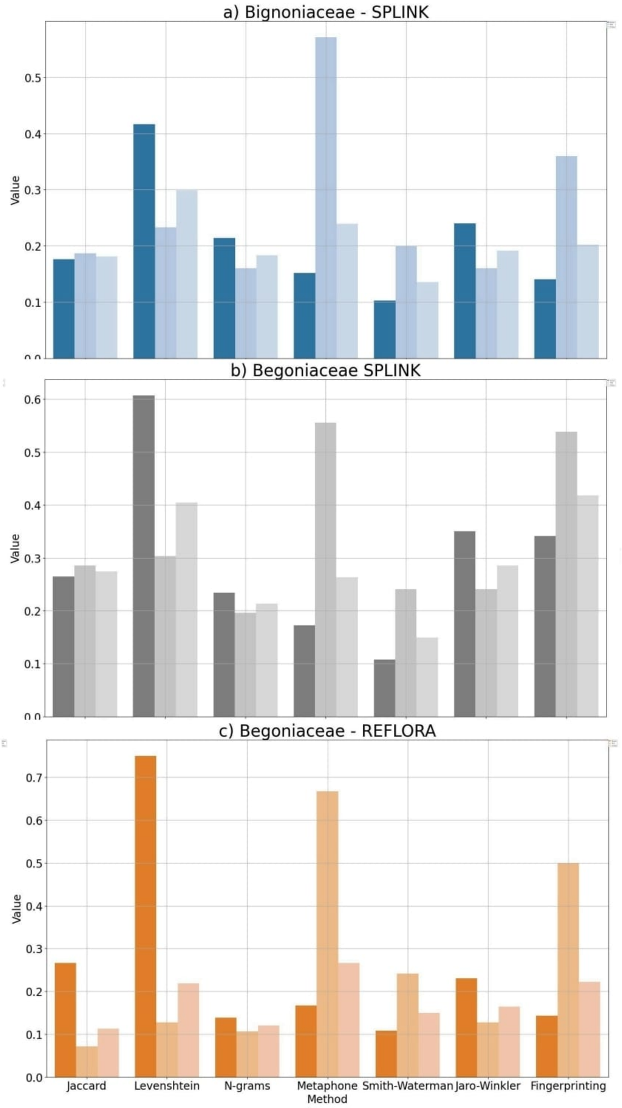
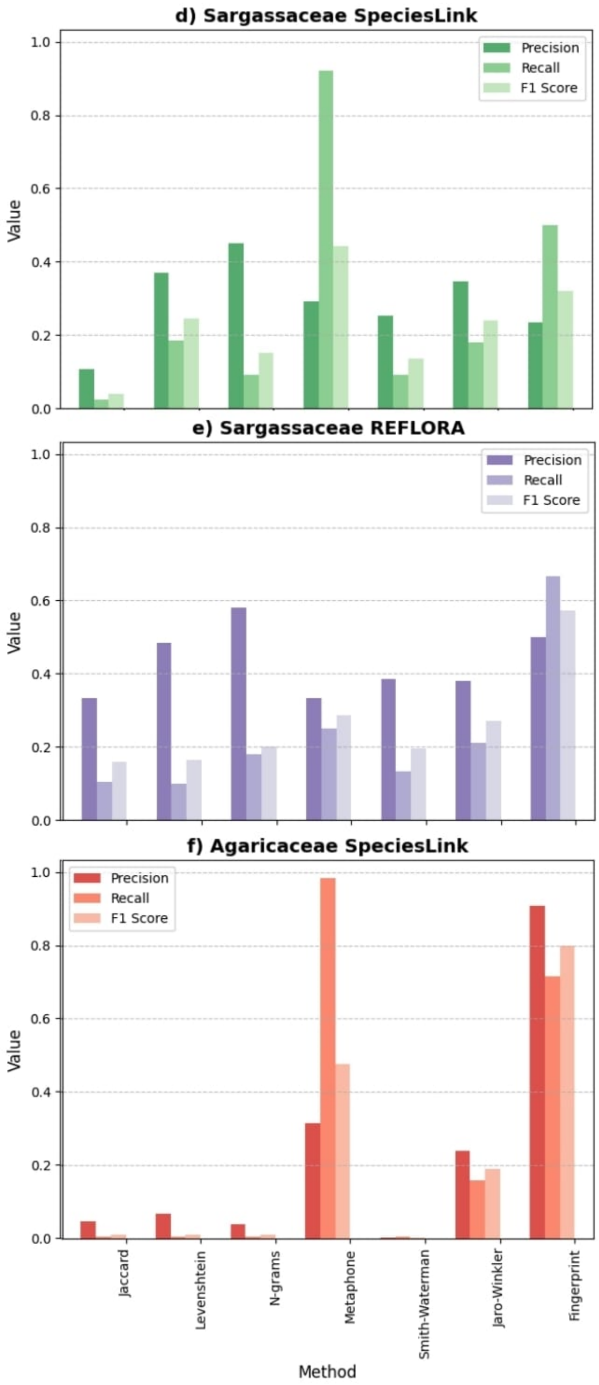


Figure 3. Comparison of text similarity methods applied to five botanical datasets. The graphs of subplots (a-f) present bar charts showing precision, recall, and F1 score for each method across the datasets.

The Levenshtein method achieved the highest precision among all methods, particularly in the *Begoniaceae* REFLORA database (Figure 5, c). However, its lower recall indicated it missed certain genuine similarities. Conversely, the Smith-Waterman method demonstrated a balanced performance with high scores in precision, recall, and F1 score across all databases (Figure 5, a, b, c), indicating robust capability in identifying true similarities while maintaining low false positives and negatives. While the Metaphone method displayed high recall across all databases, especially in *Begoniaceae* REFLORA and SPLINK (Figure 5, b, c), but its lower precision suggested a higher incidence of false positives. Similarly, the Jaccard index showed consistent performance with moderate precision and recall, leading to balanced F1 scores (Figure 5, a, b, c), while the Jaro-Winkler method had high recall but lower precision, indicating more false positives (Figure 5, a, b, c).

[3] Yacouby and Axman (2020)



Comparison of text similarity methods applied to two algae families and one fungi family. The bar charts present precision, recall, and F1-score for each dataset across the similarity functions.

For *Begoniaceae* in the SPLINK database, the Fingerprinting method achieved high precision and recall but performed lower in the REFLORA database, suggesting variability based on dataset (Figure 5, b, c). The N-grams method demonstrated moderate precision and recall, resulting in moderate F1 scores (Figure 5, a). Both Jaccard and Smith-Waterman showed high precision for *Bignoniaceae* in SPLINK, with Smith-Waterman achieving better balance (Figure 5, a). The Metaphone method's highest recall suggests it effectively identifies relevant similarities without false negatives, despite its lower precision (Figure 5, b, c). On the other hand, the Levenshtein method provided balanced performance, excelling in both precision and recall, and achieving a good F1 score (Figure 5, a, b, c). The Jaccard index was robust in precision and recall for *Bignoniaceae* in SPLINK (Figure 5, a), whereas Jaro-Winkler's high precision but lower recall indicated more false negatives (Figure 5, a, b, c).

A particular observation for the N-grams method in REFLORA (Figure 5, c) was its moderate precision and recall, highlighting the importance of dataset size and threshold settings. These results underscore the necessity of selecting appropriate text similarity methods based on the specific requirements of precision, recall, and F1 score. The Metaphone and Smith-Waterman methods demonstrated superior performance in this comparative analysis.

In addition, Fig. **??** presents the performance comparison of seven text similarity functions applied to three additional datasets: *Sargassaceae* from SpeciesLink, *Sargassaceae* from REFLORA, and *Agaricaceae* from SpeciesLink, as detailed in Section 5.2. Each similarity function was evaluated in terms of precision, recall, and F1-score.

The Fingerprinting method achieved the highest recall in *Sargassaceae* from REFLORA, while the Metaphone method exhibited the highest recall in *Sargassaceae* from SpeciesLink and *Agaricaceae* from SpeciesLink. These high recall values indicate that both methods effectively retrieve potential matches, although the expense of precision.

The Levenshtein method demonstrated high precision in *Sargassaceae* from REFLORA but suffered from low recall, indicating a conservative matching approach that minimizes false positives while potentially missing relevant matches. A similar trend was observed in *Agaricaceae* from SpeciesLink, where precision remained moderate but recall was significantly lower.

The Metaphone method achieved the highest recall in *Sargassaceae* from SpeciesLink and *Agaricaceae* from SpeciesLink, but its lower precision contributed to an increased number of false positives, reducing the overall F1-score.

The Jaccard index maintained a balanced performance with relatively moderate precision and recall across all datasets, particularly in *Sargassaceae* from REFLORA precision. The Jaro-Winkler method showed high precision in *Sargassaceae* from REFLORA (and *Agaricaceae* from SpeciesLink, but its recall values were lower, leading to a trade-off in retrieval performance.

The Smith-Waterman method exhibited relatively low recall across all datasets, except for *Sargassaceae* from REFLORA. Its precision values remained stable but did not outperform other methods significantly, this could be explained by the very small size of this additional datasets, which leads to small issues about authorship deduplication

7 Discussion

7.1 Results for *Begoniaceae* and *Bignoniaceae*

The comparative analysis of text similarity methods underscores the criticality of selecting appropriate techniques tailored to specific application needs, particularly regarding precision, recall, and F1 Score. The Metaphone method exhibited exceptional recall, achieving perfect scores in both *Begoniaceae* and *Bignoniaceae* on the SPLINK database, as well as in the REFLORA database for *Begoniaceae*. It's high recall indicates its effectiveness in capturing all potential matches, making it particularly suitable for applications where minimizing false negatives is crucial. However, its lower precision suggests a higher incidence of false positives, necessitating its combination with other methods to ensure accurate duplicate identification.

Conversely, the Levenshtein method demonstrated a balanced performance, with notable scores in precision, recall, and F1 Score, suggesting a robust capability to identify true similarities while maintaining a lower rate of false positives and negatives. Levenshtein's high precision is possibly due to its sensitivity to small differences between strings, making it particularly effective at identifying exact or near-exact matches. However, this same sensitivity can lead to lower recall, as the method may fail to capture legitimate variations in strings that represent the same entity, especially when dealing with spelling errors or alternative abbreviations.

The Jaccard index presented consistent performance across different datasets, with moderate precision and recall scores leading to balanced F1 Scores. The Jaro-Winkler method also showed relatively high precision scores in most datasets, indicating its strength in identifying accurate matches. However, its recall was lower, which may point to a higher incidence of false negatives. In the assessment of *Begoniaceae* species within the SPLINK database, the N-grams method demonstrated moderate performance with lower precision and recall scores, leading to a lower F1 score. The Fingerprinting method, while achieving high precision in both the SPLINK and REFLORA databases, had a significantly lower recall, highlighting a tendency to miss genuine similarities. It's high recall is due to Fingerprinting's ability to recognize and match a broad spectrum of similar patterns across different names. However, like Metaphone, its broad approach can result in lower precision because it may overgeneralize, grouping distinct names together based on shared features that do not necessarily indicate identical entities.

Analyzing the *Bignoniaceae* species within the SPLINK database, the Smith-Waterman method showed high precision and recall scores across all databases, achieving a harmonious balance as evidenced by its F1 score. This balance indicates its robust capability in identifying true duplicates while minimizing false positives and negatives, making it a versatile choice for various datasets and applications.

7.2 Results for *Sargassaceae* and *Agaricaceae*

An extended analysis incorporating *Sargassaceae* from SpeciesLink, *Sargassaceae* from REFLORA, and *Agaricaceae* from SpeciesLink reinforced previous trends. Metaphone achieved the highest recall in *Sargassaceae* from SpeciesLink and *Agaricaceae* from SpeciesLink, while Fingerprinting had the highest recall in *Sargassaceae* from REFLORA. However, both methods exhibited lower precision, leading to increased false positives.

Levenshtein maintained high precision in *Agaricaceae* from SpeciesLink, demonstrating its effectiveness in structured datasets, though its recall remained low. Jaccard exhibited a balanced performance, while Jaro-Winkler achieved high precision in *Sargassaceae* from SpeciesLink but suffered from low recall. Smith-Waterman showed stable performance, particularly in *Sargassaceae* from REFLORA.

Some of these issues are influenced by the small dataset sizes, which amplify variations in precision and recall across methods. The results highlight the need for adaptive thresholding and hybrid approaches. Dataset completeness influenced performance, reinforcing the role of threshold tuning. Future work should explore hybrid models and machine learning techniques to optimize text similarity in data deduplication.

The dataset-specific variations further highlight the need for adaptive thresholding and hybrid models. For example, while Fingerprinting was highly effective in recall, its lower precision suggests it may need to be combined with another method to reduce false positives. Similarly, Metaphone's high recall but lower precision reinforces its potential role in complementing other similarity metrics.

A key challenge was abbreviation inconsistencies, impacting character-based methods like Levenshtein and Jaro-Winkler, which performed well in structured datasets but struggled with irregular abbreviations. Hybrid approaches, combining phonetic and character-based metrics, could enhance deduplication accuracy. Threshold tuning was also crucial, with Smith-Waterman and Jaccard benefiting from it. Dataset completeness influenced performance, reinforcing the need for preprocessing strategies. Future work should explore hybrid models and machine learning techniques to optimize text similarity for botanical data deduplication.

These results underscore the importance of selecting appropriate text similarity methods based on the specific requirements of precision, recall, and F1 score. The superior performance of the Metaphone and Smith-Waterman methods in our comparative analysis highlights their potential as robust solutions for improving database integrity.

8 Conclusion and Future Works

This analysis of text similarity methods reveals performance variations based on precision, recall, and F1 Score metrics, underscoring the importance of selecting methods that align with specific application needs. The Smith-Waterman method emerged as a balanced and versatile choice, performing reliably across all metrics and highlighting its applicability to diverse text similarity tasks, ensuring data integrity across botanical datasets. Overall, these findings emphasize the necessity for tailored approaches in text similarity assessments. Future work will focus on developing a technique to address these challenges in the specific context of botanical databases using Large Language Model - LMM.

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