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Development of Common Names Modifier Arrangement Template Extraction Procedure

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***Abstract*—This study presents the development of a structured linguistic procedure known as the Common Name Modifier Arrangement Template Extraction Procedure. The objective is to provide a systematic method for identifying and extracting modifier arrangement templates in common names, particularly those rich in cultural and ecological knowledge. The procedure was developed using the ADDIE model, which consists of five sequential phases: Analysis, Design, Development, Implementation, and Evaluation. In the Analysis phase, the research team examined the necessity and focus areas for the procedure's development through an extensive literature review using databases such as ScienceDirect, JSTOR, Semantic Scholar, and Google Scholar. In the Design phase, the procedure was designed based on the adapted Structured Design principles of Yourdon and Constantine. The Development phase involved constructing the full procedure, integrating insights and design structures formulated in the previous stages. During the Implementation phase, the developed procedure was applied to actual linguistic data comprising Malay bird common names from the MyBIS 2024 database. In the Evaluation phase, the procedure's usability and effectiveness were assessed by six subject-matter experts. Each expert was provided with a structured open-ended questionnaire guided by Nielsen's 10 Usability Heuristics. Findings suggest that the procedure is practical, usable, and adaptable for linguistic, educational, and documentation purposes.**

***Index Terms*—common names, modifier, arrangement template, extraction procedure**

I. Introduction

The Common Names Modifier Arrangement Template Extraction Procedure is important for systematically identifying the core meanings of modifiers that describe the characteristics of the item referred to in a common name. Knowledge of these core meanings is necessary to evaluate the quality of existing names in terms of accuracy, precision,

and interpretability (Gilreath, 1993), particularly for purposes such as legislation, policy-making, conservation promotion, and educational materials. In addition, this procedure is essential for providing information on the arrangement patterns of descriptors and specifiers found in common names. This information is crucial for the development of new common names, especially for species that do not yet have a common name. This is important to ensure that the newly created common names align with the naming norms of the community and users of a language. According to Deikumah (2015), a common name that aligns with the naming norms of a language community can effectively reflect and describe an organism.

Furthermore, this procedure is important in providing information about the basic meaning of a modifier found in a common name. Understanding this basic meaning is essential for translators to determine the actual meaning of the modifier (Saridaki, 2025). It also helps in identifying whether a modifier conveys a literal or figurative meaning, especially in cases of homonymy and polysemy. Additionally, the procedure aids in producing templates that illustrate the segments of core meaning within a common name. Segment-by-segment translation can result in higher-quality outcomes (Briakou, 2024). Through these segments, translators can more easily observe the position and arrangement of meanings within the common name. This helps translators avoid errors in the translation process.

This procedure is also essential in the effort for documentation of information about organisms, community knowledge, and cultural values embedded in common names. Based on this procedure, the variety of information contained in common name modifiers that reflect natural characteristics can be identified and highlighted. This, in turn, can help zoologists, botanists, and conservationists record the uniqueness of an organism and its relationship with a language community. Such records of uniqueness are highly valuable for improving conservation strategies for both the organism and its environment (Basnet & Dendup, 2021). At the same time, this procedure can also guide in identifying the position of information categories embedded in common names. These information categories can reveal the placement of certain values that should be highlighted and prioritized when introducing a species or type of organism through a common name.

Therefore, the development of the Common Names Modifier Arrangement Template Extraction Procedure is carried out to meet the needs and interests of various stakeholders. The development of this procedure is expected to assist in the analysis and documentation of modifier arrangements in common names, especially those rich in cultural elements and the knowledge of the language community.

II. Literature Review

The system of common names remains unclear and lacks a detailed explanation (Tsukamoto, 2020). In addition, according to Phaka et al. (2019), some parts of this common name system are still undocumented. More concerning is that some documentation efforts carried out have deviated from the original principles and formation systems of common names, ignoring the culture and knowledge of communities (Driver, 2021). Many of these efforts are bound to formal language systems or artificially constructed rules (Gillman & Wright, 2020). Therefore, a procedure that can aid in clarifying and documenting the system of common names needs to be developed. According to Furlano and Troendle (2022), the use of procedures can help obtain information more accurately and in greater detail. Furthermore, procedures can prevent disruptions or deviations from the intended purpose of a process (Coupry et al., 2021). Additionally, Javaid et al. (2022) state that the use of procedures can facilitate workflow organization and save time.

Based on the study by Lei et al. (2014), naming patterns and information about naming systems can be derived through a procedure of extracting lexical arrangement templates in names. These lexical arrangement templates can be extracted based on the lexical domain of the lexemes present in a name (Lei et al., 2014). In common names, especially specific common names, some lexemes consist of a head and a modifier lexeme (Berlin, 1973; Singnoi, 2011; Soyolt et al., 2013). The head lexeme comprises a generic name that is described by the modifier lexeme, while the modifier lexeme provides a description and specification for what is referred to by the generic name in the specific common name (Fontaine, 2012).

To determine the lexical domain of modifier lexemes, various lexical features must be taken into consideration. Among these are meronymic and hyponymic lexemes. According to Flanery (2008), a meronymic lexeme refers to a part or component of a complex object or entity. These lexemes can be grouped based on a shared hypernym. Hyponymic lexemes, on the other hand, refer to members that belong to a particular category or group (Jaszczolt, 2002), and can be grouped according to a superordinate. In addition, attention must also be focused on words that exhibit homonymy and polysemy. According to Wardani (2020), and Chalker and Weiner (1998), homonyms words are lexemes that differ in meaning but share the same spelling and pronunciation. Polysemous words, by contrast, are lexemes that have related meanings within the same conceptual domain or core sense, even though their specific meanings may differ (Marios, 2019). The core meanings of homonymous and polysemous words must be carefully analyzed to accurately determine their lexical domains.

Initially, the identification of the lexical domain of a lexeme relies on the theory of semantic fields (David, 1995). However, this theory's concept of semantic fields is not particularly robust in defining the boundaries of lexeme membership (Faber & Uson, 1997). This is because the semantic field of a lexeme does not have fixed meaning limits or boundaries. To address this issue, Faber and Uson (1997) introduced the Functional-Lexematic Model, which includes the Principle of Lexical Domain Membership. According to this principle, the lexical domain of a lexeme can

be identified through the genus present in its definition. This genus represents the core meaning contained within the lexeme's definition (Seppälä et al., 2017), indicating the semantic boundary of the lexeme being defined. According to Jinsha and Zuoyan (2015), the genus is also known as the hypernym or superordinate for the lexeme. This genus can serve as a guide in determining the lexical domain of modifier lexemes found in common names.

Furthermore, the study by Herlambang et al. (2023) demonstrates that a procedure can be developed based on the ADDIE model. This model has also been used as a foundation in the development of guidelines (Kacher et al., 2023; Ab Latif & Mat Nor, 2020), guidebooks (Nikijuluw et al., 2024; Hakim et al., 2024), apps (Norouzkhani et al., 2025; Saeidnia et al., 2022), and assessment instruments (Maxnun et al., 2024). The model is not limited to module development alone. According to Johnston (2024), this model involves five phases: Analysis, Design, Development, Implementation, and Evaluation. The Analysis phase is the first stage in the ADDIE model which is conducted to gain a comprehensive understanding of the system to be developed (Norouzkhani et al., 2025). The main objective of this phase is to identify the general needs and characteristics of the procedure to be designed. Next, the Design phase is carried out after the analysis is completed. In this phase, the design, also known as the "blueprint," is drafted (Maxnun et al., 2024). According to the principles of Structured Design by Yourdon and Constantine (1979), the design process must be done step-by-step, beginning with an overall outline of the procedure, and then progressing into more detailed structures and smaller components. The interrelationships between these structures and components are then identified and mapped in the form of a flowchart to ensure smooth task execution.

In the Development phase, the complete procedure is built based on the knowledge and information obtained during the analysis and design phases (Saeidnia et al., 2022). As shown in the study by Herlambang et al. (2023), the developed procedure is presented in the form of a complete flowchart. During the Implementation phase, the completed procedure is tested and applied to real data processing (Saeidnia et al., 2022). One database containing real data and a collection of common names is the Malaysia Biodiversity Information System (MyBIS), managed by the Malaysia Biodiversity Centre (2024). Finally, the Evaluation phase is conducted to determine whether the developed procedure successfully meets its intended objectives (Maxnun et al., 2024). Evaluation in this phase can be carried out by obtaining feedback from experts (Norouzkhani et al., 2025). Expert-based evaluation elements can be structured based on Nielsen’s 10 Usability Heuristics (Matrol, 2019). According to Alexandrini et al. (2022), these evaluation principles include “(1) visibility of system status, (2) match between the system and the real world, (3) user control and freedom, (4) consistency and standards, (5) error prevention, (6) recognition rather than recall, (7) flexibility and efficiency of use, (8) aesthetic and minimalist design, (9) help users recognize, diagnose, and recover from errors, and (10) help and documentation” (p. 3170).

III. Methodology

The ADDIE Model guided the development of the procedure for extracting modifier arrangement templates. According to Johnston (2024), this model involves five phases: Analysis, Design, Development, Implementation, and Evaluation.

A. Phase 1: Analysis

The specific needs and goals related to modifier extraction were identified. The analysis was conducted through a literature review sourced from databases: ScienceDirect, JSTOR, Semantic Scholar, and Google Scholar.

B. Phase 2: Design

The design of the procedure was carried out based on the Principles of Structured Design by Yourdon and Constantine (1979), which were adapted for the current work. According to this method, the design process is performed step-by-step, beginning with an overall outline of the procedure, and then progressing into more detailed structures and smaller components.

C. Phase 3: Development

In this phase, a complete version of the procedure was developed based on the analyses and design completed in Phases 1 and 2. The developed procedure is illustrated in Figure 3.

D. Phase 4: Implementation

The developed procedure was applied to extract modifier arrangement templates from real data. The dataset used for processing and extraction consisted of Malay bird common names sourced from the Malaysia Biodiversity Information System (MyBIS) database.

E. Phase 5: Evaluation

Six experts evaluated the developed procedure. Each expert was provided with the full procedural documentation, information about its implementation, and a set of structured open-ended questions based on Nielsen’s 10 Usability Heuristics. Feedback was collected through interviews.

IV. Results and Discussion

To provide a structured and systematic overview, this section presents and explains the findings corresponding to each stage of the procedure development, as guided by the ADDIE model.

A. Analysis

Based on the conducted analysis, several issues and problems have indicated that the Common Names Modifier Arrangement Template Extraction Procedure should be developed. Additionally, the analysis revealed important aspects that need to be addressed in the development of this procedure.

(a). Needs

The common naming system, especially in certain languages, remains undefined or lacks detailed descriptions (Tsukamoto, 2020). This is far behind compared to scientific names, which are well-defined by clear guidelines (Ruedas et al., 2025). Some of these common naming systems are also undocumented (Phaka et al., 2019). Where documentation exists, it often does not reflect the original principles and formation systems of common names, neglecting the culture and knowledge of earlier communities, and is instead bound by formal language systems or contrived rules (Driver & Bond, 2021; Gillman & Wright, 2020). Therefore, an approach that contributes to transparent description, detailing, and documentation of the common name formation system needs to be developed, particularly an approach for extracting modifier arrangement templates in common names.

Furthermore, existing extraction approaches that rely on pre-defined templates fail to detect certain language patterns that do not match the templates that were created earlier (Jurafsky & Martin, 2009). Moreover, these approaches struggle to process large volumes of language data effectively when limited or insufficient pre-defined templates are used (Shaier et al., 2024). They also face challenges handling natural language data beyond standard language forms (Plank, 2016). Therefore, the developed extraction approach must be suitable for the characteristics of common names, which exist in various non-standard forms and may occur in both small and large datasets.

(b). Important Information

Common names are divided into four structural levels: the unique beginner level, such as ‘animal’; the life-form level, such as ‘bird’; the generic name level, such as ‘robin’; and the specific name level, such as ‘American robin’ (Berlin, 1973). Besides English, these levels also exist in common names in languages such as Malay (Rifin et al., 2023), Thai (Singnoi, 2011), and Mongolian common names (Soyolt et al., 2013). The structure of specific common names consists of a combination of a generic name with modifier lexemes (Berlin, 1973; Singnoi, 2011; Soyolt et al., 2013). For example, the specific common name ‘blue spruce’ consists of the generic name ‘spruce’ combined with the modifier lexeme ‘blue’. Research conducted by Zariquiey (2018) found that modifier lexemes in specific common names can appear both before and after the generic name. For instance, the modifier lexeme ‘chaxun’ in the Kakataibo common name ‘chaxun mais’ appears before the generic name ‘mais’, whereas the modifier lexeme ‘kuru’ appears after the generic name ‘chuna’ in the animal common name ‘chuna kuru’. These studies provide insights and information about the structure and components of common names necessary for designing the process of selecting modifier lexemes found in common names.

Furthermore, various characteristics of lexemes must be considered when designing the process of determining the lexical domain for modifier lexemes in common names. Among these are meronymic and hyponymic lexemes. Meronymic lexemes refer to parts or components of a complex object or entity (Flanery, 2008). Meanwhile, hyponymic lexemes refer to members belonging to a certain category or group (Jaszczolt, 2002). Additionally, determining the lexical domain for lexemes exhibiting homonymy and polysemy also requires attention. This is because homonymous lexemes are different lexemes that share the same spelling and pronunciation (Wardani, 2020; Chalker & Weiner, 1998). In contrast, polysemous lexemes are lexemes related in terms of domain or core meaning, despite having different specific meanings (Marios, 2019).

Moreover, most lexical domain identification processes initially rely on semantic field theory (David, 1995). However, the concept of semantic fields in this theory presents problems in defining the boundaries of lexeme membership (Faber & Uson, 1997). Following this problem, Faber and Uson (1997) introduced the Functional-Lexematic Model, which includes the Lexical Domain Membership Principle. Based on this principle, the lexical domain of a lexeme can be identified by its genus. According to Seppälä et al. (2017), the genus is the core of the definition of a lexeme. It indicates the primary boundaries of the meaning of a lexeme being defined. The genus is also known as the hypernym and superordinate of a lexeme (Jinsha & Zuoyan, 2015). This genus can be used as a guide to identify the lexical domain of modifier lexemes found in common names.

B. Design

The design process of this procedure began with an overview, outlining its purpose and scope. Subsequently, the input, output, and limitations of the procedure to be developed were detailed as follows:

Purpose:	To extract modifier arrangement templates in common names
Focus:	Modifier arrangement in common names based on lexical domains
Input:	Common names from databases, field guides, dictionaries, or lists

Output: Templates indicating the arrangement of modifiers in common names
Limitations: Used manually or integrated with other systems, not fully automated

Next, the general structure of the procedure was outlined in more detail. The components and sub-components that form the complete structure of this procedure were identified. All these elements were then organized and mapped in a structural chart as follows:

General Structure:
Extracting Modifier Arrangement Templates

- Selection of Common Names
  - Language standardization
  - Form standardization
  - Specific name standardization
- Segmentation of Common Names
  - Lexeme separation
  - Marking of lexeme sequences
- Identification of Lexeme Features
  - Identification of generic names
  - Identification of modifiers lexeme
- Matching Modifiers with Lexical Domains
  - Listing of modifier lexemes
  - Collecting of lexeme genus
    - Collecting of genus from monolingual dictionaries
    - Collecting of genus from foreign language dictionaries
    - Verification of genus-definition-organism relationship
    - Expert validation
  - Listing of modifier-domain matches
- Lexeme Substitution in Names
  - Substitution of generic names with generic markers
  - Substitution of modifiers with lexical domain markers
- Template Recording

Figure 1. The Components and Sub-Components of the Procedure

These components were then briefly defined and organized to form smaller process structures, each with its specific function. These structures are presented in the form of flowcharts that illustrate the more detailed execution of each process, such as the following:

Selection of Common Names

Input (Common names) → Language standardization (Only names in a single language) → Form standardization (Only uniform forms are retained) → Specific name standardization (Only names composed of a combination of generic + modifier are retained) → Output (Selected common names)

Segmentation of Common Names

Input (Selected common names) → Lexeme separation (Compound words or hyphenated forms are separated) → Marking of lexeme sequences (Spaces in names are replaced with the symbol '+') → Output (Segmented common names)

Figure 2. Flow of Small Process Structure

C. Development

Based on the analysis and design, the Common Names Modifier Arrangement Template Extraction Procedure was developed as shown in Fig. 3. This procedure consists of two parts. The first part is a flowchart representing the overall procedure, while the second part is a table containing specific instructions for each component within the procedure.

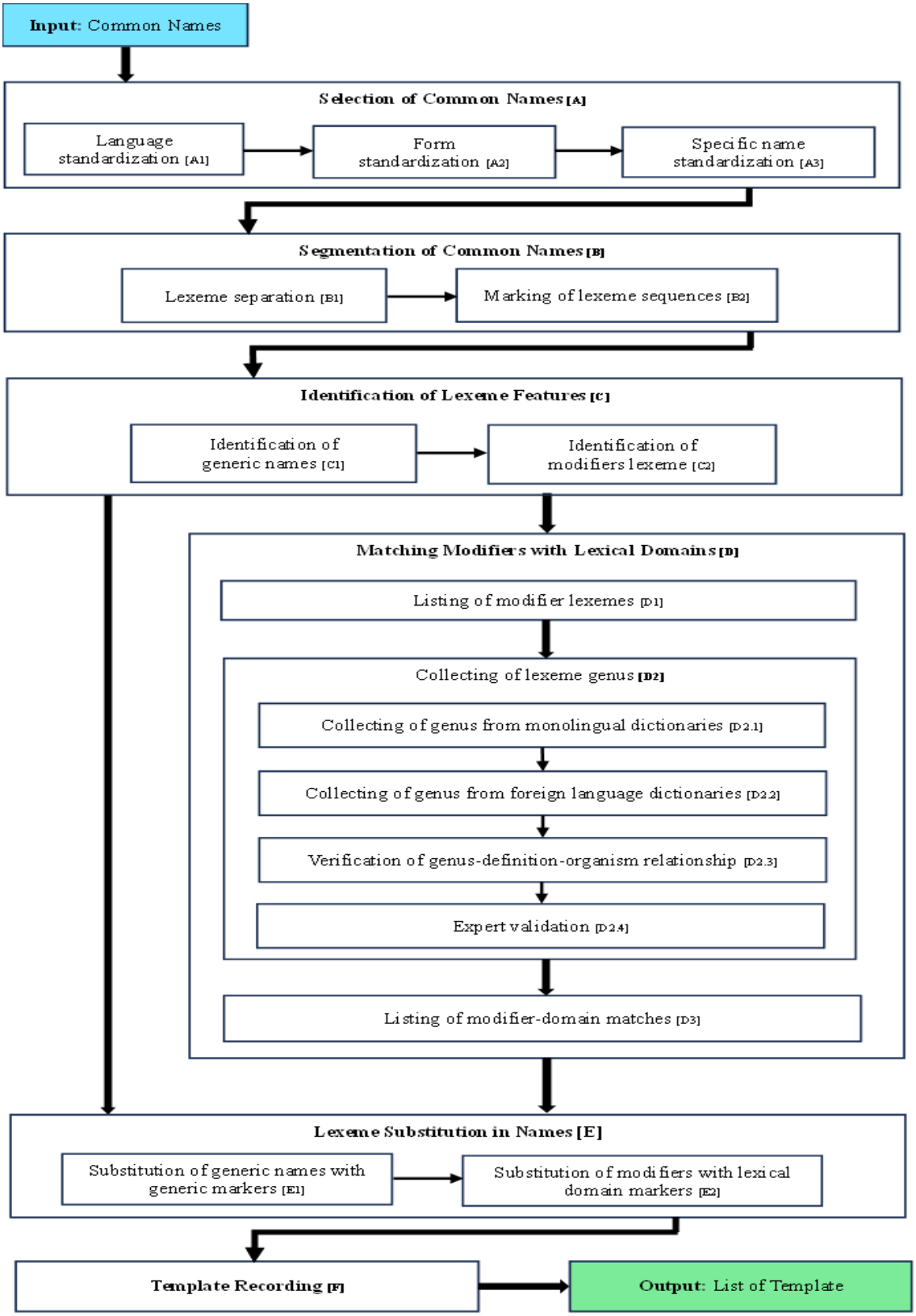

Figure 3. Flowchart of Common Names Modifier Arrangement Template Extraction Procedure

TABLE 1
SPECIFIC INSTRUCTIONS FOR MICRO-PROCESSES WITHIN THE PROCEDURE

Input:		Common names in the form of a database or a list.
A	**Selection of Common Names**	
A1	Language standardization	Select names that are in a single language only. Names from other languages should be excluded, although well-established loanwords may be considered.
A2	Form standardization	Standardize the spelling of names to ensure accuracy and consistency. Variations should be harmonized, and redundancies in meaning—such as overlaps between local and standard language names—should be removed.
A3	Specific name standardization	Select only specific names, i.e., names consisting of a combination of a generic name and a descriptive lexeme. Specific names containing a "life-form" lexeme may also be considered, but this lexeme must first be removed to standardize the common name. Afterward, duplicate names should be eliminated.
B	**Segmentation of Common Names**	
B1	Lexeme separation	Separating words in common names that contain compound meanings, whether in the form of close compounds or those joined with hyphens. Next, distinct lexemes that share the same word form are differentiated using different numbers at the end of the lexeme.
B2	Marking of lexeme sequences	Replace spaces between lexemes with the '+' symbol to indicate the sequence of lexemes within the name.
C	**Identification of Lexeme Features**	
C1	Identification of generic names	The generic name, which serves as the core being described in the specific name, is marked in bold.
C2	Identification of modifiers lexeme	The modifier lexeme, which describes the core in the specific name, is marked in regular font.
D	**Matching Modifiers with Lexical Domains**	
D1	Listing of modifier lexemes	List the modifier lexemes found in all listed names.
D2	Collecting of lexeme genus	Collect the genus of the modifier lexemes from dictionaries and glossaries. The genus refers to the core meaning in the definition of a lexeme.
D2.1	Collecting of genus from monolingual dictionaries	Collect the genus of the modifier lexemes from dictionaries and glossaries in the same language as the listed names.
D2.2	Collecting of genus from foreign language dictionaries	Collect the genus of the modifier lexemes from dictionaries and glossaries in a different language from the listed names. The genus is then translated back into the language of the listed names.
D2.3	Verification of genus-definition-organism relationship	Verify the relationship between genus, definition, and the modifier lexeme with the characteristics of the organism referred to, using reference materials.
D2.4	Expert validation	Obtain expert validation of the relationship between the genus, modifier, and the organism.
D3	Listing of modifier-domain matches	List the mapping of modifier lexemes to lexical domains, based on the genus of the modifier lexemes.
E	**Lexeme Substitution in Names**	
E1	Substitution of generic names with generic markers	Replace the generic name marked in bold with the generic name tag ‘GN’.
E2	Substitution of modifiers with lexical domain markers	Replace the modifier lexeme marked in regular font with the lexical domain tag based on the list of modifier-domain mappings.
F	**Template Recording**	
Output:		List of recorded templates based on the needs and intended purpose of the procedure.

D. Implementation

To examine how the procedure can be applied and evaluated, a real data set was processed using the developed procedure to extract modifier arrangement templates from common names. The data comprised Malay bird common names sourced from the MyBIS database. This data processing demonstrated how each microstructure and component of the procedure functions in practice.

The process began with the selection of common names. Malay bird common names were compiled from the MyBIS 2024 database. Names in other languages, such as English, were excluded. Next, the spelling of each name was standardized according to current and correct Malay spelling. Duplicate names with overlapping meanings were also removed. Then, specific names, those consisting of a combination of a generic name and a modifier lexeme were selected. The life-form lexeme ‘burung’ means ‘bird’, was removed to standardize the specific names. Once harmonized, any remaining redundant names were excluded.

Next, the name segmentation process was carried out. Compound words or hyphenated forms were split into separate lexemes. The spaces between lexemes in the common bird names were replaced with the ‘+’ symbol.

TABLE 2
NAME SEGMENTATION PROCESS

Original Common Name		**Segmentized Common Name**
belatuk bakau		belatuk + bakau
belatuk belacan		belatuk + belacan
belatuk belakang kuning	→	belatuk + belakang + kuning
belatuk berjalur		belatuk + berjalur
belatuk besar tengkuk kuning		belatuk + besar + tengkuk + kuning
belatuk biji nangka		belatuk + biji + nangka
belatuk bintik		belatuk + bintik

Subsequently, lexeme feature identification was conducted. According to Criteria C1 and C2, generic names serving as the core of specific names were marked in bold, while modifier lexemes that described the core were indicated in regular non-bold font.

TABLE 3
GENERIC NAMES AND MODIFIER LEXEMES MARKING

Unmark generic name		**Marked generic name**
belatuk bakau		**belatuk** + bakau
belatuk belacan		**belatuk** + belacan
belatuk belakang kuning		**belatuk** + belakang + kuning
belatuk berjalur		**belatuk** + berjalur
belatuk besar tengkuk kuning		**belatuk** + besar + tengkuk + kuning
belatuk biji nangka		**belatuk** + biji + nangka
belatuk bintik		**belatuk** + bintik

In the process of matching modifiers with lexical domains, the first step was to list all modifier lexemes marked in regular font. The genus which is the core meaning of each modifier lexeme was then collected from monolingual dictionaries and glossaries. This was followed by the collection of genus data from dictionaries and glossaries in other languages, such as Indonesian and English, which were then translated back into the original language of the common names. Next, the relationship between the genus, definition, and the characteristics of the organism referenced by the modifier lexeme was verified based on reference materials such as book, field guide and encyclopedia. Following this, six experts were consulted to confirm the accuracy of the relationship between the genus, modifier, and organism. Based on the genus data verified by the experts, a list of modifier-lexical domain pairings was compiled.

TABLE 4
MODIFIER-LEXICAL DOMAIN PAIRINGS BASED ON GENUS

Lexeme	**Genus**	**Lexical Domain**
…	…	…
uban	*anggota*	Body_part
ubun	*anggota*	Body_part
timur	*arah mata angin*	Compass point
utara	*arah mata angin*	Compass point
biji	*bahagian buah*	Fruit_part
injap	*bahagian bubu*	Bubu_part
akar	*bahagian tumbuhan*	Tree_part
…	…	…

Subsequently, generic names marked in bold in the segmented common names were replaced with the generic name tag ‘GN’. Modifier lexemes in regular font were replaced with lexical domain tags based on the verified modifier-domain pairing list.

TABLE 5
LEXEME SUBSTITUTION IN COMMON NAMES

Common Name		**Template extracted**
belatuk + bakau		**GN** + plant
belatuk + belacan		**GN** + food
belatuk + belakang + kuning		**GN** + body_part + colour
belatuk + berjalur		**GN** + pattern
belatuk + besar + tengkuk + kuning		**GN** + size + body_part + colour
belatuk + biji + nangka		**GN** + fruit_part + plant
belatuk + bintik		**GN** + pattern

Finally, the extracted templates were recorded and compiled into a list. The extracted templates reveal the lexical domains of the modifier lexemes found in Malay bird common names. These templates can also show the arrangement of modifier lexemes in Malay bird common names according to their lexical domains.

E. Evaluation

Based on feedback from experts, the effectiveness of the developed procedure for extracting the template modifier arrangement in common names can be evaluated based on the following ten aspects:

(a). Visibility of System Status

This procedure divides each step. For example, Step A: Selection of common names, Step B: Segmentation of common names, and Step C: Identification of lexeme characteristics. This allows users to understand their position within the process. In addition, the procedure uses reference codes to facilitate navigation during the extraction of the modifier arrangement.

(b). Match Between the System and the Real World

The terms used are consistent and relevant to the context of linguistics, such as modifier, lexeme, and common names. These terms are commonly used by experts in lexicography, terminology, language planning, and linguistic research. However, one of the experts has emphasized that the procedure does not provide actual examples for the concepts explained. The absence of such examples is intentional, to avoid any influence that could restrict or limit the selection of data by users of the procedure.

(c). User Control and Freedom

Users of the procedure are free to use common name data from any language, variety, or organism for extraction. In addition, the procedure enables users to independently determine a suitable domain for the descriptive modifier lexeme within the common name. The generation of the modifier arrangement template through this procedure can be controlled and customised to meet the specific needs of the users.

(d). Consistency and Standards

The writing format in the instruction and flowchart of the procedure are consistent. The procedure also uses uniform typography. Besides, the term used is also consistent without using synonyms which could confuse users.

(e). Error Prevention

This procedure contains instructions that emphasize the need to separate words composed of combined meanings. The purpose of this instruction is to prevent errors that may cause the actual modifier present in a common name to become undetected. The procedure also provides guidance to mark different lexemes that share the same word distinguished with different numbers. This helps to avoid errors in determining modifier-domain pairings, which could otherwise fail to accurately extract the actual template of a common name.

(f). Recognition Rather Than Recall

Each process can be viewed and referred to using the flowchart provided in the procedure. Users are not required to memorise the sequence and order of the processes.

(g). Flexibility and Efficiency of Use

The process of extracting modifier arrangement in common names can be carried out flexibly through this procedure. Experienced users can complete the entire process using a simplified flowchart, while new or non-expert users may follow the full process with the aid of a detailed flowchart and supporting instruction tables.

(h). Aesthetic and Minimalist Design

The layout of this procedure is neat and uncluttered. Only relevant instructions and information are presented at each step, which helps to reduce cognitive load. In addition, the steps in this procedure are arranged according to a visual hierarchy that supports readability.

(i). Help Users Recognize, Diagnose, and Recover From Errors

This procedure is implemented either entirely manually or in integration with a computer system, but it is not fully automated. It is not equipped with mechanisms or methods that allow it to detect errors or inconsistencies.

(j). Help and Documentation

The procedure developed is entirely in document form, providing detailed guidance from the beginning to the end of the process of extracting modifier arrangements in common names. However, this document procedure does not include any help section and does not offer explanations on how to resolve issues that may arise during the process.

V. Conclusion

The development of the Common Name Modifier Arrangement Template Extraction Procedure demonstrates the potential of structured linguistic tools in supporting language documentation, lexicography, and education. Designed with usability in mind, the procedure allows users to systematically extract, analyze, and record modifier arrangements in common names. Its step-by-step format, developed using the ADDIE model and evaluated through Nielsen's 10 Usability Heuristics, ensures clarity, accessibility, and adaptability for manual application.

The procedure offers several key values:

- Enhances consistency in descriptive naming patterns
- Supports language teaching and learning by modeling accurate modifier structures
- Facilitates documentation of vernacular knowledge and folk taxonomies
- Enables cross-linguistic comparison of modifier arrangements
- Promotes standardization in terminology and naming practices

While initial testing through expert review confirmed the procedure's relevance and clarity, further empirical validation is recommended. Future work should include pilot testing with different user groups, like educators, community language workers, and students, and application to additional language datasets. This will help assess the

procedure's effectiveness in real-world settings and refine it for broader linguistic, educational, and cultural documentation initiatives.

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