

Visual Comparison of Biological Taxonomies: A Task Characterization

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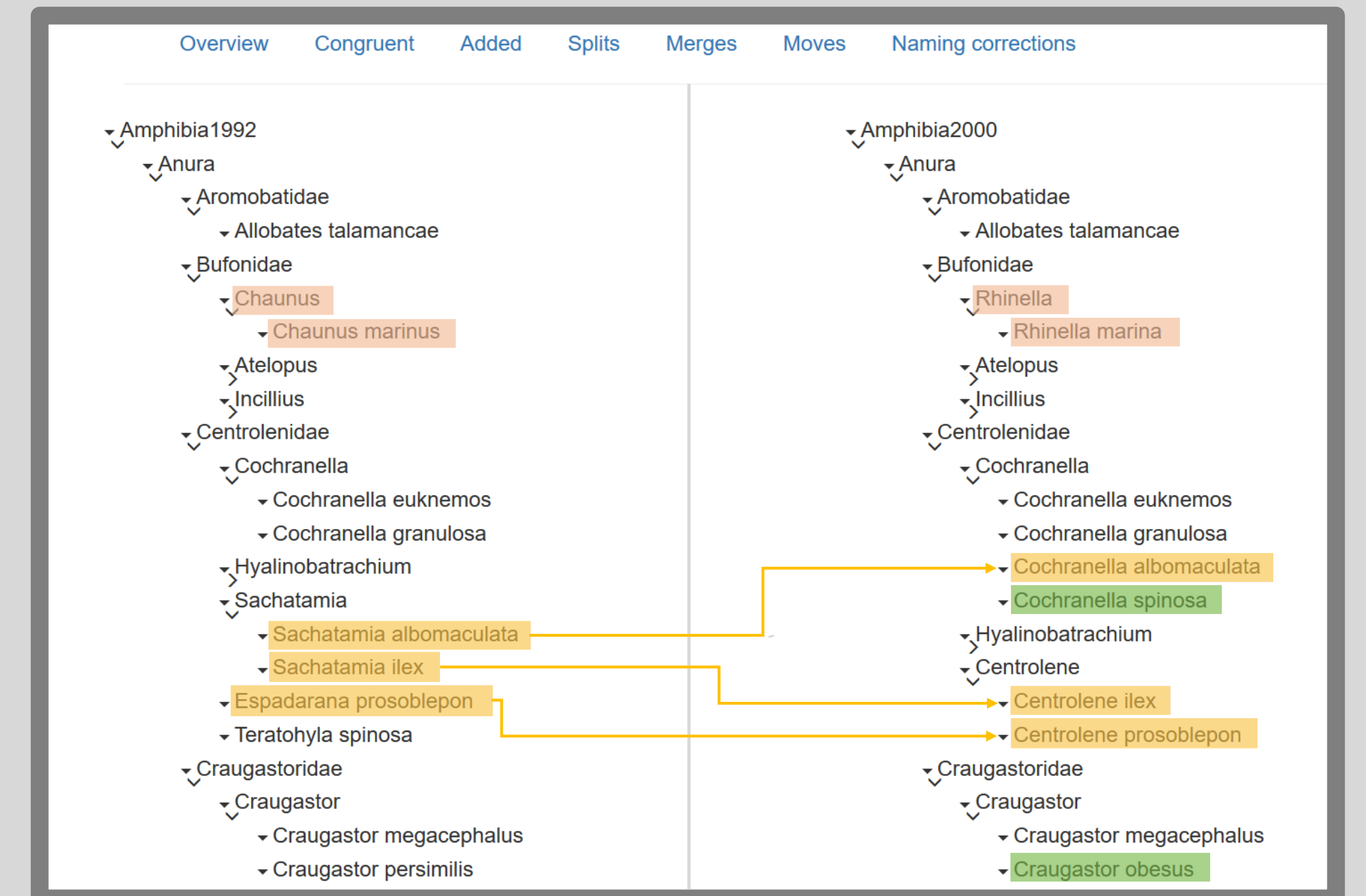
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The domain



- ≈ 10 million species in the planet.
- ≈ 2 million have been identified.
- Taxonomies change.

Two versions of a taxonomy?
How different are they?



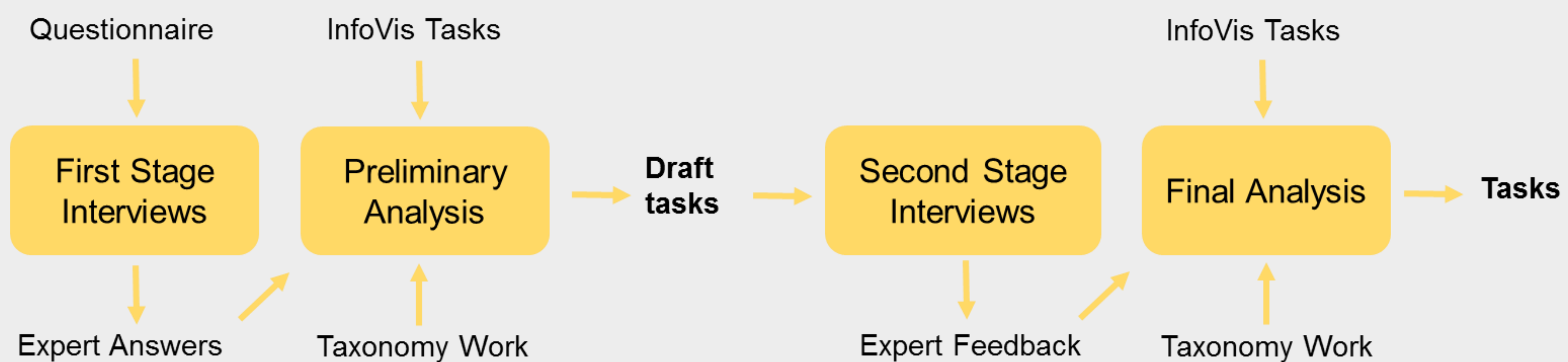
Method

First stage

- Interviews based on delivered questionnaire.
- Experts from United States, Spain, and Costa Rica.
- Literature review, taxonomic databases, software tools.
- Iterative task analysis to obtain a list of draft tasks.

Second stage

- Interviews with experts based on draft tasks.
- Iterative analysis and refinement.
- Re-group tasks and clarify descriptions.
- Organized tasks in a two-level model.



Results

Categories	User Visualization Tasks	Description
Pattern Identification	1. Identify congruence	Identify topological and taxonomic naming congruence.
	2. Identify corrections	Identify splits, merges, moves, and naming corrections.
	3. Identify additions	Identify new nodes added.
	4. Overview changes	Obtain an overview of different types of change.
	5. Summarize	Obtain a numerical understanding of change.
Query	6. Find inconsistencies	Recognize violations of rules (e.g., repeated or missing names).
	7. Filter	Find cases that satisfy certain conditions.
	8. Retrieve details	Retrieve attributes of a particular node.
	9. Focus	Navigate to an area of interest.
Edit	10. Edit	Perform taxonomic alignment and data updates.

Contact

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Future work

Compare and visualize biological taxonomies by systematically considering the characterization of users' tasks.

Abstract

Although biological taxonomies are a prevalent use case in hierarchy visualization, there has been little research on the characterization of users' tasks for taxonomy comparison. Task identification is very relevant as a start point to design effective information visualization solutions for taxonomic work. We performed a systematic domain characterization that involved interviews with experts, literature review, the identification of data sources, and a survey of existing software tools. We did iterative analysis until we reached a satisfactory list of users' tasks.