# Attribute Mining for Discrete Choice Experiments Across Diseases Using Gen-AI: Replication and Validation Objectives

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**KEY MESSAGE**

**AI-supported attribute mining can efficiently support traditional DCE attribute identification processes across disease areas and serve as a resource efficient starting point for attribute development.**

## BACKGROUND

Attribute development for discrete choice experiments (DCEs) is a multi-step process that is traditionally resource-intensive and context-specific, relying on manual qualitative synthesis of literature and expert input. [1-4]

In health-related DCEs, the formative phase of attribute and level development is widely regarded as a major determinant of study validity because poorly specified attributes can distort trade-offs respondents are asked to make and weaken policy relevance. [1,3] Recent literature has highlighted substantial heterogeneity in how attributes are developed, reinforcing the need for more transparent and reproducible approaches. [2,3] However, because these processes are often resource-intensive and iterative, the specific methods used are not always fully reported.

*This work examined whether Gen-AI-enabled mining of published evidence could provide a more resource-efficient starting point for identifying common and disease-specific concepts before expert review. [5]*

## OBJECTIVES

1. Evaluate an AI-supported attribute mining approach across multiple disease areas
2. Assess replicability, validity, and limitations relative to conventional qualitative methods
3. Examine whether Gen-AI-enabled mining could provide a resource-efficient starting point for common and disease-specific concepts

## METHODS

### Study design

An AI-based text mining and clustering pipeline using retrieval augmented generation (RAG) was applied to published qualitative studies, patient-reported outcomes literature, and HTA documents across three disease areas (addiction, autoimmune diseases, and asthma)

### Data processing

Candidate attributes and levels were extracted, normalized, and grouped thematically. Outputs were compared against attributes derived through traditional qualitative research for the same diseases. [2]

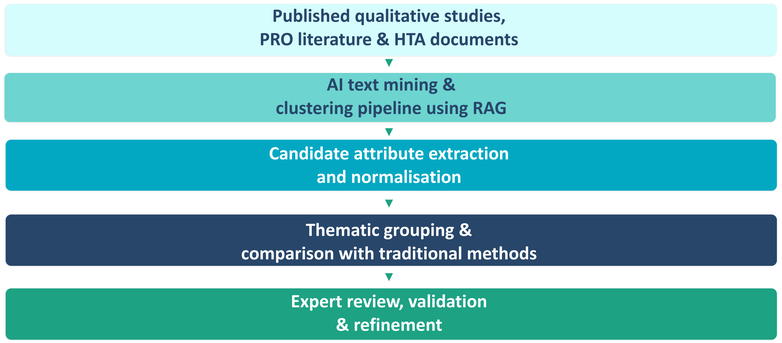
### Validation focus

(1) Attribute overlap and coverage
(2) Conceptual consistency with established DCE approaches [2,3,6]
(3) Disease-specific vs. cross-cutting attributes

Expert review was used to assess face validity and identify false positives or missing concepts. This analytic logic is aligned with established DCE development which commonly describe sequential stages of evidence collection, data reduction, removal of unsuitable concepts, wording/refinement, and stakeholder validation. [2,3]

Normalisation and clustering steps reduced lexical variation across source documents, aggregated semantically related terms, and generated candidate concepts assessed at the attribute rather than sentence level. As automated extraction can inherit ambiguity from source texts, expert review remained a prespecified component, consistent with established approaches to handling unstructured health data. [5]

## METHODS (Pipeline)




**Source selection rationale:**
Qualitative studies and PRO literature preserve patient-centred language. HTA documents provide structured synthesis of benefits, harms, comparators, and use conditions for healthcare decision making.

## RESULTS

✓ Cross disease commonalities identified

✓ Core attributes replicated

\+ Additional attributes found

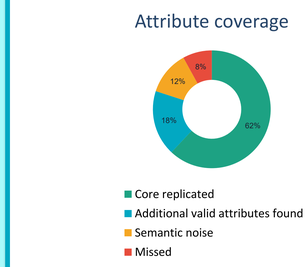



Fig 1: Percentage of attribute coverage using AI

The AI-supported approach replicated a majority of core attributes, particularly treatment effectiveness, safety, and burden of administration. (Fig 1)

Cross-disease commonalities were consistently identified. Disease-specific attributes showed greater variability and required expert refinement.

Additional candidate attributes were generated, some conceptually relevant, others reflecting semantic noise.

Replication performance was highest where source literature was rich and well-structured.

| Attribute category | AI coverage | Expert input |
|---|---|---|
| Treatment effectiveness | High | Confirmed |
| Safety profile | High | Confirmed |
| Administration Burden | High | Confirmed |
| Disease-specific | Moderate | Refinement needed |
| Cross-disease commonalities | High | Confirmed |

The pipeline was most effective for concepts repeatedly and explicitly described across evidence sources, especially when terminology is relatively standardised. By contrast, disease-specific concepts may be more vulnerable to fragmentation across small literatures, locally specific phrasing, or contextual nuances. (Fig 2)

## RESULTS (continued)

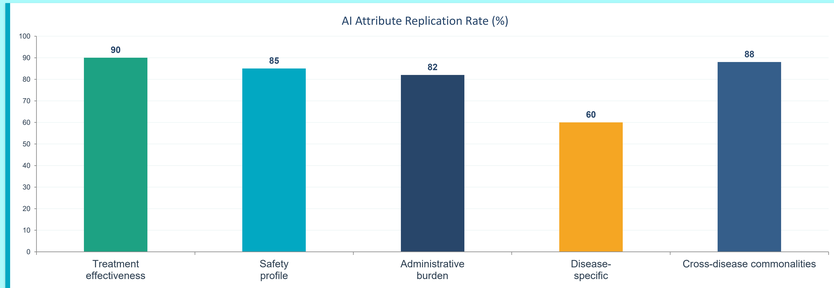



Fig 2: AI attribute replication rate across categories

## KEY FINDINGS & LIMITATIONS

Extraction quality depends on source-text structure, corpus heterogeneity, and terminology stability.

Disease-specific concepts are vulnerable to fragmentation across small literatures and due to variation in language/definition.

Additional candidate attributes are both a strength (broadens concept pool) and a limitation (requires adjudication before DCE instrument inclusion).

Contextual salience requires iterative validation with subject-matter and methods experts.

## DISCUSSION and CONCLUSIONS

AI-supported attribute mining can efficiently support traditional DCE attribute identification processes across disease areas and serve as a resource efficient starting point for attribute development.

Expert validation remains essential, particularly for disease-specific concepts and level refinement.

These findings support AI as an assistive tool in DCE design rather than a replacement for qualitative research.

**Recommended hybrid workflow:**

Gen-AI is used for rapid evidence harvesting, preliminary concept aggregation, and identification of cross-cutting themes, followed by human-led review to establish contextual relevance, remove false positives, and refine respondent-facing wording.

Such an approach may improve transparency and reproducibility in early-stage attribute development while preserving the interpretive strengths of qualitative methods necessary for final instrument design.

**Future directions:**

Future applications should focus on documentation of prompts, corpus selection, clustering decisions, and expert adjudication.

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