

Sahil Sharma¹, George Xylopoulos², Larisa Gofman³, Nils Fisher⁴, Molebedi Segwagwe⁵¹ZS Associates, New Delhi, India, ²ZS Associates, Cambridge, UK, ³ZS Associates, Princeton, NJ, USA, ⁴ZS Associates, Boston, MA, USA, ⁵ZS Associates, London, UK

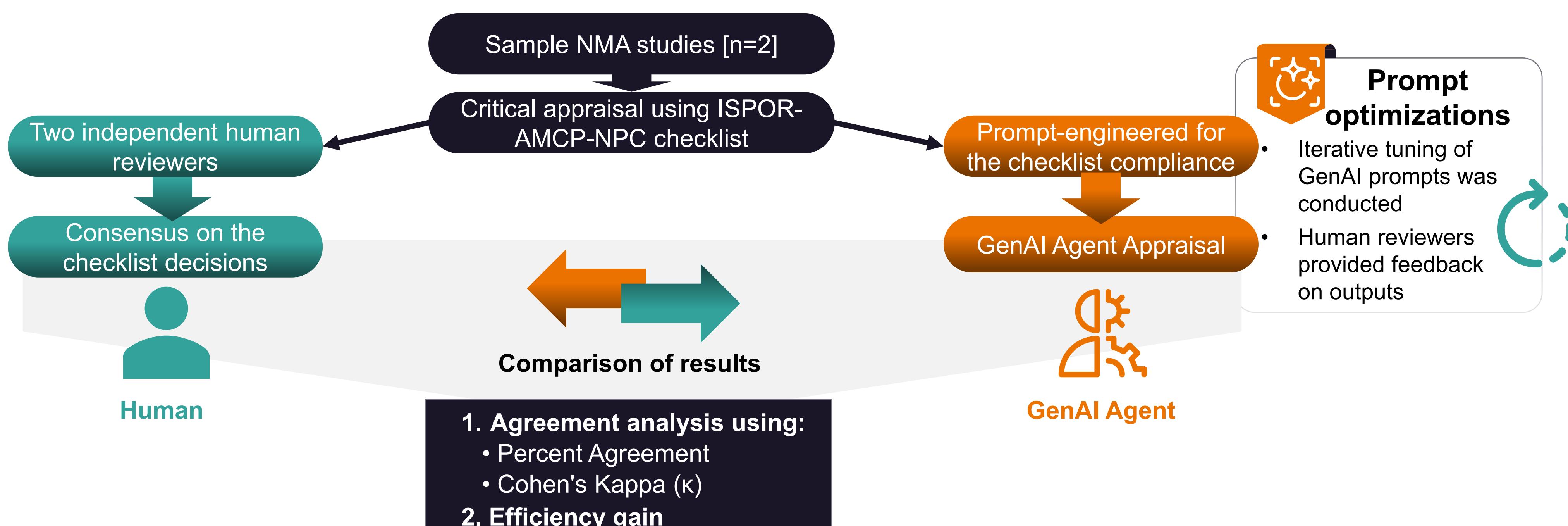
Background & Objectives

- HTAs and EU JCAs** emphasize on **transparent and credible evidence**. Given the importance of **Indirect Treatment Comparisons (ITCs)** and **Network Meta-Analyses (NMAs)** in comparative effectiveness research, **structured, high-quality appraisal** of these studies is essential for reliable decision-making
- The vast and complex nature of NMA literature presents a challenge to ensuring consistent evaluation
- Our primary objective was to overcome the hurdles of scaling and standardizing NMA appraisal. We **developed and piloted a GenAI agent** trained on the **ISPOR-AMCP-NPC Checklist**¹
- The goal was to use this agent to **support consistent and scalable appraisal** by testing its ability to reliably match human expert judgment, thus streamlining the evidence synthesis process

Methods

- The GenAI agent was developed using prompt engineering, embedded with guardrails, and informed by detailed training on the checklist's structure and interpretative guidance
- The agent was piloted on two published NMA studies in hormone receptor-positive (HR+)/HER2-negative advanced breast cancer (ABC)^{2,3}
- Independent assessments by an experienced human reviewer served as the gold standard
- The agent's responses were compared with human evaluations across six checklist domains using percent agreement and Cohen's kappa⁴

Fig 1: Methodology for pilot testing of GenAI agent



Results

- High overall agreement:** The GenAI agent demonstrated strong concordance with human reviewers, achieving an overall raw agreement of **84%** across all checklist items
- Moderate inter-rater reliability:** The **Cohen's Kappa coefficient was 0.581 (95% CI: 0.336–0.827)**, indicating moderate agreement after accounting for chance
- Consistent agreement across domains:** Domain-level agreement ranged from **80% to 90%**, with the highest alignment observed for **conflict of interest (90%)** and **interpretation (85%)** domains
- Most overlap was observed in the "Yes–Yes" category (**72 out of 104 observations**), indicating strong consensus between GenAI and human reviewers, with minimal disagreement across "No" and "Other" responses

Table 1. Confusion Matrix Comparing GenAI Agent and Human Reviewers Judgments

| Confusion Matrix | | | | |
|----------------------|-----|----|--------|-------|
| Human vs GenAI Agent | Yes | No | Other* | Total |
| Yes | 72 | 4 | 2 | 78 |
| No | 7 | 10 | 1 | 18 |
| Other* | 1 | 2 | 5 | 8 |
| Total | 80 | 16 | 8 | 104 |

*Other responses included 'not applicable', 'not enough information' & 'not reported'

Table 2. Agreement between GenAI and human reviewers on the checklist response

| | | |
|----------------------------|----------------|--------------------|
| Cohen's Kappa (κ) | 0.581 | Moderate agreement |
| Standard error | 0.125 | |
| 95% CI | 0.336 to 0.827 | |

High prevalence of "Yes" responses by both GenAI and human reviewers' limits variability, lowering Kappa despite strong agreement⁵

Fig 2: Raw agreement between GenAI agent and human reviewers on critical appraisal of the NMA studies using ISPOR-AMCP-NPC checklist

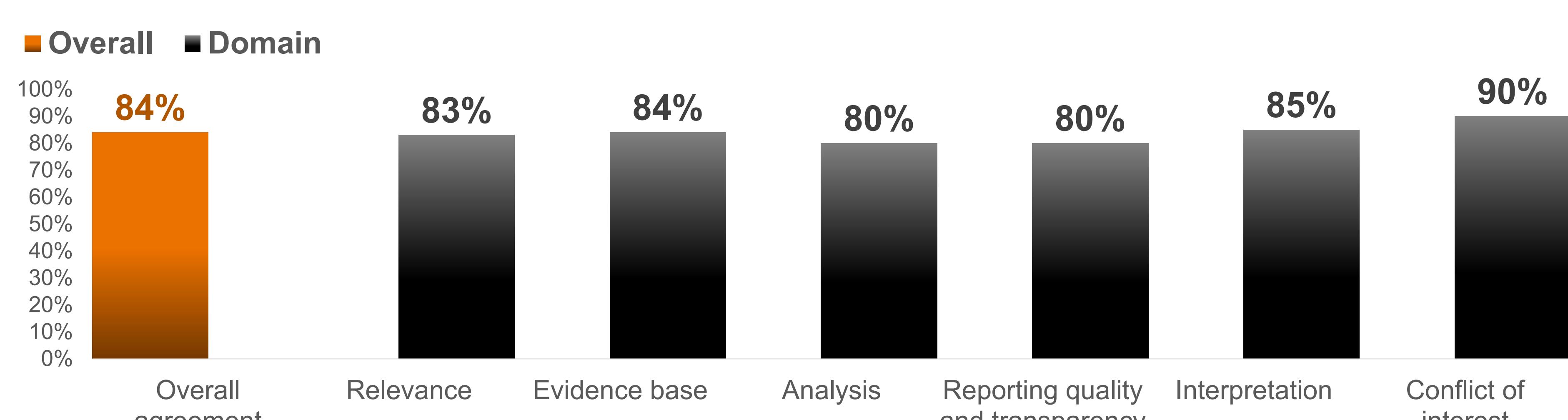
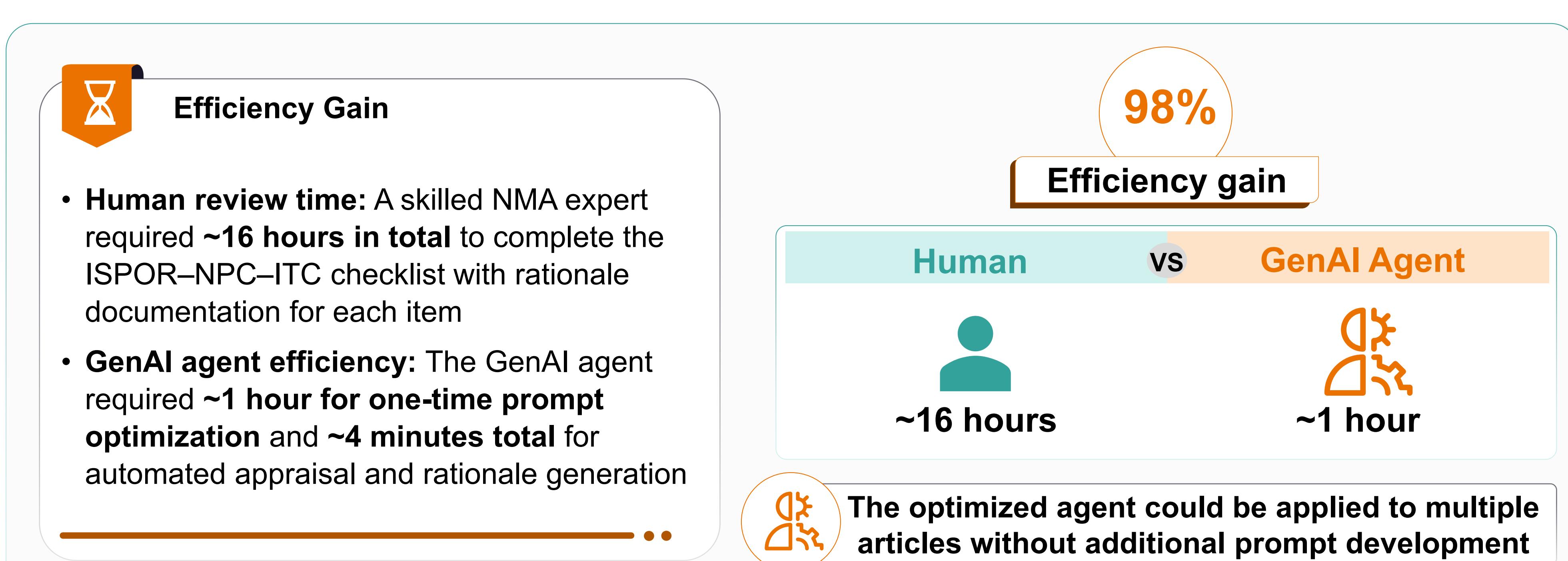


Fig 3. Time Investment Comparison – Human Reviewers vs. GenAI Agent for Critical Appraisal (2 Studies)



Conclusion

- This pilot demonstrates the feasibility of deploying a GenAI agent to support quality assessment of NMAs using established checklists
- While early results are promising in core domains, further optimization is underway to improve performance in complex or assumption-prone areas
- The approach shows strong potential to enhance efficiency and consistency in HTA/JCA evidence review processes, ultimately supporting timely access to innovative therapies

References

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