

# Responsible Use of AI/LLMs for Literature Reviews

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# Overview

- Best Practices for Responsible AI Usage
- Common Tools for Literature Review
- Using NotebookLM
- Do's & Dont's of Using Generative AI

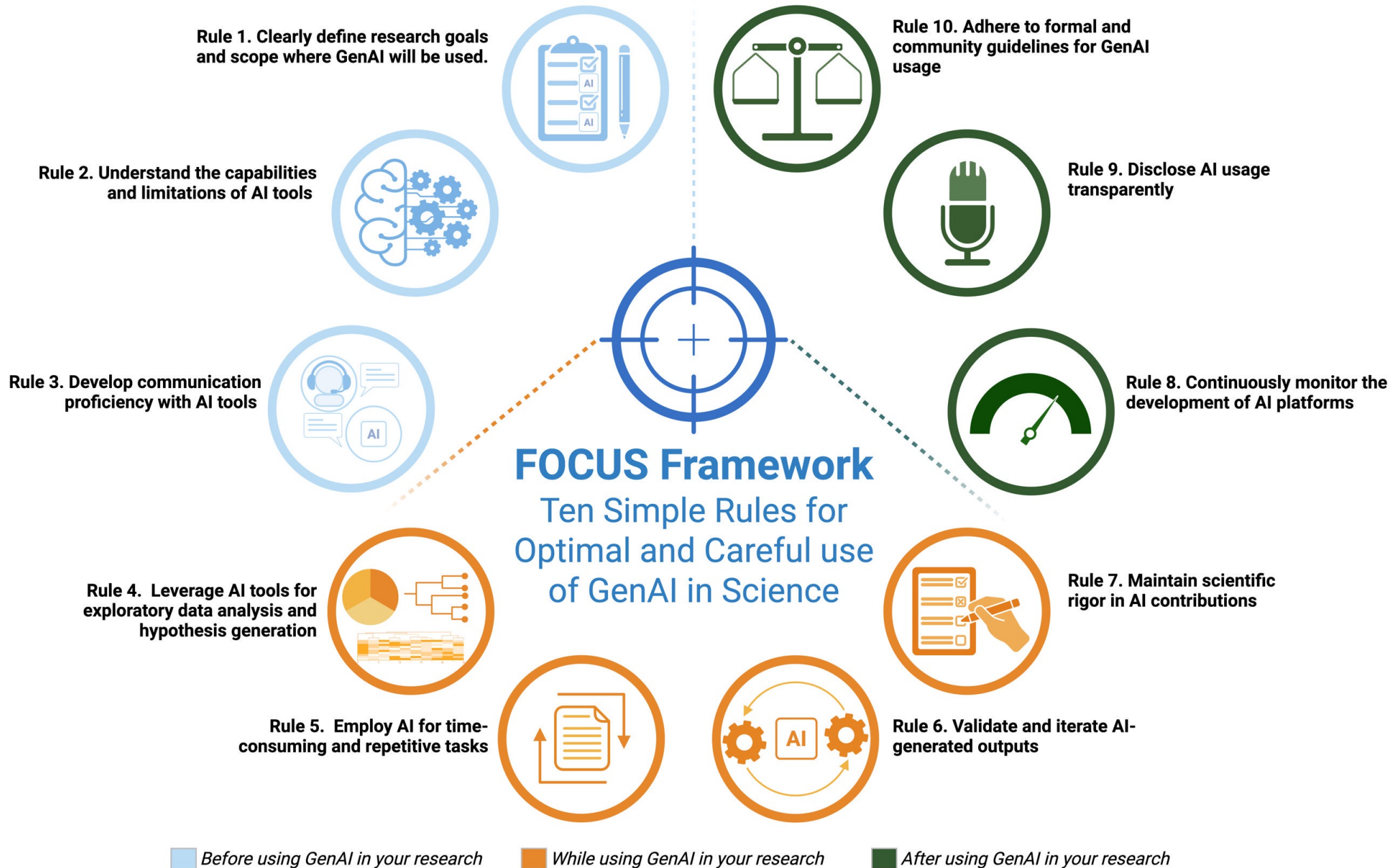
# Best Practices for Responsible AI Usage

- Clearly define research goals and scope where GenAI will be used
- Understand the capabilities and limitations of AI tools
- Employ AI for time-consuming and repetitive tasks
- Do not lose yourself in AI
- Practice FAIR (Findable, Accessible, Interoperable, Reusable) principles

**Ten simple rules for optimal and careful use of generative AI in science**

Mohamed Helmy , Lingling Jin, Amr Alhossary, Tamer Mansour, Diogo Pellagrina, Kumar Selvarajoo

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# Common Tools for Literature Review

- VOSviewer - a software tool for constructing and visualizing bibliometric networks
- CitNetExplorer - a software tool for visualizing and analyzing citation networks of scientific publications.
- Covidence - a systematic reviews production tool for title/abstract screening, full-text screening, data abstraction, and quality assessment
- AI ???
  - Scite ??
  - NotebookLM?

# What is NotebookLM?

- AI-powered research and content organization tool by Google
- Helps users streamline their workflow, enhance learning, and boost creativity by integrating multiple sources like PDFs, websites, mp3s, and videos.
- Free version lets you query up to 50 curated sources
- Generates summaries, FAQs, reports, flashcards, videos, mind maps, and audio “podcasts”



# Examples of Using Notebooklm

- Combine related papers to summarize pathways, mechanisms, or gene functions
- Build lab training guides or protocol FAQs from internal documents
- Create structured literature reviews for grant or manuscript prep
- Produce teaching materials or podcasts explaining technical concepts
- Generate comparative summaries of analytical methods or datasets

# Using NotebookLM Effectively

- Upload high-quality, relevant sources to keep insights accurate and specific
- Use suggested questions to reveal trends or gaps
- Always verify citations before citing or sharing results
- Regularly save the best AI responses into Notes and restructure them manually
- Notebooks can be shared publicly or with others
- Add written/typed notes to help contextual other sources



# Ways It's Being Use at UAB

- CPAM grant
  - Inputting hundreds of variant or gene related papers identify functional associations
- QE prep
- Variant Analysis

# Example: Studying all QE References

The screenshot displays the QE References application interface, which is organized into three main panels: Sources, Chat, and Studio.

**Sources Panel:** This panel on the left contains a search bar with the text "Search the web for new sources" and a "Web" dropdown menu. Below the search bar is a list of sources, each with a PDF icon and a checkmark. The sources include:

- 1953048.2078195.pdf
- Ahsan\_Emerging biologics for the tr...
- Alkahtani\_Heritable Pulmonary Arter...
- Anders\_Moderated estimation of fol...
- Archer\_Pulmonary arterial hypertens...
- Austin\_The Genetics of Pulmonary A...
- Bailly\_Hereditary hemorrhagic telan...
- Beltran\_The RD-Connect Genome-P...

**Chat Panel:** The central panel is titled "QE References" and features a red lung icon. It displays a summary of 142 sources, stating: "The provided sources predominantly focus on **Pulmonary Arterial Hypertension (PAH)**, examining its genetic underpinnings, particularly mutations in the **BMPR2** and **ALK1** genes, and the resulting clinical outcomes, including disease severity and survival differences between mutation carriers and non-carriers. A significant portion of the text discusses **drug repositioning**—identifying new uses for existing drugs—as a strategy for treating rare diseases like PAH, utilizing various computational methods such as **signature-based** and **network-based** approaches, often enhanced by **Artificial Intelligence (AI)** and **machine learning**. Complementing these themes, other sources address **bioinformatics methodologies** for genetic and molecular analysis, including statistical packages like **DESeq2** for **RNA-seq data analysis**, the use of **molecular networks** and **gene regulatory networks** for disease understanding, and best practices for interpreting **somatic and germline variants**." Below the text is a "Save to note" button and a chat input area with the placeholder "Start typing...".

**Studio Panel:** The right panel is titled "Studio" and contains a grid of interactive tools: Audio Overview, Video Overview, Mind Map, Reports, Flashcards, and Quiz. Below this grid is a list of notes, including "Key Driver Analysis for HPAH...", "GRN Refinement with Co-...", and "PAH: Genetic to Network-Based...". At the bottom right is an "Add note" button.

# Do's & Dont's of Using Generative AI

- **Don't** copy and paste from llms into manuscripts.
- **Do** paraphrase.
- **Don't** treat AI output as evidence.
- **Do** validate AI results.
- **Don't** let automation dictate findings or override domain expertise.
- **Do** use AI to assist reasoning.