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KEGGaNOG: A Streamlined Solution for KEGG Pathway Annotation

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The Kyoto Encyclopedia of Genes and Genomes (KEGG) is a foundational resource for annotating and understanding the metabolic pathways of microbes and microbial communities, particularly in gut microbiome research. Despite its value, leveraging KEGG pathway annotations often involves time-intensive workflows or reliance on commercial tools like DRAM [1] , which can limit accessibility for many researchers. Tools such as eggNOG-mapper offer rapid and comprehensive functional annotation, which includes the annotation of KEGG pathways of novel sequences but lack built-in visualization capabilities [2]. Conversely, KEGG-Decoder excels in visualizing KEGG pathways but requires outputs from KEGG-Koala – a web-based tool with extended processing times and limited flexibility [3]. These limitations can create bottlenecks for researchers, particularly those working on large-scale studies. To bridge this gap, we introduce KEGGaNOG, an open-source tool that integrates eggNOG-mapper annotations with KEGG-Decoder for a seamless annotation and visualization workflow.

KEGGaNOG is designed to parse eggNOG-mapper outputs and format them to be compatible with KEGG-Decoder, enabling researchers to generate heatmaps of KEGG pathway presence and completeness efficiently. This integration transforms the annotation and visualization process into a single, streamlined workflow that minimizes the need for manual intervention or complex post-processing. Furthermore, when paired with a Snakemake pipeline [4], KEGGaNOG and eggNOG-mapper enable one-click metabolic profiling, significantly reducing the complexity and time required for analyzing gut microbiome datasets.

KEGGaNOG is a versatile tool with broad applicability. It can be used to annotate individual microbial genomes, including probiotics, as well as metagenome-assembled genomes, providing valuable insights for both targeted studies of specific microbes and community-level functional analyses. This capability is particularly valuable for microbiome research, where understanding the functional roles of both individual species and entire communities is essential.

When tested with *Lp. plantarum* IS-10506 complete genome [5], KEGGaNOG reliably identified key metabolic pathways, including those central to carbohydrate metabolism and short-chain fatty acid synthesis, which are critical to gut health research. Its visualization capabilities greatly enhanced the interpretability of results, enabling researchers to quickly and effectively translate genomic data into actionable biological insights.

KEGGaNOG's user-friendly manual [5], local functionality, and open-source nature make it a versatile and accessible tool for researchers of varying expertise levels. By bridging the gap between eggNOG-mapper and KEGG-Decoder, KEGGaNOG provides universal access to KEGG pathway annotations and visualizations, fostering new opportunities in gut microbiome and microbial ecology research. Future updates aim to expand compatibility with additional annotation tools and enhance visualization features to further broaden its utility.

References

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