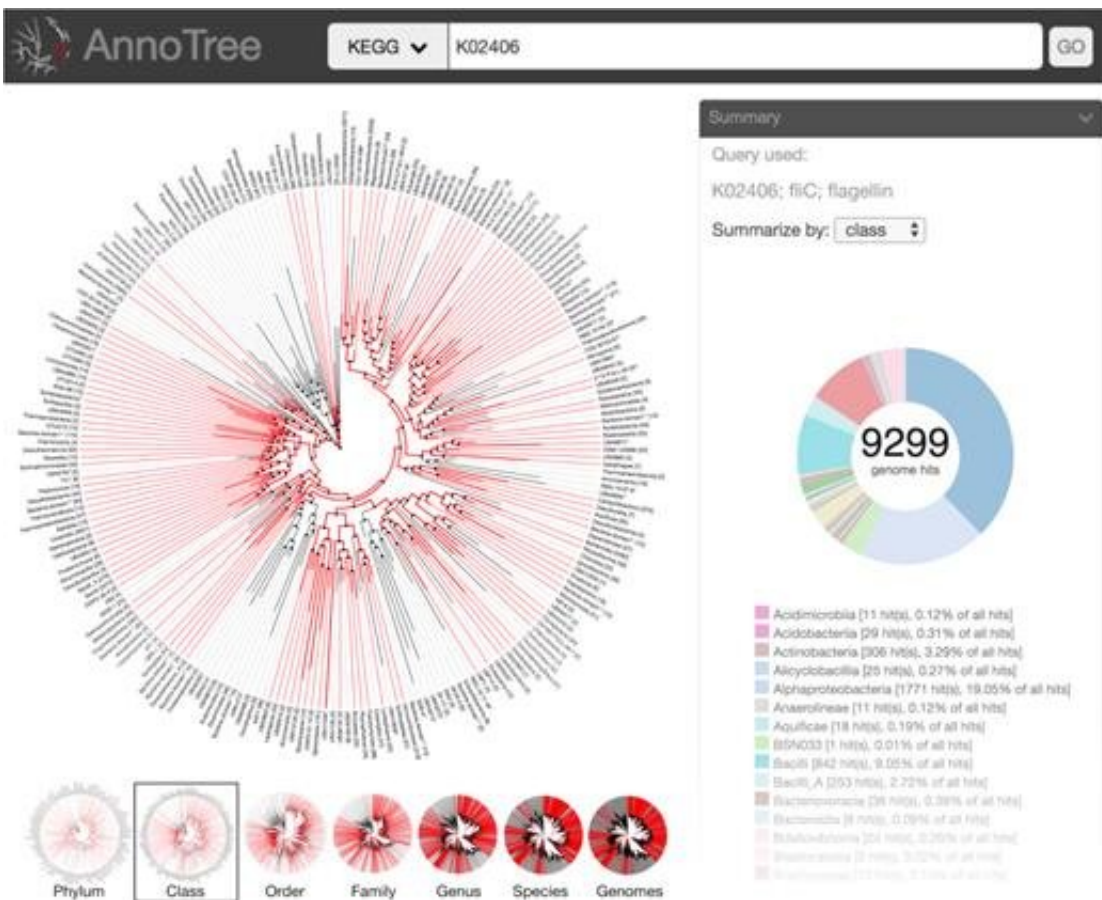


Powerful online tool will help researchers make new genomic discoveries

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Screenshot from AnnoTree. Credit: University of Waterloo

University of Waterloo researchers have developed a powerful new online tool that allows users to navigate through an interactive microbial tree of life, and to generate new scientific hypotheses and discoveries.

By integrating data across thousands of [microbial genomes](#), "AnnoTree" provides a comprehensive framework for exploring the evolution of microbial [genes](#) and functions, and can be used to advance research across a wide range of industries including microbiology, biotechnology, industrial products, biofuels, and food science.

Increased understanding of gene function and diversity in microbes can lead to the identification of important biological phenomena, including the spread of antibiotic resistance, the evolution of bacterial pathogens, the origin of new gene families, and instances of gene transfer between specific bacterial genomes. AnnoTree is freely available at annotree.uwaterloo.ca.

"Genomics has greatly expanded our understanding of the tree of life, but what a lot of researchers ultimately want to know is how [specific genes](#) and [biological functions](#) are distributed on the tree. While previously this type of analysis could take a substantial amount of time and effort, with AnnoTree it takes minutes or seconds," said Prof. Andrew Doxey, a bioinformatician at the University of Waterloo and member of the Waterloo Centre for Microbial Research (WCMR).

Through AnnoTree's Web-based interface, users may query any gene of interest. The presence or absence of the gene will then be "painted" onto the microbial tree of life to highlight species that do or do not contain the gene. Users can then "zoom in" further and explore specific lineages of interest. Users may download publication-quality images, phylogenetic trees, gene sequences, and other information.

AnnoTree uses the recently developed Genome Taxonomy Database (GTDB), which provides a standardized, thorough description of the phylogeny and taxonomic nomenclature for over 27,000 Bacteria and 1,500 Archaea. All 28,941 microbial genomes in the GTDB were re-analyzed, and functional annotations were assigned to [protein sequences](#)

during the development of AnnoTree. The resulting data is stored in an online database that is open and accessible to the research community. The AnnoTree database will be automatically updated to incorporate ongoing revisions to the GTDB taxonomy.

The AnnoTree application provides a reliable, automated tool for users to explore genes and functions of interest across microbes. The resulting genetic snapshots will enable researchers to quickly generate hypotheses, and identify genes and functions that are suitable for further study and application.

A paper on AnnoTree was recently published in the May 2019 issue of *Nucleic Acids Research*.

More information: Kerrin Mendler et al. AnnoTree: visualization and exploration of a functionally annotated microbial tree of life, *Nucleic Acids Research* (2019). [DOI: 10.1093/nar/gkz246](https://doi.org/10.1093/nar/gkz246)

Provided by University of Waterloo

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