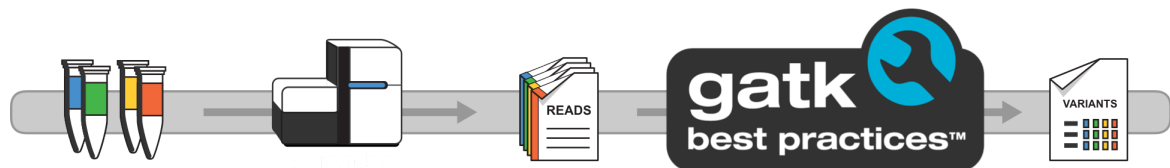


GATK

 gatk.broadinstitute.org/hc/en-us

Genome Analysis Toolkit

Variant Discovery in High-Throughput Sequencing Data



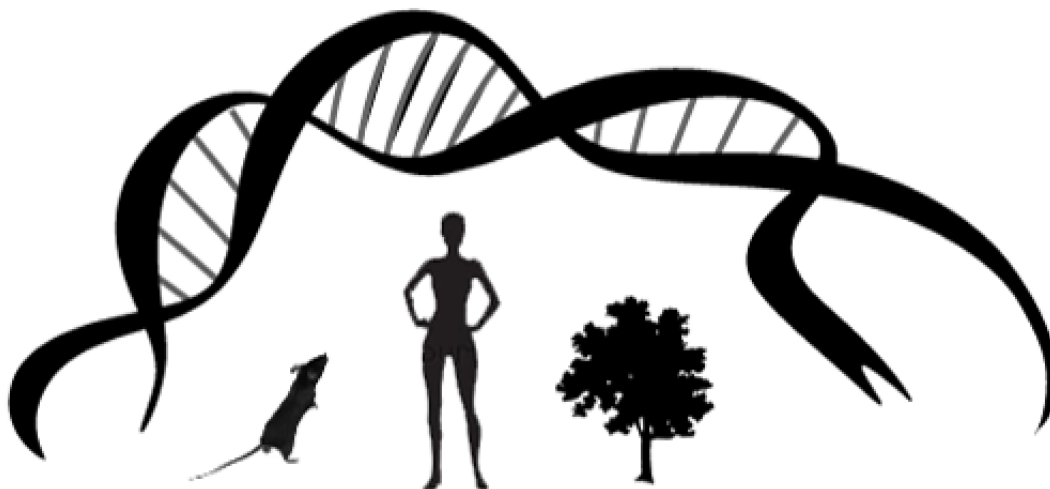
Developed in the Data Sciences Platform at the [Broad Institute](#), the toolkit offers a wide variety of tools with a primary focus on variant discovery and genotyping. Its powerful processing engine and high-performance computing features make it capable of taking on projects of any size. [Learn more](#)

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A genomic analysis toolkit focused on variant discovery.

The GATK is the industry standard for identifying SNPs and indels in germline DNA and RNAseq data. Its scope is now expanding to include somatic short variant calling, and to tackle copy number (CNV) and structural variation (SV). In addition to the variant callers themselves, the GATK also includes many utilities to perform related tasks such as processing and quality control of high-throughput sequencing data, and bundles the popular Picard toolkit.

These tools were primarily designed to process exomes and whole genomes generated with Illumina sequencing technology, but they can be adapted to handle a variety of other technologies and experimental designs. And although it was originally developed for human genetics, the GATK has since evolved to handle genome data from any organism, with any level of ploidy.



*The GATK, designed for human genome and exome analysis
and extended to handle other organisms.*

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