

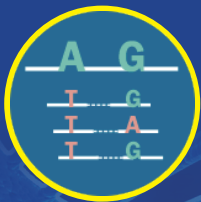


# BMKGENE BMKCloud



The BMKCloud Bioinformatics Analysis platform independently developed by BMKGENE is a powerful tool for bioinformatics analysis, covering mainstream bioinformatic analysis apps in genomics, transcriptomics, and microbiomics. These include WGS, GWAS, BSA, Evolutionary Genetics, mRNA, Full-length transcriptome (PacBio and Nanopore), SmallRNA, LncRNA, CircRNA, Amplicon (16S/18S/ITS), and Metagenomics (NGS), etc.

Even without a background in bioinformatics, you can use and analyze the bioinformatics data that you want. Simple and clear operations of the BMKCloud platform can help researchers search for data in the direction of demand. With the software analysis supporting and training, researchers can easily connect with the data platform.



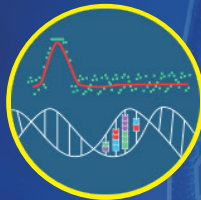
## ● **NGS-WGS(Illumina/BGI)** ●

The app of NGS-WGS facilitates the swift completion of tasks like data quality control, sequence alignment, SNP/InDel/SV variation detection, annotation, and mutation gene identification.



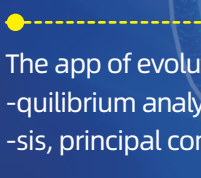
## ● **GWAS** ●

The app of GWAS uses specific statistical methodologies, GWAS analysis aims to uncover genome-wide nucleotide variations correlated with phenotypic differences.



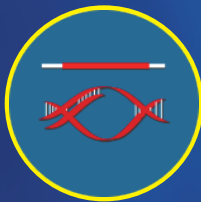
## ● **BSA** ●

BSA analysis involves pooling individuals with extreme phenotypic traits from a segregating population. Widely used in the genetic mapping of plants and animals, it is a valuable tool for marker-assisted breeding and gene positional cloning.



## ● **Evolutionary Genetics** ●

The app of evolutionary genetics is able to achieve phylogenetic tree construction, linkage disequilibrium analysis, genetic diversity assessment, selective sweep identification, kinship analysis, principal component analysis, and population structure characterization.



## ● **mRNA (Reference)** ●

The app of mRNA (Reference) is able to perform identify the boundaries of exon/intron, analyze the gene variant splicing, explore the gene regions and new transcripts, identify the SNP sites of the transcribed region, the boundary between the 3' and 5' genes, and the functional annotation and enrichment analysis of different samples (groups).

## ● **LncRNA** ●

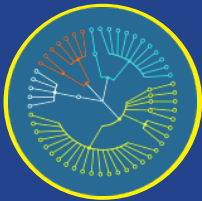
LncRNA analysis includes differential expression analysis on genes, gene structure analysis, novel lncRNA, and target prediction. Customized analysis includes expression-based data mining, Venn diagram on expression, lncRNA expression based data mining, differential expressed gene search, Venn diagrams on DEG, WGCNA analysis, etc.



## Amplicon (16S/18S/ITS)



Amplicon (16S/18S/ITS) analysis covers the mainstream analysis content of current microbial re- search, the analysis content is rich and comprehensive. Species classification, community structure, phylogenetic evolution, gene function analysis, and interspecies metabolic network analysis can be satisfied.



## Metagenomics (NGS)

The app of Metagenomics (NGS) provides detailed information on species diversity and abund- ance, population structure, phylogenetic relationship, functional genes, and correlation network with environmental factors.

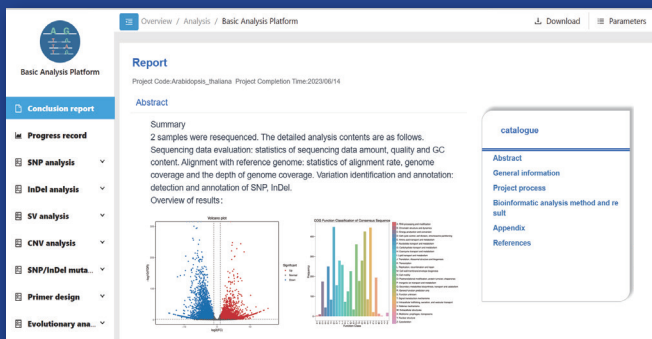
## BMKCloud platform contains standardized basic analysis and personalized analysis:

Basic analysis covers the current standard analysis content, the analysis content is rich and comprehensive; The content of personalized analysis is diverse. Samples can be selected and parameters can be set flexibly according to the basic analysis report and research purpose, to realize personalized requirements.

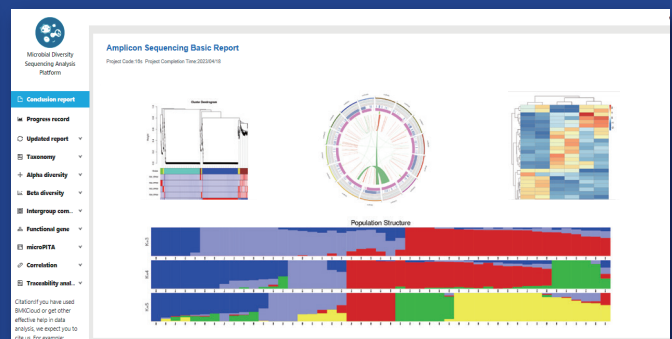
After setting parameters, click submit for analysis, and after the analysis is completed, a standardized conclusion report will be generated under the process customization page to realize one-click generation. Windows operating system is simple and fast.

One-stop solution for genomics, transcriptomics, and microbiomics research, enabling you to extract valuable insights quickly and accurately.

## Demo Report



## Visual Graphics



## Making Data Mining Effortless



## Advantages

Seamlessly integrate and analyze multi-omics data

Advanced data visualization

Powerful analysis tools

14 years of experience