

# MicroWorldOmics motivation



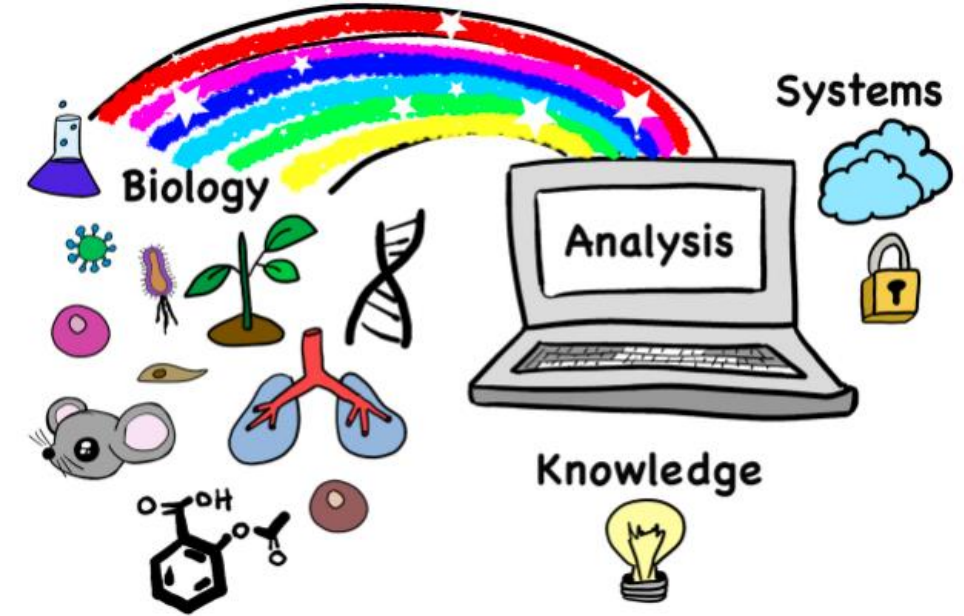
## Island Effect



Source

Method

Technology



- Need more interdisciplinary background
- Basic programming language is required

# Research Status of Integrated Bioinformatics Analysis Platforms at Home and Abroad



- Galaxy, an open-source web-based bioinformatics analysis platform developed by Pennsylvania State University in the United States, is widely used throughout North America and even around the world
- Hiplot rewrote biomedical data analysis in 28 months and was acknowledged by over 2,100 papers from 15 national laboratories around the world
- Tbtools, as a user-friendly graphical interface software tool, integrates multiple bioinformatics tools

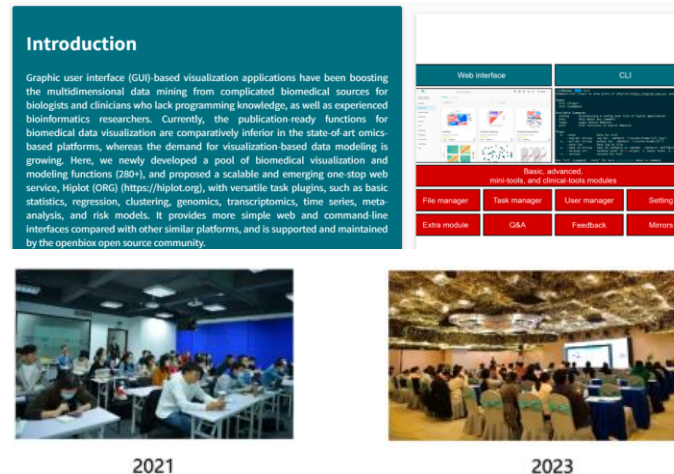
**Join us!**  
**Galaxy Training Academy**  
One week of Free, Global, Online Galaxy Training

**WHEN?** From the 12th to 16th of May 2025

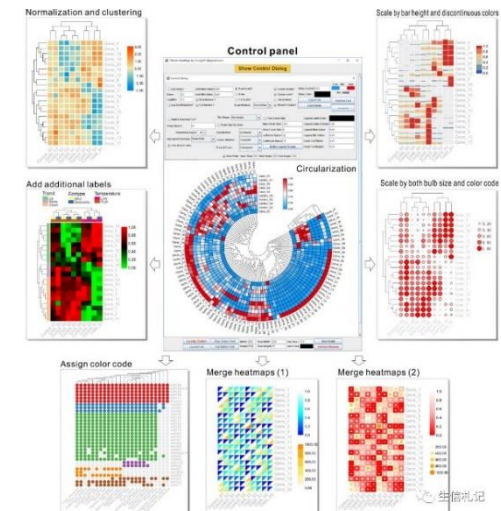
Learn about : Introduction to Galaxy, Assembly, Proteomics, Transcriptomics, Single Cell, Microbiome, Machine Learning, Python Intro, and much more!

**REGISTER NOW!** <http://gxy.io/GTA2025>

Galaxy



Hiplot



TBtools

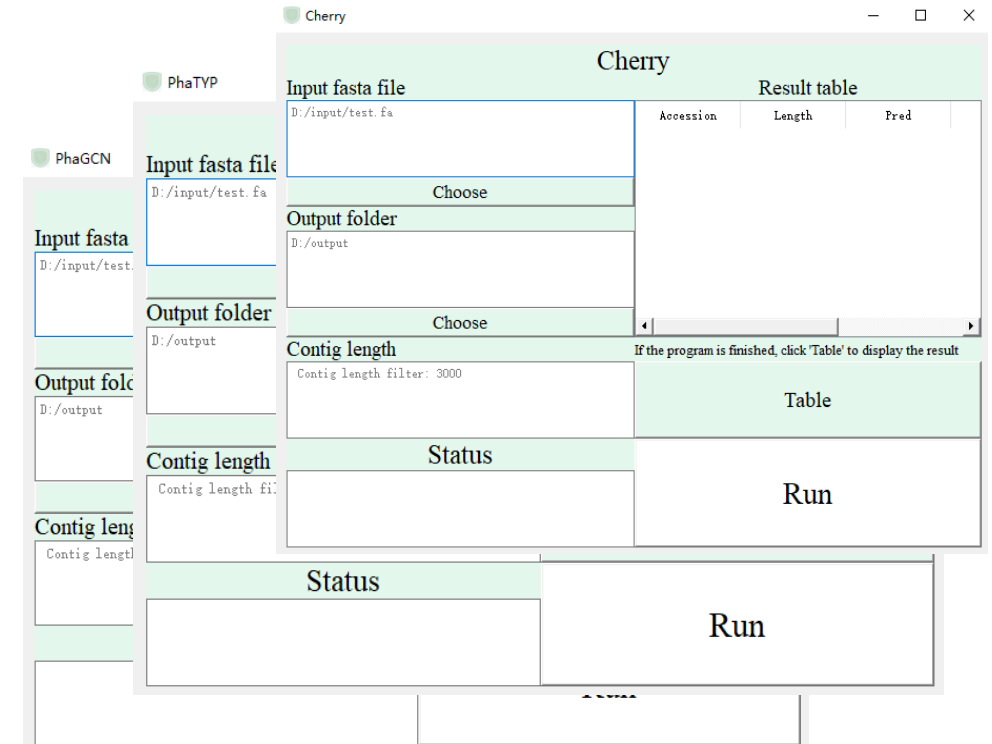
# Drive bioinformatics software towards convenience



UI



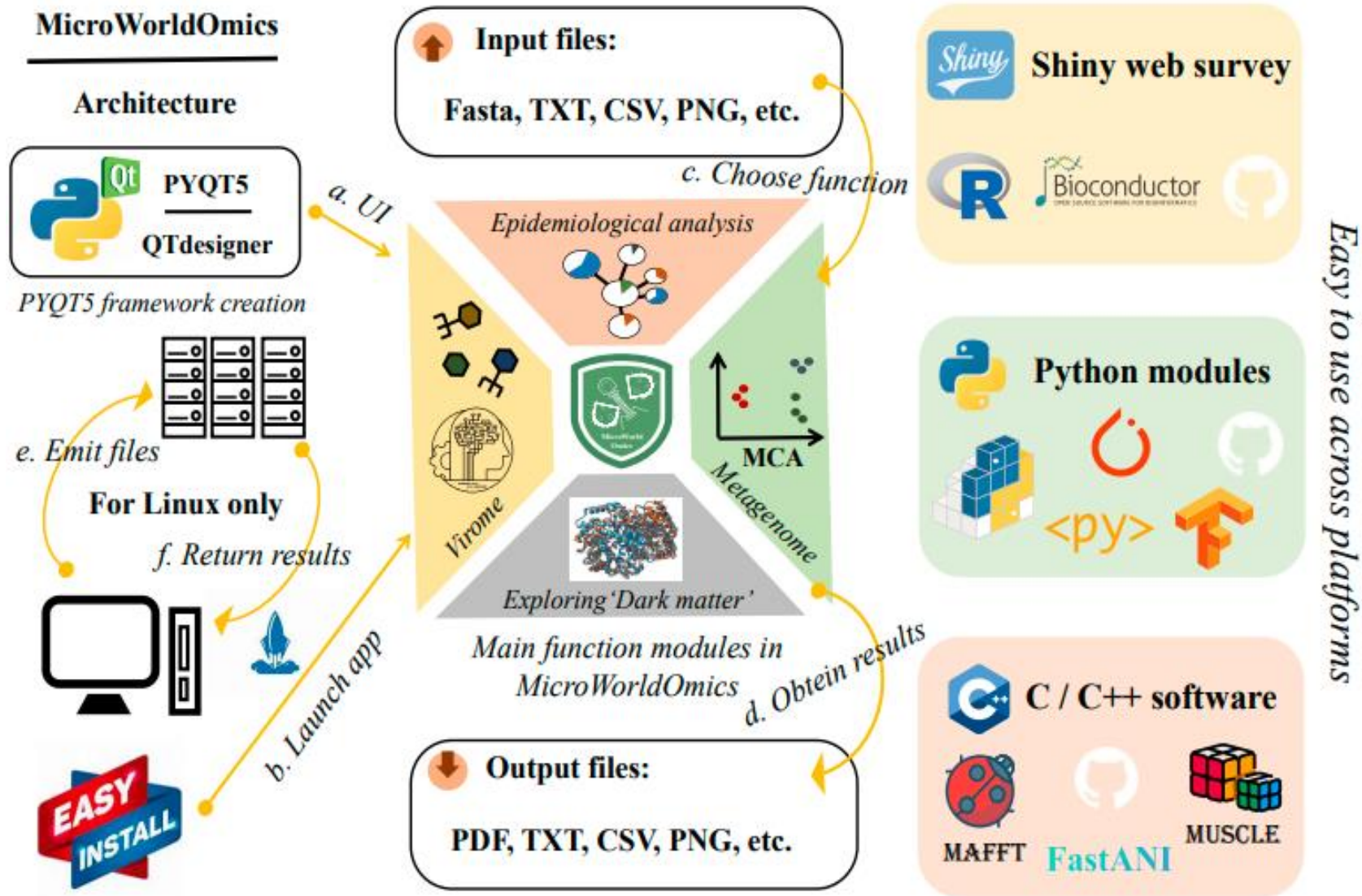
Plugins



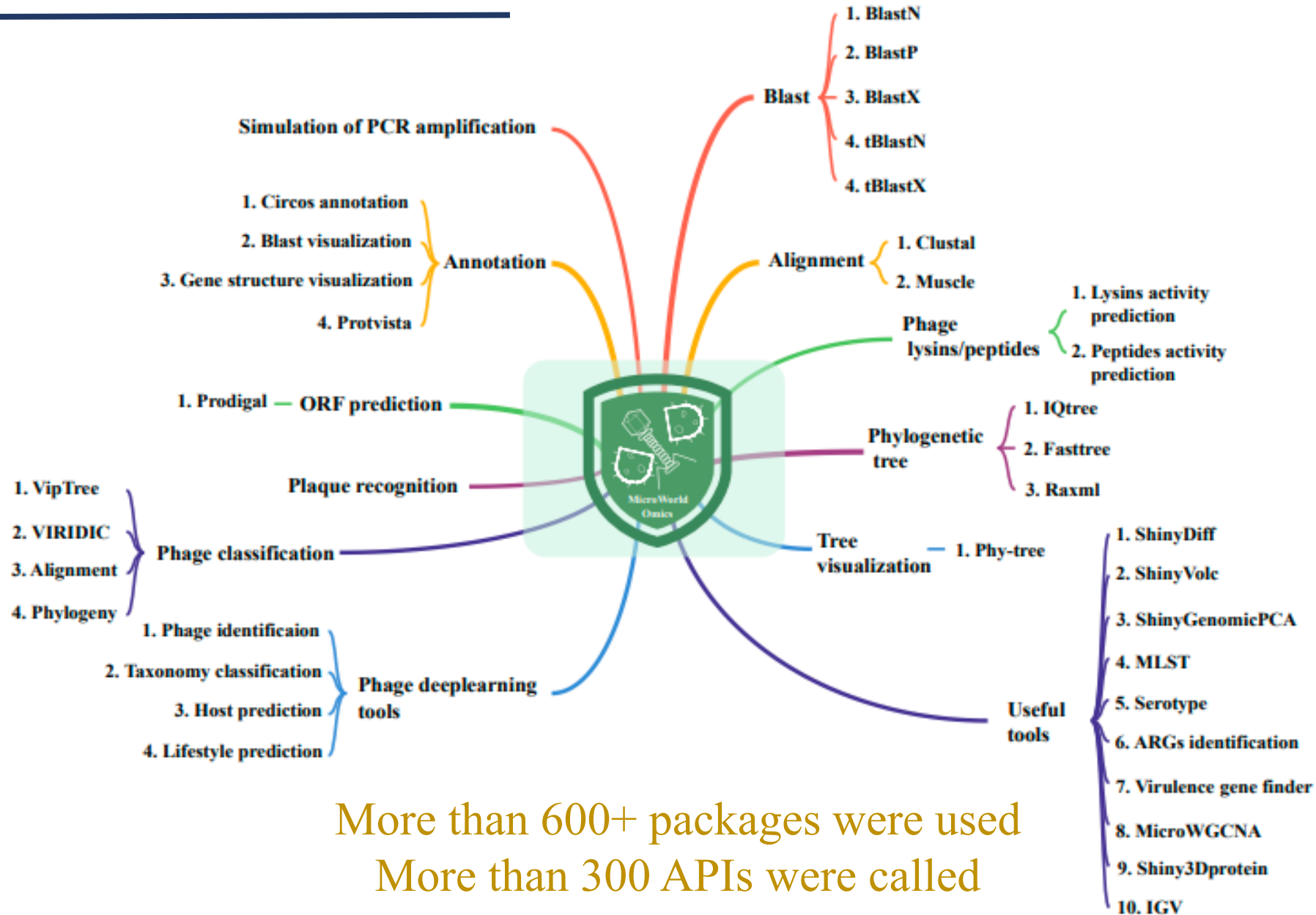
MicroWorldOmics



# MicroWorldOmics design framework

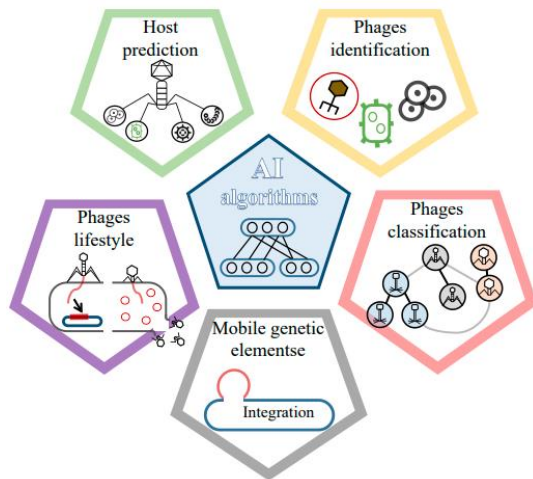


# MicroWorldOmics functional function

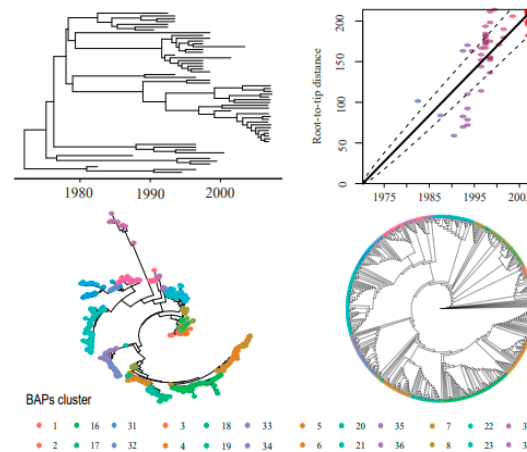


More than 600+ packages were used  
More than 300 APIs were called

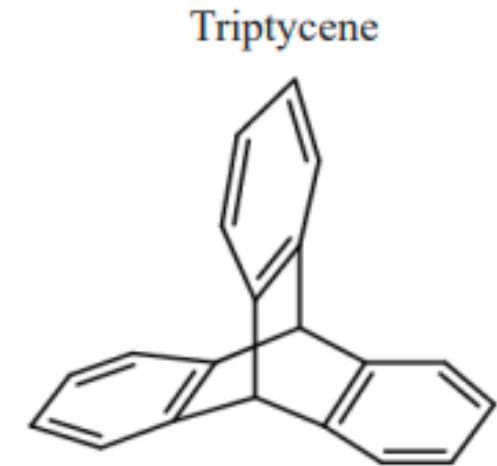
# MicroWorldOmics main modules



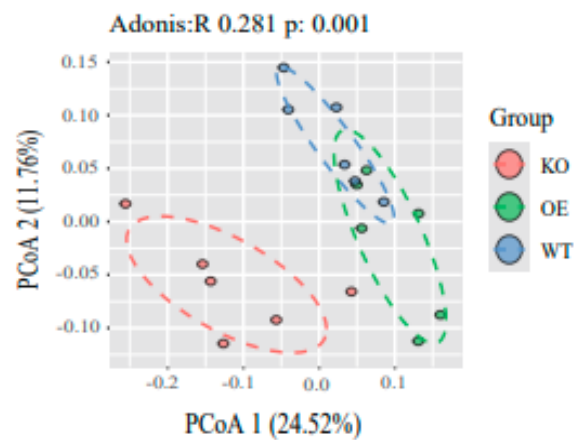
Comprehensive analysis of phages



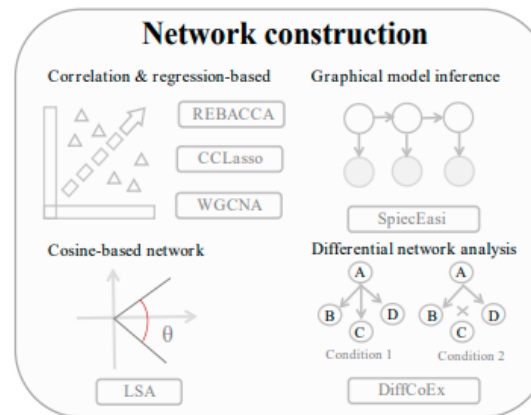
Genomic analysis of bacteria/fungi



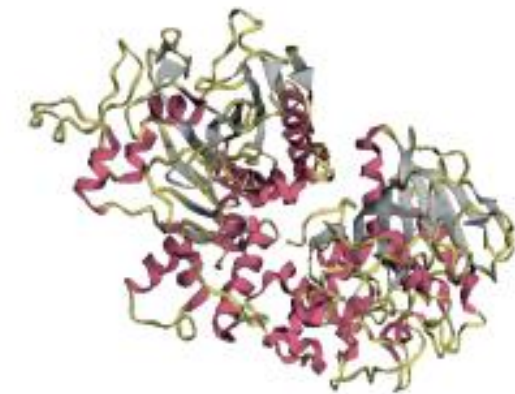
Chemical structure drawing



Metagenomic/16s downstream analysis



Network construction



Protein alignment/visualization



# MicroWorldOmics differential network



## Network construction

Correlation & regression-based

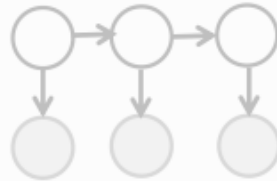


REBACCA

CCLasso

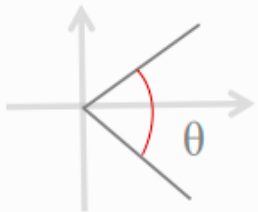
WGCNA

Graphical model inference



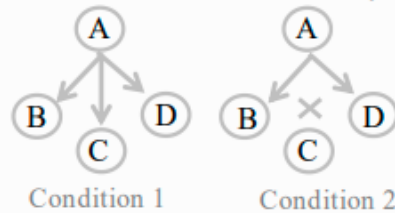
SpiecEasi

Cosine-based network



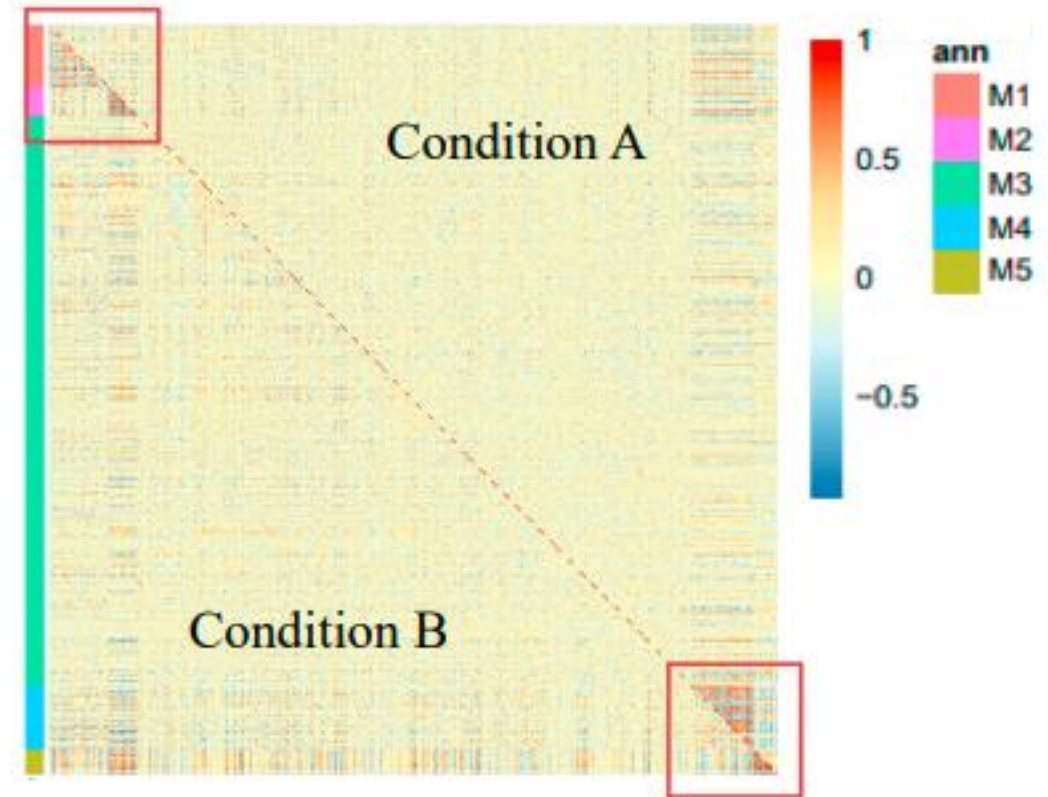
LSA

Differential network analysis



DiffCoEx

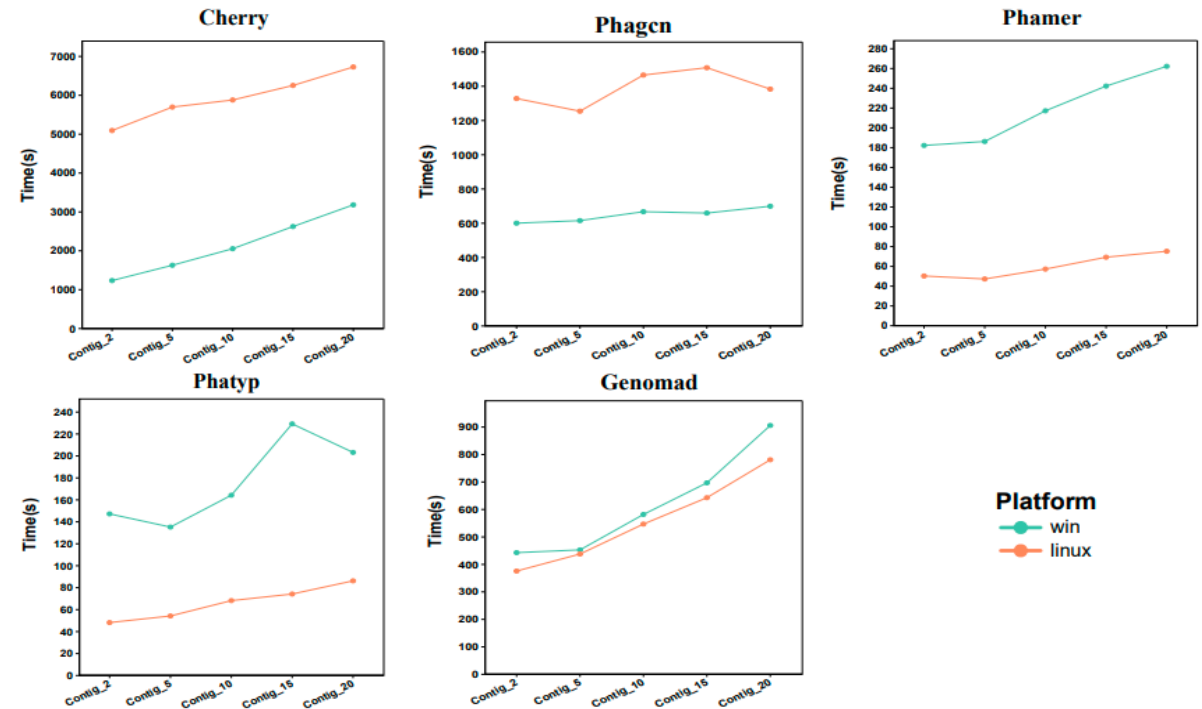
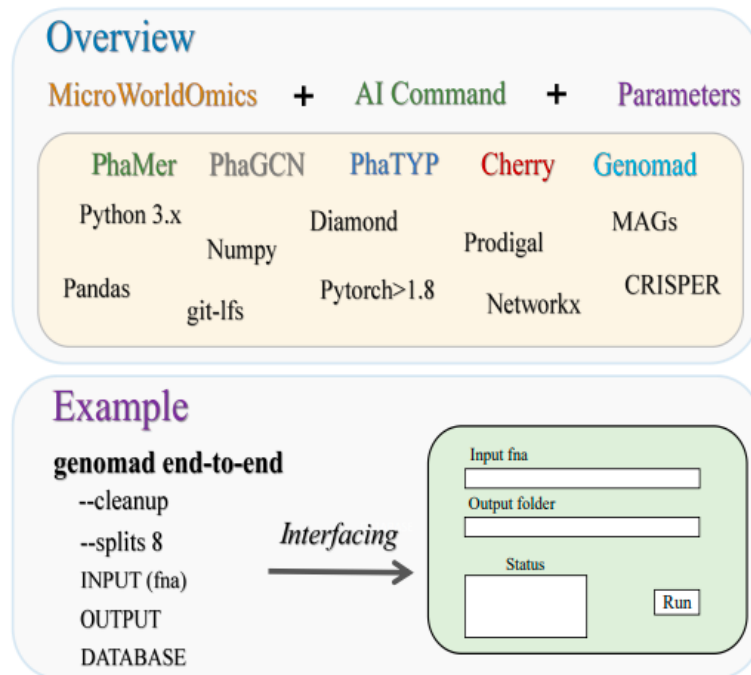
## Difference networks analysis





# MicroWorldOmics transplant deep learning algorithms

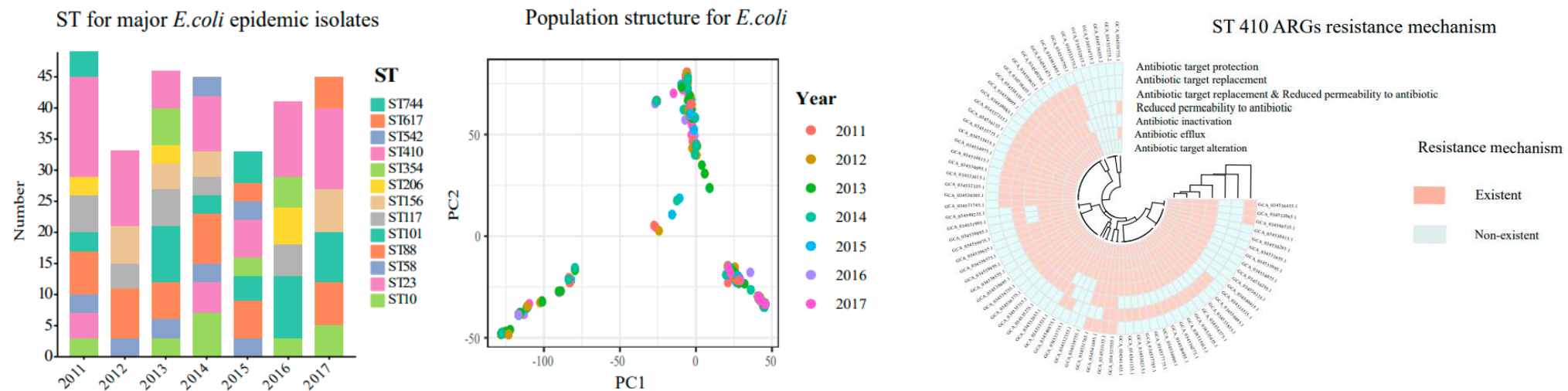
- Transplant the deep learning tools related to the **discrimination of phage sequences, life style, species classification** and **host prediction**
- After the algorithm was rewritten, the running time of some methods in Windows was **less** than that on the workstation





# MicroWorldOmics Use Case - ExPEC as an example

- Multilocus sequence typing (MLST), the demonstration output shows from different sources (sick pigs, healthy pigs and patients)
- After obtaining the core genomes of all strains, PCA dimensionality reduction clustering was performed using the plugin ShinyGenomePCA
- The plug-in can be used to describe the carriers of drug resistance genes, the distribution of serotypes and the distribution of sampling areas



Data from Xudong Li et al 2024 *Nat Commun*



# MicroWorldOmics Use Case - Optimizing MLST Identification

- The identification of ST types of parenteral pathogenic Escherichia coli using the plug-in MLST is more accurate than that of SRST2

	Position :	320		443		470
		↓		↓		↓
A1 (strain contig)		C	G ... A	T	G ... C	A
purA_8 (For reference)		T	G ... A	C	G ... C	C
purA_12 (MicroWorldOmics)		C	G ... A	T	G ... C	A

Strain A1

	Position :	27	28		472	473
		↓	↓		↓	↓
A103 (strain contig_1)		A	C	A ... T	T	C
recA_6 (For reference)		A	T	A ... T	C	C
recA_44 (MicroWorldOmics)		A	C	A ... T	T	C

	Position :	330		334		338
		↓		↓		↓
A107 (strain contig)		A	C A G	C	T T C	C
mdh_20 (For reference)		A	C A G	G	T T C	C
mdh_411 (MicroWorldOmics)		A	C A G	C	T T C	C

Strain A107

	Position :	238		240		242
		↓		↓		↓
A103 (strain contig_2)		G	A	C	T	T
gyrB_15 (For reference)		G	A	G	T	T
gyrB_1542 (MicroWorldOmics)		G	A	C	T	T

# MicroWorldOmics is widely promoted

- 2023年10月, 由Hiplot和开发者刘灶渠开发的泛癌分析BEST网站发布并发表于 Journal of Big Data.
- 2023年12月, Hiplot开发团队参加首届BioOS开源开放大赛, 攻克最难赛题, 以“符合GA4GH标准的支持多流程语言的任务调度引擎”拿下三等奖。
- 2024年6月, 由开发者彭炳明开发的工具idbview发布更新, 后发表于Frontiers in Immunology杂志。
- 2024年7月, 开发者董伟和李润泽联合开发了MicroWorldOmics工具, 用于微生物组和病毒组多组学分析。
- 2024年10月, 开发者陈俊宏主导开发的影像组学分析工具TEAR及苗奔奔、董伟等人联合开发StereoHub空间转录组分析应用, 分别在2024“猛犸杯”国际生命科学数据创新大赛赢得周提交奖、决赛二等奖和最佳人气奖。
- 2025年2月, 由Hiplot与戴晓峰老师合作开发的世界首个冷大气等离子体(CAP)肿瘤治疗的多组学数据分析网站发布。



## MicroWorldOmics: A Comprehensive Toolkit for Microbiome and Virome Exploration

Imagine a software suite that can handle all your microbiome and virome analysis needs without coding skills. This is what we developed this desktop application.

**User-Friendly Interface:** For easy navigation, MicroWorldOmics provides a simple input, output, parameters, and analysis workflow.

**Plugin Powerhouse:** More than just a toolkit, MicroWorldOmics comes with a variety of plugins that allow you to analyze your data in different ways, no matter if you want to make a simple analysis or a more complex one.

**Platform Agnostic:** Operate MicroWorldOmics can run smoothly on Windows, Linux, and Mac machines for researchers using different platforms.

**Data Visualization and Statistics:** Apps, which are easily incorporated into your workflow, analyze your data interactively and generate diagrams to understand better.

**A variety of Formats for Data:** MicroWorldOmics software supports a wide range of data formats, including TXT, CSV, PNG, etc.

**Sample Data Playground:** more! These sets of sample data and refer back for any clarification.



Image Description: The MicroWorldOmics innovative design concept, framework architecture, and main functions. Image Source: <https://doi.org/10.1101/2024.06.24.600528>

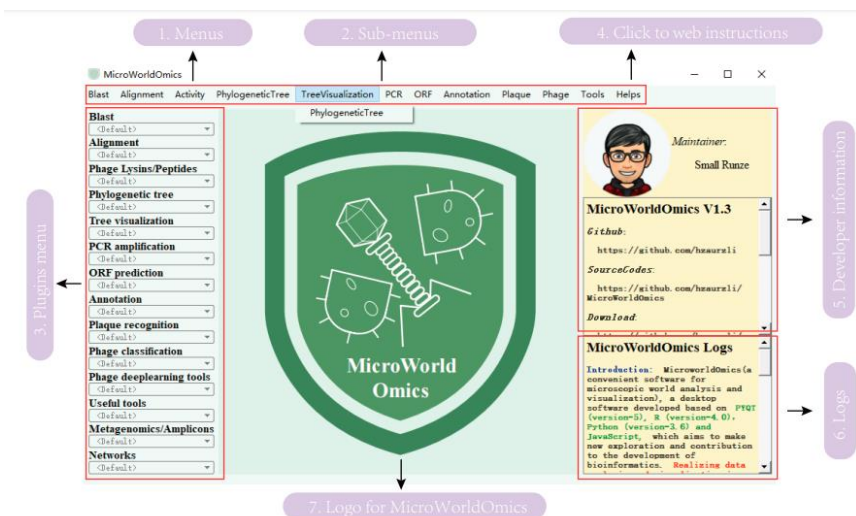
Received promotion from the development team of Hiplot, a large domestic biomedicine platform

The software developed by MicroWorldOmics has been promoted by the International Centre for Bioinformatics Research and Technology (CBIRT)

# Summarize the work of MicroWorldOmics



- A one-stop desktop application suite (with over 90 functional modules) for downstream bioinformatics analysis of the microbiome and virome has been established, making the related bioinformatics analysis more "user-friendly". Meanwhile, some plugins have been optimized to further enhance the analysis efficiency
- Adopting the design concept of modular development makes the update and maintenance of the software more convenient. A software forum has been established to facilitate cloud developers to offer suggestions for the upgrade of MicroWorldOmics



Forum: <https://hzaurzli.github.io/index.html>

Github: <https://github.com/hzaurzli/MicroWorldOmics>