## Comprehensive analysis of phages





# Comprehensive analysis of the virome



PhaMer - Identify the phage sequence

PhaGCN - Species identification

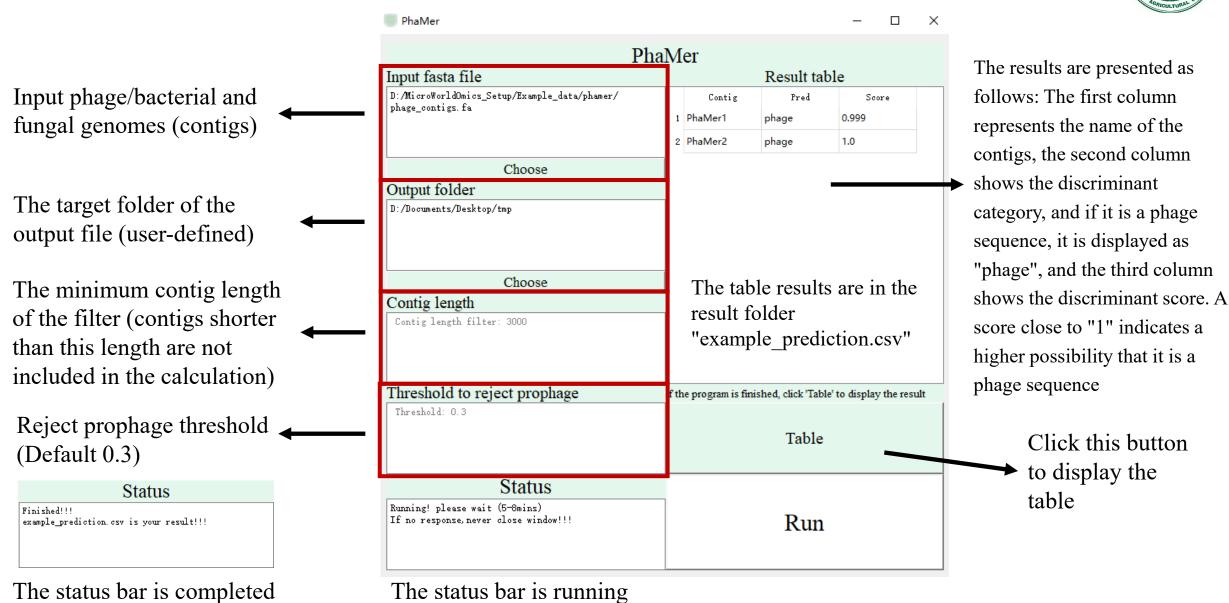
PhaTYP – Life style identification

Cherry – Host prediction

Genomad – Mobile elements identification

#### PhaMer - Identify the phage sequence

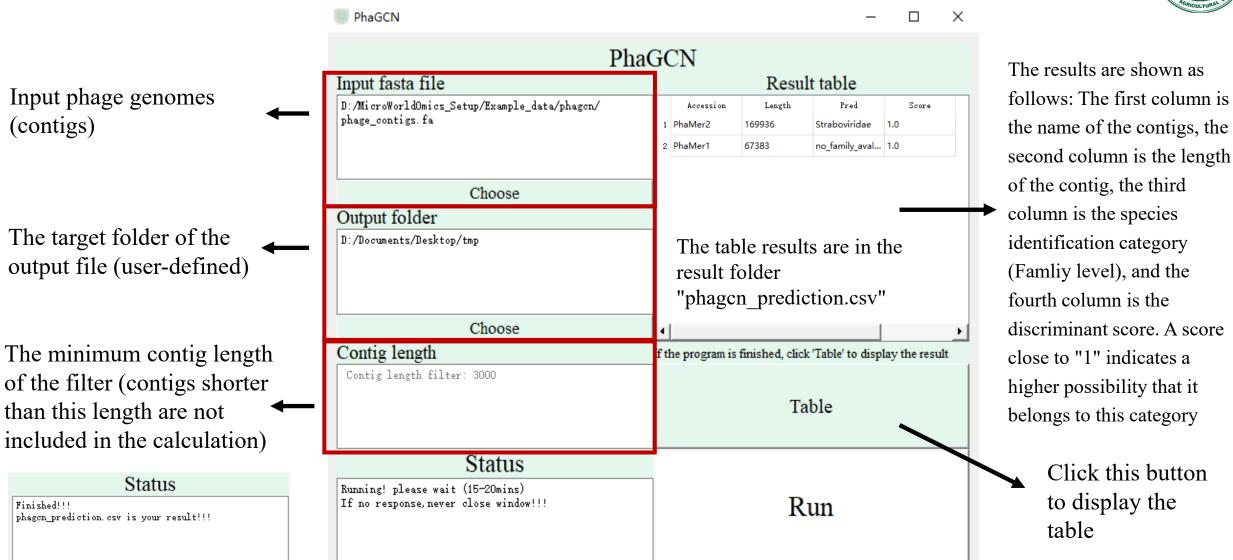




#### PhaGCN - Species identification

The status bar is completed

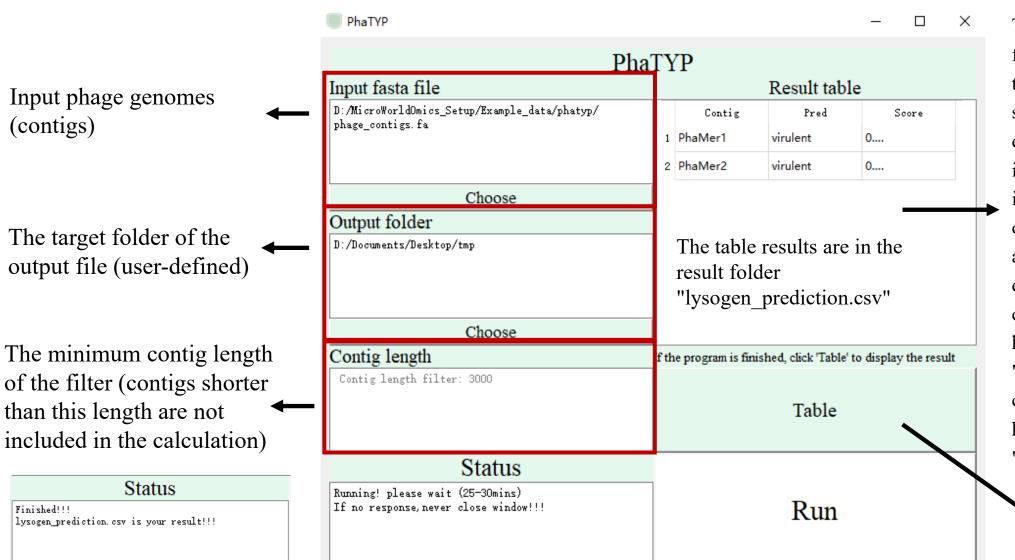




The status bar is running

## PhaTYP – Life style identification





The results are shown as follows: The first column is the name of the contigs, the second column is the discriminant category, and if it is a virulent bacteriophage, it is displayed as "virulent"; otherwise, it is "Lysogen", and the third column is the discriminant score. A score close to "1" indicates a higher possibility that it is "Lysogen", and a score close to "0" indicates a higher possibility that it is "virulent"

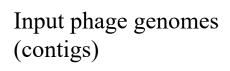
Click this button to display the table

The status bar is completed

The status bar is running

#### Cherry – Host prediction





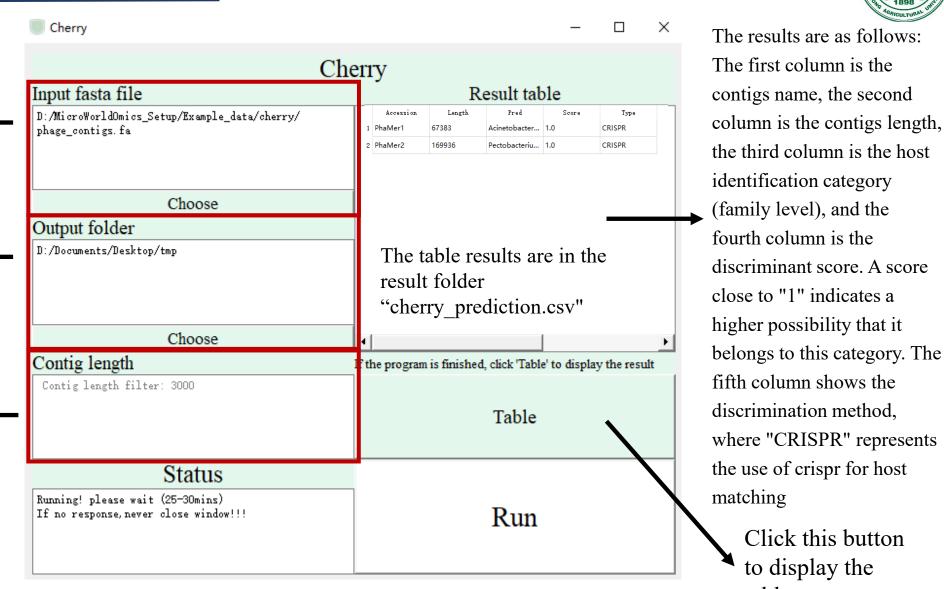
The target folder of the output file (user-defined)

The minimum contig length of the filter (contigs shorter than this length are not included in the calculation)

#### Status

Finished!!! cherry\_prediction.csv is your result!!!

The status bar is completed



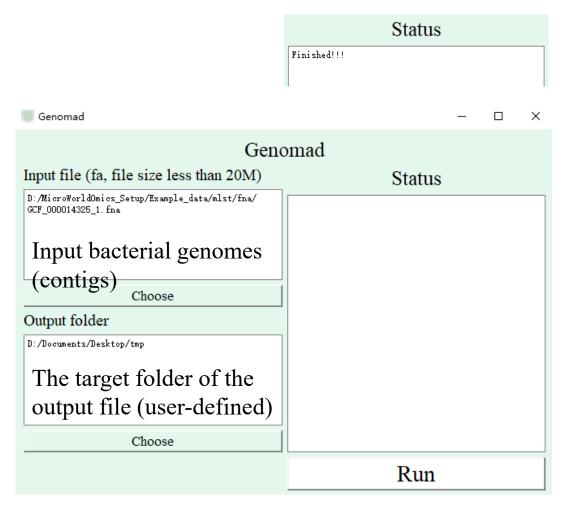
matching Click this button to display the table

The status bar is running

#### Genomad – Mobile elements identification



#### The status bar is completed



								Act of the	189
GCF_00001432	25_1_agg	gregated	_classif	2025/6	/26 12:16	文件夹		AGI	PICULT
GCF_000014325_1_annotate				2025/6	/26 12:16	文件夹			
GCF_000014325_1_find_proviruses				2025/6	/26 12:16	文件夹			
GCF_000014325_1_marker_classificati				2025/6	/26 12:16	文件夹			
GCF_000014325_1_nn_classification					/26 12:16	文件夹			
GCF_000014325_1_summary				2025/6	6/26 12:16	文件夹			
GCF_000014325_1_aggregated_classif					5/26 12:16	文本文档		4 KB	
GCF 000014325 1 annotate.log					5/26 12:16	文本文档		3 KB	
GCF_000014325_1_find_proviruses.log					, 5/26 12:16	文本文档		4 KB	
GCF_000014325_1_marker_classificati					/26 12:16	文本文档		5 KB	
GCF 000014325 1 nn classification.log				2025/6/26 12:16		文本文档		5 KB	
GCF_000014325_1_summary.log				2025/6/26 12:16		文本文档		4 KB	
_ GCI_00001402	.5_1_5411	u.yc	9	2025/0	720 12110	~+~1		7 10	
gene	start	end	length	strand	gc_content	genetic_code	rbs_motif	marker	٢
NZ CP045018.1 1	1	399	399	1	0.536	11	None	GENOMAD.1	
NZ CP045018.1_1	401	1111	711	1	0.568	11	AGGAG	GENOMAD.1	
NZ CP045018.1 3	1143	1493	351	1	0.382	11	AGGAG	GENOMAD.1	
NZ_CP045018.1_4	1509	2120	612	1	0.477	11	GGA/GAG/AGG	GENOMAD.1	
NZ_CP045018.1_5	2183	13516	11334	1	0.566	11	None	GENOMAD.1	
NZ_CP045018.1_6	13585	15084	1500	1	0.550	11	AGGAG	GENOMAD.1	
NZ_CP045018.1_7	15163	16128	966	-1	0.469	11	GGAGG	NA	
	_							<b>•</b>	

Interpretation results can be reference:

https://github.com/apcamargo/genomad/