

mGPS Interface Tutorial

1. Introduction

mGPS interface is a web program based on the mGPS application created by Shiny. It can build a microbial origin prediction model and predict the origin of microbes. To learn more about mGPS, please visit [mGPS](#). For the specific usage of the mGPS interface, please check the Readme file on [mGPS interface Github](#).

2. Function and Output

2.1 Welcome page

A brief introduction to the functions of mGPS interface and how to start using it

Geographical origin prediction of microbiome

Prediction program

Build a new prediction model using mGPS ▾

Input file

☒ Merged metadata and abundance file
☐ Separate metadata and abundance file

Upload the reference merged dataset file

Browse...

No file selected

Enter the main locality level

Enter the locality hierarchy

Column range of abundance data

☐ Locality sample size cut off (Optional)
☐ Subsets in feature elimination (Optional)

Start

Welcome

HELP

Result Plot

Output

Welcome to mGPS application

This is a web program based on the mGPS application created by Shiny. It can build a microbial origin prediction model and predict the origin of microbes.

To learn more about mGPS, please visit: [mGPS](#)

Function

This program contains three functions. These function can be performed by selected **Prediction program** in the left side bar. The detail usage will be introduced in **HELP** tab for each function.

- 1. Build a new prediction model using mGPS**

This mode can use the mGPS tool to build a microbial source prediction model based on the microbial abundance data and coordinates data uploaded by the user. To learn more about mGPS, please visit: [mGPS](#)
- 2. Build a new prediction model using mGPS and predict new samples**

This mode can train the microbial origin prediction model based on the reference data set uploaded by the user. The constructed prediction model will be used to predict the new sample to be tested provided by the user and report the prediction result of the sample source. (If user want to visualize the accuracy of the model, please use function: *Build a new prediction model using mGPS*)
- 3. Use an existing model to predict new samples**

This mode can predict new sample origin based on an exsiting prediction model. Model can be downloaded in **Output** tab of function: *Build a new prediction model using mGPS* or *Build a new prediction model using mGPS and predict new samples*

2.2 Function 1: Build a new prediction model using mGPS

Geographical origin prediction of microbiome

Prediction program
Build a new prediction model using mGPS

Input file
☒ Merged metadata and abundance file
☐ Separate metadata and abundance file

Upload the reference merged dataset file
Browse... No file selected

Enter the main locality level

Enter the locality hierarchy

Column range of abundance data

☐ Locality sample size cut off (Optional)
☐ Subsets in feature elimination (Optional)

Start

WelcomeHELPResult PlotOutput

Build a new prediction model using mGPS

Function description

This model can use the mGPS tool to build a microbial source prediction model based on the microbial abundance data and coordinates data uploaded by the user.

Usage

In left side bar:

1. Select **Prediction program** as *Build a new prediction model using mGPS*
2. **Input file(s)**: Upload data file(s) (in .csv format) containing microbial abundance data and metadata.

In metadata, at least one locality (eg. continent, city) and coordinates (necessary) data columns should be included. The metadata and abundance data of the sample can be merged into one file (*Merged metadata and abundance data*), or uploaded as two files (*Separate metadata and abundance data*)

When *Separate metadata and abundance file* is selected. **Merge column name in metadata/abundance file**: Input the header name of column which is the merged column in two files.
3. **Enter the main locality level**: Input the main locality target. It should same as that column header. (eg. city)
4. **Enter the locality hierarchy**: The locality chain used in mGPS to construct the prediction model (same column headers). It should contain one or two locality information, latitude and longitude. Use ',' as separator. (eg. continent,city,latitude,longitude)

2.2.1 Function 1 introduction

In this mode, you can use the mGPS tool to build a microbial source prediction model based on the microbial abundance data and coordinates data uploaded by the user.

2.2.2 Output plots

Geographical origin prediction of microbiome

Prediction program
Build a new prediction model using mGPS

Input file
☒ Merged metadata and abundance file
☐ Separate metadata and abundance file

WelcomeHELPResult PlotOutput

longitude range:
-165 -131 -97 -63 -29 5 39 73 107 141 168

latitude range:
-90 -69 -48 -27 -6 15 36 57 78 99 120

Whether pull points to land/marine
☐ Pull to land
☐ Pull to waterbody
☒ Default

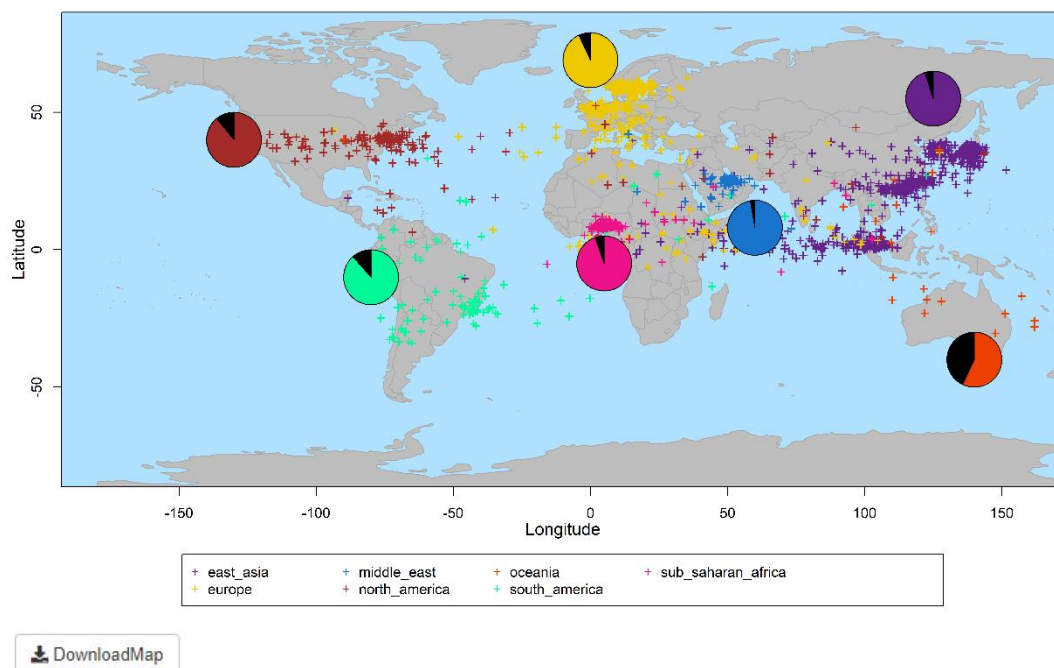
The "Result Plot" of this mode will show the accuracy of the prediction model trained by the mGPS tool and based on the reference microbial database you uploaded.

If you want to zoom in on a specific area of the map, you need to adjust both the longitude and latitude ranges. "Pull to land" refers to pushing the predicted point to the nearest land, and "Pull to waterbody" refers to pushing the predicted point to the nearest water body.

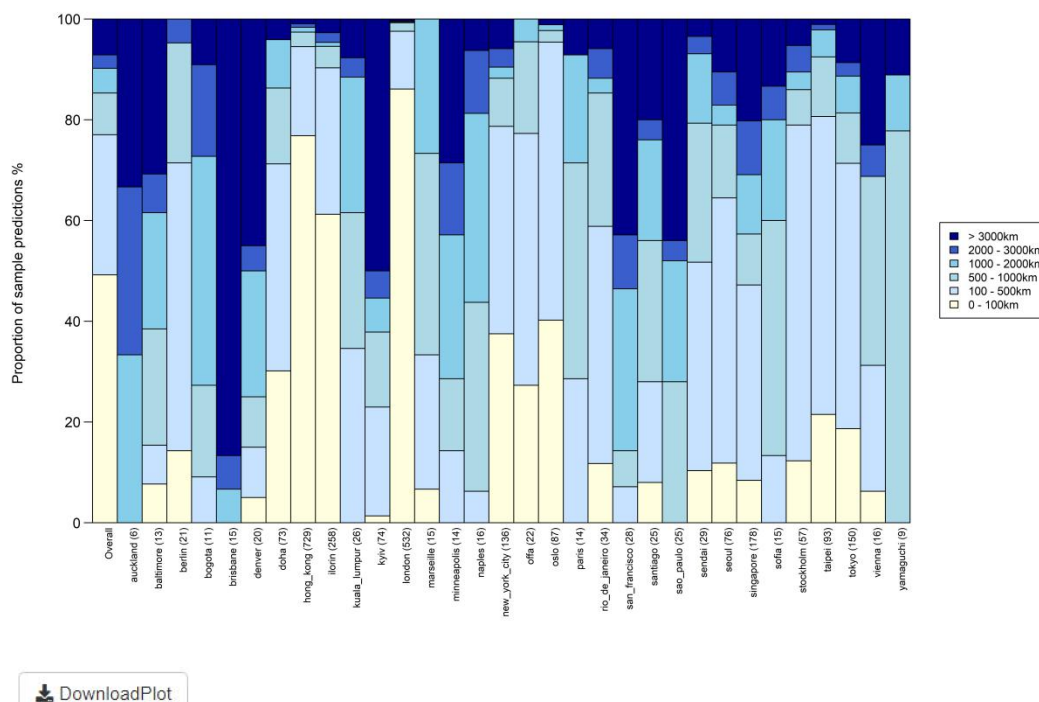
How the algorithm detects the accuracy of model: The original database will be divided into 5 folds, and mGPS will use 4 of these folds to train the model, and the resulting model will be used to predict the microbial source of the remaining fold. Iteratively obtain the prediction result of the original database and compare it with the actual location of the microorganism.

Example output plot:

a. World map: samples' prediction origins are plotted on the world map. By adjusting the range of longitude and latitude, you can select the plotting area of the figure on the map. In addition, you can choose whether to pull the predicted point into the continent or the ocean. The predicted origin of original samples will be mapped onto the world map. The pie charts with colors divided by geographic area represent the proportion of samples in the area whose origin region is predicted to be the same continent as the true location. You can download and save the png file of this map through the button 'DownloadMap' below the figure.



b. Prediction accuracy bar plot: The prediction accuracy of the model is shown per-site as the distances between the predicted and true sampling sites for the reference samples. The average prediction accuracy across all samples with each population given equal weight is shown on the left. You can download and save the png file of this plot through the button 'DownloadPlot' below the figure.



2.2.3 Output files

Data processing: Please wait while output files are being generated. When the prompt bar (*Data loading...*) disappears you can see the results and download files.

Geographical origin prediction of microbiome

Data loading....

Prediction program

Build a new prediction model using mGPS

Input file

☒ Merged metadata and abundance file

☐ Separate metadata and abundance file

Welcome HELP Result Plot **Output**

Predicted original coordinates of samples can be downloaded. Prediction model in RDA format can be downloaded

Download prediction data

Download feature subsets accuracy in feature elimination

Download optimal features in prediction model DownloadModel

a. “Downlad prediction data” button - *Predicted_origin.csv*: Records the predicted original coordinates of the reference samples (columns: LatPred and LongPred). Also contains the distance between the predicted and true sampling site for the reference samples (column: Distance_from_origin). The original metadata and abundance data will be merged.

	A	B	C	D	E	F	G	H	I	J	K	L	M
1		uuid	continent	city	latitude	longitude	taxal_abundance	taxan_abundance	cityPred	latPred	longPred	Distance_from_origin	
2	1	1	africa	offa	8.1548483	4.7263633	0.00017	0	offa	7.881690979	11.71926498	771.4253212	
3	2	2	africa	offa	8.15485	4.726465	9.00E-05	0	offa	8.323236465	-0.264049619	550.1233564	
4	3	3	africa	offa	8.1556609	4.7244244	8.00E-05	0	offa	7.446023464	4.620732784	79.81995773	
5	4	4	america	new_york_city	40.70670433	-74.0111377	7.00E-05	2.00E-05	new_york_city	40.67137527	-72.10720062	160.7544161	
6	5	5	america	new_york_city	40.67953148	-73.9035273	0.00016	0	new_york_city	18.32634163	-43.18954086	3843.356172	

b. “Download feature subsets accuracy in feature elimination” button -

Features_subsets_accuracy.csv: Records the accuracy of the prediction model with different features (microorganisms) subset size (column: n_vars). You can manually enter a specific range

or value of subset size in the option '*Subsets in feature elimination (Optional)*' .The algorithm will use the subset size with the highest accuracy (column: accuracy) to select the number of feature. For example, the subset with a size of 100 has the highest accuracy value, and then the algorithm will select most important 100 features to construct the model, and these features are recorded in the file *Optimal_features.csv*.

	A	B	C
1		n_vars	accuracy
2	1	50	0.643030303
3	2	100	0.764242424
4	3	150	0.723838384
5	4	200	0.731919192
6			

Hint: In addition to checking the given subset sizes, the algorithm also tries to use all features(taxa) to predict the origin. If the accuracy of the subset sizes uploaded by the user is lower than the accuracy of using all features, the algorithm will still choose to use all features for prediction to improve the accuracy. If the user still wants to use a specific number of features, the feature columns in the input file can be manually filtered according to the order of importance of the features in the output file "**Optimal_features.csv**" (Download optimal features in prediction model).

c. “Download optimal features in prediction model” button - *Optimal_features.csv*: Records the optimal features (microorganism) used to predict the original coordinates that selected by the mGPS algorithm. The number of features is equal to the subset size with highest accuracy value (n_vars) recorded in the *Features_subsets_accuracy.csv* file.The column “Overall” records the importance value of each feature. The higher the value, the more important the feature in the prediction algorithm.

	A	B	C	D	E
1		Overall	taxa		
2	Acetobacter. pasteurianus	0.0889962	Acetobacter. pasteurianus		
3	Acetobacter. aceti	0.0728943	Acetobacter. aceti		
4	Acetobacterium. woodii	0.0474666	Acetobacterium. woodii		
5	Acholeplasma. brassicae	0.0429964	Acholeplasma. brassicae		

d. “DownloadModel” button - *Prediction_model.Rda*: The origin prediction model built by mGPS algorithm saved in Rda format. You can download the model to view the details of the model through load into r. Also, this model can be uploaded to predict the origin of new samples through function 3 “Use an existing model to predict new samples”.

```
load('Outputs/Prediction_model.R')
```

2.3 Function 2: Build a new prediction model using mGPS and predict new samples

Geographical origin prediction of microbiome

Prediction program
Build a new prediction model using mGPS and predict new samples

Upload new sample abundance file(s)
Browse... No file selected

Upload reference file(s)
☒ Merged metadata and abundance file
☐ Separate metadata and abundance file

Upload the reference merged dataset file
Browse... No file selected

Enter the main locality level

Enter the locality hierarchy

Column range of abundance data

☐ Locality sample size cut off (Optional)

HELPResult PlotOutput

Build a new prediction model using mGPS and predict new samples

Function description

This mode can train the microbial origin prediction model based on the reference data set uploaded by the user. The constructed prediction model will be used to predict the new sample to be tested provided by the user and report the prediction result of the sample source. (If user want to visualize the accuracy of the model, please use function: *Build a new prediction model using mGPS*)

Usage

In left side bar:

1. Select **Prediction program** as *Build a new prediction model using mGPS and predict new samples*
2. **Upload new sample(s) abundance file**: Upload file (in .csv format) containing abundance data of new sample(s).
3. **Upload reference file(s)**: Upload data file(s) (in .csv format) containing microbial abundance data and metadata.

In metadata, at least one locality (eg. continent, city) and coordinates (necessary) data columns should be included. The metadata and abundance data of the sample can be merged into one file (*Merged metadata and abundance data*), or uploaded as two files (*Separate metadata and abundance data*)

When *Separate metadata and abundance file* is selected. **Merge column name in metadata/abundance file**: Input the header name of column which is the merged column in two files.

2.3.1 Function 2 introduction

In this mode, you can train the microbial origin prediction model based on the reference data set uploaded by the user. The constructed prediction model will be used to predict the new sample to be tested provided by you and report the prediction result of the sample source. (If you want to visualize the accuracy of the model, please use the function: Build a new prediction model using mGPS)

2.3.2 Output plot

Geographical origin prediction of microbiome

Prediction program
Build a new prediction model using mGPS and predict new samples

Upload new sample abundance file(s)
Browse... No file selected

HELPResult PlotOutput

longitude range:

-165 -131 -97 -63 -29 5 39 73 107 141 168

latitude range:

-90 -72 -54 -36 -18 0 18 36 54 72 90

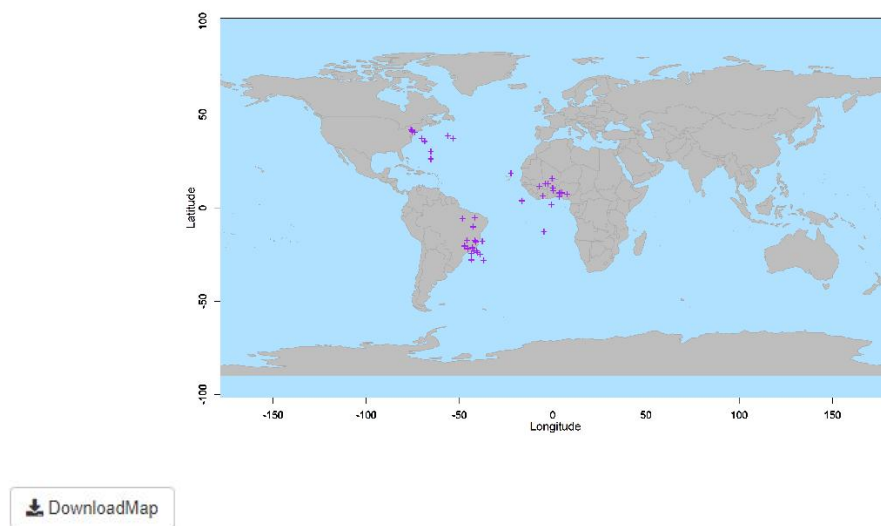
Whether pull points to land/marine
☐ Pull to land
☐ Pull to waterbody
☒ Default

The reference datasets will be used to construct an origin prediction model by mGPS. Then this model will be used to predict the origin of new samples.

If you want to zoom in on a specific area of the map, you need to adjust both the longitude and latitude ranges. "Pull to land" refers to pushing the predicted point to the nearest land, and "Pull to waterbody" refers to pushing the predicted point to the nearest water body.

Example output plot:

a. World map: samples' prediction origins are plotted on the world map. By adjusting the range of longitude and latitude, you can select the plotting area of the figure on the map. In addition, you can choose whether to pull the predicted point into the continent or the ocean. You can download and save the png file of this map through the button 'DownloadMap' below the figure.



2.3.3 Output files

Data processing: Please wait while output files are being generated. When the prompt bar (*Data loading...*) disappears you can see the results and download files.

Geographical origin prediction of microbiome

Data loading....

Prediction program

Build a new prediction model using mGPS and predict new samples

Upload new sample abundance file(s)

Browse... No file selector

HELP Result Plot Output

Predicted original coordinates of samples can be downloaded. Prediction model in RDA format can be downloaded

Download prediction data

Download feature subsets accuracy in feature elimination

Download optimal features in prediction model DownloadModel

a. "Download prediction data" button - Prediction data: Records the predicted original coordinates of the new samples. (columns: LatPred and LongPred).

	A	B	C	D	E	F	G
1		taxa1_abundance	taxa2_abundance	taxan_abundance	cityPred	latPred	longPred
2	1	0.00017	0	0	offa	7.881690979	11.71926498
3	2	9.00E-05	0.00023	0	offa	8.323236465	-0.264049619
4	3	8.00E-05	0	0	offa	7.446023464	4.620732784
5	4	7.00E-05	2.00E-05	2.00E-05	new_york	40.67137527	-72.10720062
6	5	0.00016	1.00E+00	0	new_york	18.32634163	-43.18954086

b. "Download optimal features in prediction model" button - Optimal features in prediction model: Same content as this file in function 1: Build a new prediction model using mGPS. [Jump](#)

c. "Download feature subsets accuracy in feature elimination" button - feature subsets accuracy in feature elimination: Same content as this file in function 1: Build a new prediction model using mGPS. [Jump](#)

d. "DownloadModel" button - Model: Same content as this file in function 1: Build a new prediction model using mGPS. [Jump](#)

2.4 Function 3: Use an existing model to predict new samples

2.4.1 Function 3 introduction

In this mode, you can predict new sample origin based on an existing prediction model. You can download the model in the Output tab of functions: Build a new prediction model using mGPS or Build a new prediction model using mGPS and predict new samples. [Jump to model](#)

2.4.2 Output plot

Geographical origin prediction of microbiome

Prediction program

Use an existing model to predict new samples

Upload sample(s) abundance file

Browse... No file selected

HELP
Result Plot
Output

longitude range:

-165 -131 -97 -63 -29 5 39 73 107 141 168

latitude range:

-90 -72 -54 -36 -18 0 18 36 54 72 90

Whether pull points to land/marine

☐ Pull to land
☐ Pull to waterbody
☒ Default

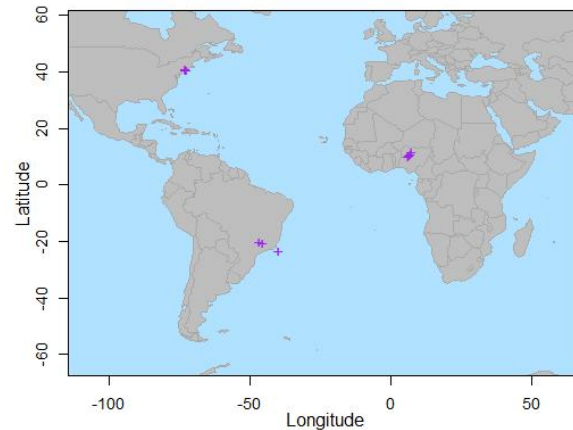
The model uploaded will be used to predict the origin of new samples.

If you want to zoom in on a specific area of the map, you need to adjust both the longitude and latitude ranges. "Pull to land" refers to pushing the predicted point to the nearest land, and "Pull to waterbody" refers to pushing the predicted point to the nearest water body.

Example output plot:

a. World map:

new samples' prediction origins are plotted on the world map. By adjusting the range of longitude and latitude, you can select the plotting area of the figure on the map. In addition, you can choose whether to pull the predicted point into the continent or the ocean. You can download and save the png file of this map through the button 'DownloadMap' below the figure.



 DownloadMap

2.4.3 Output files

Data processing: Please wait while output files are being generated. When the prompt bar (*Data loading...*) disappears you can see the results and download files.

Geographical origin prediction of microbiome

Data loading....

Prediction program


Use an existing model to predict new samples

Upload sample(s) abundance file

Browse... No file selected

[HELP](#) [Result Plot](#) [Output](#)

Here you can download the predicted original coordinates of samples in your uploaded file. (Reference microbiome locations are based on MetaSub project microbiome database)

 DownloadData

a. "Download prediction data" button - Prediction data: Prediction data: Records the predicted original coordinates of the new samples. (columns: LatPred and LongPred).

	A	B	C	D	E	F	G
1		taxa1_abundance	taxa2_abundance	taxan_abundance	cityPred	latPred	longPred
2	1	0.00017	0	0	offa	7.881690979	11.71926498
3	2	9.00E-05	0.00023	0	offa	8.323236465	-0.264049619
4	3	8.00E-05	0	0	offa	7.446023464	4.620732784
5	4	7.00E-05	2.00E-05	2.00E-05	new_york	40.67137527	-72.10720062
6	5	0.00016	1.00E+00	0	new_york	18.32634163	-43.18954086

3. FAQ

3.1 If you meet error:

```
> runApp('mGPS_interface.r')
```

```
Warning in file(con, "w") :  
cannot open file 'C:\\Users\\Temp\\...': No such file or directory  
Error in file(con, "w") : cannot open the connection
```

Try to restart the R (Rstudio). Sometimes this error is due to caching in Rstudio.

3.2 If you meet error:

```
Error in file(file, ifelse(append, "a", "w")) :  
Cannot open the file:'.....' : Permission denied  
Warning: Error in file: cannot open the connection
```

Try to see if you have the file open in another program, so the file cannot be modified by the R application.

3.3 Figure problem on interface page

Figure on interface has extra space or the map latitude and longitude range is different from the selected one. Due to the shiny page settings, the figure will be automatically expanded to a certain size, that is, it fills the entire screen. So sometimes there is extra space on the map. At the same time, to prevent serious deformation of the world map, the aspect ratio is locked when the map is plotted.

Workarounds: If you want to get a zoomed-in portion of the map, you need to adjust both longitude and latitude.

3.4 The figure downloaded via the button does not match what you see on the interface

Since the figure displayed on the shiny is forced to resize, the deformation is more serious when the interface page is enlarged. The downloaded figure is directly generated by the R code and is not forced to be deformed by shiny, so the downloaded figure will be inconsistent with the seen figure.

Workarounds: If you want to keep what you see consistent with what you download, it is recommended to use the shiny original size interface instead of enlarging the webpage. Or directly click the right mouse button on the figure to save it.