



ImageGP 2 for enhanced data visualization and reproducible analysis in biomedical research

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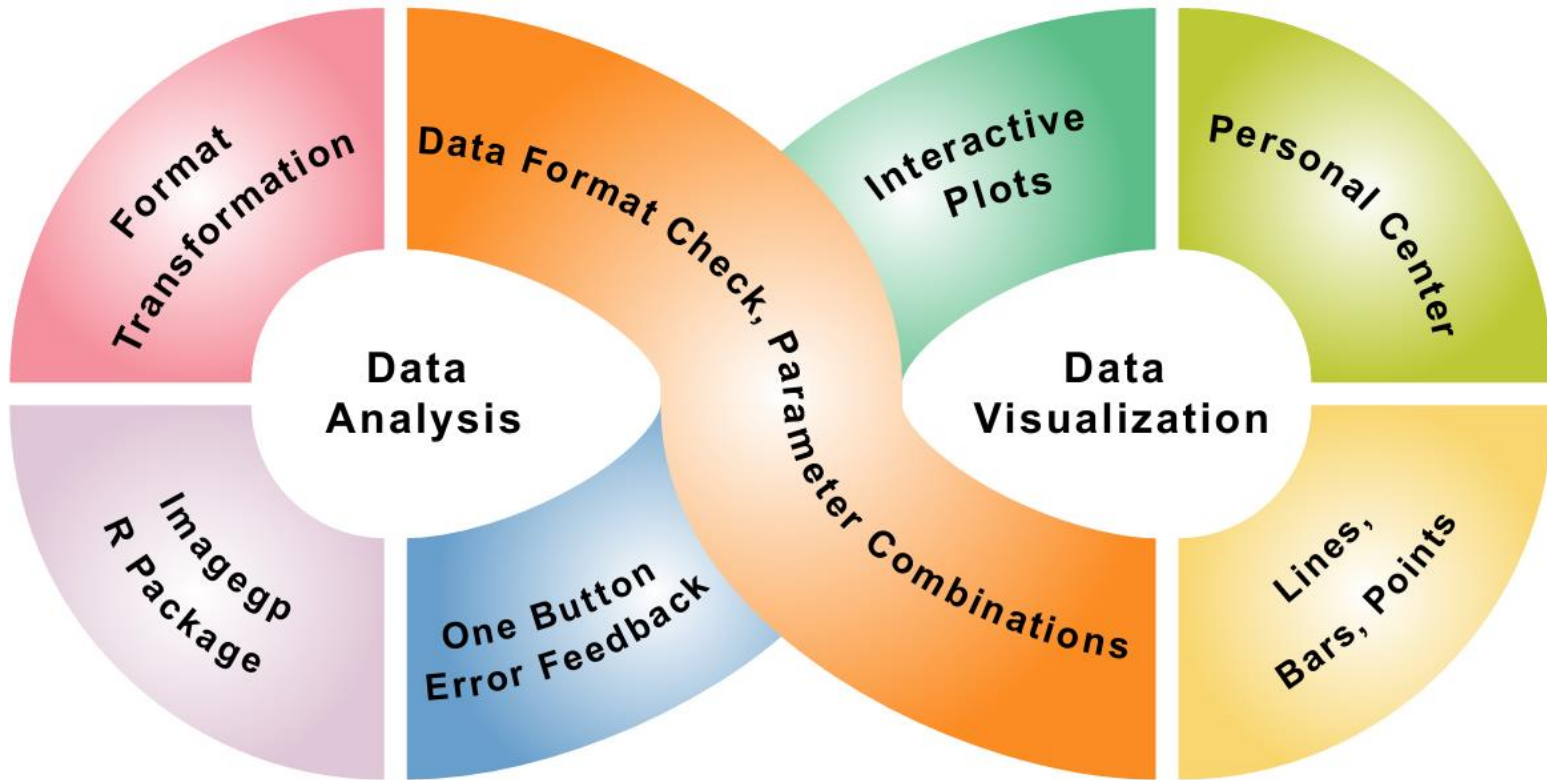


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<https://doi.org/10.1002/imt2.239>



Introduction



1. The infinity symbol illustrates the seamless workflow of ImageGP 2, encompassing essential functions such as data format transformation, data validation, and parameter combination. This process culminates in the generation of diverse visual outputs, including line, point, and bar plots.

2. Key features include a personalized user center for managing large datasets, interactive visualizations, and streamlined error feedback mechanisms.

3. Additionally, the introduction of the ImageGP R package enables local and batch analyses.

4. Overall, the infinity symbol embodies the limitless potential for data analysis and visualization offered by ImageGP 2.



Highlights

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The boxplot on the left shows the expression of gene ENSG00000109689 for two conditions: trt (blue) and untrt (yellow). The y-axis ranges from 8 to 12. The untrt condition shows a higher median expression (around 10.1) compared to the trt condition (around 8.6). Individual data points are connected by lines between the two conditions. A legend indicates conditions (trt, untrt) and individuals (N052611, N061011, N080611, N61311).

The line graph on the right shows the expression of five genes (Pou5f1, Sox2, Gata2, cMyc, Tet1, Tet3) across developmental stages: Zygote, 2_cell, 4_cell, 8_cell, Morula, and ICM. The y-axis is labeled 'Expression' and ranges from 0 to 30. Pou5f1 and Sox2 show high expression in the Zygote stage, which decreases as development progresses. Tet1 and Tet3 show low expression in the Zygote stage, which increases significantly in the ICM stage.

Citation: Chen, Tong, Yong-Xin Liu, Luqi Huang. 2022. "ImageGP: An easy-to-use data visualization web server for scientific researchers." iMeta 1: e5. <https://doi.org/10.1002/imt2.5>.

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Professional plots in seconds

- Pretty heatmap
- Boxplot
- Bar plot
- Enrichment plot
- PcOA analysis
- Volcano plot

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Matrix Formats and Transformations

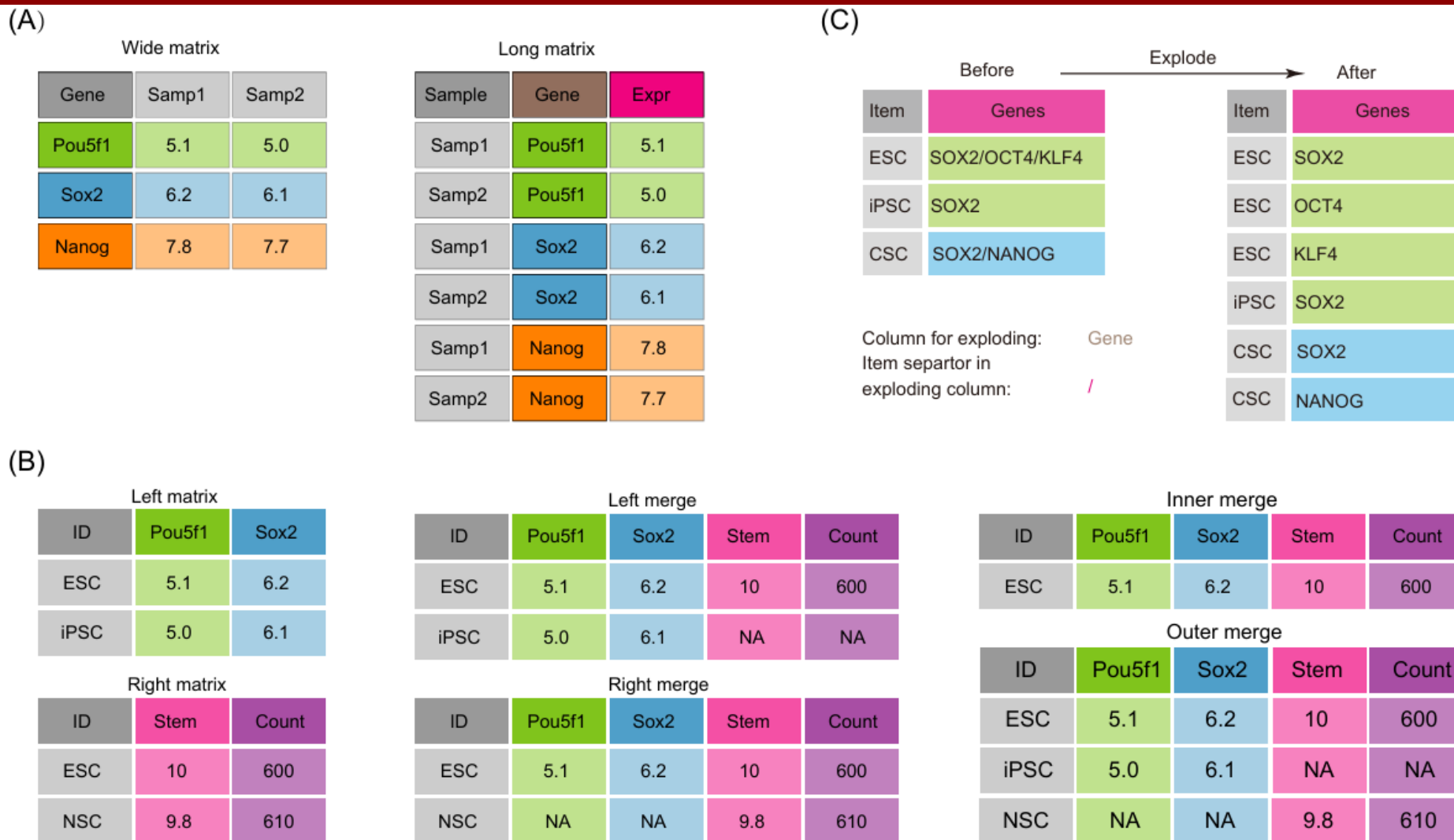


Figure 1. Matrix Formats and Transformations. (A) Illustration of the transformation between wide and long format matrices. (B) Overview of matrix merging capabilities, demonstrating five modes: left, right, inner, outer, and horizontal stacking (hstack). (C) Description of the "explode matrix" function, which expands matrix dimensions by splitting elements in a single column and duplicating values from another columns.

Complex analysis generates result reports

WGCNA

Data matrix (tab separated text file)

Main expression data

ID	Zygote	2_cell	4_cell	8_cell	Morula	ICM
Pou5f1	1	0.5	0.3	10.4	16	32
Sox2	2	1	0.6	5.2	8	16
Gata2	4	2	1.3	2.6	4	8
cMyc	8	4	2.6	1.3	2	4
Tet1	16	8	5.2	0.6	1	2
Tet3	32	16	10.4	0.3	0.5	1

Wait for several minutes



Trait data

ID	Attribute
Zygote	1
2_cell	2
4_cell	4
8_cell	8
Morula	16
ICM	32

- 1 WGCNA analysis
 - 1.1 Expression data preprocess
 - 1.2 Soft power detection
 - 1.3 WGCNA module plot
 - 1.4 WGCNA module correlation plot
 - 1.5 WGCNA module trait correlation plot
 - 1.6 WGCNA module gene trait correlation plot
 - 1.7 Interested genes for each module
 - 1.7.1 Interested genes for each module (brown.weight_g)
 - 1.7.2 Interested genes for each module (red.length_cm)

WGCNA basic usages (video tutorial)

WGCNA trait-module heatmap (video tutorial)

WGCNA basic concepts (text tutorial)

Thanks for citing: ImageGP: An easy-to-use data visualization web server for scientific researchers. iMeta 1: e5.

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Example result

Demo1

Demo2



File Management and Tools Records

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Personal Center

File management: Here to manage files like uploading, moving, and renaming files

Workflow records: Check the running status of workflows and get/download the results

Tools records: Check the running status of tools and get/download the results of tools


File management

Workflow records

Tools records

File management

Back root



Select files in your local computer for uploading

<input type="checkbox"/>	Name ↕	Size ↕	Modification time ↕	Operation
<input type="checkbox"/>	result_output			Rename Copy Cut Delete
<input type="checkbox"/>	1.bt	0B	2023/04/02 04:22	Rename Copy Cut Delete
<input type="checkbox"/>	etbio_simpler.DESeq2.t1_vs_tntr1.results.bt	1.59M	2024/01/06 17:00	Rename Copy Cut Delete
<input type="checkbox"/>	sd_sdsd	5.92K	2022/11/11 19:14	Rename Copy Cut Delete
<input type="checkbox"/>	python.log	39B	2023/05/26 20:56	Rename Copy Cut Delete
<input type="checkbox"/>	TMPa.bt	4.14M	2023/09/11 10:22	Rename Copy Cut Delete
<input type="checkbox"/>	ptam.table.bt	5.52M	2022/12/14 11:00	Rename Copy Cut Delete

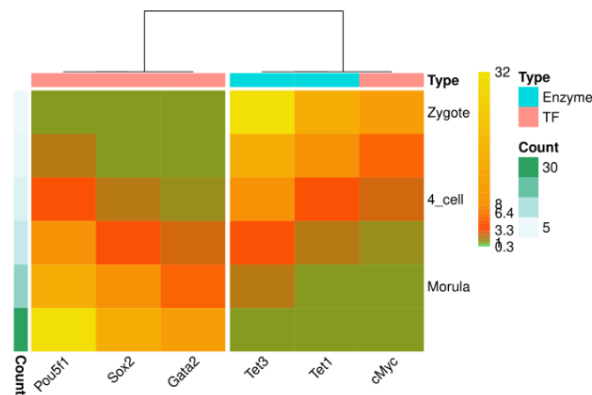
Tools records

<input type="checkbox"/>	Name ↕	Tag ↕	Create Time ↕	Results ↕	Status ↕	Reanalysis ↕	Reanalysis In Same Path ↕	删除
<input type="checkbox"/>	LEfSe	<input type="text"/> submit	2024-09-04 08:17:04.356085	Click to check	SUCCESS	Click to check	Click to check	Delete
<input type="checkbox"/>	WGCNA	<input type="text"/> submit	2024-07-31 09:34:09.004054	Click to check	SUCCESS	Click to check	Click to check	Delete
<input type="checkbox"/>	Histogram	<input type="text"/> submit	2024-07-31 07:45:33.136536	Click to check	SUCCESS	Click to check	Click to check	Delete
<input type="checkbox"/>	Convert GTF/GXF file into bed file	<input type="text"/> submit	2024-07-30 14:55:05.104567	Click to check	SUCCESS	Click to check	Click to check	Delete



ImageGP script runs locally

1 Pretty heatmap result



Click to download PDF format pictures

Click to download R script for generating this picture

Click to download data after clustering or filtering

Click to download column-cluster data

```

1 #!/usr/bin/env Rscript
2
3
4
5 data = "C:/Users/yangm/Downloads/a.txt"
6 display_numbers = "NULL"
7 outputprefix = "a"
8 outputpictype = "pdf"
9 renameDuplicateRowNames = FALSE
10 logv = "NULL"
11 log_add = 0
12 scale = "none"
13 top_n = 1
14 statistical_value_type = "mad"
15 annotation_row = "C:/Users/yangm/Downloads/row.txt"
16 annotation_col = "C:/Users/yangm/Downloads/col.txt"
17 cluster_rows = FALSE
18 cluster_cols = TRUE
19 clustering_method = "complete"
20 clustering_distance_rows = "pearson"
21 clustering_distance_cols = "pearson"

```

```

> cat(sp_current_time(), "Success.\n")
[2024-09-11 16:01:21] Success.
> #sink()
> |

```

The R package ImageGP retains the same parameters as its online counterpart. Each data visualization tool generates an R script tailored to user inputs and parameters. Users have the option to download these scripts, open them in RStudio or other R Integrated Development Environments (IDEs), and customize file paths and output prefixes for local execution.

<https://www.bic.ac.cn/BIC/#/>



Summary



- ❑ In this paper, we introduced ImageGP 2, an upgraded version of a popular online data visualization and analysis cloud platform.
- ❑ ImageGP 2 advanced user interface, expanded analytical capabilities, seamless data handling. New modules for data transformation and pre-parameter selection data validation. Personalized user center, reproducible scripts, seamless error debugging, introduction of local analysis capabilities.
- ❑ The ImageGP 2 platform will continue to be updated and maintained, integrating individual tools into workflows that enable users to initiate analyses directly from raw data.
- ❑ Website: <https://www.bic.ac.cn/BIC/#/>



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