

# Comprehensive Evaluation of the BioPareto Analyzer Tool: Usability (SUS), Utility and Interpretability.

Thank you for participating in the evaluation of the **BioPareto Analyzer**. All responses are **strictly anonymous** and will be used solely for academic thesis research.

\* Indica que la pregunta es obligatoria

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## Participant Information and Instructions

Unique Identifier (Traceability Code)

**Purpose:** To ensure the integrity of the evaluation, we need to link your feedback across different survey sections and future follow-up assessments.

**Instructions:** Please create a **unique, anonymous code (Token)** using two memorable words. This code is **not** linked to your identity and is used strictly for data tracing. The only requirement is to make sure that it is a code that you can easily remember, since you will be asked to use the same code in the following tests.

**Example Format(you can choose any, this is just an example):**

**YourFavoriteColor / FavoritePet:** greencat

or

**YourFavoriteColor / SignificantNumber:** red15

- 1.- Please enter the unique, anonymous code (Token) you created for this evaluation.

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## 2. 2.- Current Role: \*

*Marca solo un óvalo.*

- ☐ Bioinformatician / Computational Biologist
- ☐ Biologist / Researcher (Wet Lab)
- ☐ Data Scientist / Statistician
- ☐ Computer Scientist/Engineering
- ☐ Student
- ☐ Otro: \_\_\_\_\_

## 3. 3.- Experience Level with Multi-Objective Optimization / Pareto Fronts: \*

*Marca solo un óvalo.*

- ☐ 1 (None)
- ☐ 2 (Beginner)
- ☐ 3 (Intermediate)
- ☐ 4 (Advanced)
- ☐ 5 (Expert)

## System Usability Scale (SUS) Questionnaire

### Instructions for the Participant:

You will find 10 statements about the system you just used. Please indicate your level of agreement or disagreement with each statement by marking the number that best represents your opinion.

**1 2 3 4 5**

**1 = Strongly Disagree**

**5 = Strongly Agree**

Questions:

4. 1.- I would like to use this system in my work. \*

*Marca solo un óvalo.*

- ☐ 1  
☐ 2  
☐ 3  
☐ 4  
☐ 5

5. 2.- I thought the system was easy to use. \*

*Marca solo un óvalo.*

- ☐ 1  
☐ 2  
☐ 3  
☐ 4  
☐ 5

6. 3.- I think that I would need the support of a technical person to be able to use this system. \*

*Marca solo un óvalo.*

- ☐ 1  
☐ 2  
☐ 3  
☐ 4  
☐ 5

7. 4.- I found the functions in this system were well integrated. \*

*Marca solo un óvalo.*

- ☐ 1  
☐ 2  
☐ 3  
☐ 4  
☐ 5

8. 5.- I think there was too much inconsistency in this system. \*

*Marca solo un óvalo.*

- ☐ 1  
☐ 2  
☐ 3  
☐ 4  
☐ 5

9. 6.- I imagine that most people would learn to use this system very quickly. \*

*Marca solo un óvalo.*

- ☐ 1  
☐ 2  
☐ 3  
☐ 4  
☐ 5

10. 7.- I felt very confident using the system. \*

*Marca solo un óvalo.*

- ☐ 1  
☐ 2  
☐ 3  
☐ 4  
☐ 5

11. 8.- I need to learn a lot of things before I could get going with this system. \*

*Marca solo un óvalo.*

- ☐ 1  
☐ 2  
☐ 3  
☐ 4  
☐ 5

Usability/Interface Feedback

**Open Question: speak freely.**

12. Did you find any specific **interface barriers, bugs, or points of confusion** while completing the tasks? Please describe them here. Or make any suggestion you can think.

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## Utility Evaluation Survey for the BioPareto Analyzer o

**Purpose:** To assess the **practical utility** of the tool's advanced analytical functionalities and its value for the gene selection workflow.

### Instructions for the Participant:

Your feedback is vital. Please indicate your level of agreement or disagreement regarding whether each functionality is useful and necessary for your work analyzing gene expression data.

**1 2 3 4 5**

**1 = Strongly Disagree**

**5 = Strongly Agree (Very Useful)**

### Questions:

13. 1.- The functionality for identifying **frequent genes** is valuable for my work and pipelines. \*

*Marca solo un óvalo.*

☐ 1

☐ 2

☐ 3

☐ 4

☐ 5

14. 2.- The **functional analysis integrated** and the presentation of **results** (e.g., g:Profiler) are key functionalities that **shorten the biological interpretation time**. \*

*Marca solo un óvalo.*

- ☐ 1  
☐ 2  
☐ 3  
☐ 4  
☐ 5

15. 3.- The **Pareto Front scatter plot** facilitates the **intuitive visualization** of the **trade-off** between objectives. \*

*Marca solo un óvalo.*

- ☐ 1  
☐ 2  
☐ 3  
☐ 4  
☐ 5

16. 4.- The **JSON** file format used makes it easy to prepare and upload my Pareto Front data. \*

*Marca solo un óvalo.*

- ☐ 1  
☐ 2  
☐ 3  
☐ 4  
☐ 5

17. 5.- The ability to export the **raw solution and gene data** in CSV or JSON format \* is useful for conducting **further analysis** and helps **interoperability** with other bioinformatic tools.

*Marca solo un óvalo.*

☐ 1

☐ 2

☐ 3

☐ 4

☐ 5

18. 6.- The functionality to export a **consolidated report** (e.g., PDF) that includes the \* Pareto plot, selected solutions, and analysis summaries **is helpful** for reporting, documentation, and sharing results with collaborators.

*Marca solo un óvalo.*

☐ 1

☐ 2

☐ 3

☐ 4

☐ 5

Usability/Interface Feedback



19. 7.- Please use this space to explain any **low scores (1 or 2)** given above, or to elaborate on the feature you found **most useful**, or proposing some new featuring you can think it would be useful.

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### Interpretability

The primary goal of this section is to measure the **clarity and effectiveness** of the BioPareto Analyzer's visualizations and analytical metrics. **Interpretabilidad** in this context is defined as your ability to **correctly understand the significance** of the analytical concepts presented in the App, allowing you to make confident decisions on the optimal solution.

**Purpose:** To assess the user's understanding of the analytical concepts they must interpret when interacting with the BioPareto Analyzer prototype.

**Instructions:** Answer "True" or "False" to the following statements, based on your experience using the tool's App.

20. 1.- When examining the **Pareto Graph**, if you move towards the **bottom-left corner**, your main objective is to find the solution with **maximum accuracy**, sacrificing simplicity. \*

*Marca solo un óvalo.*

☐ True

☐ False

21. 2.- A solution that is on the **Pareto Front** means we cannot improve it in **any of its objectives** (e.g., more accuracy, fewer genes) without making the other objective worse. \*

*Marca solo un óvalo.*

☐ True

☐ False

22. 3.- If two solutions you are exploring in the data table have an **identical Accuracy**, the most efficient selection criterion is to choose the solution with the **lowest 'Number of Genes'**. \*

*Marca solo un óvalo.*

☐ True

☐ False

23. 4.- If you apply a filter to the 'Number of Genes' column with the condition **'greater than or equal to ( $\geq$ ) 50'**, the main objective is to select solutions that prioritize **simplicity**. \*

*Marca solo un óvalo.*

☐ True

☐ False

24. 5.- A **high selection frequency** (e.g., 95%) for a gene implies that said gene is **irrelevant** to the model. \*

*Marca solo un óvalo.*

☐ True

☐ False

25. 6.- If the **"Total Number of Unique Genes"** is **much less** than the total genes in the entire Pareto Front, this indicates that the selected solutions are **very similar** genetically. \*

*Marca solo un óvalo.*

☐ True

☐ False

26. 7.- When comparing two pathways in the g:Profiler results, a p-value adjusted of **1.5e-10** is **more significant** than a value of **3.2e-4**. \*

*Marca solo un óvalo.*

☐ True

☐ False

27. 8.- **METRIC INTERPRETATION:** The **adjusted p-value column** you see in the g:Profiler results is the most important metric for **controlling the number of false positives** in the biological analysis. \*

*Marca solo un óvalo.*

☐ True

☐ False

28. 9.- **FUNCTIONAL VALUE:** The main benefit of the **direct integration** with g:Profiler is to **transform gene IDs** into **relevant biological and functional information** for your research. \*

*Marca solo un óvalo.*

☐ True

☐ False

## Open Questions(optional):

29. 10.-What **value or main utility** does the interactive Pareto graph offer you for understanding the solution **trade-off**? How would you **improve** its visualization or interactivity?

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30. 11.- What **analytical value** does the **Gene Frequency** metric provide for determining robustness? What **other metric or graph** related to robustness/diversity would you include in this module?

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31. 12.- How useful is the direct integration with g:Profiler for **shortening your interpretation time**? If you could **integrate another biological analysis service** (e.g., Enrichr, DisGeNET), which one would you choose and why?

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32. 13.- Here you can leave a free comment about anything you consider relevant, something that caught your attention about the app, something that could be improved, or a new feature that could be added.

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