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# Grape selector: a Shiny application for grapevine breeding

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## Summary

Both variety and clonal selection programs require the study of many traits. Selecting the best accession becomes a challenge when the number of accessions and traits being studied increases. Grape selector is a user-friendly tool that allows finding the best compromises according to a set of criteria (selection index). This tool can be used with phenotypic data at the variety or clone scale. The application was tested with existing phenotypic data from a breeding program and provided consistent selection with the one done manually.

## Keywords

Grapevine breeding, R Shiny application, selection index, clonal selection.

## Introduction

Varietal breeding, involving the selection of new grapevine varieties, is a proven method to reduce the use of phytosanitary products and develop varieties better adapted to climate change while preserving organoleptic qualities and typicity of wine (Töpfer & Trapp, 2022). Like clonal selection, varietal selection requires defining a selection criterion. When the number of accessions to be evaluated remains small, the selection is typically done by an expert who considers multiple criteria simultaneously. However, this becomes quickly impractical as the number of accessions to be evaluated increases. This issue has been extensively addressed in the field of genetic breeding with selection indices (Hazel, 1943; Smith, 1936). In these indices, a set of traits of interest and their relative weights are defined. This results in a weighted index and a score for all individuals based on their phenotype or genetic value. It enables the identification of individuals that represent the best compromises for the various target traits. Further developments have been made to account for genetic correlations between traits or to maintain traits at desired levels. However, these methodologies have not been applied

to grapevine so far due to the complexity of defining a selection index that can encompass dozens of traits.

In this article, we adapted an algorithm called MGIDI (multivariate genotype-ideotype distance index) (Olivoto & Nardino, 2021) to be more adapted to grapevine selection. Unlike most improved species, determining a selection index in grapevine is complex and focused on product quality, and maximization or minimization are not the only two objectives in grapevine selection.

## Material and methods

### Algorithm description

The MGIDI algorithm is of interest as it does not require assigning weights to different variables and can account for correlations between traits. Prior to using the algorithm, an ideotype, which represents the characteristics of the ideal accession, needs to be defined to establish the selection index. In practice, the selection index comprises a list of traits and the desired selection direction (e.g., decrease for disease symptoms or increase for productivity traits, or an optimal value for quality traits). The algorithm operates in three steps:

1. Phenotypic data for each trait are rescaled to a range of 0 to 100, with 100 being the optimal desired value.
2. Factors combining multiple traits are extracted to summarize the information.
3. A sum of distances is measured between the selection objective (ideotype) and the observed value for each factor.

Consequently, the algorithm determines a score (corresponding to a distance) for each accession from the selection objective. It is also possible to study the strengths and weaknesses of each variety for each factor.

### Shiny application

The MGIDI algorithm was already freely available as the R package *metan* (Olivoto, 2023). However, using the statisti-



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cal software R may not be easy for all users. Therefore, we created the R Shiny application Grape Selector to make the tool user-friendly and accessible to a broader community. It enables loading a table of phenotypic data, sorting rows, displaying graphs, and performing selection of the best individuals based on a user-defined selection index. It is also possible to successively filter individuals using discrete filters (such as berry color or flower sex) and continuous filters.

The application requires you to fill (or copy paste) a table containing the selection index for all traits of interest, with direction of selection, optimal value if necessary, and optional relative weights (between 0 and 1 for less important or predominant traits, respectively). Moreover, the proportion of retained individuals can be fixed in advance. The application can be accessed at the following: <https://charlottebrault.shinyapps.io/grapesel/>, or downloaded from a Zenodo repository: (<https://doi.org/10.5281/zenodo.7987889>), instructions on how to run the application locally is available as supplemental data.

## Results and discussion

### Outputs

Several graphs and result tables are available:

- Comparison Strength/Weakness Graph of selected individuals based on the factors. The larger the contribution of a factor to the MGIDI (distance to the ideotype), the worse the individual is for that specific factor.

- Summary table of variables: display the grouping of traits into factors, the average phenotypic value for the whole and the selected individuals, and the selection objective.
- Correlations between variables: display the correlations between the variables studied in the index. This graph helps to identify any potential trade-offs when two variables are correlated in a direction different from that of the selection index.
- Ranking of all individuals with their associated MGIDI score (searchable).
- Selection of a trait present in the index, followed by displaying the distribution of the population and highlighting the position of the selected individuals and other individuals (Figure).

### Usefulness of Grape Selector

We used Grape Selector with a real dataset used in the varietal selection of a reciprocal cross between Syrah and Grenache. Data was obtained in Orange by the ‘Syndicat des Côtes du Rhône’ for 4 vintages and 28 offspring. The selection index includes eight criteria, applied to the data for each vintage. The MGIDI scores were summed across all vintages, and the selection was consistent with that carried out by the ‘Syndicat des Côtes du Rhône’. MGIDI has been recently used in the context of grapevine breeding in two other breeding programs (Brault *et al.*, 2024).

Grape Selector can also be used for clonal selection to find the most relevant accessions or selecting the better oenological process to final product desired. The selected varieties

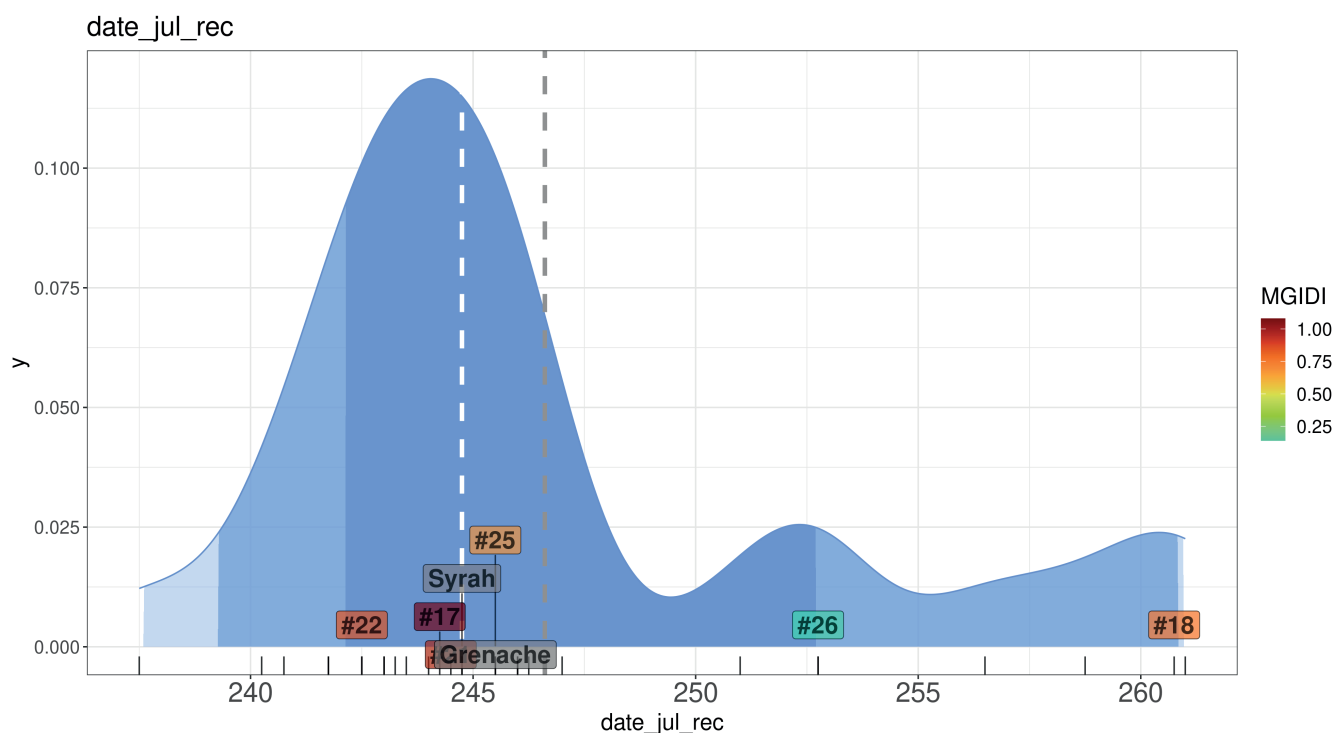


Figure: Distribution of the whole population for the selected trait, year day of harvest, and position of the selected individuals. The color indicates the MGIDI score obtained with the whole selection index on all traits. We chose here to display the position of Syrah and Grenache (parents of the cross).

and the selection index will differ depending on the wine region, wine typology, and climate adaptation for instance.

### Data availability

The example dataset in the application consists of a table comprising 783 genotypes of diverse genetic origin from (Laucou *et al.*, 2018). The studied traits include phenology, productivity, sugar quantity, and acidity in the must.

The code for the R Shiny application is publicly available in Zenodo: (<https://doi.org/10.5281/zenodo.7987889>) (Brault, 2023).

### Conflicts of interest

The authors declare that they do not have any conflicts of interest.

### References

**Brault, C., 2023:** Grape selector: A Shiny application for grapevine breeding. Zenodo. DOI: 10.5281/zenodo.7987889.

**Brault, C., Segura, V., Roques, M., Lamblin, P., Bouckenoghe, V., Pouzalgues, N., Cuntz, C., Breil, M., Frouin, M., Garcin, L., Camps, L., Ducasse, M. A., Romieu, C., Masson, G., Julliard, S., Flutre, T., Cunff, L. L., 2024:** Enhancing grapevine breeding efficiency through genomic prediction and selection index G3

Genes|Genomes|Genetics, jkae038, DOI: 10.1093/g3journal/jkae038.

**Hazel, L. N., 1943:** The genetic basis for constructing selection indexes. *Genetics*, 28(6), 476-490. DOI: 10.1093/genetics/28.6.476.

**Laucou, V., Launay, A., Bacilieri, R., Lacombe, T., Adam-Blondon, A. F., Bérard, A., Chauveau, A., Andrés, M. T. de, Hausmann, L., Ibáñez, J., Paslier, M. C. L., Maghradze, D., Martinez-Zapater, J. M., Maul, E., Ponnaiah, M., Töpfer, R., Péros, J.-P., Boursiquot, J. M., 2018:** Extended diversity analysis of cultivated grapevine *Vitis vinifera* with 10K genome-wide SNPs. *PLOS ONE*, 13(2), e0192540. DOI: 10.1371/journal.pone.0192540.

**Olivoto, T., Nardino, M. 2021.** MGIDI: Toward an Effective Multivariate Selection in Biological Experiments. *Bioinformatics* 37 (10): 1383–89. DOI: 10.1093/bioinformatics/btaa981.

**Olivoto, T., 2023:** metan : Multi Environment Trials Analysis (1.18.0) [Software]. <https://cran.r-project.org/web/packages/metan/index.html>.

**Smith, H. F., 1936:** A Discriminant Function for Plant Selection. *Annals of Eugenics*, 7(3), 240-250. DOI: 10.1111/j.1469-1809.1936.tb02143.x.

**Töpfer, R., Trapp, O., 2022:** A cool climate perspective on grapevine breeding: Climate change and sustainability are driving forces for changing varieties in a traditional market. *Theoretical and Applied Genetics*, 135(11), 3947-3960. DOI: 10.1007/s00122-022-04077-0.