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Application Note

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| Subject Section  The Genetic Map Comparator: a quick and easy way to visualize your genetic maps  Yan Holtz1, Jacques David1, Vincent Ranwez1\*  1*1Montpellier SupAgro, UMR AGAP, 34060 Montpellier, France*  \*To whom correspondence should be addressed.  Associate Editor: XXXXXXX  Received on XXXXX; revised on XXXXX; accepted on XXXXX  Abstract  **Motivation:** Genomic selection strongly relies on genetic map to accelerate breeding programs. Thanks to high throughput sequencing high density maps are now available for numerous species. Comparing several maps require dedicated tools able to summarize the key characteristics of high density maps and to pinpoint their differences and similarities.  **Results:** We developed GeneMap Comparator a web based application allowing to easily compare different maps by depicting their key statistics and the relative position of their common markers.  **Availability:** The genetic map comparator is available online: <http://www.agap-sunshine.inra.fr/holtz-apps/GenMap-Comparator/>. Source code is freely available on GitHub for non-commercial use only. (<https://github.com/holtzy/GenMap-Comparator>).  **Contact:** ranwez@supagro.fr  **Supplementary information**: Supplementary data are available at *Bioinformatics* online. |

# Introduction

*Why drawing and comparing?*

Drawing and visualizing genetic maps is now a common task for whoever works on genetics.

Summary table are coded by hundreds of people

*What tools are available yet?*

In this study, we investigated the genetic basis of WSSMV resistance in 2 RILs population of durum

*Why building a new one?*

With expansion of new technologies such as NGS and constant decrease of genotyping process, more and more genetic maps have been created. These maps

Faire du multi pop est devenu courant et les consensus aussi.

With NGS, genetic map are denser 🡪 harder to compare and visualize.

Physical position are now available

reaching thousands of markers per genetic map. Currently, no tool seems to be adapted to such a density. Provided charts for comparison often get unreadable.

The Gene Map Comparator use

Comparing such maps needs an adapted tool, since the majority of - Permet de comparer des cartes plus denses (NGS). Exemple: map chart deviant illisible avec >100 marqueurs par chromosomes ( avérifier)

- Permet des comparaisons inter-chromosomiques.

- Utilisation sur le WEB -> 0 installation.

- Utilisation des outils de visualisation interactive actuels !

# Technology and installation

R, shiny. Web interface or easy local installation It is a shiny application available online. No installation needed. Works on every device. Several example datasets are available. User can load its own dataset if located in his computer. Several classical input formats are available. R code is available on github. Proposition of improvement are thus easy to do and more than welcome.

# Key functionalities

Several sheets are available. The **Home page** allows uploading user’s dataset. Two example datasets are also available. **Basic statistics** provides general information such as number of markers, total length, number of unique positions and inter marker distances. Statistics are provided for the whole map and chromosome per chromosome. Summary tables are available to download in .csv format, ready for publication purpose. The **comparison** page displays the selected map in a desired order. A black line represents each map. Each dot represents a genetic marker and information concerning it is available hovering the dot. Purple lines link every common marker between two adjacent maps. To have a more global view and detect inter-chromosomal inconsistencies of chromosomal assignment, the **inter-chromosomal analyses** page displays a scatter plot with genetic positions of two selected maps only. The **raw map** is also made available for reading, with extended exploration tools such as ordering, filtering and searching.

with parallele representation / interchromosomal analyses / rough map. It is possible to export figures to pdf or other format with publication quality.

# Case study

This tool has been developed to soutenir a study concerning durum wheat. Two populations were genotyped. Two individual maps and a consensus map were built, with respectively xx, xx and xx SNP markers). A physical map with the putative position of markers was also available. To investigate the consistency of markers assignments and positions, an important number of comparisons were needed. Existing tools were not adapted for reasons presented above.

The genetic map comparator revealed to be really efficient to explore data quickly and in a really easy way. It permitted to pass fluently from the genetic map building to the visualization step, thus improving the genetic map building efficiency. Several of the published figures were synthetized exporting charts from the tool.

Fig. 1: Parallele comparison of 4 genetic maps.

A representation of the third sheet of the application. Each vertical black line illustrates the selected chromosome of the 4 populations, with a point for each marker. Numbers on the left side specifies positions in cM. Names of markers are available on hover. Common markers between 2 adjacent maps are represented by a purple line.

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*Conflict of Interest:* none declared.

References