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P19.005.D · Polygenic risk score comparator (*PRScomp*): tested population *vs.* worldwide populations

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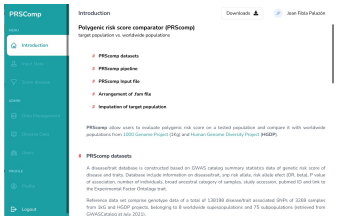
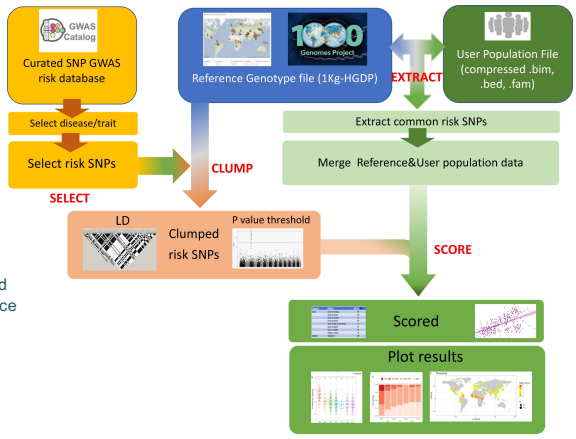
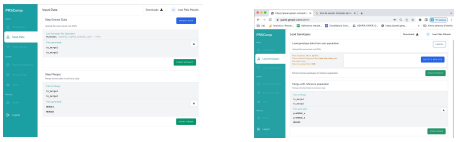
We have developed a web service "***Polygenic Risk Score Comparator (PRScomp)***", which allows users to assess the polygenic risk score of their own population and compare it with worldwide populations from the 1000 Genome Project (1Kg) [1] and the Human Genome Diversity Project (HGDP) [1].



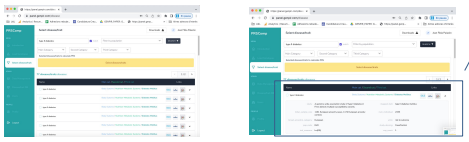


1 The user loads the genotypes of his population

2 Genotypes are merged with data from reference populations



3 User selects one or more disease/trait database entries (based on GWAS Catalog summary statistics [2])

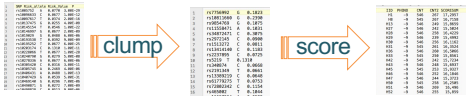


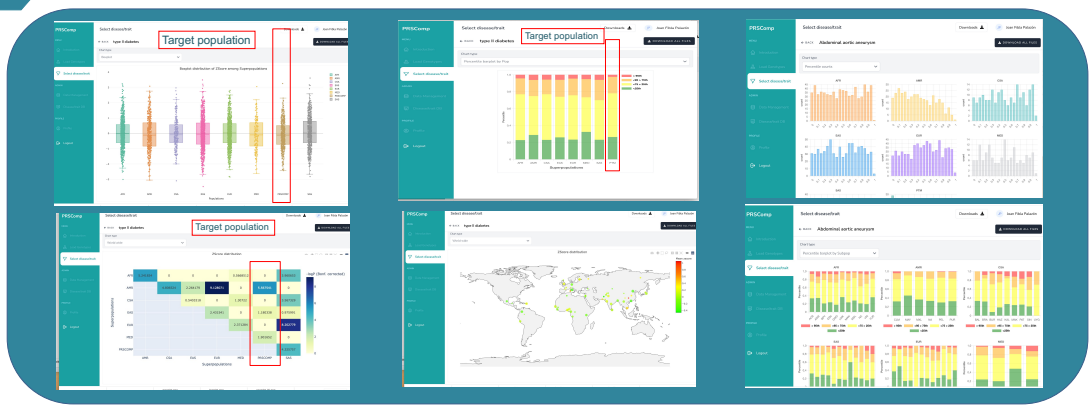
4 A file is generated with the selected risk markers (SNPs), which will be used by the Plink1.9[3] program to obtain the risk score (***PRS***) of the user's population together with the reference world populations.

5 The distribution of ***PRS*** z-score values of the user's population and of the 1Kg and HGDP populations are represented by a box plot, a bubble plot on the world map (mean values) and a bar plot for the distribution of percentile values.

Differences among populations are tested by paired-test with Bonferroni correction.

6





PRScomp offers the opportunity to assess the risk associated with diseases in a population that could be of great interest in the planning and monitoring of public health strategies.

References:
1. Birney, E., Soranzo, N. The end of the start for population sequencing. *Nature* **526,** 52–53 (2015)
2. Welter, D. et al. The NHGRI GWAS Catalog, a curated resource of SNP-trait associations. Nucleic Acids Res 42, D1001–D1006 (2013).
3. Purcell, S. et al. PLINK: A Tool Set for Whole-Genome Association and Population-Based Linkage Analyses. The American Journal of Human Genetics 81, 559–575 (2007).

All authors declare no conflicts of interest

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How to test PRScom:

Download to your computer example genotype file from:
https://figshare.com/s/5c52c34cf097a2ccf039

Login at PRScom as: (select one of them)
email: anonymous1@genpir.com **password:** anonymous1
email: anonymous2@genpir.com **password:** anonymous2
email: anonymous3@genpir.com **password:** anonymous3
email: anonymous4@genpir.com **password:** anonymous4
email: anonymous5@genpir.com **password:** anonymous5
email: anonymous6@genpir.com **password:** anonymous6
email: anonymous7@genpir.com **password:** anonymous7
email: anonymous8@genpir.com **password:** anonymous8
email: anonymous9@genpir.com **password:** anonymous9

Go to “Load Genotypes” and click on “Import data” and load example genotype (example_geno.zip) file from your computer.
Fill required data:
Population identifier: (ie. Example genotype file)
Pop code: (ie. “EXA”) (use a three-letter code)
Coordinates lat/lon
Lat: (ie -12)
Lon: (ie -12)
Upload file and perform “extract” and “merge” steps

Your file is ready to be analyzed by PRScom. “Go to disease” and select the disease/trait of your interest.

Thanks for your interest.

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