

# A web-interface for the detection of selection signatures: development and testing

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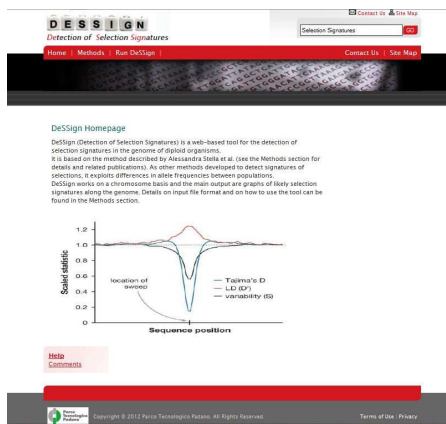
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## Introduction

Signatures of selection are of great interest and practical use both in population genetics, for the understanding and characterization of the evolution and genetic background of populations, and in animal and plant breeding, where their detection may help increase the efficiency of selection. We have been developing DeSSign (Detection of Selection Signatures), a web-interface for the on-line detection of signatures of selection based on the calculation of the composite-log likelihoods (CLL) of the difference in allele frequency between contrasting populations along the genome (Stella et al., 2010).

## Development



The basic structure of the interface has been developed with Php and XML/XHTML + CSS technologies; the programming language Python is used for data editing and to create the input files; client- and server-side asynchronous requests are handled with JQuery and Ajax; SQL is used to create and manage the database of the analyses. DeSSign returns as output interactive graphs of the CLL at each locus per chromosome, and a list with the names and positions of the most significant marker loci. DeSSign can be applied to data of any diploid species.

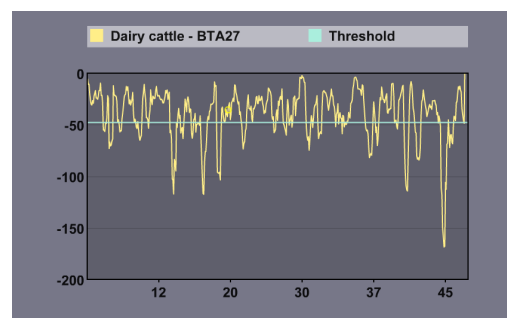
The core programme for the detection of selection signatures is written in Fortran 77: it computes CLLs at each location (sliding windows of variable size) along the chromosomes, and performs a permutation test to obtain a robust significance threshold against which results can be compared.

In order to make the programme available to a broader audience and easy to use, a web-interface has been developed (snapshot of the home page, beside). It allows for the guided uploading (snapshot below) and automatic formatting of the data, prior to the launching of the statistical analysis, which will run independently on a separate server.



## Testing

DeSSign was first tested with the same data as in Stella et al (2010), obtaining the same results (see graph on the right for an example). It is now being tested with an available dataset of Piedmontese cattle genotyped with the 54k bovine SNP chip: animals affected by congenital arthrogyrosis and macroglossia are being compared to healthy animals in a cases/controls design to detect signatures of selection for these malformations. Preliminary results did not show any significant signature of selection, thus confirming previous GWAS results that did not report significant associations for arthrogyrosis or macroglossia. DeSSign will undergo a few further tests before official release of its Beta version.



## REFERENCES

Stella, A., P. Ajmone-Marsan, B. Lazzari and P. Boettcher (2010). Identification of selection signatures in cattle breeds selected for dairy production. *Genetics*, **185**:1451-1461

