

# How Bioinformatics Enables Livestock Applied Sciences in the Genomic Era

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**Abstract.** This review paper presents the three main approaches currently used in livestock genomic sciences where the bioinformatics plays a critical role.

- They are named as Genomic Selection (GS), Genome Wide Association Study (GWAS) and Signatures of Selection (SS). The subsidies for the construction of this article were generated in a current project (started in 2011), so called Zebu Genome Consortium (ZGC), which joins researchers from different institutions and countries, aiming to scientifically explore genomic information of *Bos taurus indicus* cattle breeds and deliver useful information to breeders and academic community, specially from the tropical regions of the world.

**Keywords:** Genomic Selection, Genome Wide Association Study, Signatures of Selection, Livestock, Tropical Environment, *Bos taurus indicus*.

## 1 Introduction

There has been much progress in genomic sciences since a draft sequence of the human genome was published just ten years ago. Due to this effort for decoding the human genome, opportunities for understanding the basic biology of animal health and production are now unparalleled for some species, as advances in genomics are exploited to obtain comprehensive foundational knowledge about the structure and function of these genomes, and about the genetic contributions to phenotypes

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underlying production, health and disease. Recent projections and modeling of population growth and food demands have suggested agribusiness must double food production in the next 40 years to successfully sustain the human population and avoid catastrophic overpopulation. Some experts predict that increases in animal protein production will have to make up about 70% of this doubling in food production due to increasing demand from consumers with more disposable income and limitations on the amount of arable land available for future crop production [1]. Thus, it is somewhat surprising at this time of the genomics revolution that opportunities afforded by advances in technology and new concepts for genetic improvement based on unique population structure in domesticated animals have been overlooked. This is especially evident when considering the return on investment already generated for DNA assisted genetic improvement from very minimal funding. More importantly, there is a large gap in expertise due to an overall lack of animal scientists that possess the knowledge and skills to apply modern genome analysis methods to problems for improving animal efficiency and product quality.

Based on these facts and observations, we believe the large-scale study of livestock genetic resources enabled by computational biology can provide the innovation needed to improve animal food production. We present three main whole genome scan approaches the Zebu Genome Consortium has been applying to the Brazilian Nellore cattle (*Bos taurus indicus*) in order to achieve this innovation: Genomic Selection (GS), Genome Wide Association Study (GWAS) and Signatures of Selection (SS).

## 2 Genomic Selection: Increasing Accuracy of Genetic Predictions in Cattle

The possibility of making accurate predictions of the genetic merit of individuals by using genotypes based on dense single nucleotide polymorphism (SNP) marker panels, a process known as genomic selection (GS), is nowadays revolutionizing the design and implementation of livestock breeding programs. Conceived by [2], who provided the theoretical basis for this approach even before the existence of high density SNP panels, and further boosted as described by [3], who highlighted potential benefits of this strategy in reducing generation intervals, increasing both accuracies of prediction and selection intensities, reducing costs of breeding organizations and making feasible genetic evaluation for difficult-to-measure traits.

The logic behind genomic selection approach is that if the SNP marker density is high enough to cover the entire genome, most of the quantitative trait loci (QTL) will be in linkage disequilibrium with some markers. Therefore, the sum of all marker effects (direct genomic value, DGV) will be a good predictor of a given animal genetic merit and should enable selection decisions as soon as genotypes of such animals are available (just after birth or even during the embryo/fetus developmental phases).

Following these expectations, the sequencing of bovine genome [4] and the availability of dense SNP marker panels [5], allowed GS to migrate from simulation to