



animals



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Machine Learning and Statistics Applied to Livestock—Omics Data

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closed (31 July 2024)

Message from the Guest Editors

Dear Colleagues,

Nowadays, the data collected in the livestock sector (phenotypes, omics data, etc.) could be considered as “big data”. For this reason, “classical” statistical methods and pipelines may no longer be sufficient to dissect the biology behind the data.

The aim of this Special Issue is to develop new pipelines and methods and to identify alternative uses for existing methods, in particular for machine learning (ML) and artificial intelligence (AI) algorithms. The results could be compared with classical statistical methods. Omics data, including genomic (WGS, SNP array, etc.), transcriptomic and metagenomic, among others, will be explored along with connected metadata from the bred animals or the hosted microorganism (in the feces, gut, rumen, etc.). The idea is to apply the aforementioned methods to different kind of analyses, for example GWAS, genomic selection and biodiversity, in general modelling and prediction.



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Special Issue



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Message from the Editor-in-Chief

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