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Quantitative Genetics and Bioinformatics Method in Animals

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Deadline for manuscript submissions:
closed (15 November 2022)

Message from the Guest Editors

Bioinformatic and statistical methods are crucial in genetic and biology studies, and advanced bioinformatic and quantitative methods/tools are becoming even more important in the rapidly developing multi-omics era. In this Special Issue, we welcome the submission of research articles and review articles on topics related to the quantitative genetics and bioinformatics method for Animal Genetics and Breeding, describing novel models, tools, software and approaches in all fields of animal genetics. Research topics among the following themes are especially welcomed:

1. Novel models and methods in genomic selection and GWAS of animals;
2. Machine learning and artificial intelligence in the bioinformatics method of animals;
3. Novel computational methods and insights for genes, biological pathways, and networks associated with different traits in animals;
4. Novel approaches and methods to assemble different animals' genome and to characterize the genome variation;
5. Biological omics-data (including RNA-seq, HiC, CHIP-seq, ATAC-seq etc.) analysis for different traits in animals;
6. New bioinformatics and statistical algorithms and software development for quantitative traits.

mdpi.com/si/102523

Special Issue

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Message from the Editor-in-Chief

Genes are central to our understanding of biology, and modern advances such as genomics and genome editing have maintained genetics as a vibrant, diverse and fastmoving field. There is a need for good quality, open access journals in this area, and the *Genes* team aims to provide expert manuscript handling, serious peer review, and rapid publication across the whole discipline of genetics. Starting in 2010, the journal is now well established and recognised.

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