

## Special Issue

# Cytogenomics and Genes Bioinformatics: Analysis, Algorithms and Applications

### Message from the Guest Editor

Cytogenetics is a field with more than a century of history. Pure observation of chromosomes and their organization in karyotypes was the main focus of cytogenetics for many years. The karyotyping and classical chromosome banding revealed that different species may have different chromosome numbers or differ in their morphology. These findings were relevant for thousands of astonishing discoveries in many fields, ranging from evolutionary biology to cancer research. In situ fluorescent hybridization approaches were a landmark in cytogenetics, improving the resolution of chromosomal analysis. Recently, the emergence of Next-Generation Sequencing (NGS) has unveiled the cytogenomics era, in which chromosomes can be analyzed even in a single-base resolution. Furthermore, NGS allowed for a deeper understanding of nuclear chromosome structure/organization and the emergence of epigenomics. Cytogenomics is dependent on bioinformatics, which allows us to analyze the extensive information generated by NGS and other OMIC approaches. Cytogenomics is still in its infancy, and many discoveries will come in future years.

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### Guest Editor

Dr. Guilherme Targino Valente  
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### Deadline for manuscript submissions

closed (25 April 2025)

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## Genes

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*Genes* is central to our understanding of biology, and modern advances such as genomics and genome editing have maintained genetics as a vibrant, diverse and fast-moving 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. Why not consider *Genes* for your next genetics paper?

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### Editor-in-Chief

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