

# Genomics Communications – an enabling platform to explore the boundless horizons

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At the heart of every living organism resides the blueprint of its essence: the genome. Whether they are large dairy cattle or small bacteria living in the human guts, wild grasses, or domesticated crops, every organism, regardless of size or complexity, harbors a unique genome that orchestrates its development, function, and adaptation. Our exploration of genomic mysteries illuminates diversity in life forms, evolution history, adaptation of organisms, hidden genomic patterns, and beyond. The journey of Genomics and Bioinformatics spans decades of extraordinary discoveries and technology innovation. From the revelation of the double helix structure of DNA to the completion of the Human Genome Project, and to decode every organism, we have witnessed remarkable strides in understanding the genetic codes of living organisms. The field has moved forward at a fast pace, unraveling the evolutionary trajectory of the tree of life, the complexities of genetic variation, gene expression, epigenomic modifications, and functional genomics at multiple dimensions across time and space. Meanwhile, computational approaches have evolved rapidly with innovative algorithms and increasing computational power. At the dawn of the integration of artificial intelligence into genomics, we stand on the brink of harnessing potential powers to achieve unprecedented discovery and innovation. The remarkable advancements in protein structure prediction and AI-empowered designs of genes, proteins, and even *de novo* biosynthesis, serve as compelling examples.

Amidst this rapidly evolving genomic landscape, up-to-date platforms for disseminating research outcomes are more necessary than ever. As such, we are thrilled to inaugurate *Genomics Communications (gComm)*, a dynamic platform — serving authors, reviewers, and readers — dedicated to transparently advancing the frontiers of genomics. As a community-driven platform, our goal is to establish *gComm* as a leader in the genomic research publication service. The platform aims to: (1) provide an open-source repository for documenting genomic studies, (2) be a reliable and high-quality source of cutting-edge information and technologies, and (3) foster inclusive and unbiased academic exchange and knowledge dissemination.


For authors, we are committed to making the publication process seamless and open access more affordable. We welcome original research results from a broad spectrum of genomic studies, such as functional genomics, quantitative and population genomics, comparative genomics, genome editing, epigenomics, phenomics, genomic laboratory technology, and artificial intelligence in genomics. We encourage the submission of review and perspective articles to stimulate healthy discussions and inspire novel ideas. We invite computational pipelines with open-source scripts to foster transparency and reproducibility in data analysis. To enhance exposure of published research, authors will be selectively invited for

short talks, and the presentations will be posted online if agreed, and linked with published papers.

For editors and reviewers, we deeply value your contributions to the publication process and aim to ensure the peer-review process is both enjoyable and rewarding. We will award 2–3 Honor *gComm* Reviewers based on the quality and quantity of reviews, as well as recommendations from editors, every three-year cycle. To streamline the editorial procedures and minimize potential biases, we actively encourage the formation of local editorial groups worldwide, providing reasonable social funds, particularly in academically underrepresented locations. We strive to continuously refine and enhance our platform operations, embracing novel ideas to improve the review procedure and strengthen the impacts.

For readers, we will enable the illustration of research results to be presented dynamically and interactively, allowing readers to interpret the results from their unique perspectives. We grant free accession of all manuscripts and support multimedia views to assist in digesting original research, experimental methodologies, and computational approaches.

We extend sincere gratitude to the passionate individuals who have contributed to the establishment of *gComm*. Without the strong support of the genomics and computational biology community, our platform's success would remain elusive. We invite our fellow researchers to embark on this inclusive platform with us and share their insights and perspectives as we navigate the ever-expanding frontiers of genomics research. With your support, we are committed to nurturing *gComm* into an impactful platform, a valuable platform that will propel genomics into uncharted realms.



## Conflict of interest

The authors declare that they have no conflict of interest.

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