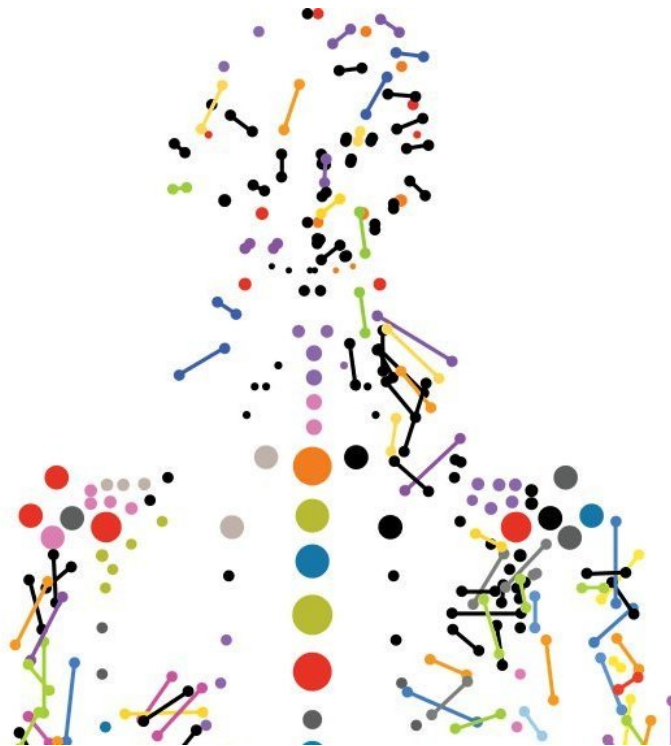


Scientists call for unified standards in 3-D genome and epigenetic data

October 31 2018



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Studying the three-dimensional structure of DNA and its dynamics is revealing a lot of information about gene expression, expanding our knowledge of how cells, tissues and organs actually work in health and disease. Properly producing and managing this large amount of data is both challenging and necessary for the progress of this field. In a

perspective paper published in *Nature Genetics*, top researchers call for unified standards and suggest guidelines in this emerging and promising research area.

Just as a map of the world is more than a list of places and street names, the [genome](#) is more than a string of letters. A complex choreography of proteins and nucleic acids interact differentially over time in the DNA, thus cells can selectively manage genetic information during development and cell differentiation or in response to physiological and environmental aspects.

Scientists worldwide are developing new technologies and making progress towards understanding the dynamics of three-dimensional organization of the nucleus. This new approach will allow researchers to map the differences between cell types, to explore how gene expression actually works in health or disease, and to discover how DNA functions are achieved even it is packed within the tiny nucleus.

"We know that genome folding and its dynamics modulates [gene expression](#) and new technologies allow us to build 3-D models to study these changes, which is currently shaking up [genome research](#) and boosting our understanding of the cell nucleus complexity," explains Marc A. Marti-Renom, ICREA research professor at the Centro Nacional de Análisis Genómico (CNAG-CRG) of the Centre for Genomic Regulation (CRG) in Barcelona, Spain. "This is an absolutely promising field and we would like to call for standards since the rapid development of methods and the increasing complexity of data pose many challenges that must be addressed now," he states.

In a perspective article published in the current issue of *Nature Genetics*, leading scientists in the field of dynamics and structural genomics have called for standards in 3-D genome and epigenetic data. They describe the main challenges in this field and provide guidelines to think about

strategies for shared standardized validation of 4-D nucleome data sets and models.

This paper comes out of their experience in the 4-D Nucleome Initiative as part of the LifeTime initiative for a new FET-Flagship in Europe to understand how genomes function within cells, and how cells form tissues and dynamically remodel their activities when tissues progress towards disease.

More information: Marc A. Marti-Renom et al, Challenges and guidelines toward 4D nucleome data and model standards, *Nature Genetics* (2018). [DOI: 10.1038/s41588-018-0236-3](https://doi.org/10.1038/s41588-018-0236-3)

Provided by Center for Genomic Regulation

Citation: Scientists call for unified standards in 3-D genome and epigenetic data (2018, October 31) retrieved 26 April 2024 from <https://medicalxpress.com/news/2018-10-scientists-standards-d-genome-epigenetic.html>

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