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

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 3D 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*, top leading scientists in the field of dynamics and structural genomics have called for standards in 3D genome and epigenetic data. They describe the main challenges in this field and provide guidelines to think about strategies for shared standardized validation of 4D nucleome data sets and models.

This paper comes out of their experience in the 4D 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.

With this call for standards, international experts at the Institut Curie in Paris, MRC Institute of Genetics and Molecular Medicine at Univeristy of Edinburgh, the Centre de Biologie Intégrative at the University of Toulouse, the Institute of Human Genetics in Montpellier, the Babraham Institute in Cambridge, the Florida State University in Forida (US), the Friedrich Miescher Institute for Biomedical Research in Basel, the Napoli

University, the Berlin Institute of Health, the Institute for Research in Biomedicine IRB Barcelona, the Max Delbruck Center for Molecular Medicine in Berlin, the Institute for Epigenetics and Stem Cells Helmholtz Zentrum Muenchen in Munich, and the Centro Nacional de Análisis Genómico (CNAG-CRG) of the Centre for Genomic Regulation (CRG) in Barcelona, want to ensure that information is properly characterized, validated and shared, and that resources are efficiently used.

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NOTES TO THE EDITOR

About the 4D Nucleome and the LifeTime Initiatives

The 4D Nucleome Initiative aims to decipher the structure-function relationships of the cell nucleus as a complex biological system at all levels, from molecules to entire genomic and epigenomic landscapes, as they respond and adapt to environmental changes, as well as changes during development, cell reprogramming and ageing.

The 4D Nucleome Initiative is one of the pillars of the larger LifeTime Initiative that calls 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.

Reference: MA. Marti-Renom et al. 4D Nucleome: challenges and guidelines towards data and model standards. Nature Genetics **50**, pages1352–1358 (2018). DOI: 10.1038/s41588-018-0236-3

For further information and media requests please, contact:
Laia Cendrós, media relations, Centre for Genomic Regulation
laia.cendros@crg.eu – Tel. +34 933160237 – Mobile +34607611798