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Objectives

Abstract: Most cardiovascular (CV) risk scores used in clinical practice predict the probability of CV events using information on the seven traditional cardiovascular risk factors: age, gender, hypertension, dyslipidemia, obesity, smoking and diabetes. These scores, however, fail to identify young, healthy individuals potentially at risk based on their extension or progression of subclinical atherosclerosis, mainly characterized using imaging techniques. By means of deep phenotyping and omics data analyzed with machine learning methods we aim to develop new risk scores to refine the prediction of 10-year cardiovascular risk in young, asymptomatic individuals. Moreover, this data-driven approach to CVD is improving our understanding about how the molecular profile and a variety of psychosocial, lifestyle, dietary and demographic variables affects the genesis of the disease and its progression and, eventually, how and when SA will lead to cardiovascular events.



Short-Bio: Dr. Fátima Sánchez Cabo graduated in Mathematics from the Universidad

Complutense de Madrid in 2000. After that, she moved to the University of Manchester where she obtained a scholarship from the BBSRC to develop her doctoral work on the statistical analysis and mathematical modeling of microarray data. In 2005, she joined the Institute of Genomics and Bioinformatics of the Graz University of Technology (Austria) where she developed her work in the field of precision medicine in cancer immunology, first as a postdoctoral researcher and later as an associate professor. In 2008 she joined CNIC and since 2017 is the Head of the Bioinformatics Unit of the center. Dr. Sánchez-Cabo has published 49 articles in peer-reviewed journals. She is especially interested in the development of statistical methods and tools for the integration of heterogeneous data to unravel complex systems such as cardiovascular disease. She is also an external professor at CEU San Pablo University and at Kaggle School.

Speakers

Dr. Sánchez-Cabo is the Head of the Bioinformatics Unit of CNIC.

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