

## Study maps human metabolism in health and disease

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Scientists have produced an instruction manual for the human genome that provides a framework to better understand the relationship between an individual's genetic make-up and their lifestyle.

The international team of researchers say their study – published in <u>Nature Biotechnology</u> – provides the best model yet to explain why individuals react differently to environmental factors such as diet or medication.

"This research is the second important stage of our understanding of the <u>human genome</u>," said study author Professor Pedro Mendes, from The University of Manchester's School of Computer Science. "If the sequencing of the human genome provided us with a list of the biological parts then our study explains how these parts operate within different individuals.

"The results provide a framework that will lead to a better understanding of how an individual's lifestyle, such as diet, or a particular drug they may require is likely to affect them according to their specific <u>genetic</u> <u>characteristics</u>. The model takes us an important step closer to what is termed 'personalised medicine', where treatments are tailored according to the patient's <u>genetic information</u>."

The research, which involved scientists from Manchester, Cambridge, Edinburgh, Reykjavik, San Diego, Berlin and others, mapped 65 different human cell types and half of the 2,600 enzymes that are known



drug targets in order to produce the network model.

Co-author Douglas Kell, Chief Executive of Biotechnology and Biological Sciences Research Council (BBSRC) and Professor of Bioanalytical Science at the Manchester Institute of Biotechnology, said: "To understand the behaviour of a system one must have a model of it. By converting our biological knowledge into a mathematical model format, this work provides a freely accessible tool that will offer an indepth understanding of <u>human metabolism</u> and its key role in many major human diseases.

"This study offers the most complete model of the human metabolic network available to date to help analyse and test predictions about the physiological and biochemical properties of human cells."

Dr Nicolas Le Novère, from the Babraham Institute in Cambridge (UK), said: "This is a model that links the smallest molecular scale to the full cellular level. It contains more than 8,000 molecular species and 7,000 chemical reactions – no single researcher could have built this alone. Having large collaborations like these, using open standards and datasharing resources, is crucial for systems biology."

**More information:** 'A community-driven global reconstruction of human metabolism,' by Ines Thiele and Neil Swainston et al, *Nature Biotechnology*, 2013.

Provided by University of Manchester

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