Statistician helps resolve dispute about how gene expression is controlled

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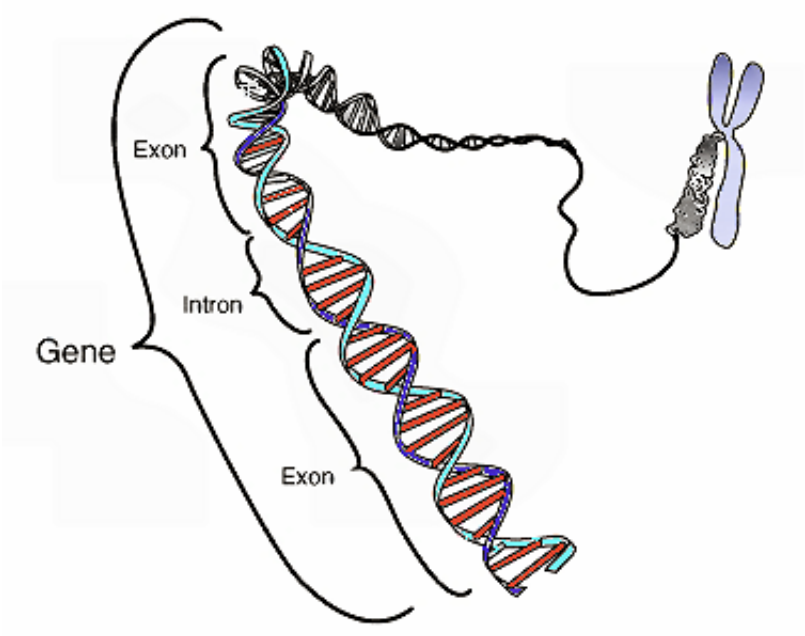

This image shows the coding region in a segment of eukaryotic DNA. Credit: National Human Genome Research Institute

The differences between different tissues, such as brain and muscle, and between healthy and unhealthy human cells are largely defined by changes in the abundance of proteins in the cells. Transcription—the process that governs the flow of genetic information from DNA to RNA—was long believed to play the dominant role in determining the quantity of proteins in a cell. But over the past decade, many studies have claimed that in animals, differences in the rate at which RNA is

translated into proteins are a more important factor.

Several new studies, one co-authored by a UCLA professor, show that transcription is in fact the most influential step in determining protein abundance. A summary of this research is published in the journal *Science*.

Jingyi Jessica Li, an assistant professor of statistics and human genetics in the UCLA College, and Mark Biggin at Lawrence Berkeley National Laboratory, reviewed these recent studies, including one they performed, and concluded that transcription makes the largest contribution to protein abundance. Their study and the other recent work they reviewed use more careful statistical methods that estimate or reduce the impact of experimental measurement errors. Li and Biggin showed that much of what was taken to be an effect of translation in the earlier studies is actually a result of experimental errors.

The researchers conclude that more accurate measurement and analysis methods are needed for gene expression to be accurately modeled by scientists.

Their research has implications for identifying pharmaceuticals that can effectively treat a variety of diseases

More information: Statistics requantitates the central dogma, *Science* 6 March 2015: Vol. 347 no. 6226 pp. 1066-1067 . DOI: 10.1126/science.aaa8332 .
www.sciencemag.org/content/347/6226/1066.full

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