

# BGRF announces OncoFinder algorithm for reducing errors in transcriptome analysis

August 18 2014

---

Scientists from the Biogerontology Research Foundation (BGRF), a UK-based charity founded to support ageing research and address the challenges of a rapidly ageing population, propose a new concept for signalome-wide analysis of changes in intracellular pathways, called OncoFinder, which allows for accurate and robust cross-platform analysis of gene expression data. This new technique will allow scientists to derive useful information from and compare the hundreds of thousands of data sets obtained using legacy equipment as well as data sets obtained from biological samples preserved in paraffin blocks and partially-degraded samples.

The original research, published in the journal *Frontiers in Molecular Biosciences*, shows that the OncoFinder method significantly reduces errors introduced by transcriptome-wide experimental techniques. Scientists compared gene expression data for the same [biological samples](#) obtained by both next generation sequencing (NGS) and microarray methods, finding that these different techniques have almost no correlation between the gene expression values for all datasets analysed. In contrast, when the OncoFinder algorithm is applied to the data, a clear correlation between next generation sequencing and microarray gene expression datasets was seen.

"For several years the potential for the use of [gene expression data](#) in research and clinical applications has been underappreciated due to the inconsistency of the data coming from the various types of equipment. There is just too much variation and complexity when comparing the

massive number of individual genes. But when this complexity is reduced and the [gene expression](#) is mapped onto signalling pathways, we can evaluate the pathway activation drift and analyse the changes and transitions much more effectively. The OncoFinder algorithm enables scientists to characterise the functional states of transcriptomes more accurately than before and we hope that this will become a method of choice in genetics, physiology, biomedicine and molecular diagnostics," said Alex Zhavoronkov, PhD, director of the BGRF and co-author of the study.

**More information:** [journal.frontiersin.org/Journal/2014.00008/abstract](https://journal.frontiersin.org/Journal/2014.00008/abstract)

Provided by Biogerontology Research Foundation

Citation: BGRF announces OncoFinder algorithm for reducing errors in transcriptome analysis (2014, August 18) retrieved 26 June 2024 from <https://medicalxpress.com/news/2014-08-bgrf-oncofinder-algorithm-errors-transcriptome.html>

<p>This document is subject to copyright. Apart from any fair dealing for the purpose of private study or research, no part may be reproduced without the written permission. The content is provided for information purposes only.</p>
--