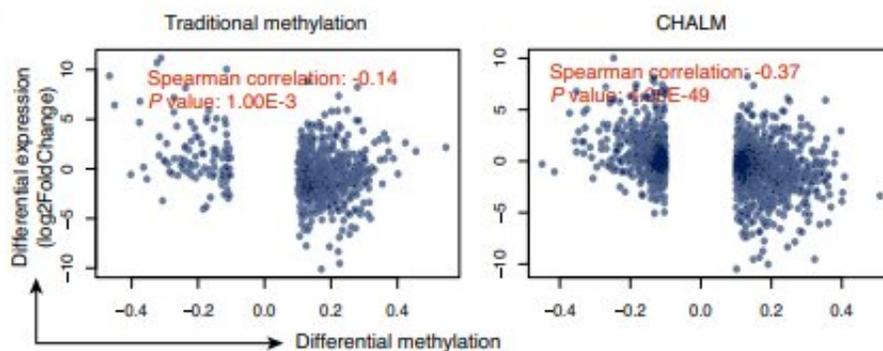


New study points to better diagnostics for cancer

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Scatter plots show the correlation between differential expression and differential methylation calculated by the traditional and CHALM methods. Credit: UCI School of Medicine

A new University of California, Irvine-led study finds a new method for identifying biomarkers may aid in early cancer diagnosis. The study focused on lung cancer, however the Cell Heterogeneity-Adjusted cLonal Methylation (CHALM) method has been tested on aging and Alzheimer's diseases as well and is expected to be effective for studying other diseases.

"We found the CHALM method may be a [valuable tool](#) in helping researchers to identify more reliable differentially methylated genes from sequence-based methylation data," said Wei Li, Ph.D., the Grace

B. Bell chair and professor of bioinformatics in the Department of Biological Chemistry at the UCI School of Medicine. "For clinicians, this method may aid in [cancer diagnosis](#) by helping them identify more useful biomarkers, which are overlooked by the traditional method."

Published in *Nature Communications*, the study, titled, "Cellular Heterogeneity-Adjusted cLonal Methylation (CHALM) improves prediction of [gene expression](#)," illustrates the importance of considering cell heterogeneity when calculating the DNA methylation level from sequencing data.

"After applying our CHALM method to a [lung cancer](#) dataset, we were able to identify more reliable and biological functions-related differentially methylated genes. Applying our CHALM method may lead to better early cancer detection," said Li.

Using traditional methods for identifying cancer biomarkers, researchers have consistently found the correlation between gene expression and promoter methylation to be weak, especially for low methylated genes. This new study found the CHALM method allowed for more reliable identification of methylated markers that cannot be detected by traditional methods.

More information: Jianfeng Xu et al, Cellular Heterogeneity–Adjusted cLonal Methylation (CHALM) improves prediction of gene expression, *Nature Communications* (2021). [DOI: 10.1038/s41467-020-20492-7](https://doi.org/10.1038/s41467-020-20492-7)

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