Docket #: S23-034

Improved cfDNA methylation profiling through correction of misrepaired jagged-ends

Stanford researchers have developed an in silico method, JEEPERS, that corrects DNA methylation errors at jagged-ends, improving cfDNA methylation profiling for early cancer detection and tissue-of-origin classification.

Cell free DNA (cfDNA) methylation profiling allows early cancer detection and tissue-of-origin classification. However, end repair process during library preparation for cfDNA sequencing may introduce changes in methylation patterns. To address this issue, Stanford researchers have developed JEEPERS (Jagged-End Error Polishing of Enzymatically misRepaired Sequences), a novel in silico method for correcting errors in methylation data resulting from the end repair process in double-stranded library preparation. It detects and corrects errors at jagged-ends (JEs) in silico, leveraging support from complementary strands and sibling reads.

Stage of Development
Proof of Concept

Applications

- Early cancer detection

Advantages

- Superior cfDNA genotyping
- Identification of allele-specific methylation, hemi-methylation, and gene expression
- Compatible with other methylation datasets

- Low cost

Publications

- Wang, R., Hamilton, E. G., Almanza, D., Hui, A., Diehn, M., & Alizadeh, A. A. (2024). Improved cfDNA methylation profiling through correction of misrepaired jagged-ends. *Cancer Research, 84*(6 Supplement), 960-960.
- Wang, R., Hamilton, E. G., Hui, A., Almanza, D., Esfahani, M. S., Diehn, M., & Alizadeh, A. A. (2023). Improved cfDNA methylation profiling through correction of misrepaired jagged-ends. *Cancer Research, 83*(7 Supplement), 1024-1024.

Innovators

- Arash Alizadeh
- Maximilian Diehn
- Rui Wang

Licensing Contact

Mona Wan

Senior Associate Director, Life Science

Email