Software and Algorithms for Optimized Molecular Inversion Probe (MIP) Design in Targeted DNA Sequencing

This technology enables efficient and scalable design of molecular inversion probes (MIPs), a cost-effective method for targeted DNA sequencing. It includes predictive modeling tools and software that improve probe performance and coverage uniformity across genomic regions.

What is the Problem?

Targeted DNA sequencing is widely used in research and clinical diagnostics to analyze specific regions of the genome. Molecular inversion probes (MIPs) enable targeted sequencing of specific genes and can be applied to detect low-frequency mutations through high-depth sequencing. However, designing probes that reliably capture these regions remains a challenge. Poor probe design can lead to uneven coverage, low specificity, and increased costs due to repeated assay optimization. As sequencing applications expand to larger cohorts and more complex targets, the need for scalable, accurate probe design tools becomes more pressing.

What is the Solution?

This technology provides a computational framework for designing molecular inversion probes (MIPs), which are short DNA sequences used to selectively capture genomic targets. The system includes algorithms that evaluate probe performance using predictive models based on empirical data. It identifies optimal probe “arms” that flank target regions and scores them for expected efficiency and specificity. The software, known as MIPgen, streamlines probe design for hundreds to thousands of targets simultaneously, reducing manual effort and improving assay reliability. These tools are especially useful for applications such as rare variant detection, gene panel sequencing, and clinical diagnostics.

What is the Competitive Advantage?

-Predictive modeling using logistic regression and support vector machines (SVMs) improves probe success rates and reduces design iterations.

-Automated scoring and selection of probe arms ensures uniform coverage and minimizes off-target effects.

-Scalable design supports large panels and high-throughput applications, making it suitable for population-scale studies.

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Category

Software/Bioinformatics

Therapeutics/Platform Technology

Selection of Available Technologies

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-The software is user-friendly and adaptable to diverse genomic targets, including coding and non-coding regions.

Patent Information:

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References

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