



Systems And Methods For Identifying Sequence Information From Single Nucleic Acid Molecule Measurements

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The Invention

Systems and methods for identifying sequence information from measurements made on single nucleic acid molecules are disclosed. The systems and methods can include binding portions of nucleic acid molecules with marker molecules, such as fluorescent molecules and/or intercalating molecules. The marker molecules provide a detectable signal that includes information about the underlying genomic information of the location on the nucleic acid molecule where a given marker molecule is bound. A profile of the detectable signal along a position of the nucleic acid is acquired for multiple different nucleic acid molecules. The PRIMR algorithm processes the data to provide a consensus profile from which a consensus underlying genomic information can be determined.

Additional Information

For More Information About the Inventors

- [David Schwartz](#)
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Tech Fields

- [Research Tools : DNA & RNA tools](#)

For current licensing status, please contact Justin Anderson at janderson@warf.org or 608-960-9853