Bisulfite sequencing is a technique used to study DNA methylation, which is an epigenetic modification involved in gene regulation. In DNA methylation, a methyl group is added to a cytosine base, usually in the context of a CpG dinucleotide. Bisulfite sequencing is based on the chemical conversion of unmethylated cytosines to uracils by treatment with sodium bisulfite, which leaves methylated cytosines unchanged. After bisulfite treatment, the DNA is amplified using polymerase chain reaction (PCR), and the resulting DNA fragments are sequenced to determine the pattern of cytosine methylation.

Bisulfite sequencing can be used to study DNA methylation patterns in a variety of contexts, including developmental processes, disease states, and environmental exposures. It can also be used to study epigenetic changes associated with aging, cancer, and other diseases.

There are two main types of bisulfite sequencing: target-based and whole-genome. Target-based bisulfite sequencing is used to analyze specific genomic regions of interest, such as promoter regions or CpG islands. Whole-genome bisulfite sequencing (WGBS) is used to analyze the methylation status of the entire genome, which allows for the discovery of novel methylation patterns and epigenetic changes.

Bisulfite sequencing has become a widely used technique in epigenetics research, and it has led to important insights into the role of DNA methylation in gene regulation and disease. However, bisulfite sequencing is a complex and labor-intensive technique that requires specialized equipment and expertise, and careful interpretation of the results is necessary to avoid false positives and false negatives.