DNA METHYLATION ANALYSIS WITH DMRCATE

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Tran Ba Thien

About me

Affiliation	OUCRU-HCM (Oxford University Clinical Research Unit) Emerging Infections group Research Assistant (Bioinformatics)
ORCID	0009-0007-2964-7747
Webpage	Trần Bá Thiên – OUCRU
Phone	+84 815451019
Email	thientb@oucru.org / thien2522k@gmail.com

Commonly Used Methods to Characterize DNA Methylation

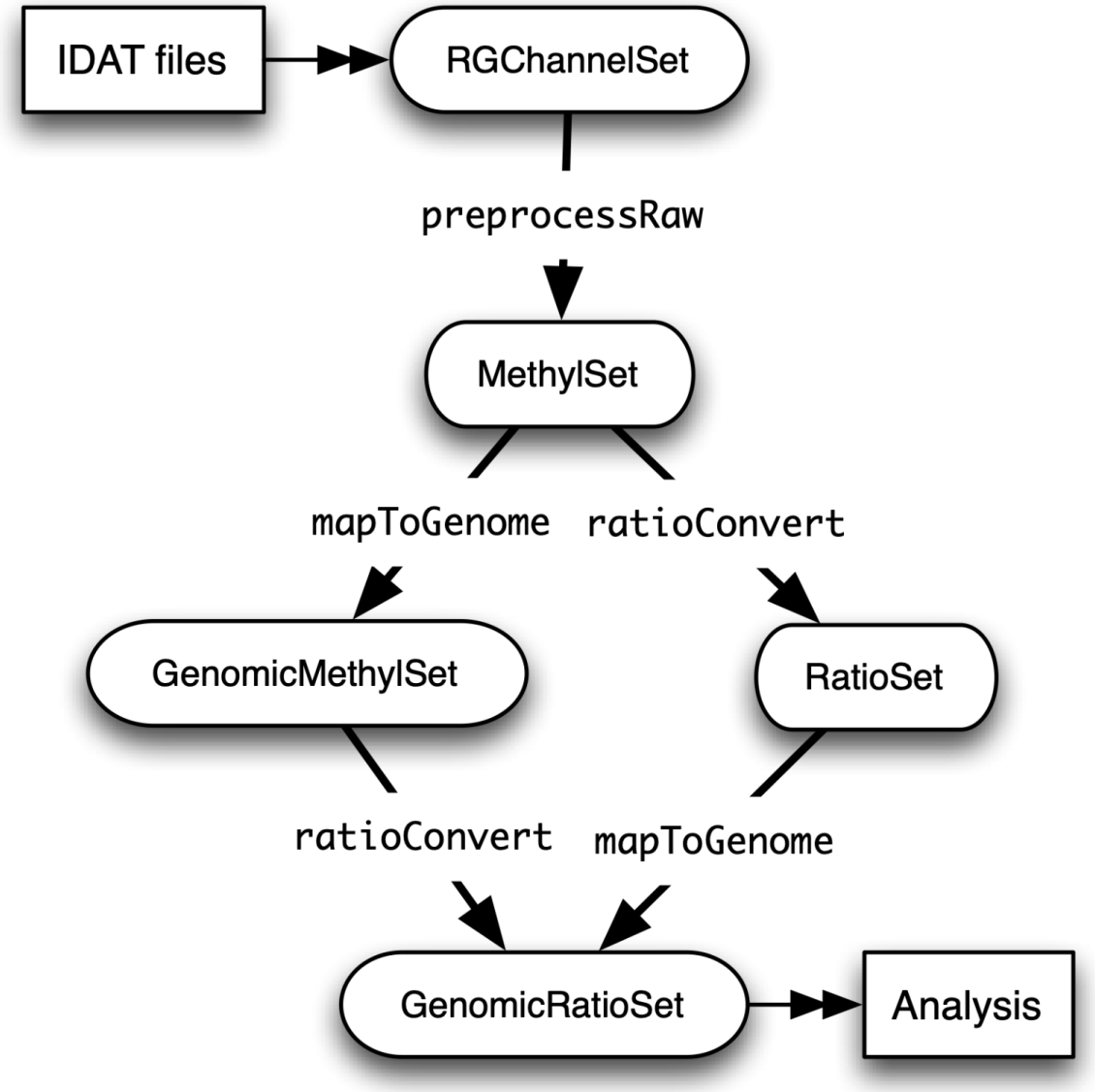
Technique	Mechanism	Genomic Targets	Advantages	Disadvantages
Whole genome bisulfite sequencing (WGBS)	Treatment of DNA with sodium bisulfite followed by next-generation sequencing	All nucleotides	The most extensive analysis of DNA methylation Nucleotide-level resolution	Expensive Confounding C/T polymorphisms Analyses are computationally intensive
Reduced representation Bisulfite Sequencing (RRBS)	Cleavage of DNA with methylation sensitive restriction enzymes followed by bisulfite sequencing	Genomic fragments within pairs of certain recognition sites	Intermediate cost Nucleotide-level resolution	Only methylation events within the recognition sites are assayed Confounding C/T polymorphisms
Methylated DNA immunoprecipitation chip (MeDIP-chip)	Sample methylated DNA fragments using 5mC antibody Assay by microarray hybridization	Genomic fragments with substantial DNA methylation	Large scale Low cost	Low resolution (1 kb) Could be affected by antibody efficiency Batch effects
Methylated DNA immunoprecipitation sequencing (MeDIP-seq)	Sample methylated DNA fragments using 5mC antibody Assay by next-generation sequencing	Genomic fragments with substantial DNA methylation	Large scale Intermediate cost	Low resolution (150–200 bp) Could be affected by antibody efficiency
CXXC affinity purification (CAP)-seq	Sample unmethylated DNA using zinc-finger CxxC affinity chromatography Assay by next-generation sequencing	Genomic fragments devoid of DNA methylation	Large scale Cost-effective to capture the unmethylated genomic fraction	Requires large amounts of input DNA Could be affected by binding efficiency
Methylation array	Treatment of DNA with sodium bisulfite and array hybridization	Preselected CpG sites via the source company	Low cost Nucleotide-level resolution	Predefined CpGs are interrogated Batch effects

https://doi.org/10.1093/gbe/evx203

Illumina Methylation Array Platforms

Platform	Release	# CpG Sites	Key Features
27K (HumanMethylation27)	~2009	~27,578	Early version; focused mostly on promoter regions of ~14,000 genes
450K (HumanMethylation450)	~2011	~485,577	Genome-wide; includes CpG islands, shores, shelves, promoters, gene bodies
EPIC (850K, MethylationEPIC)	~2015	~865,918	Improved version of 450K; adds enhancer CpGs (ENCODE, FANTOM5, etc.)
EPIC v2.0 (MethylationEPIC v2.0)	~2022	~935,000	Expanded coverage of regulatory regions, enhancers, and TSSs
Custom Infinium Arrays	Variable	Variable (10K–>1M+)	Tailored to specific genes, diseases, or CpG regions

Illumina Methylation Array Processing Workflow



DNA Methylation: Array Workflow — Epigenomics Workshop 2024 1 documentation

Outline

1. Raw data downloading and processing
2. DMRcate: DMPs and DMRs calling
3. DMPs and DMRs visualizing
4. DMRs annotating
5. Gene ontology calling

› Mol Clin Oncol. 2022 Sep 2;17(4):149. doi: 10.3892/mco.2022.2582. eCollection 2022 Oct.

Searching for the methylation sites involved in human papillomavirus type 16 and 18-positive women with cervical cancer

Yanyun Ma [1], Chunxia Wang [1], Mengqi Shi [2], Mingshan Li [2], Lin Li [3], Tuanjie Che [3], Jing Qu [2]

Affiliations + expand

PMID: 36157320 PMCID: PMC9468798 DOI: 10.3892/mco.2022.2582

DMPs: Differential Methylation Positions
DMRs: Differential Methylation Regions
https://doi.org/10.3892/mco.2022.2582

Before we start

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