

Steps in a DNA methylation analysis

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Background on DNA Methylation

DNA

ACTGACCTAGATCAGTGTAGCGATCGTATACGAGACCGATTTCATCGGCAT



transcription

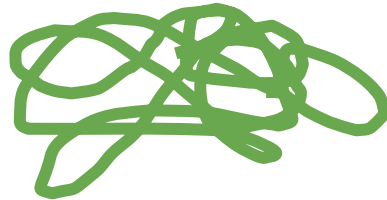
RNA

AUCAGUCGAUCACCGAU



translation

protein



DNA

ACTGACCGTTCGATCGATCGTATACGATTACAAAATCATCGGCAT



transcription

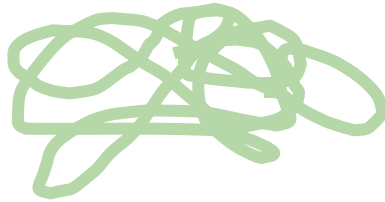
RNA

AUCAGUCGAUCACCGAU



translation

protein



M M
ACGACTACGC

M M
ACGACTACGC

Split DNA into two aliquots
(identical samples)

ACGACTACGC



ACGAUTACGU



Bisulfite conversion converts
unmethylated C to U

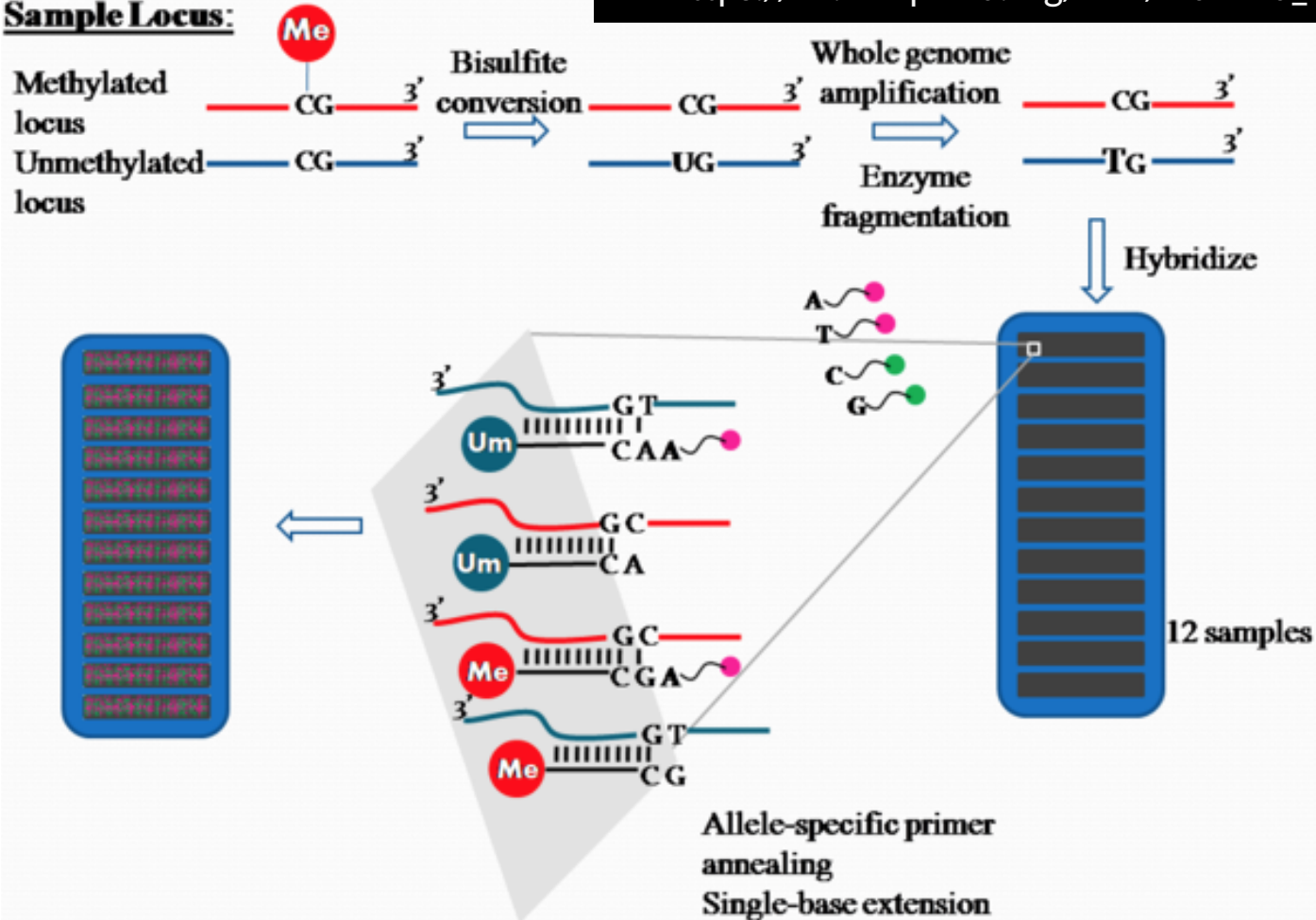
ACGACTACGC

ACGAUTACGU

Sequence and compare



Sample Locus:



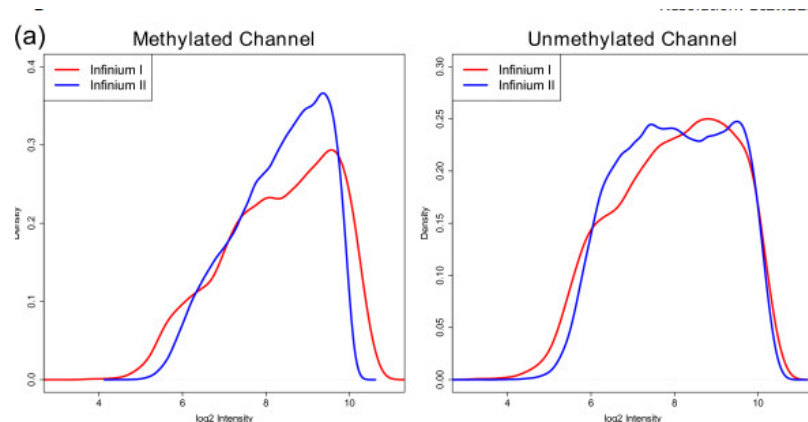
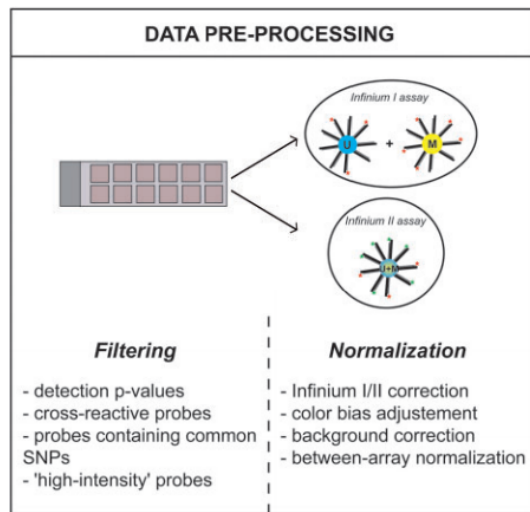
Steps

1. Normalization
2. Smoothing
3. Region finding
4. Annotation

Step 1: Normalization

Software:

- [minfi](#) (bisulfite seq + array)
- [charm](#)

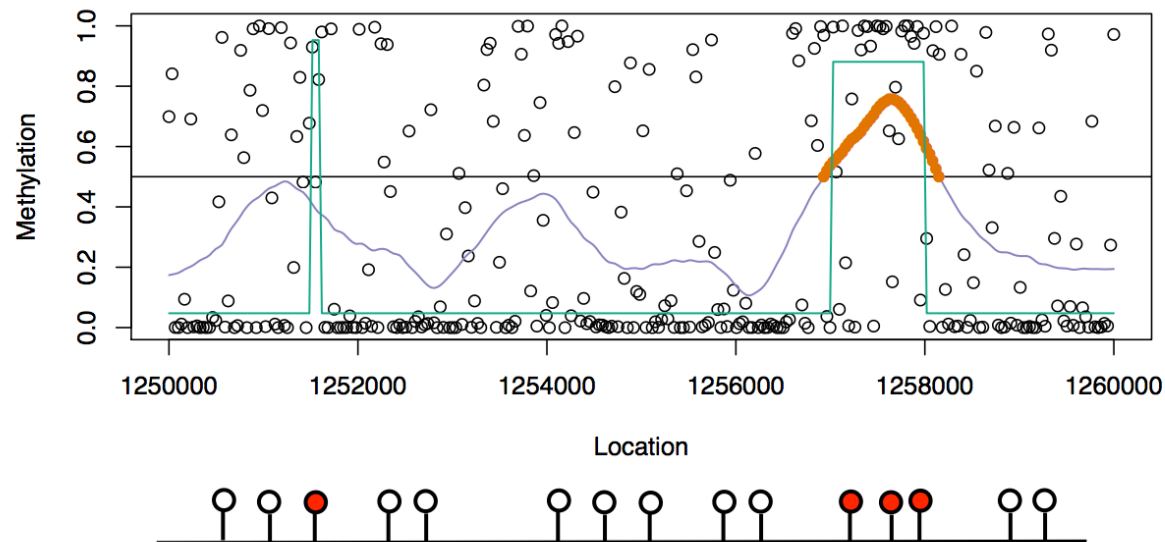


<http://bib.oxfordjournals.org/content/early/2013/08/27/bib.bbt054.full>
<http://www.genomebiology.com/2012/13/6/r44>

Step 2: Smoothing

Software:

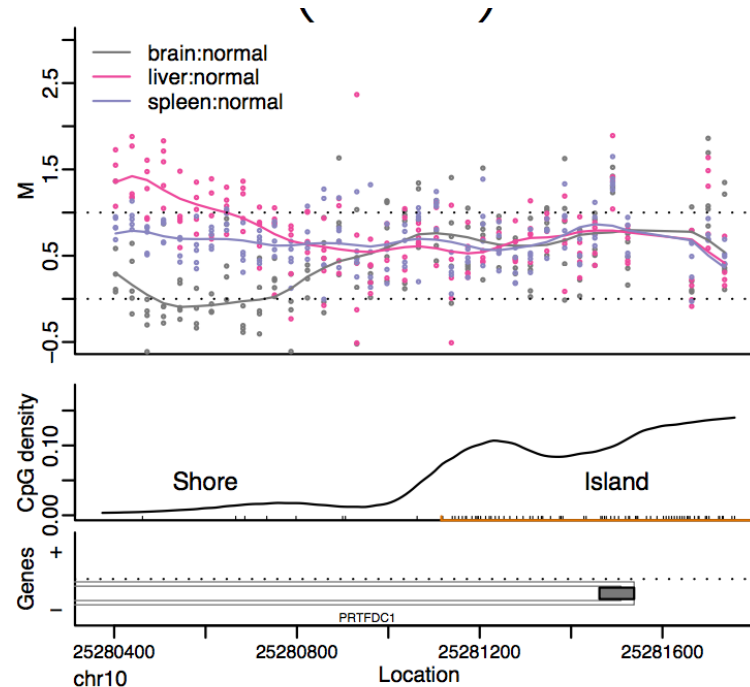
- [charm](#)
- [bsseq](#) (bisulfite seq)



Step 3: Region finding

Software:

- [charm](#)
- [bsseq](#) (bisulfite seq)



Step 4: Annotation

Software:

- [charm](#)
- [bsseq](#) (bisulfite seq)
- [BioC Annotation Workflow](#)

<http://www.ncbi.nlm.nih.gov/pubmed/19151715>

