BMIQ:

A beta-mixture quantile normalization method for correcting probe design bias in Illumina Infinium 450k DNA methylation data

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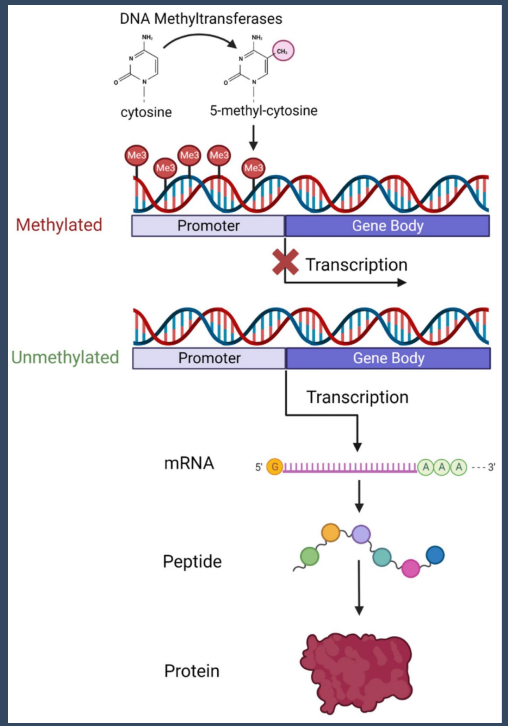
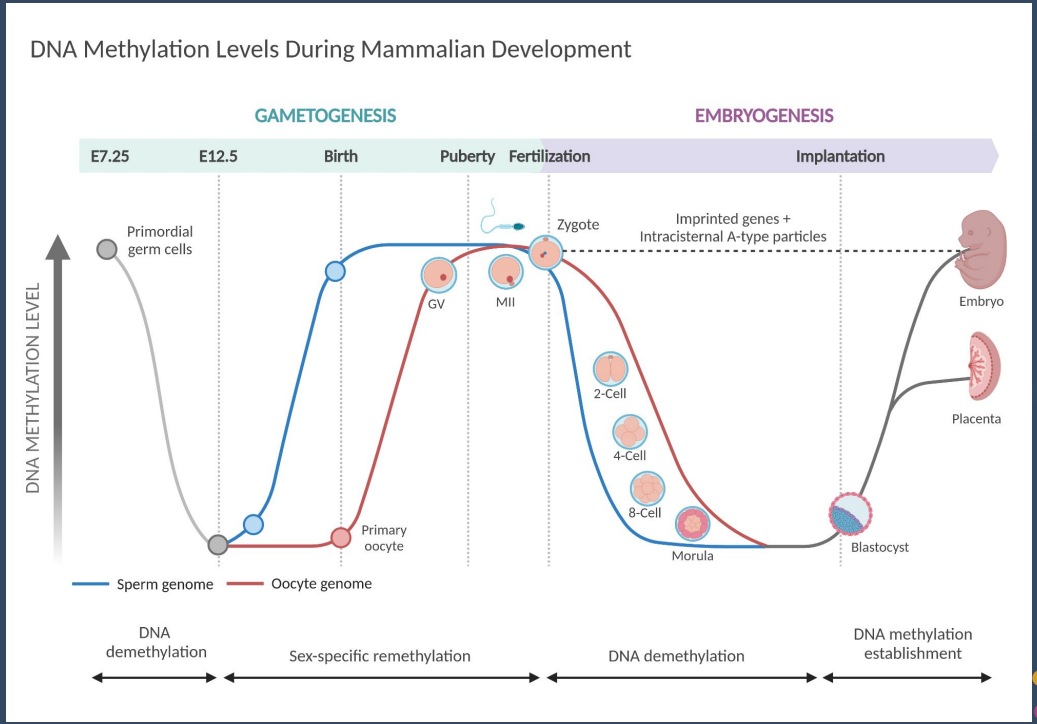
DNA Methylation

- DNA methylation is an epigenetic modification affecting gene expression without altering the DNA sequence.



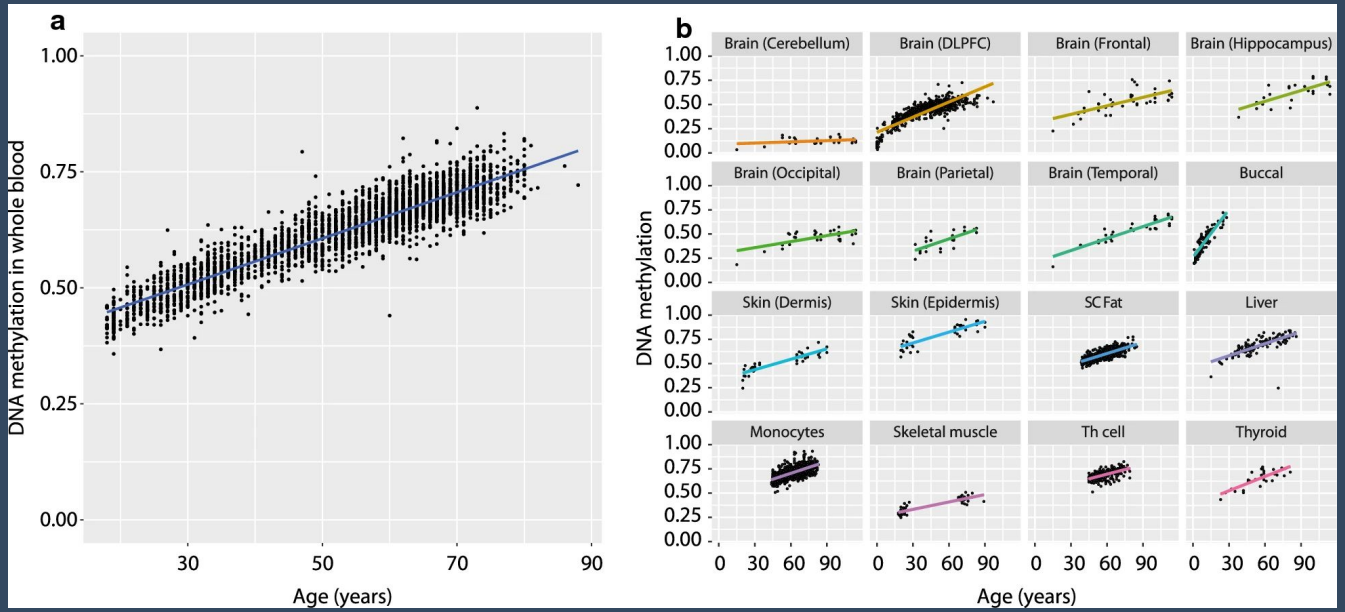
Wang et al, 2023



Smallwood et al, 2012

Study DNA methylation is challenging

- DNA methylation is highly variable between cell types and developmental stages.
- Technical variability can introduce bias and noise to the biological differences.



Zhang et al, 2013

How to address this challenges?

With Normalization :)

BMIQ

Beta Mixture Quantile normalization (BMIQ) is a method developed particularly for **Illumina methylation array data**.

BMIQ Assumption

Methylation level distributions of **Type I** and **Type II probes** should be the **same** for the **same biological sample**.

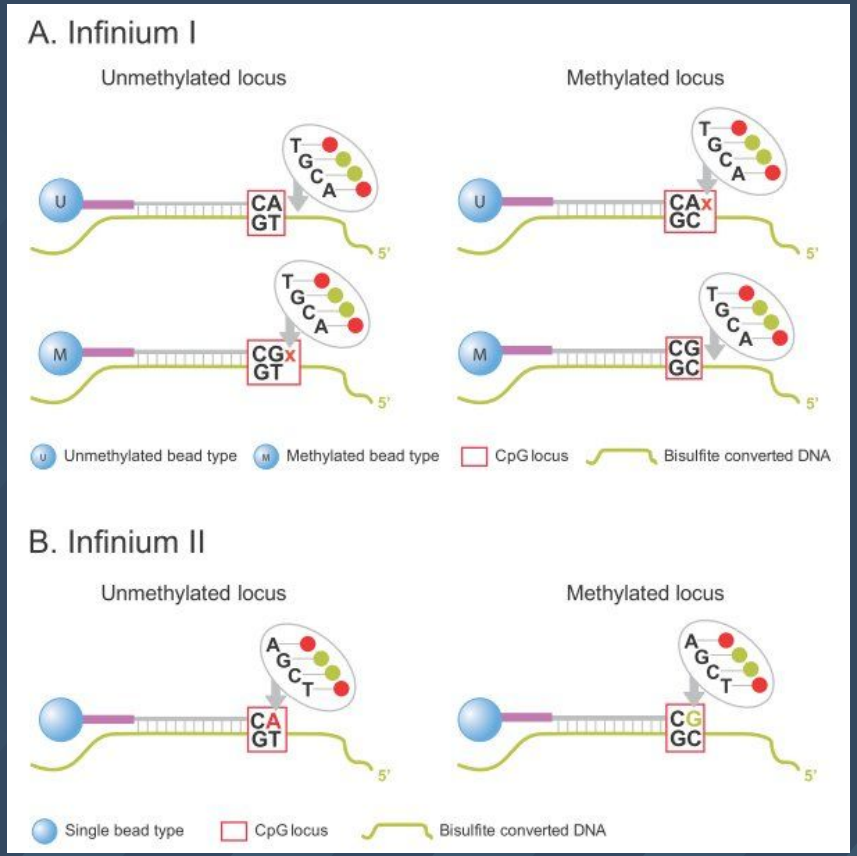
Illumina methylation arrays

Type I

Fluorescent signal

Type II

Colorimetric readout



Papst, 2019

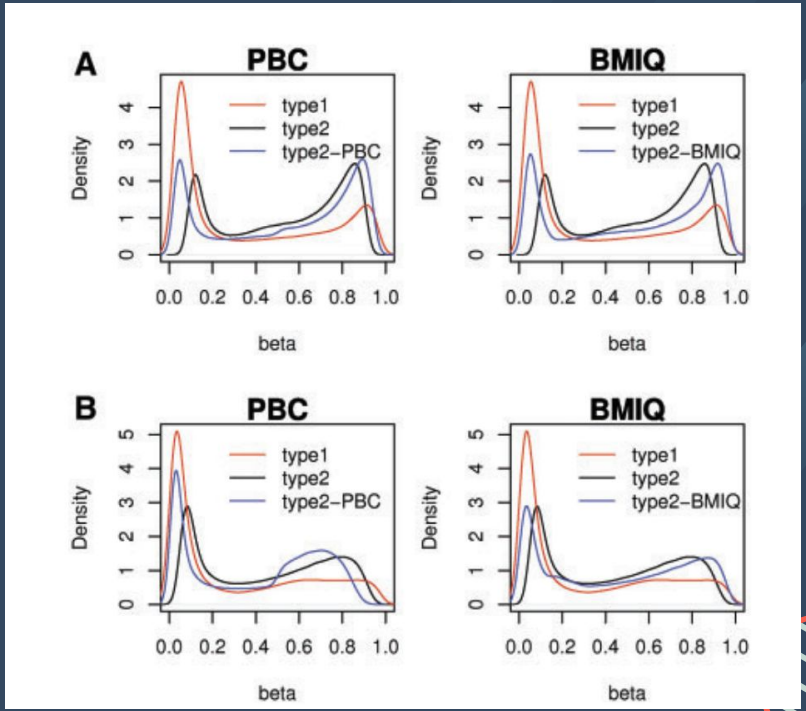
Specificity
Sensitivity

BMIQ adjustment

Dynamic range
variance

BMIQ Key Steps

1. Data segregation and analysis
2. Distribution Modeling
3. Normalization Process
4. Evaluation and adjustment



Teschendorff et al, 2013

Where to find BMIQ

Multiple R packages integrate BMIQ normalization:

- waterMelon (https://bioconductor.org/packages/wateRmelon)
- ChAMP (https://bioconductor.org/packages/ChAMP)
- Minfi (https://bioconductor.org/packages/minfi)
- ENmix (https://bioconductor.org/packages/ENmix)

Thanks!

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