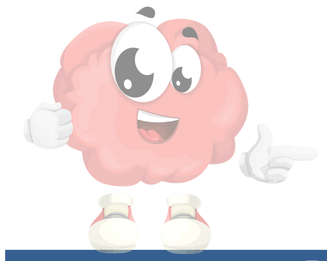

Normalizing for cell type: Does it matter?

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Team: Methylhomies

BACKGROUND

- DNA methylation (DNAm) plays a crucial role in maintaining patterns of gene expression during human development and aging.
- Understanding the human methylome is important for determining both biomarkers for - and direct pathways implicating - health and disease [1].
- Aberrant DNAm patterns have been correlated with common neurodegenerative disorders, including Alzheimer's Disease and Parkinson's Disease [2], as well as with mental disorders such as schizophrenia [3,4].
- However, much of the literature on either the diseased or healthy brain methylome fails to separate DNAm data by cell type composition - a major driver of DNAm variability - or by brain region [5-8].
- **Dataset:** We are using publically available data that is used and described in the Hannon *et al.* paper.

AIM

1. To determine whether cell type correction between brain regions is necessary in the analysis of Illumina HumanMethylation450 BeadChip array data
2. To investigate genes differentially methylated between cerebellum and cortex regions

METHODS

- Filler…..

Pipeline:

Image of pipeline (hilary is making) or PCA?

RESULTS

1. BMIQ normalization may be more appropriate than Dasen

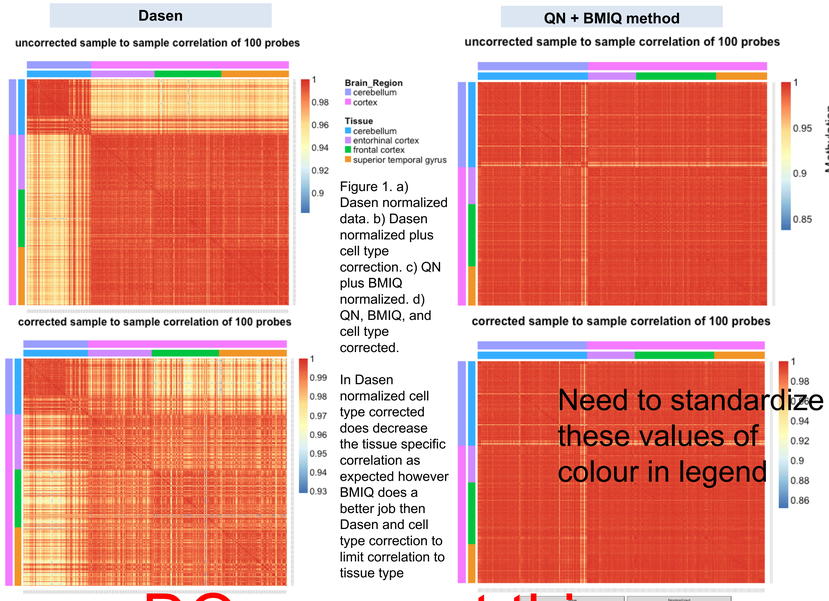
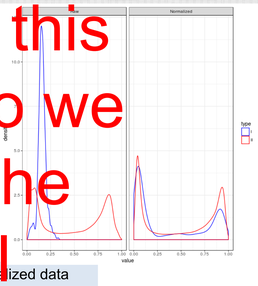


Figure 1. a) Dasen normalized data. b) Dasen normalized plus cell type correction. c) QN plus BMIQ normalized. d) QN, BMIQ, and cell type corrected.

In Dasen normalized cell type corrected does decrease the tissue specific correlation as expected however BMIQ does a better job then Dasen and cell type correction to limit correlation to tissue type

Need to standardize these values of colour in legend

DO we want this also? If so do we have it with the dasen model

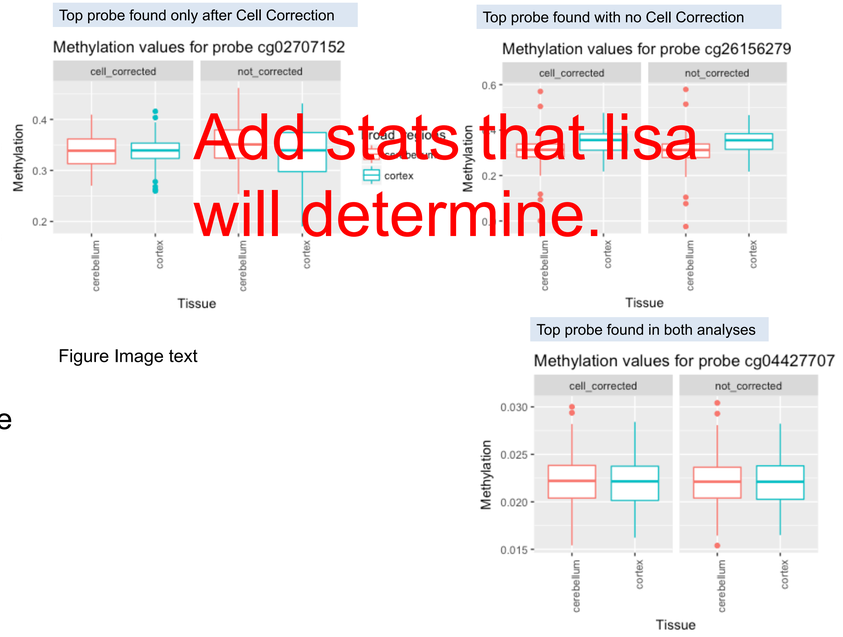


Our analysis moved forward with the BMIQ normalized data

2. Differential expression analysis found… Filler

Vendiagram + volcano? List of most intersting genes

3. Cell type correction has greater effect in certain probes and brain regions



Add stats that lisa will determine.

Figure Image text

5.

CONCLUSIONS

- Guidelines for those doing DNA methylation studies.. How to normalize and such.

FUTURE WORK

Filler Text

References: [1] Bernstein *et al. Cell* (2007). [2] Sanchez-Mut *et al. Transl Pysch.* [3] Huang *et al. PloS one* (2007). [4] Huang *et al. Journal of Neuroscience* [5] Shin *et al. Nat Neurosci* (2014). [6] Jaffe *et al. Genome Biology* (2014). [7] Guintivano *et al. Epigenetics* (2013). [8] Montano *et al. Genome Biol* (2013).