# Epigenomic Aging Eric Kramer 1 June 2015

#### Introduction

DNA methylation is the binding of a methyl-group to guanine on DNA. It is well-known that DNA methylation affects gene expression, and that it is a strong contributor to differences in gene expression during tissue differentiation. More recent work has shown that DNA methylation is also affected by aging, socio-economic status and ancestral background.

## Assembly of DNA methylation database from GEO

I assembled a database of 7247 GEO samples of the Illumina 450k array. This database contains samples from 18 tissues, and ages ranging from neonates to 105 years old.

Table 1: Number of samples for each tissue

Tissue	Count
Adipose Tissue	174
Bone Marrow	72
Brain	832
Breast	14
Buccal	96
Colon	53
Leukocytes	923
Liver	231
Lung	11
Lymphoblasts	322
Lymphocytes	614
Monocytes	1202
Muscle	86
Neuronal	145
Pancreas	221
T-cells	262
Thyroid	82
Whole Blood	1907

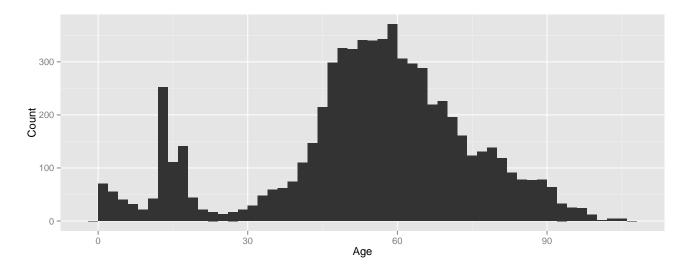


Figure 1: Age distribution of GEO samples

### Normalization

BMIQ normalization was used on each sample. Downstream analysis found that this normalization minimized batch effects between different GEO entries.

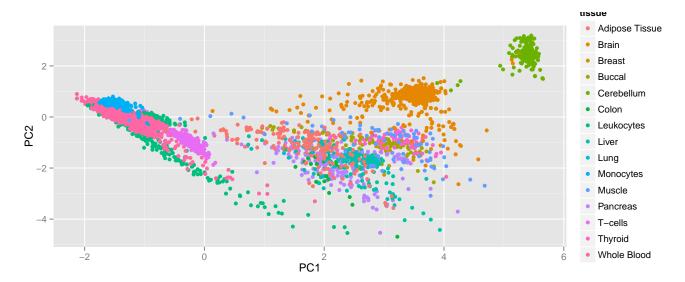


Figure 2: PCA of GEO samples, excluding outliers

### **Figures**

#### Margin Figures

Images and graphics play an integral role in Tufte's work. To place figures or tables in the margin you can use the fig.margin knitr chunk option. For example:

```
library(ggplot2)
qplot(Sepal.Length, Petal.Length, data = iris,
    color = Species)
```

Note the use of the fig.cap chunk option to provide a figure caption. You can adjust the proportions of figures using the fig.width and fig.height chunk options. These are specified in inches, and will be automatically scaled down to fit within the handout margin.

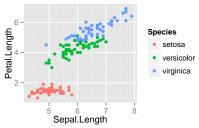


Figure 3: Sepal length vs. petal length, colored by species

#### Full Width Figures

You can arrange for figures to span across the entire page by using the fig.fullwidth chunk option.

```
qplot(wt, mpg, data = mtcars, colour = factor(cyl))
```

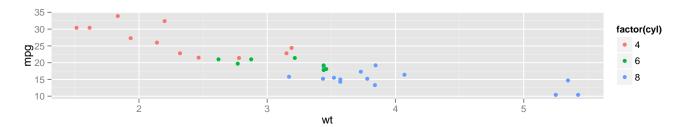


Figure 4: Full width figure

Note the use of the fig.width and fig.height chunk options to establish the proportions of the figure. Full width figures look much better if their height is minimized.

#### Main Column Figures

Besides margin and full width figures, you can of course also include figures constrained to the main column.

```
qplot(factor(cyl), mpg, data = mtcars, geom = "boxplot")
```

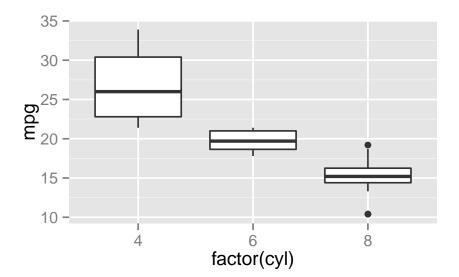


Figure 5: Another figure

#### Sidenotes

One of the most prominent and distinctive features of this style is the extensive use of sidenotes. There is a wide margin to provide ample room for sidenotes and small figures. Any use of a footnote will automatically be converted to a sidenote. 1

If you'd like to place ancillary information in the margin without the sidenote mark (the superscript number), you can use the \marginnote command.

Note also that the two footnote references (tufte\_latex and books\_be, both defined below) were also included in the margin on the first page of this document.

#### **Tables**

You can use the **xtable** package to format LATEX tables that integrate well with the rest of the Tufte handout style. Note that it's important to set the xtable.comment and xtable.booktabs options as shown below to ensure the table is formatted correctly for inclusion in the document.

<sup>1</sup> This is a sidenote that was entered using a footnote.

This is a margin note. Notice that there isn't a number preceding the note.