A Tale of Two Mice: Why DNA is Not Necessarily Your Destiny
Molecular Structure of Nucleic Acids
A Structure for Deoxyribose Nucleic Acid

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An Epigenome

Reading the chart
The outer ring represents 35 million base pairs in Chromosome 22. Orange marks highlight areas of the chromosome that were tested for CpG methylation in a pilot study by the Human Epigenome Project.

Measuring CpG methylation
Bar charts indicate the average amount of CpG methylation found within the tested areas. Each chart covers 100,000 base pairs. Some charts have been shifted, shown with connecting lines.

AMOUNT OF METHYLATION
- 0 to 20%
- 20 to 80%
- 80 to 100% of CpG sites
Epigenetic Switches

The two main components of the epigenetic code

DNA methylation
Methyl marks added to certain DNA bases repress gene activity.

Histone modification
A combination of different molecules can attach to the ‘tails’ of proteins called histones. These alter the activity of the DNA wrapped around them.
Bisphenol A (BPA) – an epigenetic toxicant?
Challenge 1: Resources & Tools to Identify Individuals at Risk
Challenge 2: Technology Development to Reverse Adverse Epigenomic Consequences
Challenge 3: Incorporating Epigenetics into Ethical, Legal, & Risk Assessment Frameworks