Epigenetics—where the environment meets the genetics of disease: Interpreting high-throughput DNA Methylation data

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> WHBRS Young Investigators Meeting Victoria University, Wellington

> > 19th November 2012

Epigenetics Overview	Illumina 450K	Some Biology	Bringing it all together	Acknowledgements
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Outline				



- 2 Illumina 450K
- Some Biology
- 4 Bringing it all together



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Epigenetics:	An Overvie	ew		

- Epi-(GREEK:over,above) genetics
 - heritable changes in gene expression/phenotype
 - functionally relevant changes, doesn't modfiy underlying genomic sequence

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ONA Methylation

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A brief overview of DNA Methylation

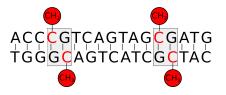
- 5'methylation of cytosine
- typically at CpG dinucleotide



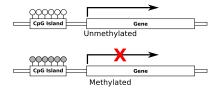
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Result is a reduction of gene expression (though there are exceptions)



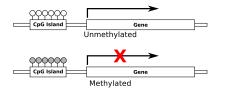
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A brief overview of DNA Methylation

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Result is a reduction of gene expression (though there are exceptions)



- Methylation is heritable imprinting
- **BUT** is also dynamic: response to environment

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- Illumina 450K Human Methylation Chip
 - Genome Wide: has >450,000 probes (individual CpG sites)
 - only recently publications starting to emerge
 - analysis needs to catch up

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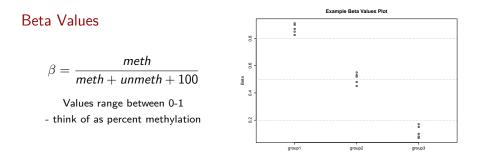
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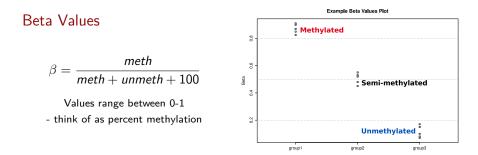
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- Same old story: Quality in equals Quality out
 - good bioinformatics will never make up for poor lab technique and/or poor study design

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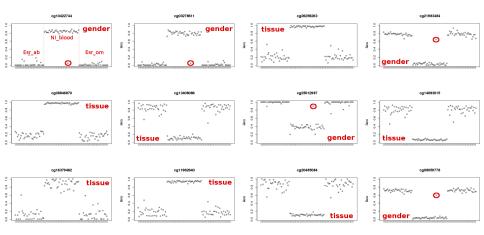
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- Case/Control? Paired-samples? Numbers?

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Example: Gender and Tissue specific markers



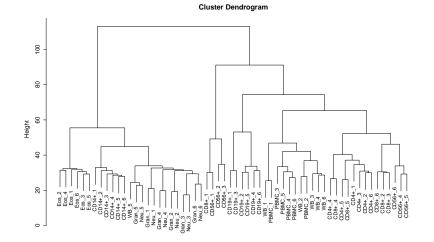
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The Biology	/			

Time for the interesting part...

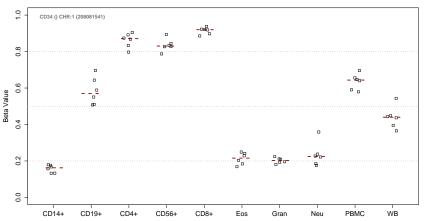
The technology in action



Publicly available data set (6 'healthy' males) - cell sorted





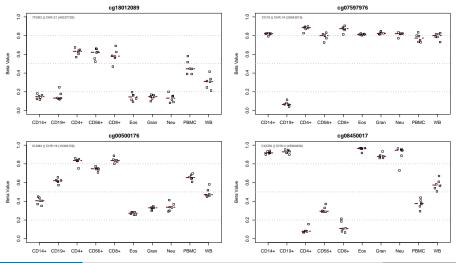


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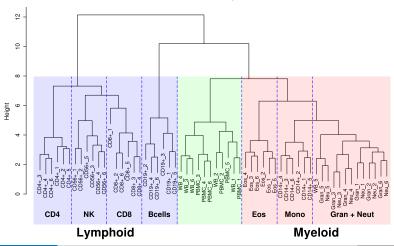


DNA Methylation



Cluster Dendrogram

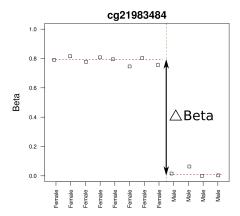
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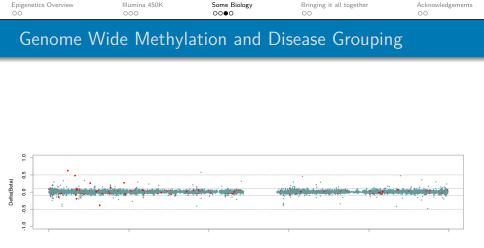


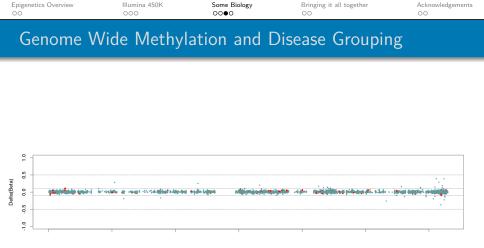
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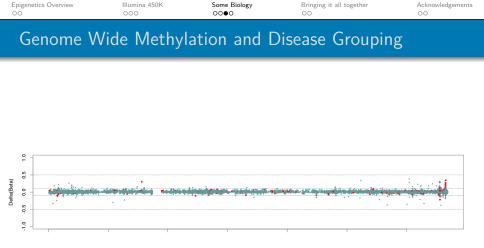
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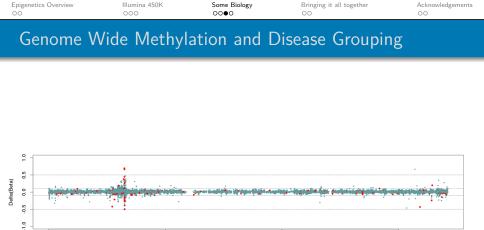
Genome Wide Methylation and Disease Grouping





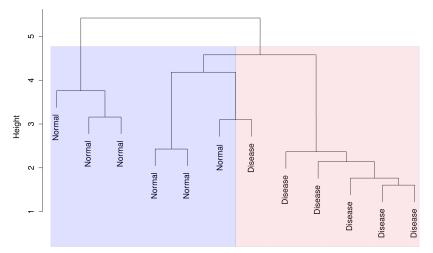






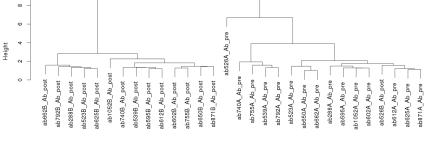
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Genome Wide Methylation and Disease Grouping



Cluster Dendrogram





d hclust (*, "complete")

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Overlaying	Genomic [Data Sets		

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- multiple layers of genomic data
 - mRNA data
 - miRNA data
 - methylation data

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- Pathways analysis indicates that 13 of the top differentially expressed mRNA are potentially regulated by the above miRNA
- We have identified significant correlations between all layers of data - suggests strong biological relevance

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Conclusions				

• We have designed and validated a novel QC and analysis pipeline

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 - able to group based on differential expressed methylation profiles

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 - able to group based on differential expressed methylation profiles
- Attention to study design will allow increased quality and application - i.e. multi-cell populations in tissue/whole blood
- Applying multiple layers of genomic data shows potential to increase our understanding of complex biological pathways/networks

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Acknowled	gements			

ESR/Wakefield Obesity Project: Dr Donia Macartney-Coxson, Prof Richard Stubbs, Angela Jones, Daniel Kay

Norfolk Island Health Study: Prof Lyn Griffiths

PHD Supervisors: Dr Rod Lea, Prof Lyn Griffiths

Co Supervisors: Dr Donia Macartney-Coxson, Dr Geoff Chambers

Obesity Project Sample Running: George Washington University, Washington DC

Genomics Research Centre: Dr Heidi Sutherland, Michelle Hanna, Dr Bridget Maher, Dr David Eccles

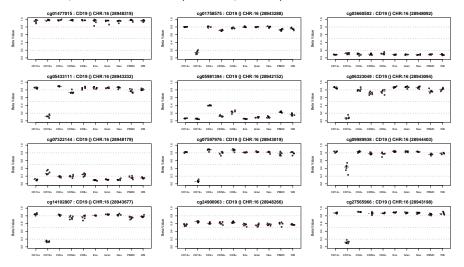
Institutes: Institute of Environmental and Scientific Research, Wakefield Hospital, Griffith University, Victoria University of Wellington

All the patients for their consent to being part of the respective studies



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