

Regression with many features

A scatter plot of age and a feature of interest.



A scatter plot of a grouping and a feature of interest.



A scatter plot of a grouping and a feature of interest.



Regression is like a normal distribution with varying mean.



The p-value for a regression coefficient represents how often it'd be observed under the null.



Relationships can be significant with small noise and small effects.



Relationships can be non-significant with large noise and large effects.



With few points, relationships can be non-significant with large noise and large effects.



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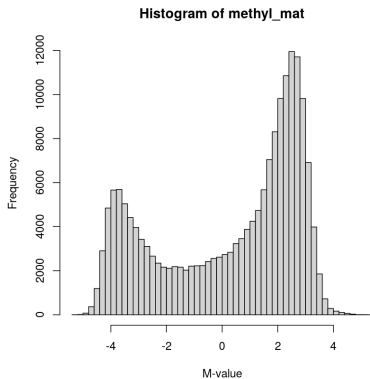
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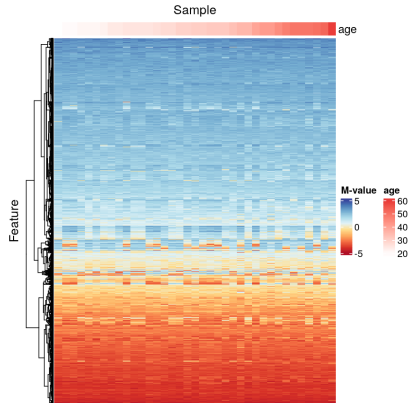
With many points, relationships can be significant with small noise and tiny effects.



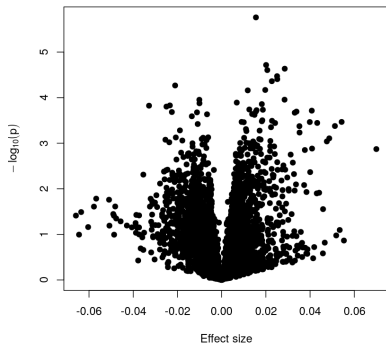
Methylation levels are generally bimodally distributed.



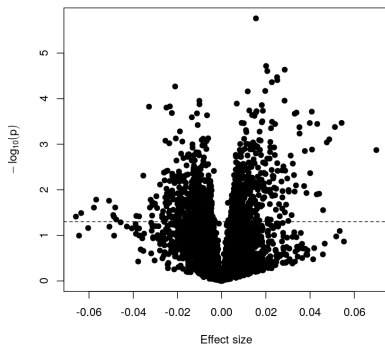
Visualising the data as a heatmap, it's clear that there's too many models to fit 'by hand'.



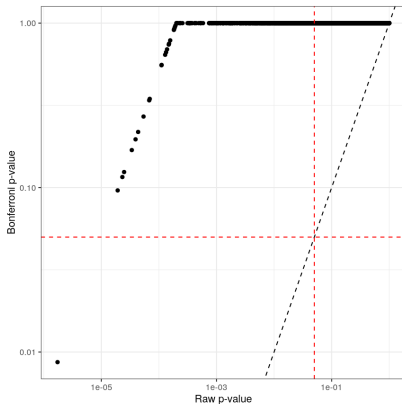
Plotting significance against effect size, it's clear that the two are related (but not 1-1).



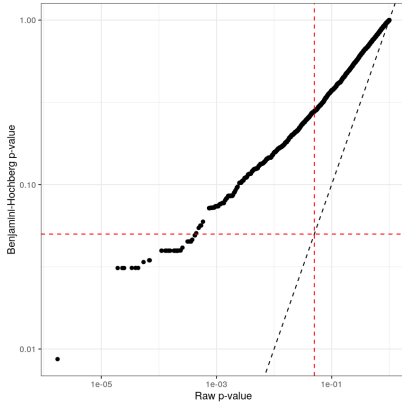
Plotting p-values against effect sizes for a randomised outcome shows we still observe 'significant' results.



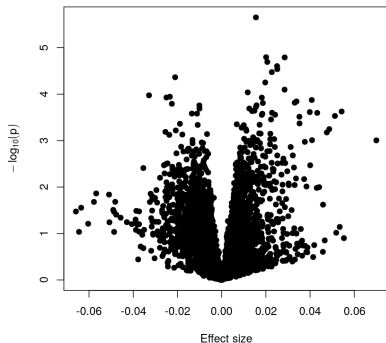
Bonferroni correction often produces very large p-values, especially with low sample sizes.



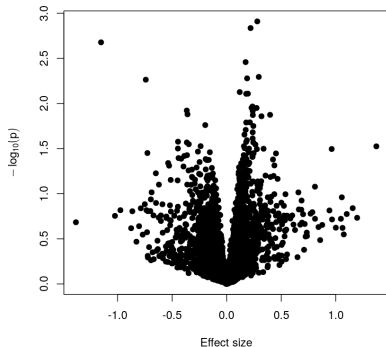
Benjamini-Hochberg correction is less conservative than Bonferroni



Plotting p-values against effect sizes using limma; the results are similar to a standard linear model.



A plot of significance against effect size for a regression of smoking against methylation.



Caption

