Introduction

Illumina Infinium MethylationEPIC Array

- Covers over 850,000 sites
- No PCR - uses whole genome amplification
- Over 98% reproducibility
- Cost effective
Introduction

DNA Methylation Array Processing

- R packages like Minfi and RnBeads allow efficient processing and high level statistics of human DNA methylation arrays
- Verification of specific loci is still an important step in the analysis process
- However, wet-lab scientists are typically uncomfortable with command-line environments but still need to visualise, compare and quantify changes at these loci against identified genomic features
Overview
CandiMeth Functions

• Two step process:
  - Methylation array results are automatically mapped to the genome allowing easy visualisation of methylation changes and integration with external tracks
  - Interrogation of specific genomic intervals for candidate genes conducted using a minimum of steps
CandiMeth
Candidate Gene Quantification within Galaxy

1. Treatment
   - Cell Line
2. Methylation
3. Wet-lab Verification
4. Analysis
   - R Studio

Blood or Saliva
Published Applications

Depletion of DNMT1 in differentiated human cells highlights key classes of sensitive genes and an interplay with polycomb repression

Widespread recovery of methylation at gametic imprints in hypomethylated mouse stem cells following rescue with DNMT3A2
Future Features

- Graphical Outputs
- UCSC Overlap
- Optional Inputs
- Statistics
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