GIMP

A Comprehensive R Package for exploring Genomic Imprinting Methylation Patterns in Imprinting Disorders

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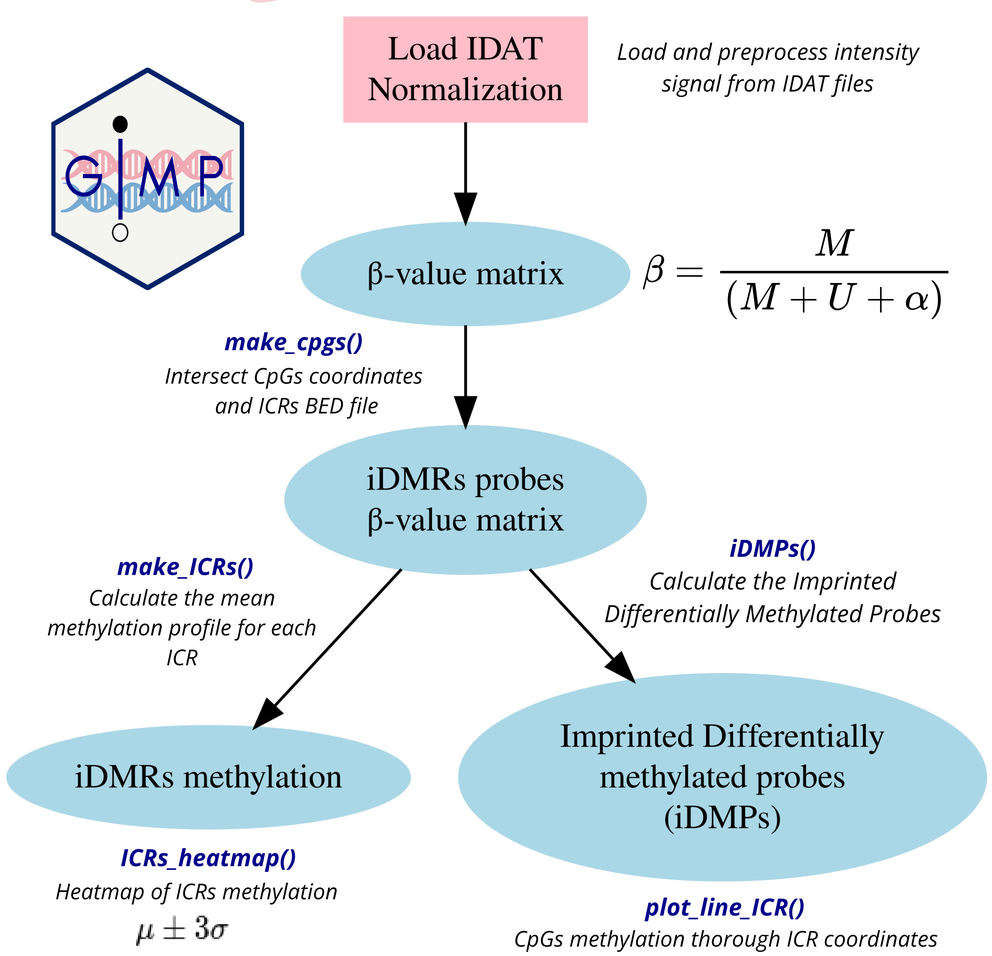
♂ Introduction ♀

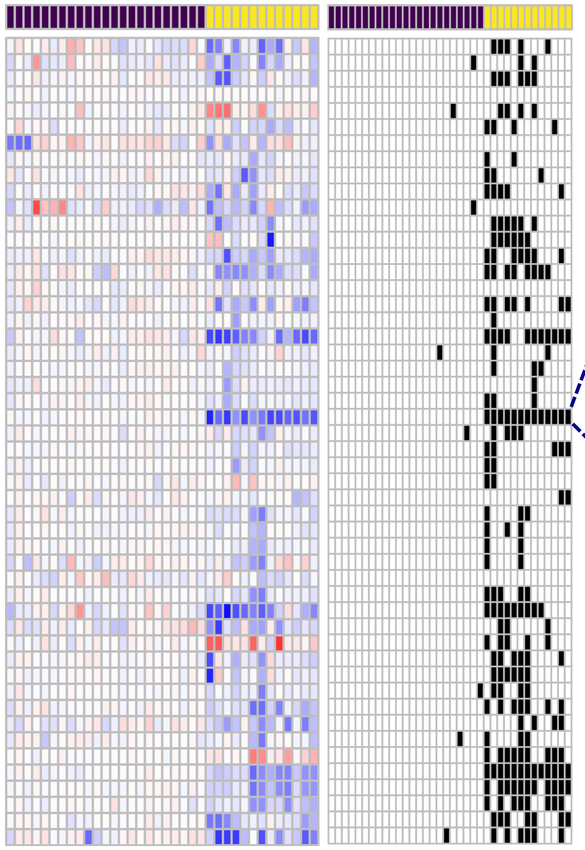
Genomic imprinting is an epigenetic phenomenon where certain genes (imprinted genes, IGs) are expressed differently depending on their parent of origin. The IGs, are controlled by epigenetic marks such as DNA methylation at Imprinting Control Regions (ICRs) differentially established during the gametogenesis in oocytes and sperms. Alterations at imprinted genes cause Imprinting Disorders (IDs), a group of congenital diseases affecting growth, development and metabolism.

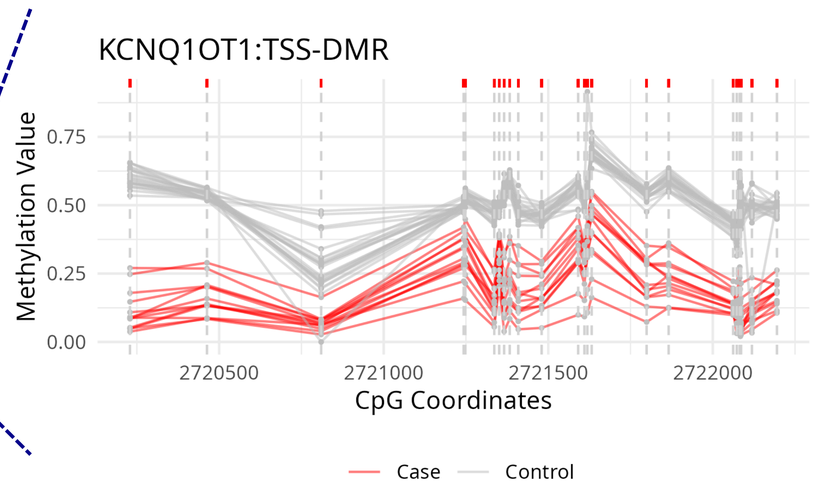
♂ Flowchart ♀



♂ Results ♀

In a typical workflow, users provide a normalized β-value matrix that represents CpG sites across samples; GIMP processes this into ICR-specific analyses. The output includes coverage plots heatmaps and lineplots that illustrate differences between experimental groups in terms of ICR defect and CpG defect (iDMPs), aiding in the identification of epigenetic changes linked to the experimental groups.





♂ Conclusion ♀

Conclusively, GIMP presents a powerful tool for studying ICRs using methylation array data while bridging an important gap in existing bioinformatics tools.