# DNA methylation analysis

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**Abstract**

This document is an automatic output of the dnapipeR pipeline. Within this report, preprocessing, quality control, normalisation, surrogate variable analysis, clock estimation, cell-type deconvolution, as well as generalized linear and linear mixed-effects modeling are presented. This script is still under development, so please excuse any formatting issues. If you have suggestions, questions, or requests, feel free to contact me at ruizpint@qut.edu.au.

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