

DNA methylation analysis

Queensland University of Technology

School of Biomedical Sciences

January 23, 2026

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.

Contents

1	Quality Control Plots	1
2	Pre-processing and Filtering	1
3	Post-processing and Filtering	1
4	Surrogate Variable Analysis	1
5	General Linear Model	1
6	Linear Mixed-Effects Model	1

1	Quality Control Plots
2	Pre-processing and Filtering
3	Post-processing and Filtering
4	Surrogate Variable Analysis
5	General Linear Model
6	Linear Mixed-Effects Model