PACMAN: PacBio Methylation Analyzer

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Pacific Biosciences sequencing allows for the simultaneous detection of DNA methylation in particular m6A and m4C (Flusberg et al., 2010). The motifs around the methylation sites are provided by the SMRT pipeline[1] in GFF format. However the visualization of these motifs methylated or non-methylated, for example on a bacterial genome, is not part of the pipeline. Circos is a software package for producing publication quality images of large scale data(Krzywinski et al., 2009), however mastering the numerous configuration files needed, requires extra skills not easy to acquire for biologists. We developed a tool written in Perl and an associated web site called PACMAN (PacBio Methylation Analyzer) allowing users to easily create images with Circos in a user-friendly interface. The required files are 1) the genome or draft in FASTA format and 2) the motifs file in GFF format (from the SMRT pipeline). The counts of each motif are calculated according to a customisable sliding window and normalised by their expected frequency. PACMAN generates a publication quality image of the selected methylated motifs counts, locations and non-methylated locations, on one or both strands of the DNA. PACMAN is available on this web site: http://www.unifr.ch/bugfri/pacman.

References

Flusberg BA, Webster DR, Lee JH, Travers KJ, Olivares EC *et al.* (2010) Direct detection of DNA methylation during single-molecule, real-time sequencing. *Nat. Methods* **7**, 461–465. http://dx.doi.org/10.1038/nmeth.1459

Krzywinski M, Schein J, Birol I, Connors J, Gascoyne R *et al.* (2009) Circos: An information aesthetic for comparative genomics. *Genome Res.* **19**, 1639–1645. http://dx.doi.org/10.1101/gr.092759.109

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[1] www.pacb.com/devnet/