Sharma and Majumdar (2017) Can J Biotech, Volume 1, Special Issue, Page 41
https://doi.org/10.24870/cjb.2017-a28

Canadian Journal of Biotechnology

ISSN 2560-8304

Poster Presentation **OPEN ACCESS**

Category: Bioinformatics

Determination of data analysis pipeline for detection of Thap-9 binding sites in human genome

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Abstract

Transposons are ubiquitously expressed DNA sequences that can move from one position within the genome to another, resulting in alteration of gene expression, mutations and generation of genome diversity. Human Thap-9 protein is homologous to *Drosophila* P-element transposase. Previous studies have reported that Human Thap-9 shows excision and integration activity in human cells. Over the past decade, the realm of biotechnology has witnessed an upsurge of computational tools available for analysing ChIP-seq data. ChIP-seq (Chromatin immunoprecipitation-sequencing) has proven to be a versatile tool for detecting protein-DNA interactions. Since its advent, several modifications of this technique have come into existence. ChIP-exo is a modification of conventional ChIP-seq, which uses lambda exonucleases to digest protruding ends of DNA in protein-DNA complexes followed by next generation sequencing. This technique gives better resolution of binding sites (20 bp-90 bp), reduces noise and can detect weaker protein-DNA interactions. We are trying to develop a data analysis pipeline for finding Thap-9 binding sites in human genome using ChIP-exo generated reads. For this purpose, we have compared the outputs of different computational tools for various steps in the analysis and have used different freely available online tools for alignment (Bowtie2 and BWA), peak calling (MACS, MACE and GEM) and visualization of the binding sites (MEME and HOMER).

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Citation: Sharma, V. and Majumdar, S. Determination of data analysis pipeline for detection of Thap-9 binding sites in human genome [Abstract]. In: Abstracts of the NGBT conference; Oct 02-04, 2017; Bhubaneswar, Odisha, India: Can J biotech, Volume 1, Special Issue, Page 41. https://doi.org/10.24870/cjb.2017-a28