

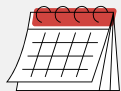
HYBRID WORKSHOP

methyIR

from sequencer to publication...



Register Here



Friday
5 May, 2023



13:00 - 15:00

Limited with
20 on-
campus
participants

13:00 - 13:15 Brief Introduction

13:15 - 13:45 Live demo of methyIR

13:45 - 14:00 Break

14:00 - 14:45 Hands on

14:45 - 15:00 Q & A

Massimiliano Volpe
&
Jyotirmoy Das

methyIR

Logged In

Welcome to methyIR: single solution from sequencer to publication

For non-commercial Academic and Research purpose only!

Here we introduce methyIR, a complete pipeline for the analysis of both 450K and EPIC Illumina arrays which not only offers data visualization and normalization but also provide additional features such as the annotation of the genomic features resulting from the analysis, pairwise comparisons of DMCs with different graphical representation plus functional and pathway enrichment as downstream analysis, all packed in a minimal, elegant and intuitive graphical user interface which brings the analysis of array DNA methylation data

NOTICE: YOUR INPUT DATA FILES AND RESULT WILL BE DELETED AS SOON AS YOU CLOSE THE BROWSER. WE DONOT READ/STORE YOUR DATA AND NOT RESPONSIBLE FOR IT.

Please NOTE - ChAMP and Minfi are two different algorithms designed and developed by Yuan Tian et al and Kasper D. Hansen & Jean-Phillipe Fortin, respectively to perform the DNA Methylation analysis from illumina 450K or EPIC HumanMethylation Array. We here added both of them (with some modifications) and using only one pipeline is enough to get the analysis result.

Publications related to MethyIR +

Other tools from Us +

Notifications +

Main Packages +

Figures generated with MethyIR

1000 most enriched pathways

Principal Component Analysis

Genes heatmap

Pairwise Intersection

Intersection Size

Venn Diagram

Heatmap

Bar chart

Scatter plot

Horizontal bar chart

Dot plot

Hosted by
Malgorzata Lysiak