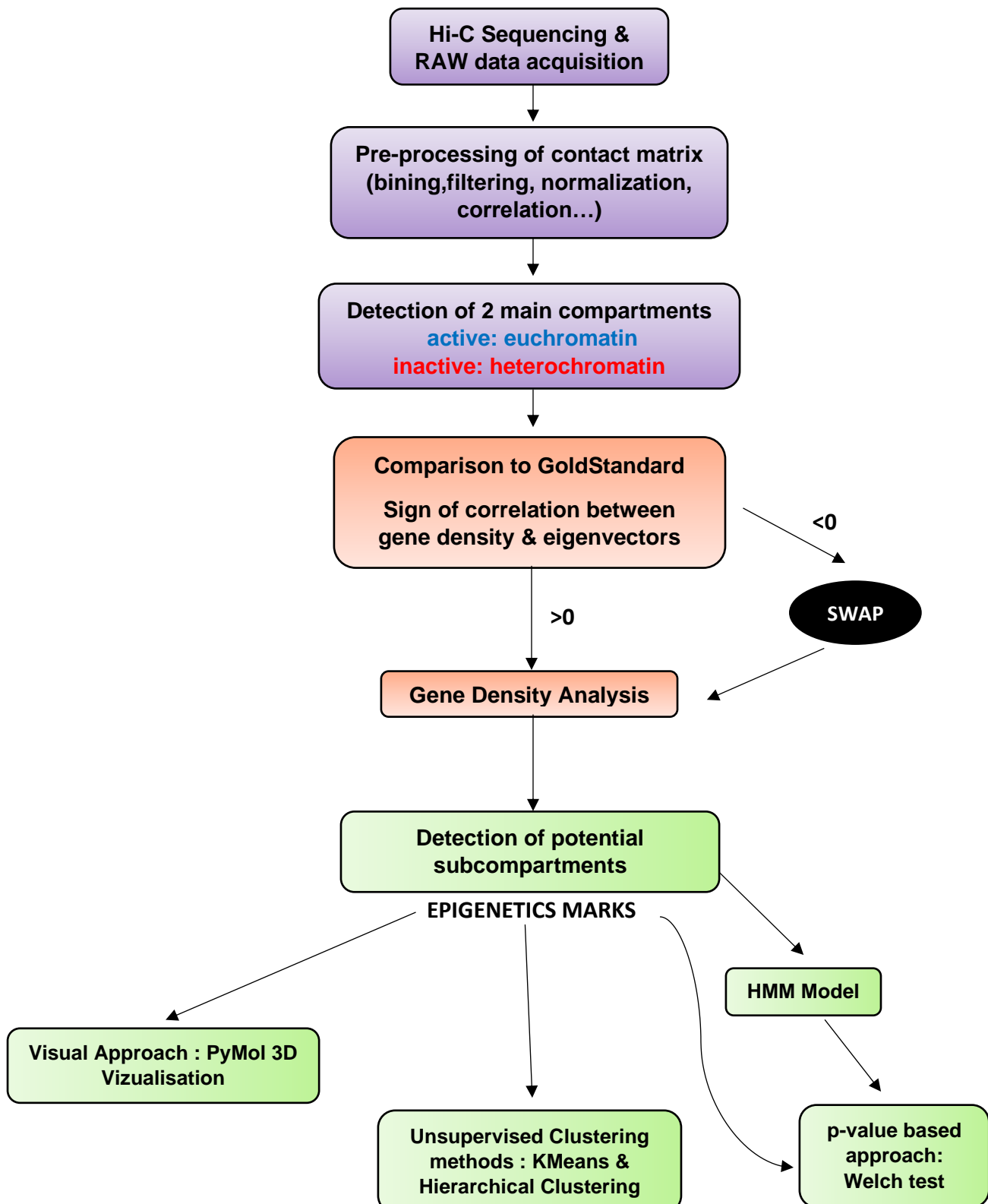


# Hi-C matrix-based pipeline for multi-scale chromatin compartmental analysis

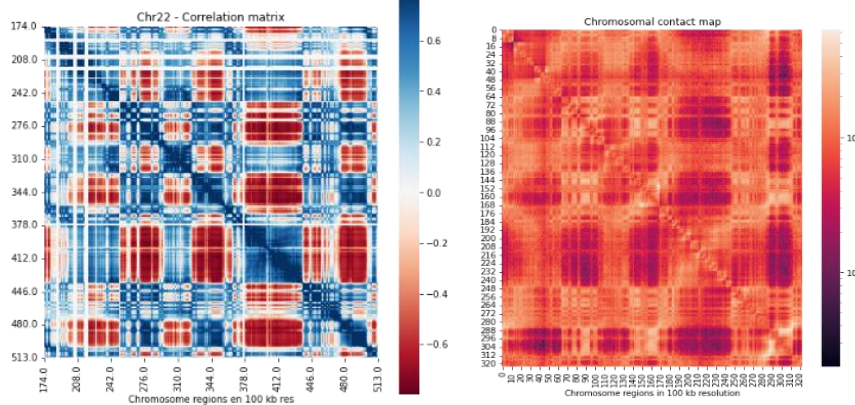
Mikal Daou, Oktavia Ścibior, Maxime Gueudré

*Based on Rao et al. (2014)*

## WORKFLOW

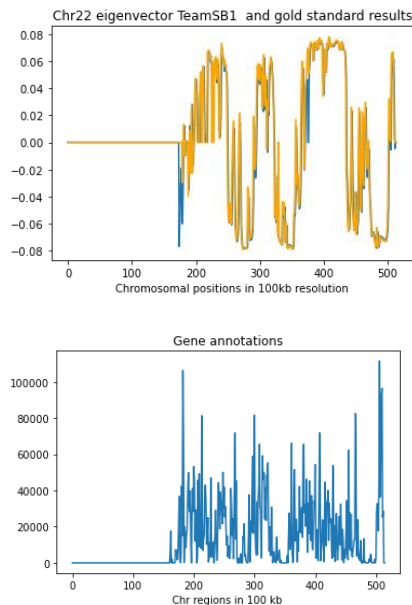


## Correlation and Contact matrix

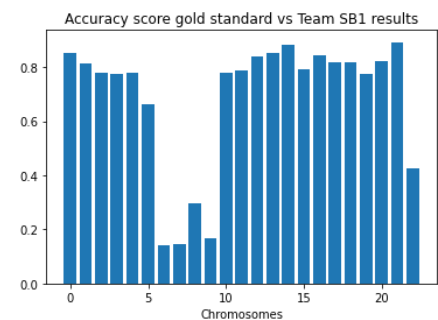


- Correlation matrix shows that compartments are **NOT** conserved across chromosomes
- Enhanced** contacts on the diagonal

## Detection of 2 main compartments



- Results matching with gold standard results
- Positive eigenvector values: **enriched** regions in intrachromosomal contact and open chromatin (compartment A)
- Enriched** gene density in compartment A

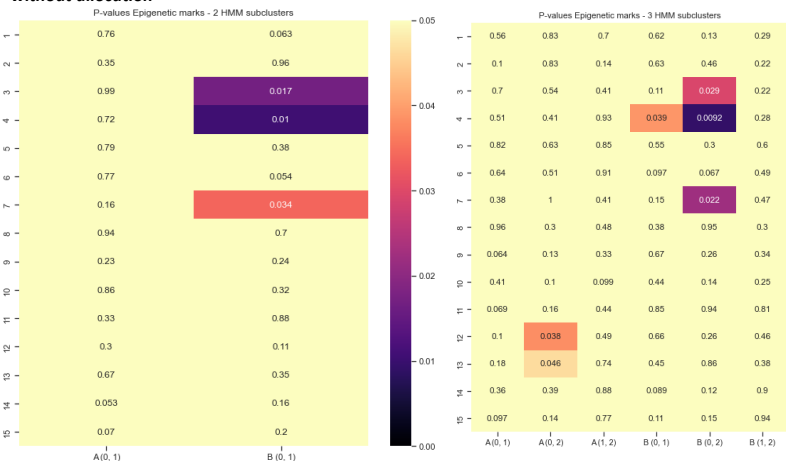


### LIMITS:

- Low accuracy: partial inversion, chromosome branches size

## Detection of more than 2 compartments

p-values for 2 subcompartments in A and 3 subcompartments in B, correlation for 5 subcompartments without allocation



- Epigenetic marks manifesting in non-active regions of chromatin
- Hierarchical organization of compartments
- Several approaches to detect optimal number of subcompartments

### LIMITS:

- only based on intrachromosomal contacts
- tested in **ONE** cell
- only in 100kb resolution

