Biomarker Identification and Tumor Classification in Cervical Cancer

An integrated approach of Methylation and Expression Analysis

Authored by: CHODREDA Team

Team Members

Chaima BenMohamed

Opeyemi De Campos

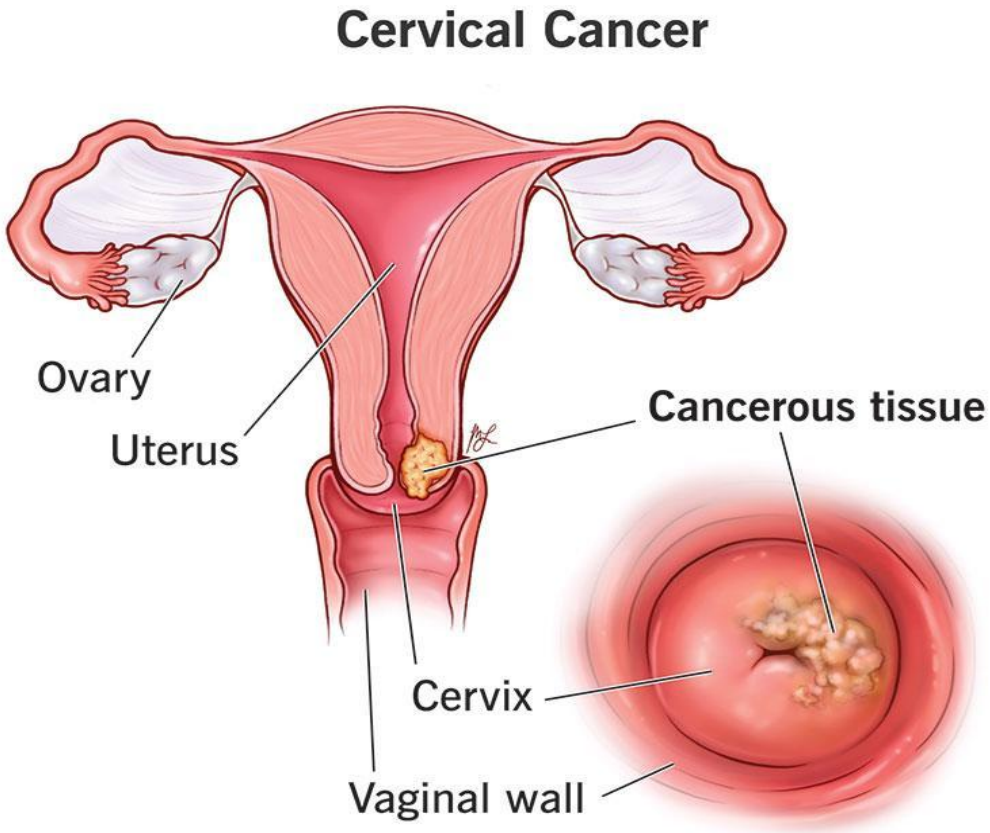
R

Reem Atawia

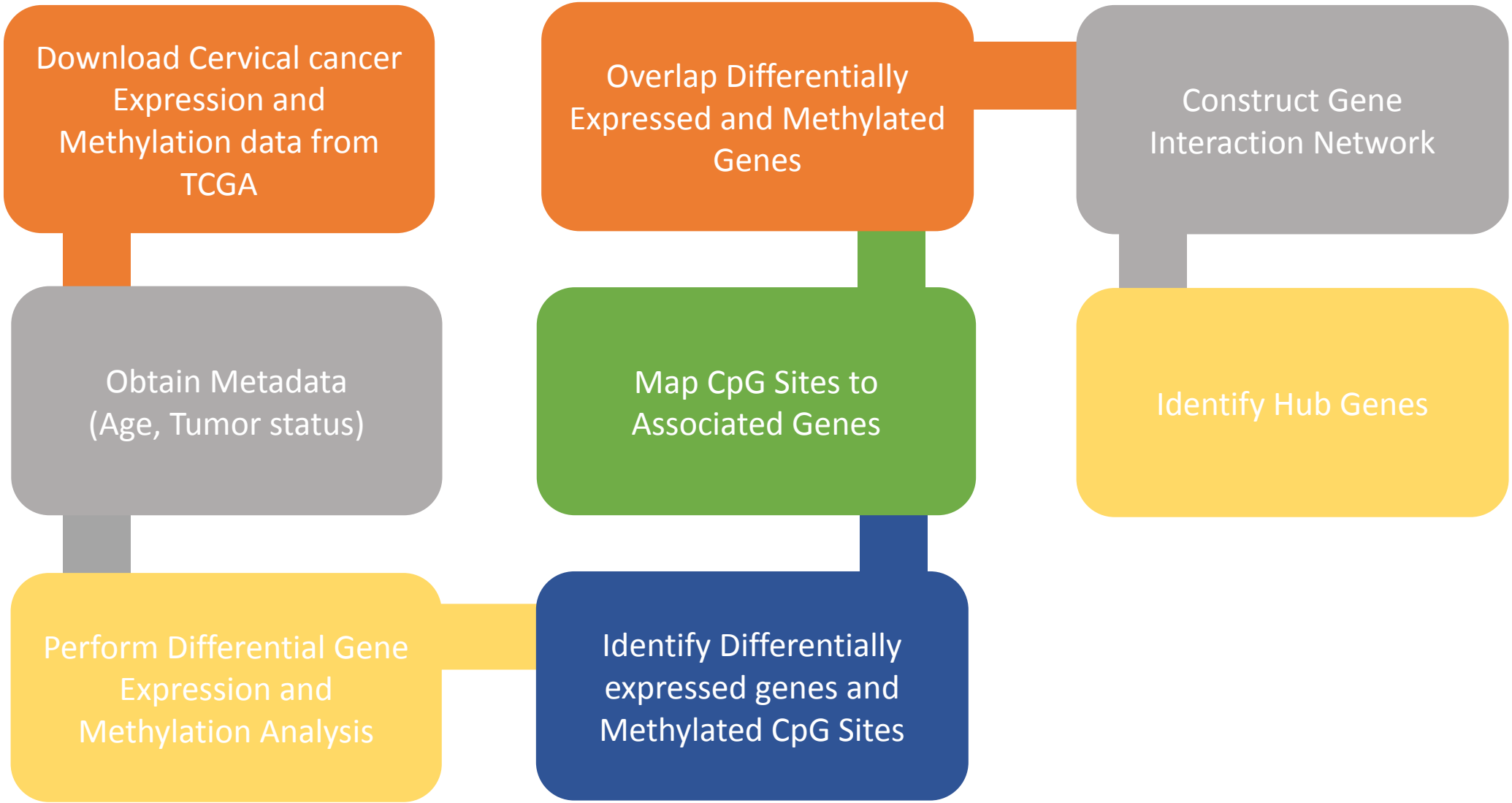
David Ojo

BACKGROUND

- Cervical cancer is the fourth most common cancer type and the fourth cause of cancer-related death among women (Bray et al., 2024).
- Despite advancements in screening and treatment, effective biomarkers for early diagnosis, prognosis, and treatment stratification remain limited.
- Integration of methylation and expression analysis will provide a more comprehensive view of the molecular mechanisms involved in cervical cancer pathogenesis.



METHOD


Download Cervical cancer Expression and Methylation data from TCGA
Obtain Metadata (Age, Tumor status)
Perform Differential Gene Expression and Methylation Analysis
Identify Differentially expressed genes and Methylated CpG Sites
Map CpG Sites to Associated Genes
Overlap Differentially Expressed and Methylated Genes
Construct Gene Interaction Network
Identify Hub Genes

EXPECTED RESULTS

- Identify differentially methylated CpG sites and genes with altered methylation status in cervical cancer
- By combining methylation and expression data, we hope that this study will uncover novel biomarkers and key hub genes with high connectivity in cervical cancer.
- Functional enrichment analysis of these hub genes is expected to reveal critical biological processes, pathways, and molecular functions impacted in cervical cancer.

References

Bray, F., Laversanne, M., Sung, H., Ferlay, J., Siegel, R. L., Soerjomataram, I., & Jemal, A. (2024). Global cancer statistics 2022: GLOBOCAN estimates of incidence and mortality worldwide for 36 cancers in 185 countries. *CA: A Cancer Journal for Clinicians*, *74*(3), 229–263. https://doi.org/10.3322/caac.21834

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THANK YOU