

Task1

Answer the following questions

2a : What is the medically relevant insight from the article?

→The article investigates the gene expression profiles of various immune cell types in patients with systemic lupus erythematosus (SLE). The study identifies distinct transcriptomic signatures associated with different immune cell populations, providing insights into the complex molecular mechanisms underlying SLE. These findings may inform the development of targeted therapeutic strategies for managing SLE.

2b : Which genomics technology / technologies were used?

→The study primarily relied on bulk RNA sequencing (RNA-seq) to analyze gene expression patterns. In addition, it incorporated complementary genomic approaches, such as genome-wide association studies (GWAS), expression quantitative trait loci (eQTL) mapping, and whole-genome sequencing (WGS), to provide a more comprehensive view of the genetic and transcriptomic landscape.

Further related research questions

3a : List and explain at least three questions / hypotheses you can think that extend the analysis presented in the paper.

→1. How does chromatin accessibility or DNA methylation in immune cells influence the observed transcriptomic patterns in SLE?

2. How do the transcriptomic profiles of immune cells change longitudinally during flare and remission periods in SLE patients?

3. Are the genetic variants identified by GWAS functionally causal in specific immune cell types, and do they influence the distinct transcriptomic signatures observed in SLE patients?

Task6

3. Read about piping from here:<https://r4ds.had.co.nz/pipes.html#pipes> (you don't have to learn everything, a basic understanding of the usage is enough). Write a short (max. 300 characters, no spaces) explanation of why, how, and when not to use pipes.

→Pipes make code cleaner by connecting steps in linear order, improving readability. Use when transforming a single dataset with short steps. Avoid for long pipelines, complex dependencies, or multiple inputs/outputs.

4. Familiarize yourself with the apply-family of functions (apply, lapply, sapply etc.) http://uc-r.github.io/apply_family Write a short explanation (max. 300 characters, no spaces) of why they could be useful in your work.

→The apply family of functions (apply, lapply, sapply, tapply) minimizes the need for loops and allows applying a function to each row, column, or list item. They make summary, transformation, and grouped calculations compact and efficient, improving code clarity and productivity.