**Case Study 16: Gene Expression (GSE5859)**

These gene expression study represents a microarray experiment – **GSE5859** – comparing Gene Expression Profiles from Lymphoblastoid cells (<http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE5859>). Specifically, the data compares the expression level of genes in lymphoblasts from individuals in three HapMap populations {*CEU, CHB, JPT* }. The study found that more than 1K genes were significantly different () in mean expression level between the {*CEU*} and {*CHB+JPT*} samples.

The data (<https://umich.instructure.com/files/folder/users_67875/BiomedHealth_CaseStudies/CaseStudy16_GeneExpression_GSE5859>) has 2 components:

1. The gene expression intensities (**exprs\_GSE5859.csv**):
   * rows represent features on the microarray (e.g., genes), and
   * columns represent different microarray samples
   * <https://umich.instructure.com/files/1997175/download?download_frd=1>
2. Meta-data about each of the samples (**exprs\_MetaData\_GSE5859.csv**)
   * rows represent samples, and
   * columns represent meta-data (e.g., sex, age, treatment status, the date the sample processing)

* <https://umich.instructure.com/files/1997177/download?download_frd=1>