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## **Project Summary:**

I selected a dataset titled "Huntington's disease: peripheral blood expression profile". The goal of the study was to identify genes that are significantly differentially expressed in the peripheral blood of patients with Huntington's Disease (HD). HD is genetic, progressive degenerative disorder that affects the central nervous system. However, the mutant huntingtin protein is found throughout the body, so it is of great interest to study gene expression levels in other tissues, such as peripheral blood. The purpose of such studies is to identify biomarkers that can be used to track the disease state in early- or pre-symptomatic HD carriers, or for clinical measurements to study the effectiveness of new treatments in clinical trials. The type of data analyzed by the authors was microarray data of total RNA using both Affymetrix GeneChips and Amersham Uniset Human I and II bioarrays for comparison. The authors also performed quantitative reverse transcription polymerase chain reaction (QRT-PCR) to further analyze genes that were found to be significantly differentially expressed. For my project, I will focus on the Affymetrix GeneChip microarray data, which is publicly available in the GEO database. The analyses they performed were a two-sided t-test, ratio of change calculation, principal component analysis (PCA), and hierarchical clustering. From the microarray data, the authors concluded that there was a subset of 12 genes that could be used to distinguish between patients with HD and healthy controls. The expression levels of these 12 biomarker genes could also be used to track the disease progression and differentiate between patients in the early-symptomatic and latesymptomatic phases.

## Reference:

Borovecki F, Lovrecic L, Zhou J, Jeong H et al. Genome-wide expression profiling of human blood reveals biomarkers for Huntington's disease. Proc Natl Acad Sci U S A 2005 Aug 2;102(31):11023-8. PMID: 16043692