Intro To Bioinformatics Final Project - Workflow Submission

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**Disease of choice**: Asthma

**Biological Question:** We would like to explore the genetic differences between patients with mild and severe asthma, and if there is any correlation with the age of diagnosis. We are interested in this question because Saar was diagnosed with mild asthma at a late age (20), despite most cases being diagnosed in childhood.

**How can gene expression data help?** We can run an analysis on Bulk RNA-Seq data to compare gene expression in samples of healthy patients and those with varying degrees of asthma severity. It is common to categorize asthma as either Mild/Moderate and Severe. We can use the genes found to identify pathways that are associated with asthma, and if any are more strongly associated with more severe forms of it.

**Other analysis:** We will also use GWAS to determine if the differentially expressed genes found in the previous step are significant markers for asthma. GWAS can also help us look for genes that are differentially expressed in those with childhood onset asthma vs. adult onset.

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| Accession ID | Location | Data Type | Count Matrix | Groups |
| GSE136587 | https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE136587 | Bulk RNA-Seq | raw counts | 39 samples: 17 mild/moderate, 6 healthy, 16 severe |
| GSE145505 | https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE145505 | Bulk RNA-Seq | raw counts | 442 samples of children with 6 respiratory phenotypes |
| GSE207751 | https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE207751 | Bulk RNA-Seq | raw counts | 50 samples: 36 asthma, 14 healthy |
| GSE158752 | https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE158752 | Bulk RNA-seq | Raw counts | 67  Healthy: 17  Mild/Moderate:25  Severe:25 |
| GSE119579 | https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE119579 | Bulk RNA-Seq | RPKM normalized | 7 non asthmatic, 6 asthmatic |