

# Workflow for Identifying Key Genes in Severe Asthma

## Gal Carmely and Ran Benayoun



### Disease of Choice

Asthma

### Biological Questions to Answer

- What are the key differentially expressed genes (DEGs) between mild-moderate and severe asthma?
- How do these genes contribute to asthma progression?
- Can specific genes be used as biomarkers for diagnosing severe asthma?
- What pathways are involved in the transition from mild-moderate to severe asthma?
- Are there potential drug interactions that may influence these genes?

### Approach Using the Dataset

- Use transcriptomic data from the **GEO** database to identify DEGs.
- Perform **Gene Set Enrichment Analysis (GSEA)** to find pathways related to asthma severity.
- Validate findings using an external dataset.

### Secondary Analysis Plan

- **Pathway enrichment analysis** to determine which biological processes are altered in severe asthma.
- **ROC (Receiver Operating Characteristic) analysis** to assess the diagnostic power of identified genes.
- Analyze potential drug interactions with the key genes using the **Comparative Toxicogenomics Database (CTD)**.

### Table of Collected Datasets

<i>Dataset Accession ID</i>	<i>Link to Dataset</i>	<i>Type of Data</i>	<i>Gene Expression Format</i>	<i>Data Description</i>
CTD Database	<a href="https://ctdbase.org/">https://ctdbase.org/</a>	Chemical-Gene Interactions	N/A	Interaction data between asthma-related genes and drugs
GSE201955	<a href="https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE201955">https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE201955</a>	Bulk RNA-Seq	Raw count	DNA methylation signatures in airway cells (epithelial) from adult children of asthmatic mothers reflect subtypes of severe asthma
GSE58434	<a href="https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE58434">https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE58434</a>	Bulk RNA-Seq	Raw Count	42 non-asthma, 88 asthma Fatal Asthma (n=6) vs. Control (n=12) Human Airway Smooth Muscle Transcriptome Changes in Response to Vitamin D or Albuterol
GSE152004	<a href="https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE152004">https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE152004</a>	Bulk RNA-Seq	Raw Count	derived from nasal epithelium cells (NECs) contains 257 asthmatic and 136 control subjects

GSE used in:

Development and validation of asthma risk prediction models using co-expression gene modules and machine learning methods

<https://www.nature.com/articles/s41598-023-35866-2#Sec2>

Based on methods:

Identification of key genes and pathways between mild-moderate and severe asthmatics via bioinformatics analysis

<https://www.nature.com/articles/s41598-022-06675-w#Sec11>