

# Supplementary Tutorial — Using the Age Effect Explorer Dashboard

## Overview

**Age Effect Explorer** is an interactive R Shiny application for systematically analyzing age- and sex-related gene expression pattern changes across 54 human tissues using GTEx v10 data.

This application enables users to explore tissue-level summaries and gene-specific age/sex effects without requiring any programming skills.

## Main Modules

### 1. Tissue-level Summary

This module provides an overview of significant age- or sex-associated genes ( $FDR < 0.05$ ) in all GTEx tissues. Users can switch between the "Age" and "Sex" summaries, and results can be exported as a .csv file.

#### Summary Table Columns

- o Sample\_Size: number of donor samples available for that tissue.
- o Up (upregulated): number of genes with a positive regression coefficient, indicating an increase in expression with age (or in males).
- o Down (downregulated): number of genes with a negative regression coefficient, indicating a decrease in expression with age (or in males).
- o Total: total number of significant genes in that tissue (Up + Down).
- o Percent\_Up\_Regulated: proportion of upregulated genes among all significant genes.

### 2. Age-effect Browser

This module allows exploration of individual genes within a selected tissue.

Steps:

- 1) Select a tissue and choose whether to rank genes by *Age FDR* or *Sex FDR*.
- 2) Click “Generate gene-level p-value table” to view and download the ranked gene list.
- 3) Select a gene and choose a plot type:
  - o Scatter plot:  $\log_2(TPM + 1)$  expression vs. age with regression lines for males and females.
  - o Boxplot: grouped by age and sex.
  - o Residual plot: with or without sex effect.
- 4) Click “Generate plot”; Download plot as PNG, PDF, SVG and JPG.
- 5) A cross-tissue table “Cross-Tissue Effects for Selected Gene” below summarizes age and sex effects for a selected gene across all GTEx tissues.