

Gene Gazer – Making RNA Sequence Data Understandable

Interactive and intuitive gene expression analysis for researchers



Why We Built RNA

Visualizer

1 RNA-seq datasets are massive and hard to interpret

2 Existing tools are:

- Complex for beginners
- Not real-time or interactive

3 Researchers need:

- Simple UI
- Quick insights (clustering, heatmaps, expression levels)





Meet RNA Visualizer



Data Input

Seamlessly upload your scRNA-seq data in common formats like CSV, .hdf5, mtx..



Interactive

Visualizations

- Gene heatmaps
- Expression-level highlights



Powerful Features

- User-friendly interface
- Fast rendering
- AI assistant powered by GEmini

How It Works – Under the Hood

Frontend:

Python 

Streamlit 

Backend:

Pandas

Scanpy

Matplotlib

Numpy

Pandas

Models/Methods:

 PCA (Principal Component Analysis)

 UMAP (Uniform Manifold Approximation)

 Clustering (Leiden algorithm)

Demo (screenshots or mockups of plots)

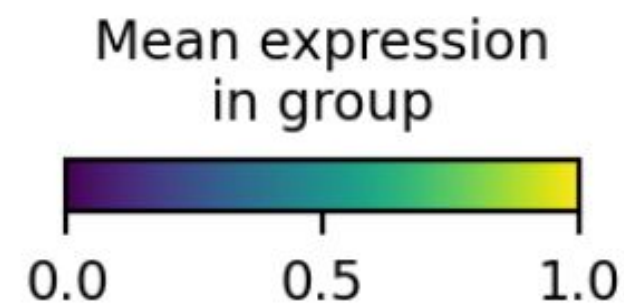
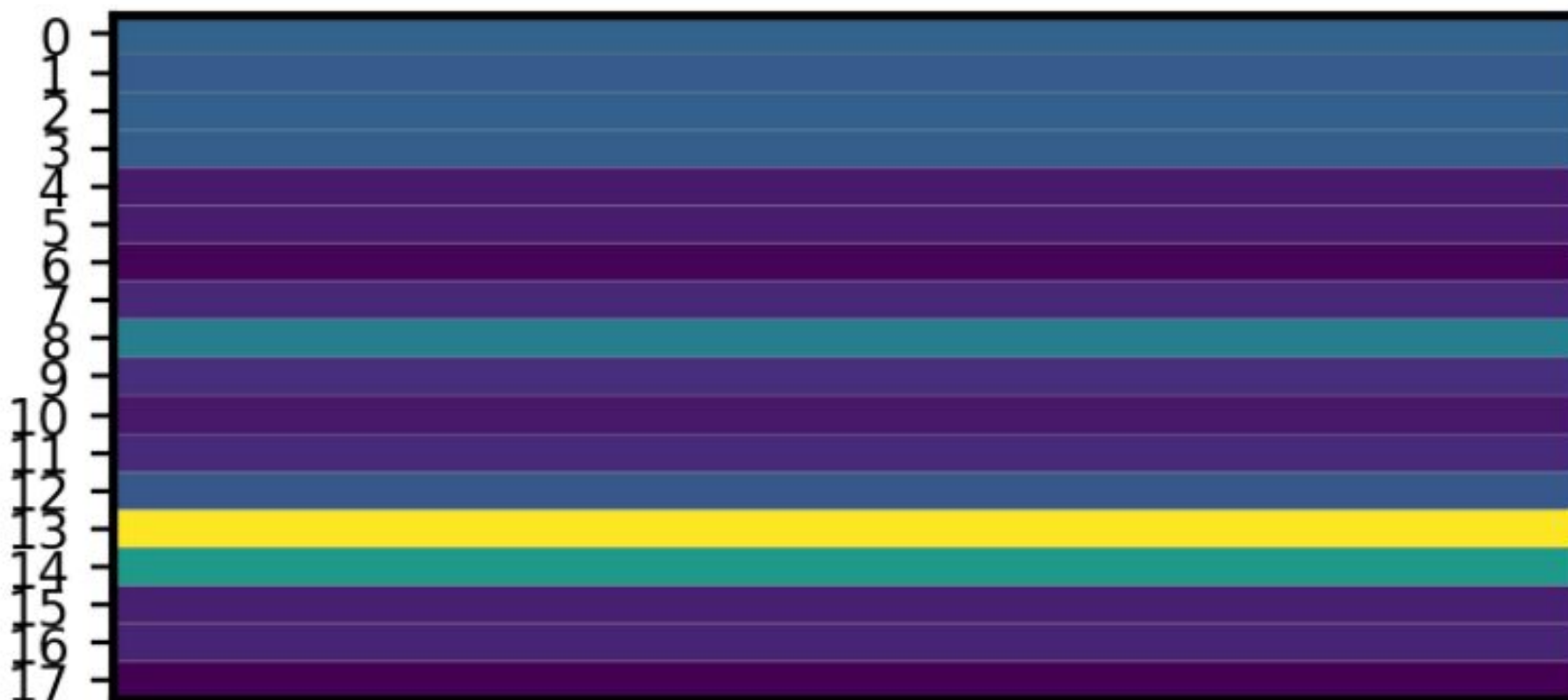
Here are some screenshots demonstrating the capabilities of the RNA Visualizer:



Gene Heatmap (by Cluster)

Type or select a gene to plot:

ENSG00000001561





Gemini AI Assistant for RNA-seq



Hi! I'm your AI assistant powered by Gemini. I can help you with:

Data Analysis: Interpret your single-cell RNA-seq results **Biology:** Explain gene functions, pathways, and cell types
 Methods: Discuss preprocessing, clustering, and visualization techniques **Statistics:** Help understand your data metrics and quality control

Feel free to ask me anything about your RNA-seq data or bioinformatics in general!



hi



Hi! It's great to hear from you. I understand you have a single-cell RNA sequencing (scRNA-seq) dataset with 1651 cells, 2423 genes, and 18 identified clusters. This is a reasonable dataset size for scRNA-seq analysis, though the number of genes detected might be considered relatively low depending on your sequencing depth and the organism you're studying. We'll need to investigate this further.

Before we proceed, to best assist you, I need more information. For example:

- **What is the biological question you are trying to answer?** This is crucial for guiding the analysis. Are you looking at cell type identification, developmental trajectories, response to a treatment, or something else?
- **What organism was the data generated from?** This is essential for gene annotation and interpretation.
- **What preprocessing steps have you already performed?** (e.g., quality control, normalization, dimensionality reduction). Knowing your current pipeline helps me avoid suggesting redundant steps.
- **What clustering method was used to obtain the 18 clusters?** (e.g., Seurat, Scanpy, etc.) Knowing this will allow me to help interpret your results more effectively.
- **What is the goal of the next step in your analysis?** Are you aiming to characterize the clusters, identify marker genes, perform differential gene expression analysis, or explore cell-cell interactions?

The list of top variable genes you provided (ENSG00000001561, etc.) is helpful, but without knowing the organism and the context of your experiment, their biological significance remains unknown. We need to map these Ensembl gene IDs to gene symbols to get a better understanding of their function.

Once I have this information, I can provide more specific and targeted advice. Let's work together to uncover the biological insights hidden in your data.

Future scope

Looking ahead, we envision several exciting enhancements for the RNA Visualizer:

1

Integration with More File Types

Expand support to include other omics data, such as ATAC-seq or spatial transcriptomics.

2

Advanced Statistical Analysis

Incorporate more sophisticated statistical methods for differential expression analysis and pathway enrichment.

3

Comparison reports of different datasets

Add feature to compare different RNA-Seq datasets side-by-side for better pattern discovery and decision-making.

Revenue Model – Turning Science into Sustainability

- ◆ Freemium SaaS Model:

Basic version free for individual researchers; paid “Pro” version offers advanced visualizations, data export, and customization.

- ◆ Educational Partnerships:

Collaborate with universities and online learning platforms to use GeneGazer in teaching and certification programs.

- ◆ Add-ons Marketplace

Sell premium features like AI-powered gene prediction, custom annotations, and publication-ready reports.

Revenue Model – Turning Science into Sustainability

Target Revenue Streams:

- Individual Researchers
- Universities & Research Institutes
- Genomics Startups
- EdTech & Course Providers