



Ragomics-Meta: An Open-Source, Scalable, Reproducible, and Extensible Multi-Omics Analysis Workflow

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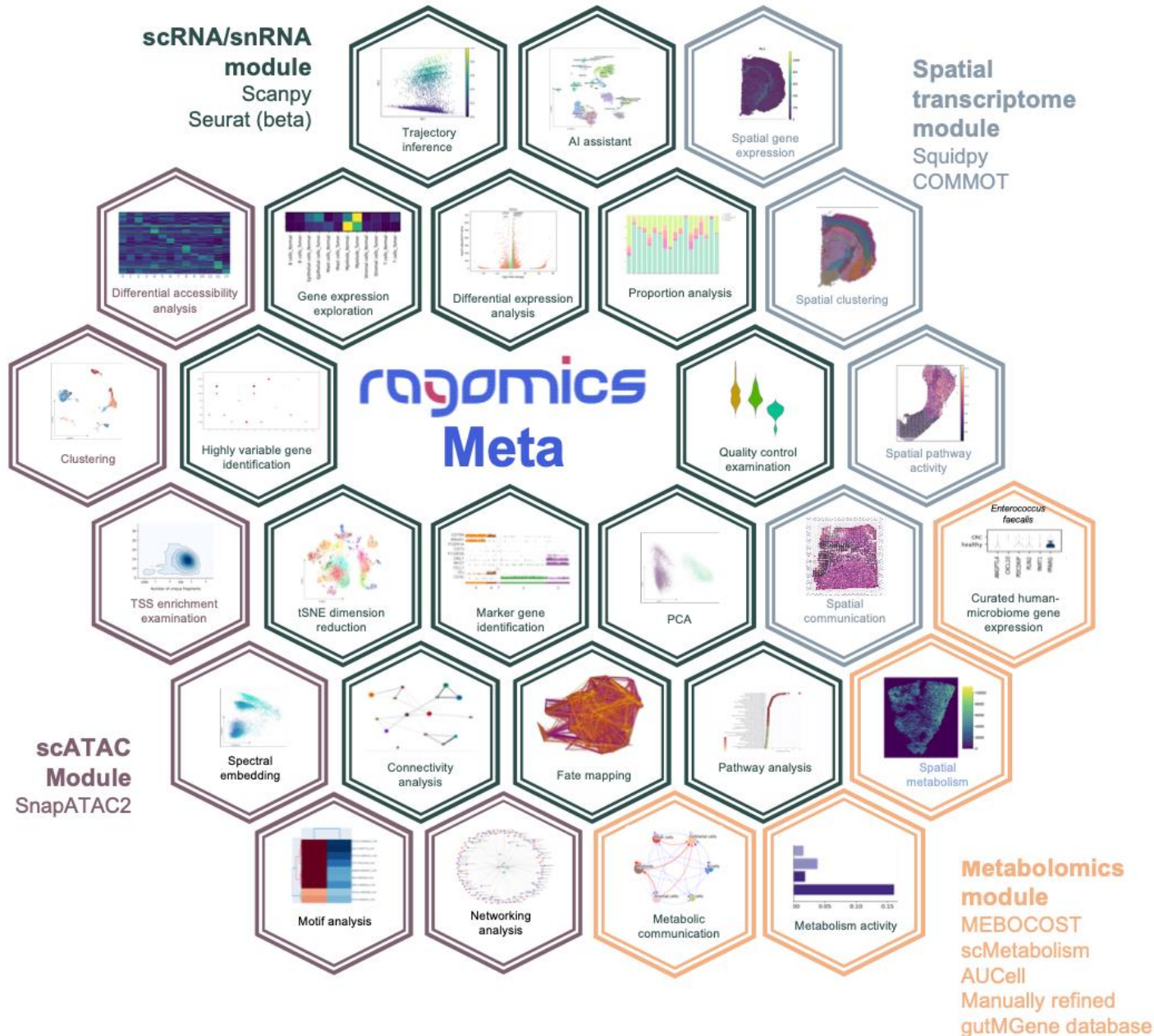
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Introduction

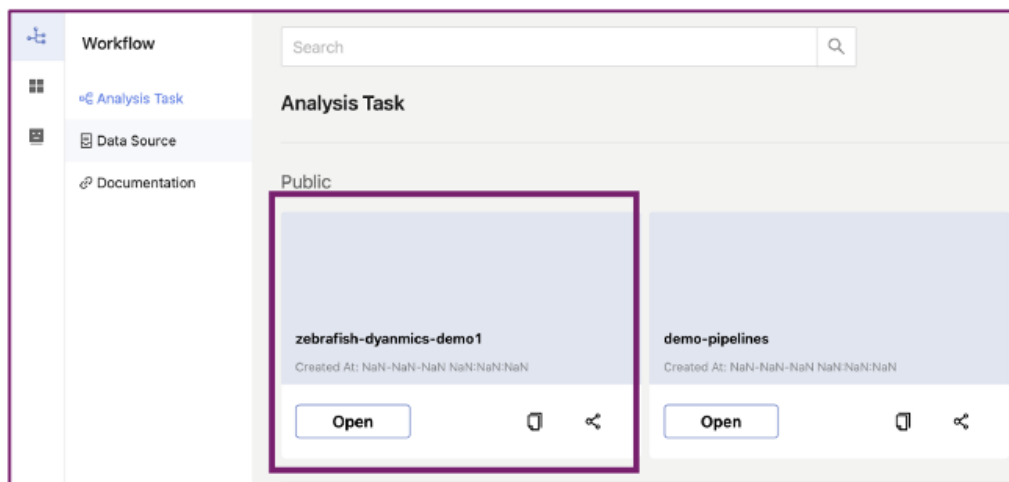


Ragomics-Meta is an open analytical workflow designed for single-cell, multi-omics, and spatial omics studies. It integrates analytical modules for scRNA/snRNA-seq, scATAC-seq, spatial transcriptomics, and spatial metabolism-related data. The platform supports quality control, dimensionality reduction, clustering, differential analysis, metabolic pathway scoring, cell-cell communication analysis, transcription factor regulatory network analysis, and host-microbiome interaction exploration.

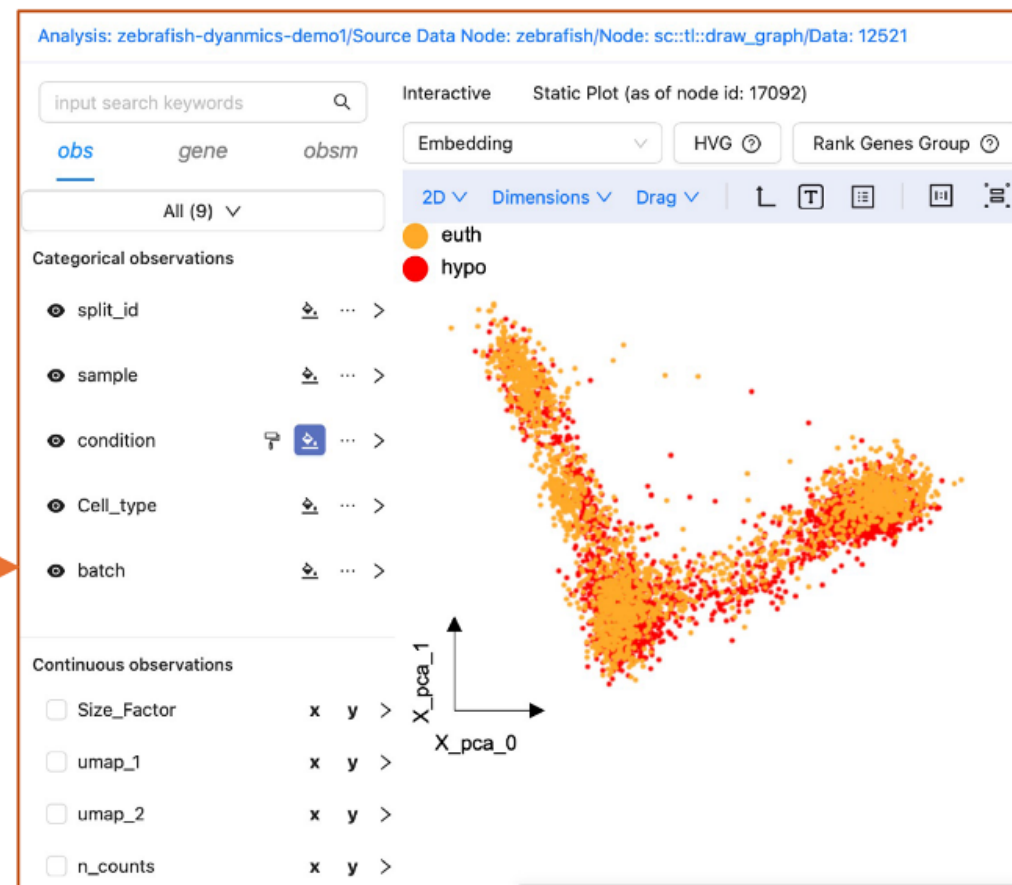


Overview of the Ragomics Cloud Platform

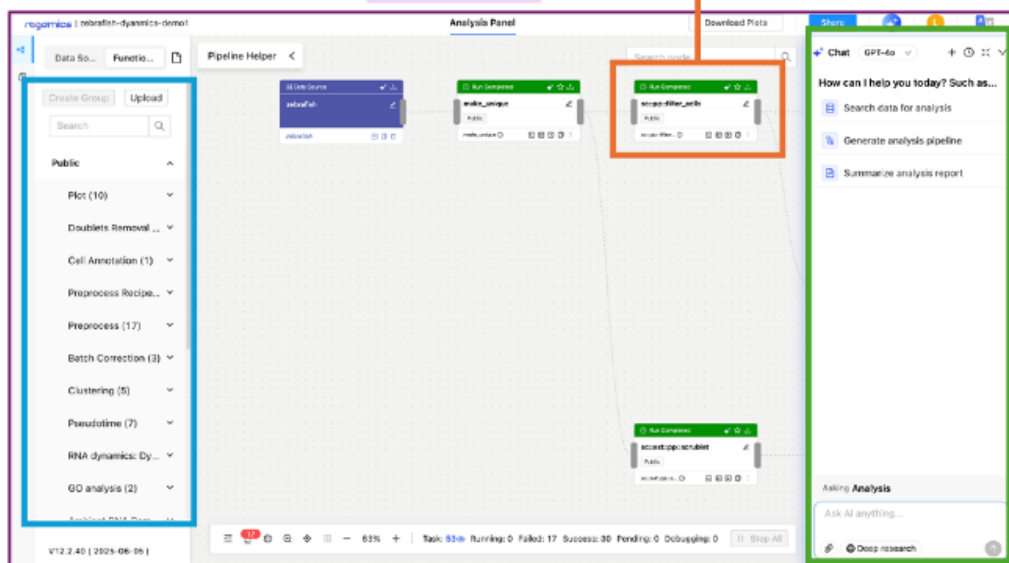
(A) Task panel



(C) Visualization panel



(B) Analysis panel



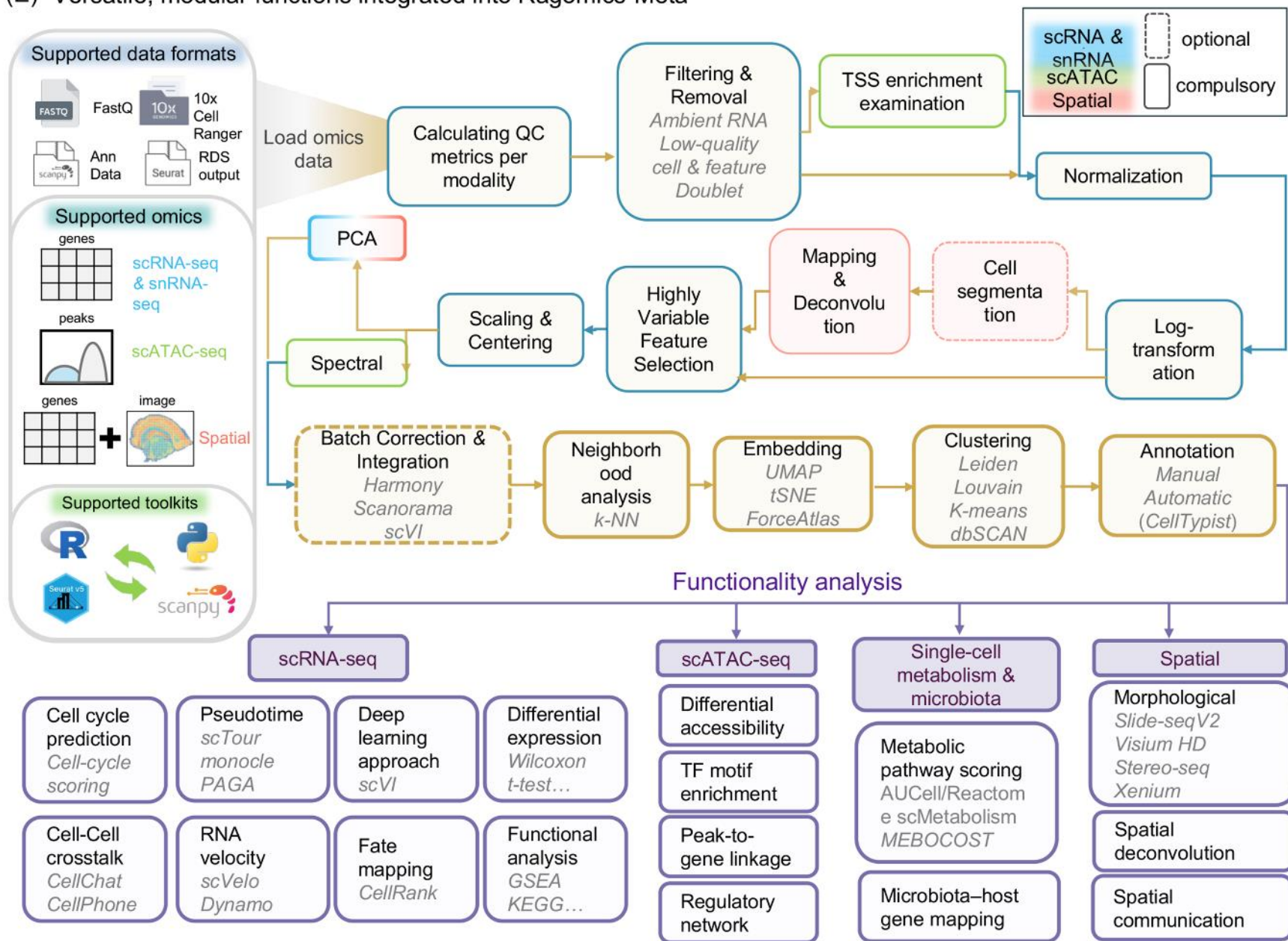
(D) Supported AI assistants





Cloud Workflow

(E) Versatile, modular functions integrated into Ragomics-Meta



Versatile, modular functions integrated into Ragomics-Meta



Cloud Tool: AI-Assisted Interpretation

Chat List

New Chat

Hello, I have a list of genes involving the interaction between human and gut microbiome, can you pinpoint which pathways are related for these genes? Here is the genelist: CCL20 DUOX2 IL10 IL12B IL12A TNF TLR2 TLR4 CXCL8 IL6 MAPK1 CCR6 CXCR6 CXCR3 TJP2 PRKCZ IL1B TLR5 TJP1 CLDN1 OCLN CGN DEFB4A CLDN4 F11R TGFB1 FOXP3 MAPK14 IKBKE MIR146A MIR155 CXCL10 PDCD6IP FFAR2 NFKB1 IL1A IL2 IL5 MYD88 RORA CXCL1 CXCL5 IL17A ANGPTL4 PLIN2 PPARG NR1H4 GLP1R VEGFA ACTB PARD6B ACTC1 ITCH JUP CNKSR3 SNAI1 HNF4A CD2AP VCL MAGI3 PALS1 CPSF2 CDK4 IFNG LEP CYP7A1 GPBAR1 TLR6 CLGN TJP3 CLDN14 IL4 SLC5A8 MUC1 MUC2 MGAT3 B4GALT1 ST6GAL1 FOS JUN PGP SLC19A2 SLC19A3 SLC9A3 RELA BCL10 SLC26A3 MGAT4B MGAT4A IL22RA2 PTGS2 IL18 HDAC3 HCAR2 CDKN1A Htr1a NBP13P RMRP RNR1 APOE CCL2 COX1 FABP2 HK2 LDHA ENO1 ENO1-IT1 IRAK1 IRAK4 TAB2 PTGER3 LPA GOT1 GPT IL11 IL24

To identify the related pathways for the genes involved in human-gut microbiome interactions, databases such as KEGG, Reactome, BioCarta, or pathway analysis tools could be used. Here is a list of some well-known pathways potentially associated with the provided genelist. Please further verify using specific databases or pathway analysis tools for precise mappings: 1. **CCL20, CXCL8, CXCL1, CXCL5, CXCL10, CCL2** – Chemokine signaling pathway. 2. **DUOX2, NOX family members** – Reactive Oxygen Species (ROS) generation and regulation. 3. **IL10, IL12B, IL12A, IL6, IL1B, IL1A, IL2, IL5, IL4, IL17A, IL24, IL22RA2** – Cytokine-cytokine receptor interaction pathways. 4. **TNF, IL10, IL6, CXCL8, TLR pathways** – TNF signaling pathway. 5. **TLR2, TLR4, TLR5, MYD88, IRAK1, IRAK4** – Toll-like receptor signaling pathway. 6. **MAPK1, MAPK14, JUN, FOS** – MAPK signaling pathway. 7. **FOXP3** – T cell receptor signaling pathway and regulation of immune response. 8. **TGFB1, FOXP3** – TGF-beta signaling pathway. 9. **PPARG, RORA, NR1H4, HNF4A** – Nuclear Receptor signaling pathways. 10. **NFKB1, MIR146A, MIR155, BCL10, RELA** – NF-kappa B signaling pathway. 11. **PLIN2, FABP2** – Lipid metabolic pathways. 12. **LEP, VEGFA** – PI3K-Akt signaling pathway. 13. **ITCH, JUP, SNAI1** – Wnt signaling pathway. 14. **CDK4** – Cell cycle regulation. 15. **ANGPTL4, VEGFA** – Angiogenesis. 16. **COX1, PTGS2** – Inflammatory response and Prostaglandin synthesis. 17. **APOE** – Cholesterol metabolism and transport. 18. **ENO1, LDHA, HK2, GOT1, GPT** – Glycolysis/Gluconeogenesis pathways. 19. **MGAT3, MGAT4A, MGAT4B, B4GALT1, ST6GAL1** – N-Glycan biosynthesis. Note that the actual involvement in these pathways can vary based on species and tissue type, and cross-referencing with specific pathway databases is recommended for research-specific accuracy.

Input your question there to get answer

AI Interpretation

Regenerate

Interpretation of Function Block Output:

- Biological Significance of Motif Enrichment:**
 - The heatmap illustrates motif enrichment analysis results showing differential enrichment of transcription factor binding motifs between two groups: CRC (colorectal cancer) and healthy cells.
 - The y-axis lists motif names along with identifiers, with colors representing the significance level of enrichment (log-transformed p-values).
 - Dark red represents significant enrichment in CRC samples, whereas blue indicates significant enrichment in healthy samples.
 - Motifs such as TCF7L2 and LEF1 are highly enriched in CRC, suggesting potential regulatory roles in cancer pathogenesis.
- Dataset Changes:**
 - The computation used differentially accessible regions (peaks) identified in previous steps, separating them into CRC and healthy groups based on log2 fold changes.
 - No major changes in sparsity or structure of the dataset are noted post-execution, indicating focus on interpretative analysis rather than data transformation.
- Historical Context:**
 - Previous clustering and differential testing identified groups and peaks underlying this analysis.
 - The analysis follows differential expression with motif enrichment, a critical step for understanding transcriptional regulatory mechanisms.
- Potential Next Steps:**
 - Validate findings with experimental methods, such as ChIP-seq, to confirm motif activity.
 - Integrate data with additional omics layers (e.g., proteomics) for a comprehensive view of molecular differences.
 - Explore motif enrichment in other conditions or cell types for broader insights into regulatory networks.

These interpretations provide insights into the transcriptional landscape differences between CRC and healthy cells, offering a pathway for further investigation into cancer biology.



Case Study 1: Validation Using ALL Single-Cell Data

(F)

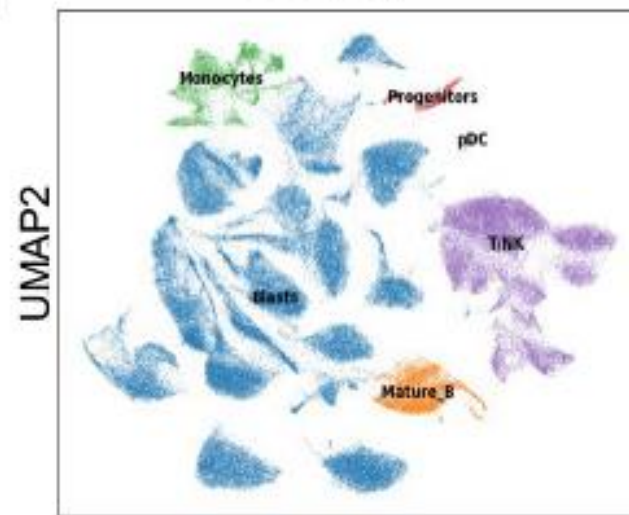


→ Ragomics
meta

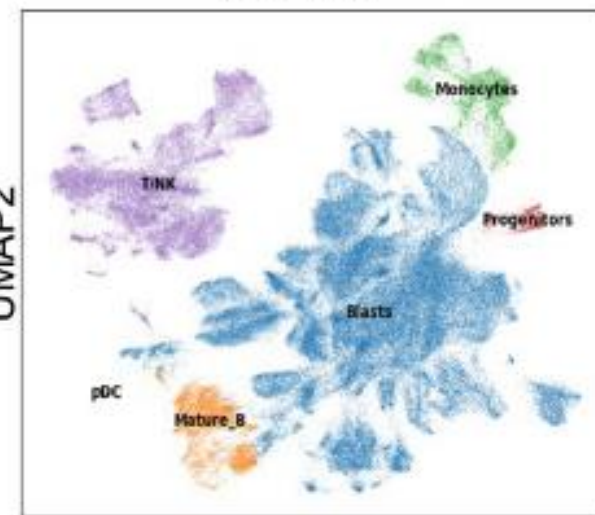
18 KMT2A-rALL infant
PBMCs

(G)

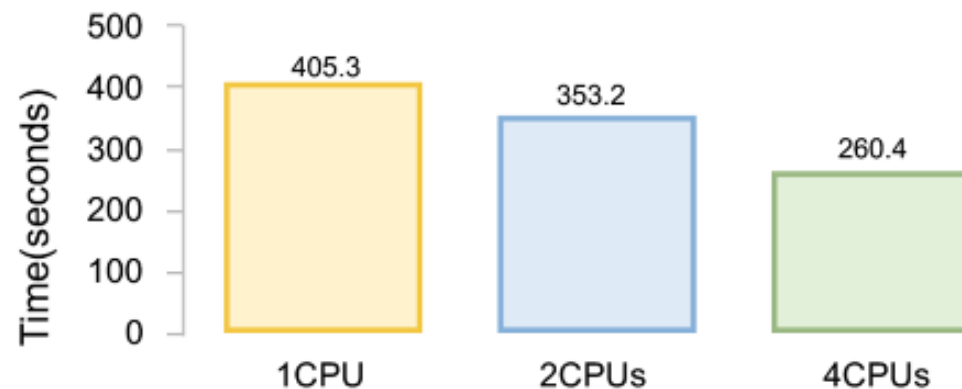
Scanpy



Seurat

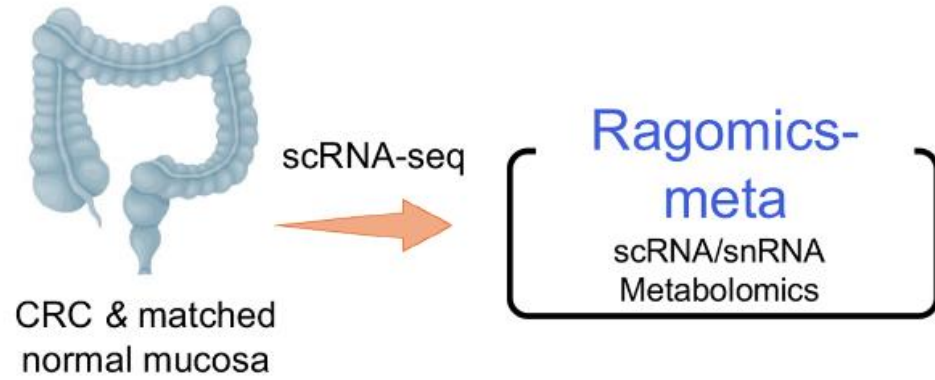


(H)

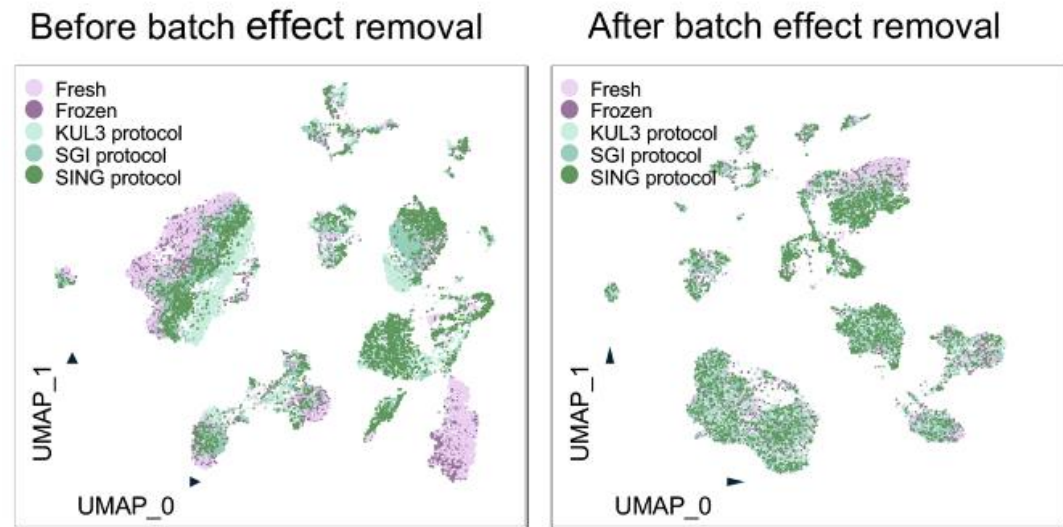


Case Study 2: Single-Cell Metabolic Analysis in Colorectal Cancer

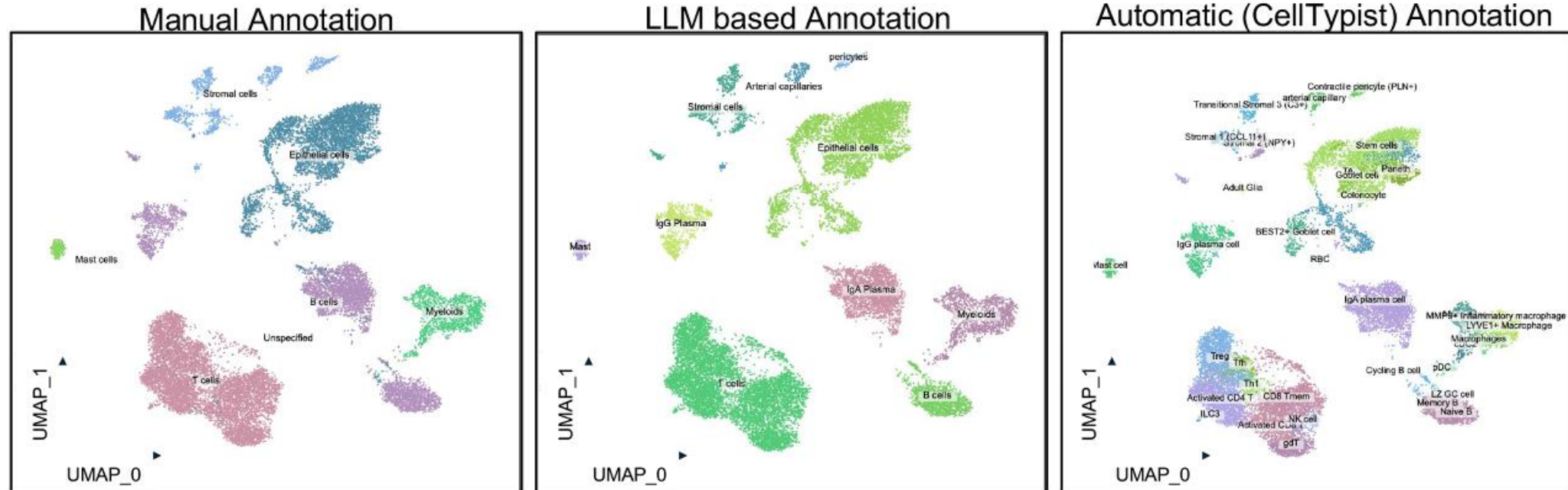
(A)



(B)

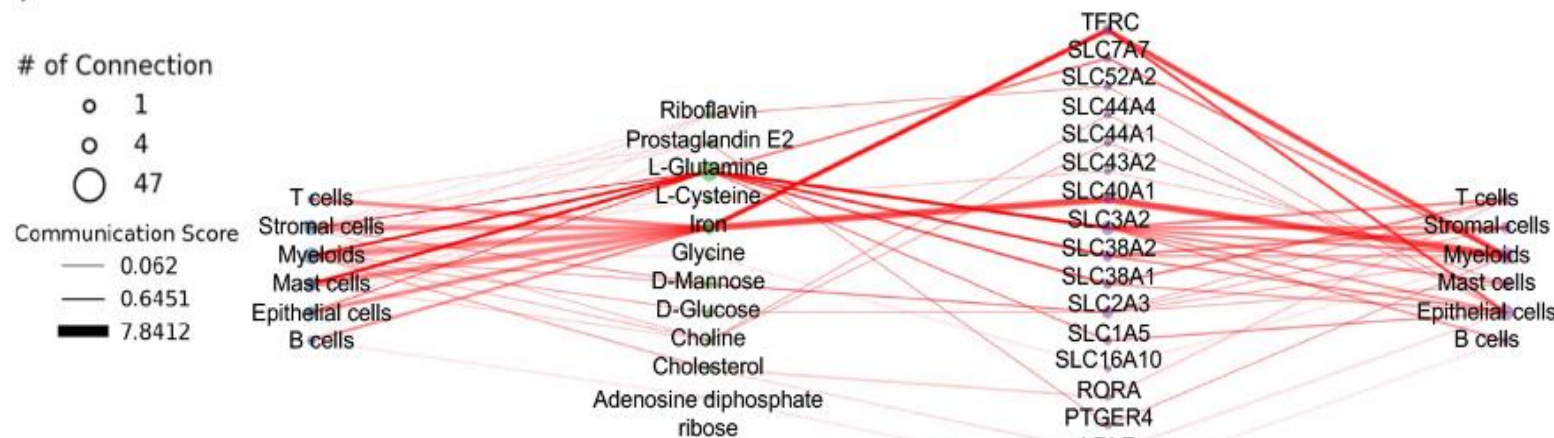


(C)

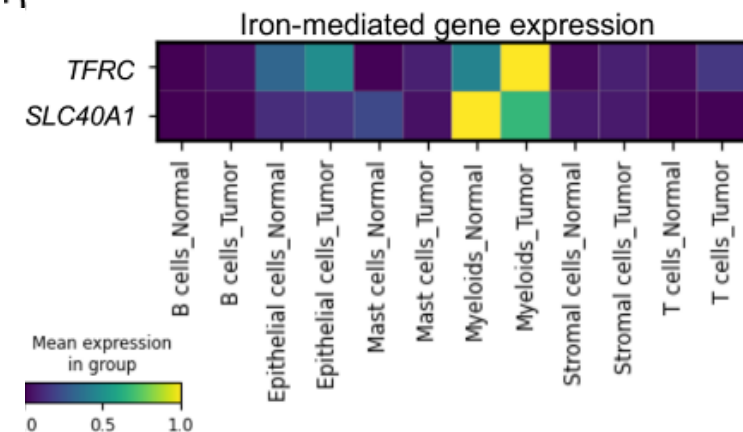


Case Study 2: Iron-Related Metabolic Communication in CRC

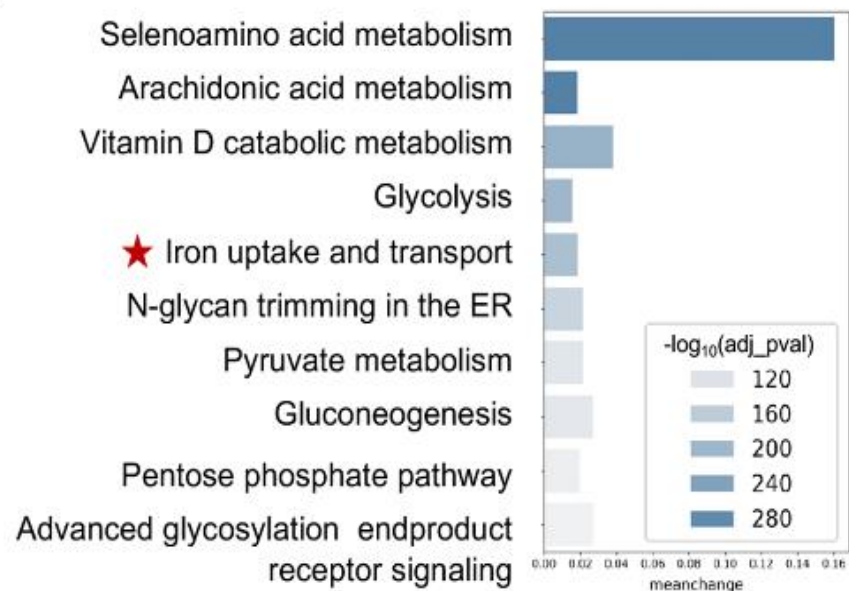
(D)



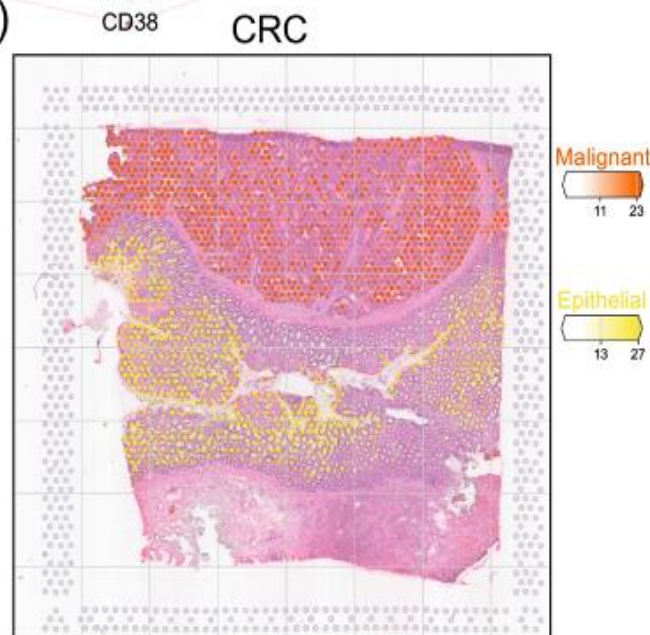
(E)



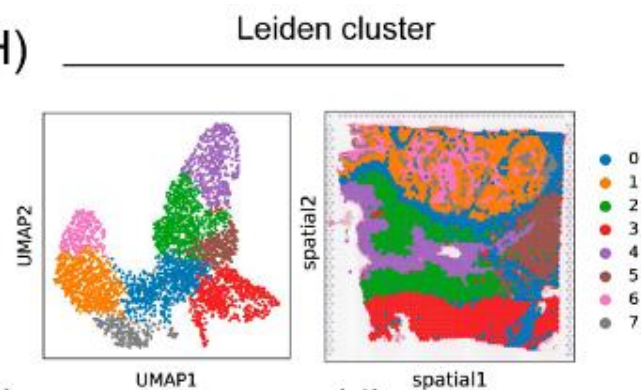
(F) CRC activated metabolic pathways in epithelium



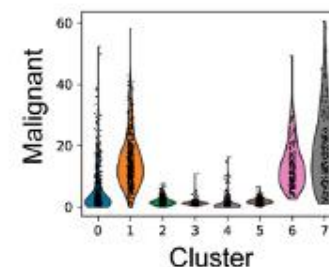
(G)



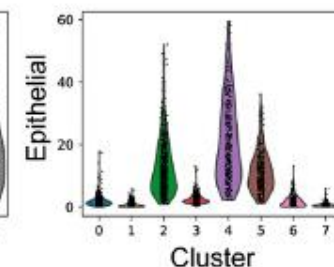
(H)



(I)



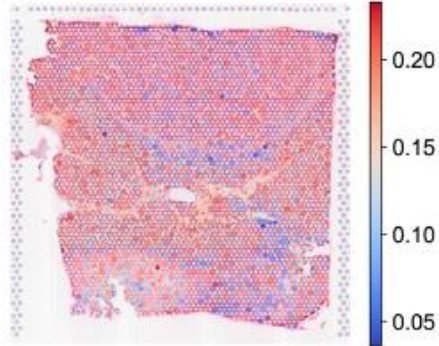
(J)



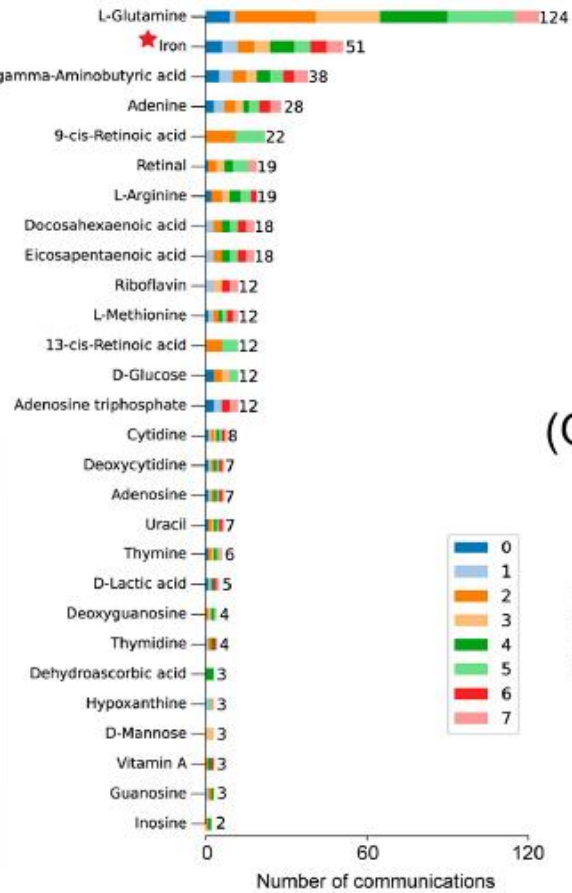


Case Study 2: Spatial Metabolism and Epigenetic Regulation

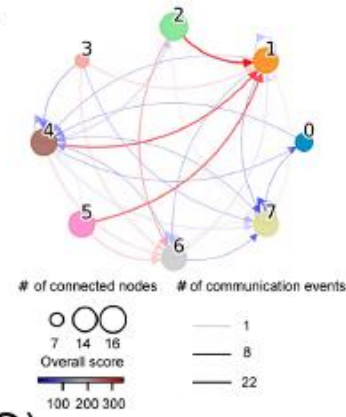
(K) Iron uptake and transport activity score



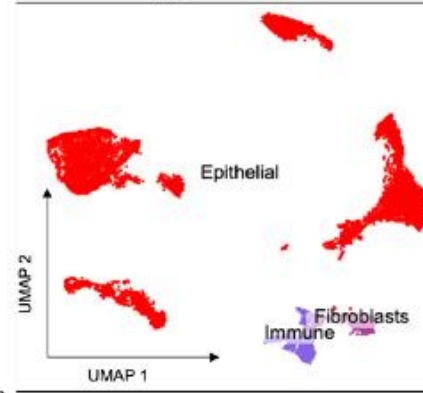
(M) Communication number of metabolite in sender



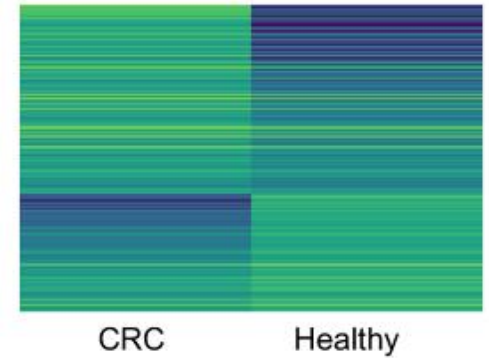
(N) Iron-mediated network



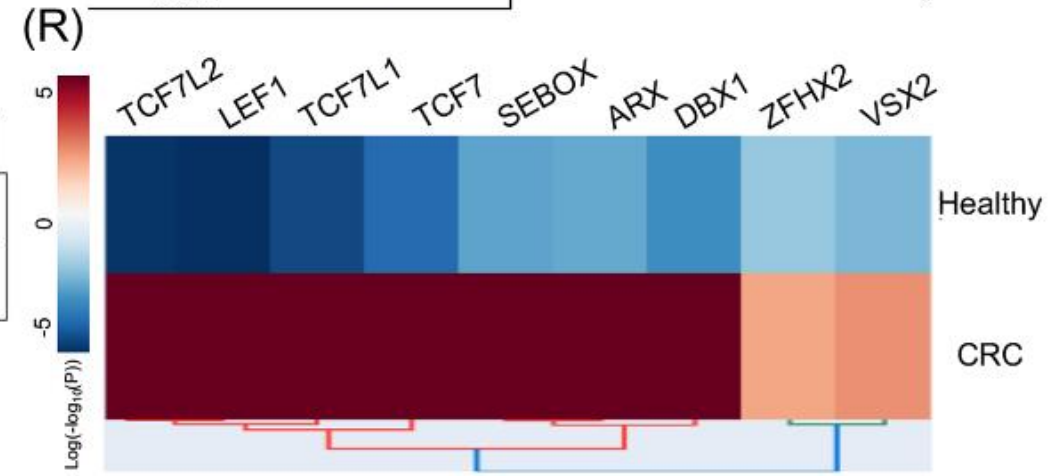
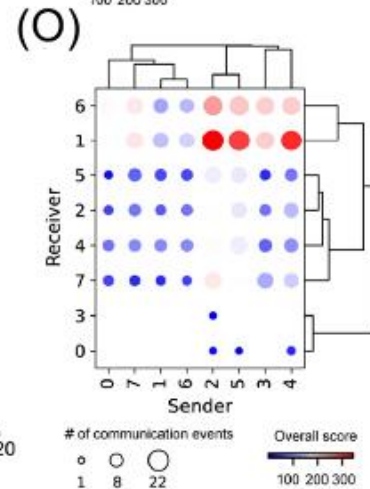
(P) Cell-type annotation



(Q) DARs in epithelial cells



(L) Spatial cell-cell communication





Summary

- ❑ In this study, we introduce **Ragomics-Meta**, an open, metabolism-centered multi-omics analysis workflow that supports multimodal data analysis, including scRNA/snRNA-seq, scATAC-seq, spatial transcriptomics, and spatial metabolomics.
- ❑ Ragomics-Meta integrates more than 100 commonly used functional modules, including mainstream tools such as Scanpy, Seurat, SnapATAC2, Squidpy, COMMOT, MEBOCOST, scMetabolism, and AUCell. These modules cover key analytical steps, including data preprocessing, clustering and annotation, differential analysis, metabolic pathway scoring, and visualization.
- ❑ The platform also supports AI-assisted analysis and interpretation. It can incorporate large language models such as ChatGPT, DeepSeek, and Grok to assist with cell-type annotation, gene list organization, pathway result interpretation, and hypothesis generation.
- ❑ Platform website: <http://www.raganetwork.com>.

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