

Evaluating Saliency Models in Motion: DeepGaze IIE Outperforms Itti-Koch on Egocentric Video but Reveals a Performance Gap Beyond Static Viewing

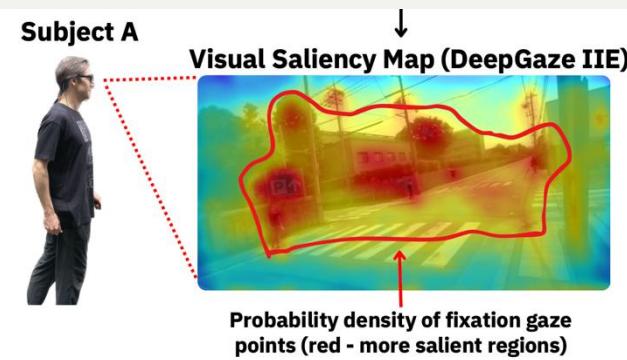
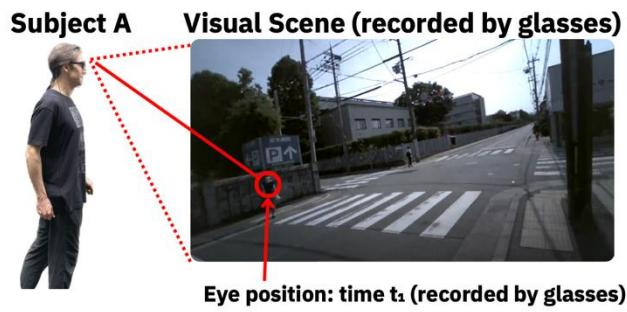
Experimental Design

Core Question

Can saliency models trained on static lab images predict human gaze in dynamic, real-world egocentric video?

Experimental Setup

7 participants walked two designated routes while wearing Tobii Pro Glasses 3, capturing natural gaze data and first-person video. No specific task instructions were given to ensure natural viewing behavior.

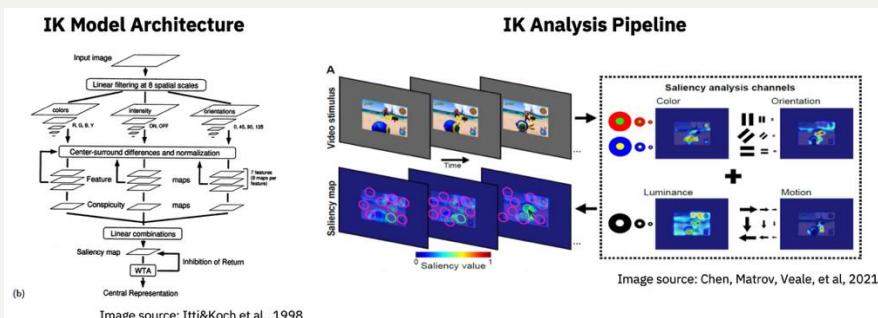


Models being compared

Classic Model

Itti-Koch (1998).

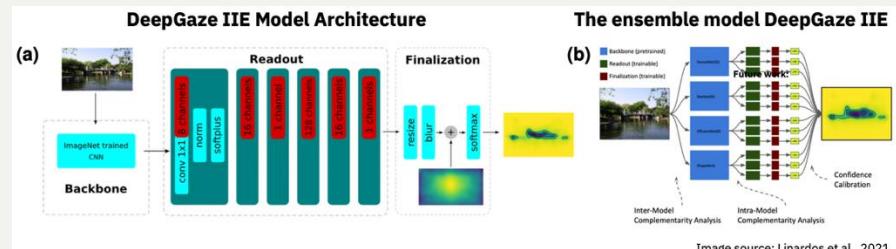
A biologically-inspired model that simulates bottom-up attention by creating a saliency map from low-level visual features like color, intensity, and orientation.



Modern Model

DeepGaze IIE (2021).

A deep learning model using a pre-trained Convolutional Neural Network (CNN) to extract high-level features. It was trained on large static image datasets (SALICON and MIT1003).



Verdict & Key Insight

Results

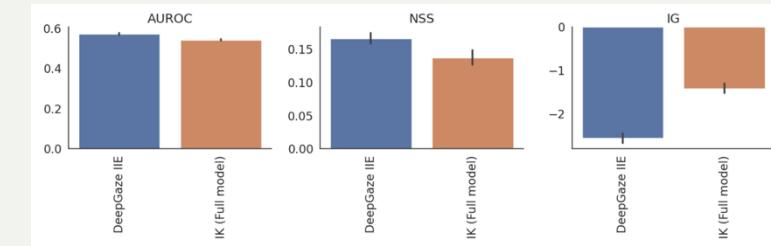
DeepGaze IIE demonstrated superior performance across key metrics, indicating a better prediction of human gaze locations in this dynamic task.

Key Insight

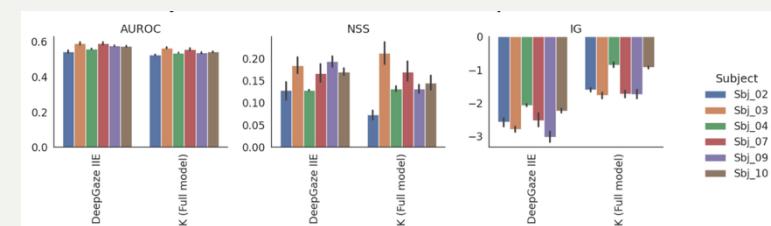
Despite outperforming the classic model, DeepGaze IIE's overall performance was modest (AUROC of 0.574).

This suggests that models trained exclusively on static, lab-based images do not fully translate to the complexities of real-world, dynamic egocentric vision.

Model Performance Comparison



Per-subject Model Performance Comparison

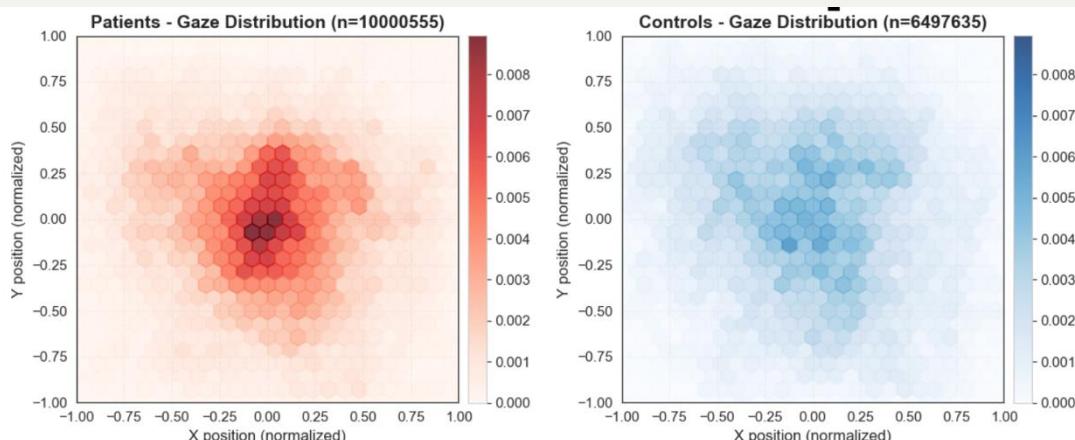


Classifying Schizophrenia with 88% AUROC Using Video-Based Eye-Tracking

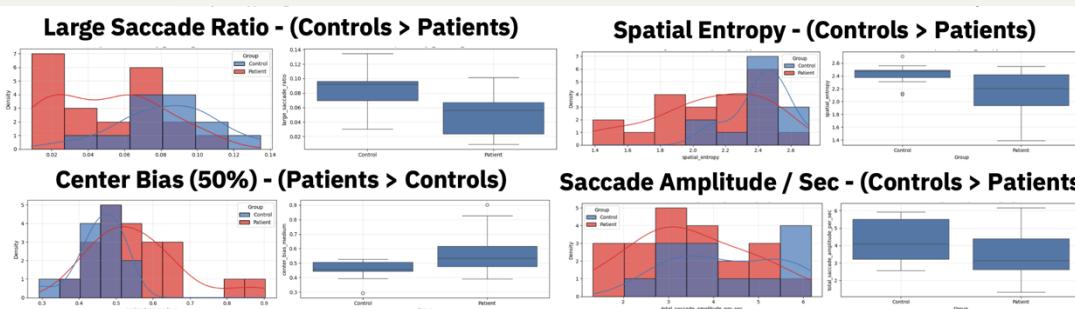
Distinct Gaze Patterns Differentiate Patients from Controls

21 schizophrenia patients and 13 healthy controls viewed videos of various scenes. Eye movements were recorded at 1000 Hz using an EyeLink 1000 Plus system.

Overall Gaze Distribution



Selected Features

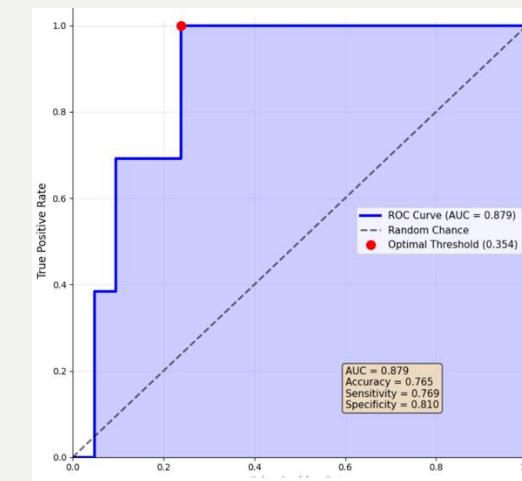


A Logistic Regression Model Achieves High Diagnostic Accuracy

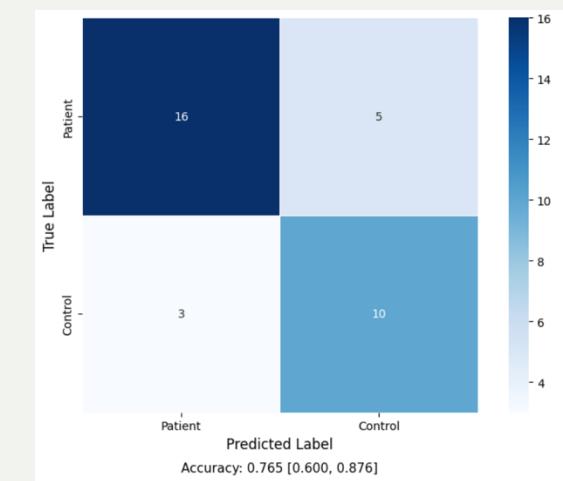
Following recursive feature elimination to identify the most discriminative signals, a Logistic Regression classifier was trained on just four key features:

- Large Saccade Ratio ($>5^\circ$) (Higher in Controls)
- Spatial Entropy (Higher in Controls)
- Center Bias (50%) (Higher in Patients)
- Total Saccade Amplitude / Sec (Higher in Controls)

ROC Curve



Confusion Matrix



This work demonstrates that features extracted from eye movements during video-viewing can serve as a robust, objective, and non-invasive biomarker for schizophrenia, achieving accuracy comparable to previous image-based methods.

DeepSpaceDB: a spatial transcriptomics atlas for interactive in-depth analysis of tissues and tissue microenvironments

2,144

Total Samples
(1361 Human, 783 Mouse)

5.4 Million

Total Spots

Published in: *Nucleic Acids Research*
(IF=17, first author)



Search & Discover

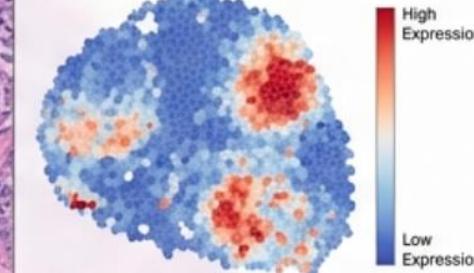
Search a comprehensive, manually curated database by tissue, organism, condition, or publication to find relevant datasets.

Metadata

- Organism: human
- Organ: breast
- Condition: cancer



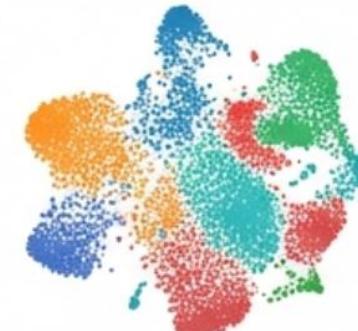
Spatially Variable Genes



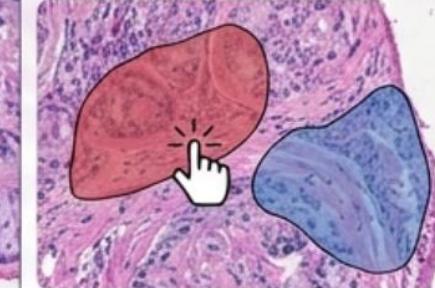
Interactive Exploration

Manually select any region of a tissue sample to perform on-the-fly differential gene expression analysis between your selections.

Spot Clustering in 2D Embedding

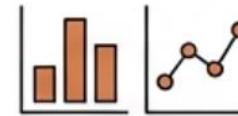


Interactive Tissue Analysis



Quality Control

Inspect and compare detailed quality metrics across thousands of samples to ensure data reliability for your analysis.



Visualize & Analyze

Explore spatially variable genes, biological pathways, and predicted cell type compositions directly on high-resolution tissue images.

DeepSpaceDB 2.0: A Standardized Pipeline and Viewer for 10x Xenium, Creating the Largest Public Single-Cell Spatial Atlas

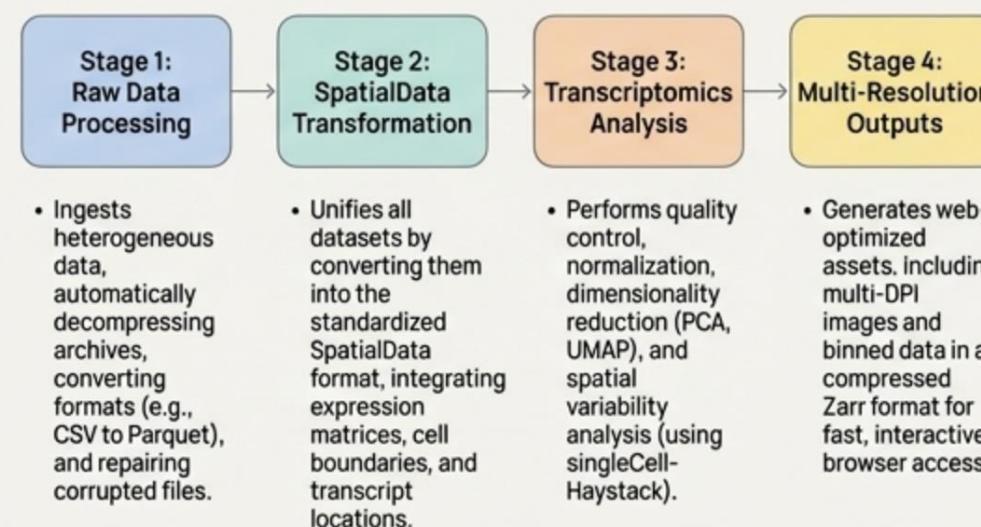
The Challenge

Publicly available 10x Xenium data is a major resource, but it's massive (>10GB per sample), highly heterogeneous, and stored in inconsistent formats.

This heterogeneity in file types, compression methods, and data structures makes large-scale analysis and direct comparison impractical.

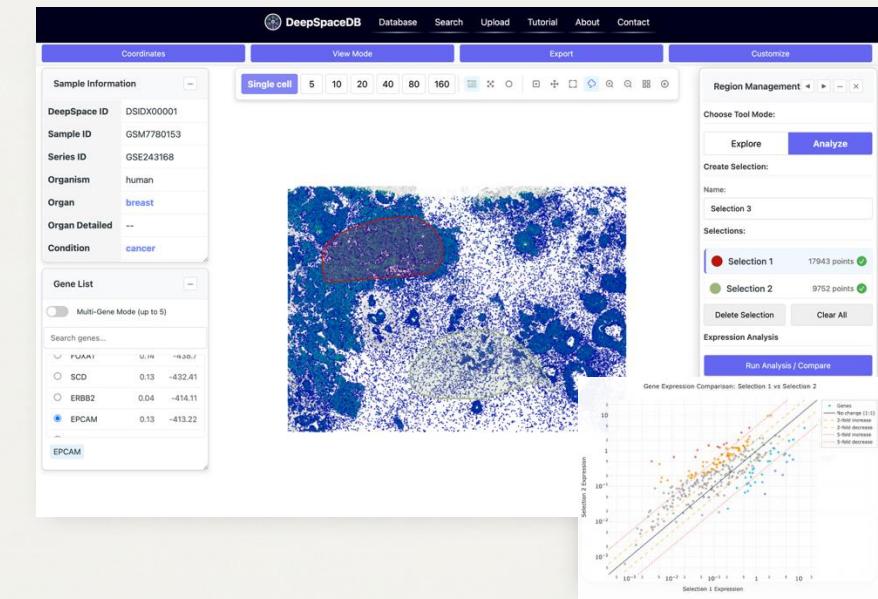
727 raw samples were collected from public repositories (GEO, 10X, DBKERO) to begin the standardization process.

The Solution



591 of 727 samples (81%) were successfully processed and standardized, forming the core of the new database.

The Result



Enables fast, interactive preview of single-cell data directly in the browser, eliminating the need to download large files. Users can **visualize gene expression**, explore UMAP clusters, and compare user-selected regions of interest.

Public release planned for early 2026.