

An Introduction to ChatGPT

Didong Li

August 4, 2024

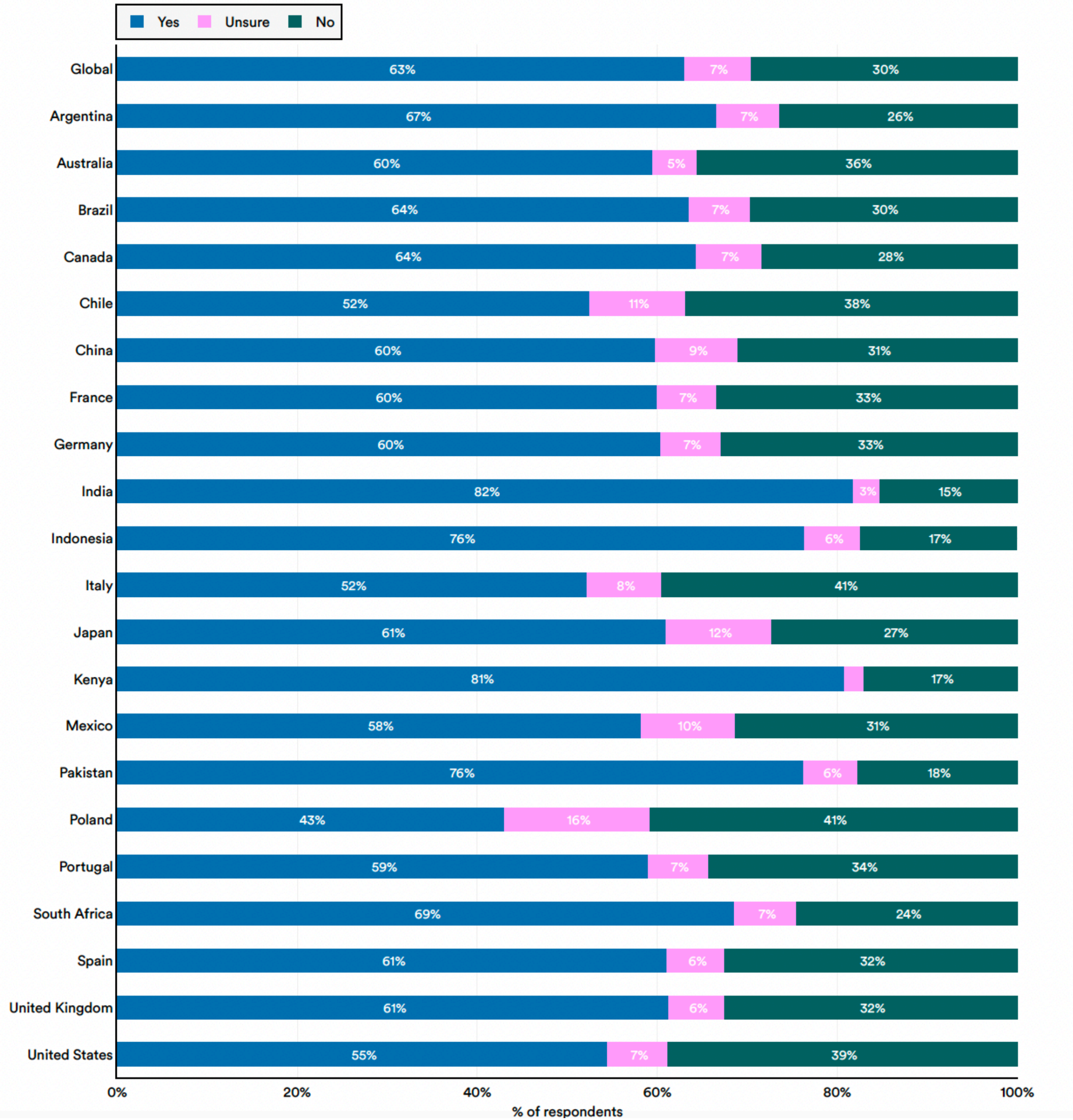
NISS Writing Workshop for Junior Researchers



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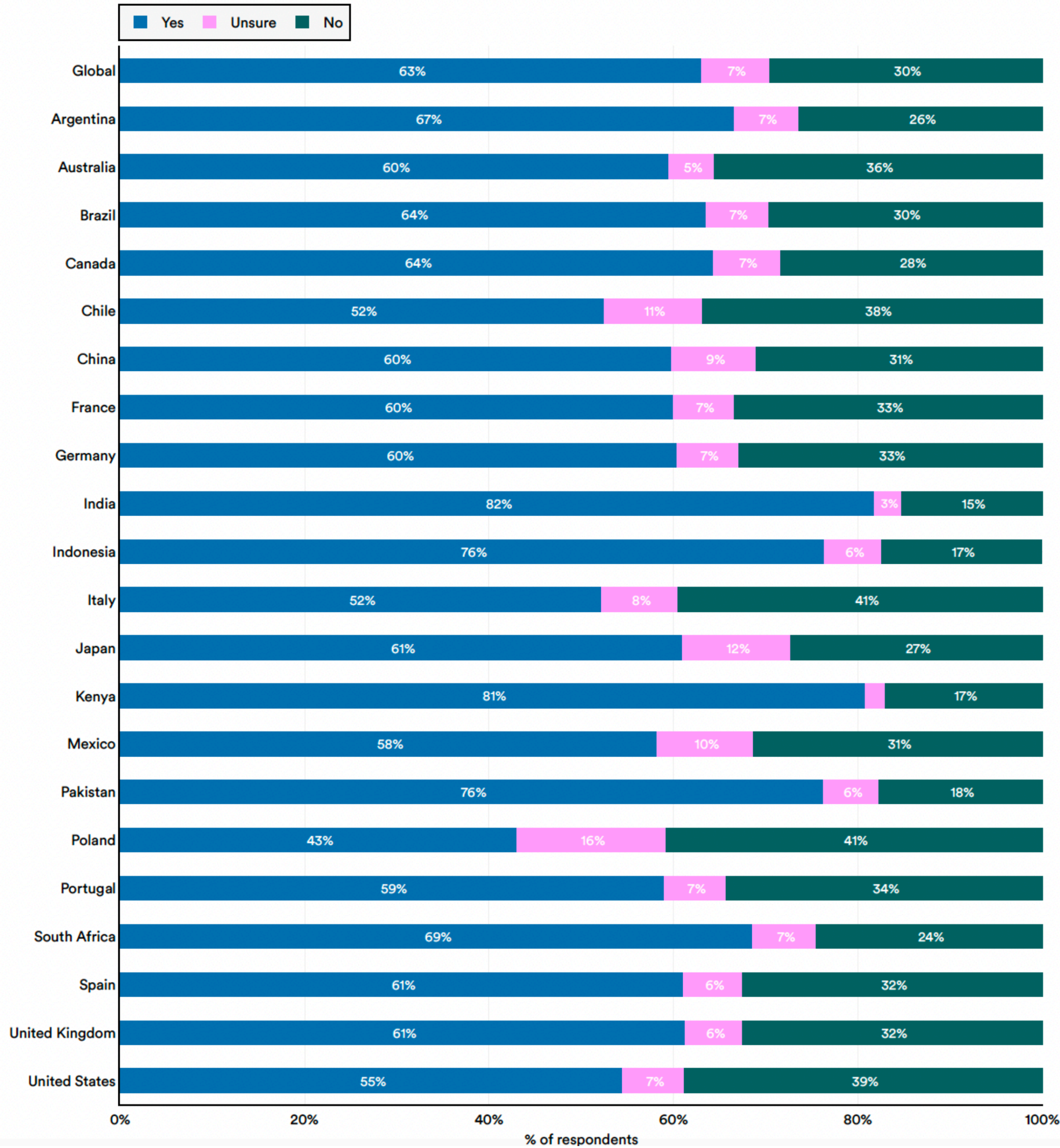
Global awareness of ChatGPT (% of total), 2023

Source: Global Public Opinion on Artificial Intelligence (GPO-AI), 2024 | Chart: 2024 AI Index report



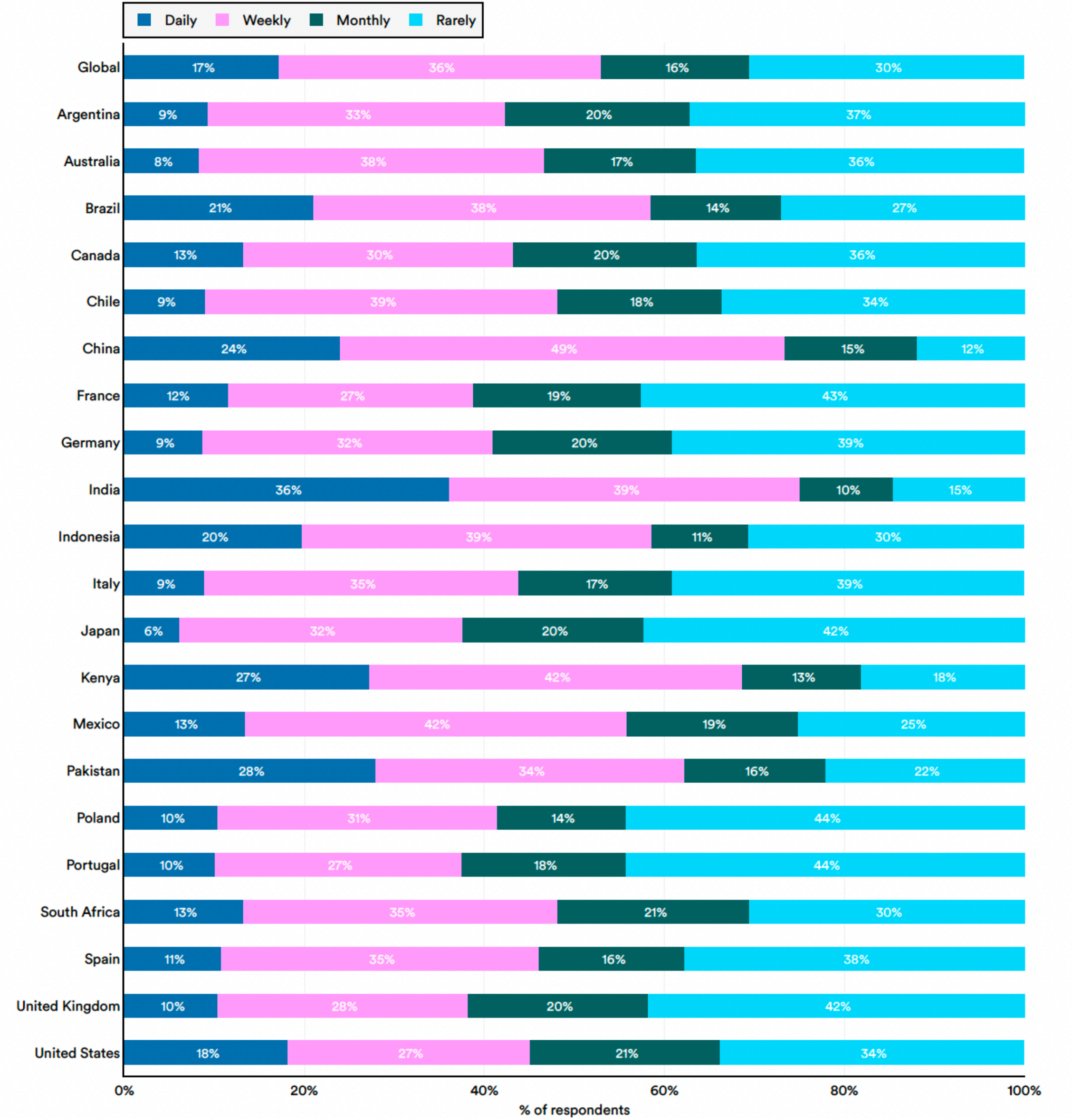
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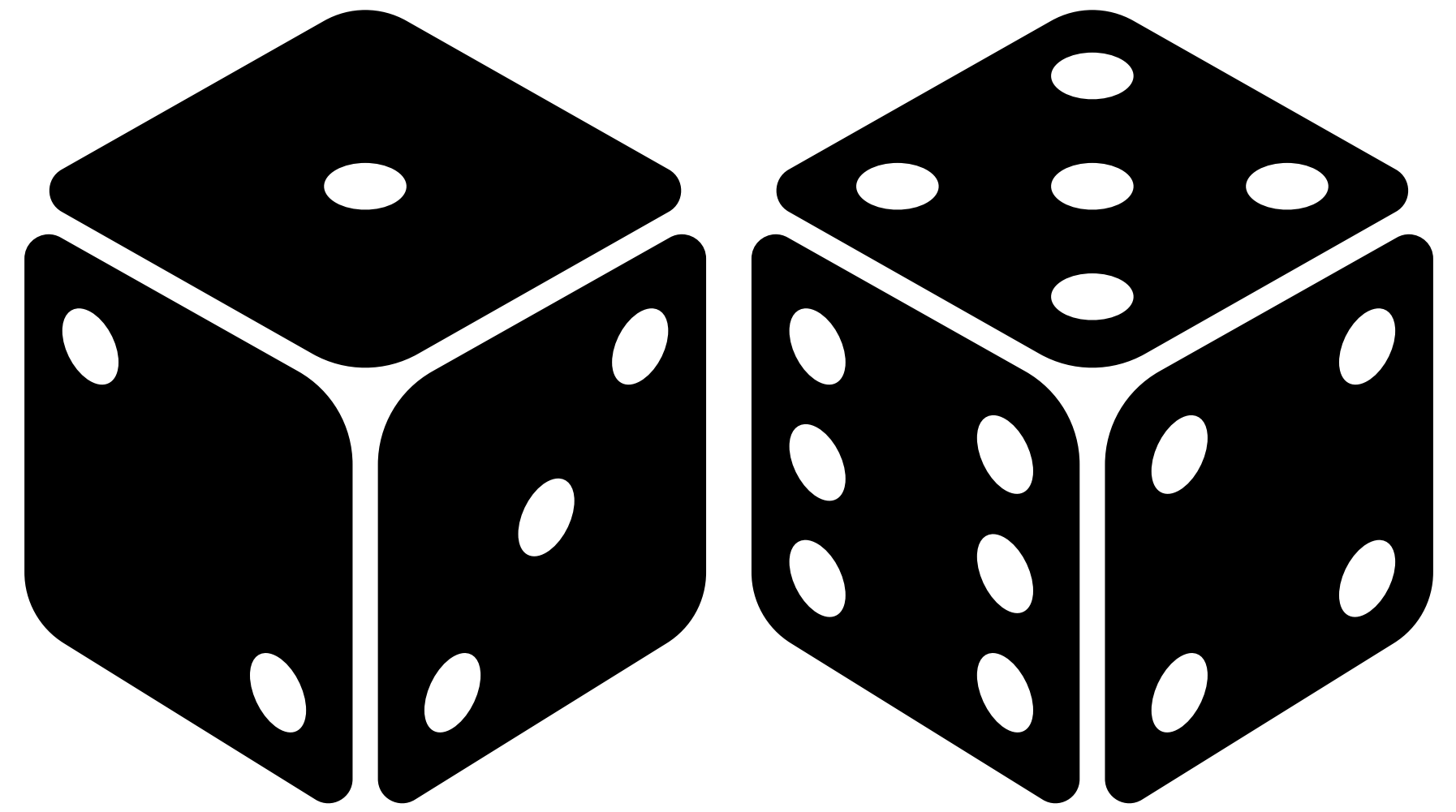
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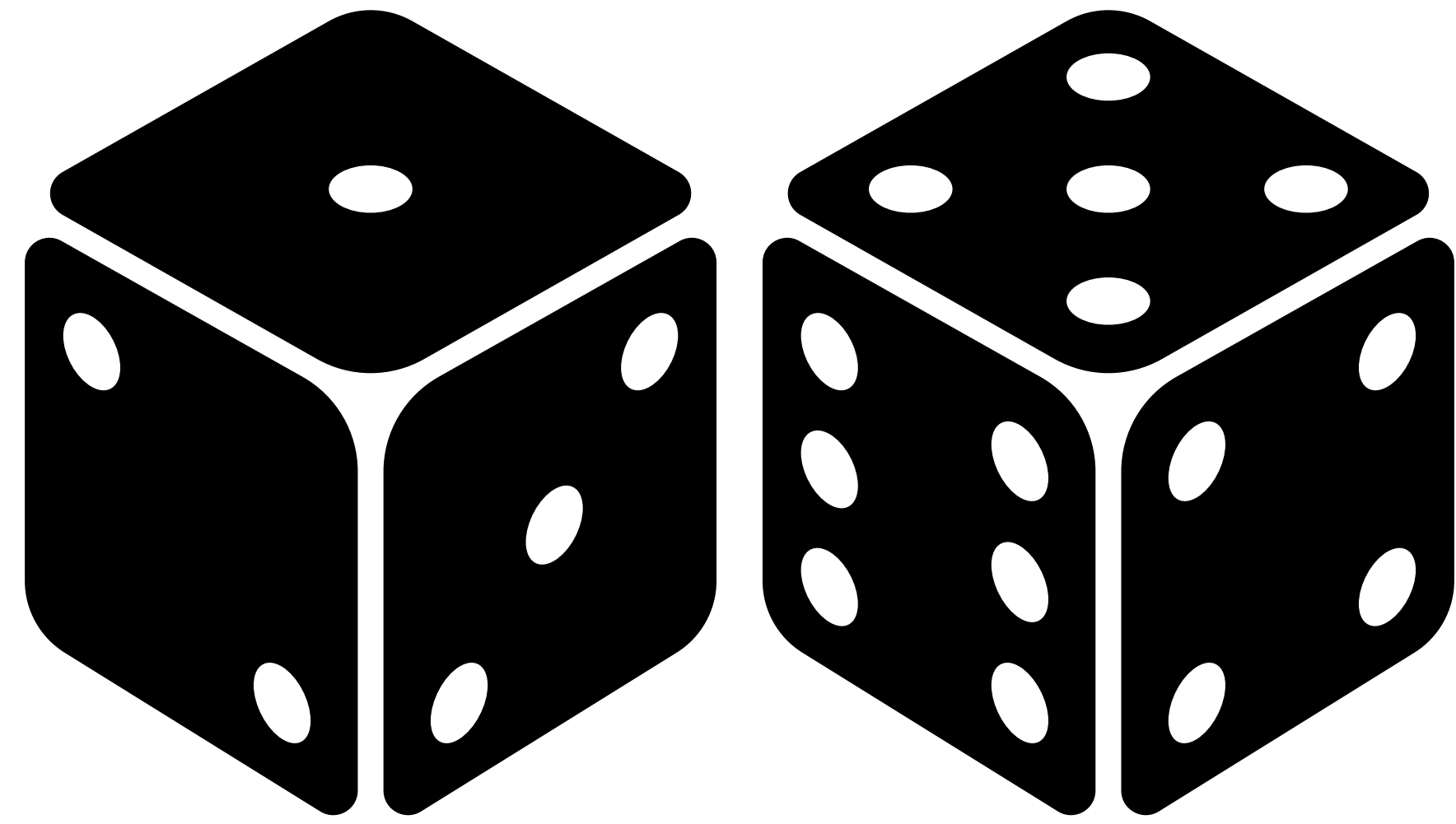


Global usage frequency of ChatGPT (% of total), 2023

Source: Global Public Opinion on Artificial Intelligence (GPO-AI), 2024 | Chart: 2024 AI Index report







Pintrest

Overview

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A brief history

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NeurIPS 2017

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NeurIPS 2017

Improving Language Understanding by Generative Pre-Training

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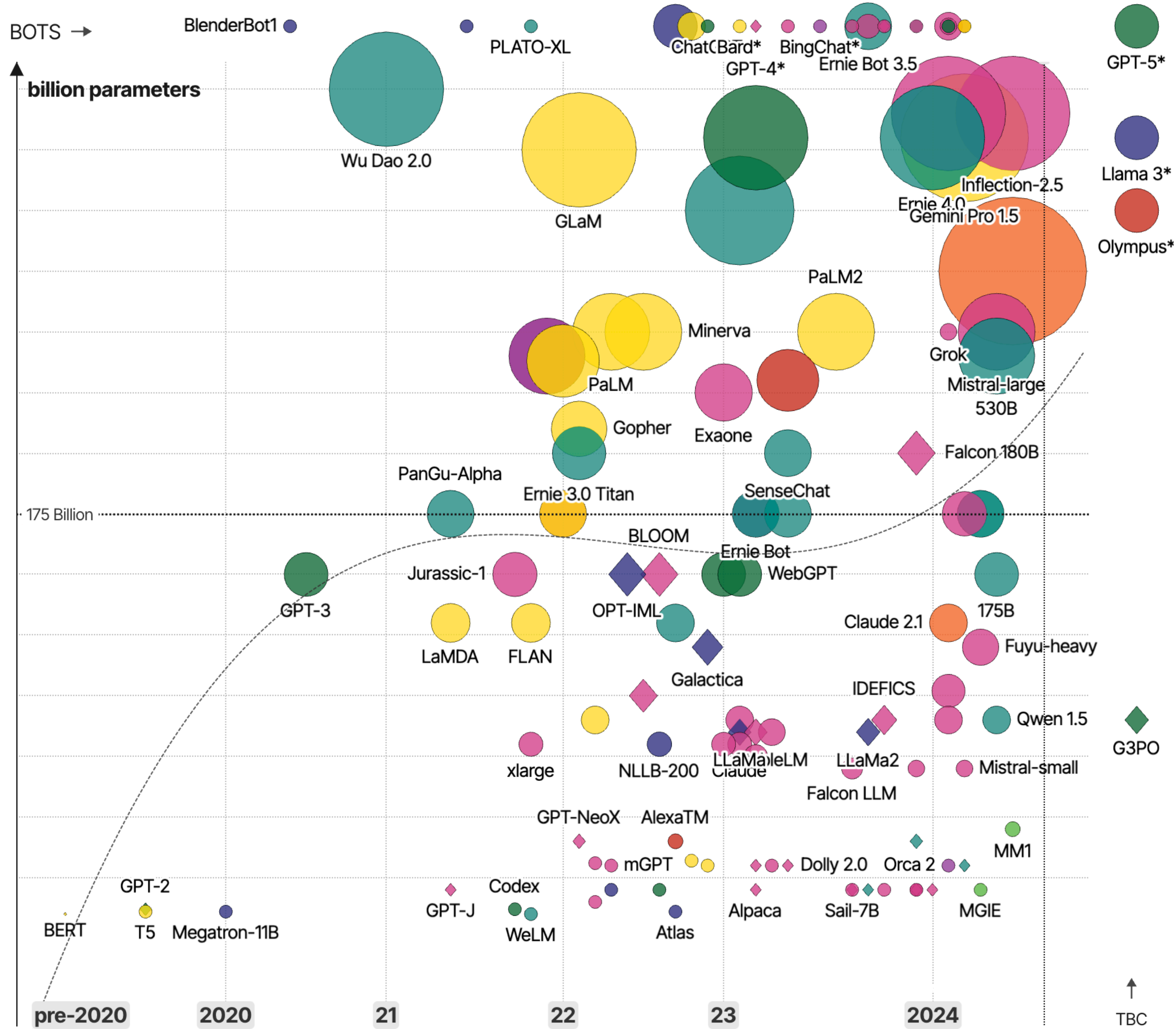
Ilya Sutskever
OpenAI
ilyasu@openai.com

Technical report 2018

OpenAI's *GPT-n* series

Model	Architecture	Parameter count	Training data	Release date	Training cost
GPT-1	12-level, 12-headed Transformer decoder (no encoder), followed by linear-softmax.	117 million	BookCorpus : ^[34] 4.5 GB of text, from 7000 unpublished books of various genres.	June 11, 2018 ^[9]	30 days on 8 P600 GPUs, or 1 petaFLOP/s-day. ^[9]
GPT-2	GPT-1, but with modified normalization	1.5 billion	WebText: 40 GB of text, 8 million documents, from 45 million webpages upvoted on Reddit .	February 14, 2019 (initial/limited version) and November 5, 2019 (full version) ^[35]	"tens of petaflop/s-day", ^[36] or 1.5e21 FLOP. ^[37]
GPT-3	GPT-2, but with modification to allow larger scaling	175 billion ^[38]	499 billion tokens consisting of CommonCrawl (570 GB), WebText, English Wikipedia, and two books corpora (Books1 and Books2).	May 28, 2020 ^[36]	3640 petaflop/s-day (Table D.1 ^[36]), or 3.1e23 FLOP. ^[37]
GPT-3.5	Undisclosed	175 billion ^[38]	Undisclosed	March 15, 2022	Undisclosed
GPT-4	Also trained with both text prediction and RLHF ; accepts both text and images as input. Further details are not public. ^[33]	Undisclosed. Estimated 1.7 trillion. ^[39]	Undisclosed	March 14, 2023	Undisclosed. Estimated 2.1×10^{25} FLOP. ^[37]

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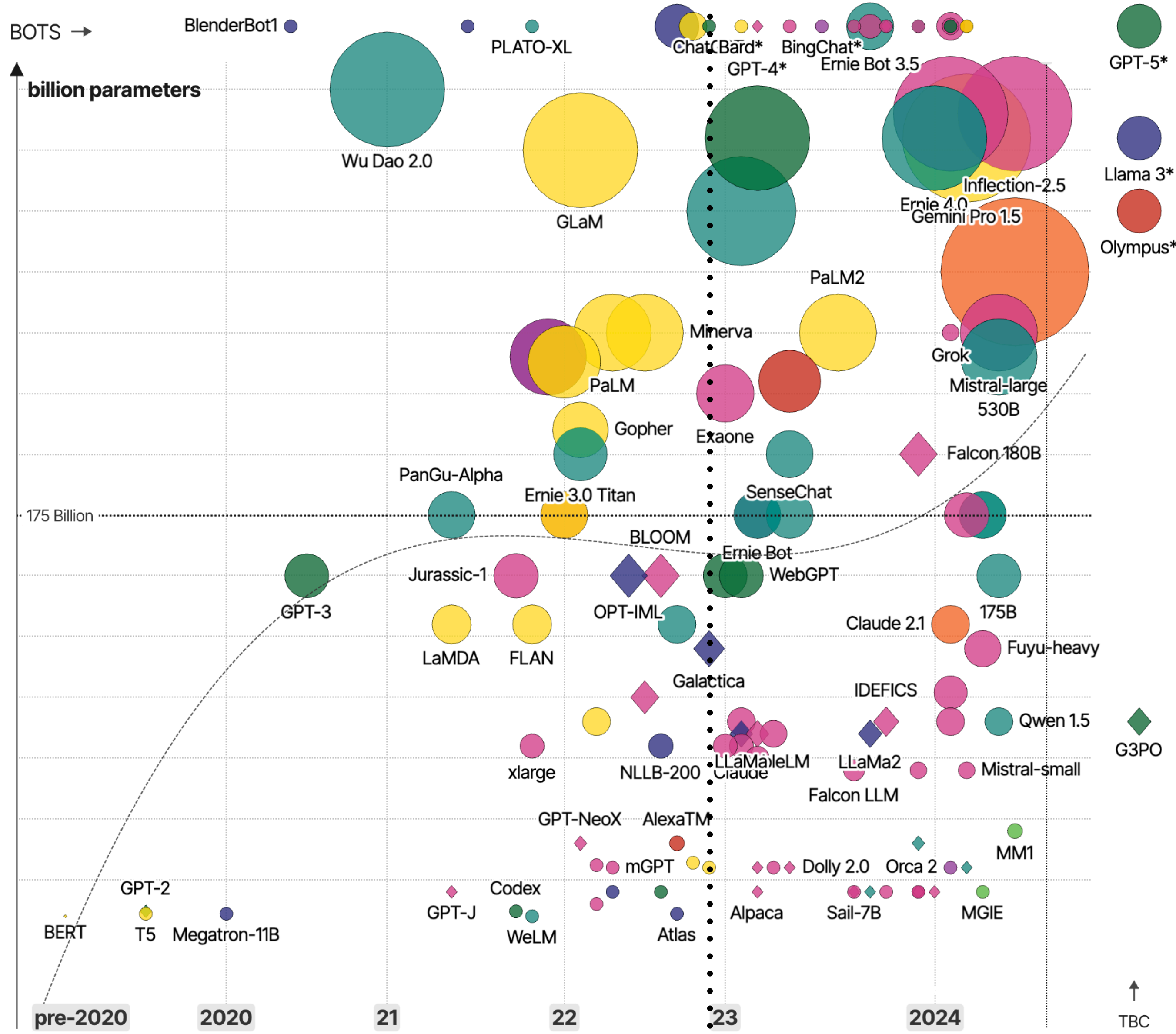


David McCandless, Tom Evans, Paul Barton
Information is Beautiful // UPDATED 20th Mar 24

source: news reports, [LifeArchitect.ai](https://life-architect.ai)
 * = parameters undisclosed // see [the data](#)

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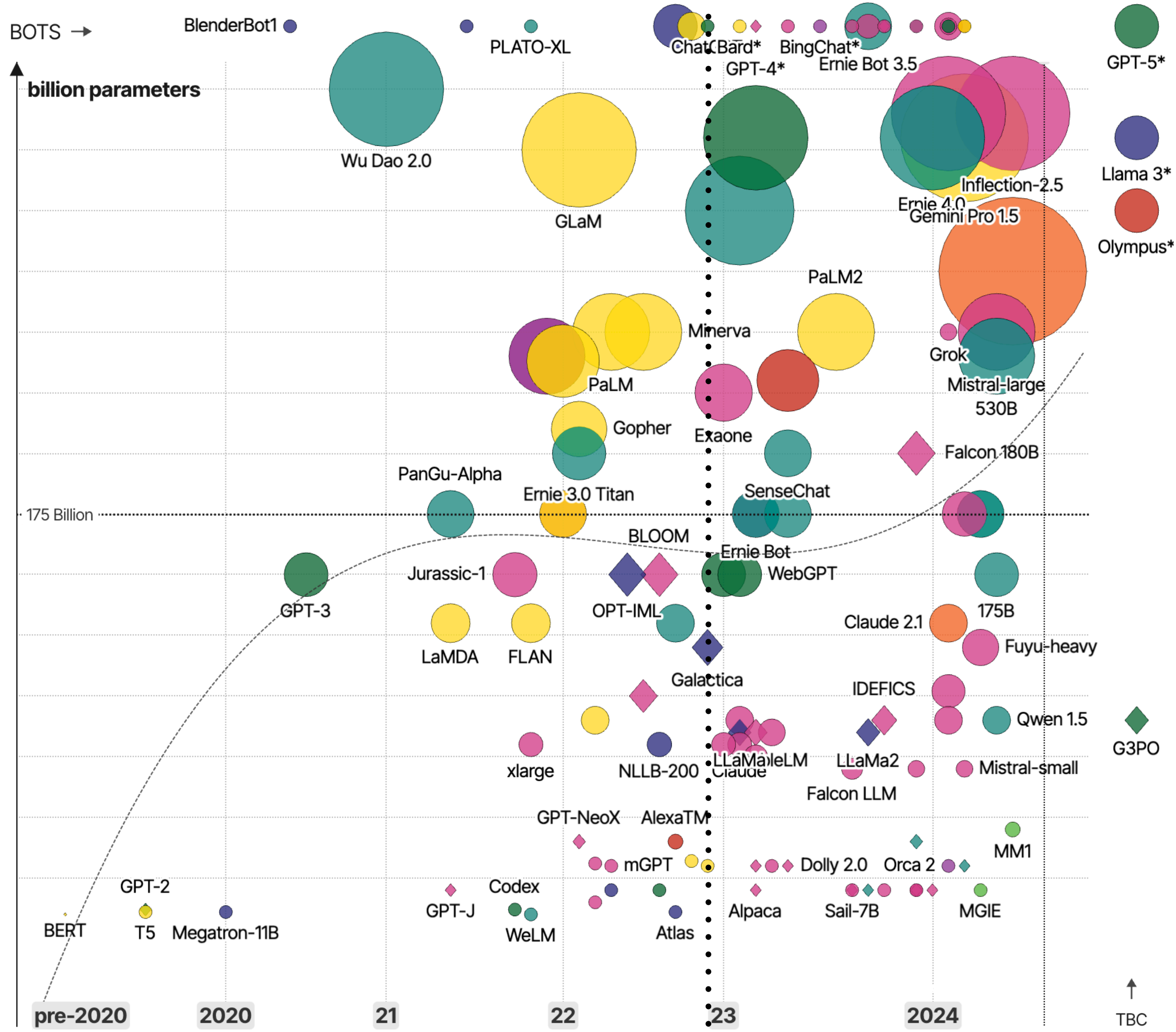


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Market Summary > NVIDIA Corp

125.83 USD

+ Follow

+121.82 (3,037.91%) ↑ past 5 years

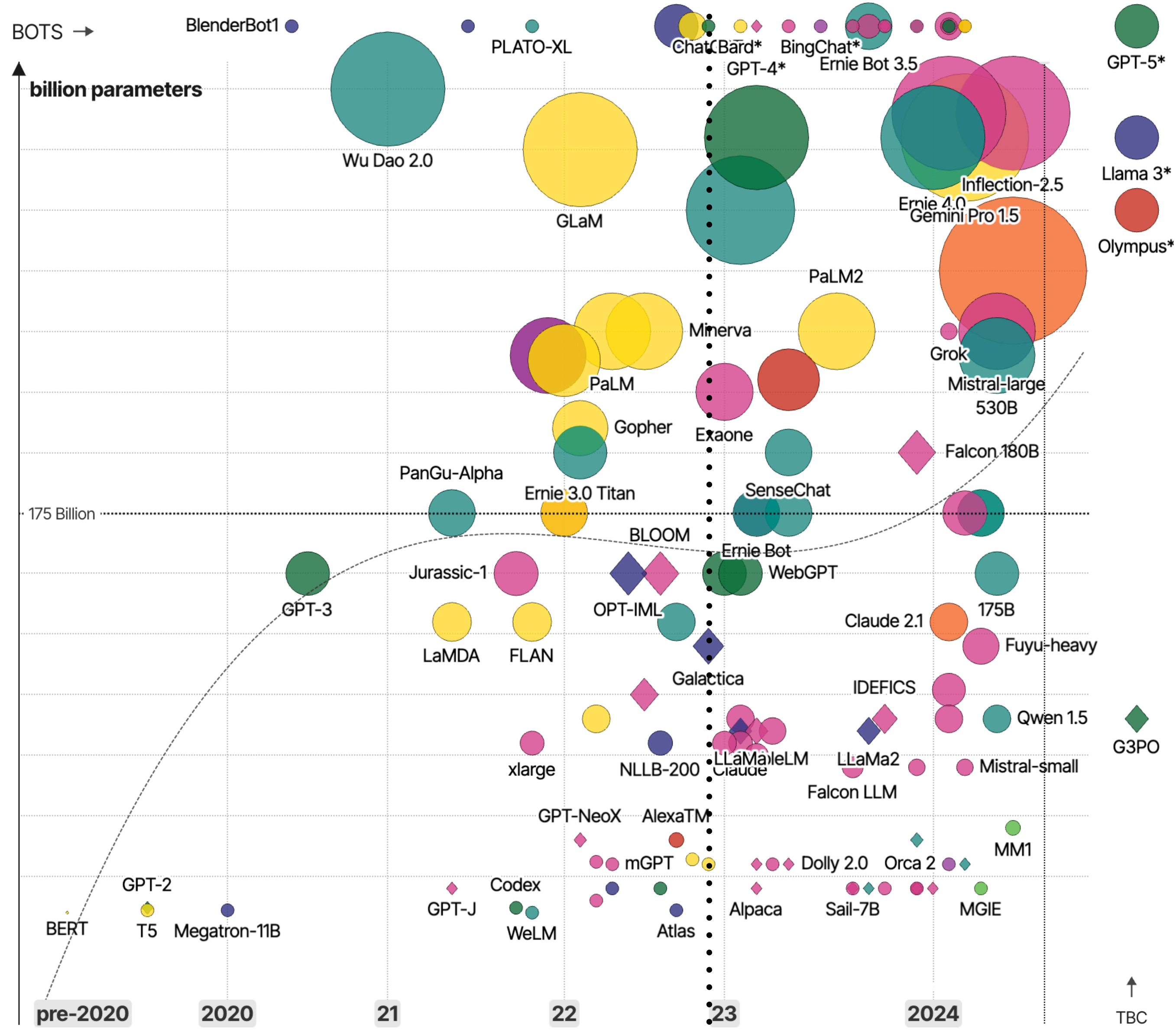
Closed: Jul 5, 8:00 PM EDT • Disclaimer

After hours 125.38 -0.45 (0.36%)

1D | 5D | 1M | 6M | YTD | 1Y | **5Y** | Max



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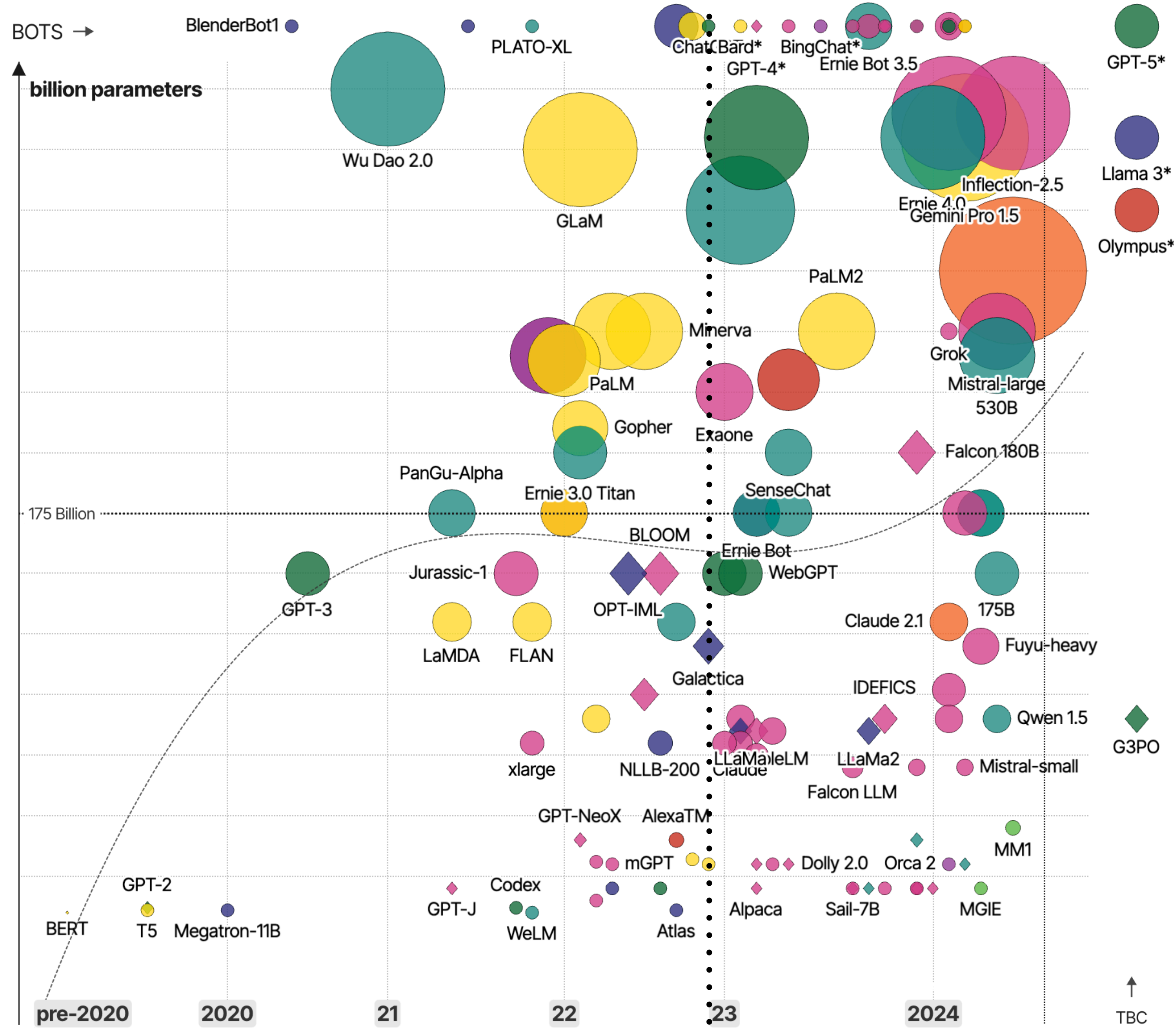
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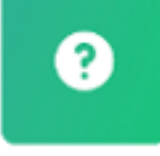






















"The more GPUs
you buy, The
more money
you save"





























- Jensen Huang
2017































Capabilities of ChatGPT

-  **Q&A**
Answer questions based on existing knowle...
-  **Grammar correction**
Corrects sentences into standard English.
-  **Advanced tweet classifier**
Advanced sentiment detection for a piece o...
-  **Explain code**
Explain a complicated piece of code.
-  **Summarize for a 2nd grader**
Translates difficult text into simpler concep...
-  **Natural language to OpenAI API**
Create code to call to the OpenAI API usin...
-  **Keywords**
Extract keywords from a block of text.
-  **Factual answering**
Guide the model towards factual answering ...
-  **Text to command**
Translate text into programmatic commands.
-  **English to other languages**
Translates English text into French, Spanish...
-  **Ad from product description**
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-  **SQL translate**
Translate natural language to SQL queries.
-  **TL;DR summarization**
Summarize text by adding a 'tl;dr:' to the en...
-  **Python bug fixer**
Find and fix bugs in source code.
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-  **Science fiction book list maker**
Create a list of items for a given topic.
-  **Calculate Time Complexity**
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Let's go



Summarize a research paper

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- Topic:

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- Topic:

Theory and Methods

Method

[Matrix Completion When Missing Is Not at Random and Its Applications in Causal Panel Data Models*](#) >

Jungjun Choi & Ming Yuan

Accepted author version posted online: 17 Jul 2024

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Matrix Completion When Missing Is ...
PDF

Can you write a summary of this paper?

- Use your own prompt:



The paper "Matrix Completion When Missing Is Not at Random and Its Applications in Causal Panel Data Models" by Jungjun Choi and Ming Yuan addresses the challenge of matrix completion when data entries are missing not at random (MNAR). Traditional matrix completion methods assume data is missing at random, which is often not the case in real-world applications.

Key Contributions and Methodology:

1. **Inferential Framework for MNAR Data:** The authors develop a framework to infer missing entries when the data is MNAR. This approach does not require strong signals and uses nuclear norm regularization for estimation.
2. **Subgroup Estimation:** They propose dividing missing entries into smaller groups and estimating each group separately. This method is shown to be effective even with weak signals, improving the accuracy of estimates compared to traditional methods that handle the entire matrix at once.
3. **Debiasing Technique:** To improve statistical inference, they introduce a debiasing technique that corrects the bias induced by nuclear norm regularization, ensuring that the proposed estimates are asymptotically normal.
4. **Application to Tick Size Pilot Program:** The framework is applied to the Tick Size Pilot Program, a study conducted by the SEC to evaluate the impact of widening the tick size on market quality. This program's data revealed significant heterogeneity across units and time, highlighting the limitations of traditional regression methods that assume invariant treatment effects.

Theoretical and Practical Implications:

- **Asymptotic Normality:** The authors demonstrate that their debiased estimator is asymptotically normal, providing a theoretical foundation for the reliability of their method.
- **Computational Efficiency:** By subgrouping missing entries, their approach balances computational cost and statistical efficiency, showing advantages over existing methods that estimate the entire matrix simultaneously.
- **Empirical Validation:** The application to the Tick Size Pilot Program data underscores the practical utility of their method, uncovering dynamics and heterogeneity in treatment effects that were previously unrecognized.

Conclusion:

The paper advances the field of matrix completion by offering a robust methodology for handling MNAR data, validated through both theoretical analysis and practical application. The proposed methods offer significant improvements in estimation accuracy and inferential power, particularly in complex panel data models like those found in the SEC's Tick Size Pilot Program.

The detailed exploration of various missing data patterns and the comprehensive theoretical underpinnings make this work a significant contribution to the statistical literature on matrix completion and causal inference in panel data models.

Step-by-step guide

Prompt: “What is the research question or objective of this paper?”

What is the research question or objective of this paper



The research question or objective of the paper "Matrix Completion When Missing Is Not at Random and Its Applications in Causal Panel Data Models" by Jungjun Choi and Ming Yuan is to develop an inferential framework for matrix completion in scenarios where data entries are missing not at random (MNAR). The objective is to provide accurate estimation and inference methods that do not rely on the strong signal assumptions typically required by traditional matrix completion techniques.

Specifically, the paper aims to:

1. Address the limitations of existing matrix completion methods by developing a technique that can handle MNAR data.
2. Introduce a subgrouping strategy to improve estimation accuracy and efficiency.
3. Propose a debiasing method to ensure the asymptotic normality of the estimators.
4. Apply the developed methodology to real-world data, exemplified by the Tick Size Pilot Program, to demonstrate its practical utility and effectiveness in uncovering treatment effects with significant heterogeneity over time and across units.

Overall, the paper seeks to bridge the gap between theoretical matrix completion techniques and their practical applications in causal panel data models, especially when data is MNAR.

Step-by-step guide

Prompt: “Summarize the methods used in this study.”

Summarize the methods used in this study.



The methods used in the study "Matrix Completion When Missing Is Not at Random and Its Applications in Causal Panel Data Models" by Jungjun Choi and Ming Yuan include several innovative techniques for handling matrix completion when data is missing not at random (MNAR). Here is a summary of the methods:

1. Nuclear Norm Regularization:

- **Estimation Framework:** The authors propose an inferential framework that leverages nuclear norm regularization to estimate missing entries in the matrix. This approach is based on the observation that a small number of missing entries relative to the panel size can be estimated well even when missing not at random.

2. Subgroup Estimation:

- **Subgrouping Strategy:** Instead of estimating the entire matrix at once, the authors divide the missing entries into smaller subgroups. Each subgroup is then estimated separately using nuclear norm regularization. This method improves estimation accuracy and efficiency, particularly in the presence of weak signals.
- **Estimation of Submatrices:** For each subgroup of missing entries, a submatrix is constructed and estimated using the nuclear norm penalization approach. The results from these submatrices are then aggregated to form the final estimate of the full matrix.

3. Debiasing Technique:

- **Bias Correction:** To improve the statistical properties of the estimators, a debiasing technique is introduced. After applying nuclear norm regularization, the bias induced by the penalty is corrected through an additional projection step.
- **Asymptotic Normality:** The debiased estimator is shown to be asymptotically normal, which ensures the reliability and interpretability of the inferential results.

4. Handling Different Missing Patterns:

- **Single Treated Period and Single Treated Unit:** The methods are tailored to handle different patterns of missing data, such as single treated periods or units, by appropriately splitting and estimating the missing entries.
- **General Block Missing Pattern:** For more complex block missing patterns, the subgrouping and estimation techniques are extended to handle larger numbers of missing entries efficiently.

5. Application to Tick Size Pilot Program:

- **Empirical Application:** The developed methodology is applied to the Tick Size Pilot Program data to evaluate the impact of widening the tick size on market quality. The application demonstrates how the proposed methods can uncover significant heterogeneity and dynamics in treatment effects over time and across different units.
- **Data and Model:** The authors use data from the Tick Size Pilot Program, including various control variables and liquidity measures. The model incorporates interactive fixed effects to capture the heterogeneity in treatment effects.

6. Statistical Inference:

- **Group-Averaged Treatment Effects:** The methods are used to estimate group-averaged treatment effects and their differences across different treatment groups and time periods.
- **Variance Estimation:** The variance of the estimators is calculated, and the asymptotic distribution of the treatment effect estimates is derived to enable robust statistical inference.

In summary, the methods used in this study combine nuclear norm regularization, subgroup estimation, debiasing techniques, and careful handling of different missing data patterns to provide a robust framework for matrix completion when data is MNAR. The empirical application to the Tick Size Pilot Program data showcases the practical utility and effectiveness of these methods in uncovering complex treatment effects in causal panel data models.

Step-by-step guide

Prompt: “What are the main findings of this paper?”

What are the main findings of this paper?



The main findings of the paper "Matrix Completion When Missing Is Not at Random and Its Applications in Causal Panel Data Models" by Jungjun Choi and Ming Yuan are as follows:

1. Effective Estimation with MNAR Data:

- **Framework for MNAR Data:** The authors develop a novel inferential framework for matrix completion that effectively handles cases where data entries are missing not at random (MNAR). This framework does not require strong signal assumptions, which are typically necessary in traditional methods.
- **Subgrouping and Estimation:** By dividing the missing entries into smaller subgroups and applying nuclear norm regularization to each subgroup, the proposed method achieves more accurate and efficient estimates compared to traditional methods that handle the entire matrix at once.

2. Debiasing and Asymptotic Normality:

- **Debiasing Technique:** The paper introduces a debiasing technique that corrects the bias induced by nuclear norm regularization, making the estimators asymptotically normal. This ensures the reliability of the inferential results.
- **Theoretical Validation:** The authors provide theoretical guarantees for the convergence rates and asymptotic normality of their estimators, even in the presence of weak signals.

3. Application to Tick Size Pilot Program:

- **Heterogeneity in Treatment Effects:** The application of the proposed methodology to the Tick Size Pilot Program reveals significant heterogeneity in treatment effects across different units and time periods. This finding challenges the assumptions made by traditional regression and difference-in-difference methods, which typically assume invariant treatment effects.
- **Dynamics of Treatment Effects:** The analysis uncovers intriguing dynamics in the treatment effects during the pilot program, providing deeper insights into the impact of widening the tick size on market quality.

4. Empirical and Practical Implications:

- **Improved Estimates:** The empirical results demonstrate that the proposed subgrouping and estimation approach performs better than traditional methods, particularly in scenarios with MNAR data.
- **Versatility of the Method:** The methods developed in the paper are versatile and can be applied to various causal panel data models beyond the Tick Size Pilot Program, making them broadly useful for real-world applications where data is often MNAR.

5. Computational Efficiency:

- **Trade-off Between Computation and Accuracy:** The subgrouping strategy not only improves the statistical accuracy of the estimates but also balances computational efficiency. The results suggest that while it may be computationally efficient to estimate all missing entries together, doing so can be statistically suboptimal compared to the proposed subgrouping method.

Conclusion:

The paper advances the field of matrix completion by providing a robust and theoretically sound framework for handling MNAR data. The proposed methods improve estimation accuracy and efficiency, offer reliable statistical inference, and are validated through an empirical application to the Tick Size Pilot Program, revealing complex dynamics and heterogeneity in treatment effects. These findings have important implications for both theoretical research and practical applications in causal inference and matrix completion.

Step-by-step guide

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Step-by-step guide

Prompt: “What are the **three** main findings of this paper?”

What are the three main findings of this paper?



The three main findings of the paper "Matrix Completion When Missing Is Not at Random and Its Applications in Causal Panel Data Models" by Jungjun Choi and Ming Yuan are:

1. Inferential Framework for MNAR Data:

The paper develops a robust inferential framework for matrix completion that effectively handles data missing not at random (MNAR). This framework leverages nuclear norm regularization and a novel subgrouping strategy, allowing for accurate estimation even with weak signals and complex missing data patterns. This method improves upon traditional matrix completion techniques that assume data is missing at random, making it more applicable to real-world scenarios.

2. Debiasing Technique and Asymptotic Normality:

The authors introduce a debiasing technique that corrects the bias induced by nuclear norm regularization, resulting in estimators that are asymptotically normal. This advancement ensures that the inferential results are statistically reliable and can be used for robust statistical inference. The theoretical validation of the convergence rates and asymptotic normality provides a strong foundation for the proposed method's effectiveness.

3. Empirical Application to Tick Size Pilot Program:

Applying the proposed methodology to the Tick Size Pilot Program data reveals significant heterogeneity and dynamics in treatment effects across different units and time periods. This finding challenges the assumptions made by traditional regression and difference-in-difference methods, which typically assume invariant treatment effects. The analysis demonstrates the practical utility of the proposed methods in uncovering complex treatment effects and provides deeper insights into the impact of widening the tick size on market quality.

Step-by-step guide

Prompt: “What are the implications of the findings?”

What are the implications of the findings



The implications of the findings from the paper "Matrix Completion When Missing Is Not at Random and Its Applications in Causal Panel Data Models" by Jungjun Choi and Ming Yuan are significant for both theoretical research and practical applications in statistics and causal inference. Here are the key implications:

1. Improved Methodologies for MNAR Data:

- **Broader Applicability:** The developed framework for handling data missing not at random (MNAR) expands the applicability of matrix completion techniques to a wider range of real-world problems where the missingness mechanism is non-random.
- **Enhanced Accuracy:** The improved estimation accuracy and efficiency provided by the subgrouping strategy and debiasing technique mean that researchers and practitioners can achieve more reliable results when dealing with incomplete data.
- **Robust Statistical Inference:** The asymptotic normality of the debiased estimators ensures that inferential procedures based on these methods are statistically sound, leading to more robust conclusions in empirical studies.

2. Impact on Causal Inference in Panel Data Models:

- **Revealing Heterogeneity:** The ability to uncover significant heterogeneity and dynamics in treatment effects across units and time periods has profound implications for causal inference. It highlights the need for models that can account for such heterogeneity, moving beyond traditional methods that assume invariant treatment effects.
- **Policy and Program Evaluation:** For policymakers and analysts, the application to the Tick Size Pilot Program demonstrates how the proposed methods can provide deeper insights into the effects of interventions. This can lead to more informed decisions and better-designed policies by capturing the true variability and dynamics of treatment effects.

3. Computational Efficiency and Practical Use:

- **Balancing Computational Cost and Statistical Efficiency:** The proposed subgrouping method strikes a balance between computational efficiency and statistical accuracy. This makes it feasible to apply these advanced techniques to large-scale datasets without prohibitive computational costs.
- **Adoption in Diverse Fields:** The methods can be adopted in various fields beyond finance, such as healthcare, marketing, and social sciences, where MNAR data is common. This broadens the impact of the research and provides tools for more accurate data analysis across disciplines.

Overall Implications:

The findings of this paper have the potential to reshape the way researchers and practitioners approach matrix completion and causal inference in the presence of MNAR data. By providing a robust, accurate, and computationally feasible framework, the study paves the way for more reliable empirical research and better-informed decision-making in diverse applications.

Step-by-step guide

Prompt: “What limitations did the authors mention?”

What limitations did the authors mention



The authors mention several limitations in their study "Matrix Completion When Missing Is Not at Random and Its Applications in Causal Panel Data Models." Here are the key limitations highlighted:

1. Assumption of Sub-Gaussian Noise:

- The noise matrix E in their model is assumed to follow a sub-Gaussian distribution. This assumption, while common in matrix completion literature, may not hold in all real-world applications where noise can exhibit different statistical properties.

2. Independence of Noise Terms:

- The independence assumption of the noise terms ϵ_{it} is another limitation. In many practical situations, noise terms can be correlated, and the model does not account for this dependency. The authors acknowledge that allowing for dependency in noise is challenging and is left for future research.

3. Extension to Heteroskedasticity:

- While the paper briefly discusses the extension of their theory to the case of heteroskedastic noise in the supplement, the primary focus remains on homoskedastic noise. This may limit the applicability of their methods in scenarios with varying noise levels.

4. Computational Trade-offs:

- The subgrouping strategy, while improving statistical efficiency, introduces a trade-off between computational cost and estimation accuracy. Estimating missing entries in smaller subgroups can be more computationally intensive compared to estimating the full matrix at once.

5. Specific Missing Patterns:

- The methods are designed to handle specific missing patterns such as block missing patterns and staggered adoption. The performance and applicability of the methods in other, more irregular missing patterns are not extensively discussed or tested.

6. Dependence on Incoherence Condition:

- The theoretical results rely on the incoherence condition of the singular vectors of the low-rank matrix M . This condition requires the singular vectors to be delocalized, which might not be satisfied in all applications, potentially limiting the method's effectiveness.

7. Empirical Application Focus:

- The empirical validation is primarily focused on the Tick Size Pilot Program. While this provides a concrete example of the method's utility, the generalizability of the results to other datasets and contexts may need further empirical exploration.

8. Leave-One-Out Technique:

- The proof strategy is based on the leave-one-out technique, which may not easily extend to scenarios with stronger dependencies in the data. The authors suggest this as an area for future research to develop more robust proof techniques that can handle dependent noise structures.

By acknowledging these limitations, the authors provide a clear direction for future research to address these challenges and further improve the robustness and applicability of their methods.

Write an outline for a manuscript

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- Outline provides a foundation, improves efficiency, and ensures clarity.

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- Topic:

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- Topic:

Theory and Methods



Method

[Matrix Completion When Missing Is Not at Random and Its Applications in Causal Panel Data Models*](#) >

Jungjun Choi & Ming Yuan

Accepted author version posted online: 17 Jul 2024

Write an outline for a manuscript

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- Try your own prompt:

Can you write an outline for the paper titled "Matrix Completion When Missing Is Not at Random and Its Applications in Causal Panel Data Models"



Certainly! Here's a detailed outline for the paper titled "Matrix Completion When Missing Is Not at Random and Its Applications in Causal Panel Data Models":

An outline from ChatGPT

An outline from ChatGPT

I. Introduction

1. Background and Motivation

- Importance of matrix completion in data science.
- Challenges posed by missing data in various applications.
- Significance of addressing missing data not at random (MNAR) in matrix completion.
- Relevance to causal panel data models.

2. Objectives and Contributions

- Develop a novel matrix completion method for MNAR scenarios.
- Apply this method to improve causal inference in panel data models.
- Demonstrate the effectiveness through theoretical analysis and empirical studies.

3. Paper Organization

- Outline the structure of the paper.

II. Related Work

1. Matrix Completion

- Overview of matrix completion methods (MCAR, MAR, MNAR).
- State-of-the-art techniques for MNAR matrix completion.

2. Causal Inference in Panel Data Models

- Brief overview of causal panel data models.
- Challenges due to missing data in causal inference.

3. Intersection of Matrix Completion and Causal Inference

- Previous work combining these fields.
- Gaps in the current literature.

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III. Methodology

1. Problem Formulation

- Define the problem of matrix completion when data is MNAR.
- Mathematical formulation and assumptions.

2. Proposed Matrix Completion Method

- Detailed description of the novel method.
- Theoretical foundation and algorithms.

3. Integration with Causal Panel Data Models

- Approach to incorporate matrix completion in causal inference.
- Adjustments and extensions to standard models.

IV. Theoretical Analysis

1. Consistency and Convergence

- Proof of consistency and convergence for the proposed matrix completion method.
- Conditions under which the method performs optimally.

2. Bias and Variance Analysis

- Examination of the bias and variance properties.
- Comparison with existing methods.

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V. Empirical Studies

1. Simulation Studies

- Design of simulation experiments.
- Results demonstrating the performance of the proposed method.

2. Real-World Applications

- Case studies from various fields (e.g., economics, social sciences).
- Application to causal panel data models with real datasets.
- Comparison with other methods.

VI. Applications in Causal Panel Data Models

1. Setup and Assumptions

- Specifics of the panel data models used in the applications.
- Assumptions and setup for causal inference.

2. Impact of Matrix Completion

- Analysis of how matrix completion improves causal inference.
- Case studies showing the practical benefits.

3. Discussion of Results

- Interpretation of findings.
- Implications for future research and practice.

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VII. Discussion

1. Strengths and Limitations

- Critical evaluation of the proposed method.
- Limitations and potential areas for improvement.

2. Broader Implications

- Broader impacts on matrix completion and causal inference fields.
- Possible extensions to other types of data and models.

VIII. Conclusion

1. Summary of Contributions

- Recap of key contributions and findings.

2. Future Directions

- Suggestions for future research.
- Potential applications in other domains.

IX. References

- Comprehensive list of all cited literature.

X. Appendices

1. Technical Proofs

- Detailed proofs of theoretical results.

2. Additional Experimental Results

- Supplementary figures and tables.
- Additional details on the simulation studies and real-world applications.

Grammar correction

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In recent years, the importance of statistical methods in research have been widely recognized. This methods provides researchers with tools to analyze data and draw meaningful conclusions. One of the most commonly used technique is regression analysis, which allows to understand the relationship between variables. However, many researchers fails to properly apply this techniques, leading to inaccurate results. It is essential for researchers to have a strong understanding of statistical principles and to use appropriate software for their analyses.

Grammar correction

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Sure, here is the corrected paragraph with changes in bold:

"In recent years, the importance of statistical methods in research **has** been widely recognized. **These** methods **provide** researchers with tools to analyze data and draw meaningful conclusions. One of the most commonly used **techniques** is regression analysis, which allows **researchers** to understand the relationship between variables. However, many researchers **fail** to properly apply **these** techniques, leading to inaccurate results. It is essential for researchers to have a strong understanding of statistical principles and to use appropriate software for their analyses."

Generate LaTeX code for tables

Detailed prompts

Generate LaTeX code for a table with the following specifications:

- The table should have 10 rows and 5 columns.
- The first column should be colored light gray.
- The third column should be colored light blue.
- The first row should be a header row spanning all columns, with the text 'Header Spanning All Columns.'
- The second column should have merged cells for specific rows.
- Include row names for all rows.
- Add a multi-row cell spanning 3 rows in the last column.
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Table 1: Complex Table Example with Advanced Features

Header Spanning All Columns				
Row Name	Column 1	Column 2	Column 3	Column 4
Row 1	Data 1.1	Merged	Data 1.3	Multi-row Cell
Row 2	Data 2.1		Data 2.3	
Row 3	Data 3.1		Data 3.3	
Row 4	Data 4.1	Merged	Data 4.3	Data 4.4
Row 5	Data 5.1		Data 5.3	Data 5.4
Row 6	Data 6.1	Merged	Data 6.3	Multi-row Cell
Row 7	Data 7.1		Data 7.3	
Row 8	Data 8.1		Data 8.3	
Row 9	Data 9.1	Merged	Data 9.3	Data 9.4
Row 10	Data 10.1	Merged	Data 10.3	Data 10.4
Footer Row Spanning All Columns				

Generate LaTeX code for tables

Example tables

Dataset	Method/ d' =	1	2	3	4
Banknote	PCA	15.6094	6.2737	1.9278	
	SPCA	15.0516	7.3182	1.5511	
	SRCA	13.2273	5.4120	1.1257	
Power	PCA	227.6291	56.0524	23.4302	3.0244
Plant	SPCA	151.7555	102.3262	44.3802	41.0081
	SRCA	151.3426	52.9769	20.0871	4.0775
User	PCA	0.1952	0.1281	0.0749	0.0306
Knowledge	SPCA	0.1478	0.0898	0.0465	0.0145
	SRCA	0.1479	0.0904	0.0462	0.0144
Ecoli	PCA	0.0761	0.0334	0.0219	0.0057
	SPCA	0.0462	0.0351	0.0187	0.0122
	SRCA	0.0758	0.0337	0.0168	0.0058
Concrete	PCA	6.8783	4.8345	3.5462	2.5046
	SPCA	5.5565	4.2051	3.1664	2.0173
	SRCA	5.5573	4.2173	3.1842	2.0389
Leaf	PCA	0.0245	0.0126	0.0062	0.0040
	SPCA	0.0163	0.0100	0.0073	0.0047
	SRCA	0.0164	0.0101	0.0062	0.0037
Climate	PCA	1.4486	1.3846	1.3167	1.2447
	SPCA	1.4265	1.3637	1.2921	1.2224
	SRCA	1.3863	1.3081	1.2278	1.1525

Table I.1: Out-of-sample mean square error (MSE) table for different experiments.

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	SRCA	151.3426	52.9769	20.0871	4.0775
	PCA	0.1952	0.1281	0.0749	0.0306
User	SPCA	0.1478	0.0898	0.0465	0.0145
Knowledge	SRCA	0.1479	0.0904	0.0462	0.0144
	PCA	0.0761	0.0334	0.0219	0.0057
	SPCA	0.0462	0.0351	0.0187	0.0122
Ecoli	SRCA	0.0758	0.0337	0.0168	0.0058
	PCA	6.8783	4.8345	3.5462	2.5046
	SPCA	5.5565	4.2051	3.1664	2.0173
Concrete	SRCA	5.5573	4.2173	3.1842	2.0389
	PCA	0.0245	0.0126	0.0062	0.0040
	SPCA	0.0163	0.0100	0.0073	0.0047
Leaf	SRCA	0.0164	0.0101	0.0062	0.0037
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	SRCA	13.2273	5.4120	1.1257	
Power	PCA	227.6291	56.0524	23.4302	3.0244
Plant	SPCA	151.7555	102.3262	44.3802	41.0081
	SRCA	151.3426	52.9769	20.0871	4.0775
	PCA	0.1952	0.1281	0.0749	0.0306
User	SPCA	0.1478	0.0898	0.0465	0.0145
Knowledge	SRCA	0.1479	0.0904	0.0462	0.0144
	PCA	0.0761	0.0334	0.0219	0.0057
	SPCA	0.0462	0.0351	0.0187	0.0122
Ecoli	SRCA	0.0758	0.0337	0.0168	0.0058
	PCA	6.8783	4.8345	3.5462	2.5046
	SPCA	5.5565	4.2051	3.1664	2.0173
Concrete	SRCA	5.5573	4.2173	3.1842	2.0389
	PCA	0.0245	0.0126	0.0062	0.0040
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Generate Latex Code for this table.



Here is the LaTeX code to generate the table from the provided image:

Generate LaTeX code for tables

Example tables

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Table 2: Out-of-sample mean square error (MSE) table for different experiments.

Generate LaTeX code for tables

Example tables



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LaTeX Transformer

By MistyBorn 

Converts PDF, handwriting, typed content etc. into LaTeX

Generate LaTeX code for tables

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Generate LaTeX code for plots

Detailed prompts

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Detailed prompts

Generate LaTeX code for a multipanel plot with the following specifications:

Generate LaTeX code for plots

Detailed prompts

Generate LaTeX code for a multipanel plot with the following specifications:

- The document should include a multipanel plot with 4 panels arranged in a 2x2 grid.

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Here is the LaTeX code for a multipanel plot with the specified requirements:

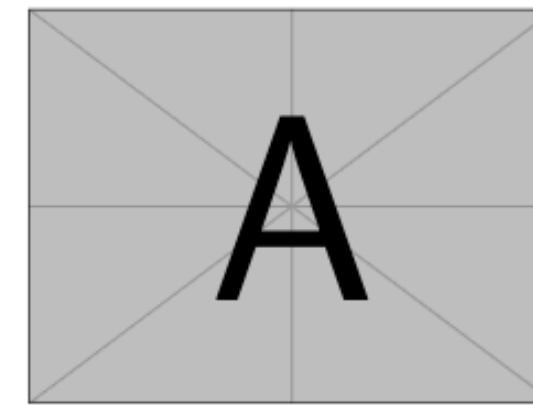
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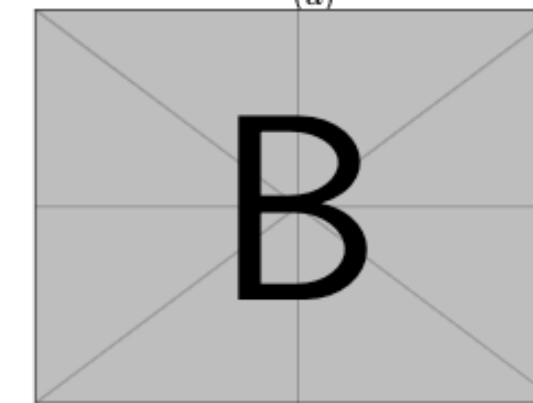
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Main Title: Multipanel Plot



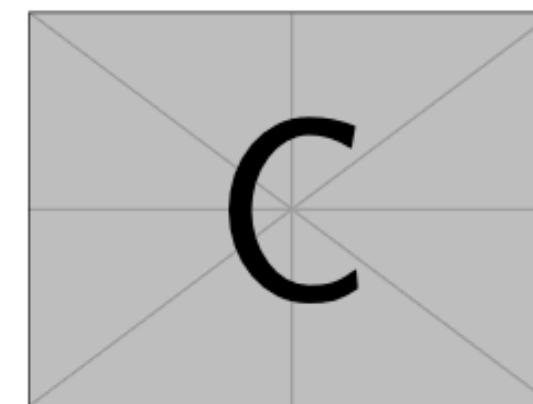
(a) Plot (a) Title

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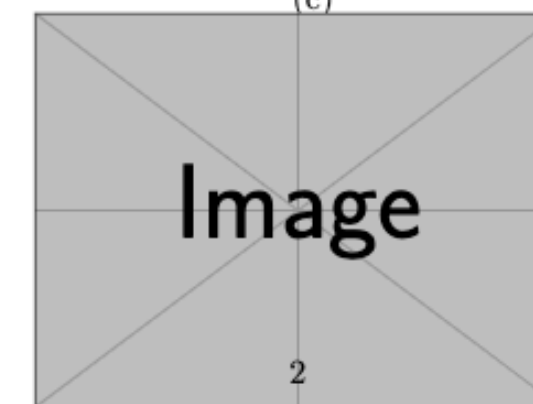
(c) Plot (b) Title

(b)



(e) Plot (c) Title

(c)



(g) Plot (d) Title

(d)

Figure 1: Multipanel plot showing different data sets



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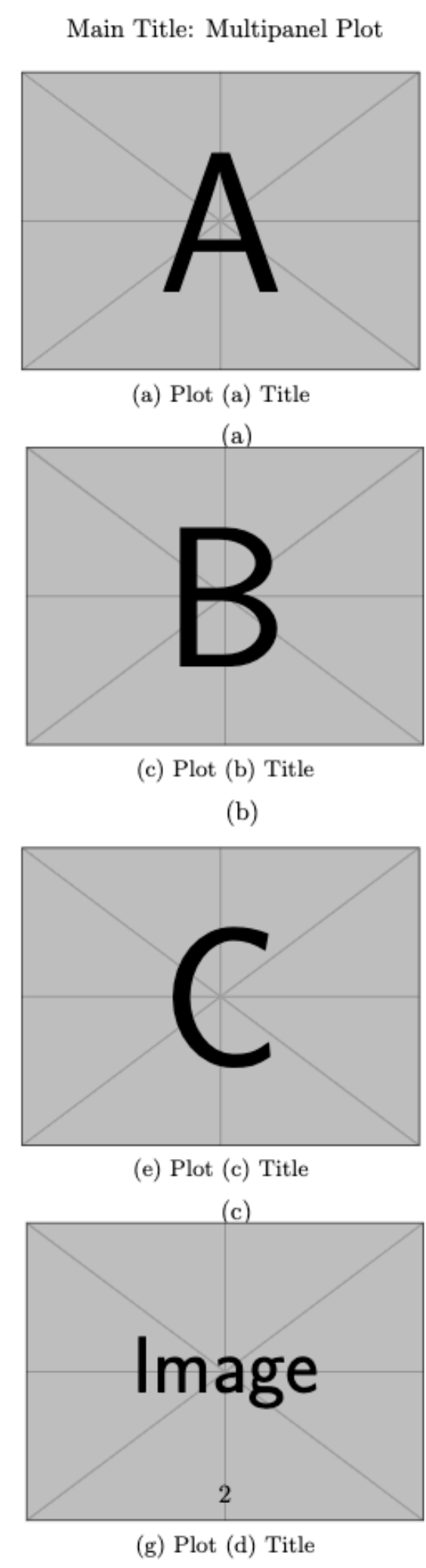


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Generate LaTeX code for plots

Detailed prompts

The document should include a multipanel plot with 4 panels arranged in a 2x2 grid.
Each panel should have a distinct plot labeled as (a), (b), (c), and (d) in the top left corner of each panel.
The multipanel plot should have a main title.
Each panel should have an individual title above the plot.
Ensure the panels are evenly spaced and aligned.
Add a caption below the multipanel plot with the text 'Multipanel plot showing different data sets'.
Include a label for referencing the multipanel plot in the document.
Ensure the code is structured and well-commented for readability



Here's the LaTeX code for creating a multipanel plot with the specified requirements:



LaTeX Transformer


By MistyBorn ʘ

Converts PDF, handwriting, typed content etc. into LaTeX

Generate LaTeX code for plots

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The document should include a multipanel plot with 4 panels arranged in a 2x2 grid. Each panel should have a distinct plot labeled as (a), (b), (c), and (d) in the top left corner of each panel. The multipanel plot should have a main title. Each panel should have an individual title above the plot. Ensure the panels are evenly spaced and aligned. Add a caption below the multipanel plot with the text 'Multipanel plot showing different data sets'. Include a label for referencing the multipanel plot in the document. Ensure the code is structured and well-commented for readability

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LaTeX Transformer

By MistyBorn 8

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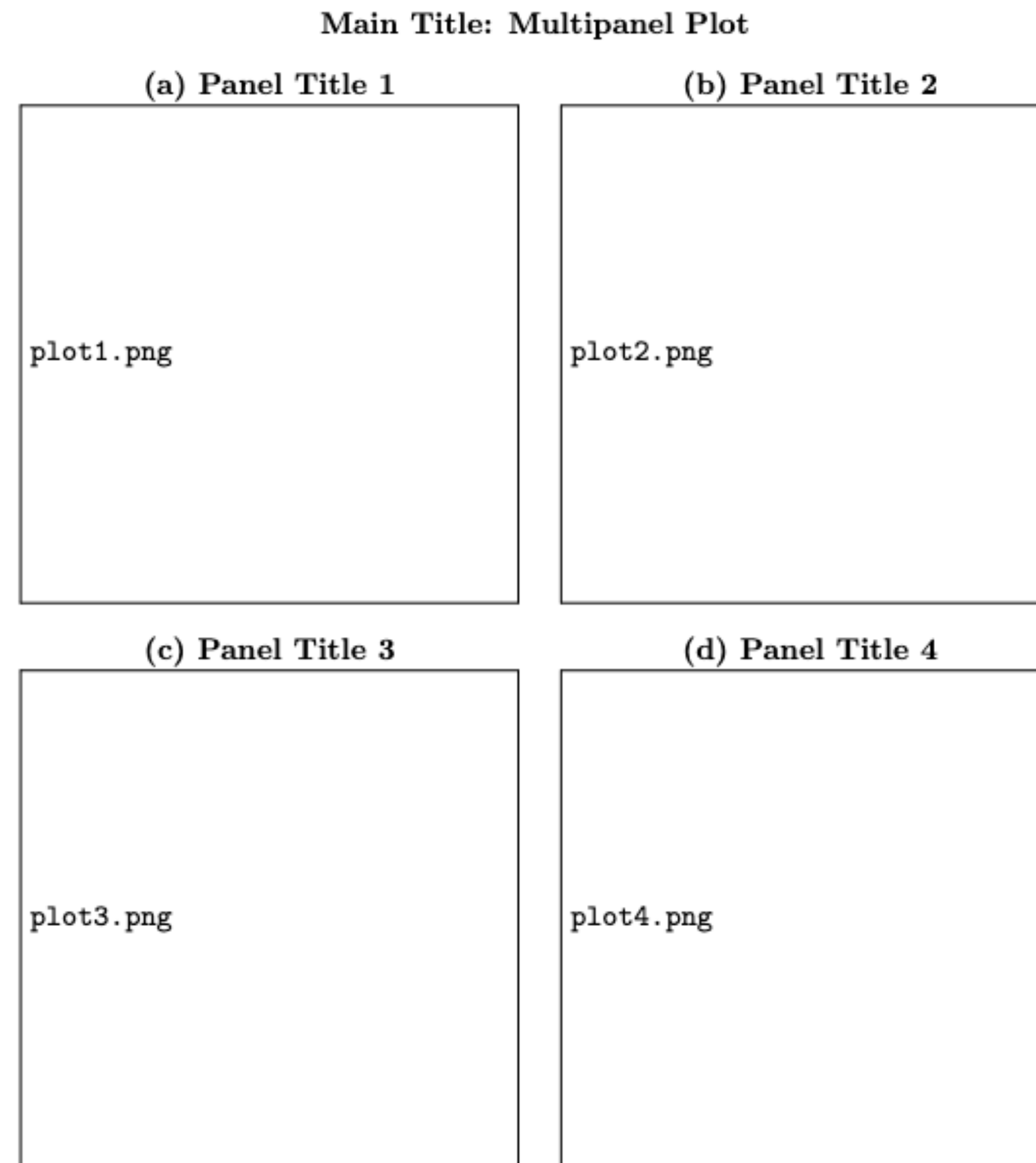


Figure 1: Multipanel plot showing different data sets.

Generate LaTeX code for plots

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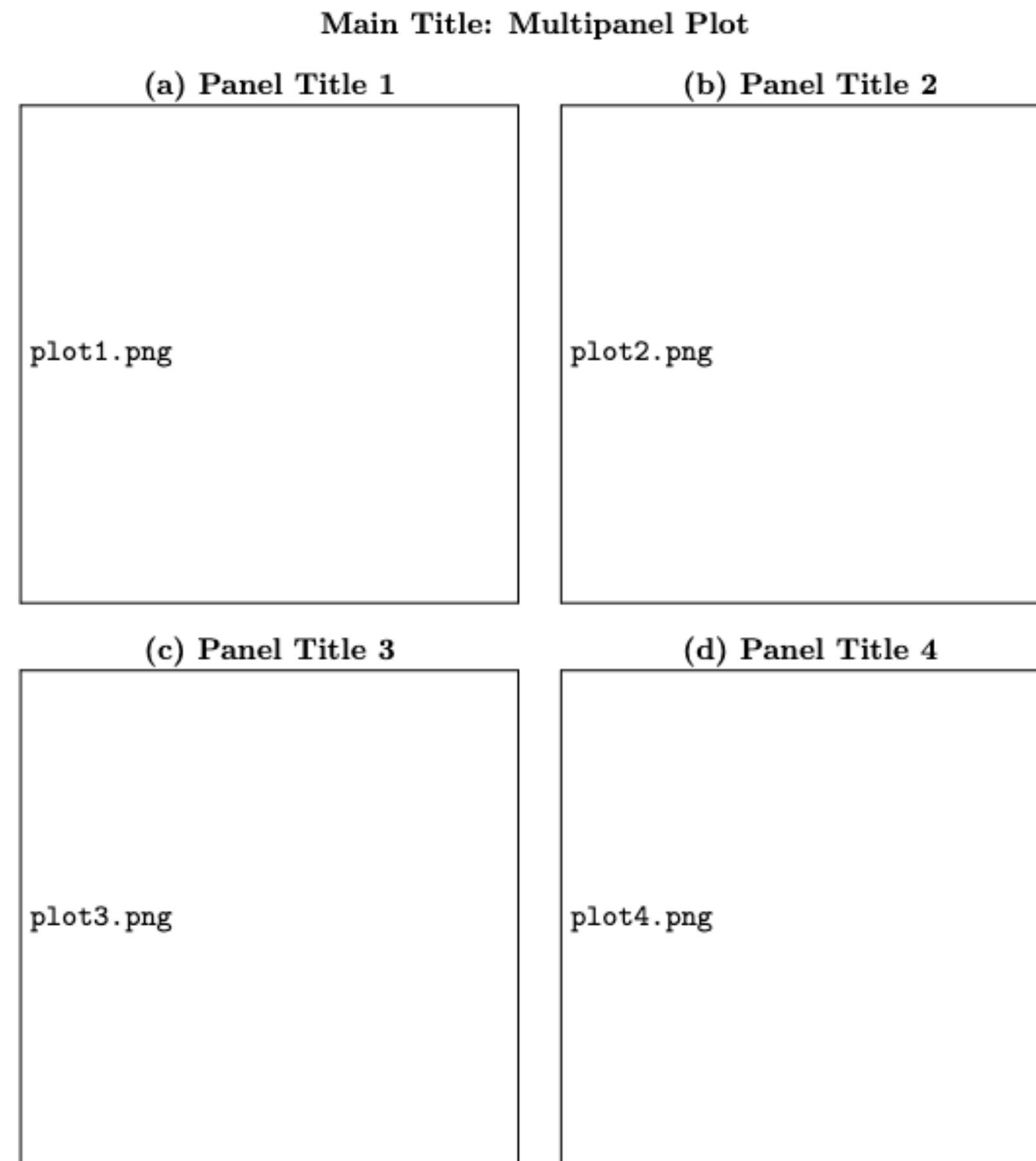
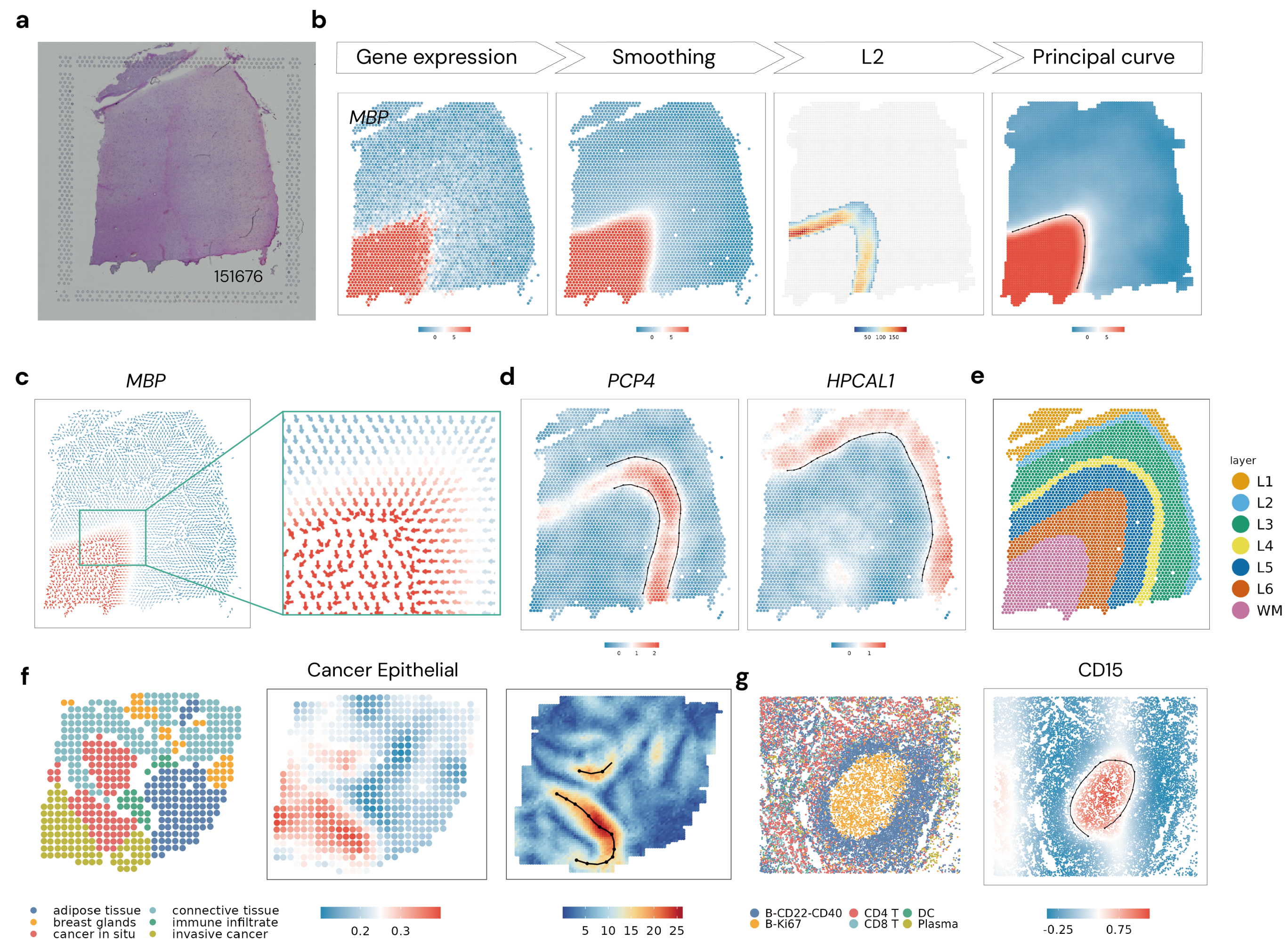


Figure 1: Multipanel plot showing different data sets.



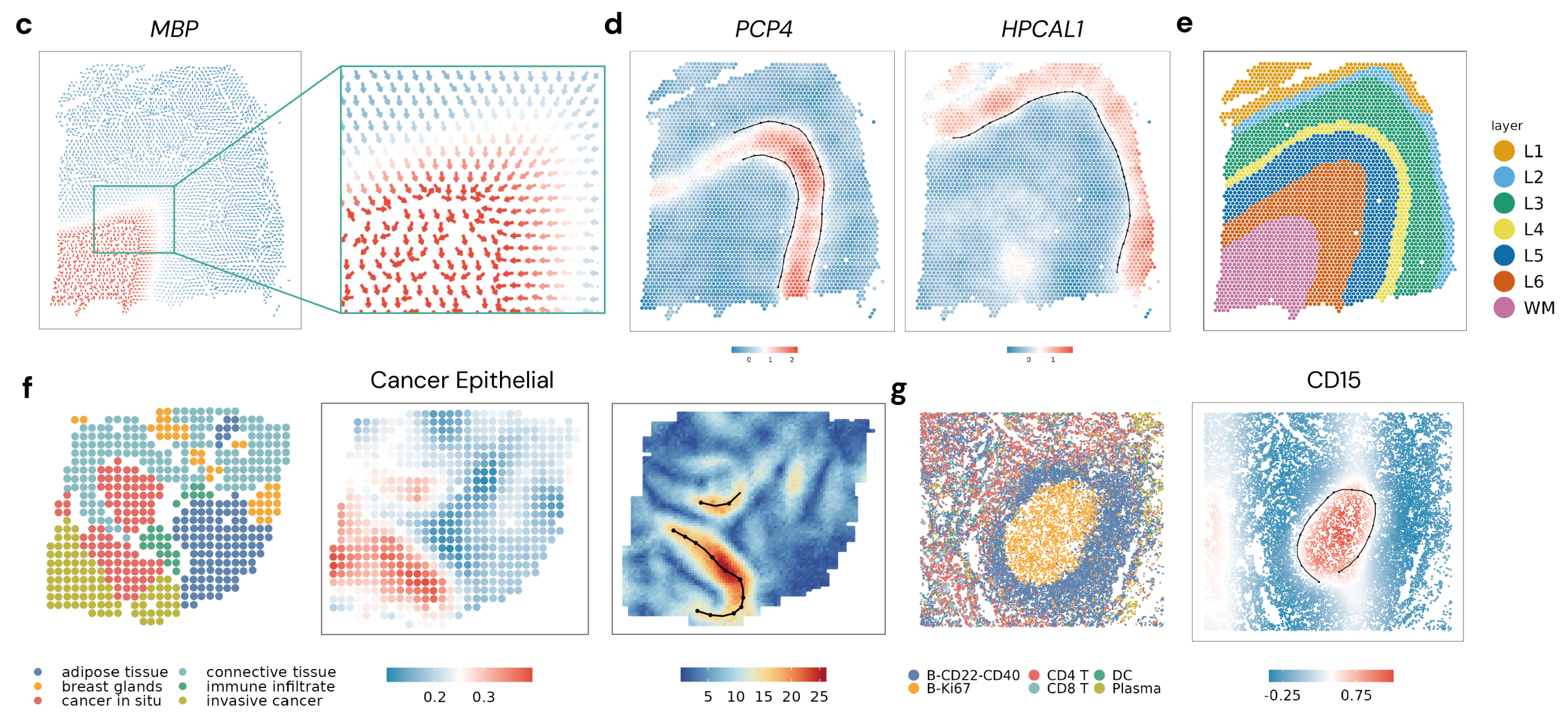
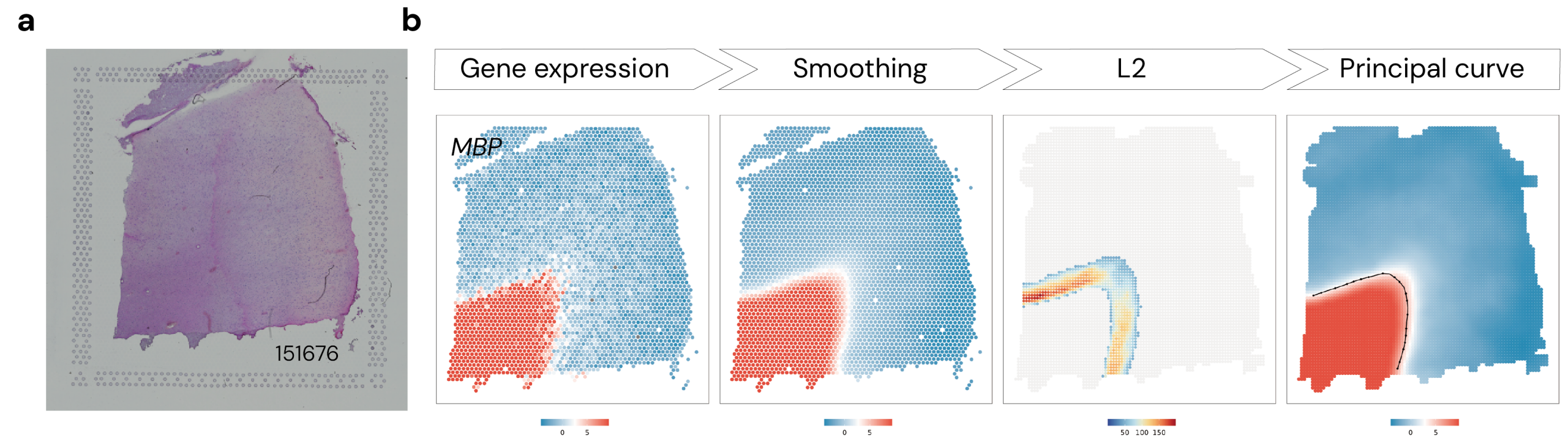
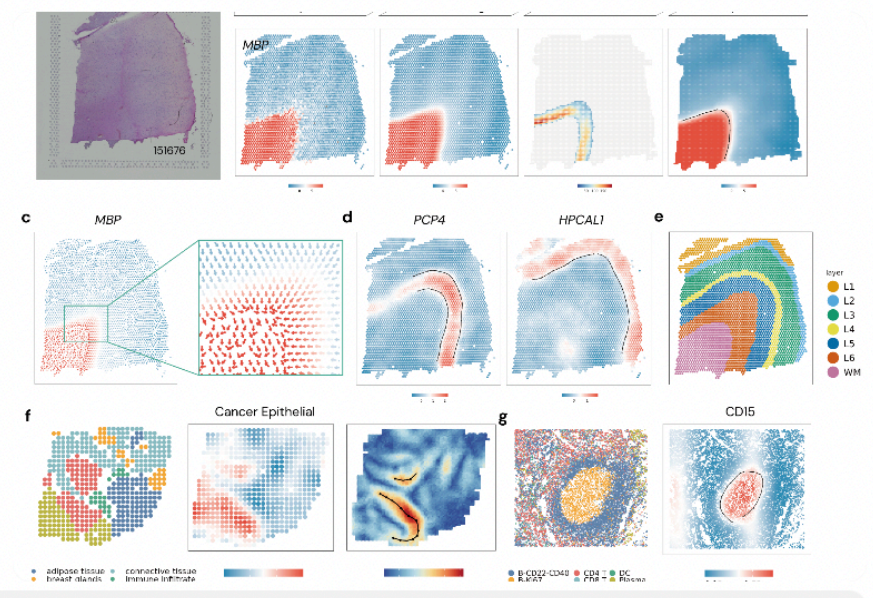
Generate LaTeX code for plots

Example plots



Generate LaTeX code for plots

Example plots

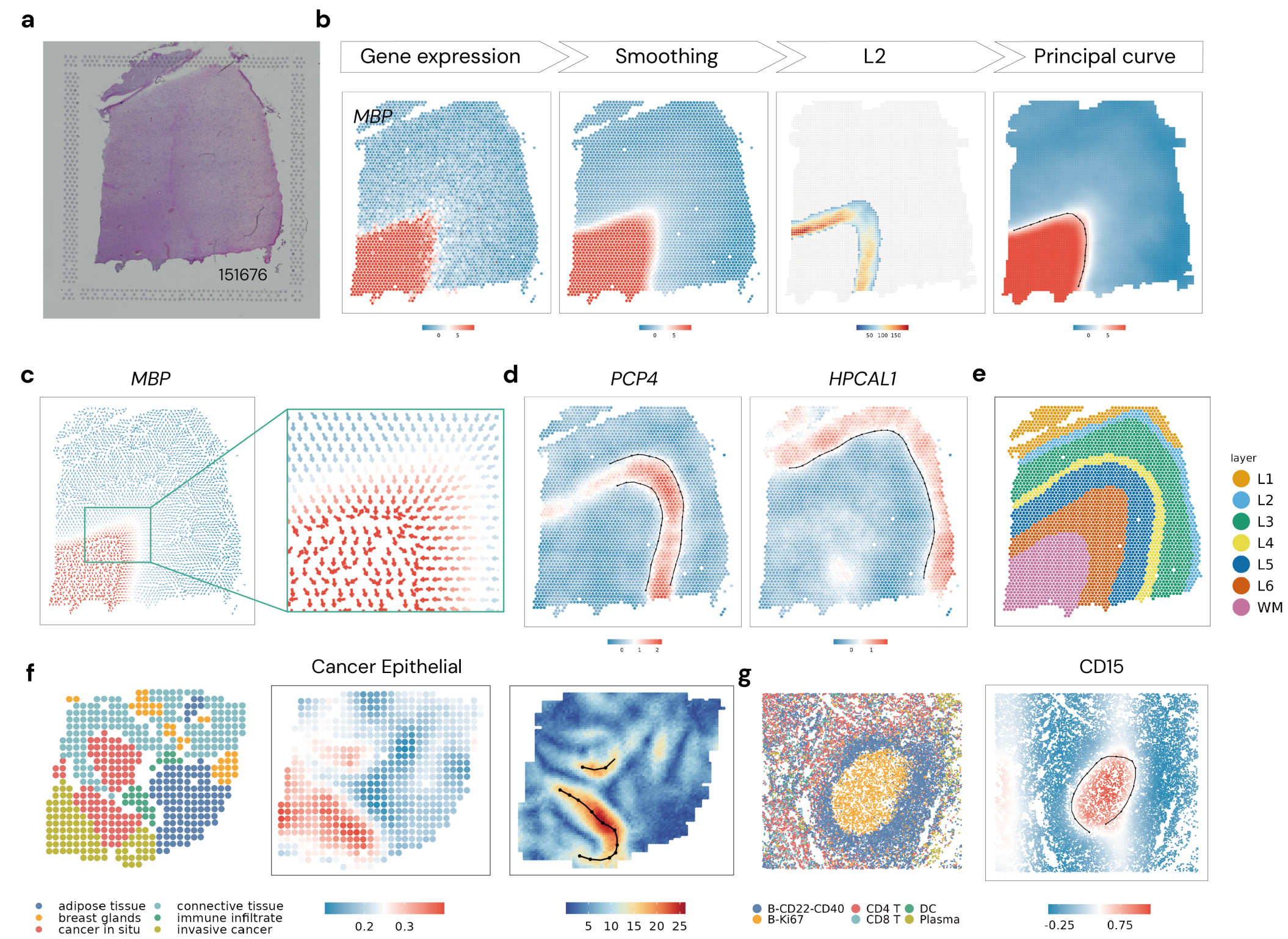


Generate latex code to make a multipanel plot like the one in this figure

To create a multipanel plot like the one in the provided figure using LaTeX, you can use the `\subfigure` package for arranging multiple images. The LaTeX code below demonstrates how to structure this:

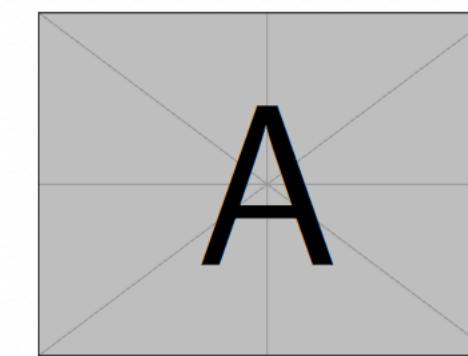
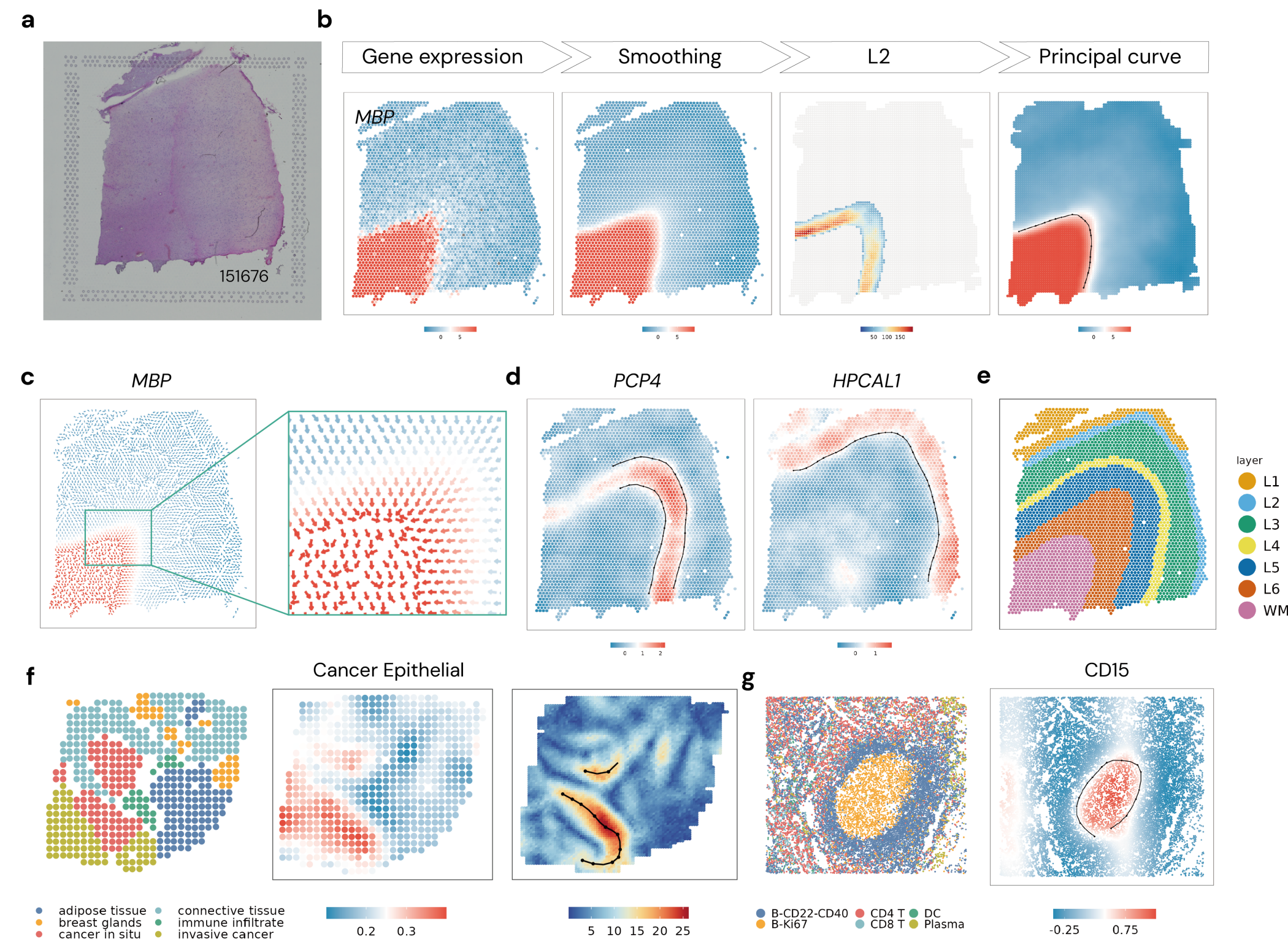
Generate LaTeX code for plots

Example plots

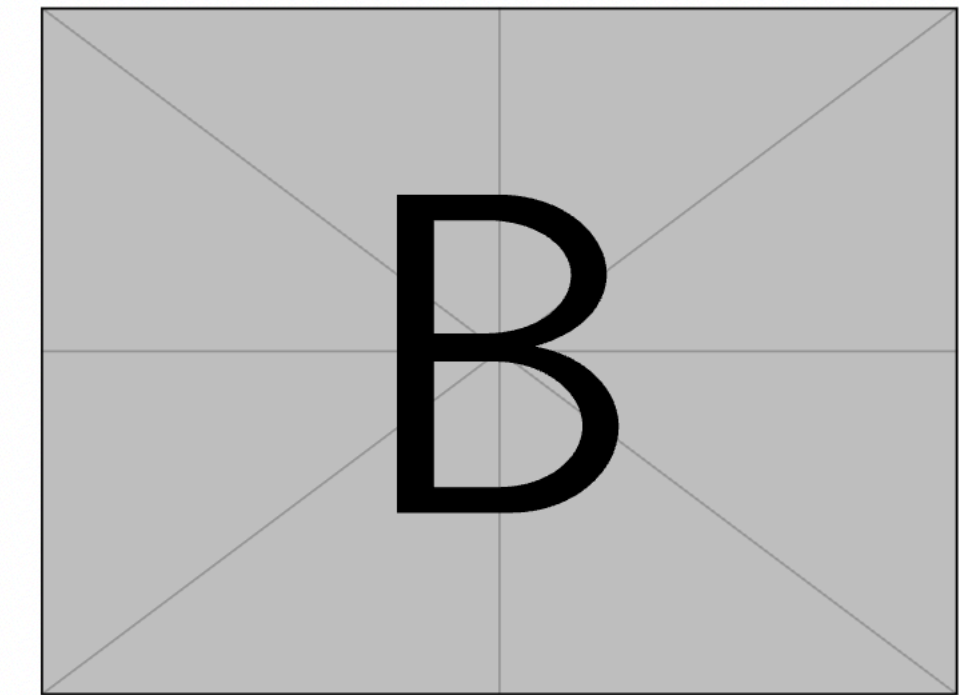


Generate LaTeX code for plots

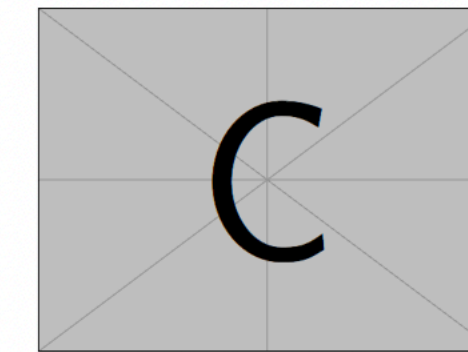
Example plots



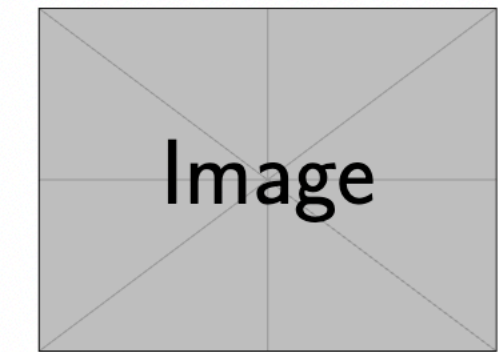
(a) a



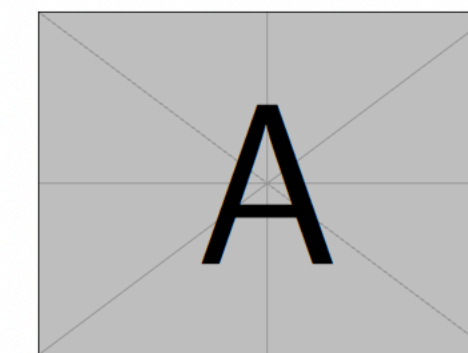
(b) b



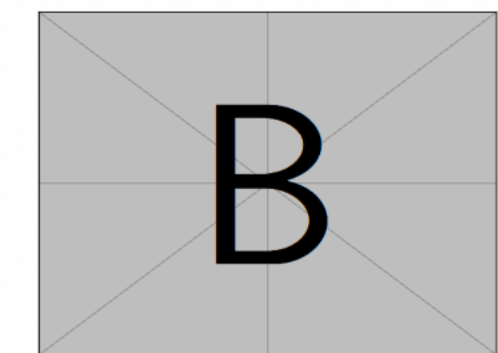
(c) c



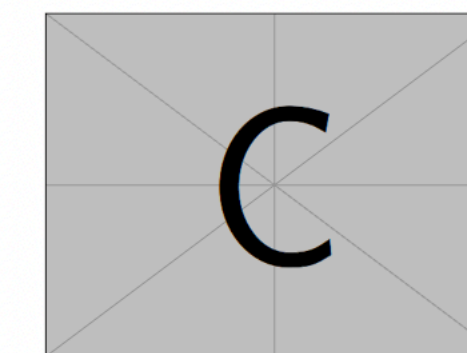
(d) d



(e) e



(f) f

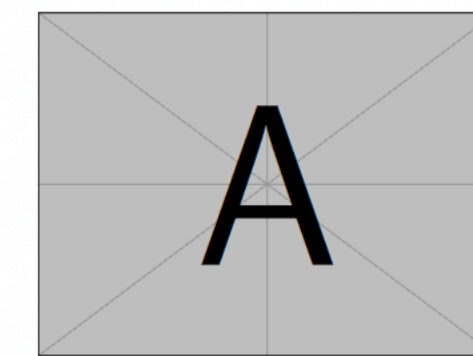
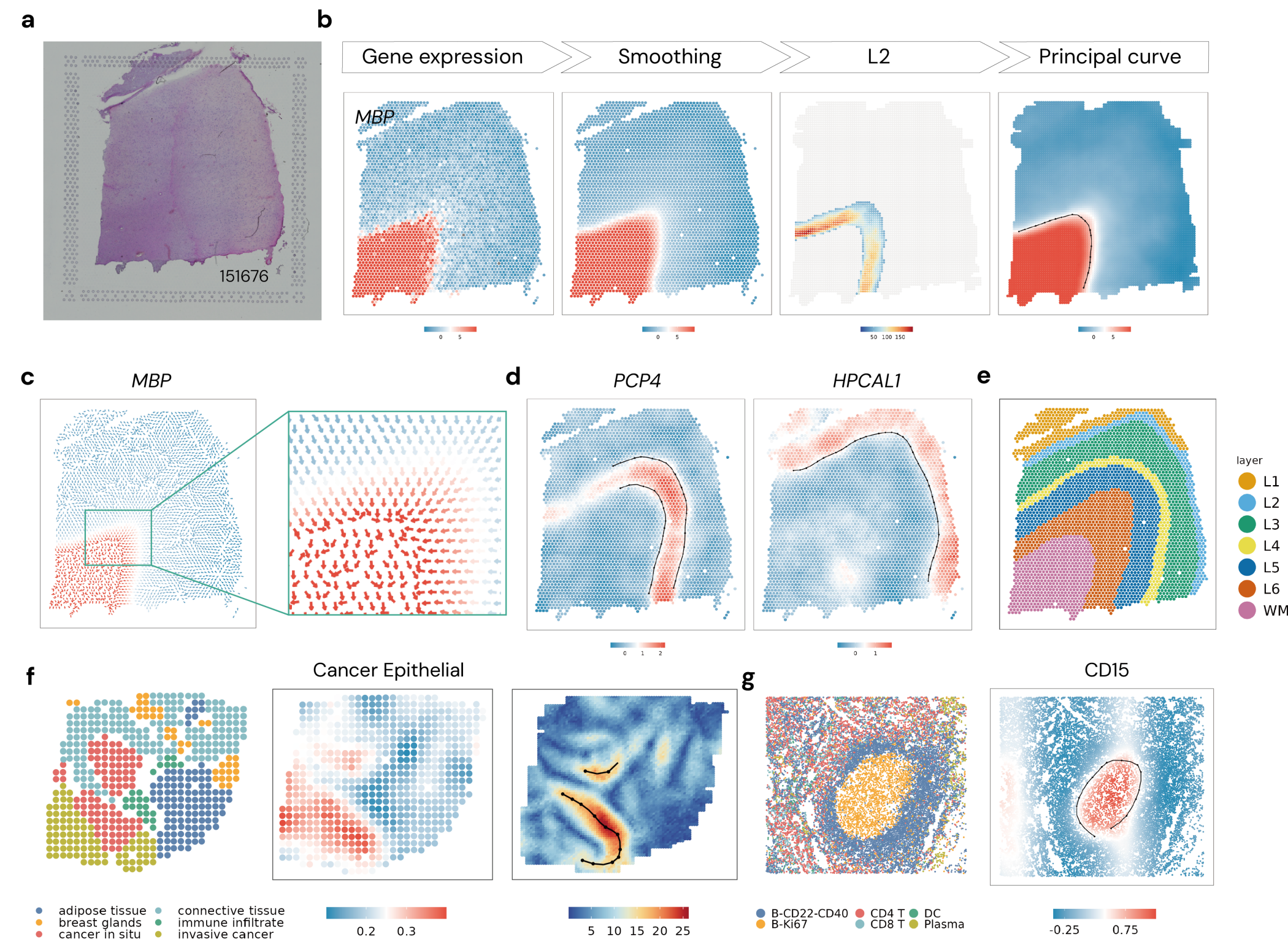


(g) g

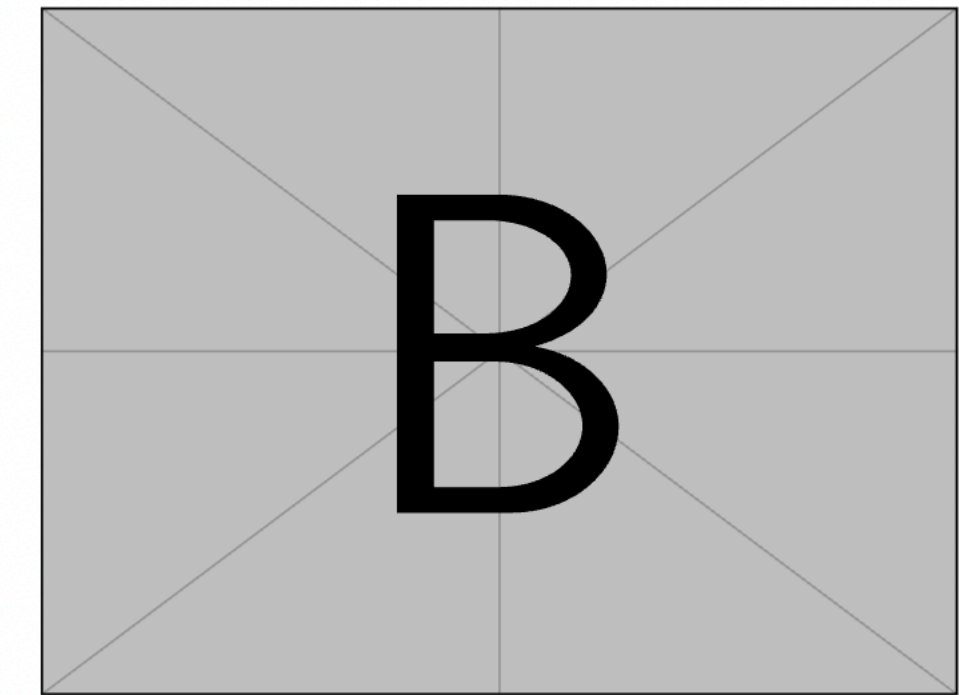
Figure 1: Multipanel plot with subfigures a to g using example images in Overleaf.

Generate LaTeX code for plots

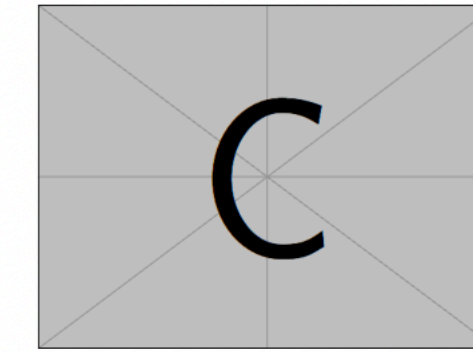
Example plots



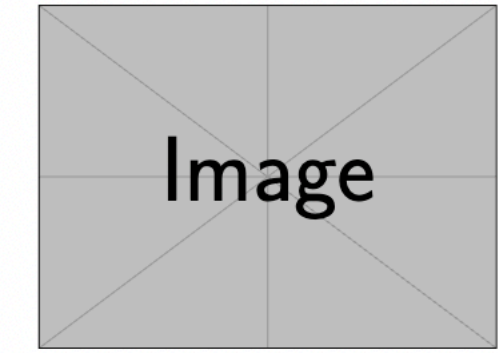
(a) a



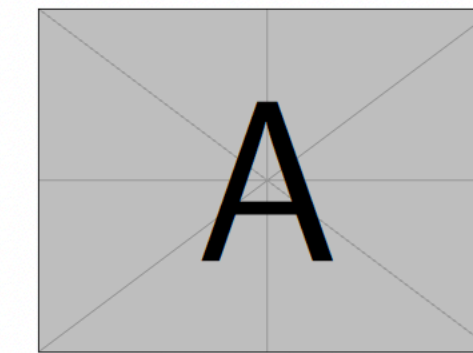
(b) b



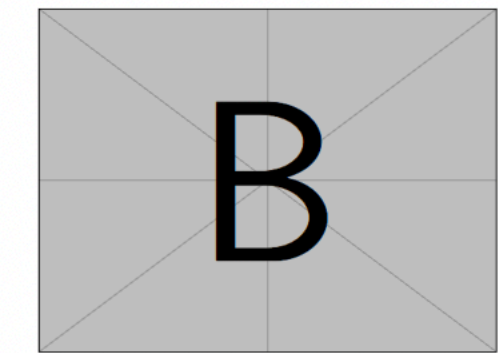
(c) c



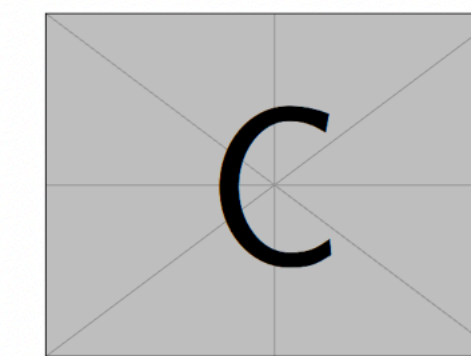
(d) d



(e) e



(f) f

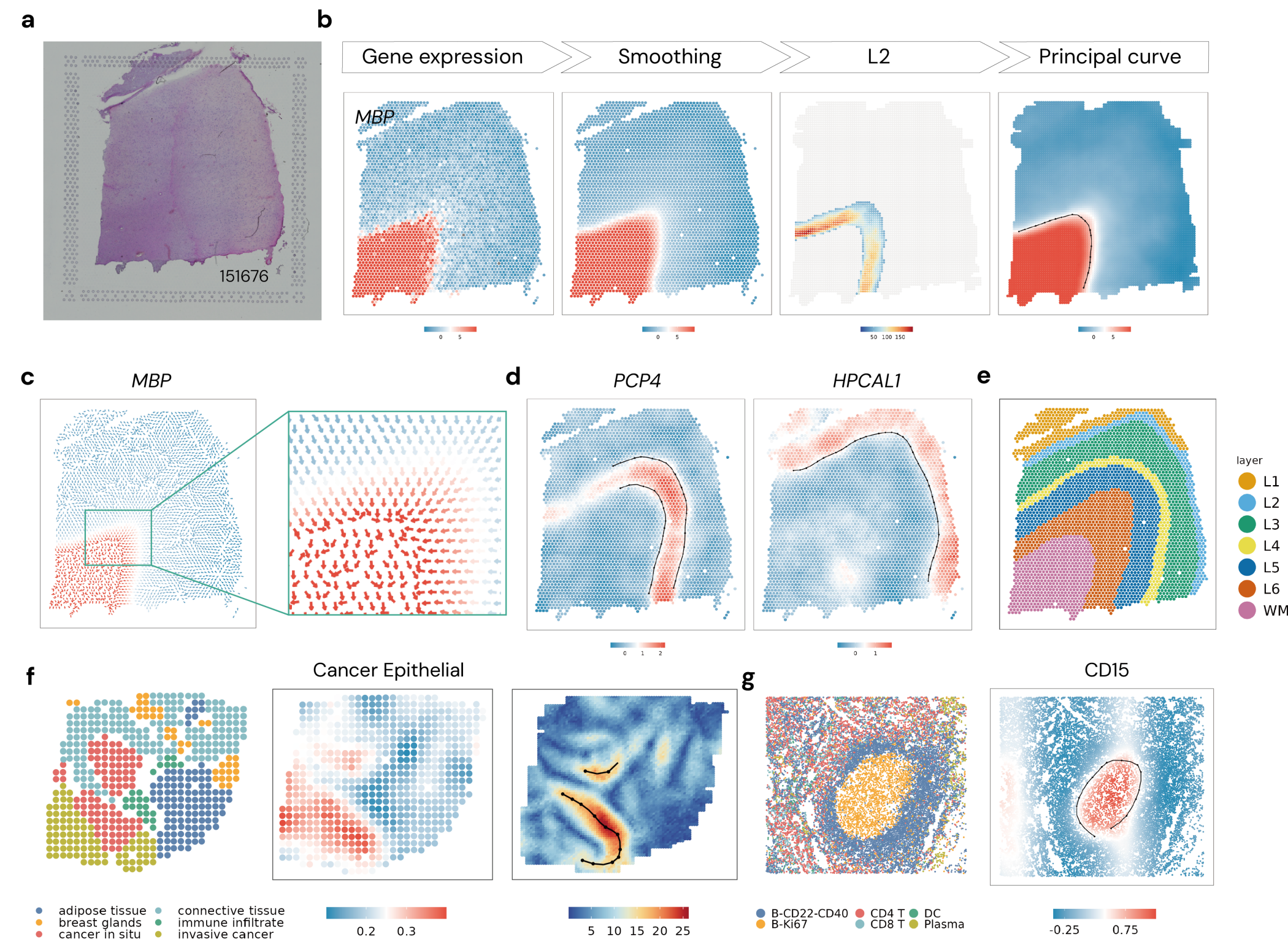


(g) g

Figure 1: Multipanel plot with subfigures a to g using example images in Overleaf.

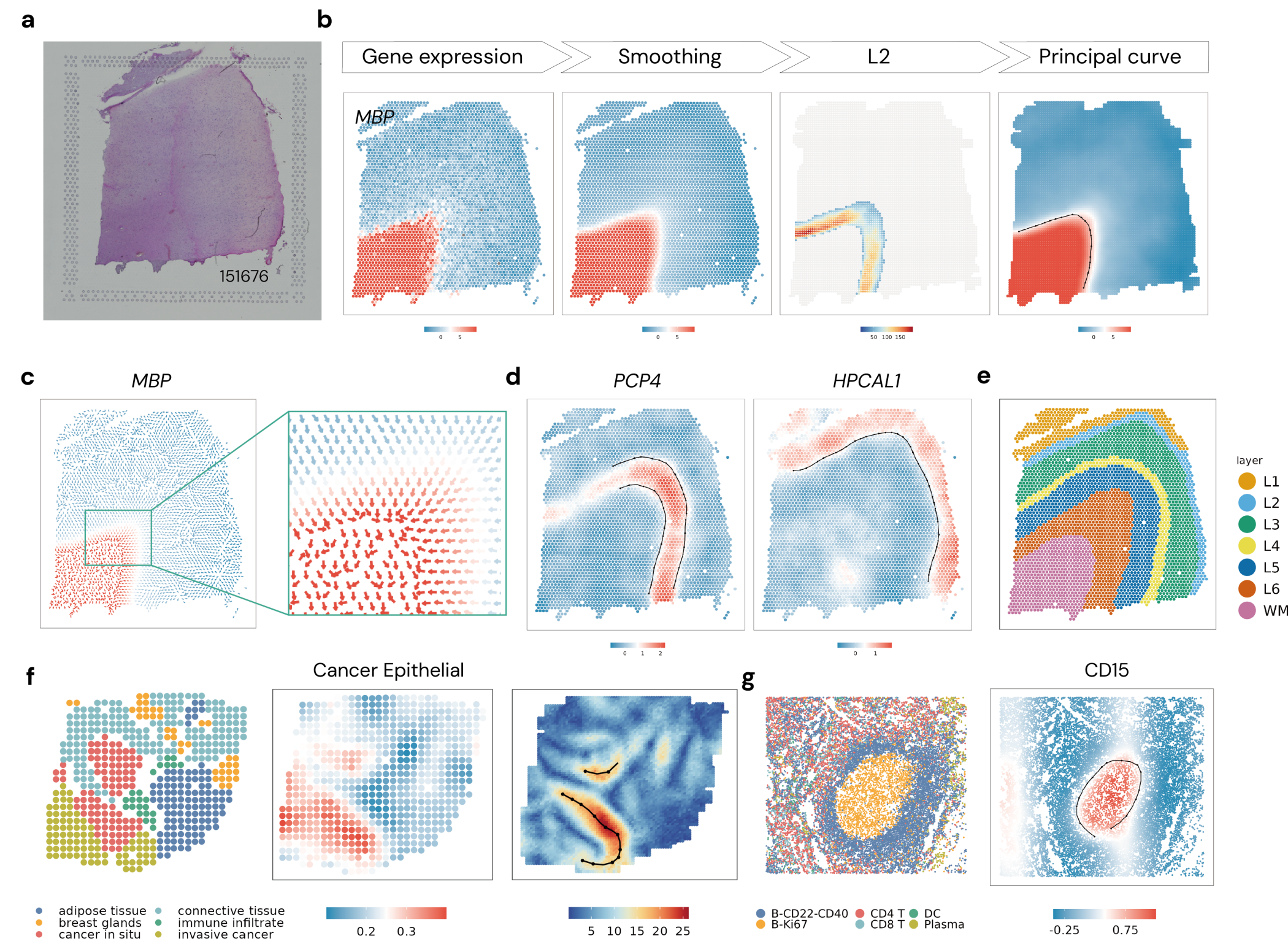
Generate LaTeX code for plots

Example plots



Generate LaTeX code for plots

Example plots



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Example plots

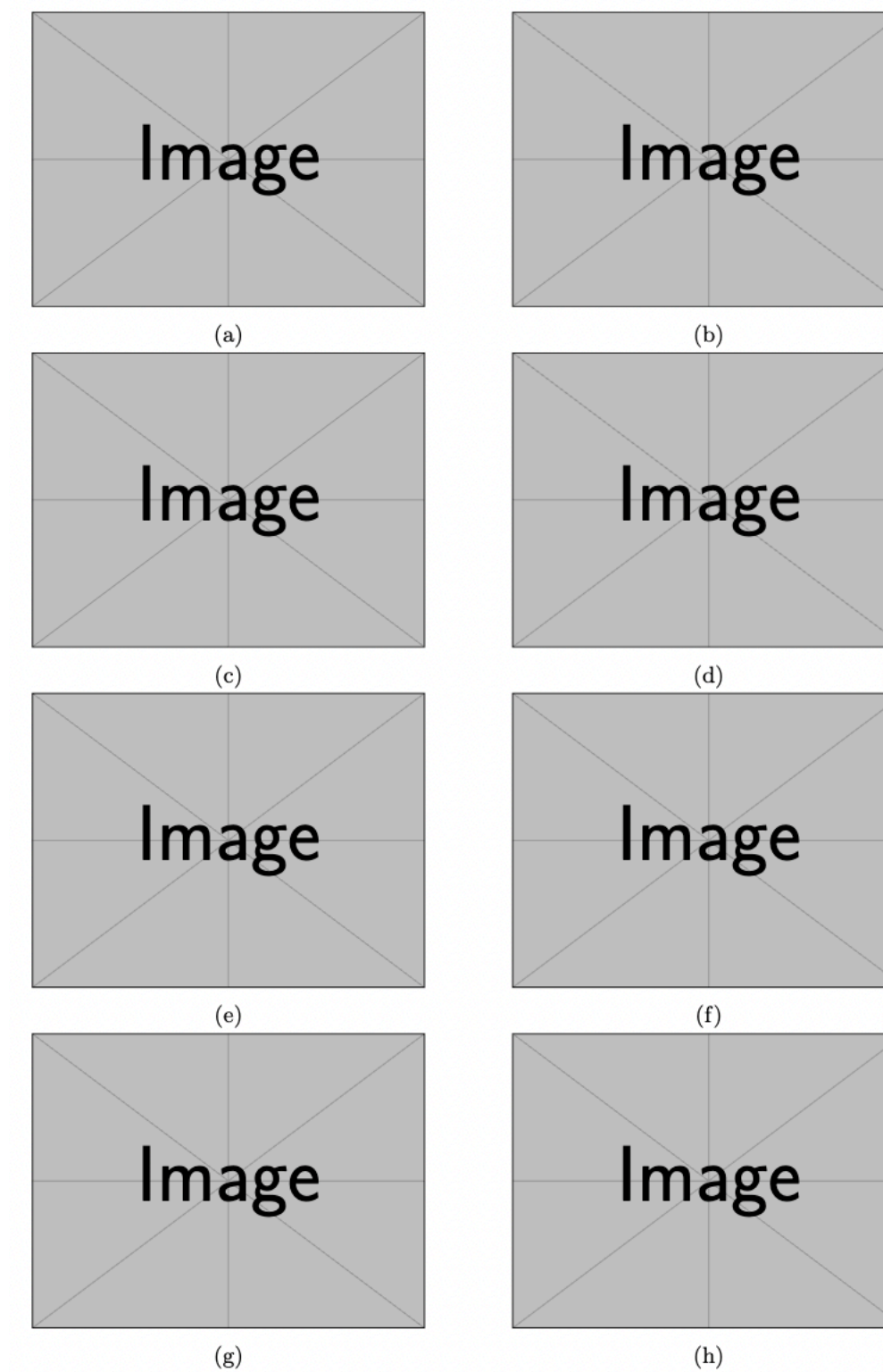
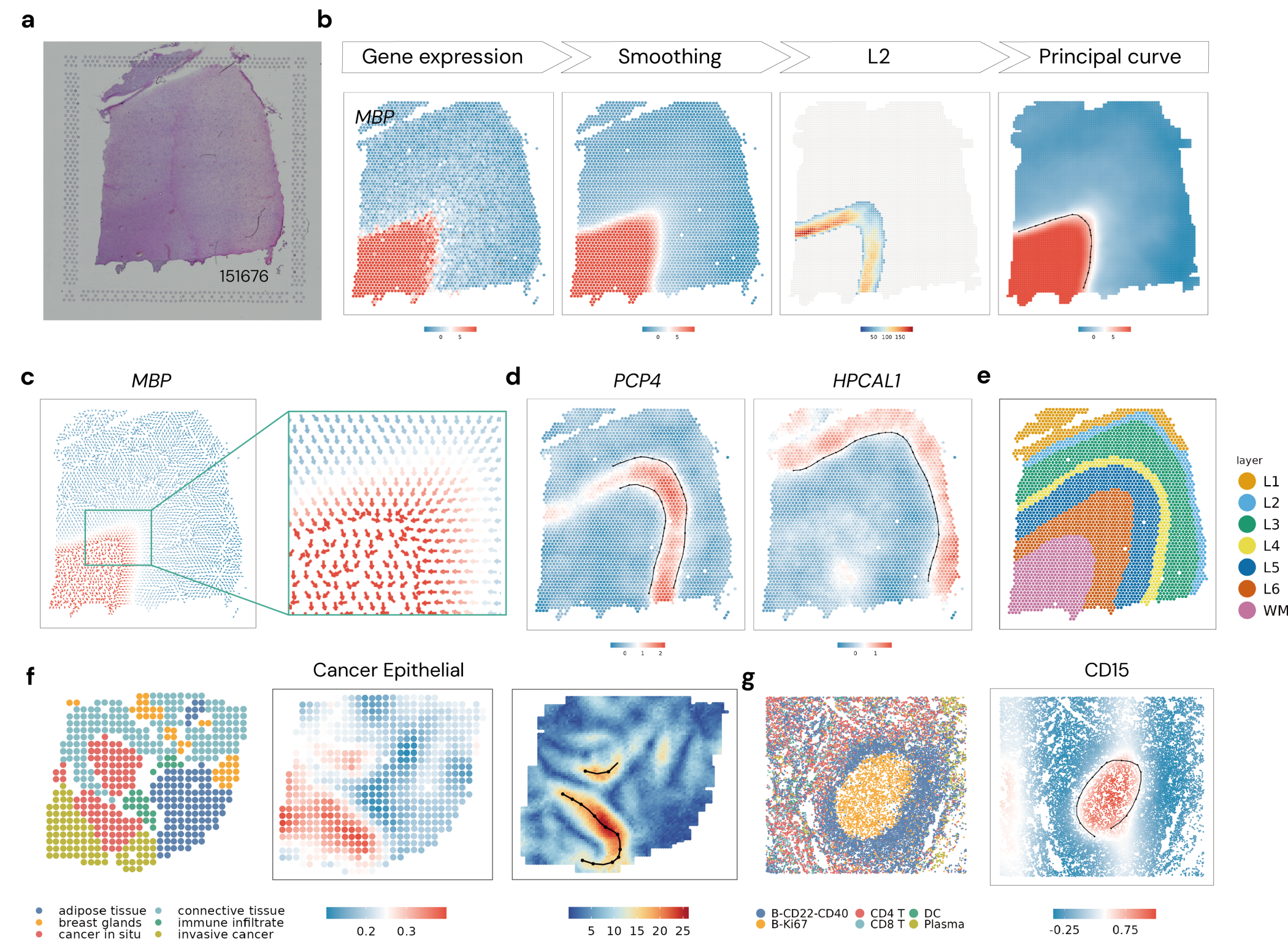
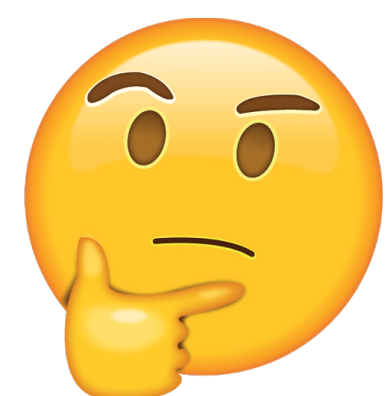


Figure 1: Multipanel figure with placeholder images.



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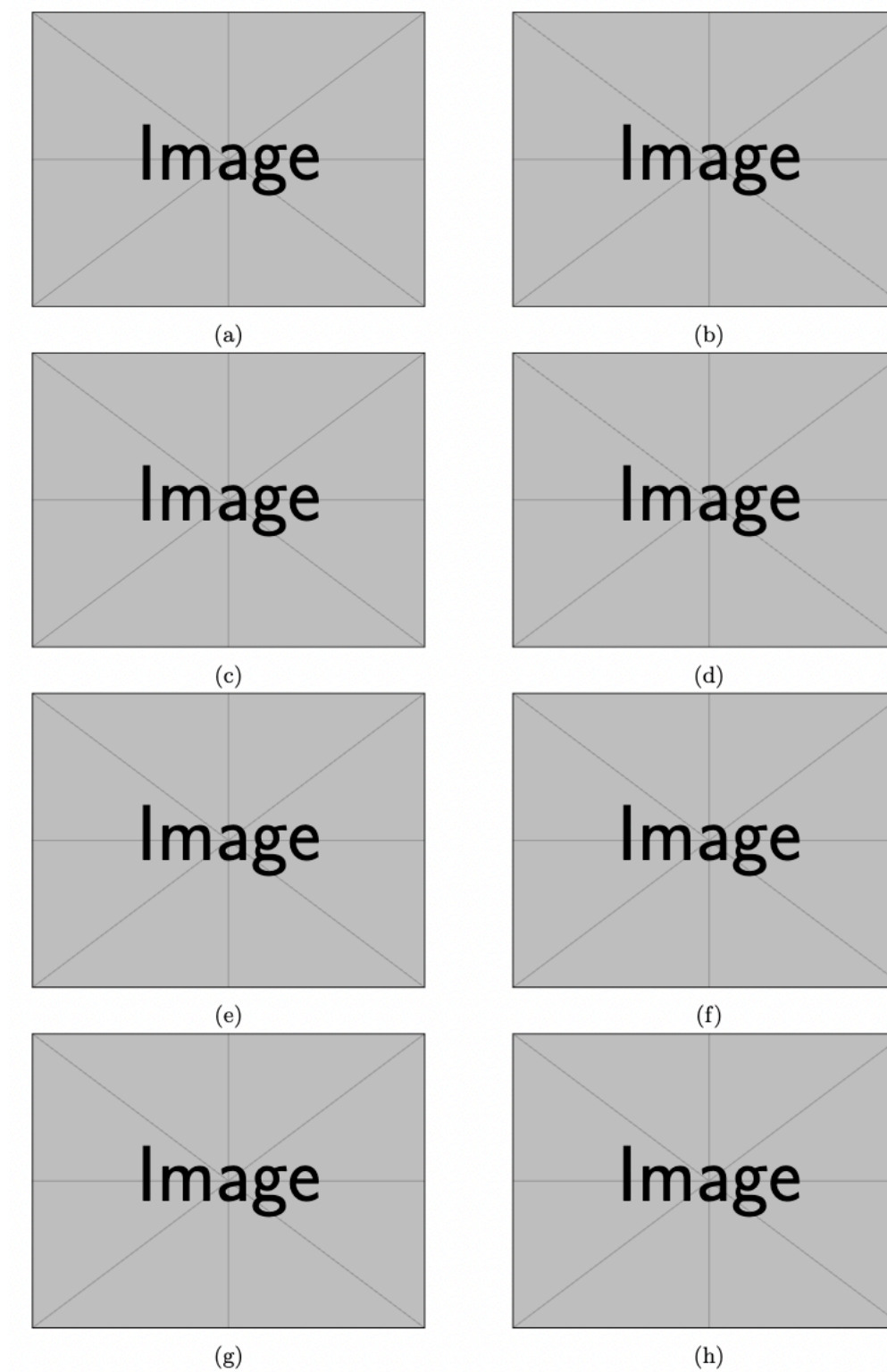
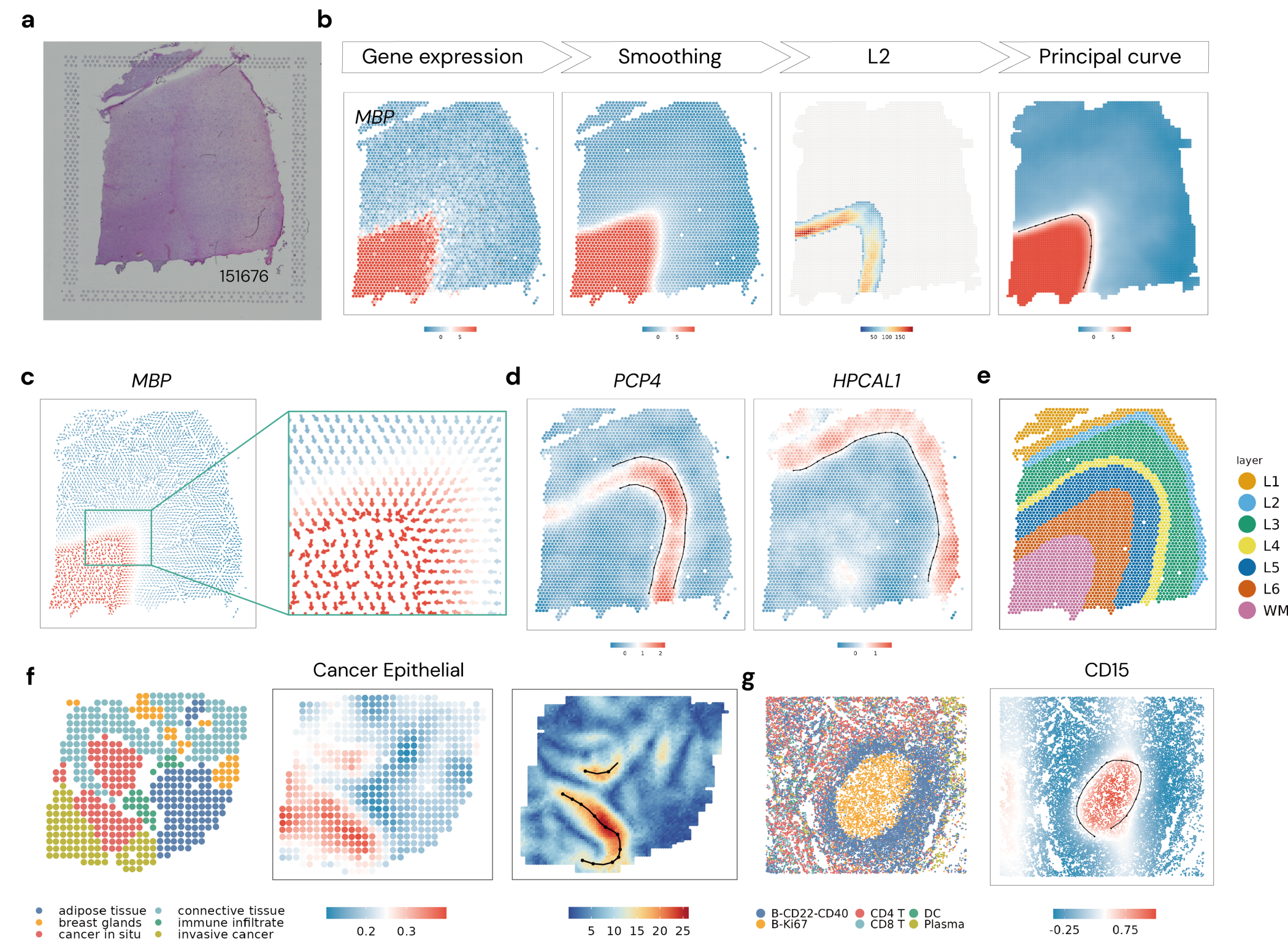
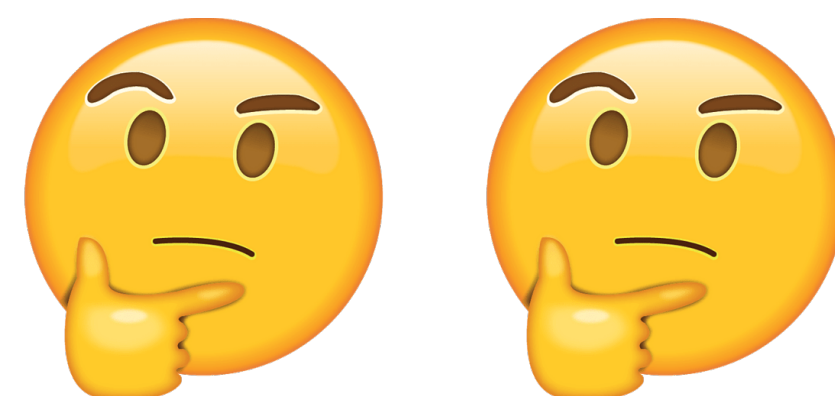


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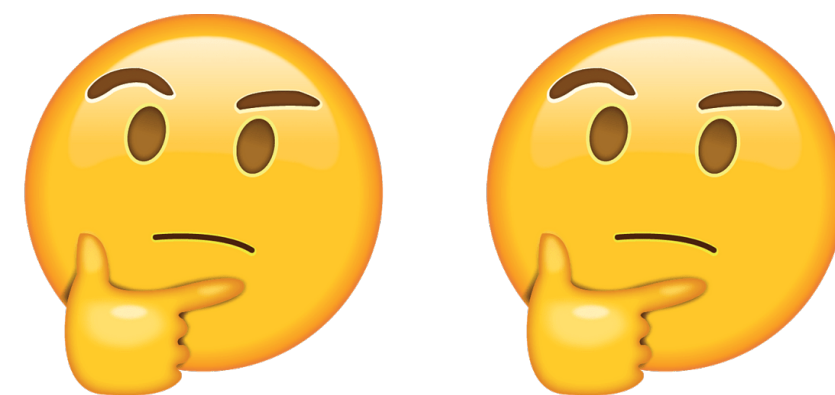
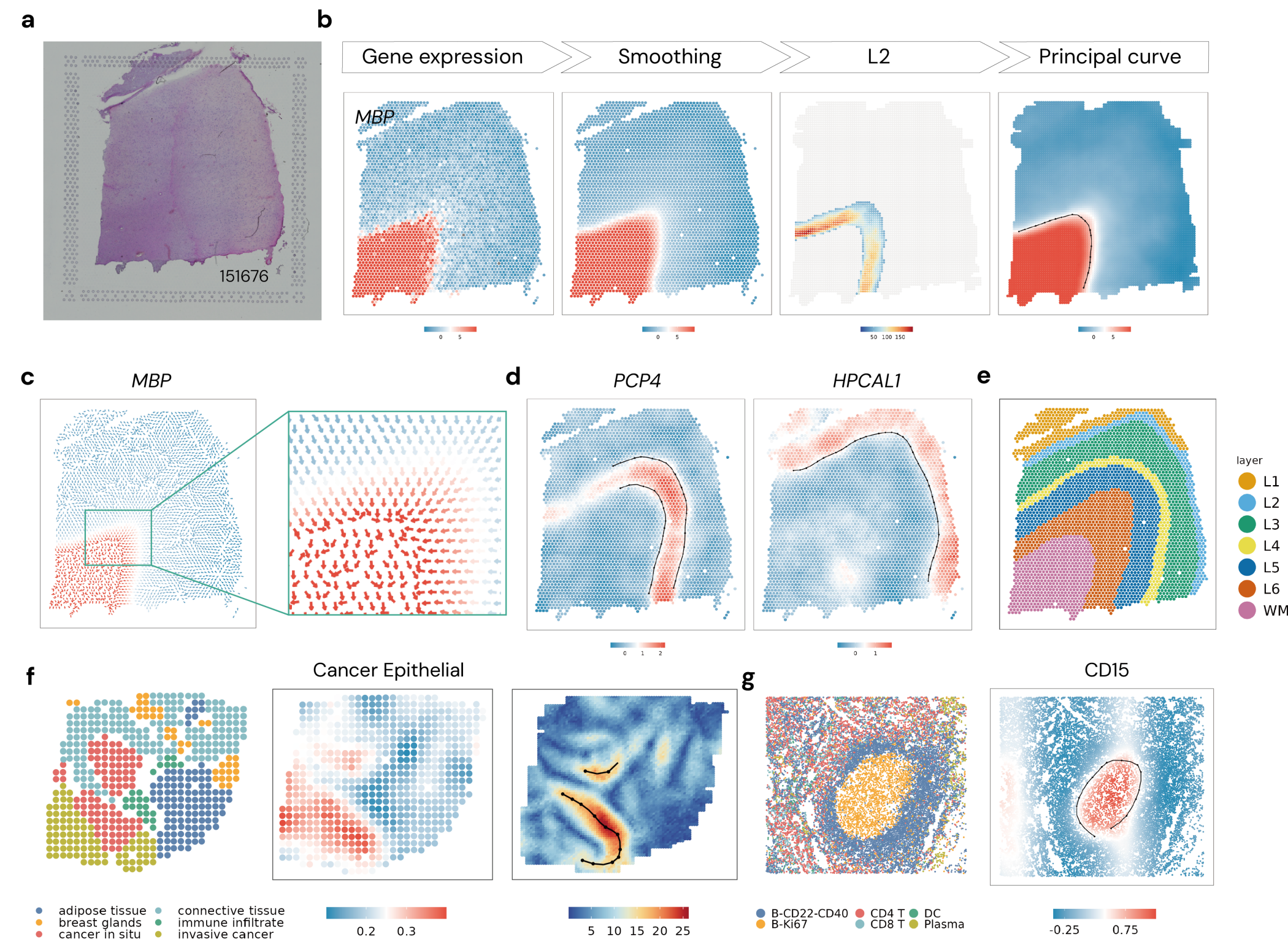
LaTeX Transformer

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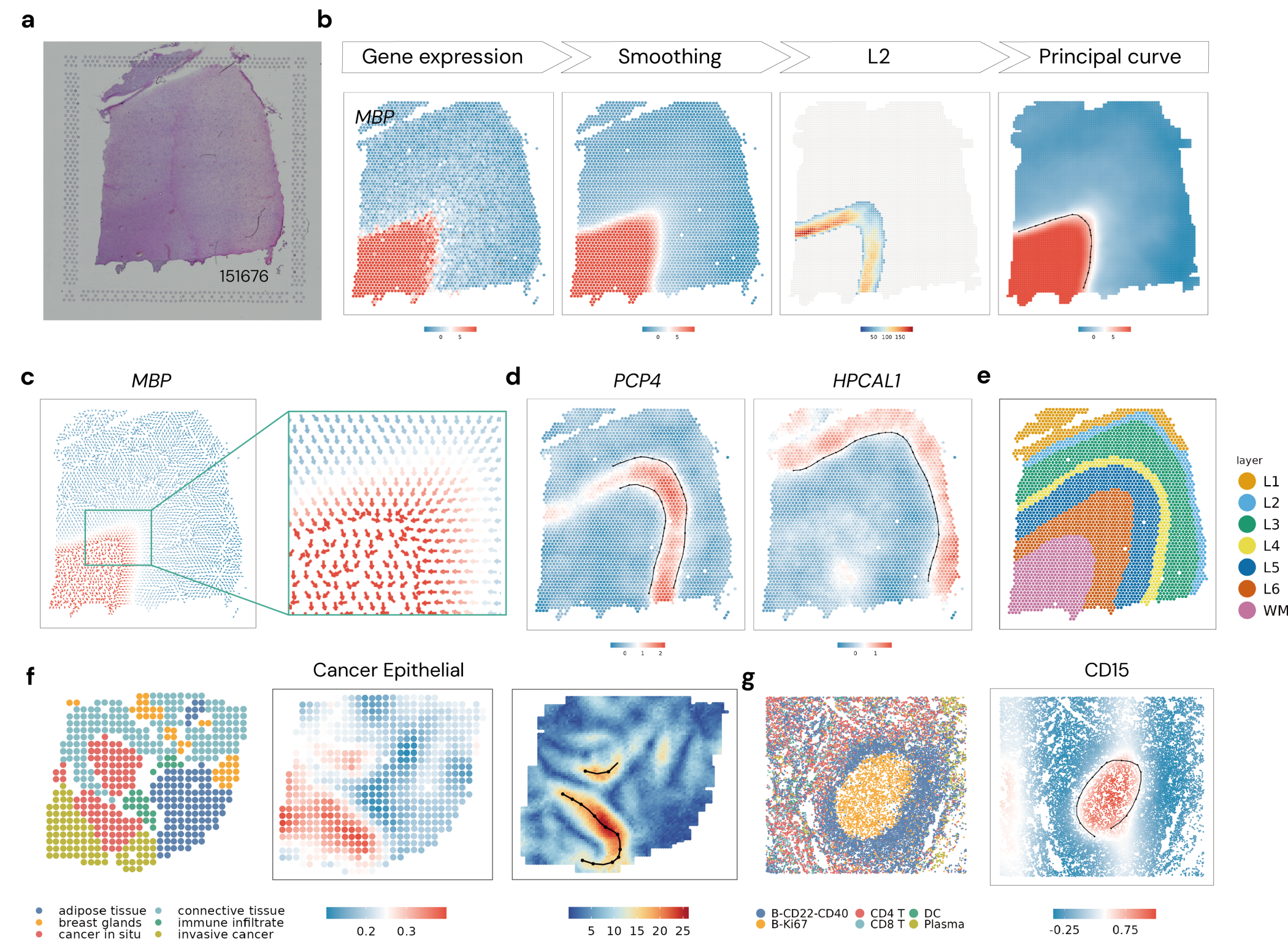
Generate LaTeX code for plots

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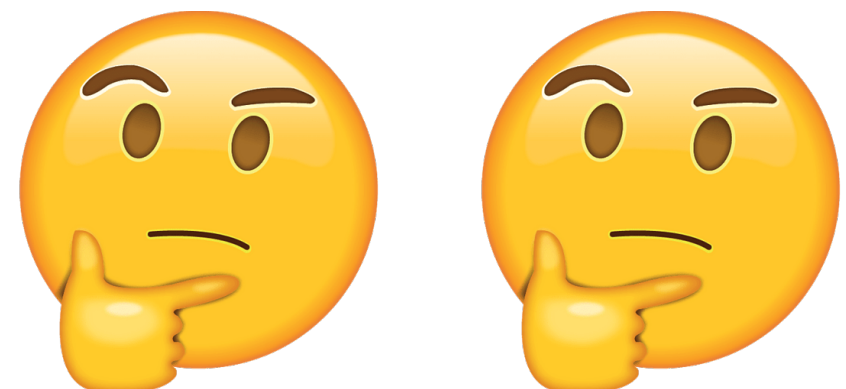


Generate LaTeX code for plots

Example plots



The locations of each panel are not correct



Understood, let's correct the layout to match the provided figure more closely. We will use a combination of `\begin{minipage}` and `\begin{subfigure}` to ensure proper placement.

Here is the updated LaTeX code:

Generate LaTeX code for plots

Example plots

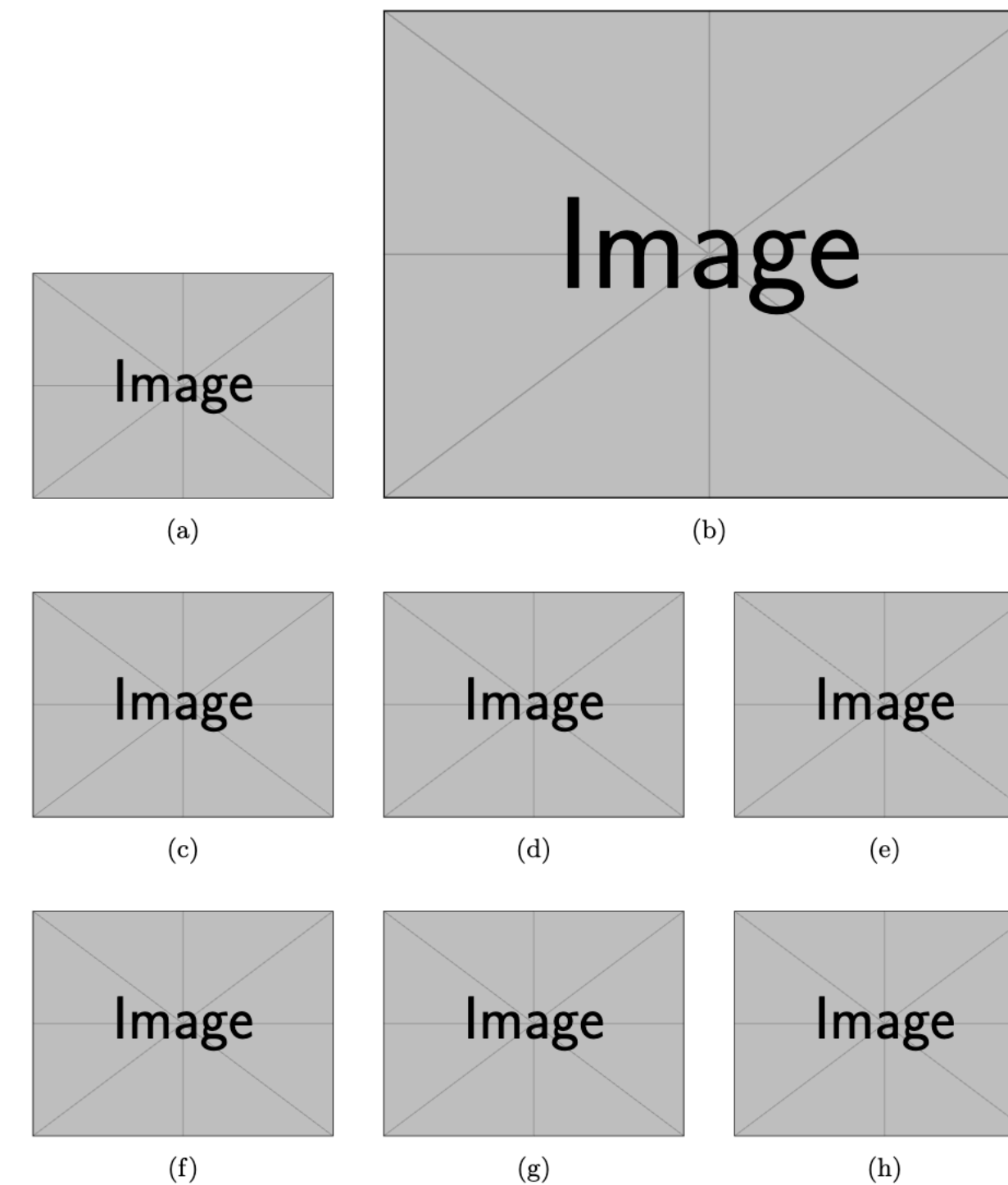
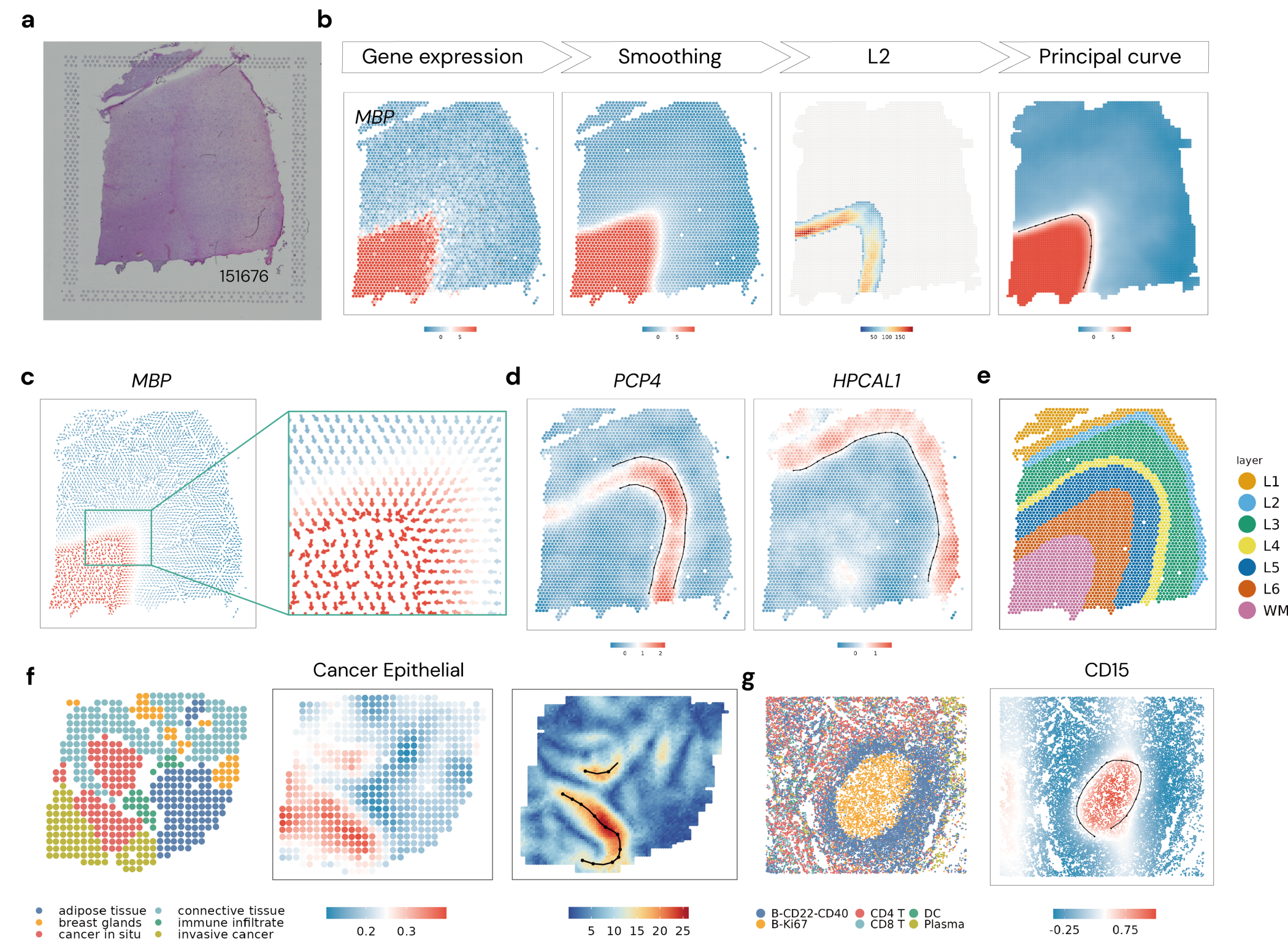
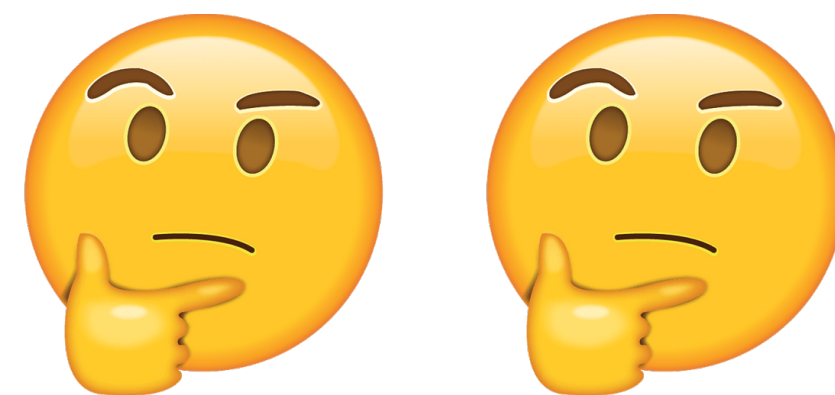


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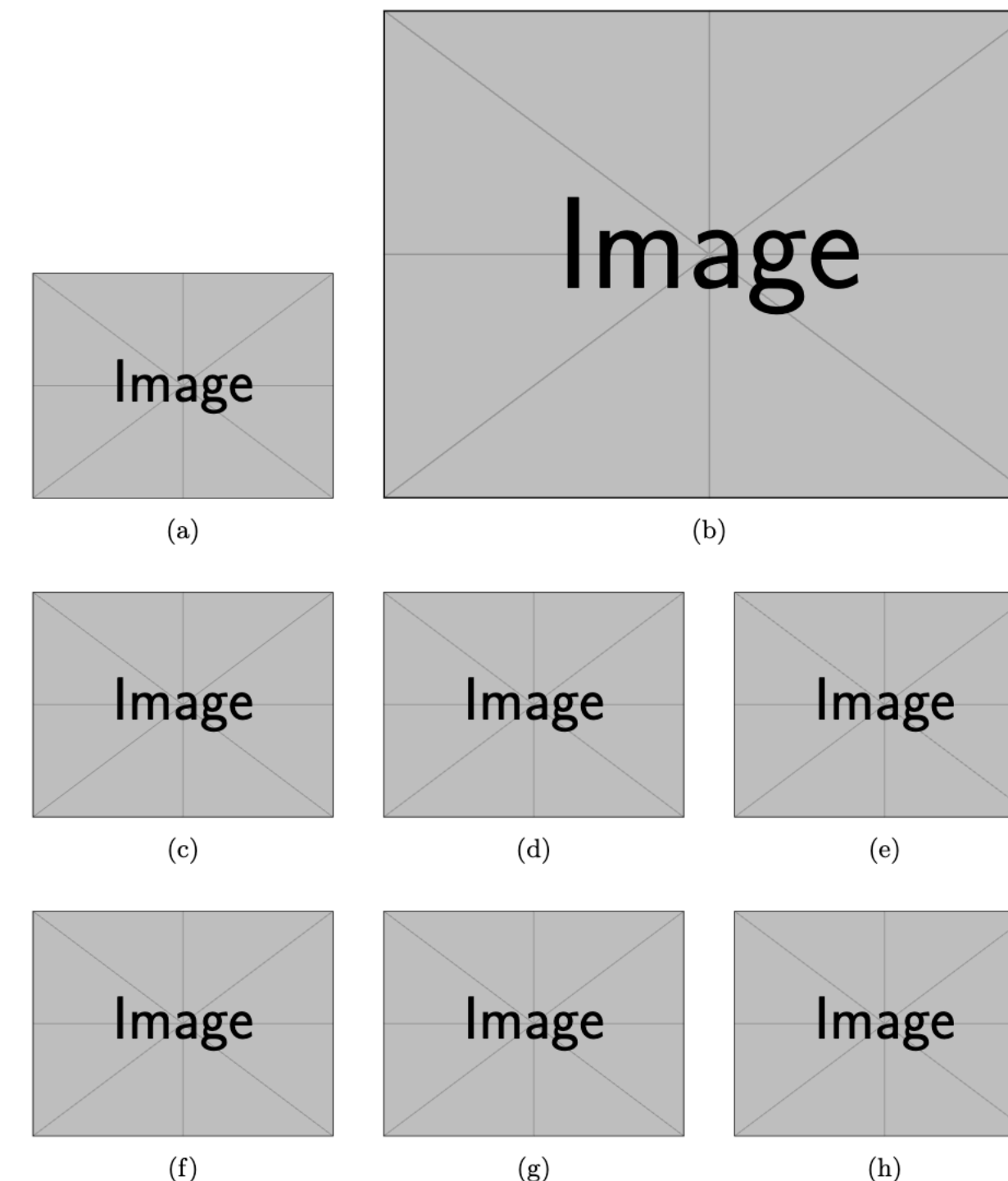
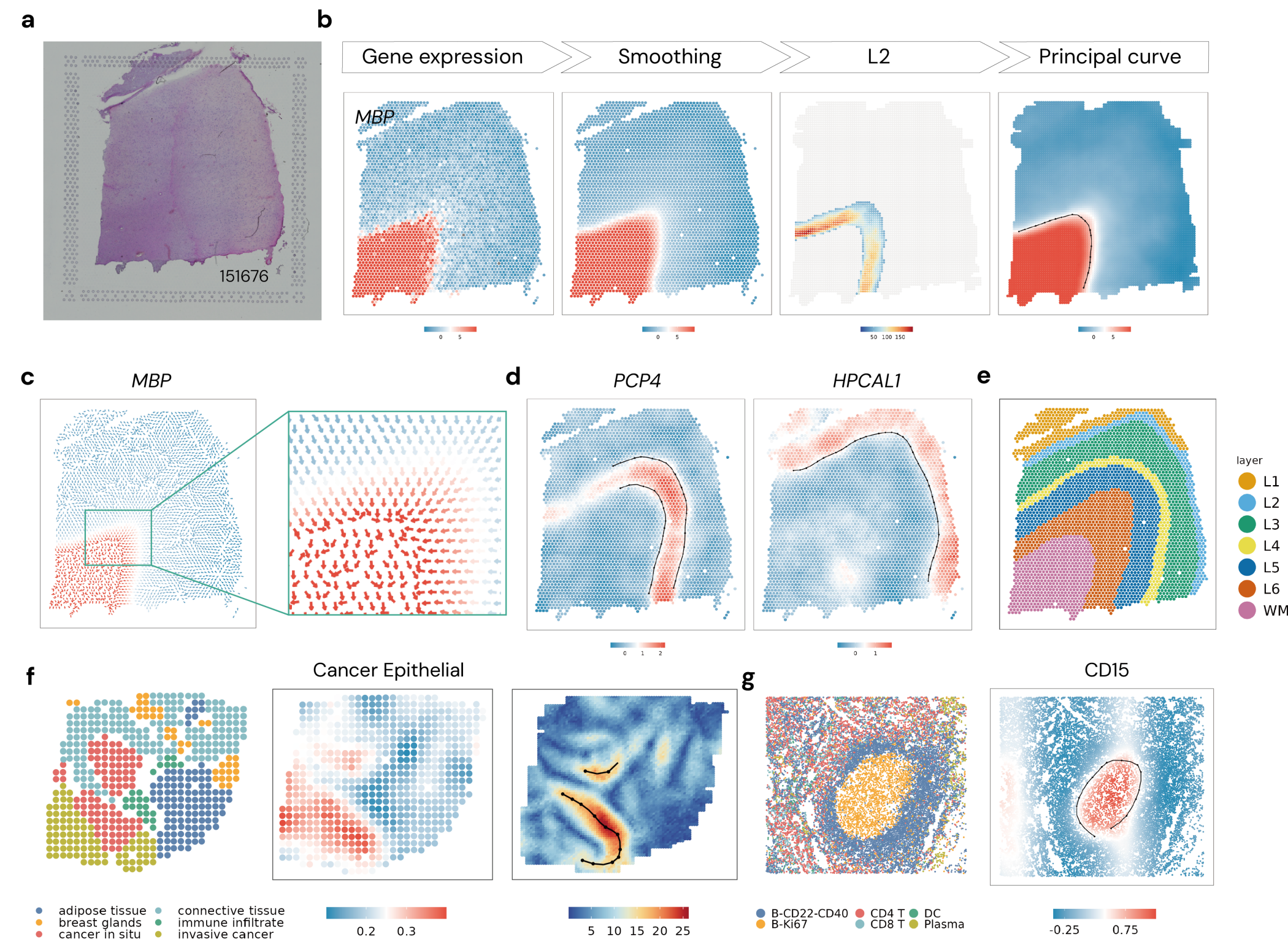


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Here is the updated LaTeX code:

Explain R code

```
Explain the following R code line by line: set.seed(123)
n <- 200
x1 <- rnorm(n)
x2 <- rbinom(n, 1, 0.5)
x3 <- runif(n, 1, 5)
eta <- 1 + 2 * x1 - 1.5 * x2 + 0.5 * x3
p <- 1 / (1 + exp(-eta))
y <- rbinom(n, 1, p)
data <- data.frame(y, x1, x2, x3)
model <- glm(y ~ x1 + x2 + x3, family = binomial(link = "logit"), data
= data)
summary(model)
predicted_probs <- predict(model, type = "response")
confusion_matrix <- table(predicted = predicted_probs > 0.5, actual
= y)
deviance_residuals <- residuals(model, type = "deviance")
plot(deviance_residuals)
```



Here's an explanation of each line of the provided R code:

Explain R code



Generate R code for simple tasks

Generate R code for simple tasks

Generate R code for the following statistical task:

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- Use the built-in `iris` dataset.

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- Use the built-in `iris` dataset.
- Perform a summary analysis of the dataset, including basic statistics for each species.

Generate R code for simple tasks

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- Use the built-in `iris` dataset.
- Perform a summary analysis of the dataset, including basic statistics for each species.
- Conduct a Principal Component Analysis (PCA) on the numeric data.

Generate R code for simple tasks

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- Use the built-in `iris` dataset.
- Perform a summary analysis of the dataset, including basic statistics for each species.
- Conduct a Principal Component Analysis (PCA) on the numeric data.
- Visualize the PCA results with a scatter plot, coloring points by species.

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- Create a pair plot (scatterplot matrix) of the numeric variables, with different colors for each species.

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- Visualize the PCA results with a scatter plot, coloring points by species.
- Create a pair plot (scatterplot matrix) of the numeric variables, with different colors for each species.
- Ensure the code is structured and well-commented for readability.

Generate R code for simple tasks



Debug in R

```
1 # Load necessary libraries
2 library(ggplot2)
3 library(dplyr)
4 library(tidyr)
5 library(GGally)
6
7 # Load the iris dataset
8 data(iris)
9
10 # Summary analysis
11 summary_analysis <- iris %>%
12   group_by(Species) %>%
13   summarize(
14     Sepal.Length.Mean = mean(Sepal.Length),
15     Sepal.Width.Mean = mean(Sepal.Width),
16     Petal.Length.Mean = mean(Petal.Length),
17     Petal.Width.Mean = mean(Petal.Width),
18     Sepal.Length.SD = sd(Sepal.Length),
19     Sepal.Width.SD = sd(Sepal.Width),
20     Petal.Length.SD = sd(Petal.Length),
21     Petal.Width.SD = sd(Petal.Width)
22   )
23 print("Summary Analysis by Species")
24 print(summary_analysis)
25
26 # Perform PCA on the numeric data
27 iris_numeric <- iris %>% select(-Species)
28 pca_result <- prcomp(iris_numeric, center = TRUE, scale = TRUE)
29
30 # Print PCA summary
31 print("PCA Summary")
32 print(summary(pca_result))
33
34 # Create a data frame with PCA results
35 pca_data <- data.frame(pca_result$x, Species = iris$species)
36
37 # Visualize PCA results with a scatter plot
38 ggplot(pca_data, aes(x = PC1, y = PC3, color = Species)) +
39   geom_point(size = 2) +
40   labs(title = "PCA of Iris Dataset", x = "Principal Component 1", y = "Principal Component 2") +
41   theme_minimal()
42
43 # Create a pair plot (scatterplot matrix) of the numeric variables
44 ggpairs(iris, aes(color = Species)) +
45   labs(title = "Pair Plot of Iris Dataset") +
46   theme_minimal()
47
```

Debug in R

" explain each bug, and explain how to fix



Sure, let's go through each bug one by one and explain how to fix them:

1. Incorrect Argument Name in PCA Function:

```
r Copy code  
pca_result <- prcomp(iris_numeric, center = TRUE, scale = TRUE)
```

- **Bug:** The correct argument name for scaling the data is `scale.`, not `scale`.
- **Fix:** Change `scale = TRUE` to `scale. = TRUE`.

```
r Copy code  
pca_result <- prcomp(iris_numeric, center = TRUE, scale. = TRUE)
```

2. Incorrect Column Name for Species in `data.frame`:

```
r Copy code  
pca_data <- data.frame(pca_result$x, Species = iris$species)
```

- **Bug:** The correct column name for species in the iris dataset is `Species`, not `species`.
- **Fix:** Change `iris$species` to `iris$Species`.

```
r Copy code  
pca_data <- data.frame(pca_result$x, Species = iris$Species)
```

3. Incorrect Component for y-axis in PCA Scatter Plot:

```
r Copy code  
ggplot(pca_data, aes(x = PC1, y = PC3, color = Species)) +
```

- **Bug:** The typical PCA plot uses the first two principal components, PC1 and PC2.
- **Fix:** Change `y = PC3` to `y = PC2`.

```
r Copy code  
ggplot(pca_data, aes(x = PC1, y = PC2, color = Species)) +
```

4. Incorrect Theme Function Name in Pair Plot:

```
r Copy code  
ggpairs(iris, aes(color = Species)) +  
  labs(title = "Pair Plot of Iris Dataset") +  
  theme_minimal()
```

- **Bug:** The function `theme_minimal()` is correct, but it needs to be part of the `ggplot2` object, not `ggpairs`.
- **Fix:** Ensure that `theme_minimal()` is applied correctly to the plot. `ggpairs` automatically applies themes, so this line can be omitted.

The pair plot section is actually correct as is, but we should ensure the correct theme application:

```
r Copy code  
ggpairs(iris, aes(color = Species)) +  
  labs(title = "Pair Plot of Iris Dataset")
```

Translate R code to Python

Translate the r code to python

```
python Copy code
# Import necessary libraries
import pandas as pd
import seaborn as sns
import matplotlib.pyplot as plt
from sklearn.decomposition import PCA
from sklearn.preprocessing import StandardScaler

# Load the iris dataset
from sklearn.datasets import load_iris
iris = load_iris()
iris_df = pd.DataFrame(data=iris.data, columns=iris.feature_names)
iris_df['species'] = pd.Categorical.from_codes(iris.target, iris.target_names)

# Summary analysis
summary_analysis = iris_df.groupby('species').agg(
    Sepal_Length_Mean=('sepal length (cm)', 'mean'),
    Sepal_Width_Mean=('sepal width (cm)', 'mean'),
    Petal_Length_Mean=('petal length (cm)', 'mean'),
    Petal_Width_Mean=('petal width (cm)', 'mean'),
    Sepal_Length_SD=('sepal length (cm)', 'std'),
    Sepal_Width_SD=('sepal width (cm)', 'std'),
    Petal_Length_SD=('petal length (cm)', 'std'),
    Petal_Width_SD=('petal width (cm)', 'std')
).reset_index()

print("Summary Analysis by Species")
print(summary_analysis)

# Perform PCA on the numeric data
iris_numeric = iris_df.drop('species', axis=1)
scaler = StandardScaler()
iris_scaled = scaler.fit_transform(iris_numeric)
pca = PCA()
pca_result = pca.fit_transform(iris_scaled)

# Print PCA summary
print("PCA Explained Variance Ratio")
print(pca.explained_variance_ratio_)

# Create a data frame with PCA results
pca_df = pd.DataFrame(data=pca_result, columns=[f'PC{i+1}' for i in range(pca_result.shape[1])]
pca_df['species'] = iris_df['species']

# Visualize PCA results with a scatter plot
plt.figure(figsize=(10, 7))
sns.scatterplot(data=pca_df, x='PC1', y='PC2', hue='species', palette='Set1')
plt.title('PCA of Iris Dataset')
plt.xlabel('Principal Component 1')
plt.ylabel('Principal Component 2')
plt.show()

# Create a pair plot (scatterplot matrix) of the numeric variables
sns.pairplot(iris_df, hue='species', palette='Set1')
plt.suptitle('Pair Plot of Iris Dataset', y=1.02)
plt.show()
```



Certainly! Here is the translated R code to Python using pandas, scikit-learn, and seaborn for visualization:

Explanation:

1. Load the dataset:

- The `load_iris` function from `sklearn.datasets` is used to load the iris dataset.
- A pandas DataFrame is created from the data and the species column is added using the target information from the dataset.

2. Summary Analysis:

- The DataFrame is grouped by species and aggregated to calculate the mean and standard deviation for each feature.

3. PCA:

- The numeric data is standardized using `StandardScaler`.
- PCA is performed using `PCA` from `sklearn.decomposition`.
- The explained variance ratio is printed to understand the amount of variance captured by each principal component.

4. PCA Visualization:

- A scatter plot of the first two principal components is created using seaborn's `scatterplot`.

5. Pair Plot:

- A pair plot of the numeric variables is created using seaborn's `pairplot`.

This Python code replicates the functionality of the original R code, allowing for summary analysis and visualization of the iris dataset using PCA and pair plots.

Translate R code to Python



August 10, 2021

OpenAI Codex

We've created an improved version of OpenAI Codex, our AI system that translates natural language to code, and we are releasing it through our API in private beta starting today.

[Start using Codex ↗](#)

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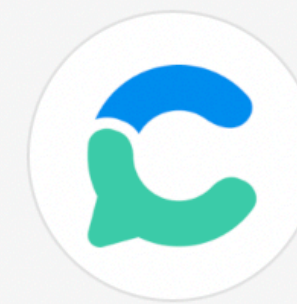
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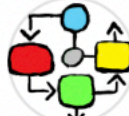

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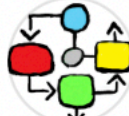

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- Used solely for the output for completing mathematical [computations](#)
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Discussion

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 - Translate R code to Python
- Extension: other “apps” and create your own GPTs

Acknowledgement



Thank you



R01 HL149683
R01 AG079291
R56 LM013784
P30 ES010126
UM1 TR004406

Choi and Yuan, Matrix Completion When Missing Is Not at Random and Its Applications in Causal Panel Data Models, JASA 2024
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