PRISM: PRIor from corpus Statistics for topic Modeling

Anonymous authors
Paper under double-blind review

Abstract

Topic modeling seeks to uncover latent semantic structure in text, with LDA providing a foundational probabilistic framework. While recent methods often incorporate external knowledge (e.g., pre-trained embeddings), such reliance limits applicability in emerging or underexplored domains. We introduce **PRISM**, a corpus-intrinsic method that derives a Dirichlet parameter from word co-occurrence statistics to initialize LDA without altering its generative process. Experiments on text and single cell RNA-seq data show that PRISM improves topic coherence and interpretability, rivaling models that rely on external knowledge. These results underscore the value of corpus-driven initialization for topic modeling in resource-constrained settings.

Code will be released upon acceptance.

1 Introduction

Topic modeling is a cornerstone technique in Natural Language Processing (NLP) for uncovering latent semantic structures in text. It infers the thematic composition of a corpus by representing each topic as a probability distribution over words. The versatility of topic modeling is evidenced by its application across a spectrum of disciplines - from analyzing customer feedback in e-commerce platforms to modeling gene expression patterns in biology by treating genes as "vocabulary" and samples as "documents". Such cross-disciplinary utility underscores topic modeling's broad relevance in both applied and scientific contexts.

Since its inception, among topic modeling techniques, Latent Dirichlet Allocation (LDA) (Blei et al., 2003) remains a foundation model, leveraging Bayesian inference to estimate document-topic and topic-word distributions while inspiring numerous generative extensions. Topic modeling research has since evolved along many directions, which can be broadly categorized into two main paradigms. The first follows LDA's corpus-intrinsic approach, relying solely on statistical patterns within the target corpus through methods including graph-based and neural models that enhance semantic representation and topic coherence. The second paradigm incorporates external knowledge—such as pre-trained embeddings from large-scale language models or domain-specific priors—to guide topic discovery beyond the statistical patterns available in the input corpus alone.

Corpus-intrinsic topic modeling offers clear advantages for knowledge discovery in emerging scientific domains, where foundation models are underdeveloped and existing knowledge is often fragmented. In fields like biology, key regulatory genes or functional proteins may be undiscovered or poorly characterized, limiting the reliability of external knowledge sources. While pre-trained models excel in established domains, they often fall short in data-scarce settings. In contrast, corpus-intrinsic methods enable unbiased pattern discovery directly from domain-specific data, supporting systematic exploration in knowledge-limited environments.

In this work, we introduce **PRISM**—a **PRI**or from corpus **S**tatistics for topic **M**odeling—which enhances LDA solely through corpus-intrinsic initialization (Figure 1). PRISM shapes the model's "initial perspective" by deriving informed topic-word distributions from statistical patterns in the data, serving as prior-like guidance, which leads to higher topic quality. Empirical results across five text corpora and a single-cell RNA sequencing dataset show that PRISM significantly improves topic coherence and interpretability, often matching or exceeding externally guided methods.

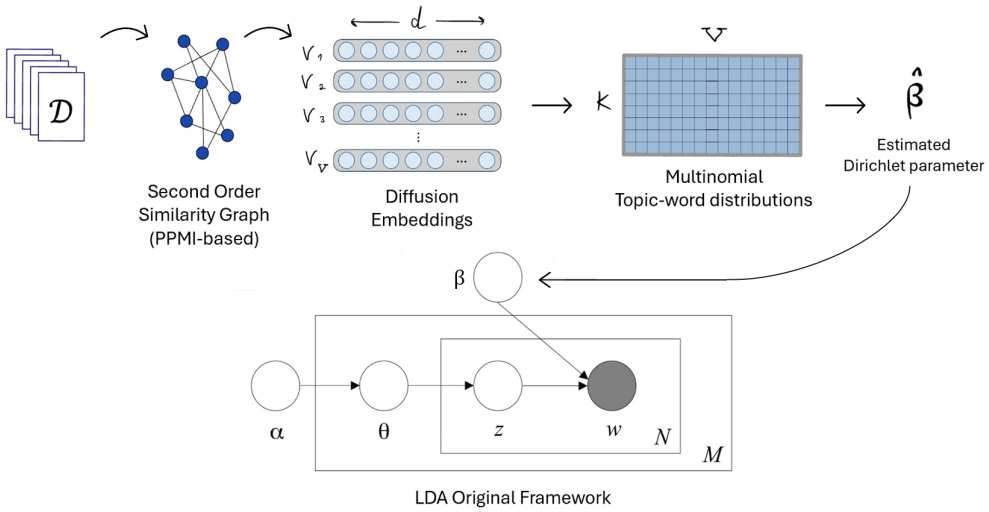

Figure 1: Overview of the PRISM framework. Given a corpus $\mathcal{D}$, we construct a second-order word similarity graph using PPMI and cosine similarity. Diffusion maps produce low-dimensional word embeddings v_i, which are softly clustered into K topics. From the resulting multinomial topic–word distributions, we estimate a Dirichlet parameter $\hat{\boldsymbol{\beta}}$ that serves as the topic–word prior in LDA. The lower panel shows the full LDA graphical model, including all parameters and variables: $\boldsymbol{\alpha}$ (document–topic Dirichlet parameter), $\boldsymbol{\theta}$ (document topic proportions), z (topic assignments), w (observed words), and $\boldsymbol{\beta}$ (topic–word Dirichlet parameter). PRISM replaces the standard symmetric $\boldsymbol{\beta}$ with the data-driven estimate $\hat{\boldsymbol{\beta}}$ while leaving the generative process unchanged.

2 Related Work

Research on topic modeling has evolved along two main paradigms: (1) methods that incorporate external semantic knowledge (typically via pretrained representations), and (2) corpus-intrinsic methods that infer structure solely from corpus statistics.

2.1 Methods Incorporating External Knowledge

A prominent line of work enhances topic modeling by integrating external semantic resources. One route augments LDA with auxiliary supervision, for instance SeededLDA (Jagarlamudi et al., 2012) guides topic assignment using predefined seed words. Another route relies on pretrained representations. The Embedded Topic Model (ETM) parameterizes each topic–word distribution as a softmax over inner products between topic embeddings and word embeddings (Dieng et al., 2020). Contextualized Topic Models (CTM) retain a BoW generative decoder while amortizing the posterior with contextualized document embeddings (Bianchi et al., 2021). A complementary line discovers topics directly in embedding space. BERTopic clusters transformer sentence embeddings and labels clusters with class-based TF-IDF (c-TF-IDF) (Grootendorst, 2022). Contextual-Top2Vec clusters pretrained contextual token embeddings and defines topics from the resulting dense regions (Angelov & Inkpen, 2024). Instead of clustering approach, FASTopic reconstructs semantic relations among pretrained-Transformer document embeddings and learnable topic/word embeddings (Dual Semantic-relation Reconstruction) (Wu et al., 2024).

2.2 Corpus-Intrinsic Methods (No External Knowledge)

Corpus-intrinsic methods work strictly with the given data, without importing pretrained semantics. Latent Dirichlet Allocation (LDA) (Blei et al., 2003) remains the canonical probabilistic formulation. An alternative with no generative assumption is Non-negative Matrix Factorization (NMF) (Lee & Seung, 2001) which factorizes the document–term matrix into non-negative parts and often yields sparse, interpretable topics.

Another strand is neural variational models that modernize inference while retaining bag-of-words (BoW) evidence. NeuralLDA and ProdLDA (Srivastava & Sutton, 2017) are examples of models that apply amortized VAE inference to BoW with a logistic-normal prior. They are closely related but differ primarily in the decoder: NeuralLDA preserves LDA's mixture structure, whereas ProdLDA uses a product-of-experts, typically sharpening topic assignments.

Complementary work has examined how Dirichlet hyperparameters affect LDA. Asuncion et al. (Asuncion et al., 2009) and Wallach et al. (Wallach et al., 2009) treat $\boldsymbol{\alpha}$ and $\boldsymbol{\beta}$ as a small set of scalar concentration parameters and use empirical Bayes updates during inference to tune their magnitude, showing that predictive performance is sensitive to the choice of symmetric or asymmetric priors. These approaches thus exploit corpus-internal signals only to rescale a global smoothing term, rather than to shape a full topic–word prior.

Taken together, these lines of work demonstrate the value of corpus-internal signals for enhancing topic models without external supervision. Building on this idea, PRISM introduces a corpus-derived prior as a data-driven initialization for LDA, constructing a full V-dimensional, semantically structured $\hat{\boldsymbol{\beta}}$ from corpus similarity. This provides a more informed starting point—a prism through which the model better captures semantic structure—while preserving LDA's generative foundations.

3 Preliminaries

This section introduces the key mathematical tools underpinning our approach.

3.1 Latent Dirichlet Allocation (LDA)

LDA (Blei et al., 2003) is a generative probabilistic model in which each document is a mixture over K latent topics, and each topic is a distribution over words. For each document d, topic proportions θ_d are drawn from a Dirichlet distribution with parameter $\boldsymbol{\alpha}$. Each word w_{dn} is then generated by first sampling a topic $z_{dn} \sim \text{Multinomial}(\theta_d)$, followed by sampling the word from the corresponding topic–word distribution, drawn from a Dirichlet distribution with parameter $\boldsymbol{\beta}$.

In the original formulation of LDA (Blei et al., 2003), $\boldsymbol{\beta}$ denotes the *multinomial topic–word distribution*. In contrast, implementations based on collapsed Gibbs sampling, including MALLET (McCallum, 2002), treat $\boldsymbol{\beta}$ as the *Dirichlet parameter* over topic–word distributions. Throughout this work we adopt the latter convention, consistent with MALLET and other Gibbs-based LDA implementations.

Inference is commonly performed using *Collapsed Gibbs Sampling* (Griffiths & Steyvers, 2004), which samples topic assignments z_{dn} based on current token counts and priors - $\boldsymbol{\alpha}$ and $\boldsymbol{\beta}$. This method, implemented efficiently in MALLET (McCallum, 2002), is a widely adopted baseline.

3.2 Pointwise Mutual Information and Variants

Pointwise Mutual Information (PMI) (Church & Hanks, 1990) quantifies the strength of association between two words w_i and w_j by comparing their joint probability to the product of their marginal probabilities. To remove noisy or uninformative associations, Positive PMI (PPMI) retains only non-negative values.

Rather than focusing solely on direct co-occurrence, prior work has shown that applying similarity metrics—such as cosine similarity—over PPMI-based word vectors effectively captures second-order semantic similarity (Bullinaria & Levy, 2012; Schütze, 1998). This approach enables the identification of semantically related words that may not co-occur directly, based on the similarity of their distributional contexts. This approach enables the model to estimate semantic relatedness between words that do not co-occur directly by leveraging overlapping associations. For example, while *surgeon* and *physician* may not co-occur, both co-occur with *patient*, *hospital*, and *diagnosis*.

3.3 Diffusion Maps

Diffusion Maps (Coifman & Lafon, 2006) provides a nonlinear dimensionality reduction technique that captures the intrinsic geometry of data represented as a similarity graph. Given an undirected word-word

similarity graph W, the method constructs a Markov transition matrix P according the following formulation: $P = D^{-1}W$, where D is the diagonal degree matrix with entries $D_{ii} = \sum_j W_{ij}$. Then, it performs eigen-decomposition over P to obtain the diffusion embedding. Each word is then embedded as a vector:

$$\Psi_t(w_i) = \left(\lambda_1^t \psi_1(i), \lambda_2^t \psi_2(i), \ldots, \lambda_m^t \psi_m(i)\right),$$

where λ_k and ψ_k are the k-th eigenvalue and eigenvector of the transition matrix, respectively; m is the embedding dimension, and t is the diffusion time controlling the decay.

4 Proposed Method

We introduce **PRISM**, a corpus-intrinsic method for improving topic modeling by providing a data-driven initialization for LDA. The approach consists of two main stages: (1) constructing word embeddings based solely on corpus statistics, and (2) estimating a Dirichlet parameter $\boldsymbol{\beta}$ over topic-word distributions derived from these embeddings. The resulting prior is used to initialize LDA, offering a principled way to guide inference without altering the model's generative process.

4.1 Rationale

While contemporary models benefit significantly from pre-trained word embeddings that capture semantic relationships, we sought to harness similar advantages without relying on external knowledge sources. To achieve this, we propose to derive our own word embeddings directly from the target corpus. Our key insight is to derive dense word embeddings from corpus-internal statistics using a semantic similarity graph constructed from PMI variants, followed by diffusion maps to capture global semantic structure embeddings. These embeddings are then softly clustered to produce a probabilistic topic-word distribution, from which we estimate a Dirichlet parameter that guides LDA initialization.

4.2 Constructing Word Embeddings

4.2.1 Similarity Graph

To capture semantic similarity between words, we construct an undirected graph W based on Positive PMI (PPMI), as described in Section 3.2. The PPMI matrix is computed using document-level co-occurrence, treating each document as a context window. Each word w_i is represented by its corresponding row vector $\mathbf{v}_i$ from the PPMI matrix, encoding its distributional context. We then define pairwise similarity using cosine similarity as $W_{i,j} = \cos(\mathbf{v}_i, \mathbf{v}_j)$, where $\mathbf{v}_i$ and $\mathbf{v}_j$ are the PPMI vectors of words w_i and w_j, respectively. The resulting similarity graph W captures both direct and indirect semantic associations by leveraging the principle that words appearing in similar contexts tend to have similar vector representations.

4.2.2 From Graph to Embeddings

To obtain dense word representations from the similarity graph, we apply diffusion maps, as defined in Section 3.3. This spectral embedding technique captures high-order semantic relationships by modeling multi-step transitions over the graph. Intuitively, if a diffusion process is initiated at two semantically similar words, their transition probabilities over time will be similar, reflecting shared contextual neighborhoods.

We embed each word using the top m diffusion components—i.e., the leading eigenvectors of the transition matrix scaled by their corresponding eigenvalues. Empirically, we find that selecting between 80 and 130 components yields the best semantic representation, with the optimal m chosen based on the highest topic coherence score for each dataset and topic configuration.

The resulting vectors serve as our corpus-specific word embeddings, encoding semantic structure without relying on any external resources.

4.3 Estimating Dirichlet Parameter β

4.3.1 Topic-Word Distributions

To compute empirical topic-word distributions from the learned word embeddings, we apply a Gaussian Mixture Model (GMM) (Reynolds, 2009) with K components to softly cluster the word representations. The GMM yields the posterior probability $p(z \mid w)$ of each word w belonging to topic z, along with the topic priors $p(z)$.

However, our goal is to obtain $p(w \mid z)$—the probability of a word given a topic—as required to estimate the Dirichlet parameter $\boldsymbol{\beta}$ over topic-word distributions. To do so, we apply Bayes' Rule:

$$p(w \mid z) = \frac{p(z \mid w)p(w)}{p(z)},$$

where $p(z \mid w)$ is given by the GMM, $p(z)$ is the mixture weight for component z, and $p(w)$ is taken from unigram distribution, computed as the frequency of word w in the corpus divided by the total number of tokens.

This yields multinomial topic-word distributions matrix $\boldsymbol{X} \in \mathbb{R}^{K \times V}$, where each row corresponds to $p(w \mid z)$ for a given topic. The matrix is grounded entirely in corpus-derived signals—capturing both contextual similarity and token-level frequency—used to estimate the Dirichlet parameter $\boldsymbol{\beta}$.

4.3.2 Parameter β Estimation

To estimate a Dirichlet parameter $\boldsymbol{\beta} \in \mathbb{R}^V$ over the vocabulary, we apply the method of moments (Minka, 2000), a classical statistical technique used for parameter estimation. The core idea is to match the theoretical moments of the Dirichlet distribution to empirical moments computed from data.
Let $\mathbf{X}^{(1)}, \ldots, \mathbf{X}^{(k)} \in \Delta^{V-1}$ be k observed samples from a $Dirichlet(\boldsymbol{\beta}_1 \ldots \boldsymbol{\beta}_V)$ distribution over the $(V-1)-$probability simplex. The method of moments estimator for $\hat{\boldsymbol{\beta}}$ is given by

$$\hat{\boldsymbol{\beta}}_i = \mathbb{E}[X_i] \left(\frac{\mathbb{E}[X_j](1 - \mathbb{E}[X_j])}{\mathbb{V}[X_j]} - 1 \right),$$

where, following Minka (2000), we set $i = j$, and

$$\mathbb{E}[X_i] \approx \frac{1}{k} \sum_{\ell=1}^{k} X_i^{(\ell)}, \qquad \mathbb{V}[X_i] \approx \frac{1}{k-1} \sum_{\ell=1}^{k} \left(X_i^{(\ell)} - \mathbb{E}[X_i] \right)^2.$$

4.3.3 Initializing LDA with $\hat{\beta}$

The estimated vector $\hat{\boldsymbol{\beta}}$ is then used to initialize the LDA model, replacing the standard uniform or fixed scalar prior. We modified the MALLET implementation to support a vector valued $\hat{\boldsymbol{\beta}}$ parameter, enabling topic-word distributions to reflect corpus-specific semantic structure from the outset. Apart from this change, the rest of the LDA inference pipeline in MALLET remains unaltered.

5 Experiments

We evaluate the effectiveness of our corpus-informed Dirichlet parameter by assessing its impact on standard LDA. Our goal is to determine whether data-driven initialization can substantially improve topic quality and bring LDA closer to, or even surpass, state-of-the-art topic modeling methods. Experiments are conducted on five diverse text corpora, using three complementary metrics. (Ablation studies appear in Appendix D.2, and the complexity analysis in Appendix D.3).

Datasets. To ensure a fair and objective evaluation, we use pre-processed datasets from the OCTIS framework (Terragni et al., 2021), thereby avoiding model-specific tuning of the preprocessing pipeline. Specifically,

we experiment with four diverse OCTIS datasets: 20NewsGroup, BBC News, M10, and DBLP, covering a range of domains and document styles.

In addition, following BERTopic (Grootendorst, 2022), we include the TrumpTweets (TT) dataset to test model performance on informal, short-form text. Since this dataset is not included in OCTIS, we apply OCTIS's preprocessing module with standard, commonly used filtering (see Appendix A for details). This setup allows us to evaluate our method both under standardized preprocessing and in a setting closer to real-world social media text. The statistical details can be seen in Appendix A.

Baselines. We evaluate our approach against a diverse set of topic models. For classical and neural baselines implemented in OCTIS (Terrone et al., 2021), we include LDA (Blei et al., 2003), NMF (Zhao et al., 2017), ProdLDA (Srivastava & Sutton, 2017), NeuralLDA (Srivastava & Sutton, 2017), and the ETM (Dieng et al., 2020). These models rely solely on corpus-internal signals and do not incorporate any external knowledge.

We further compare against recent embedding-based methods that leverage pretrained representations: BERTopic (Grootendorst, 2022), FASTopic (Wu et al., 2024), and Contextual Contextual-Top2Vec (Angelov & Inkpen, 2024). These models utilize external knowledge, typically through pretrained sentence embeddings such as MiniLM or the Universal Sentence Encoder. We follow each method's official implementation and recommended configuration as provided in their respective GitHub repositories.

Additionally, we include MALLET (McCallum, 2002), a highly optimized Gibbs-sampling-based LDA implementation, and our proposed model, PRISM. Both were run using the MALLET framework with default hyperparameters, enabling internal parameter optimization (e.g., `optimizeInterval`). For PRISM, we further supplied the model with estimated $\hat{\boldsymbol{\beta}}$ as described in Section 4.

Metrics. We evaluate topic models using statistical and human-aligned metrics that capture different dimensions of quality: c_v *Coherence*, normalized pointwise mutual information (NPMI) and the word intrusion detection (*WID*) task. Formal definitions appear in Appendix B. c_v *Coherence* (Röder et al., 2015) and NPMI (Bouma, 2009) measure the semantic relatedness of top words within a topic, based on co-occurrence statistics. While both are widely used, we tend to favor c_v due to its empirically stronger correlation with human judgments. *WID* (Chang et al., 2009) evaluates topic interpretability via the identification of an out-of-place word among a topic's top words. To scale this human-centric task, we follow (Garg et al., 2023) and use large language models (LLMs) as automated judges. WID implementation details are provided in Appendix B.2.

Setup. To enable fair and robust comparison, we evaluate all models under a unified protocol. For each dataset, we select three values of K near the reference number of ground-truth topics, along with slightly larger values to support finer-grained topic discovery. For TrumpTweets, which lacks labels, we use comparable K values to those in labeled datasets (See Table 4). This protocol reflects a weakly-supervised topic modeling paradigm, in which coarse supervision guides model behavior without enforcing strict topic-label alignment, following the principles outlined by (Zhao et al., 2017). All models are evaluated using the top 10 words per topic, and each configuration is run 10 times to account for stochastic variation; final scores are averaged across runs and topic counts.
Models with adaptive topic selection are evaluated accordingly. For BERTopic, we report the best result across runs with and without a fixed K; for Contextual-Top2Vec, which infers K automatically, we evaluate its output as-is. Further implementation details appear in Appendix C.

Our Results. We evaluate PRISM across five benchmark datasets, focusing on two key questions: (1) whether it provides consistent improvements over classical LDA as implemented in MALLET, and (2) how it compares to recent topic models, including both corpus-intrinsic approaches and those that leverage external semantic knowledge. The following results address both aspects. Models above the dashed line are direct baselines; those below use external embeddings and represent an upper bound (Table 1, Table 2).

Table 1: Model performance across datasets. Each entry is mean (std) over three topic settings. Best is **bold**, second-best is underlined. † indicates PRISM outperforms MALLET for that metric.

MODELS	20NG		BBC News		M10		DBLP		TrumpTweets	
	c_v	NPMI	c_v	NPMI	c_v	NPMI	c_v	NPMI	c_v	NPMI
ProdLDA	.5976 (.0216)	.0569 (.0057)	.6427 (.0059)	−.0046 (.0110)	.4218 (.0336)	−.0951 (.0954)	**.4733** (.0196)	.0072 (.0464)	.5373 (.0099)	.0758 (.0029)
NeuralLDA	.5339 (.0049)	.0425 (.0010)	.5720 (.0234)	−.0532 (.0274)	.4179 (.0183)	−.1950 (.0459)	.3833 (.1022)	−.0207 (.0768)	.4252 (.0159)	−.0249 (.0037)
LDA	.5321 (.0078)	.0457 (.0033)	.4924 (.0150)	−.0409 (.0153)	.3833 (.0116)	−.1602 (.0455)	.3647 (.0148)	−.0273 (.0262)	.4188 (.0196)	−.0109 (.0041)
ETM	.5242 (.0079)	.0433 (.0049)	.4963 (.0062)	−.0176 (.0103)	.3659 (.0150)	−.1255 (.0384)	.2828 (.0581)	−.0389 (.0152)	.4133 (.0338)	.0203 (.0136)
NMF	.5497 (.0087)	.0550 (.0029)	.4564 (.0369)	−.0037 (.0110)	.3536 (.0019)	−.0943 (.0487)	.3663 (.0213)	.0102 (.0188)	.4358 (.0103)	.0326 (.0120)
BERTopic	.5557 (.0155)	.0887 (.0113)	**.7124** (.0073)	**.1694** (.0022)	.4030 (.0131)	**.1310** (.0095)	.3862 (.0075)	−.0039 (.0051)	.4461 (.0025)	−.0287 (.0043)
C-Top2Vec	.5632 (.0327)	.0682 (.0152)	.5108 (.0484)	−.5750 (.0262)	.3543 (.0033)	−.1675 (.0036)	.3185 (.0005)	−.1328 (.0019)	.3653 (.0028)	−.2349 (.0045)
FASTopic	.5744 (.0258)	.0223 (.0078)	.6572 (.0314)	.0236 (.0136)	.4473 (.0081)	−.2065 (.0172)	.3239 (.0027)	.0012 (.0102)	.3804 (.0243)	−.1319 (.0380)
MALLET	.6381 (.0015)	.1106 (.0081)	.6371 (.0047)	.1128 (.0104)	.4639 (.0080)	.0718 (.0026)	.4394 (.0175)	.0443 (.0082)	.5044 (.0122)	.0721 (.0057)
PRISM (ours)	**.6581**†(.0073)	**.1169**†(.0050)	.6763†(.0149)	.1309†(.0186)	**.5269**†(.0021)	.0831†(.0128)	.4638†(.0156)	**.0736**†(.0110)	**.5557**†(.0046)	**.0952**†(.0104)

Table 2: Word Intrusion Detection accuracy across five datasets (mean (std) over three topic settings). Best is **bold**, second-best is underlined; † indicates PRISM outperforms MALLET.

MODELS	20NewsGroup	BBC	M10	DBLP	TrumpTweets
ProdLDA	.4561 (.0165)	.4556 (.0681)	.2232 (.0322)	.2528 (.0638)	.2759 (.0722)
NeuralLDA	.2533 (.0518)	.3259 (.0060)	.1194 (.0211)	.1667 (.0667)	.1296 (.0414)
LDA	.1472 (.0202)	.1333 (.3615)	.1139 (.4885)	.0833 (.9211)	.1611 (.5625)
ETM	.3422 (.0301)	.4592 (.0726)	.0889 (.3713)	.1194 (.6224)	.1130 (.9177)
NMF	.1411 (.0196)	.0630 (.3148)	.0010 (.8161)	.0010 (.8161)	.2426 (.3977)
BERTopic	.3811 (.0452)	.5537 (.0092)	**.4907** (.0227)	.3584 (.0118)	.3139 (.0103)
C-Top2Vec	.6022 (.0309)	.5915 (.0618)	.3875 (.0188)	**.4928** (.0356)	**.3554** (.1016)
FASTopic	.5844 (.0265)	**.6315** (.0500)	.3379 (.0442)	.2722 (.0278)	.2352 (.0466)
MALLET	.5744 (.0305)	.4667 (.0330)	.3750 (.0276)	.3111 (.0788)	.2741 (.0226)
PRISM (ours)	**.6078**†(.0374)	.6137†(.0453)	.3915†(.0176)	†.3361 (.0742)	†.3028 (.0410)

Quantitative Results. As shown in Table 1, PRISM consistently outperforms the original MALLET implementation, achieving substantial gains in both c_v and NPMI. Beyond improving upon MALLET, PRISM frequently closes the gap to, or even surpasses, recent embedding-based methods. This is particularly evident on the BBC News, M10, and TrumpTweets datasets, where PRISM not only significantly outperforms MALLET but also achieves the best or second-best scores across both metrics—demonstrating competitiveness with SOTA methods. PRISM obtains the best c_v score on three out of five datasets (20NG, M10, TrumpTweets), and ranks second on BBC News and DBLP. Given that c_v is widely regarded as more reflective of human topic judgments, these results suggest that PRISM produces more interpretable and semantically coherent topics across diverse domains. While NPMI improvements are somewhat more modest, PRISM still achieves the best scores on 20NewsGroup, M10 and TrumpTweets and remains competitive throughout.

To further assess topic interpretability, we employ the Word Intrusion Detection (WID) task (detailed in Appendix B.2). As shown in Table 2, PRISM ranks among the top two models on three out of five datasets and remains highly competitive on the remaining two. Among corpus-intrinsic models (above the dashed line), PRISM consistently achieves the highest accuracy—outperforming MALLET and all other classical baselines. It also competes strongly with embedding-based methods (below the dashed line), outperforming all of them on 20NG and several on BBC and M1. Overall, these results show that PRISM not only dominates traditional models in both coherence and interpretability but also matches—and at times exceeds—the performance of state-of-the-art models that rely on external knowledge.

Qualitative Analysis. Over BBC dataset, we show a comparison of PRISM to BERTopic, which achieved the highest c_v and NPMI scores, and to ProdLDA, the strongest corpus-intrinsic baseline in c_v (Table 1) over BBC. The dataset contains five ground-truth topic labels. As shown in Figure 2, PRISM successfully recovers all five topics—politics, business, sports, technology, and entertainment—with minimal off-topic words. In contrast, BERTopic fails to recover the business category and exhibits redundancy across two overlapping technology topics. ProdLDA clearly captures politics and business, while entertainment and technology are only partially distinguishable, and sports is entirely missing. These observations align with the WID results (Table 2), where PRISM ranks second overall, while BERTopic and ProdLDA rank fourth

Topic 1	Topic 2	Topic 3	Topic 4	Topic 5
government	film	win	game	virus
election	good	play	phone	mail
party	award	player	mobile	site
labour	music	match	technology	software
plan	win	game	device	program
tory	show	final	service	security
rise	star	club	music	user
country	include	good	video	attack
tax	actor	back	search	computer
economy	band	team	gadget	net

(a) BERTopic: top-10 words

Topic 1	Topic 2	Topic 3	Topic 4	Topic 5
mobile	category	bug	rise	election
game	victory	yesterday	quarter	government
phone	aviator	shrink	interest	plan
player	album	navigate	investment	party
technology	film	keynote	rate	labour
firm	goal	fate	growth	issue
service	performance	declaration	analyst	tory
user	great	finnish	figure	leader
music	ball	excitement	price	conservative
system	band	inevitable	stock	public

(b) ProdLDA: top-10 words

Topic 1	Topic 2	Topic 3	Topic 4	Topic 5
government	film	company	win	technology
election	good	market	game	computer
party	award	firm	play	phone
labour	music	rise	player	mobile
plan	win	sale	good	service
tory	show	price	back	user
law	include	economy	match	game
issue	star	share	team	firm
public	top	growth	club	net
minister	actor	month	final	music

(c) PRISM: top-10 words

Figure 2: Top-10 words per topic on the **BBC** dataset with $K = 5$. Each column is a distinct topic. Colors denote manually interpreted categories (politics, entertainment, business, sports, technology); lighter shades indicate weaker relevance and white indicates no clear association. Panels: (a) BERTopic, (b) ProdLDA, (c) PRISM.

Topic
gene
expression
protein
datum
sequence
cluster
dna
microarray
model
fold

(a) **BERTopic**

Topic	Topic
gene	protein
expression	structure
datum	sequence
microarray	dna
analysis	model
cluster	motif
regulatory	fold
model	prediction
method	algorithm
classification	bind

(b) **PRISM**

Topic	Topic
gene	protein
expression	sequence
datum	model
model	structure
network	dna
cluster	motif
analysis	base
microarray	fold
regulatory	prediction
paper	bind

(c) **MALLET**

Figure 3: Top-10 words for biology topics in M10.

Topic
soil
water
crop
yield
climate
irrigation
remote
change
agriculture
production

(a) **BERTopic**

Topic
soil
water
crop
yield
change
area
climate
effect
production
remote

(b) **PRISM**

Topic
water
soil
diesel
change
engine
model
climate
effect
production
fuel

(c) **MALLET**

Figure 4: Top-10 words for a climate/agriculture topic in M10.

and seventh, respectively. This suggests that PRISM produces more coherent and uniquely identifiable topics. A supplementary example is included in Appendix D.1.

On M10, we compare PRISM to BERTopic and MALLET. PRISM achieves the highest c_v and second-best WID score, while BERTopic leads in WID and NPMI, and MALLET ranks second in c_v (Table 1, Table 2). As shown in Figure 3, all models capture biologically meaningful themes, though MALLET includes a few less relevant terms (e.g., "paper," "network"). BERTopic merges gene-related and protein-related concepts into a single broad topic, whereas both PRISM and MALLET separate them into two distinct but related topics, one focused on gene expression and microarray, the other on protein structure and binding. This finer-grained separation reflects PRISM's stronger topical coherence and is also evident in its ranking of more meaningful terms (e.g., "microarray," "regulatory," "structure") with higher probability than MALLET. Interestingly, BERTopic's broader topic structure may contribute to its higher WID score: in the WID task, intruder words are sampled from other high-probability topics (details in Appendix B.2), and when topics overlap semantically, as with genes and proteins, intruders may feel topically adjacent rather than clearly out of place. PRISM's more specific topics make intruder detection more challenging, which may explain its slightly lower WID despite better topic distinctiveness. Figure 4 presents another M10 topic, likely related to climate and agriculture. PRISM and BERTopic show high overlap in top-ranked words ("soil," "water," "crop," "yield," etc.), with strong topic focus. In contrast, MALLET's output contains

generic or loosely related terms ("engine," "fuel," "model"), leading to reduced coherence. These results support the quantitative findings, where PRISM outperforms MALLET across all metrics and approaches the interpretability of BERTopic without using external knowledge.

6 Biological Experiments

Motivation and Analogy. We investigate the applicability of PRISM to biological data, aiming to uncover latent Biological Processes (BPs) from single-cell RNA sequencing (scRNA-seq) data. This task naturally parallels topic modeling: cells correspond to documents, genes to words, and BPs to topics. As in text, where documents often span multiple topics and words can take on different meanings depending on context, each cell may be involved in multiple BPs, and individual genes may participate in several biological functions, reflecting the many-to-many relationships captured by topic models. Furthermore, scRNA-seq data is organized as a count matrix, where each entry denotes the expression level of a gene in a cell, directly analogous to the word-document count matrix in LDA.

Datasets. We evaluate our approach on three scRNA-seq datasets spanning human and mouse tissues. BreastCancer comprises human breast tumor samples provided by a collaborating laboratory in a preprocessed form,[1] PBMC3k contains peripheral blood mononuclear cells (PBMCs) from a healthy donor,[2] and Zeisel brain profiles cells from the mouse cerebral cortex.[3]. All datasets were preprocessed using a standard Scanpy workflow; no provider-specific preprocessing was applied. Details are given in Appendix E.1).

Baselines. As a proof of concept, we compare PRISM to the standard LDA implementation in MALLET to test whether our corpus-intrinsic initialization improves the interpretability of biological processes in scRNA-seq data. We also include two widely used text-topic baselines: ProdLDA (Srivastava & Sutton, 2017) and NMF (Lee & Seung, 2001). Finally, we benchmark against two single-cell–specific factorization models: scHPF (single-cell hierarchical Poisson factorization) (Levitin et al., 2019) and cNMF (consensus NMF) (Kotliar et al., 2019).

Evaluation Metrics. We assess biological plausibility with an LLM-based scoring procedure following Hu et al. (2025). For each topic, we submit its top 20 genes to GPT-4 using a fixed prompt asking how likely the genes are to co-participate in a Biological Process (BP), and record the returned confidence as the topic's score. Averaging over topics yields a proxy for biological coherence (details in Appendix E.2.2). In addition, we report conventional gene-set quality metrics; definitions and full results appear in Appendix E.2.1 (definitions) and Appendix E.3 (results).

Experimental Setup. We evaluate all baselines and PRISM on the same scRNA-seq datasets under a matched configuration: the number of topics is fixed to $K = 5$, and each model is trained for 10 independent runs per dataset. For PRISM, the $\boldsymbol{\beta}$ prior is estimated exactly as in our text-corpus experiments, with a minor adjustment to the PPMI graph construction tailored to gene–gene co-occurrence (see Appendix E.1 for details).

Table 3: LLM-based evaluation scores (mean and std over 10 runs) across biological datasets.

Models	BreastCancer	pbmc3k	zeisel_brain
cNMF	<u>.8000</u> (.0505)	**.9021** (.0401)	<u>.9330</u> (.0172)
scHPF	.7712 (.0240)	.8326 (.0235)	.8980 (.0658)
NMF	.7880 (.0331)	.6590 (.0141)	.6670 (.0435)
ProdLDA	.7600 (.0469)	.4950 (.1862)	.5950 (.0282)
MALLET	.7920 (.0352)	.8392 (.0276)	.8920 (.0268)
PRISM	**.8320**†(.0171)	<u>.8997</u>†(.0167)	**.9350**†(.0206)

[1] https://zenodo.org/records/10620607
[2] https://scanpy.readthedocs.io/en/stable/generated/scanpy.datasets.pbmc3k.html
[3] https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE60361

Results. As shown in Table 3, PRISM attains the highest GPT-4 confidence on two of three datasets (BreastCancer, zeisel_brain) and is a close second on pbmc3k, consistently outperforming MALLET. Together with the gene-set metrics (see Appendix E.3), these results may indicate that corpus-intrinsic LDA variants are well-suited to scRNA-seq: PRISM and MALLET clearly surpass generic text models (NMF, ProdLDA), while PRISM is competitive with single-cell baselines (cNMF, scHPF) and reliably improves over MALLET. Since GPT-4 scores track biological plausibility (Hu et al., 2025), PRISM's gains suggest more coherent, biologically meaningful topics.

7 Conclusion

We introduced PRISM, a corpus-driven initialization method for LDA that integrates semantic structure derived directly from the data, without relying on external embeddings. Across five diverse datasets—spanning news, social media, and biomedical texts—PRISM consistently improves coherence and interpretability over classical baselines and rivals embedding-based models. Its strong performance, despite operating entirely on corpus-internal signals, highlights the underexplored potential of structure-aware initialization in probabilistic models. This work opens new directions for enhancing topic models through data-intrinsic semantics—bridging the gap between classical transparency and modern representational strength.

7.1 Limitations and Future Directions

PRISM, like classical topic models, requires a priori selection of K, treated as a tunable hyperparameter; while this may limit full automation across heterogeneous corpora, our experiments indicate robustness across a practical range of K. A natural extension is a corpus-driven initialization for the document–topic prior $\boldsymbol{\alpha}$, aiming to adapt sparsity and enhance interpretability, and potentially further stabilizing training across datasets.

References

Meta AI. Llama 3.3-70b instruct, 2024. URL `https://huggingface.co/meta-llama/Llama-3.3-70B-Instruct`. Accessed: 2024-02-10.

Dimo Angelov and Diana Inkpen. Topic modeling: Contextual token embeddings are all you need. In *Findings of the Association for Computational Linguistics: EMNLP 2024*, 2024.

Arthur Asuncion, Max Welling, Padhraic Smyth, and Yee Whye Teh. On smoothing and inference for topic models. In *Proceedings of the Twenty-Fifth Conference on Uncertainty in Artificial Intelligence (UAI)*, pp. 27–34, 2009.

Yoav Benjamini and Yosef Hochberg. Controlling the false discovery rate: A practical and powerful approach to multiple testing. *Journal of the Royal Statistical Society: Series B*, 57(1):289–300, 1995.

Federico Bianchi, Silvia Terragni, and Dirk Hovy. Pre-training is a hot topic: Contextualized document embeddings improve topic coherence. In *Proceedings of the 59th Annual Meeting of the Association for Computational Linguistics (ACL)*, pp. 759–766, 2021.

David M. Blei, Andrew Y. Ng, and Michael I. Jordan. Latent dirichlet allocation. *Journal of Machine Learning Research*, 3:993–1022, 2003. URL `https://jmlr.org/papers/v3/blei03a.html`.

Gerlof Bouma. Normalized (pointwise) mutual information in collocation extraction. In *Proceedings of the Biennial GSCL Conference*, pp. 31–40, 2009.

John A. Bullinaria and Joseph P. Levy. Extracting semantic representations from word co-occurrence statistics: A computational study. *Behavior Research Methods*, 44(3):510–526, 2012.

Jonathan Chang, Jordan Boyd-Graber, Sean Gerrish, Chong Wang, and David M. Blei. Reading tea leaves: How humans interpret topic models. In *Advances in Neural Information Processing Systems (NeurIPS)*, volume 22, 2009. URL `https://proceedings.neurips.cc/paper_files/paper/2009/file/dfeb1a3aef17961ee3e6a5a89a6c0708-Paper.pdf`.

Kenneth W Church and Patrick Hanks. Word association norms, mutual information, and lexicography. *Computational Linguistics*, 16(1):22–29, 1990.

Ronald R Coifman and Stéphane Lafon. Diffusion maps. *Applied and Computational Harmonic Analysis*, 21(1):5–30, 2006.

Adji B. Dieng, Francisco J. R. Ruiz, and David M. Blei. Topic modeling in embedding spaces. *Transactions of the Association for Computational Linguistics*, 8:439–453, 2020. doi: 10.1162/tacl_a_00325.

Siddhant Garg, Dinesh Balasubramaniam, Aniruddha Guha, Dipankar Das, and Shubham Jain. Llm reading tea leaves: Automatically evaluating topic models with large language models. In *Findings of the Association for Computational Linguistics (ACL)*, 2023. URL `https://aclanthology.org/2023.findings-acl.550/`.

Thomas L. Griffiths and Mark Steyvers. Finding scientific topics. *Proceedings of the National Academy of Sciences*, 101(suppl 1):5228–5235, 2004. doi: 10.1073/pnas.0307752101.

Maarten Grootendorst. Bertopic: Leveraging bert and c-tf-idf to create easily interpretable topics. *arXiv preprint*, 2022. URL `https://arxiv.org/abs/2203.05794`.

Minji Hu, Safa Alkhairy, Irene Lee, Ryan T Pillich, Daniel Fong, Kevin Smith, Rebecca Bachelder, Trey Ideker, and Daniel Pratt. Evaluation of large language models for discovery of gene set function. *Nature Methods*, 22(1):82–91, 2025. doi: 10.1038/s41592-024-02525-x.

Jagadeesh Jagarlamudi, Hal Daumé III, and Raghavendra Udupa. Incorporating lexical priors into topic models. In *Proceedings of the 13th Conference of the European Chapter of the Association for Computational Linguistics*, pp. 204–213. Association for Computational Linguistics, 2012.

Aobo Kong, Shiwan Zhao, Hao Chen, Qicheng Li, Yong Qin, Ruiqi Sun, Xin Zhou, Enzhi Wang, and Xiaohang Dong. Better zero-shot reasoning with role-play prompting. *arXiv preprint arXiv:2308.07702*, 2023.

D. Kotliar, A. Veres, M. A. Nagy, S. Tabrizi, E. Hodis, D. A. Melton, and P. C. Sabeti. Identifying gene expression programs of cell-type identity and cellular activity with single-cell rna-seq using cnmf. *eLife*, 8:e43803, 2019. doi: 10.7554/eLife.43803.

Daniel D. Lee and H. Sebastian Seung. Algorithms for non-negative matrix factorization. In *Advances in Neural Information Processing Systems 13 (NIPS 2000)*, pp. 556–562, 2001.

H. M. Levitin, J. Yuan, Y. L. Cheng, F. J. Ruiz, D. Pe'er, and et al. De novo gene signature identification from single-cell rna-seq with hierarchical poisson factorization (schpf). *Molecular Systems Biology*, 15(2): e8577, 2019. doi: 10.15252/msb.20188557.

Malte D. Luecken and Fabian J. Theis. Current best practices in single-cell rna-seq analysis: a tutorial. *Molecular Systems Biology*, 15(6):e8746, 2019. doi: 10.15252/msb.20188746.

Andrew Kachites McCallum. Mallet: A machine learning for language toolkit. Technical software, University of Massachusetts Amherst University of Pennsylvania, 2002. URL `http://mallet.cs.umass.edu`.

Thomas P. Minka. Estimating a dirichlet distribution. Technical Report MSR-TR-2000-7, Microsoft Research, 2000. `https://tminka.github.io/papers/dirichlet/`.

Douglas A Reynolds. Gaussian mixture models. *Encyclopedia of biometrics*, 741:659–663, 2009.

Michael Röder, Andreas Both, and Alexander Hinneburg. Exploring the space of topic coherence measures. In *Proceedings of the eighth ACM international conference on Web search and data mining*, pp. 399–408, 2015.

Hinrich Schütze. Automatic word sense discrimination. *Computational linguistics*, 24(1):97–123, 1998.

scverse. Scanpy documentation: `pp.highly_variable_genes`. `https://scanpy.readthedocs.io/en/stable/generated/scanpy.pp.highly_variable_genes.html`, accessed 2025.

Akash Srivastava and Charles Sutton. Autoencoding variational inference for topic models. In *International Conference on Learning Representations (ICLR)*, 2017. URL `https://openreview.net/forum?id=BybtVK9lg`.

Timothy Stuart, Andrew Butler, and et al. Comprehensive integration of single-cell data. *Cell*, 177(7): 1888–1902.e21, 2019. doi: 10.1016/j.cell.2019.05.031.

Silvia Terragni, Xuan Tien Doan, Brian Davis, Bedoor AlShebli, Suppawong Tuarob, Pascal Frossard, Javier Borge-Holthoefer, Raheel AlGhamdi, and Peter Gloor. Octis: Comparing and optimizing topic models is simple! In *Proceedings of the 16th Conference of the European Chapter of the Association for Computational Linguistics: System Demonstrations*, pp. 263–270, 2021.

Leonardo Terrone, Federico Bianchi, Elisabetta Fersini, and Matteo Palmonari. Octis: Comparing and optimizing topic models is simple! In *Proceedings of the 16th Conference of the European Chapter of the Association for Computational Linguistics: System Demonstrations*, pp. 263–270, 2021.

Isaac Virshup, Sergei Rybakov, Fabian J. Theis, Philipp Angerer, and F. Alexander Wolf. anndata: Access and store annotated data matrices. *Journal of Open Source Software*, 9(101):4371, 2024. doi: 10.21105/joss.04371.

Hanna Wallach, David Mimno, and Andrew McCallum. Rethinking LDA: Why priors matter. In *Advances in Neural Information Processing Systems*, volume 22, pp. 1973–1981. Curran Associates, Inc., 2009.

Jason Wei, Xuezhi Wang, Dale Schuurmans, Maarten Bosma, Brian Ichter, Fei Xia, Ed Chi, Quoc V Le, and Denny Zhou. Chain of thought prompting elicits reasoning in large language models. In *Advances in Neural Information Processing Systems (NeurIPS)*, 2022.

F. Alexander Wolf, Philipp Angerer, and Fabian J. Theis. Scanpy: large-scale single-cell gene expression data analysis. *Genome Biology*, 19(1):15, 2018. doi: 10.1186/s13059-017-1382-0.

Xiaobao Wu, Thong Nguyen, Delvin Ce Zhang, William Yang Wang, and Anh Tuan Luu. Fastopic: Pretrained transformer is a fast, adaptive, stable, and transferable topic model. *arXiv:2405.17978*, 2024.

Wayne Xin Zhao, Songbo Tan, Rui Zhang, Xueqi Li, Yongdong Zhang, and Ji-Rong Liu. Weakly-supervised text classification with topic modeling. In *Proceedings of the 2017 ACM on Conference on Information and Knowledge Management (CIKM)*, pp. 2235–2238. ACM, 2017.

A Datasets

As described in Sec 5, we evaluate on five benchmarks. Four are standard corpora from `OCTIS` (preprocessed by its internal pipeline). We also include *TrumpTweets*, following BERTopic (Grootendorst, 2022), to assess performance on short, noisy social media text. Summary statistics are in Table 4.

Table 4: Dataset statistics. Avg. Len. denotes average document length in tokens; K lists the topic counts used.

Dataset	**#Docs**	**Vocab**	**Avg. Len.**	**#Labels**	K
20NewsGroup	16,309	1,612	48.0	20	20, 25, 50
BBC	2,225	2,949	12.1	5	5, 10, 15
M10	8,355	1,696	5.9	10	10, 15, 20
DBLP	54,595	1,513	5.4	4	4, 10, 15
TrumpTweets	18,239	1,988	9.0	–	10, 15, 20

The *TrumpTweets* dataset was obtained from the same source cited by BERTopic.[4] To ensure consistency across datasets, we applied the `OCTIS` preprocessing module with basic filtering:

```
Preprocessing(
    vocabulary=None,
    lowercase=True,
    remove_numbers=True,
    min_words_docs=3,
    min_chars=3,
    min_df=.01,
    max_df=.9,
    max_features=2000,
    remove_punctuation=True,
    lemmatize=True,
    stopword_list="english"
)
```

This configuration balances document retention and vocabulary quality, which is especially important for short texts such as tweets.

B Metrics

We assess topic quality using corpus-intrinsic coherence (c_v) and normalized pointwise mutual information (NPMI), plus a language-model–assisted interpretability evaluation.

B.1 Standard Topic Modeling Metrics

c_v **Coherence.** The c_v metric (Röder et al., 2015) combines pairwise NPMI with cosine similarity over context vectors derived from a sliding window:

$$C_v = \frac{1}{|W|(|W|-1)} \sum_{i<j} \mathrm{NPMI}(w_i, w_j) \cdot \cos(\mathbf{v}_i, \mathbf{v}_j), \tag{1}$$

where W is the set of top-N words per topic and $\mathbf{v}_i \in \mathbb{R}^{|C|}$ encodes co-occurrence statistics of w_i across the corpus C. We compute c_v with `Gensim`'s `CoherenceModel` (defaults).

[4] `https://www.thetrumparchive.com/faq`

NPMI. Following (Bouma, 2009),

$$\mathrm{NPMI}(w_i, w_j) = \frac{\log \frac{P(w_i, w_j)}{P(w_i)P(w_j)}}{-\log P(w_i, w_j)}, \tag{2}$$

which normalizes PMI to $[-1, 1]$ for comparability across corpora.

B.2 Word Intrusion Detection (WID)

To complement statistical metrics with a proxy for human interpretability, we use the Word Intrusion Detection (WID) task. General framework of the metric can be viewed in Figure 5.

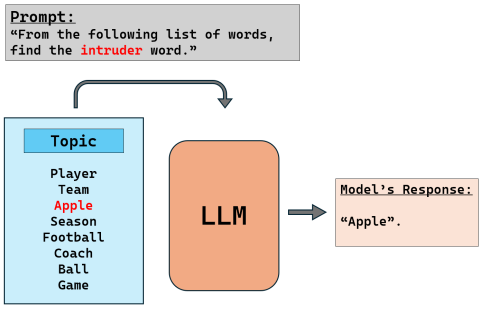

Figure 5: Illustration of the Word Intrusion Detection (WID) framework. A large language model is prompted to identify the word that does not belong in a list of top topic words (a.k.a. the intruder). The prompt shown here is illustrative; actual prompts used in our experiments follow a more structured format.

The Word Intrusion Detection (WID) task (Chang et al., 2009) is a widely adopted human-centered evaluation method for assessing topic interpretability. In this task, annotators are shown the top-N words of a topic, one of which is an intruder—i.e., a word drawn from another topic that appears with low probability in the target topic but is prominent elsewhere. The annotator is asked to identify the word that does not semantically belong. Higher topic coherence typically results in easier and more consistent intruder identification, making WID an indirect yet effective proxy for human interpretability.

Recent studies have proposed leveraging large language models (LLMs) to automate WID (Garg et al., 2023), enabling scalable, consistent, and human-aligned evaluation. We adopt this paradigm by employing a LLM as an automatic evaluator within our WID framework (see Figure 5). This model is prompted to identify the intruder from each modified topic word list, effectively simulating human judgment without the need for manual annotation.

Pipline. Our pipeline leverages HuggingFace's `transformers` library. We initialize the tokenizer via `AutoTokenizer.from_pretrained`, explicitly setting the end-of-sequence (`eos`) token as the padding token to ensure consistent handling of short text inputs. The LLM is integrated with the `pipeline` API using `device_map="auto"` for efficient hardware mapping and `torch_dtype=torch.bfloat16` to reduce memory overhead.

During inference, each topic's word list is modified by injecting one intruder word. The model is then prompted to identify the semantic outlier. Its success in this task reflects the semantic cohesion of the topic, thus serving as an indirect interpretability metric that complements statistical scores.

The task involves identifying an intruder word inserted into an otherwise coherent topic word list. We evaluate performance using the Meta-LLaMA-3.3-70B-Instruct model (AI, 2024), which demonstrates strong alignment with human judgment.

```
"You are an assistant in a word intrusion detection task.

From the following list of tokens, identify the one token that does not belong
with the others.
For example: for 1. Banana 2. Orange 3. Japan 4. Strawberry 5. Tree The expected
answer is index 3.

The reason 3 is the intruder's index is since Banana, Orange, Strawberry and
Tree are related to fruits in a way, but Japan is a country.

Another example: for 1. Dog 2. Cat 3. Horse 4. Apple 5. Pig The expected answer
is index 4.

The reason 4 is the intruder's index is since Dog, Cat, Horse and Pig are
different kinds of animals, while Apple is a fruit.

Here are your words:  {numbered_word_list}.

In your response, you have to provide only one index between 1 to {len(words_list)},
where the index is the intruder word's index from the given list. Without any
additional explanations."
```

Figure 6: Prompt template for the Word Intrusion Detection (WID) task, with instructions, two illustrative examples, and a structured response format. The input variable `numbered_word_list` is inserted at evaluation time to test different word sets.

Algorithm 1 Word Intrusion Detection (WID) Pipeline

Input: set of topic models $\mathcal{M}$; prompt template
Output: saved LLM outputs; model-wise accuracy scores

for each model $M \in \mathcal{M}$ **do**
  for each topic $T \in M.\textsc{Topics}$ **do**
    for each word list size $s \in \{10, 15, 20\}$ **do**
      $W \leftarrow \textsc{TopWords}(T, s)$
      $W_{\text{idx}} \leftarrow \textsc{AddIndices}(W)$
      $\textit{prompt} \leftarrow \textsc{FormatPrompt}(W_{\text{idx}})$
      $\textit{result} \leftarrow \textsc{QueryLLM}(\textit{prompt})$
      $\textsc{SaveOutput}(\textit{result})$

$\textsc{EvaluateAccuracy}(\mathcal{M})$ ▷ Eq. 3

Prompt Engineering. Inspired by chain-of-thought prompting (Wei et al., 2022) and role-play prompting (Kong et al., 2023), we crafted prompts to guide the large language model (LLM). The template includes two examples that demonstrate both intruder identification and the expected output format (Figure 6).

Evaluation Metric. Accuracy is computed as the proportion of correct intruder identifications:

$$\text{Accuracy} = \frac{\text{Count}(\text{LLM response} = \text{true intruder})}{K}, \tag{3}$$

where K is the number of topics. We report accuracy separately for top-10, top-15, and top-20 word lists.

This pipeline evaluates topic coherence by detecting intruder words—terms that do not fit within topic word lists—using an LLM. For each model, we form top-10/15/20 word lists per topic, index the words (AddIndices), format a structured prompt (FormatPrompt), query the LLM (QueryLLM), and save outputs. We then compare predictions to the known intruders to compute accuracy (EvaluateAccuracy).

C Setip

C.1 Models

To ensure fair and reproducible comparisons, we evaluate a diverse set of topic modeling baselines using publicly available implementations under their recommended configurations.

OCTIS Models. We run `LDA`, `NMF`, `ETM`, `ProdLDA`, and `NeuralLDA` via the `OCTIS` framework, using its standardized preprocessing pipeline and default hyperparameters unless noted.

ETM configurations. We consider two ETM variants:

- **Without pretrained embeddings:** the default `OCTIS` configuration.
- **With pretrained embeddings:** GloVe initialization:

```
ETM(num_topics=TOPICS_NUM,
    embeddings_path="filtered_glove.100d.vec",
    embedding_size=100)
```

Results were similar across the two settings (no detectable improvement from GloVe), so we report the corpus-only variant in the main tables.

BERTopic. We use the official implementation[5] with default parameters, except we explicitly set the number of topics to match our experimental setup; when applicable, we report the better of auto-detected vs. fixed-K configurations.

Contextual Top2Vec. We run C-Top2Vec in contextual-embedding mode with:

```
Top2Vec(
    documents,
    split_documents=True,
    contextual_top2vec=True,
    embedding_model="all-MiniLM-L6-v2",
    speed="deep-learn",
    workers=2
)
```

This follows the recommended usage from the official repository.[6] We also tested a custom tokenizer, which did not improve performance; therefore, we use default tokenization in reported results.

FASTopic. We use the `TopMost` implementation[7] with the recommended preprocessing utility:

```
preprocessing = Preprocess(stopwords="English")
model = FASTopic(num_topics=topic_num, preprocess=preprocessing)
```

Hyperparameters follow the defaults in the official GitHub repository,[8] with no additional tuning.

C.2 Computing Infrastructure

Local (WSL). ASUS Vivobook S 15/16 OLED; Windows 11 + WSL2 (Ubuntu). CPU: *Intel Core Ultra 9 185H* (11 cores / 22 threads); RAM: *16 GB*. GPU: not utilized. Used for PRISM, MALLET, and OCTIS models (LDA, NMF, ProdLDA, ETM, NeuralLDA), and BERTopic.

[5] https://github.com/MaartenGr/BERTopic
[6] https://github.com/ddangelov/Top2Vec
[7] https://github.com/yfsong0709/TopMost
[8] https://github.com/bobxwu/FASTopic

Server. Linux (Ubuntu). GPUs: *4× NVIDIA L40S*, each with ∼46 GiB VRAM (driver *575.57.08*, CUDA *12.9*). Example utilization snapshot (from `nvidiasmi`): GPU 0/1/3 active (≈28.6/17.9/17.1 GiB). (Host CPU/RAM not recorded.) Used for FASTopic and Contextual-Top2Vec.

C.3 Licenses of External Assets

We list the license for each third-party asset used.

Table 5: Licenses / terms for third-party software and assets.

Asset	**License / Terms**
Software / libraries	
OCTIS	MIT License[9]
Gensim	LGPL v2.1 (or later)[10]
MALLET	Apache License 2.0[11]
BERTopic	MIT License[12]
Contextual-Top2Vec (Top2Vec)	BSD 3-Clause[13]
FASTopic / TopMost	Apache License 2.0[14]
ETM (reference implementation)	MIT License[15]
CTM (Contextualized Topic Models)	MIT License[16]
Text datasets	
OCTIS preprocessed corpora (20NG, BBC, M10, DBLP)	Original source terms via OCTIS dataset cards[17]
TrumpTweets (The Trump Archive)	Site terms / Twitter TOS[18]
Biological datasets	
PBMC3k (10x Genomics)	CC BY 4.0[19]
Zeisel mouse brain (GSE60361, GEO)	GEO usage policy (no explicit license)[20]
BreastCancer (Zenodo: 10.5281/zenodo.10620607)	CC BY 4.0[21]

D Additional Experiments

D.1 More Qualitative Findings

To complement the qualitative findings presented in the main paper, we include additional quantitative analysis for BBC dataset here.

BBC Dataset. Figure 7a (MALLET) and Figure 7b (PRISM) display the top words for each topic on the BBC dataset with 5 topics. While MALLET produces reasonable topics, it redundantly captures politics in two separate themes and fails to isolate the entertainment domain. In contrast, PRISM yields distinct and semantically meaningful topics, effectively covering all major themes in the corpus. These results suggest that while MALLET offers a solid inference framework, our initialization method pushes the model further

[9] `https://github.com/MIND-Lab/OCTIS/blob/master/LICENSE`
[10] `https://github.com/RaRe-Technologies/gensim/blob/develop/LICENSE`
[11] `http://mallet.cs.umass.edu/` (see `LICENSE` in the distribution)
[12] `https://github.com/MaartenGr/BERTopic/blob/master/LICENSE`
[13] `https://github.com/ddangelov/Top2Vec/blob/master/LICENSE`
[14] `https://pypi.org/project/fastopic/` (license field)
[15] `https://github.com/adjidieng/ETM/blob/master/LICENSE`
[16] `https://github.com/MilaNLProc/contextualized-topic-models/blob/master/LICENSE`
[17] `https://github.com/MIND-Lab/OCTIS`
[18] `https://www.thetrumparchive.com/faq`; `https://developer.x.com/en/developer-terms`
[19] `https://www.10xgenomics.com/resources/datasets`
[20] `https://www.ncbi.nlm.nih.gov/geo/info/disclaimer.html`
[21] `https://zenodo.org/records/10620607`

Topic 1	Topic 2	Topic 3	Topic 4	Topic 5
company	technology	law	win	election
market	phone	case	good	government
rise	mobile	court	play	party
sale	game	government	game	labour
firm	service	rule	film	plan
price	music	claim	award	tory
share	user	legal	player	public
growth	computer	charge	back	country
economy	net	police	show	work
month	firm	ban	world	minister

(a) MALLET Top 10 words

Topic 1	Topic 2	Topic 3	Topic 4	Topic 5
government	film	company	win	technology
election	good	market	game	computer
party	award	firm	play	phone
labour	music	rise	player	mobile
plan	win	sale	good	service
tory	show	price	back	user
law	include	economy	match	game
issue	star	share	team	firm
public	top	growth	club	net
minister	actor	month	final	music

(b) PRISM Top 10 words

Figure 7: Top-10 words per topic on the **BBC** dataset with $K = 5$. Each column is a distinct topic. Colors in the panels denote manually interpreted categories (**politics**, **entertainment**, **business**, **sports**, and **technology**); lighter shades indicate weaker relevance and white indicates no clear association. Panels: (a) MALLET, (b) PRISM.

toward more coherent and semantically distinct topics, indicating that the observed improvements stem from our approach rather than the base model alone.

D.2 Ablation: Priors and Embeddings

To assess the contribution of individual components of our method, we conducted ablation studies focusing on priors and embeddings. Specifically, we evaluated four variants: (1) replacing our custom word embeddings (constructed via soc-PPMI and diffusion maps) with pretrained GloVe embeddings; (2) introducing a random prior within the MALLET framework to test whether improvements arise solely from enabling an asymmetric $\boldsymbol{\beta}$ prior (unsupported in the original MALLET, which assumes a scalar $\boldsymbol{\beta}$); (3) using the raw PPMI matrix without applying cosine similarity, to test whether the latter indeed enhances the capture of indirect semantic associations beyond direct co-occurrence; and (4) substituting diffusion maps with SVD to examine whether SVD alone provides more effective embeddings. For each variant, we report both standard statistical metrics (c_v, NPMI) in Table 6 and WID task performance in Table 7. Overall, the ablations consistently underperformed the full model, confirming that both the embedding construction and the asymmetric $\boldsymbol{\beta}$ prior are necessary to achieve the observed gains.

D.2.1 Statistic Metrics

We report ablation results using two standard coherence metrics, c_v and NPMI, consistent with the evaluation used in the main paper.

Table 6: Coherence across datasets for ablation variants. Each entry is mean (std). Best is **bold**, second-best is underlined.

MODELS	20NewsGroup		BBC		M10		DBLP		TrumpTweets	
	c_v	NPMI	c_v	NPMI	c_v	NPMI	c_v	NPMI	c_v	NPMI
GloVe + GMM Prior	.6324 (.0021)	.1133 (.0076)	.6395 (.0119)	.1100 (.0099)	.4839 (.0129)	.0658 (.0169)	.4503 (.0310)	.0588 (.0177)	.4968 (.0085)	.0699 (.0091)
Random Prior	.6230 (.0053)	.1104 (.0104)	.6420 (.0096)	.1131 (.0137)	.4822 (.0484)	.0717 (.0332)	.4539 (.0476)	.0591 (.0214)	.4910 (.0078)	.0678 (.0028)
No SOC (PPMI→DM)	.6482 (.0103)	.1164 (.0058)	.6540 (.0219)	.1250 (.0072)	.5132 (.0018)	.0734 (.0231)	**.4879** (.0209)	**.0742** (.0114)	.5194 (.0037)	.0840 (.0079)
SVD in place of DM	.6436 (.0117)	.1159 (.0051)	.6456 (.0141)	.1115 (.0128)	.4814 (.0115)	.0694 (.0129)	.4611 (.0359)	.0616 (.0169)	.4969 (.0169)	.0697 (.0072)
PRISM (reference)	**.6581** (.0073)	**.1169** (.0050)	**.6763** (.0149)	**.1309** (.0186)	**.5269** (.0021)	**.0831** (.0128)	.4638 (.0156)	.0736 (.0110)	**.5557** (.0046)	**.0952** (.0104)

The results in Table 6 highlight the consistent advantage of our method. Across all datasets, PRISM achieves the highest coherence scores, with the sole exception of DBLP, where it ranks second. Notably, the variant that omits cosine similarity (No SOC) emerges as the most competitive ablation, frequently attaining the

second-best results. This suggests that the overall framework of our method effectively captures meaningful similarities, while the cosine-similarity step further enhances performance.

D.2.2 Word Intrusion Detection

We also evaluate the ablation variants on the Word Intrusion Detection (WID) task, which was used in the main paper to assess topic interpretability. Results are reported in Table 7. Across all datasets, PRISM consistently outperforms the ablation baselines, achieving the highest WID accuracy. These findings indicate that PRISM produces more coherent and interpretable topics, enabling intruder words to be more reliably identified.

Table 7: Word Intrusion Detection (WID) accuracy for ablations across datasets. Each entry is mean accuracy (std) over 10 runs. Ablations: **GloVe Embed** (GloVe term embeddings → GMM; MoM to Dirichlet prior), **Random Prior** (random vector prior), **No SOC** (PPMI → DM; cosine-similarity step removed), **SVD in place of DM** (SOC-PPMI → SVD → GMM).

MODELS	20NewsGroup	BBC	M10	DBLP	TrumpTweets
GloVe Embed	.5590 (.0480)	.5778 (.0072)	.3672 (.0492)	.2844 (.0376)	.2733 (.0618)
Random Prior	.5277 (.0494)	.5467 (.0091)	.3161 (.0547)	.2506 (.0448)	.2328 (.0627)
No SOC (PPMI→DM)	.5637 (.0492)	.5233 (.0145)	.3633 (.0577)	.2750 (.0467)	.2744 (.0687)
SVD in place of DM	.5543 (.0514)	.5533 (.0132)	.3589 (.0615)	.3133 (.0455)	.2411 (.0714)
PRISM (reference)	**.6078** (.0374)	**.6137** (.0453)	**.3915** (.0176)	**.3361** (.0742)	**.3028** (.0410)

D.3 Complexity Analysis

Table 8: Dominant time and space complexities.

Model	**Time (dominant)**	**Space (dominant)**
BoW topic/factor models		
LDA	$O(\mathrm{nnz}(X)\,K) + O(\lvert V\rvert K)$	$O(\mathrm{nnz}(X) + NK + \lvert V\rvert K)$
NMF	$O(\mathrm{nnz}(X)\,K)$	$O(\mathrm{nnz}(X) + NK + \lvert V\rvert K)$
ProdLDA	$O(\mathrm{nnz}(X)\,K) + O(\lvert\Theta\rvert)$	$O(\mathrm{nnz}(X) + NK + \lvert V\rvert K + \lvert\Theta\rvert)$
ETM	$O(\mathrm{nnz}(X)\,K) + O(\lvert V\rvert K)$	$O(\mathrm{nnz}(X) + NK + \lvert V\rvert K)$
CTM	$O(\mathrm{nnz}(X)\,K) + O(\lvert\Theta\rvert)$	$O(\mathrm{nnz}(X) + NK + \lvert V\rvert K + \lvert\Theta\rvert)$
MALLET	$O(\mathrm{nnz}(X)\,\bar{K}_{\mathrm{act}})$	$O(\mathrm{nnz}(X) + NK + \lvert V\rvert K)$
Embedding → clustering pipelines		
BERTopic	$O(N\,c_{\mathrm{enc}}) + O(N \log N) + O(N^2) + O(\lvert V\rvert K)$	$O(N\,d_{\mathrm{emb}} + \lvert V\rvert K)$
Contextual-Top2Vec	$O(N\,c_{\mathrm{enc}}) + O(N \log N) + O(N^2)$	$O(N\,d_{\mathrm{emb}})$
FASTopic	$O(\mathrm{nnz}(X)) + O(\lvert V\rvert K^2) + O(\lvert V\rvert K)$	$O(\mathrm{nnz}(X) + \lvert V\rvert K)$
Our model		
PRISM (ours)	$O(\mathrm{nnz}(X)\,\bar{K}_{\mathrm{act}}) \;+\; O(\lvert V\rvert^3)$	$O(\mathrm{nnz}(X) + NK + \lvert V\rvert K) + O(\lvert V\rvert^2)$

Reading Table 8. *Symbols.* N: #documents; $|V|$: vocabulary size; K: #topics; $X \in \mathbb{R}^{N\times|V|}$ sparse with $\mathrm{nnz}(X)$ nonzeros; $|\Theta|$: number of trainable neural parameters (encoder/decoder); c_{enc}: per-document embedding cost of the text encoder; d_{emb}: embedding dimension; $\bar{K}_{\mathrm{act}}$: average number of *active* topics per token under SparseLDA (typically $\bar{K}_{\mathrm{act}} \ll K$). Time entries are per iteration/epoch for iterative models and per pipeline for embedding→clustering methods; space lists dominant stored objects.

BoW models. LDA: $O(\mathrm{nnz}(X)\,K)$ from local doc–topic variational/sufficient–statistic updates (each nonzero token touches K topic scores); $O(|V|K)$ from global topic–word updates/normalization; space $O(\mathrm{nnz}(X)+NK+|V|K)$ for sparse data plus doc–topic and topic–word matrices. NMF: $O(\mathrm{nnz}(X)\,K)$ from multiplicative updates touching nonzeros per factor; same space pattern as BoW factorization. ProdLDA: $O(\mathrm{nnz}(X)\,K)$ (local BoW term) $+\,O(|\Theta|)$ from backprop through amortized encoder/decoder per epoch; space adds $|\Theta|$. ETM: $O(\mathrm{nnz}(X)\,K)$ (local inference) $+\,O(|V|K)$ for topic–embedding softmax/global updates; BoW space. CTM: $O(\mathrm{nnz}(X)\,K)$ (local) $+\,O(|\Theta|)$ (backprop); BoW space $+\,|\Theta|$. MALLET: $O(\mathrm{nnz}(X)\,\bar{K}_{\mathrm{act}})$ since per-token sampling operates only over nonzero counts for the (few) topics active in that context; space as BoW.

Embedding→clustering. BERTopic: $O(N\,c_{\mathrm{enc}})$ for encoder forward passes; $O(N\log N)$ from ANN/kNN graph (UMAP build); $O(N^2)$ worst-case from HDBSCAN; $O(|V|K)$ from c-TF-IDF labeling; space $O(N\,d_{\mathrm{emb}})$ for embeddings $+\,O(|V|K)$ for cluster-term weights. Contextual-Top2Vec: same $O(N\,c_{\mathrm{enc}})+O(N\log N)+O(N^2)$ (encoder+UMAP+HDBSCAN); no c-TF-IDF term; space $O(N\,d_{\mathrm{emb}})$. FASTopic: $O(\mathrm{nnz}(X))$ to build word co-occurrences; $O(|V|K^2)$ for anchor selection; $O(|V|K)$ for recovery; space $O(\mathrm{nnz}(X)+|V|K)$.

PRISM (ours). Inference matches MALLET: $O(\mathrm{nnz}(X)\,\bar{K}_{\mathrm{act}})$ time; $O(\mathrm{nnz}(X)+NK+|V|K)$ space. The one-time word-embedding pre-step (dense case) is dominated by the diffusion-maps spectral decomposition on a $|V|\times|V|$ kernel: $\approx O(|V|^3)$ time and $O(|V|^2)$ space (the PPMI transform and all-pairs similarities are subsumed).

E Biological Experiments

E.1 Biological Technical Details

Bio Preprocessing. We first filtered lowly detected genes, retaining only those expressed in at least m cells using `scanpy.pp.filter_genes` (Wolf et al., 2018). Counts were normalized per cell to a fixed library size (`scanpy.pp.normalize_total`) and log-transformed (`scanpy.pp.log1p`) (Wolf et al., 2018; Luecken & Theis, 2019). Highly variable genes (HVGs) were then selected with the Seurat v3 method (`flavor=seurat_v3`), using raw counts via `layer="counts"` and, where applicable, merging HVGs across batches via `batch_key` (scverse, accessed 2025; Stuart et al., 2019). Analyses were performed in Scanpy with AnnData as the primary container (Wolf et al., 2018; Virshup et al., 2024).

PRISM adaptation for scRNA-seq. Our workflow matches the text-corpus setup except for the PPMI construction. In text, the sliding window is an entire document; in scRNA-seq, we first construct a cell–cell k-NN (here $k=30$) on PCA features (Euclidean distance), a standard step in single-cell pipelines, and treat each cell's neighborhood as the PPMI 'window'. We then compute gene–gene PPMI from co-occurrences across these neighborhoods. The intuition is that genes co-expressed across similar cells (often sharing cell type/state) better capture shared programs than mere co-occurrence within a single cell, where multiple unrelated programs may be intermixed.

E.2 Biological Evaluations

E.2.1 Gene-Set Quality Metrics

We assess the biological plausibility of inferred gene expression programs using three complementary criteria: (i) enrichment—overrepresentation of curated pathways/functions (e.g., GO/KEGG/MSigDB) relative to a fixed gene universe; (ii) coherence—within–gene-set co-variation of expression across cells; and (iii) coverage–the extent to which programs collectively recover pathway members. Metrics are computed per program and then aggregated per model and dataset. We control the false discovery rate (FDR)–the expected proportion of false positives among rejected hypotheses–using the Benjamini–Hochberg procedure and report BH-adjusted q-values (Benjamini & Hochberg, 1995).

Enrichment strength ($-\log_{10} q$). Let U be the gene universe ($|U| = N$). For a program $S \subseteq U$ ($|S| = K$) and a curated pathway $P \subseteq U$ ($|P| = M$), with overlap $x = |S \cap P|$, we test overrepresentation using a one-sided hypergeometric (Fisher's exact) test:

$$p = \sum_{i=x}^{\min(K,M)} \frac{\binom{M}{i}\binom{N-M}{K-i}}{\binom{N}{K}}.$$

We then correct the collection of p-values across all tested pathways for S using FDR (Benjamini–Hochberg) to obtain q, and report the strength as $-\log_{10}(q)$ (higher is better).

Coherence (mean within-set Spearman correlation). Given the cells×genes expression matrix, compute Spearman correlations ρ_{ij} across cells for all gene pairs $i < j$, $i, j \in S$, and average:

$$\text{coherence} = \frac{2}{K(K-1)} \sum_{i<j,\ i,j \in S} \rho_{ij}.$$

Higher values indicate coordinated expression consistent with a functional program.

Coverage (pathway completeness). Per-pathway coverage is the recovered fraction of members:

$$\text{cov}(P \mid S) = \frac{|S \cap P|}{|P|}.$$

Aggregate over the set $\mathcal{P}^*$ of pathways significantly enriched for S (post-FDR), e.g., by a simple mean:

$$\text{coverage} = \frac{1}{|\mathcal{P}^*|} \sum_{P \in \mathcal{P}^*} \text{cov}(P \mid S),$$

or a size-weighted mean (specified in the Supplement). Higher is better.

E.2.2 LLM Confidence Score

To assess the biological relevance of gene sets derived from topic models, we follow the LLM-based evaluation protocol introduced by (Hu et al., 2025).[22] The core idea is to query a large language model (GPT-4) with each gene set and evaluate whether it can (1) identify a coherent biological process (BP) associated with the gene set, and (2) express high confidence in that association.

Prompt Design. Each gene set is presented in a natural language prompt, instructing the model to infer a shared biological process based on the listed genes. Prompts are carefully crafted to be neutral and avoid leading the model toward specific functions. The model is then asked to (i) name the most likely BP, and (ii) rate its confidence on a scale from 0 to 1.

Scoring. The model's textual output is manually inspected to verify whether the inferred BP matches a plausible biological function supported by external evidence (e.g., GO annotations). Confidence scores are recorded for each gene set and aggregated to assess overall coherence across topics.

Interpretation. As shown in prior work, gene sets yielding low confidence often correspond to functionally inconsistent or noisy groups, whereas high-confidence predictions align with known biological pathways. Thus, the LLM confidence score serves as a proxy for functional coherence and interpretability of the gene sets.

[22] https://www.ncbi.nlm.nih.gov/pmc/articles/PMC11725441

E.3 Biological Quality Results

Table 9: Gene-set quality metrics for biological datasets. Each entry is the mean over 10 runs with $K = 5$. Coherence = mean within-set Spearman correlation; Coverage = fraction of pathway members recovered (averaged over significant pathways); Strength = $-\log_{10}(q)$ (FDR-adjusted). "—" indicates no significant pathway enrichments ($q \geq 0.05$). Best scores are **bold**; second-best are underlined; † indicates PRISM significantly outperforms MALLET for that metric (test details in the Supplement).

Models	BreastCancer			PBMC3k			Zeisel brain		
	Coherence	Coverage	Strength	Coherence	Coverage	Strength	Coherence	Coverage	Strength
cNMF	0.2695	0.0	—	**0.3867**	**0.8**	10.2447	**0.6306**	**0.8**	**4.1679**
scHPF	0.2423	**0.2**	**1.4056**	0.1694	0.6	6.0057	0.4049	0.6	3.4919
ProdLDA	0.0956	0.0	—	0.0091	0.0	—	0.0273	0.0	—
NMF	0.0918	0.0	—	0.0068	0.0	—	0.0395	0.0	—
MALLET	0.2471	0.0	—	0.2952	**0.8**	9.0515	0.5541	**0.8**	2.2903
PRISM	**0.2906**†	0.0	—	0.3488†	**0.8**	**11.8848**†	0.5987†	**0.8**	3.7403†

As shown in Table 9, two factors largely explain the observed patterns. **(i) Dataset scale.** The BreastCancer matrix contains only 297 genes (vs. 5,000 for PBMC3k/Zeisel), which limits the pathway universe and reduces statistical power for enrichment testing; accordingly, most methods show no significant enrichments on BreastCancer despite reasonable within-set coherence. **(ii) Model suitability.** Methods geared toward text without biological inductive bias (ProdLDA, NMF) perform poorly across datasets–exhibiting low coherence and no enrichment–whereas corpus-intrinsic, count-based topic models (MALLET, PRISM) and single-cell specific baselines (scHPF, cNMF) recover biologically meaningful structure. Across datasets, PRISM is consistently competitive with - and often exceeds - scRNA-seq baselines, while also outperforming MALLET on every dataset, yielding higher coherence and stronger enrichments wherever pathways are detectable. Overall, these results may indicate that LDA (as implemented in MALLET) is a strong choice for biological gene-program discovery, and that domain-appropriate, corpus-intrinsic initialization, as in PRISM, further improves the biological interpretability of the inferred programs.