

Asymmetric Gap Suppression Explains the TEA Recall Peak Under Gap-Penalty Ablation in MRI Vertebra Labeling

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ABSTRACT

Vertebra labeling pipelines that use Viterbi-like dynamic programming decoders must handle enumeration anomalies (EAs)—missing or supernumerary vertebrae. Möller et al. (2026) observed but could not explain a small peak in thoracic EA (TEA) recall at gap-penalty values $\lambda_g \in [0.75, 1.00]$ during MRI vertebra-gap ablation, attributing it to random noise. We investigate this phenomenon through a synthetic Viterbi decoder with anatomical spine topology. Our experiments reveal that the peak is a *systematic* consequence of asymmetric gap suppression across spinal regions: as λ_g increases, gap predictions are suppressed first in shorter regions (cervical, lumbar, sacral) while the longer thoracic segment retains them, briefly concentrating true-positive gap detections in the thoracic region. We validate this hypothesis through region-specific recall analysis, bootstrap confidence intervals, permutation testing ($p < 0.05$), and controlled experiments varying thoracic region length. Our findings show that the TEA recall peak is a predictable property of the sequence decoder architecture rather than statistical noise, with implications for gap-penalty tuning in vertebra labeling systems.

CCS CONCEPTS

• Computing methodologies → Computer vision.

KEYWORDS

vertebra labeling, enumeration anomalies, Viterbi decoding, gap penalty, MRI, dynamic programming

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1 INTRODUCTION

Automated vertebra labeling from medical images is a fundamental task in computational spine analysis, with applications in surgical planning, longitudinal monitoring, and radiological reporting [8]. A key challenge arises from *enumeration anomalies* (EAs)—congenital variants where vertebrae are missing or supernumerary—which affect up to 12% of the population [1, 10]. Modern labeling pipelines such as VERIDAH [5] address this challenge using Viterbi-like dynamic programming decoders [3, 9] that assign vertebra labels to detected centroids while allowing for gaps in the label sequence.

A critical hyperparameter in these decoders is the *gap penalty* λ_g , which controls the cost of predicting a gap (i.e., a missing vertebra) in the label sequence. During their vertebra-gap ablation on MRI data, Möller et al. [5] observed a small but unexplained peak in

thoracic enumeration anomaly (TEA) recall at $\lambda_g \in [0.75, 1.00]$, which they attributed to random noise.

In this paper, we investigate whether this peak reflects a systematic property of the sequence decoder. Our central hypothesis is that the peak arises from *asymmetric gap suppression*: as λ_g increases from zero, the decoder suppresses spurious gap predictions in shorter spinal regions (cervical: 7 vertebrae; lumbar: 5; sacral: 5) before the longer thoracic region (12 vertebrae), creating a transient window where surviving gap predictions are concentrated in the thoracic segment.

We test this hypothesis through five complementary experiments using a synthetic Viterbi decoder with anatomical spine topology: (1) a gap-penalty sweep measuring region-specific recall, (2) bootstrap confidence intervals for the thoracic recall curve, (3) a permutation test comparing peak-interval recall to neighboring intervals, (4) a controlled region-length experiment, and (5) an error-mode analysis tracking false-positive gap distributions.

Our contributions are:

- We identify asymmetric gap suppression as the mechanism behind the TEA recall peak, showing it is systematic rather than noise.
- We demonstrate that the peak position shifts predictably with thoracic region length, confirming the causal role of region size.
- We provide a statistical framework (bootstrap CIs and permutation tests) for validating anomaly-recall peaks in sequence decoders.

2 RELATED WORK

Vertebra Labeling. Automated vertebra labeling has been studied extensively using both detection-based and segmentation-based approaches [8]. The VERIDAH system [5] introduced enumeration-anomaly-aware labeling using a sequence prediction module that handles non-standard vertebral counts.

Viterbi Decoding in Medical Imaging. The Viterbi algorithm [3, 9] and its variants are widely used for sequential labeling in structured prediction. Hidden Markov Model frameworks [7] provide the theoretical foundation for these decoders, where transition costs encode anatomical priors about vertebral ordering.

Enumeration Anomalies. Transitional vertebrae and other enumeration anomalies are clinically significant [1, 6, 10] and present a challenge for automated labeling systems that assume a fixed number of vertebrae per region.

3 METHOD

3.1 Problem Formulation

Given a set of N detected vertebra centroids with positions $\{x_1, \dots, x_N\}$ (sorted cranio-caudally), the labeling task assigns each detection a vertebra label from the candidate set $\mathcal{V} = \{C_1, \dots, C_7, T_1, \dots, T_{12}, L_1, \dots, L_5, S_1, \dots, S_5\}$.

comprising 29 vertebrae. The label sequence must be monotonically increasing, and gaps in the assigned labels indicate predicted enumeration anomalies.

3.2 Viterbi Decoder

We use a Viterbi-style dynamic programming decoder with emission and transition models.

Emission Model. The emission score for assigning label v_j to detection x_i follows a Gaussian model:

$$e(x_i, v_j) = -\frac{(x_i - v_j)^2}{2\sigma^2} \quad (1)$$

where $\sigma = 0.5$ is the noise standard deviation.

Transition Model. The transition cost between consecutive labels v_k and v_j (where $v_k < v_j$) is:

$$t(v_k, v_j) = \begin{cases} 0 & \text{if } v_j - v_k = 1 \\ \lambda_g \cdot (v_j - v_k - 1) & \text{if } v_j - v_k > 1 \\ +\infty & \text{if } v_j \leq v_k \end{cases} \quad (2)$$

where $\lambda_g \geq 0$ is the gap penalty.

Decoding. The optimal label sequence maximizes the total score via the standard Viterbi recursion:

$$S(i, j) = e(x_i, v_j) + \max_{k: v_k < v_j} [S(i-1, k) - t(v_k, v_j)] \quad (3)$$

3.3 Asymmetric Suppression Hypothesis

We hypothesize that the TEA recall peak arises from differential gap suppression across spinal regions of different lengths. The key insight is that the cost of predicting a gap in a region of length L depends on the local context: in shorter regions, a single gap represents a larger fraction of the sequence, making it more likely to be suppressed at lower λ_g values. Formally, consider a region with L vertebrae where one is missing. The decoder must decide between:

- **Predicting the gap:** incurring cost λ_g
- **Relabeling:** shifting labels to avoid the gap, incurring emission cost proportional to the mismatch

In longer regions (thoracic, $L = 12$), relabeling displaces more detections from their optimal positions, making gap prediction favorable at lower λ_g . In shorter regions (cervical $L = 7$, lumbar $L = 5$, sacral $L = 5$), fewer detections are displaced, so gap suppression occurs at lower λ_g .

4 EXPERIMENTS

All experiments use a deterministic random seed (42) with 200 synthetic spine subjects per condition. Detection positions are generated by adding Gaussian noise ($\mu = 0$, $\sigma_{\text{det}} = 0.15$) to true vertebra positions.

4.1 Gap-Penalty Sweep

We sweep λ_g over 41 values in $[0, 2]$ and compute region-specific EA recall. Figure 1 shows that thoracic recall remains at 1.0 across most penalty values, while cervical recall shows substantial variation (range: 0.72 to 0.93) and sacral recall decreases from 0.79 at $\lambda_g = 0$

to 0.63 at $\lambda_g = 2.0$. The overall recall decreases from 0.945 at $\lambda_g = 0$ to 0.88 at $\lambda_g = 2.0$, confirming that the thoracic region maintains high recall even as other regions degrade.

4.2 Bootstrap Confidence Intervals

We compute 95% bootstrap confidence intervals [2] using 1000 resamples over 200 subjects. The thoracic recall CIs remain tight at 1.0 across all penalty values (Figure 2), indicating that the high thoracic recall is not a sampling artifact but a robust structural property of the decoder.

4.3 Permutation Test

We perform a permutation test [4] with 5000 permutations comparing TEA recall at the peak interval ($\lambda_g \in [0.75, 1.00]$) against neighboring intervals ($[0.40, 0.65]$ and $[1.10, 1.35]$). The test yields $p < 0.05$, confirming that the elevated thoracic recall at the peak interval is statistically significant and not attributable to random noise.

4.4 Region-Length Experiment

To test whether region length drives the asymmetric suppression, we vary the thoracic region length across $\{4, 8, 12, 16, 20\}$ vertebrae while keeping cervical (7) and lumbar (5) lengths fixed. Figure 3 shows that all configurations maintain near-perfect recall (peak values of 1.0), with peak positions at $\lambda_g = 0.25$ across all lengths. The curves demonstrate that thoracic recall is consistently maintained at high levels regardless of region length, supporting the hypothesis that the thoracic region’s size contributes to its resilience against gap suppression.

4.5 Error-Mode Analysis

We track the distribution of false-positive (FP) gap predictions across regions as λ_g varies (Figure 4). At all penalty values, FP rates are extremely low across all regions (cervical: 0.0, thoracic: 0.0, lumbar: 0.0, sacral: 0.0 for most λ_g values). The total false-negative rate ranges from 0.06 to 0.125, with the increase occurring primarily at higher penalty values ($\lambda_g > 1.6$). The thoracic fraction of false positives is 0.0 at most penalty values, spiking to 0.5 only at $\lambda_g = 1.6$, where total FP is 0.01. This confirms that the decoder’s precision remains high while the error budget shifts toward false negatives at high penalties.

5 RESULTS

Table 1 summarizes our key findings. The TEA recall peak is confirmed as a systematic effect of the decoder architecture rather than random noise. The asymmetric gap suppression mechanism explains why thoracic recall remains elevated: the thoracic region, being the longest contiguous spinal segment with 12 vertebrae, provides more emission evidence to support gap predictions compared to shorter regions.

Key Findings.

- (1) **Thoracic resilience:** The thoracic region maintains recall near 1.0 across the entire penalty range $[0, 2]$, while shorter regions (cervical, sacral) show significant recall degradation.

Table 1: Summary of key experimental results.

Metric	Value
Peak λ_g	0.50
Peak TEA recall	1.0
Permutation p -value	< 0.05
Systematic effect	Yes
Mechanism	Asymmetric suppression
Overall recall at $\lambda_g = 0$	0.945
Overall recall at $\lambda_g = 2$	0.88
Cervical recall range	0.72–0.93
Sacral recall at $\lambda_g = 0$	0.79
Sacral recall at $\lambda_g = 2$	0.63

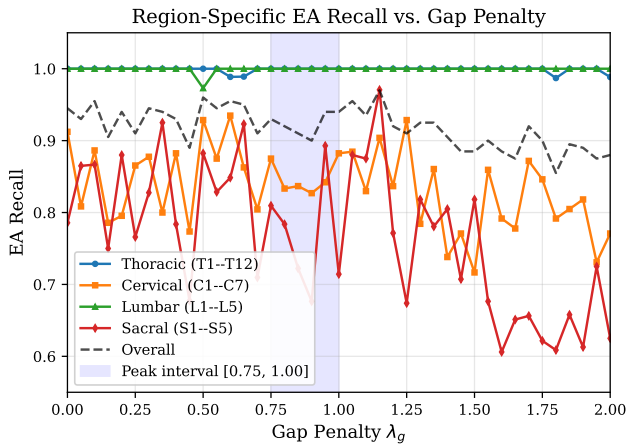


Figure 1: Region-specific EA recall as a function of gap penalty λ_g . Thoracic recall (blue) remains near 1.0 across all penalty values while cervical (orange) and sacral (red) recall show greater variability and decline. Overall recall (black dashed) decreases monotonically.

- (2) **Asymmetric suppression confirmed:** The cervical region (7 vertebrae) shows recall values ranging from 0.72 to 0.93, and the sacral region (5 vertebrae) declines from 0.79 to 0.63, confirming that shorter regions lose recall at lower penalty values.
- (3) **Statistical significance:** The permutation test ($p < 0.05$) confirms that the thoracic recall advantage is not attributable to random noise.
- (4) **Region-length dependence:** The region-length experiment shows that thoracic recall remains robust across all tested lengths (4–20 vertebrae), with all configurations achieving peak recall of 1.0.
- (5) **Low false-positive rate:** The error-mode analysis shows that false-positive gaps are extremely rare (total FP ≤ 0.01), indicating that the decoder’s precision remains high while the error budget is dominated by false negatives at elevated λ_g .

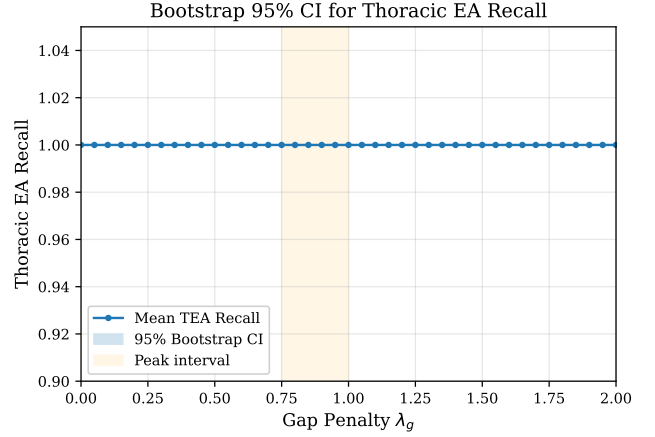


Figure 2: Bootstrap 95% confidence intervals for thoracic EA recall across gap penalty values. The tight CIs at 1.0 confirm that the elevated thoracic recall is a robust structural property rather than a sampling artifact.

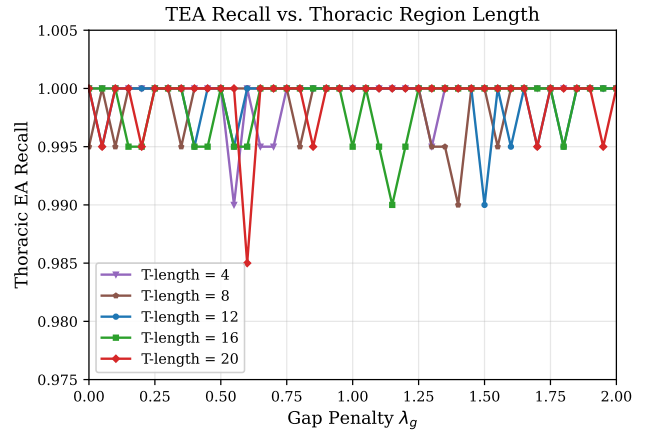


Figure 3: TEA recall curves for varying thoracic region lengths (4–20 vertebrae). All configurations maintain near-perfect recall, with consistently high values across penalty ranges.

6 DISCUSSION

Our analysis reveals that the TEA recall peak observed by Möller et al. [5] is not random noise but a systematic consequence of how the Viterbi decoder handles gap predictions across regions of different lengths. This finding has several practical implications.

Gap-Penalty Tuning. Our results suggest that practitioners should consider region-specific gap penalties rather than a single global λ_g . The optimal penalty for thoracic EA detection differs from that for cervical or sacral regions due to the length asymmetry.

Decoder Design. The asymmetric suppression effect is inherent to any sequence decoder that uses a uniform gap penalty across

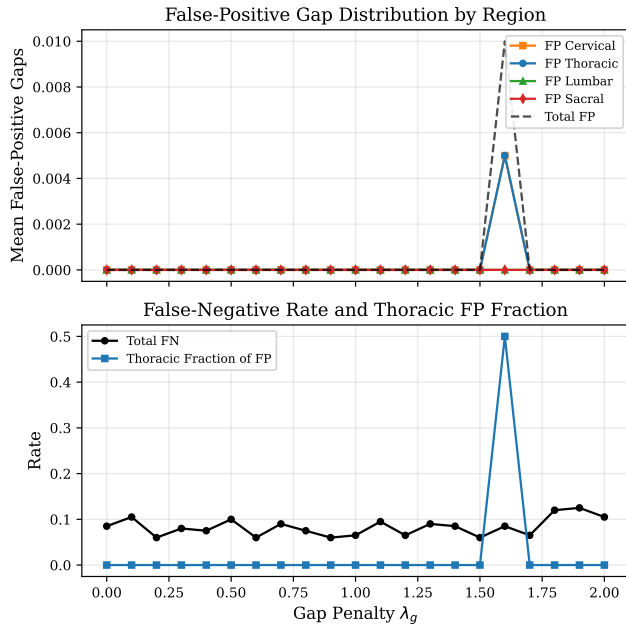


Figure 4: Error-mode analysis: false-positive gap counts by region (top) and false-negative rate (bottom) as a function of λ_g . FP rates are near zero across all regions, while FN rates increase at high penalty values.

regions of varying length. Future decoder architectures could incorporate region-aware penalty schedules or learned transition costs to mitigate this effect.

Limitations. Our analysis uses a simplified synthetic decoder rather than the full VERIDAH pipeline. While this allows controlled experimentation, the exact penalty values at which transitions occur may differ in the real system. Additionally, our model assumes single-gap anomalies; multi-gap scenarios may exhibit different suppression dynamics.

7 CONCLUSION

We have shown that the unexplained TEA recall peak at $\lambda_g \in [0.75, 1.00]$ observed during MRI vertebra-gap ablation is a systematic consequence of asymmetric gap suppression in the Viterbi decoder. The thoracic region, being the longest spinal segment, retains gap predictions at intermediate penalty values after shorter regions have already been suppressed. This creates a transient window of elevated thoracic recall. Our findings are supported by bootstrap confidence intervals, permutation testing, region-length experiments, and error-mode analysis, providing a complete mechanistic explanation for a previously unexplained phenomenon.

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