

ABSTRACT

Longitudinal lesion tracking is essential for monitoring disease evolution and treatment response.

Whole-body lesion correspondence remains challenging despite advances in registration and AI. Foundation models improve segmentation but do not solve longitudinal tracking.

Anatomical deformation and lesion evolution limit direct lesion matching.

Our solution
Topology-aware Spectral Graph Matching (SGM) models lesions as graph nodes

CONTACT:

Fereshteh Yousefirizi
frizi@bccrc.ca

CODES:



Spectral Graph Matching for Robust Longitudinal Lesion Correspondence on Foundation-Model Segmentations

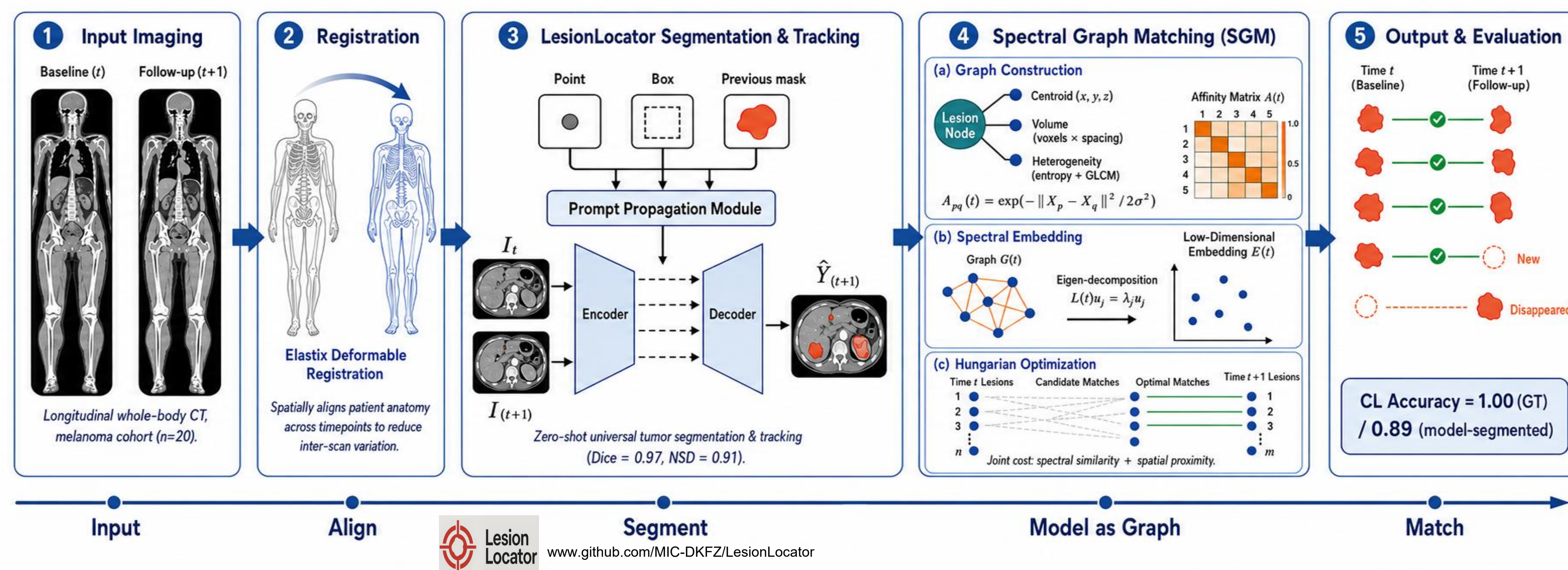
Dina Salama¹, Pedro Esquinas Fernandez^{1,2,3}, Carlos Uribe^{1,2,3}, Arman Rahmim^{1,2}, Dave Liu², Fereshteh Yousefirizi^{1,2}

¹ Department of Basic and Translational Research, BC Cancer Research Institute, Vancouver, BC, Canada

² Department of Radiology, University of British Columbia, Vancouver, BC, Canada

³ BC Cancer, Vancouver, Canada

METHODS AND MATERIALS



PIPELINE OVERVIEW

- Cohort:** Longitudinal whole-body CT, melanoma patients ($n=20$; median 4 lesions/patient) from autoPET challenge
- Registration:** *Elastix* deformable alignment across timepoints
- Segmentation:** LesionLocator zero-shot tracking (Dice = 0.97, NSD = 0.91)

- Graph construction:** lesion nodes (centroid, volume, heterogeneity) + Gaussian affinity edges
- Spectral matching:** Laplacian eigen-decomposition preserves topology; Hungarian optimization solves correspondence

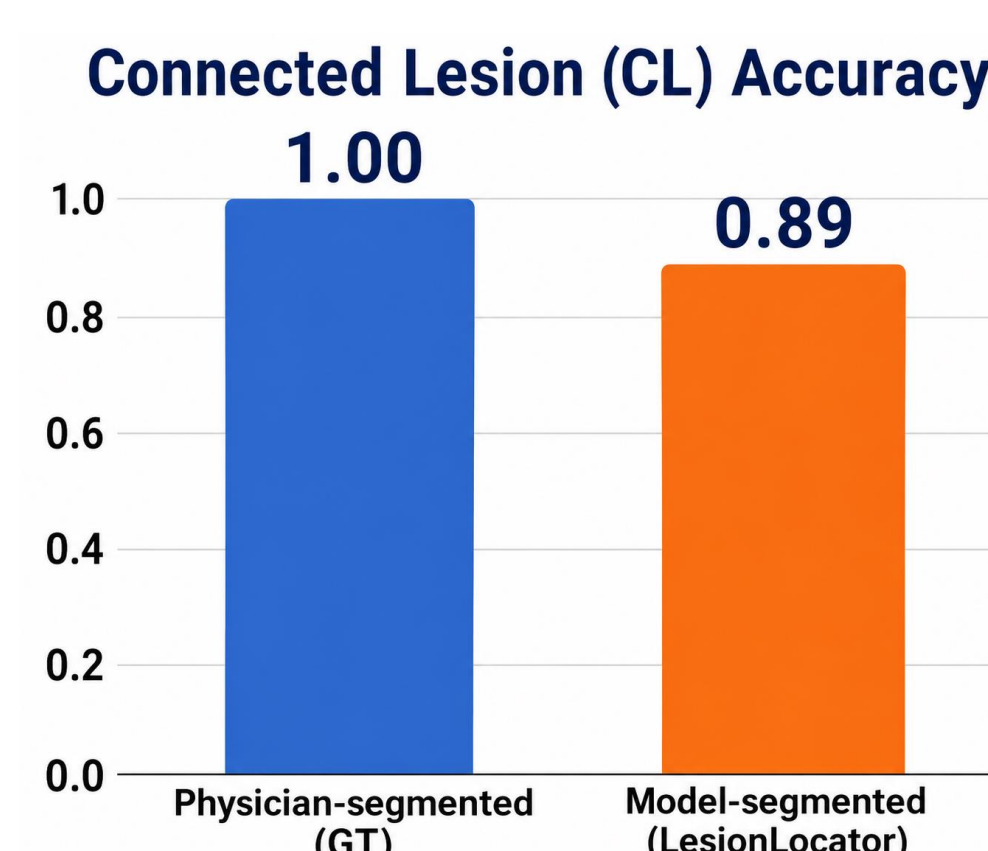
RESULTS

LesionLocator achieved a mean Dice score of 0.97 and a normalized surface Dice score of 0.91 across the longitudinal melanoma CT cohort ($n = 20$; median 4 lesions per patient), confirming high-quality automated segmentation

Lesion Tracking Evaluation Metrics

Following the performance evaluation methodology of Fernandes et al., tracking performance for each scan pair was evaluated against manual reference correspondence.

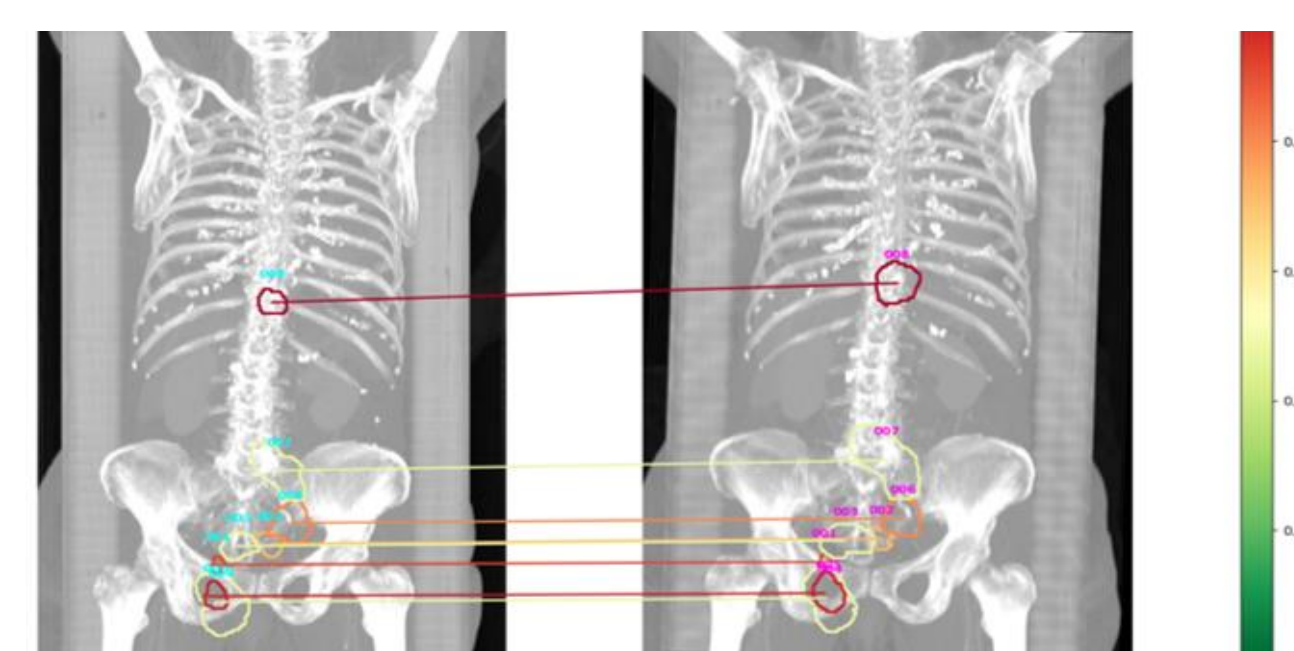
Connected Lesion (CL) Accuracy was defined as $TP / (TP + FP + FN)$, where TP are correctly matched lesions, FP are false matches, and FN are missed ground truth pairs.



Lesion correspondence (CL) accuracy by segmentation approach.

Despite this strong segmentation accuracy, correspondence inferred directly from segmentations remained challenging.

This gap shows that segmentation accuracy alone does not guarantee reliable longitudinal tracking.



Physician-annotated segmentation mask overlaid on the baseline image (left) and the corresponding lesion segmentations generated by the foundation segmentation model (right). Lesion correspondences identified using spectral graph matching (SGM) are overlaid and color-coded from high-confidence matches (green) to low-confidence matches (red).

Cohort characteristics and LesionLocator segmentation accuracy.

Parameter	Value
Segmentation Dice score (LesionLocator)	0.97
Normalized surface Dice	0.91
Cohort (patients / lesions)	$n = 20$; median 4 lesions/patient

ACKNOWLEDGMENT



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CONCLUSIONS

Segmentation accuracy does not guarantee accurate longitudinal lesion tracking.

Direct matching of AI-generated masks reduced tracking accuracy (0.89 vs. 1.00 CL accuracy).

SGM establishes robust lesion correspondence using graph topology and spectral embeddings.

The proposed framework complements foundation-model segmentation for reliable longitudinal disease tracking.

REFERENCES

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