

# Incorporating morphology via deep learning improves classification performance of MALDI imaging for skin lesions

Wanqiu Zhang; Nathan Heath Patterson; Nico Verbeeck; Jessica Moore; Alice Ly; Richard M. Caprioli;  
Bart De Moor; Jeremy L. Norris; Marc Claesen

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*Does combining histopathology data with MALDI IMS improve the unimodal classification results on melanoma diagnosis?*

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Benign nevus  
vs.  
Malignant melanoma

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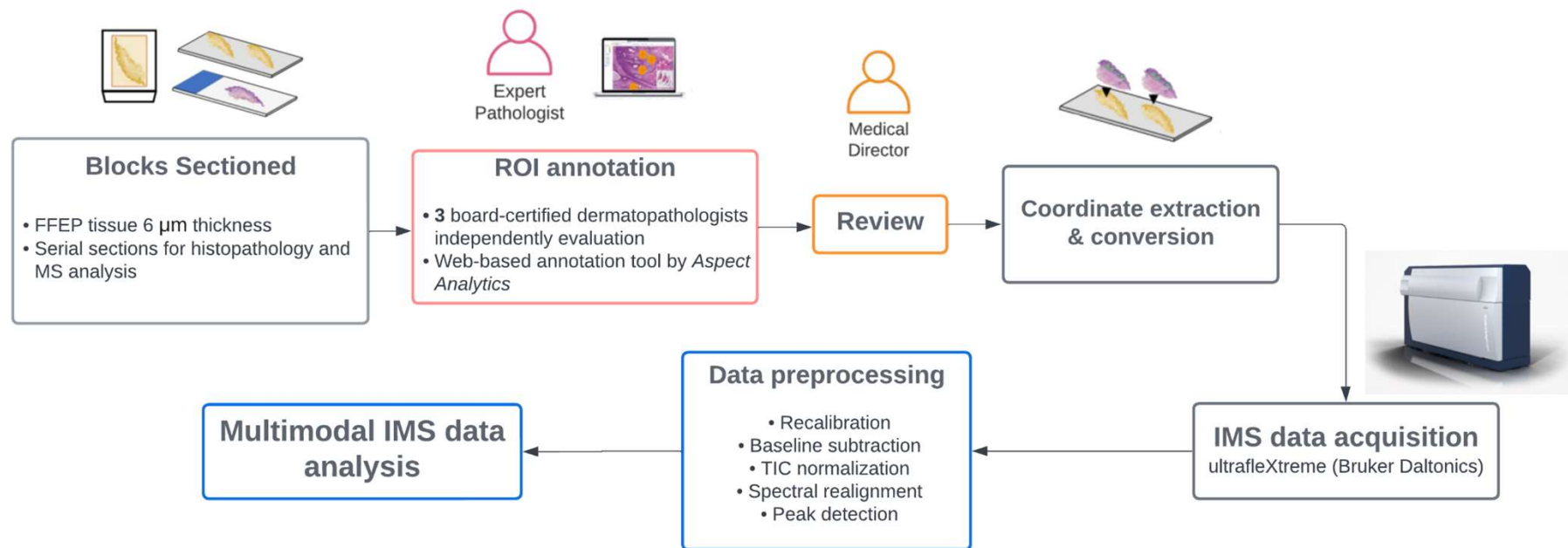


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Yes!

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# Histology-guided IMS sample preparation pipeline



ANNOTATION STUDIO

Home

Annotations

Layers

MM-200

Annotation

Review

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Annotations

Point annotation radius: 25.000  $\mu\text{m}$

MELANOMA VS BENIGN

MELANOMA IN SITU

INVASIVE MELANOMA

JUNCTIONAL NEVUS

INTRADERMAL NEVUS

EPIDERMIS STROMA

DERMIS STROMA

OTHER

0

0

0

55

36

31

0

Sample info

Lesion location: Forehead

Patient age: 48.0

Patient gender: Female

Feedback

1 Message

Most nevus are not pure and have dermis or epidermis mixed with them.

5 months ago

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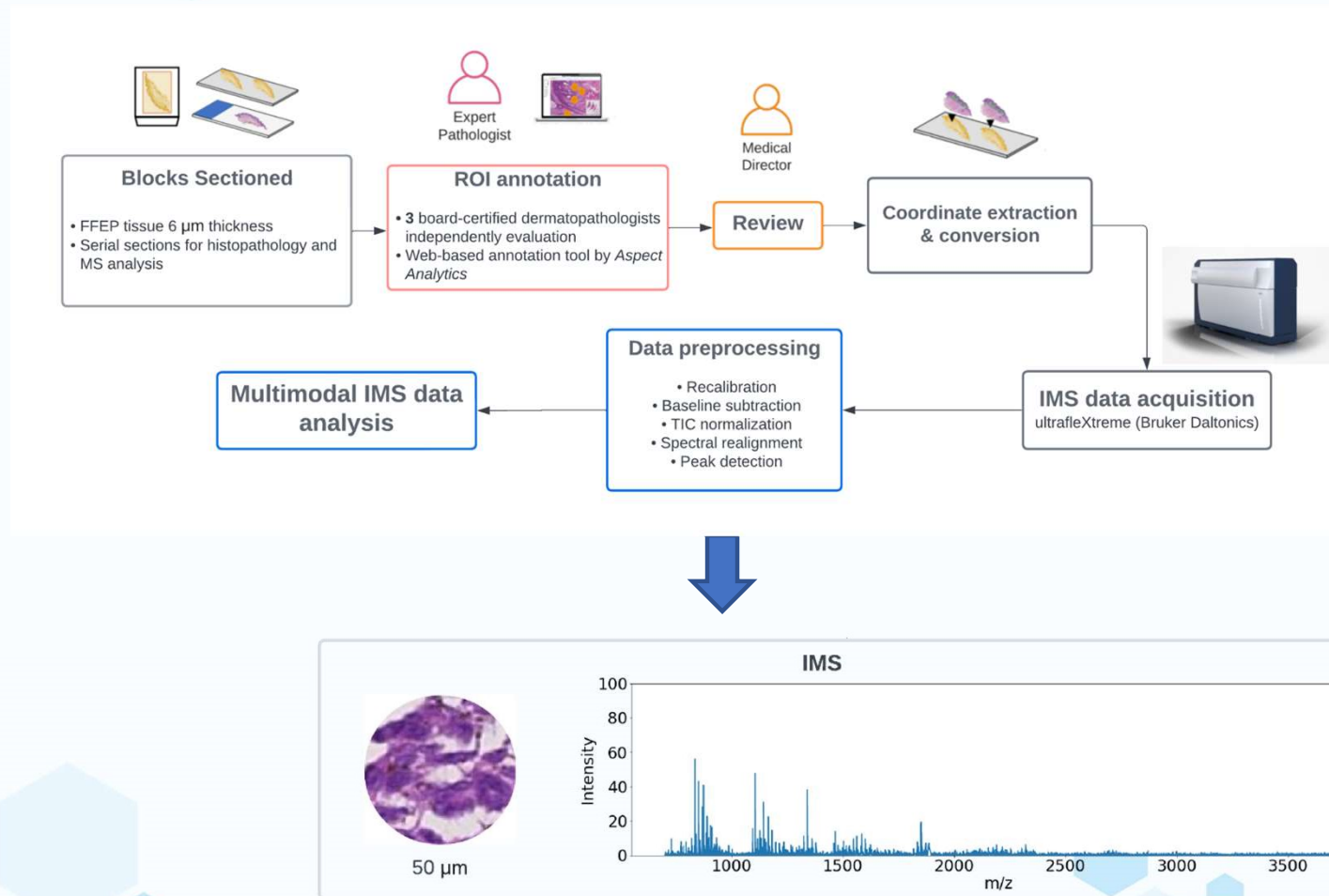
69

70

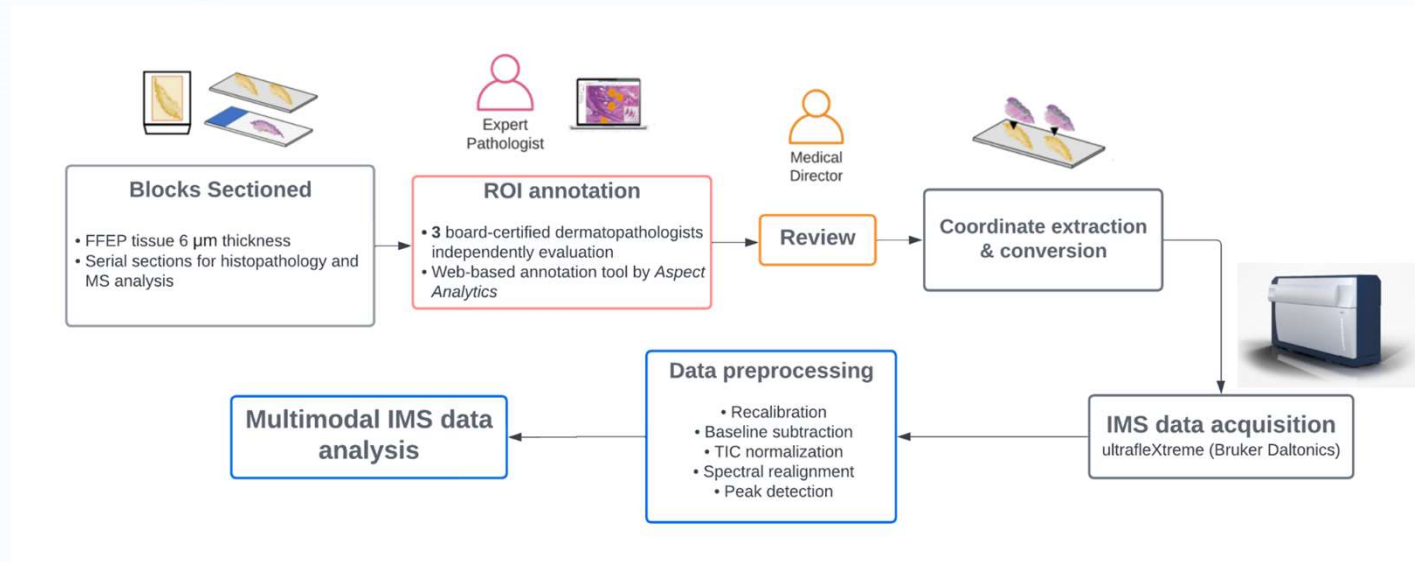
250  $\mu\text{m}$

Developed by Aspect Analytics  
Booth 324

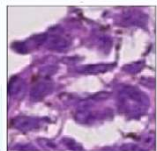
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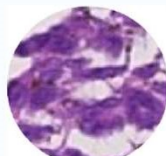


Microscopy

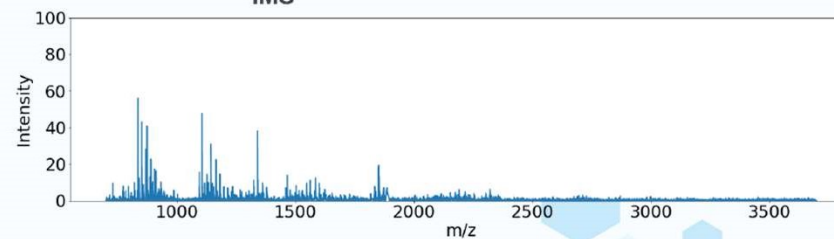


48  $\mu\text{m}$  \* 48  $\mu\text{m}$

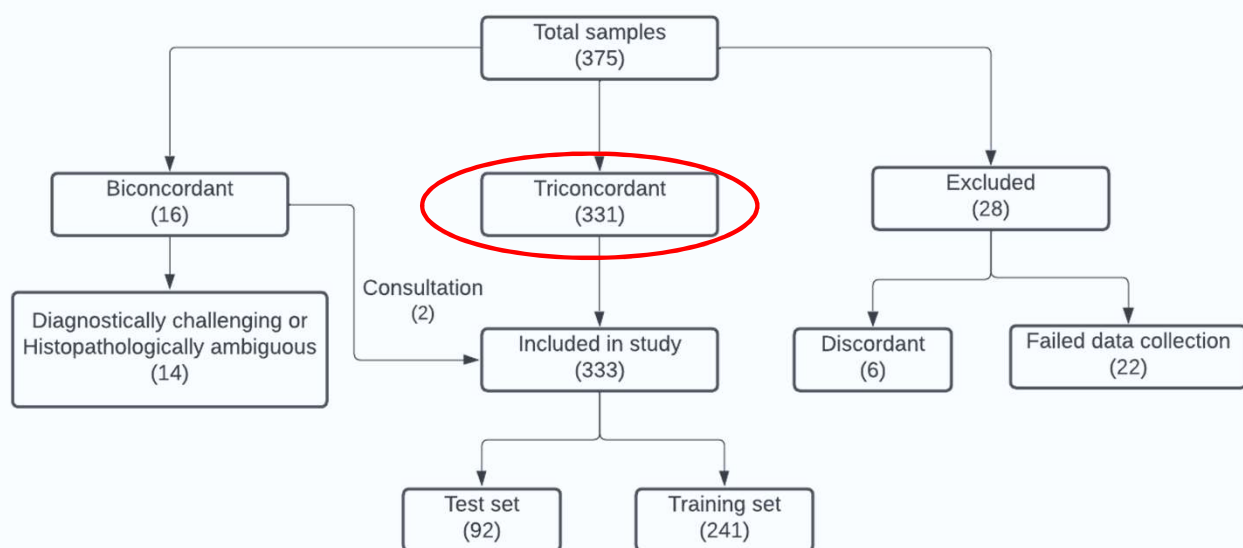
IMS



50  $\mu\text{m}$



# IMS data sample selection



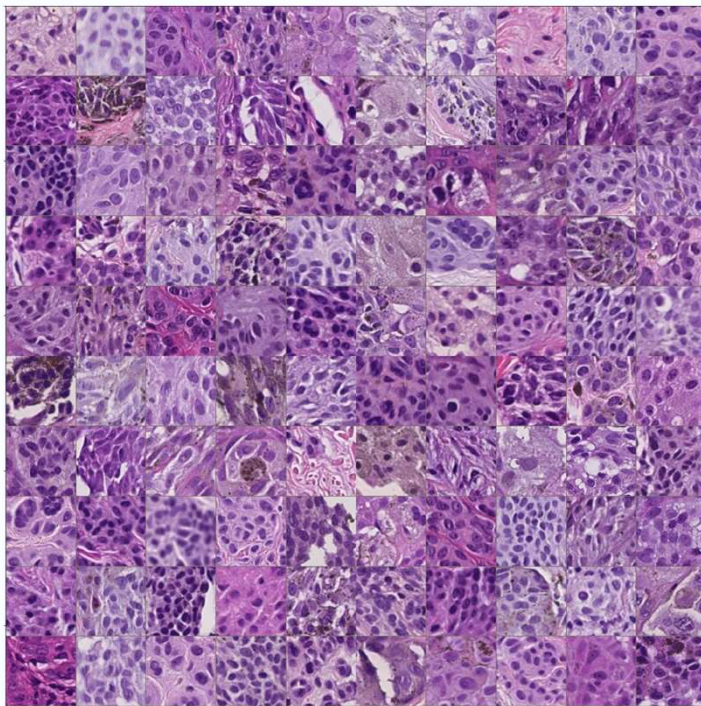
*Note: Each sample has 21 annotation spots on average*

**TABLE 1** Patient demographics for training and test sets

	Training set	Test set
Benign subtype		
Intradermal nevus	75	25
Compound nevus	65	24
Blue nevus	1	0
<b>Total benign</b>	<b>141</b>	<b>49</b>
Melanoma subtype		
Superficial spreading	47	23
Lentigo maligna	26	11
Mel-NOS	9	5
Nodular	8	2
Spitzoid	3	1
Desmoplastic	3	0
Spindle cell	2	1
Nevoid	1	0
Acral	1	0
<b>Total melanoma</b>	<b>100</b>	<b>43</b>
Other clinical parameters		
Mean patient age		
Benign	44.4	39.9
Melanoma	61.3	63.9
Patient sex		
Benign		
Male	52	18
Female	89	31
Melanoma		
Male	55	28
Female	45	15
Mean Breslow depth		
Benign	—	—
Melanoma	1.42 mm	1.12 mm

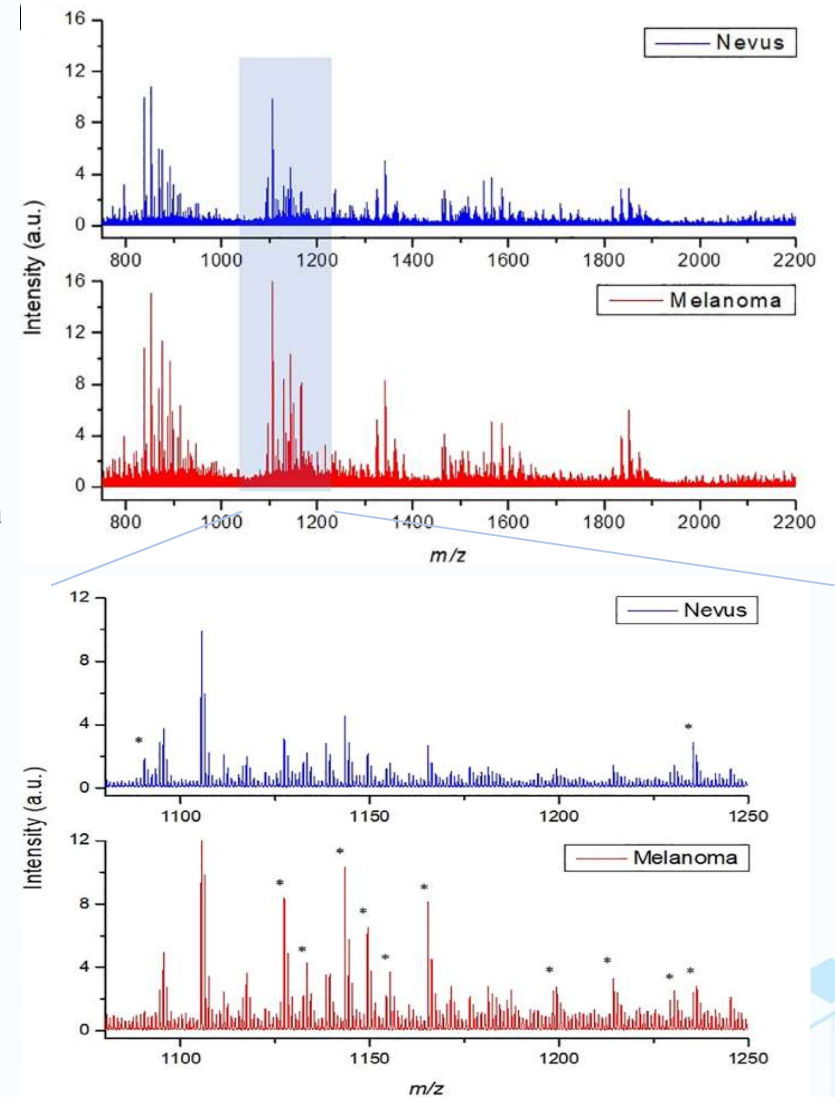
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# Data visualization



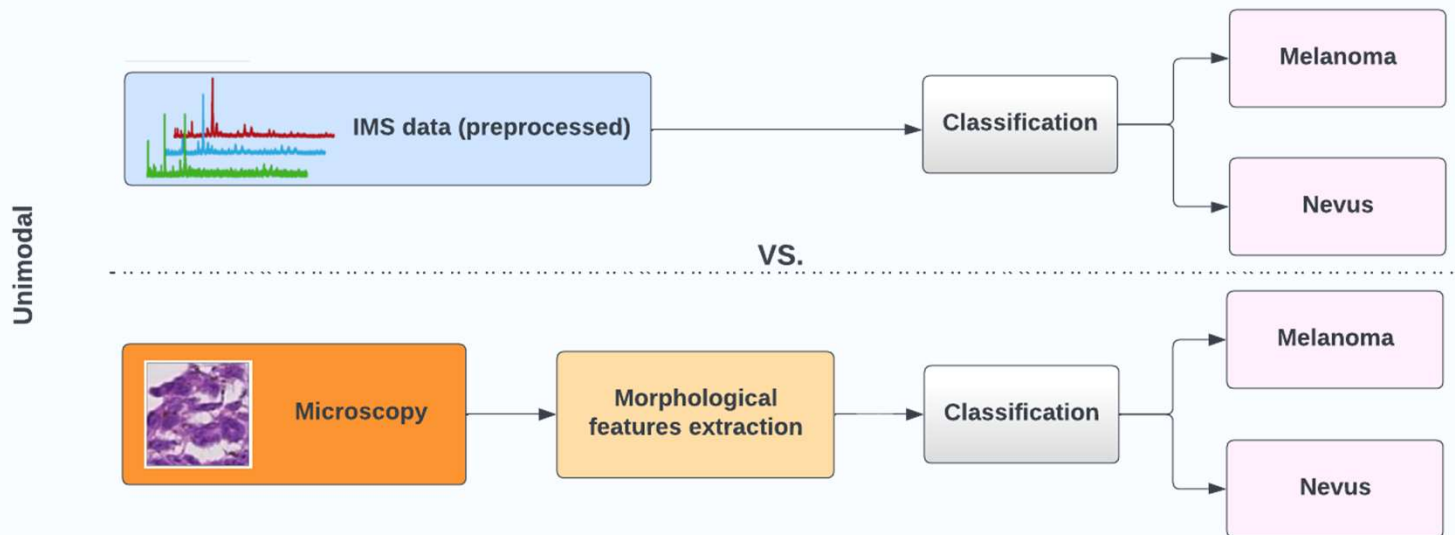
Randomly sampled microscopy data

IMS data

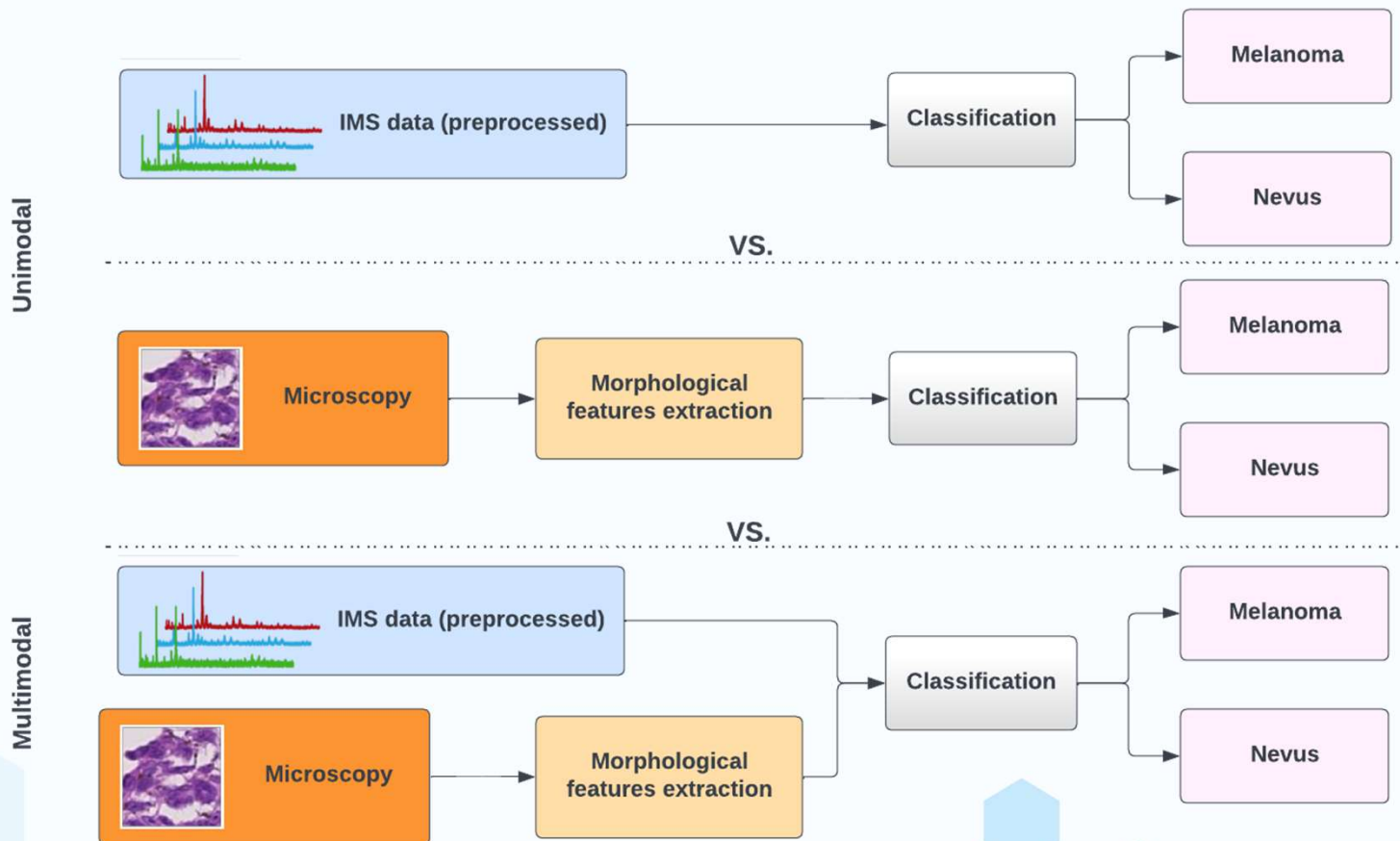


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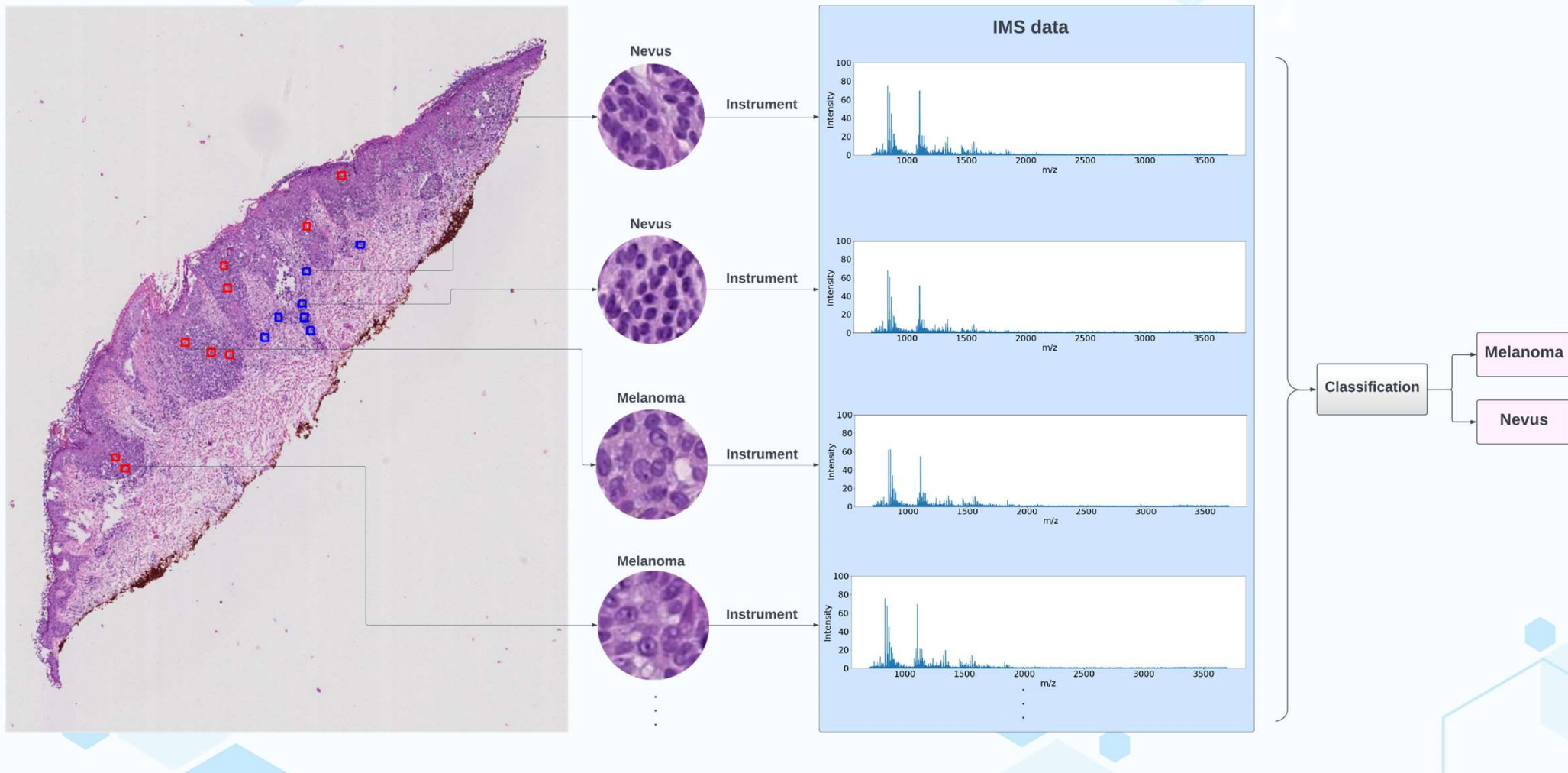
# Data analysis pipeline (Study design)



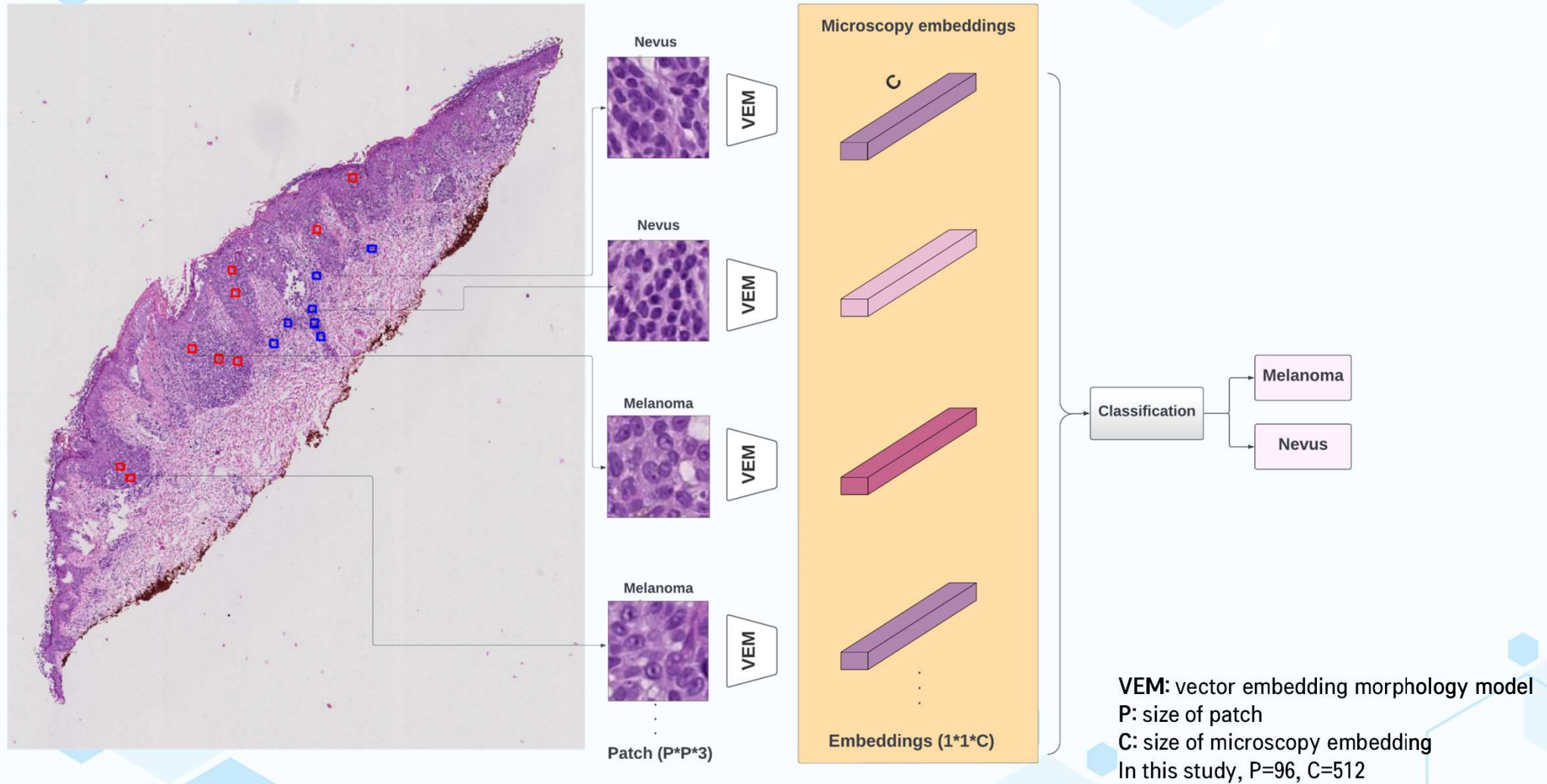
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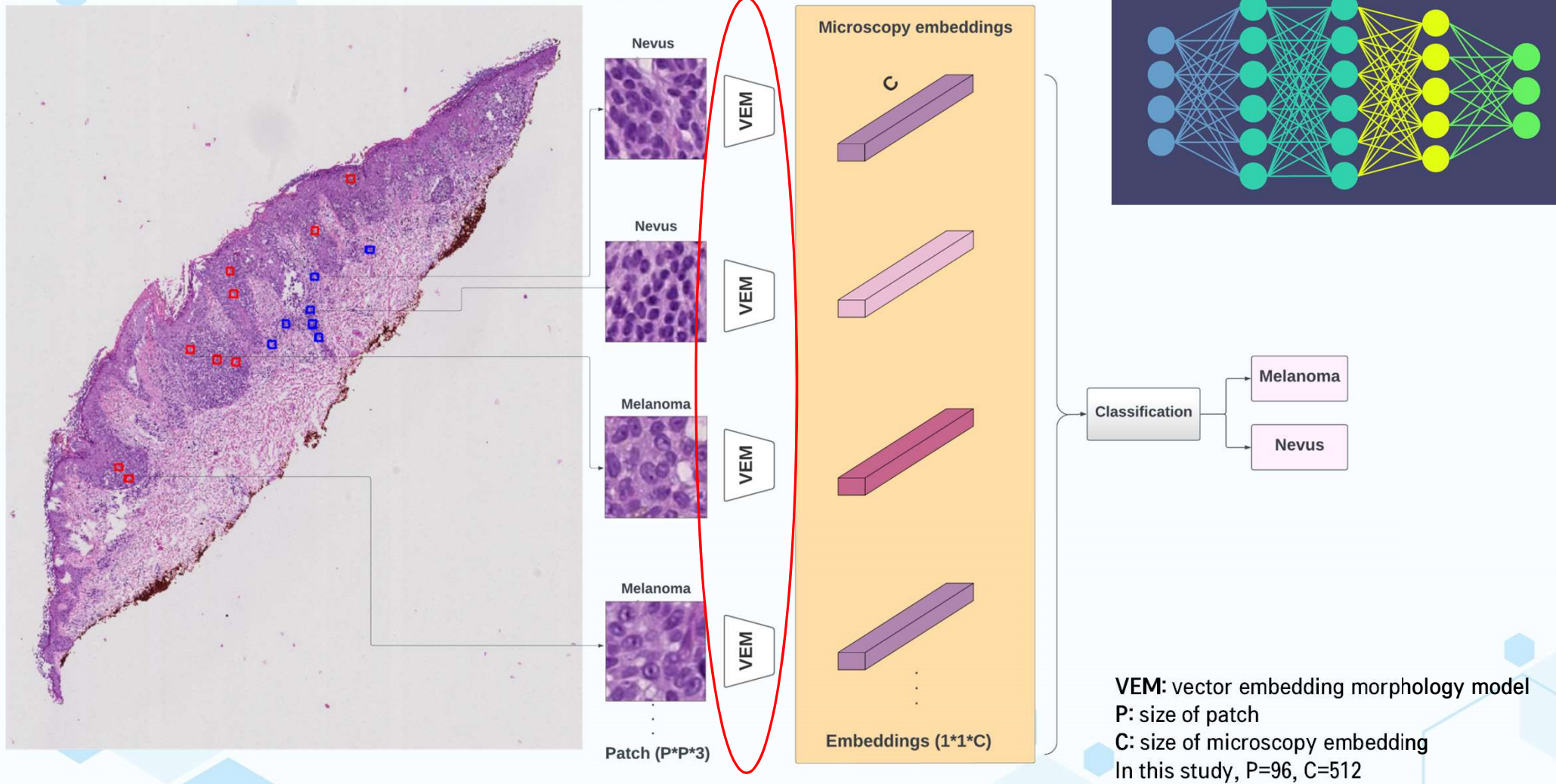
# Unimodal IMS pipeline



# Unimodal Microscopy pipeline



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# Pre-trained neural networks

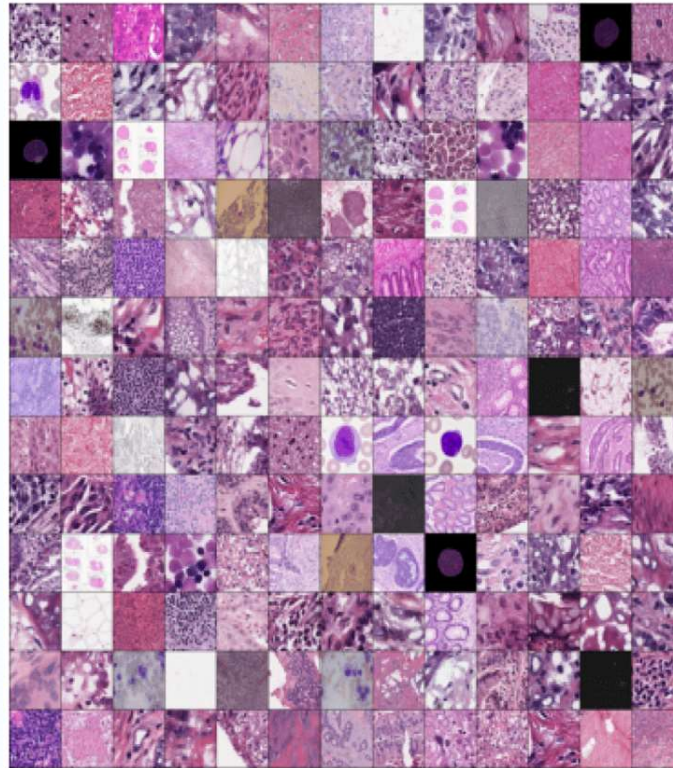


Before training

# Pre-trained neural networks

57 histopathology multi-organ datasets<sup>1</sup>:

- 206,000 patches in 23 datasets;
- 25,000 giga-resolution images in 35 datasets



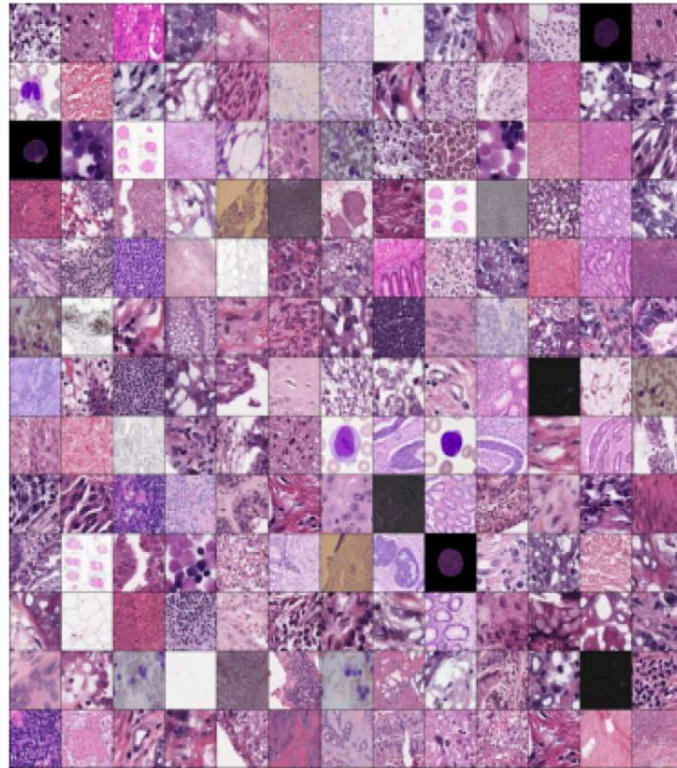
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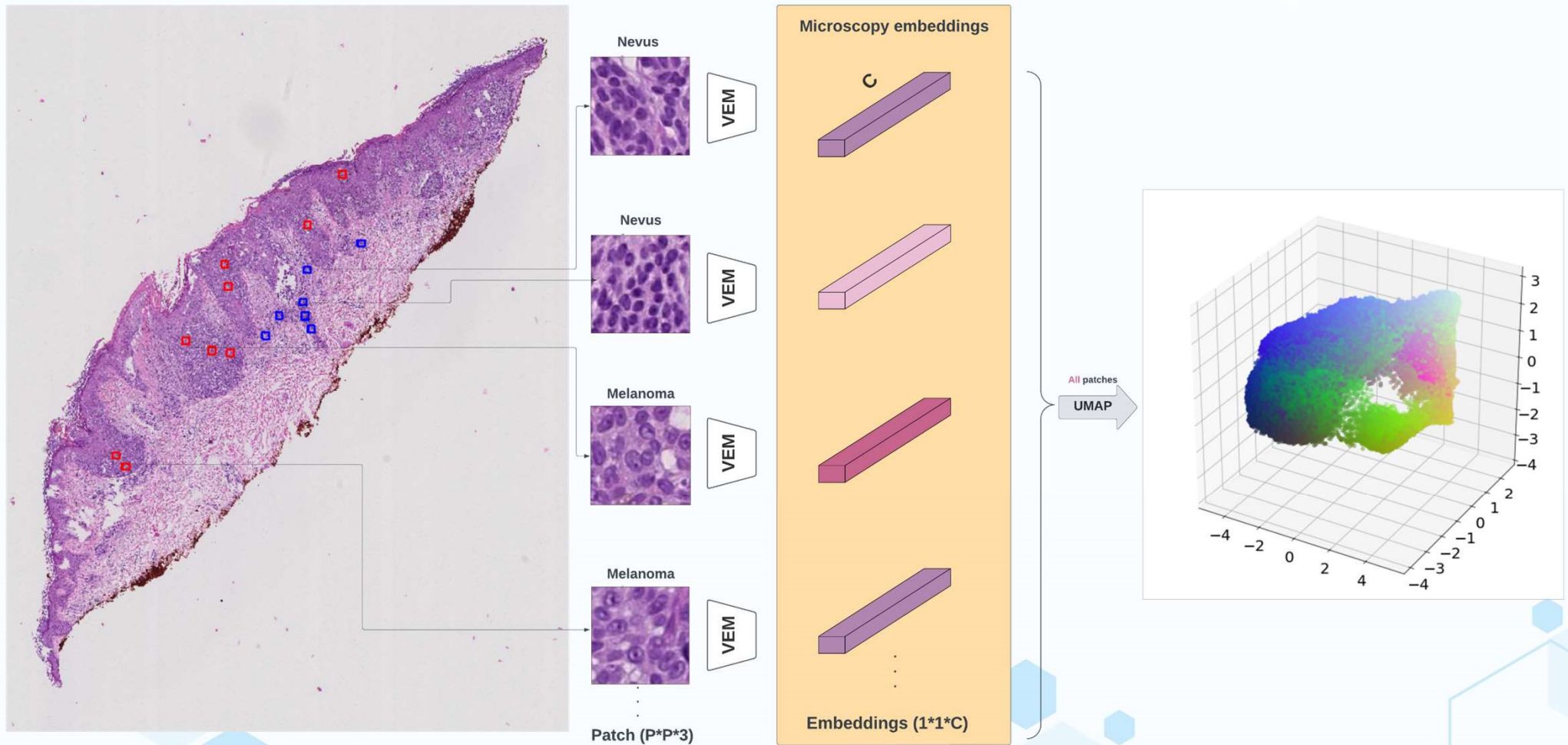


Before training

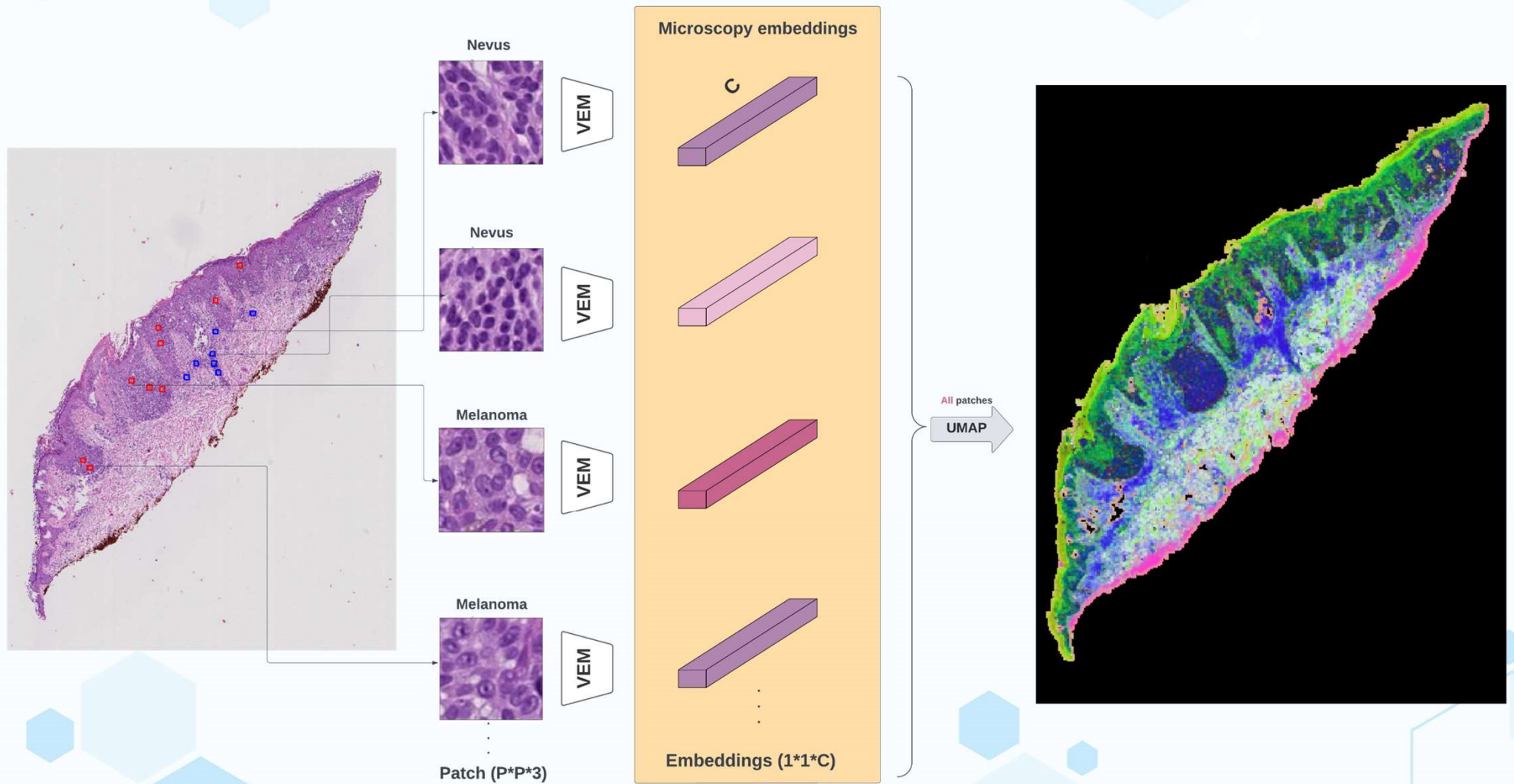
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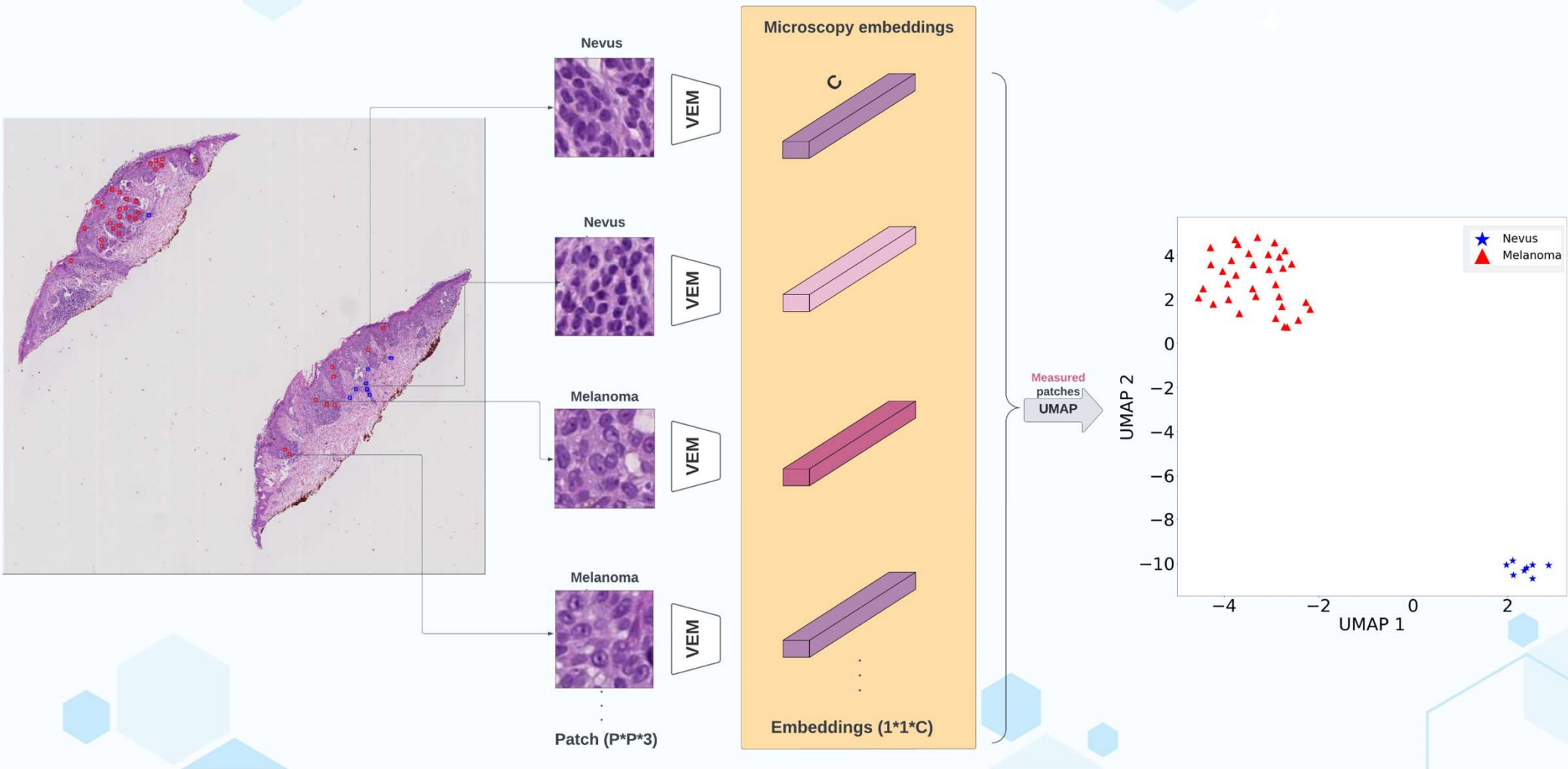
# Unimodal Microscopy pipeline



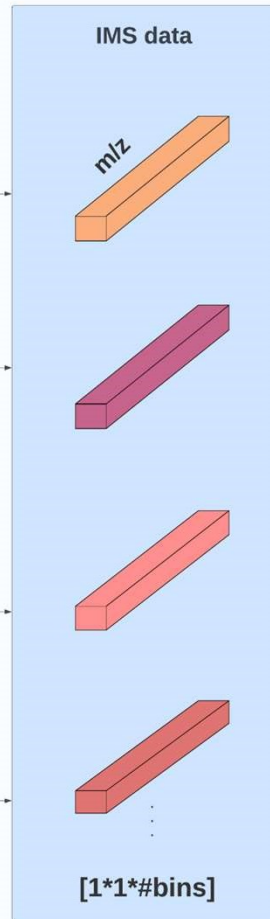
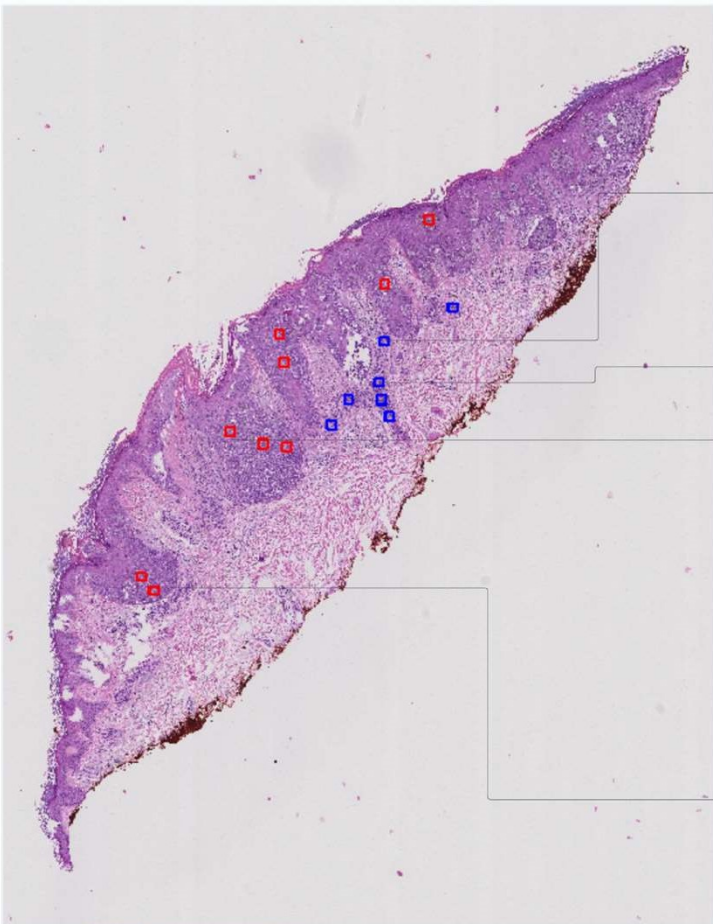
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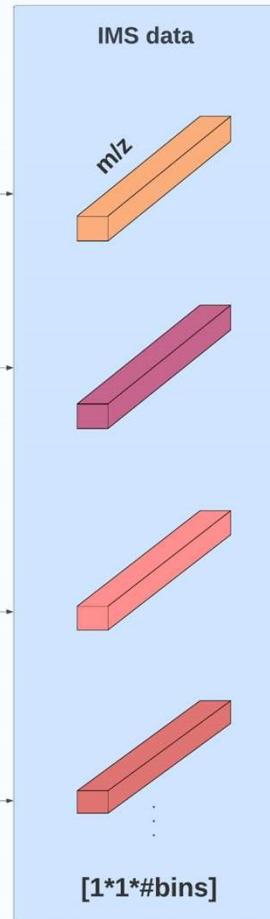
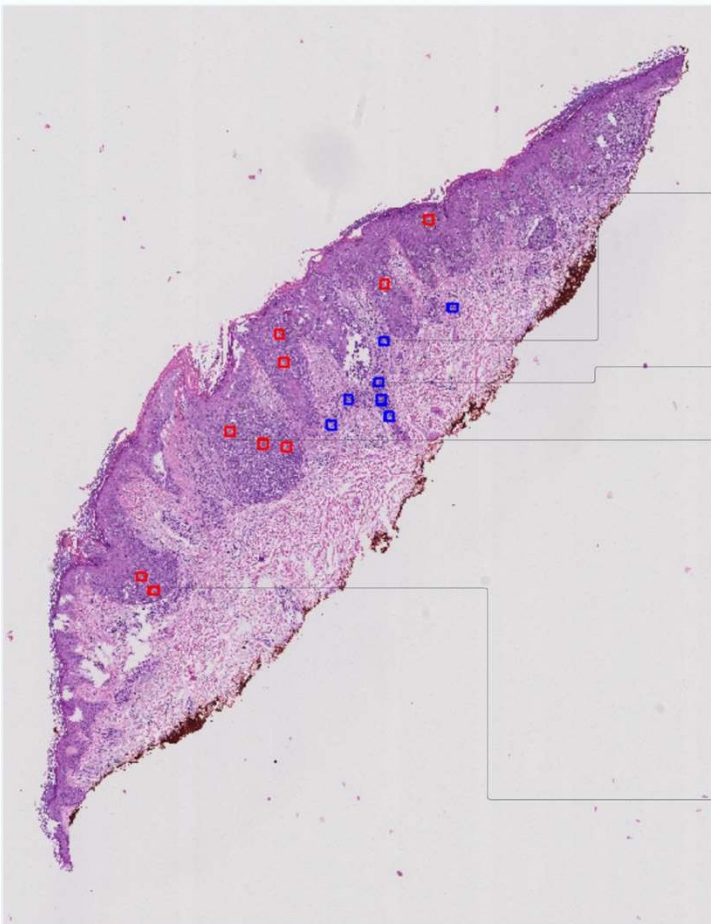


# Multimodal pipeline

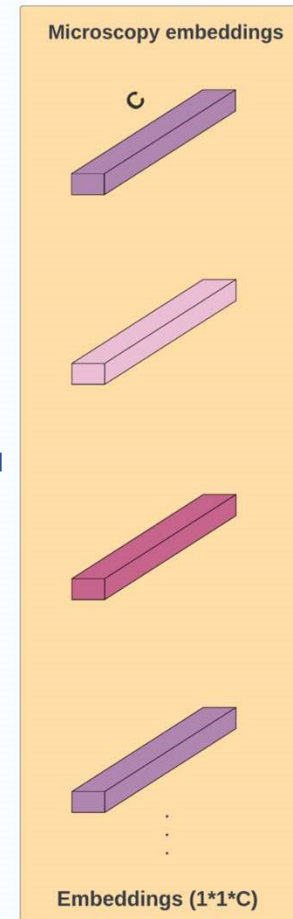


**VEM:** vector embedding morphology  
**P:** size of patch  
**C:** size of microscopy embedding  
In this study, P=96, C=512,  
**#bins = 5558**

# Multimodal pipeline

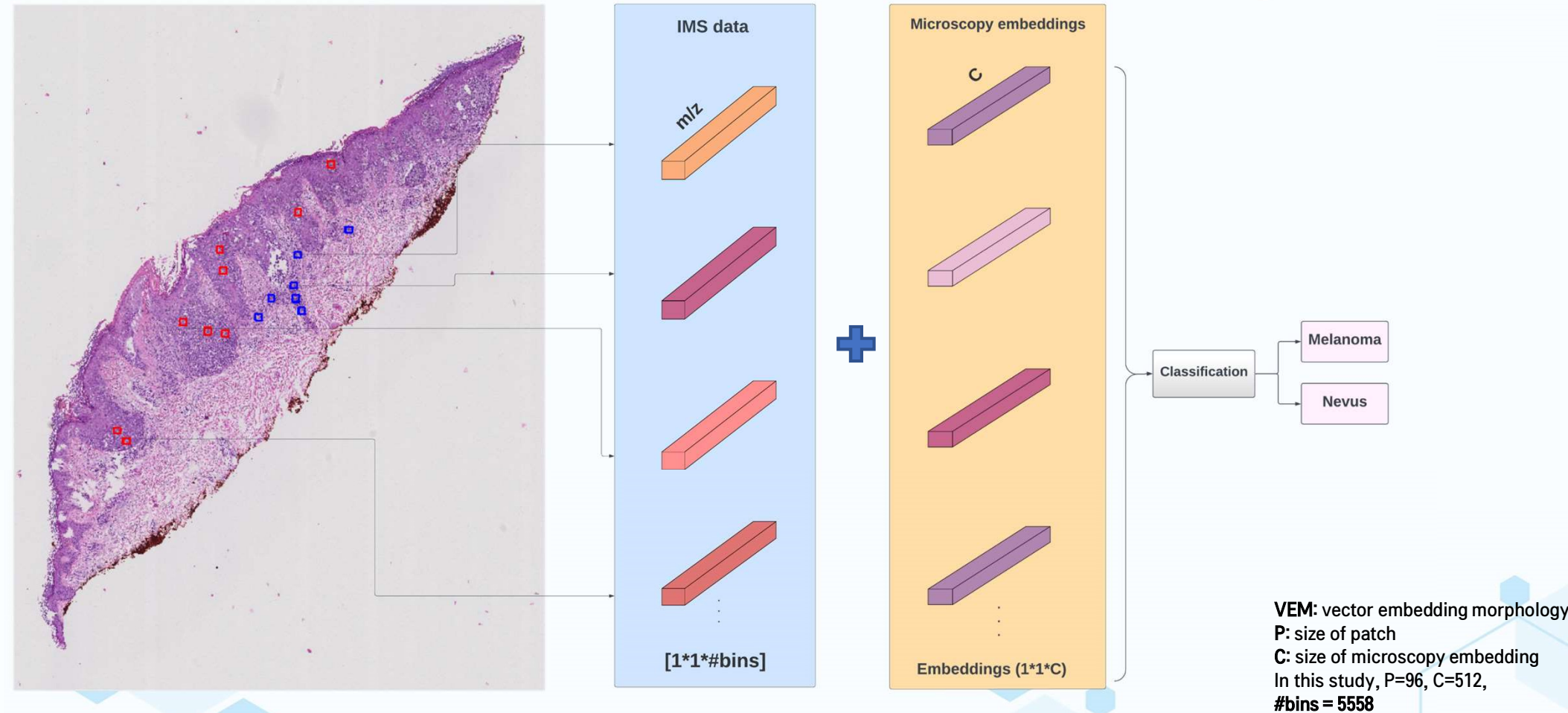


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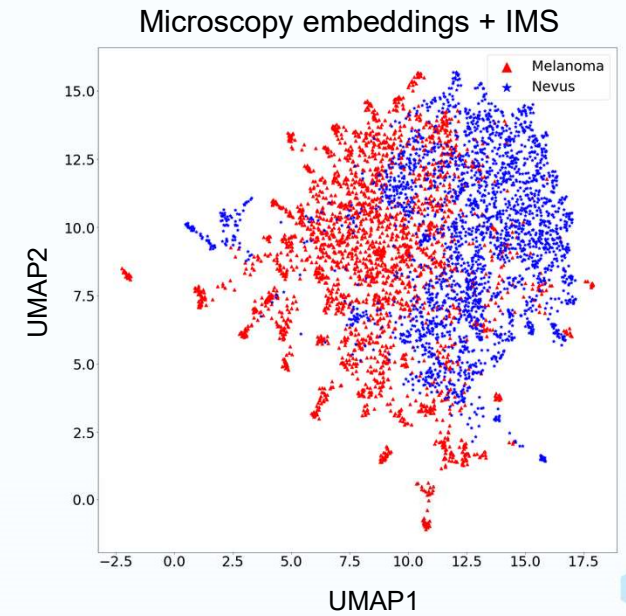
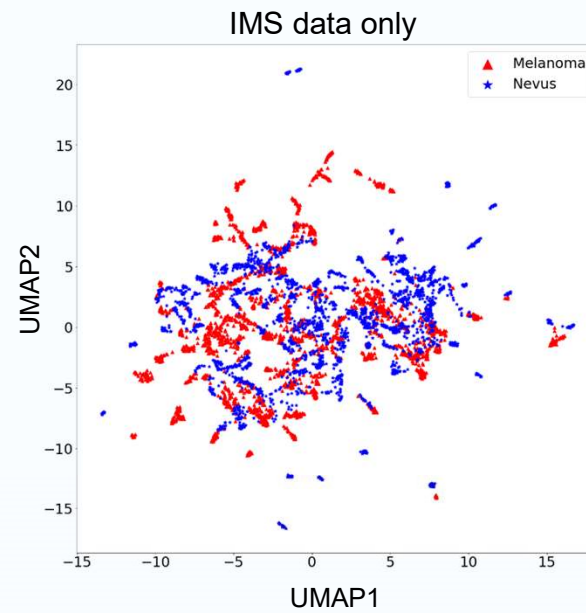
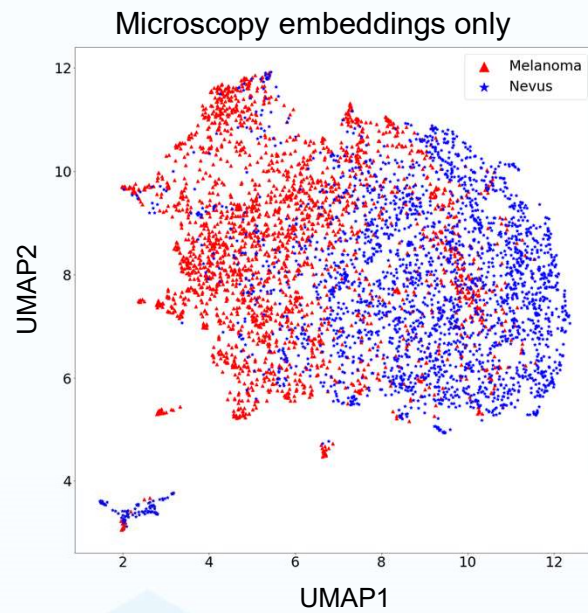
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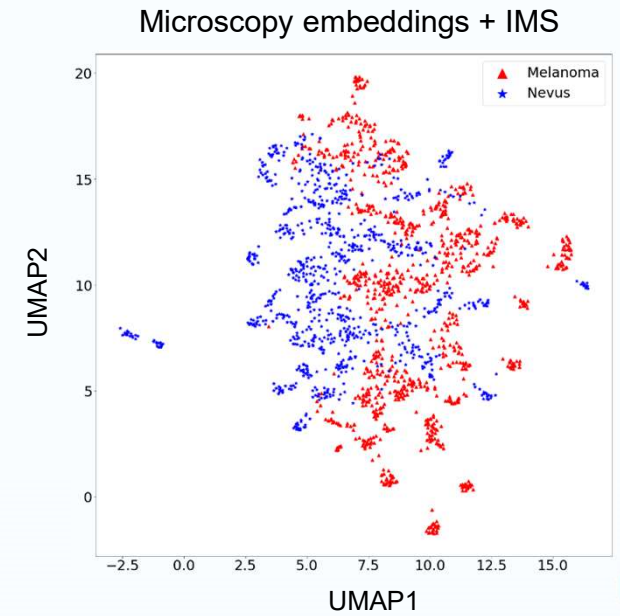
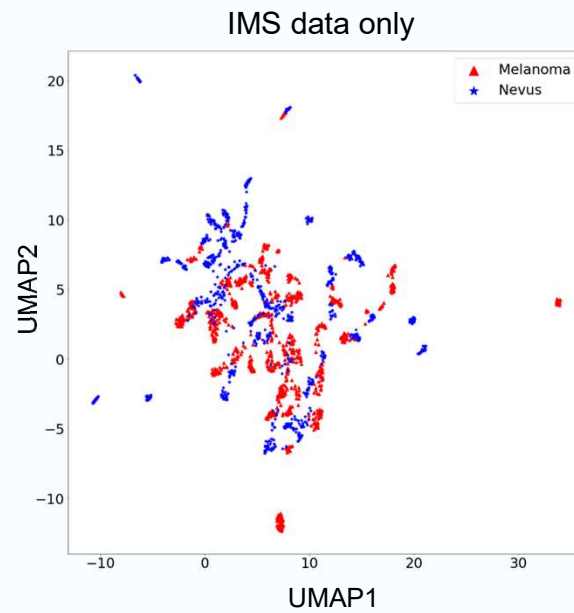
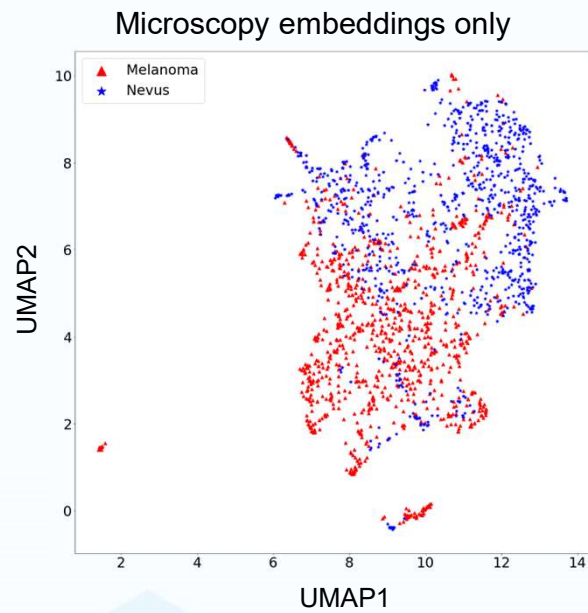
# Results

## UMAP on training data



# Results

## UMAP on test data



# Results

## Experiments details:

- Classification model: linear support vector machine (SVM)
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  - Inner cross validation: 10 folds
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*Spots that measured in the same tissue were grouped in the same fold, during each iteration*

Final Multimodal IMS and Microscopy data		
Number	Training set	Test set
Samples/Patients	239	92
Spots	5080	1924
Diagnosis Melanoma	2476	999
Diagnosis Nevus	2604	925

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Nested cross validation results on training data:

Model	Mean ROC-AUC		Mean F1 score		Mean Precision		Mean Recall	
Unimodal IMS	0.915	0.049	0.823	0.067	0.846	0.085	0.815	0.11
Unimodal Microscopy	0.937	0.03	0.82	0.056	0.857	0.104	0.805	0.111
Multimodal	<b>0.968</b>	0.023	<b>0.866</b>	0.056	<b>0.920</b>	0.051	<b>0.83</b>	0.112

*Note: Melanoma is negative; all results are based on spots-level; Standard deviation are in grey, ROC-AUC = 1 means the classifier can distinguish between all Positive and Negative class points perfectly correctly.*

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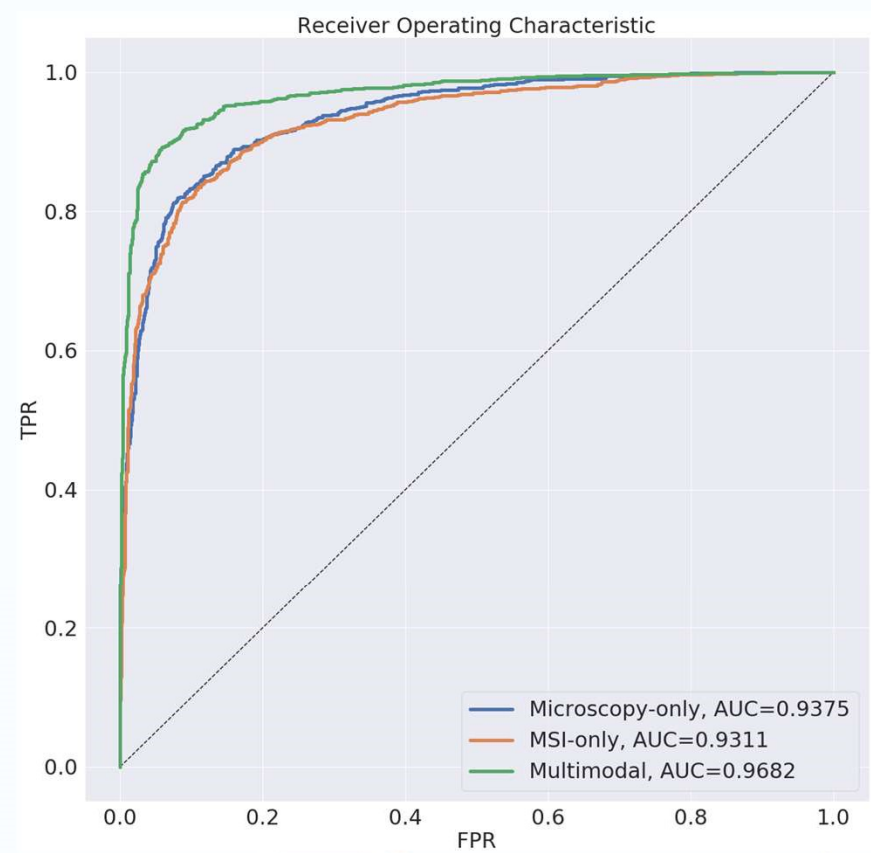
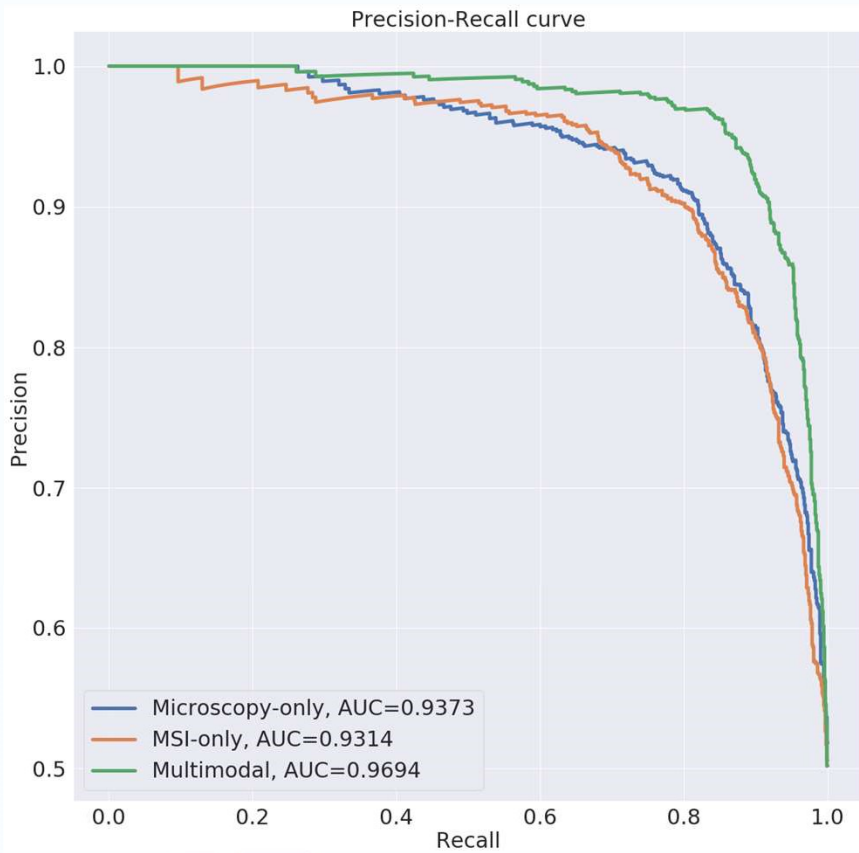
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Results on independent test data (with optimized parameters):

Model	ROC-AUC	F1 score	Precision	Recall	Specificity
Unimodal IMS	0.931	0.856	0.828	0.886	0.83
Unimodal Microscopy	0.938	0.861	0.871	0.851	0.883
Multimodal	<b>0.968</b>	<b>0.91</b>	<b>0.924</b>	<b>0.90</b>	<b>0.932</b>

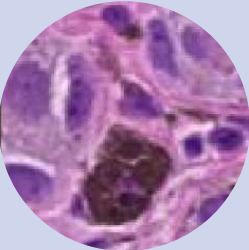

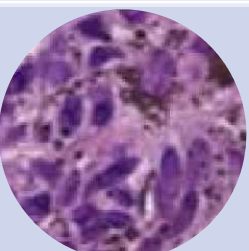

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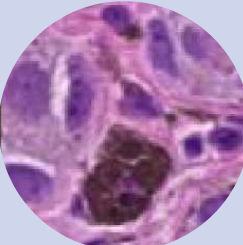
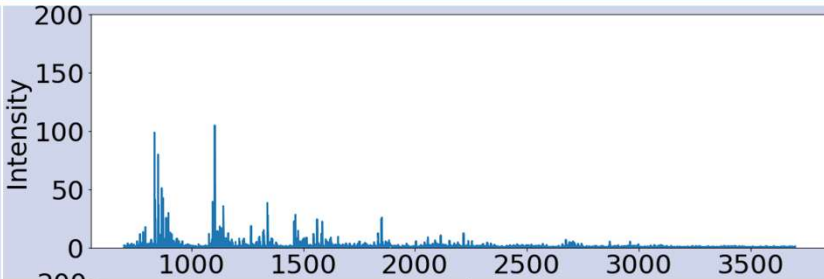

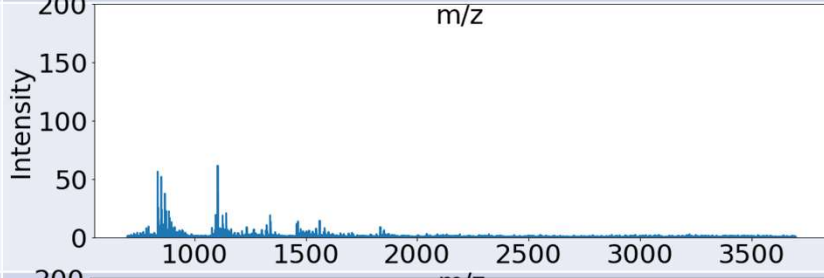

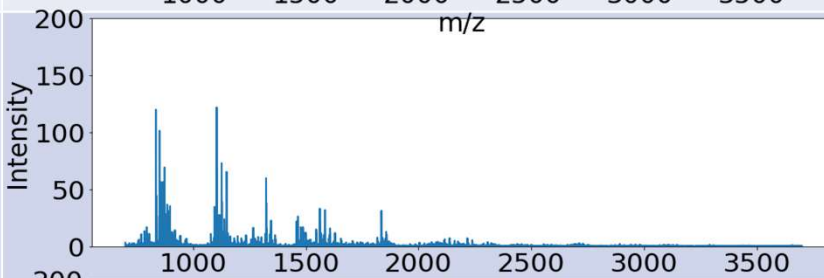

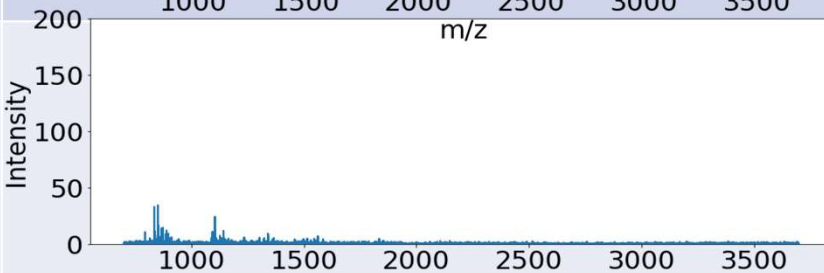
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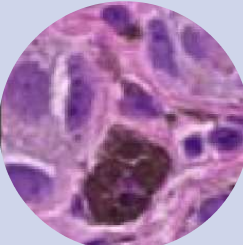
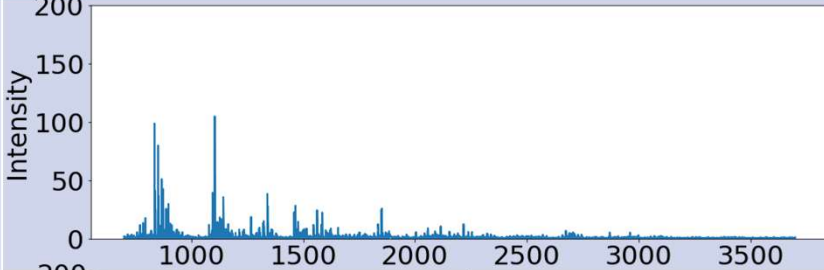

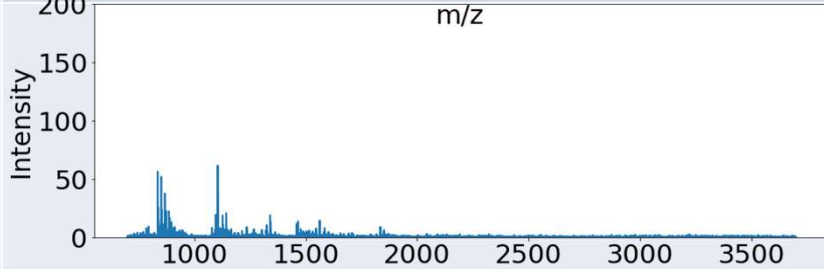

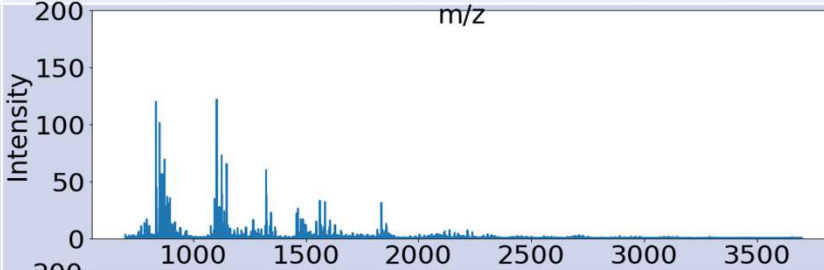
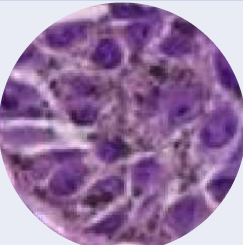
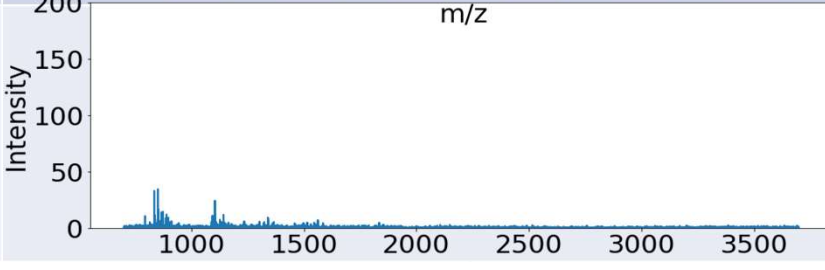


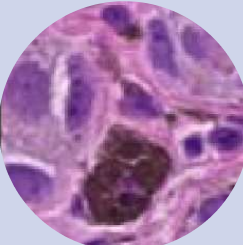
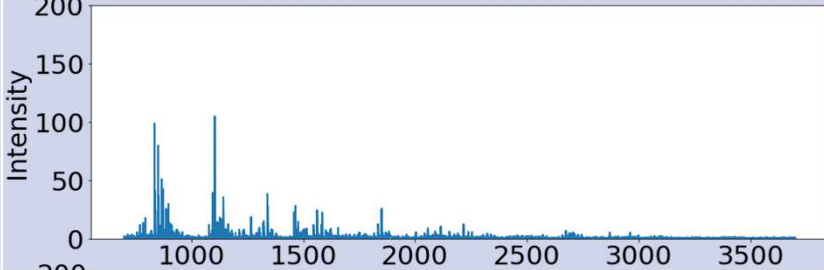

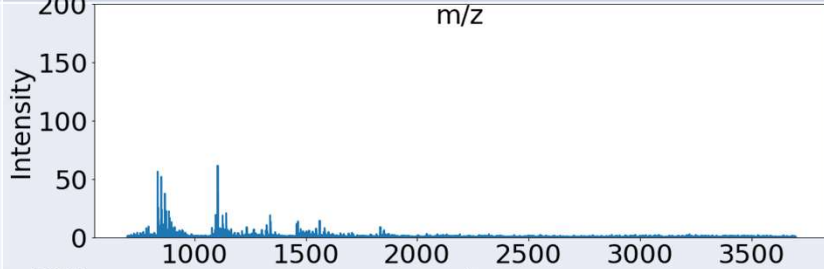

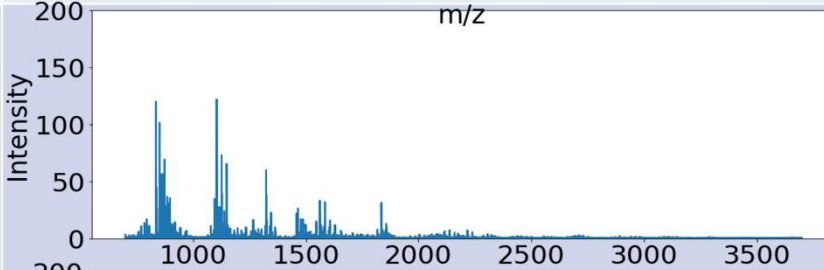
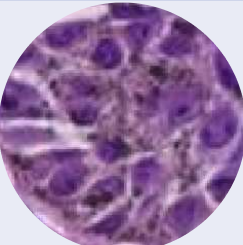
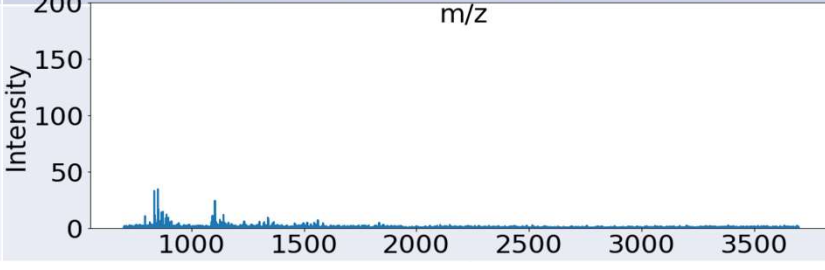
# Interesting cases

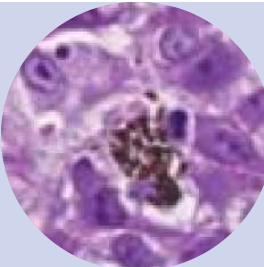
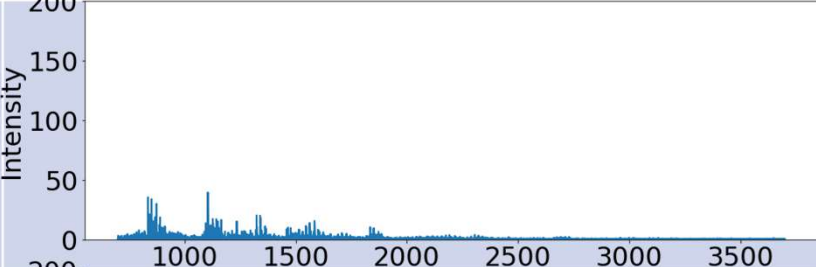

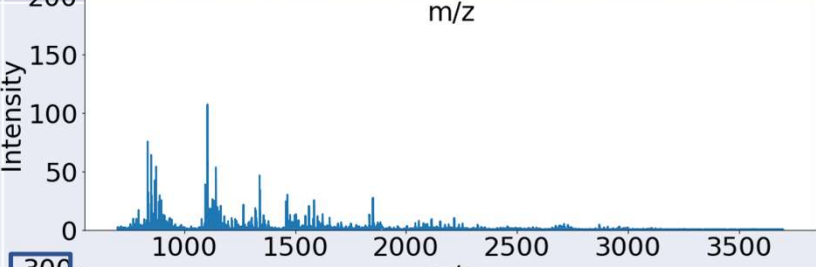
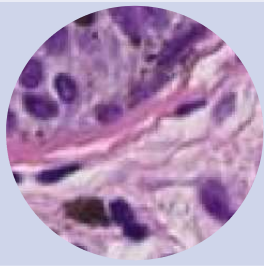
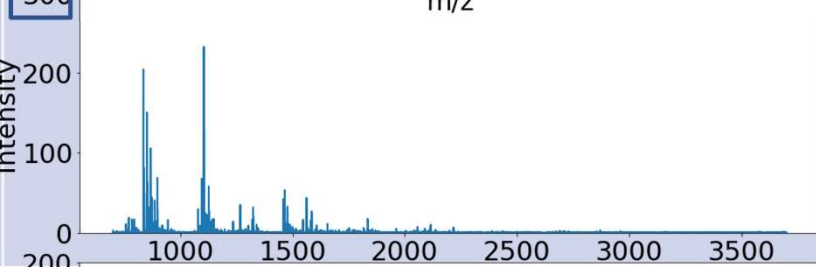

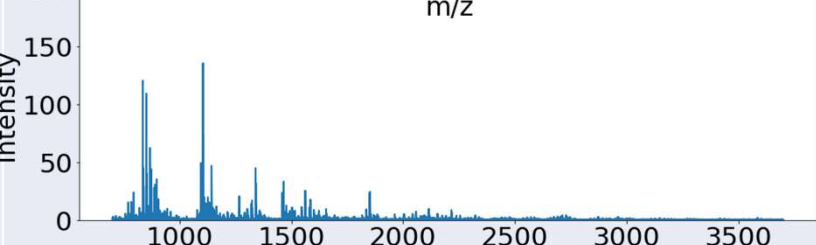
Misclassified cases from unimodal pipelines


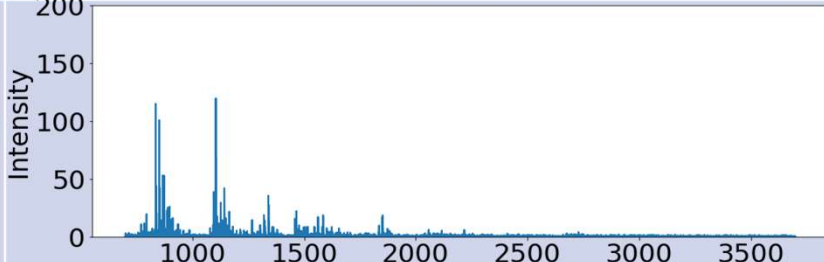

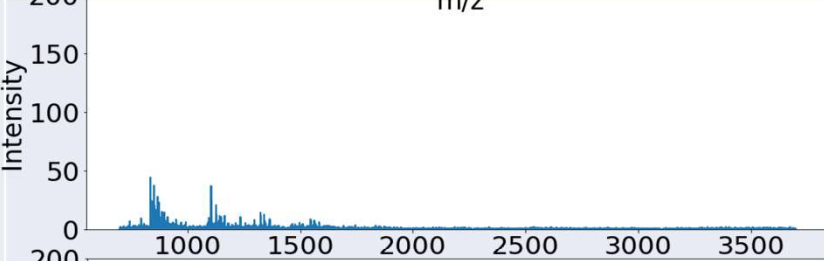

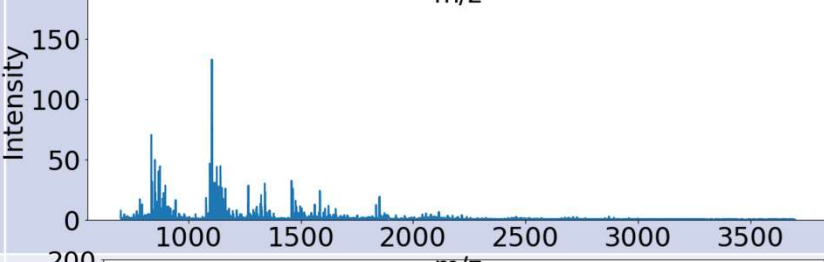

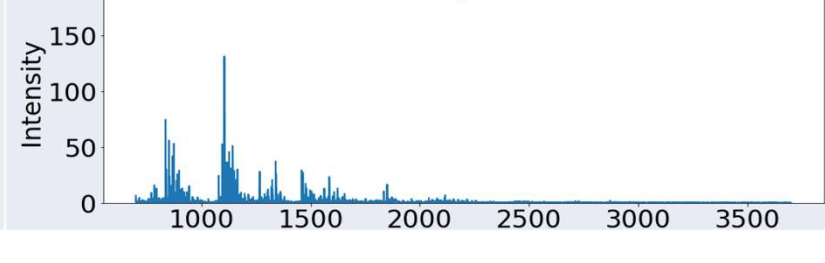
Microscopy data	IMS data	Unimodal Microscopy prediction	Unimodal IMS prediction	Multimodal prediction	Experts evaluation
					Melanoma
					Melanoma
					Nevus
					Nevus


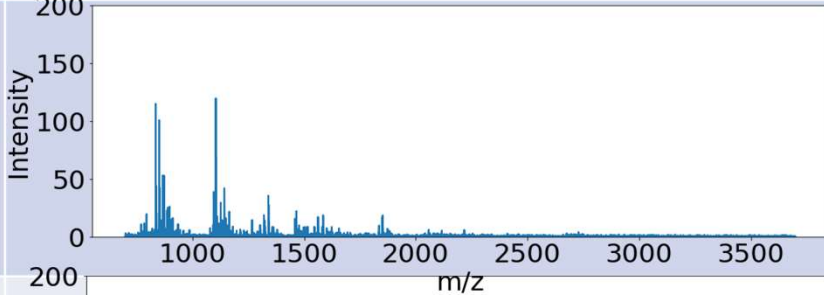

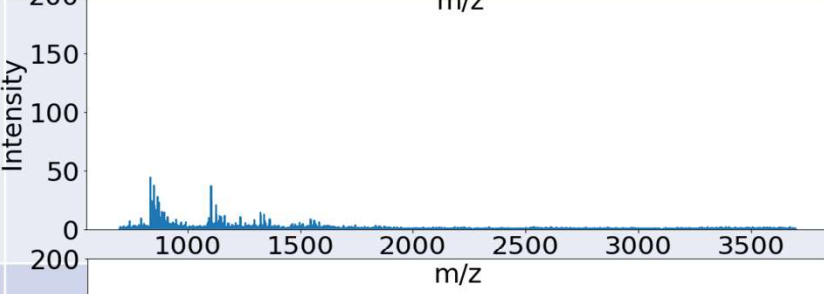
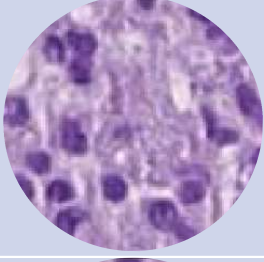
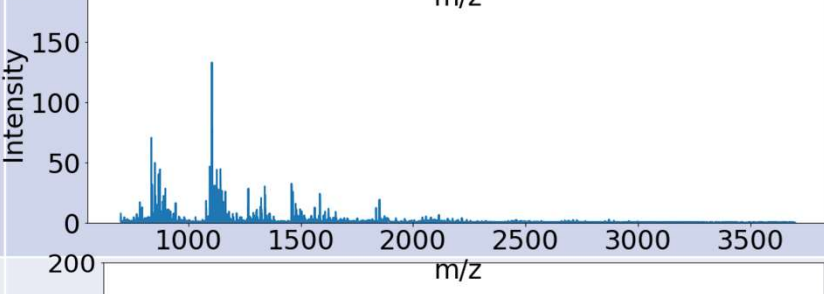

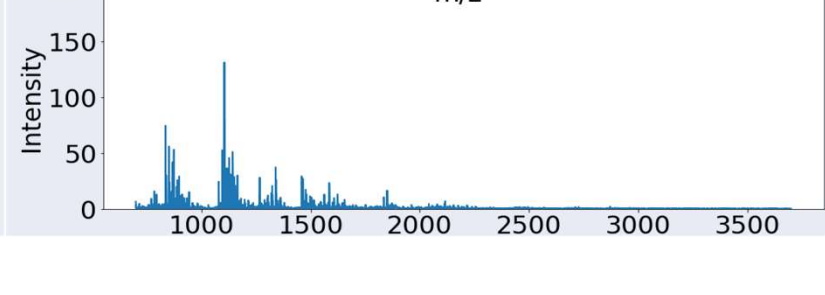
Microscopy data	IMS data	Unimodal Microscopy prediction	Unimodal IMS prediction	Multimodal prediction	Experts evaluation
					Melanoma
					Melanoma
					Nevus
					Nevus

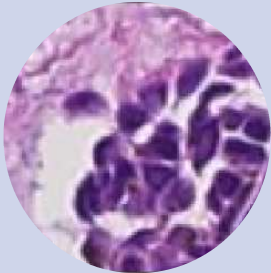
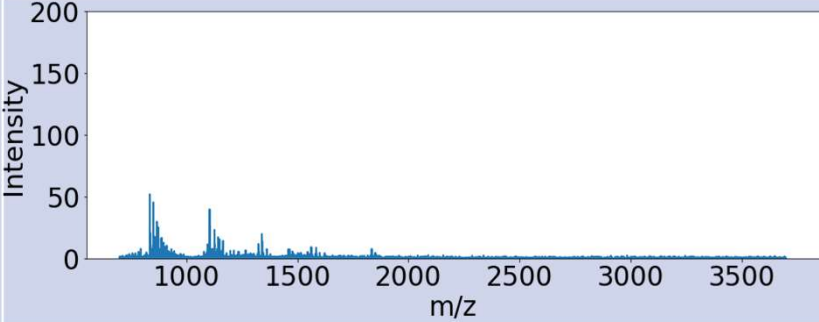

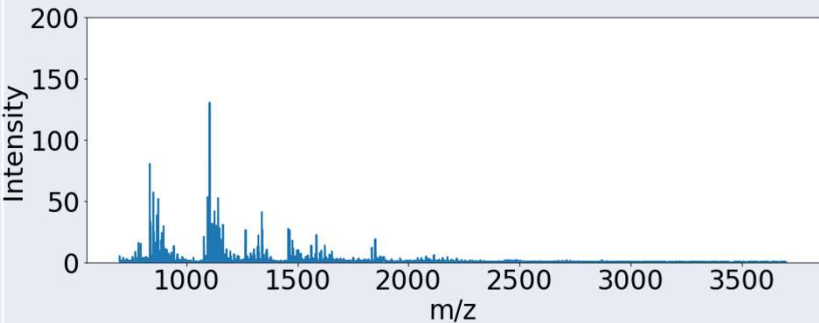

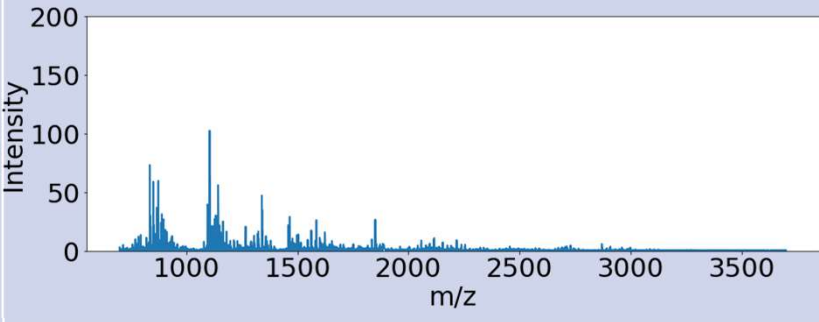
Microscopy data	IMS data	Unimodal Microscopy prediction	Unimodal IMS prediction	Multimodal prediction	Experts evaluation
		Nevus	Melanoma		Melanoma
		Nevus	Melanoma		Melanoma
		Melanoma	Nevus		Nevus
		Melanoma	Nevus		Nevus

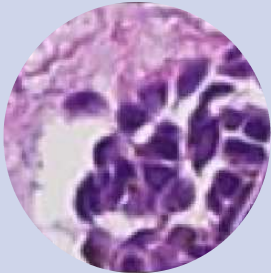
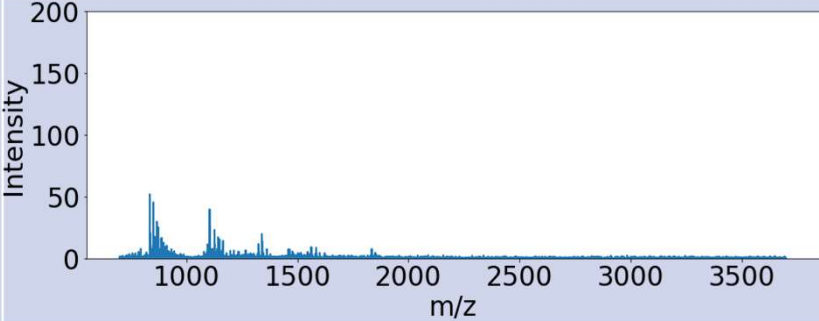

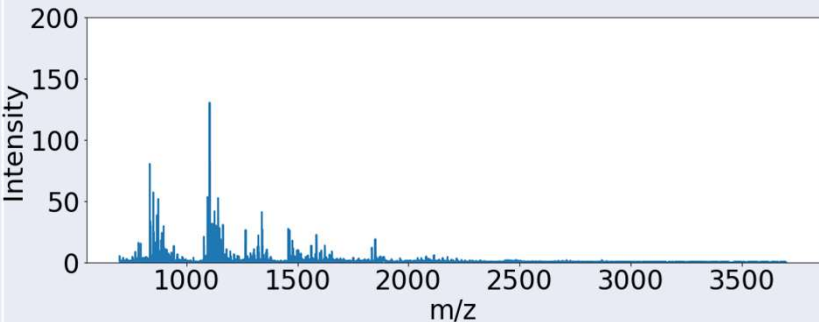

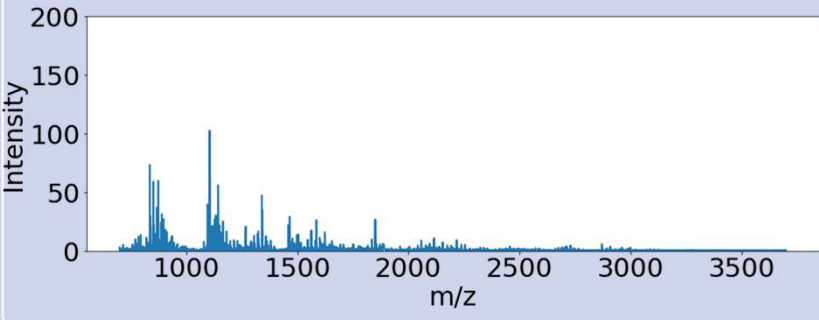
Microscopy data	IMS data	Unimodal Microscopy prediction	Unimodal IMS prediction	Multimodal prediction	Experts evaluation
		Nevus	Melanoma	Melanoma	Melanoma
		Nevus	Melanoma	Melanoma	Melanoma
		Melanoma	Nevus	Nevus	Nevus
		Melanoma	Nevus	Nevus	Nevus

Microscopy data	IMS data	Unimodal Microscopy prediction	Unimodal IMS prediction	Multimodal prediction	Experts evaluation
	 <p>Intensity</p> <p>m/z</p>	Melanoma	Nevus	Melanoma	Melanoma
	 <p>Intensity</p> <p>m/z</p>	Melanoma	Nevus	Melanoma	Melanoma
	 <p>Intensity</p> <p>m/z</p>	Nevus	Melanoma	Nevus	Nevus
	 <p>Intensity</p> <p>m/z</p>	Nevus	Melanoma	Nevus	Nevus

Microscopy data	IMS data	Unimodal Microscopy prediction	Unimodal IMS prediction	Multimodal prediction	Experts evaluation
		Melanoma	Melanoma		Nevus
		Nevus	Nevus		Melanoma
		Nevus	Nevus		Melanoma
		Nevus	Nevus		Melanoma

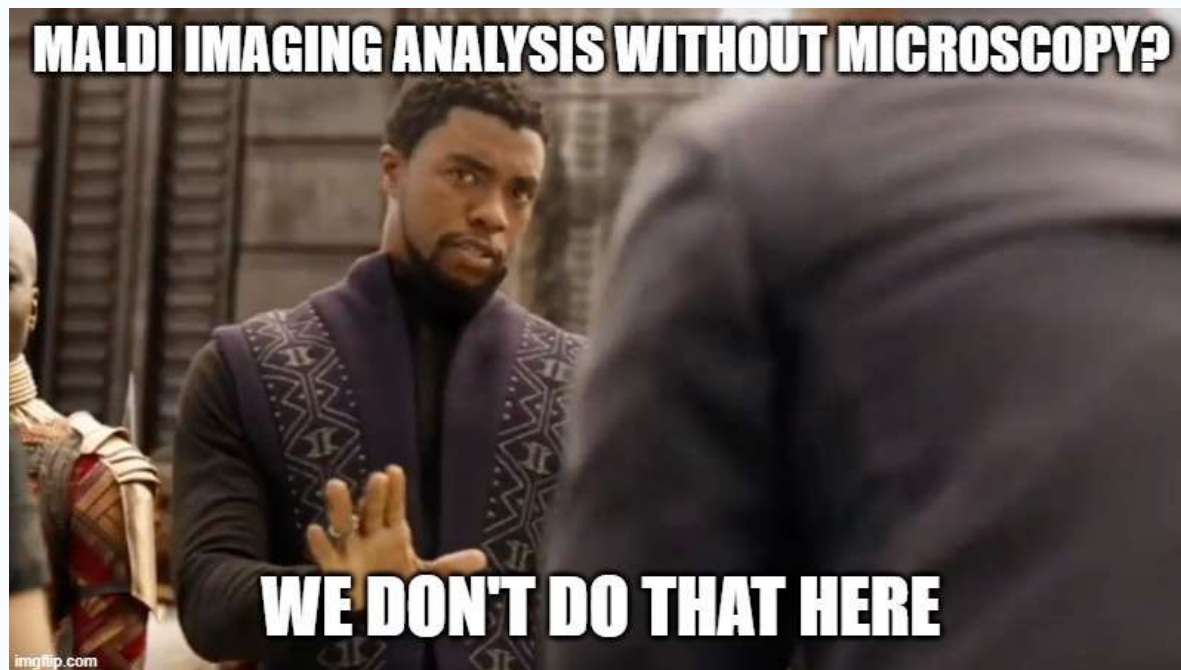
Microscopy data	IMS data	Unimodal Microscopy prediction	Unimodal IMS prediction	Multimodal prediction	Experts evaluation
		Melanoma	Melanoma	Nevus	Nevus
		Nevus	Nevus	Melanoma	Melanoma
		Nevus	Nevus	Melanoma	Melanoma
		Nevus	Nevus	Melanoma	Melanoma

Microscopy data	IMS data	Unimodal Microscopy prediction	Unimodal IMS prediction	Multimodal prediction	Experts evaluation
		Nevus	Nevus		Melanoma
		Nevus	Nevus		Melanoma
		Nevus	Nevus		Melanoma

Microscopy data	IMS data	Unimodal Microscopy prediction	Unimodal IMS prediction	Multimodal prediction	Experts evaluation
		Nevus	Nevus	Melanoma	Melanoma
		Nevus	Nevus	Melanoma	Melanoma
		Nevus	Nevus	Melanoma	Melanoma

## Conclusion

- Multimodal is great!
- Do not throw your microscopy data away 😊



# Want to know more?



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# Want to know more?



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## Acknowledgements

Wanqiu Zhang was supported by a Baekeland PhD grant from Flanders Innovation and Entrepreneurship (VLAIO)

Nathan Heath Patterson; Jessica Moore; Richard M. Caprioli; Jeremy L. Norris;  
Nico Verbeeck; Alice Ly; Bart De Moor; Marc Claesen

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### Conflict of Interest

JM, NHP, RMC, and JLN disclose a financial interest in Frontier Diagnostics, LLC (FDx). FDx has issued and pending patent applications in the US Patent Office that include part of the methods described in paper<sup>1</sup>. NV and MC, principals of Aspect Analytics NV, are paid consultants and provide services to FDx. WZ declares no competing interests.

<sup>1</sup>Al-Rohil, Rami N., Jessica L. Moore, Nathan Heath Patterson, Sarah Nicholson, Nico Verbeeck, Marc Claesen, Jameelah Z. Muhammad et al. "Diagnosis of melanoma by imaging mass spectrometry: Development and validation of a melanoma prediction model." *Journal of cutaneous pathology* 48, no. 12 (2021): 1455-1462.