

Reducing Annotation Need in Self-Explanatory Models for Lung Nodule Diagnosis (cRedAnno)

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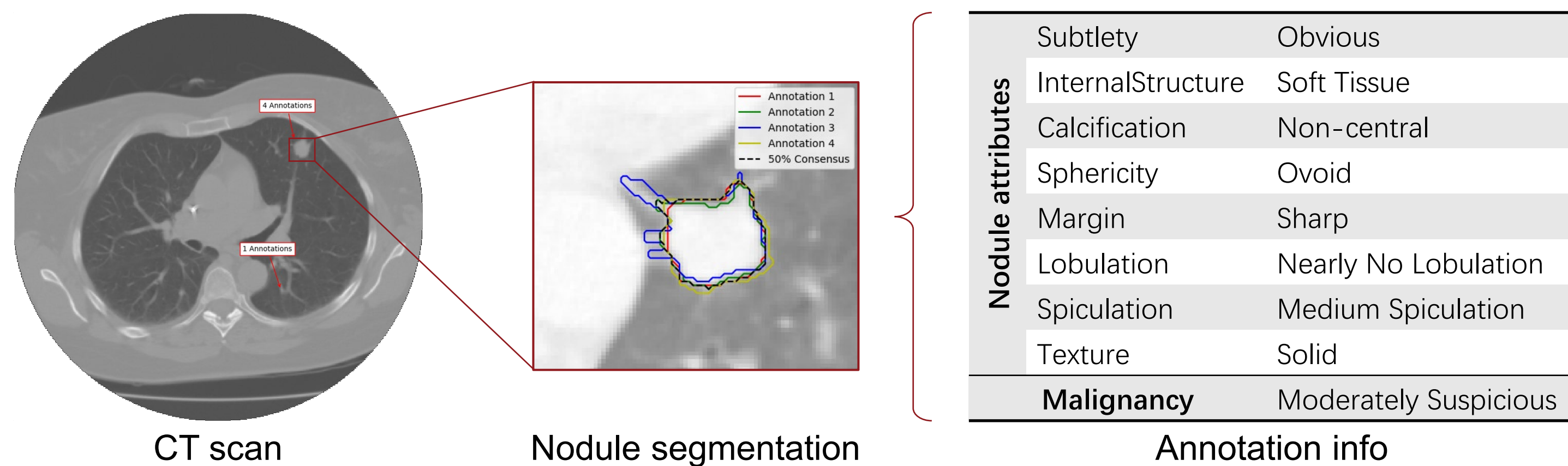


github.com/diku-dk/credanno

Background

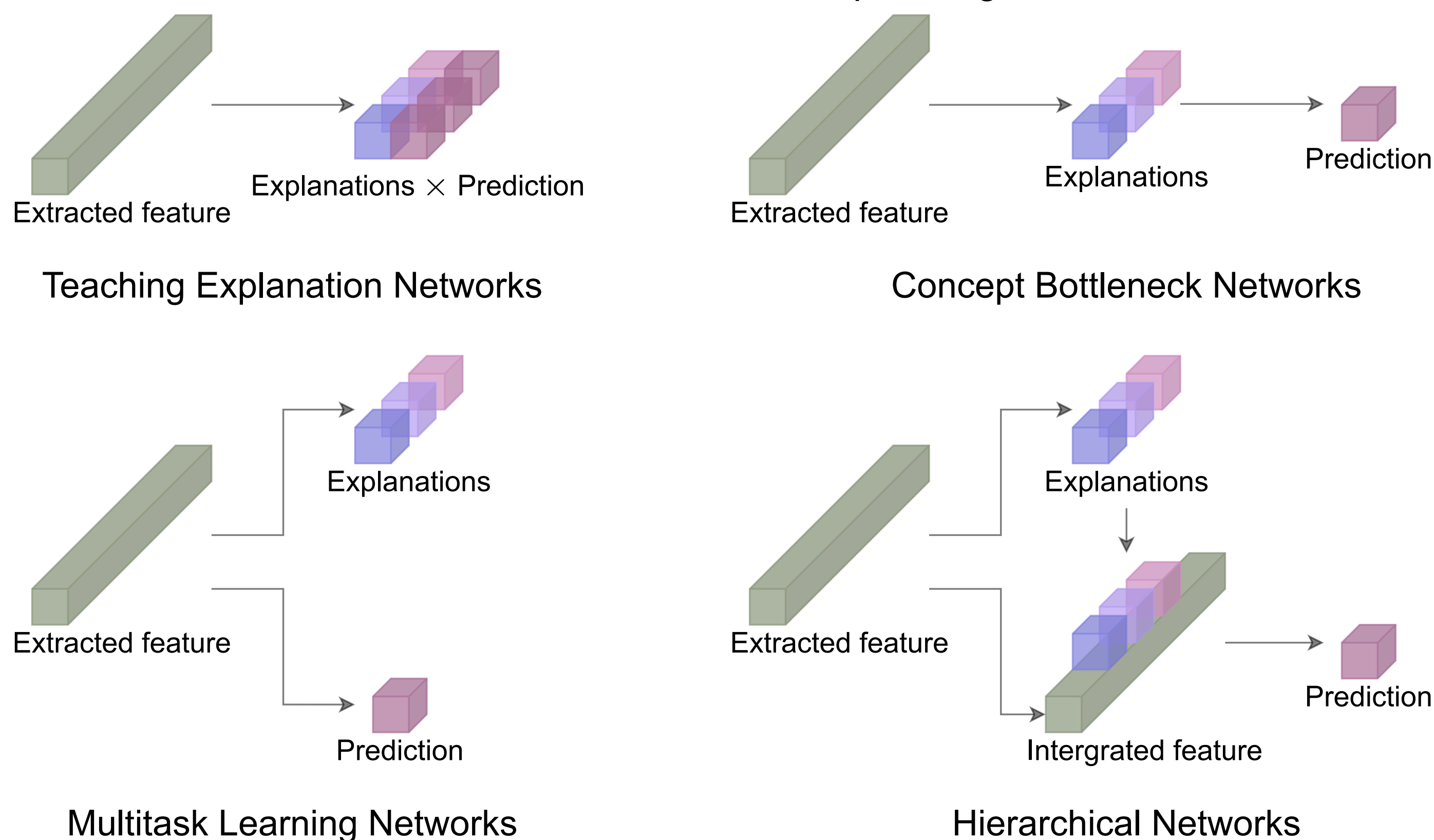
Lung nodule diagnosis

In clinical practice, accurate **characterisation of pulmonary nodules** in CT images is an essential step for effective lung cancer screening. Modern deep-learning-based “black box” algorithms, although achieving accurate classification performance, are hardly acceptable in high-stakes medical diagnosis.



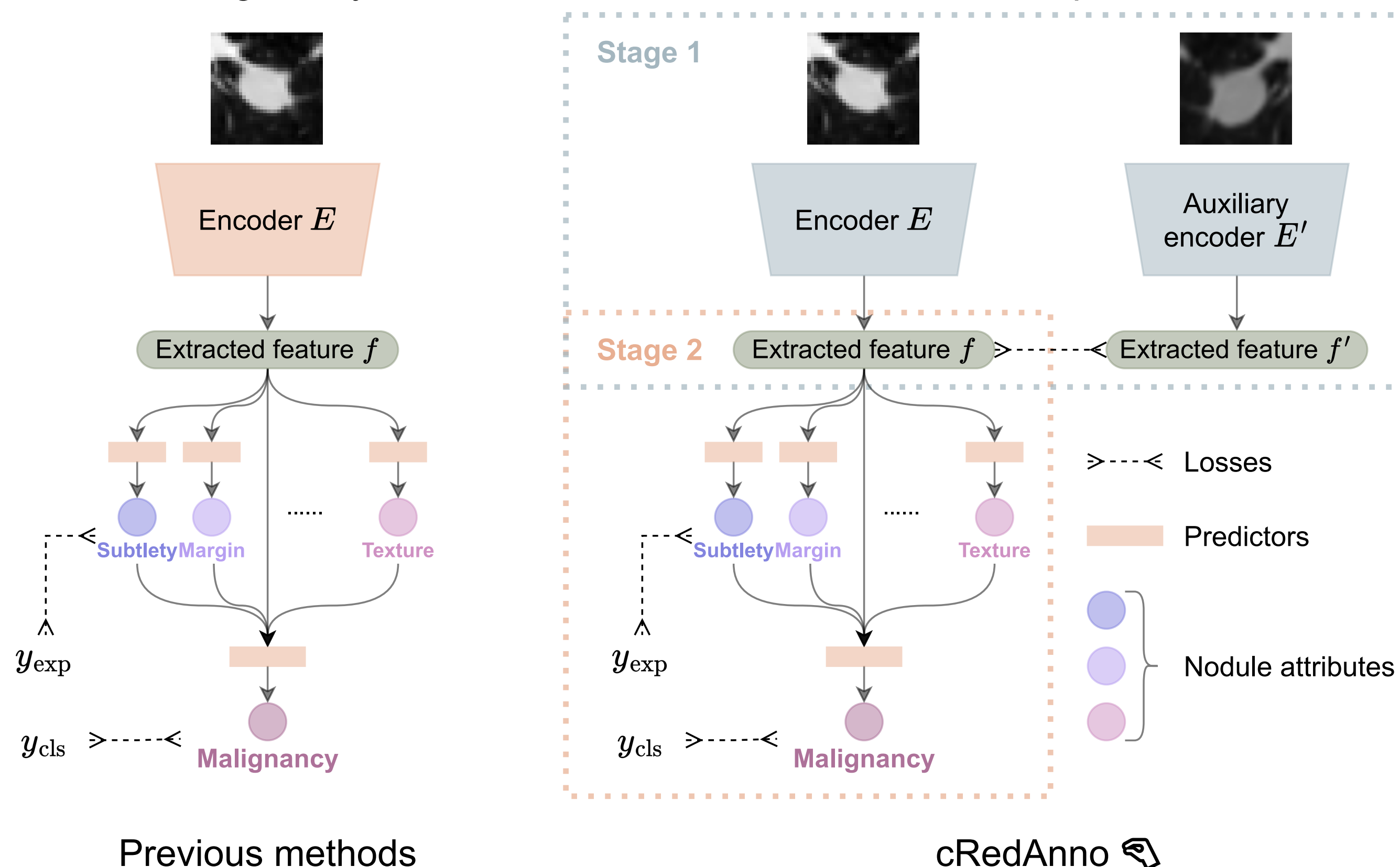
Self-explanatory models

Feature-based self-explanatory methods explain their classification in terms of human-understandable features. In medical applications, this **semantic matching of clinical knowledge** adds significantly to the trustworthiness of the AI. However, the **cost of additional annotation of features** remains a pressing issue.



Method

(a) Previous works are trained end-to-end, where all parameters are learned from the annotations. (b) Our proposed cRedAnno uses **two-stage training**, where most of the parameters are learned during the first stage in a self-supervised manner. Therefore, in the second stage, only few annotations are needed to train the predictors.



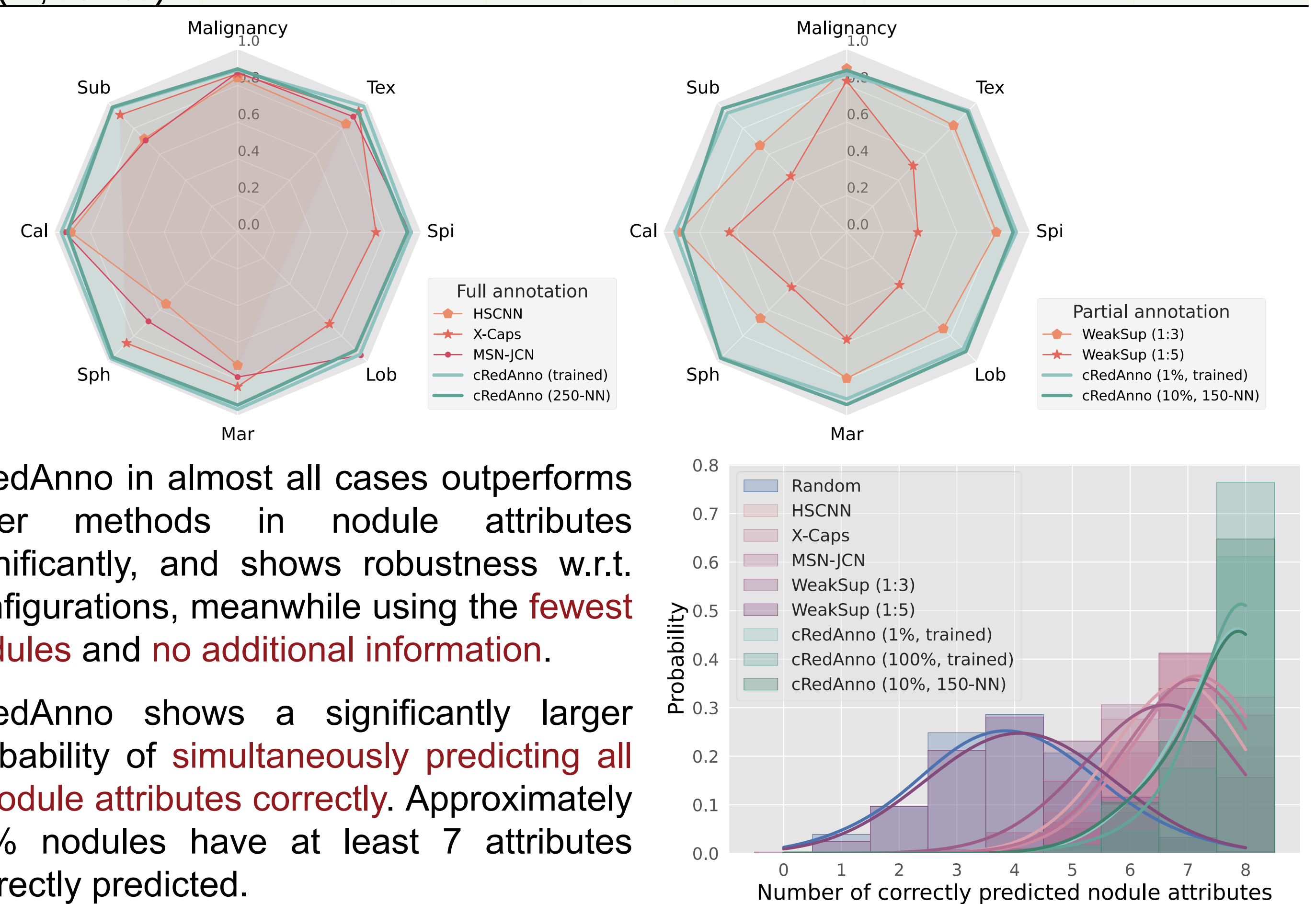
Stage 1: unsupervised feature extraction. The majority of parameters are trained using self-supervised contrastive learning as an encoder to map the input images to a latent space that complies with radiologists' reasoning for nodule malignancy.

Stage 2: supervised prediction. A small random portion of labelled samples is used to train a simple predictor for each nodule attribute. Then the predicted human-interpretable nodule attributes are used jointly with the extracted features to make the final classification.

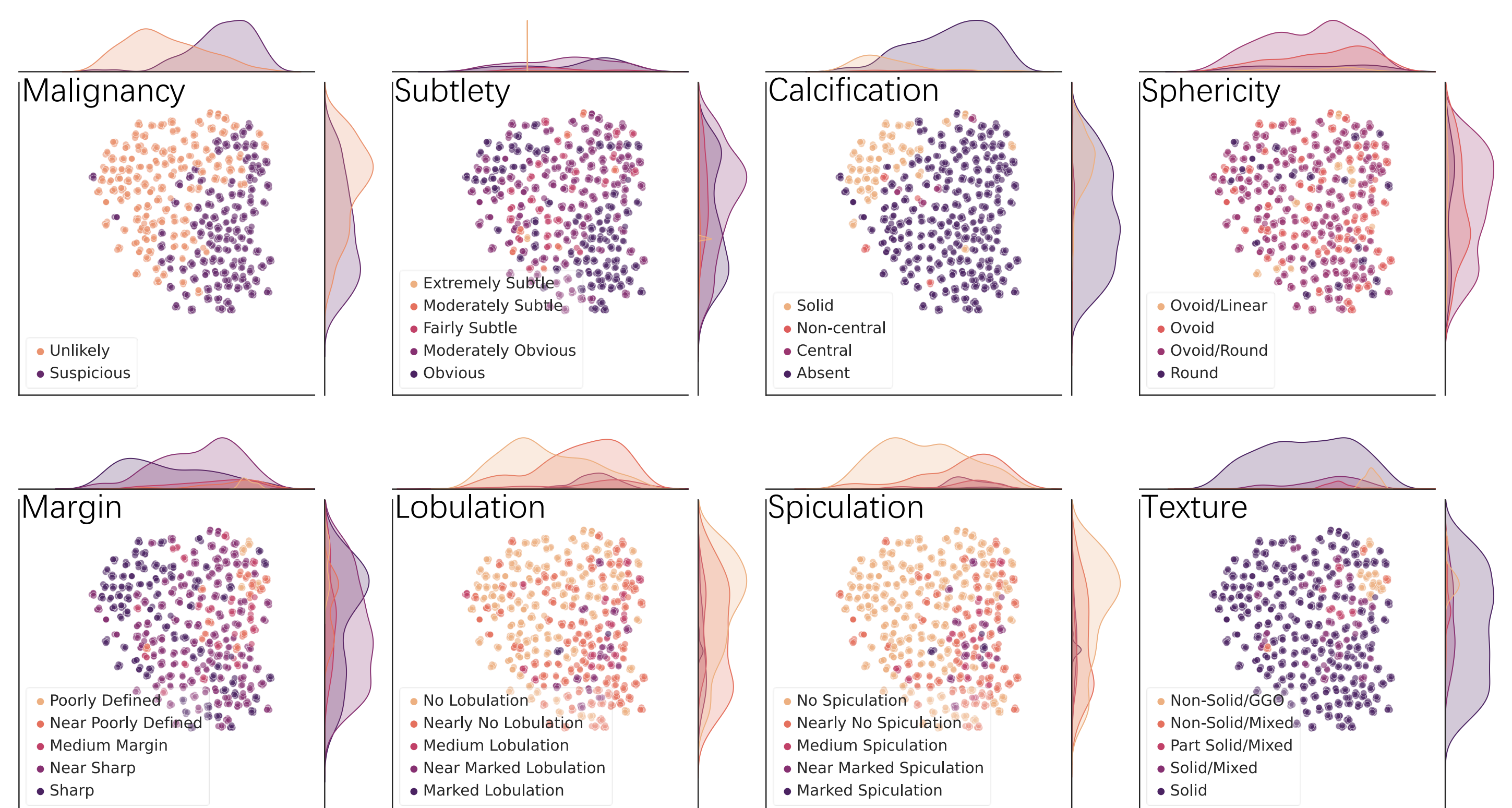
Results

Prediction performance

	Nodule attributes						Malignancy	#nodules	No additional info	
	Sub	Cal	Sph	Mar	Lob	Spi				Tex
Full annotation										
HSCNN ^[1]	71.90	90.80	55.20	72.50	-	-	83.40	84.20	4252	X
X-Caps ^[2]	90.39	-	85.44	84.14	70.69	75.23	93.10	86.39	1149	✓
MSN-JCN ^[3]	70.77	94.07	68.63	78.88	94.75	93.75	89.00	87.07	2616	X
MTMR ^[4]	-	-	-	-	-	-	-	93.50	1422	X
(50-NN)	94.93	92.72	95.58	93.76	91.29	92.72	94.67	87.52		
(250-NN)	96.36	92.59	96.23	94.15	90.90	92.33	92.72	88.95	730	✓
* (trained)	95.84	95.97	97.40	96.49	94.15	94.41	97.01	88.30		
Partial annotation										
WeakSup ^[5] (1:5)	43.10	63.90	42.40	58.50	40.60	38.70	51.20	82.40	2558	X
WeakSup ^[5] (1:3)	66.80	91.50	66.40	79.60	74.30	81.40	82.20	89.10		
(10%, 50-NN)	94.93	92.07	96.75	94.28	92.59	91.16	94.15	87.13		
* (10%, 150-NN)	95.32	89.47	97.01	93.89	91.81	90.51	92.85	88.17	730	✓
* (1%, trained)	91.81	93.37	96.49	90.77	89.73	92.33	93.76	86.09		



Analysis of extracted features



Malignancy shows highly separable in the learned space and correlates with the clustering in each nodule attribute.

Conclusion

- We propose cRedAnno, a **data-/annotation-efficient** self-explanatory approach for lung nodule diagnosis.
- When training with **hundreds of nodule samples** and only **1% of their annotations**, cRedAnno significantly outperforms previous works in predicting nodule attributes, meanwhile achieving competitive accuracy in predicting malignancy.
- Visualisation of the learned space further indicates that the correlation between the clustering of malignancy and nodule attributes **coincides with clinical knowledge**.

References
 [1] S. Shen et al., “An interpretable deep hierarchical semantic convolutional neural network for lung nodule malignancy classification,” Expert Systems with Applications, 2019.
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 [3] W. Chen et al., “End-to-End Multi-Task Learning for Lung Nodule Segmentation and Diagnosis,” ICPR, 2021.
 [4] L. Liu et al., “Multi-Task Deep Model With Margin Ranking Loss for Lung Nodule Analysis,” IEEE Trans. Med. Imaging, 2020.
 [5] A. Joshi et al., “Lung nodule malignancy classification with weakly supervised explanation generation,” J. Med. Imag., 2021.