#### (considerably) **Red**ucing **Anno**tation Need in Self-Explanatory Models for Lung Nodule Diagnosis (cRedAnno �)

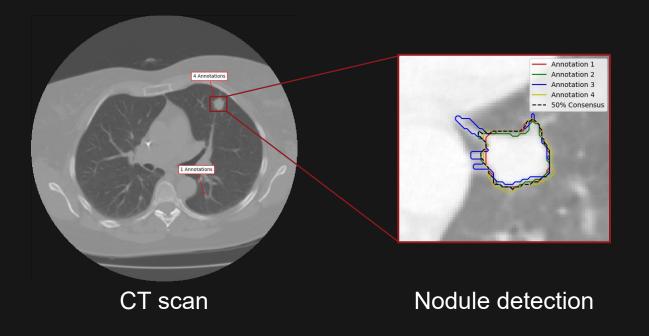
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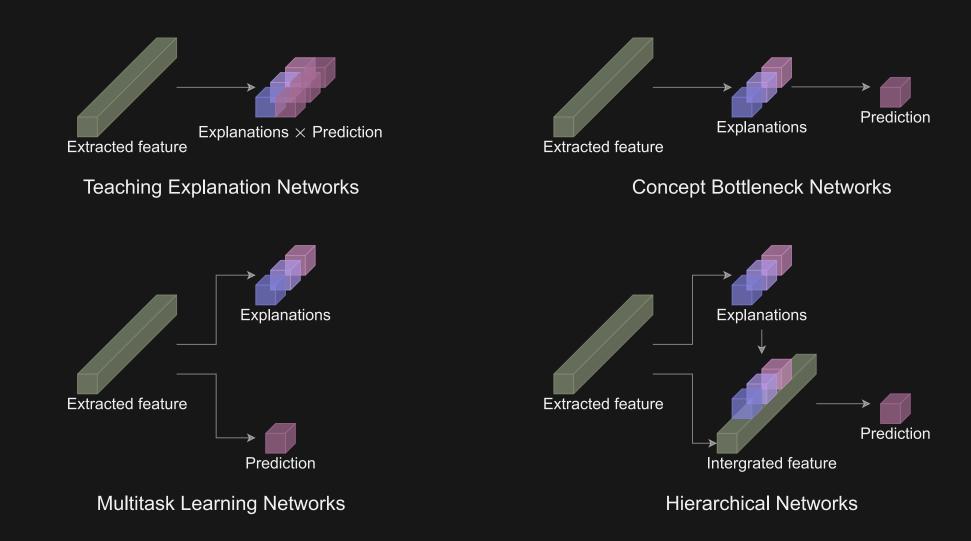
## Background: Lung nodule diagnosis



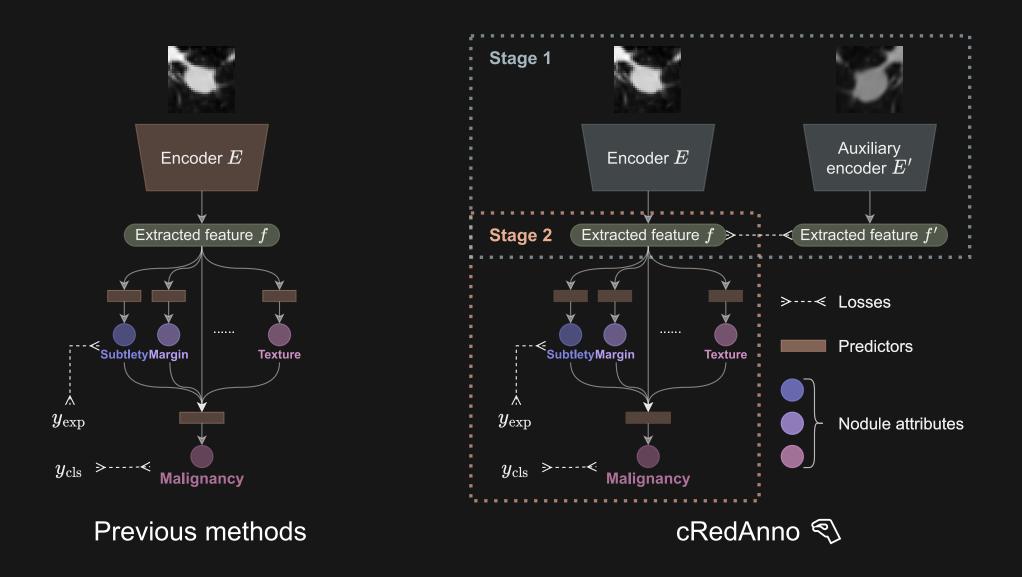
	Malignancy	Moderately Suspicious			
Nodule attributes	Texture	Solid			
	Spiculation	Medium Spiculation			
	Lobulation	Nearly No Lobulation			
	Margin	Sharp			
	Sphericity	Ovoid			
	Calcification	Non-central			
	InternalStructure	Soft Tissue			
	Subtlety	Obvious			

Annotation info

## Related work: Feature-based self-explanatory models



# Method

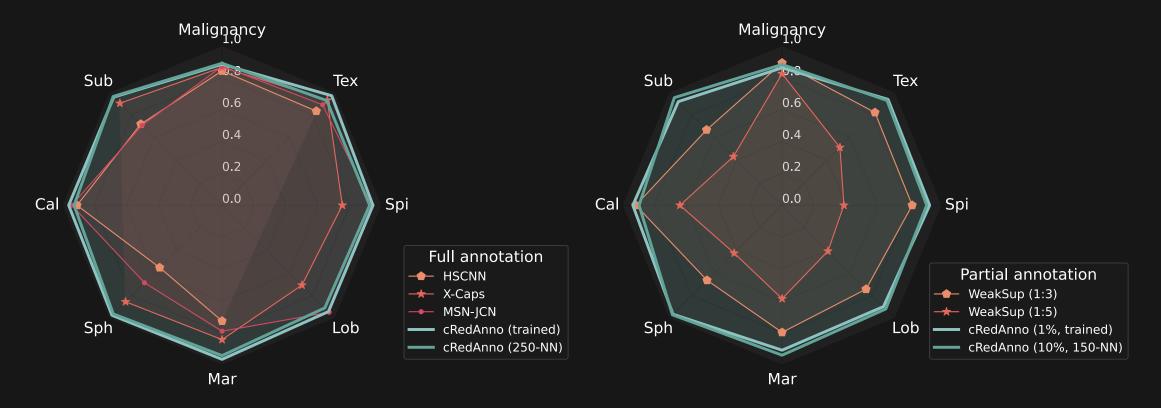


## Results: Predicting nodule attributes and malignancy

	Nodule attributes							Malignancy	#nodules	Additional information	
	Sub	Cal	Sph	Mar	Lob	Spi	Тех		#nouules		
Full annotation											
HSCNN <sup>[1]</sup>	71.90	90.80	55.20	72.50			83.40	84.20	4252	3D volume data	
X-Caps <sup>[2]</sup>	90.39		85.44	84.14	70.69	75.23	93.10	86.39	1149	None	
MSN-JCN <sup>[3]</sup>	70.77	94.07	68.63	78.88	94.75	93.75	89.00	87.07	2616	segmentation mask + diameter + OTSU + SLIC	
MTMR <sup>[4]</sup>								93.50	1422	all 2D slices in 3D volumes	
<b>cRedAnno</b> (50-NN)	94.93	92.72	95.58	93.76	91.29	92.72	94.67	87.52		$\boxed{\begin{array}{c c} \hline \\ \hline $	
<b>cRedAnno</b> * (250-NN)	96.36	92.59	96.23	94.15	90.90	92.33	92.72	88.95	730 -	train 276 242 <b>518</b> <b>val</b> 108 104 <b>212</b>	
<b>cRedAnno</b> * (trained)	95.84	95.97	97.40	96.49	94.15	94.41	97.01	88.30		sum 384 346 730	
Partial annotation											
<b>WeakSup</b> <sup>[5]</sup> (1:5)	43.10	63.90	42.40	58.50	40.60	38.70	51.20	82.40	2558	multi-scale 3D volume data, all malignancy annotations, 1/(1+N) attribute annotations	
<b>WeakSup</b> <sup>[5]</sup> (1:3)	66.80	91.50	66.40	79.60	74.30	81.40	82.20	89.10	2000		
<b>cRedAnno</b> (10%, 50-NN)	94.93	92.07	96.75	94.28	92.59	91.16	94.15	87.13			
<b>cRedAnno</b> * (10%, 150-NN)	95.32	89.47	97.01	93.89	91.81	90.51	92.85	88.17	730	None	
<b>cRedAnno</b> * (1%, trained) 🔊	91.81	93.37	96.49	90.77	89.73	92.33	93.76	86.09			

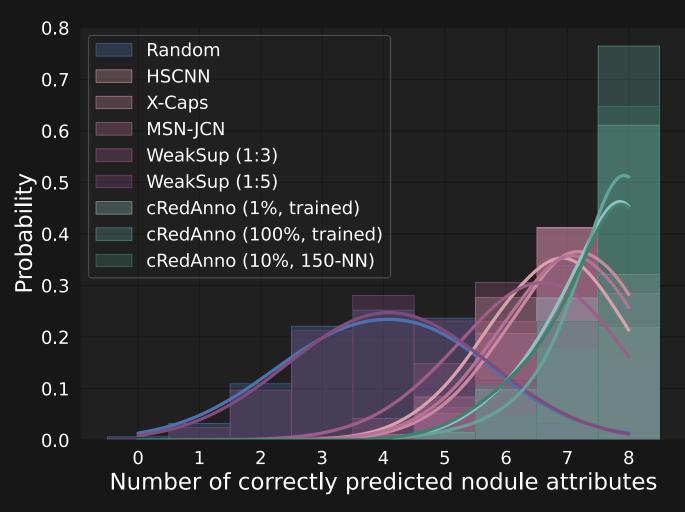
[1] S. Shen *et al.*, "An interpretable deep hierarchical semantic convolutional neural network for lung nodule malignancy classification," *Expert Systems with Applications*, vol. 128, pp. 84–95, Aug. 2019.
[2] R. LaLonde *et al.*, "Encoding Visual Attributes in Capsules for Explainable Medical Diagnoses," in *Medical Image Computing and Computer Assisted Intervention – MICCAI 2020*, Cham, 2020, pp. 294–304.
[3] W. Chen *et al.*, "End-to-End Multi-Task Learning for Lung Nodule Segmentation and Diagnosis," in *2020 25th International Conference on Pattern Recognition (ICPR)*, Milan, Italy, 2021, pp. 6710–6717.
[4] L. Liu *et al.*, "Multi-Task Deep Model With Margin Ranking Loss for Lung Nodule Analysis," *IEEE Trans. Med. Imaging*, vol. 39, no. 3, pp. 718–728, Mar. 2020.
[5] A. Joshi et al., "Lung nodule malignancy classification with weakly supervised explanation generation," *J. Med. Imag.*, vol. 8, no. 04, Aug. 2021.

## Results: Predicting nodule attributes and malignancy Full annotation Partial annotation



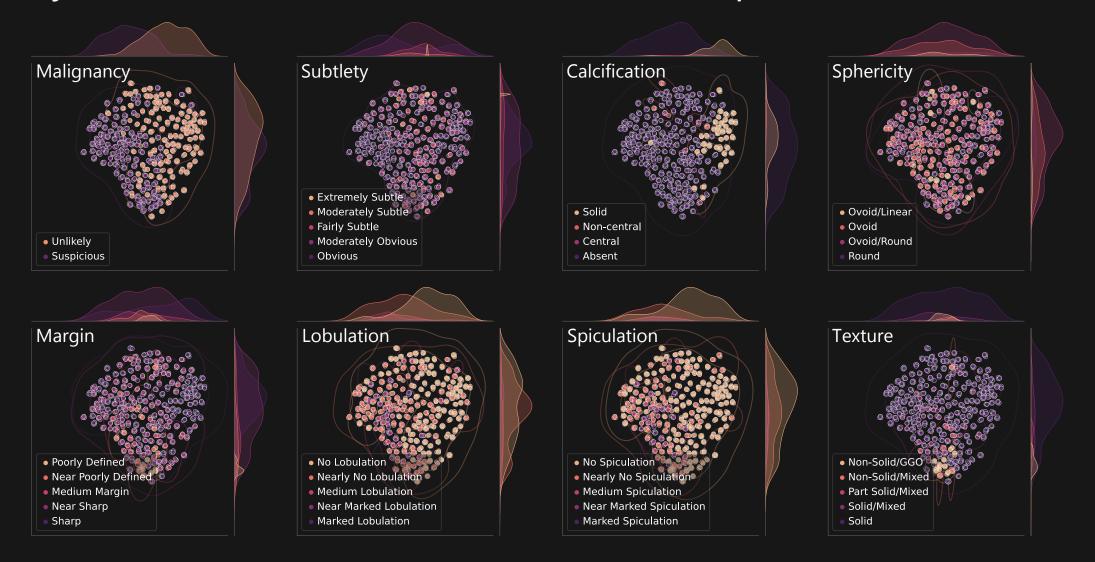
Simultaneously high accuracy in predicting malignancy and all nodule attributes.

# Results: Predicting nodule attributes



- cRedAnno shows a significantly larger probability of simultaneously predicting all 8 nodule attributes correctly.
- Approximately 90% nodules have at least 7 attributes correctly predicted.

## Results: Analysis of extracted features in learned space



## Results: Ablation study

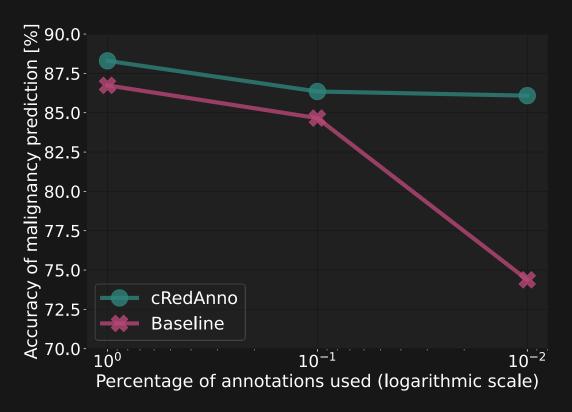
#### Validation of components

Accuracy of malignancy prediction (%). All annotations are used during training.

Arch	#params	Training strategy	ImageNet pretrain	Acc
		end-to-end		86.74*
ResNet-50	23.5M	two-stage	×	70.48
		two-stage	$\checkmark$	70.48
ViT		end-to-end	×	64.24
	21.7M	two-stage	×	79.19
		two-stage	$\checkmark$	88.30

Representative setting and performance of previous works using CNN architecture

#### Annotation reduction



# Conclusion

- A data-/annotation-efficient selfexplanatory approach for lung nodule diagnosis
- Comparing with SOTA:
  - 1% annotation, fewer samples
  - comparable in malignancy prediction
  - significantly better in predicting all nodule attributes as explanations
- Visualising the learned space:
  - extracted features are highly separable
  - clustering coincides with clinical knowledge

• Open-source code



github.com/diku-dk/credanno

- Implementation
- Sample selection
- Pre-processing
- Experiments
- Plots

#### Considerably **Red**ucing **Anno**tation Need in Self-Explanatory Models for Lung Nodule Diagnosis (cRedAnno <a>)</a>



