Disentangling Disease-related Representation from Obscure for Disease Prediction

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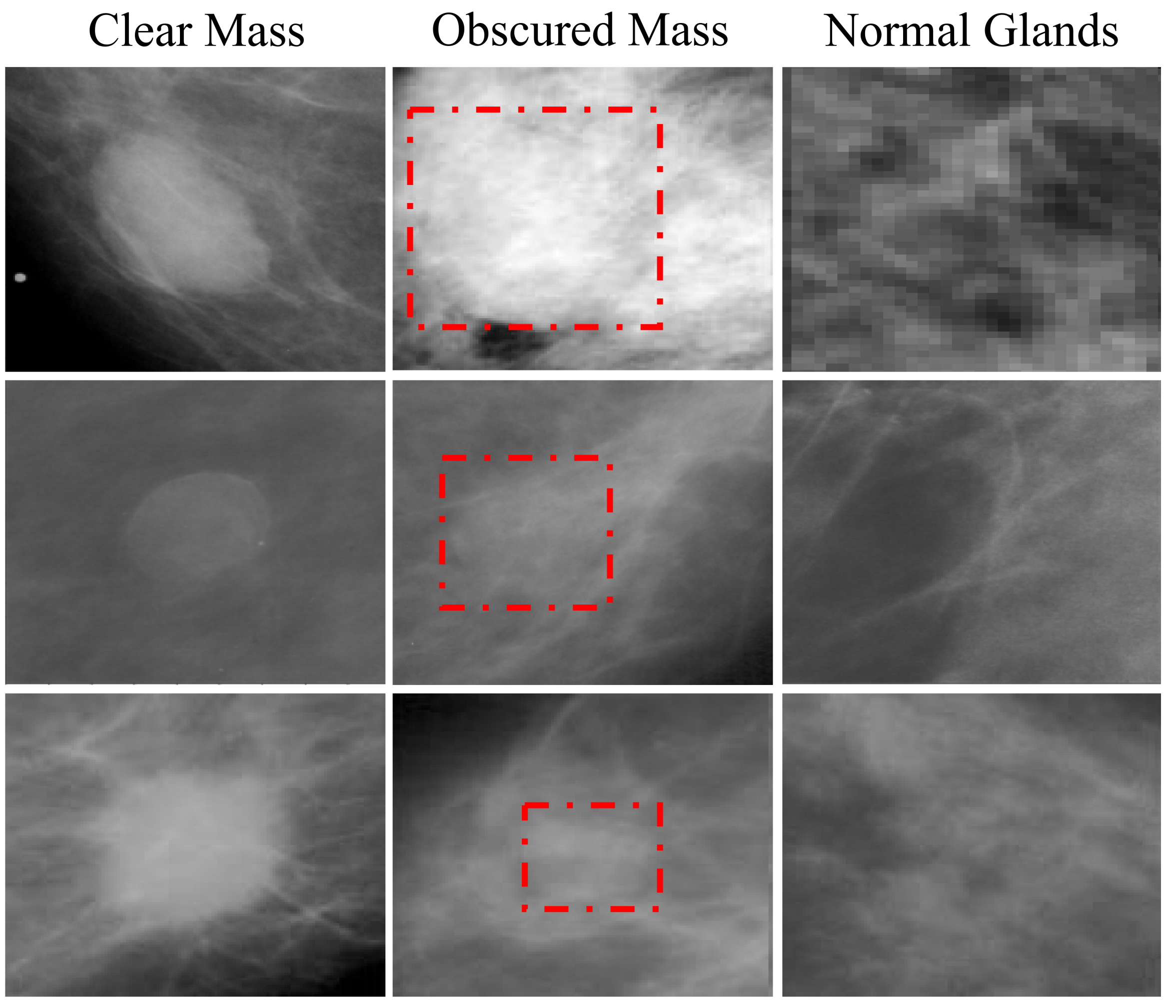
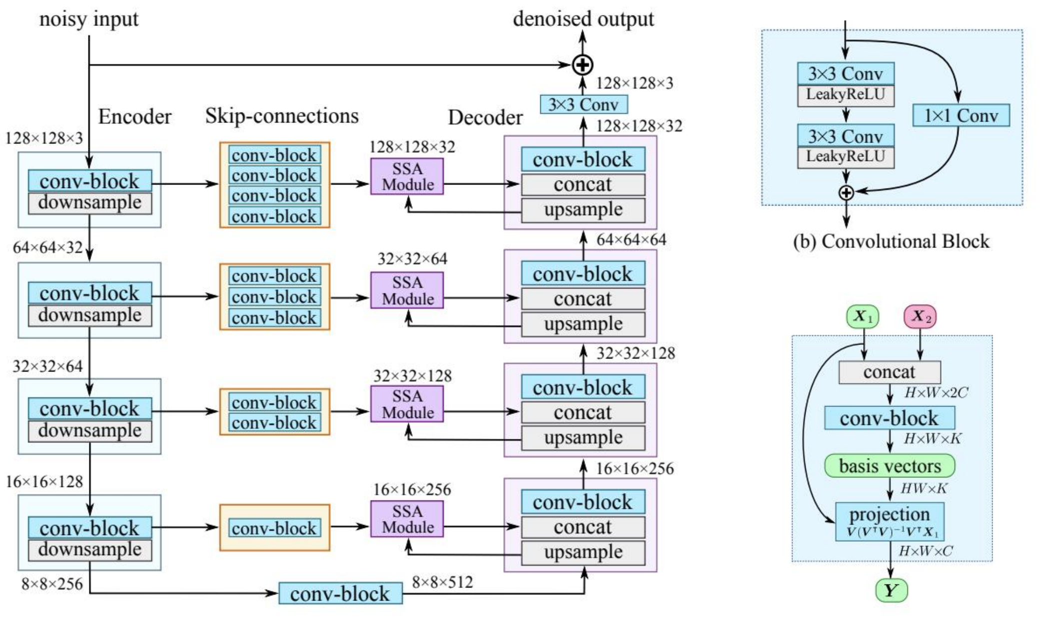
Motivation

- **Goal：** Eliminate the effect of redundant content (inter-ference of other tissues) and mine the essential content (disease-related features) hidden in the image.
- **Clinical scenario:** A considerable proportion of lesions are obscured by other normal tissues such as glandular and fibrous tissues, especially in the imaging modality of X-ray with the principle of projection overlay imaging
- **Challenge：** **It is still a challenge to identify lesion characteristics in obscured images, as many lesions are obscured by other tissues.**

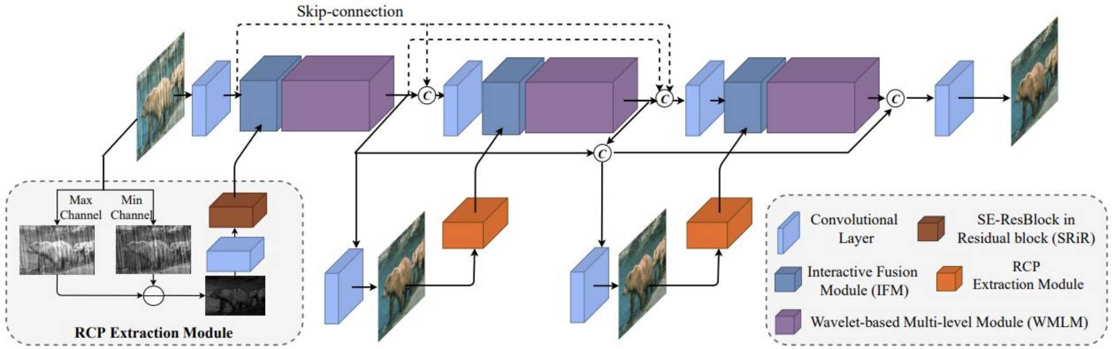


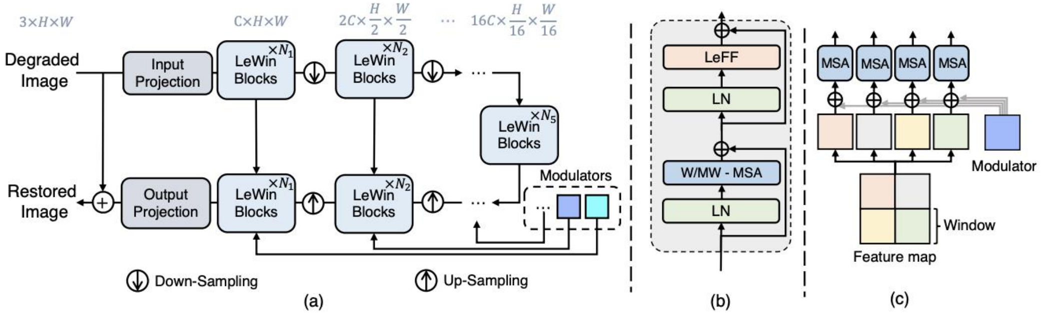
Related Work



(a) Overall Network Architecture

(c) Subspace Attention (SSA) Module

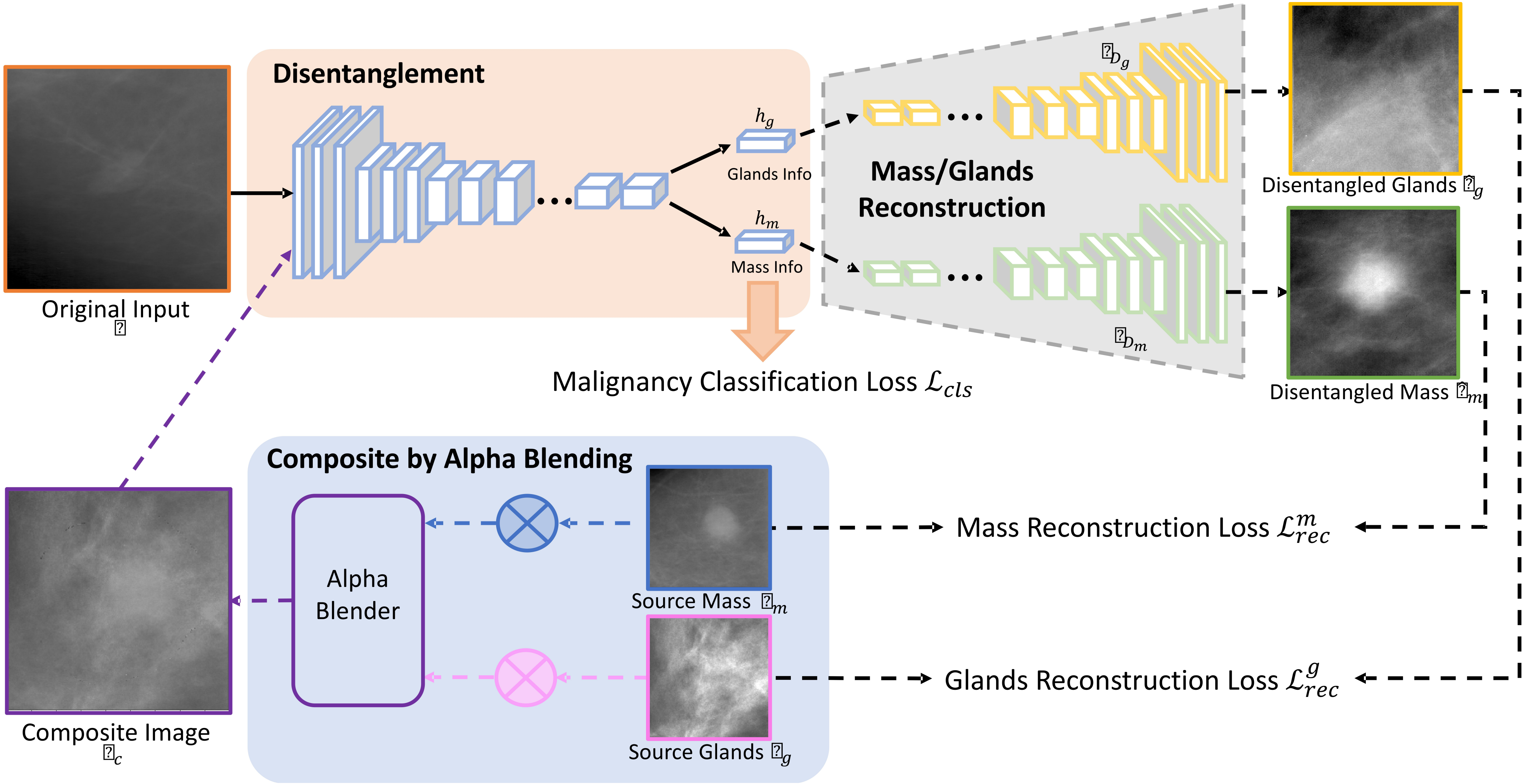




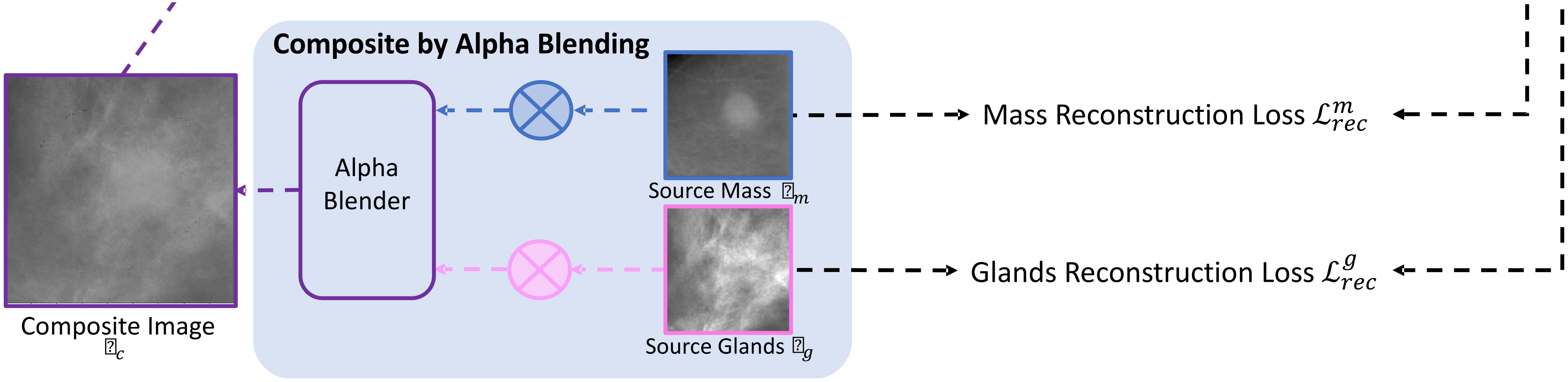
With the advances of computer vision, a number of methods in natural images processing, particularly for image restore[1,2,3], are designed to remove the redundant noise (such as haze, rain, and *etc.*) and enhance the main content in the image.

[1] Cheng S, Wang Y, Huang H, et al. Nbnet: Noise basis learning for image denoising with subspace projection[C]//Proceedings of the IEEE/CVF Conference on Computer Vision and Pattern Recognition. 2021: 4896-4906.
[2] Wang Z, Cun X, Bao J, et al. Uformer: A general u-shaped transformer for image restoration[J]. CVPR, 2021.
[3] Yi Q, Li J, Dai Q, et al. Structure-Preserving Deraining with Residue Channel Prior Guidance[C]//Proceedings of the IEEE/CVF International Conference on Computer Vision. 2021: 4238-4247.

Overview of Proposed Pipeline



Compositing by Alpha Blending

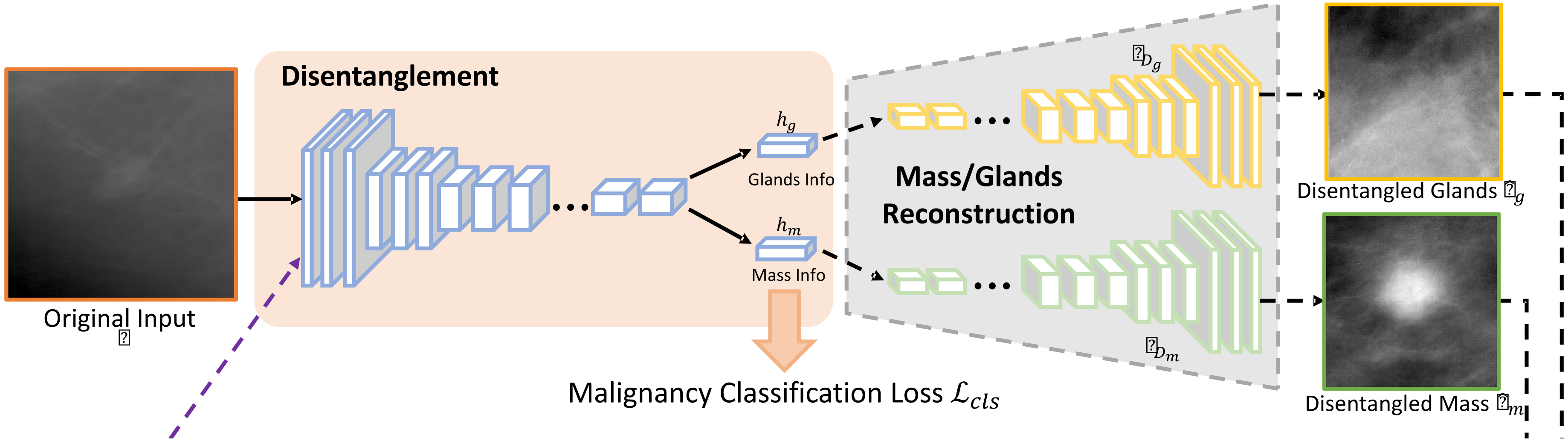


For learning disease related features of obscured masses, we try to composite obscured data and get disentangle training supervision meanwhile. We employ a parsimonious mechanism, alpha blending, for obscured mass generation.

$$x_c^{ij} = x_g^{ij}(1 - A^{ij}) + x_m^{ij} A^{ij}$$

where x^{ij} is a vector of pixel values in position (*i*, *j*)
and A^{ij} is a scalar alpha value of the same position.

Learning Disentanglement with Composite



Two-Branch Decoder

$$\mathcal{L}_{rec}^{m}(\theta_E, \theta_{D_m}) := \| x_m - \hat{x_m}(\theta_E, \theta_{D_m}) \|_1$$

$$\mathcal{L}_{rec}^{g}(\theta_E, \theta_{D_g}) := \| x_g - \hat{x_g}(\theta_E, \theta_{D_g}) \|_1$$

Disease Classifier

$$\mathcal{L}_{cls}(\theta_E, \theta_C) := -\log(1 - f_C(\theta_{f_C}))$$

$$\boxed{\mathcal{L} = \mathcal{L}_{rec}^{m}(\theta_E, \theta_{D_m}) + \mathcal{L}_{rec}^{g}(\theta_E, \theta_{D_g}) + \mathcal{L}_{cls}(\theta_E, \theta_C)}$$

Experimental Setup

- **DDSM Dataset & Inhouse1 & Inhouse2 & Inhouse3**

We randomly divide the whole set into training, validation and testing as 8:1:1 in patient-wise.

		DDSM	Inhouse1	Inhouse2	Inhouse3
train	the number of patients	571	292	410	271
	the number of ROIs	1165	684	840	565
valid	the number of patients	68	38	50	33
	the number of ROIs	143	87	104	70
test	the number of patients	75	33	52	34
	the number of ROIs	147	83	105	70
total	the number of PID	714	363	512	338
	the number of patients	1455	854	1049	705

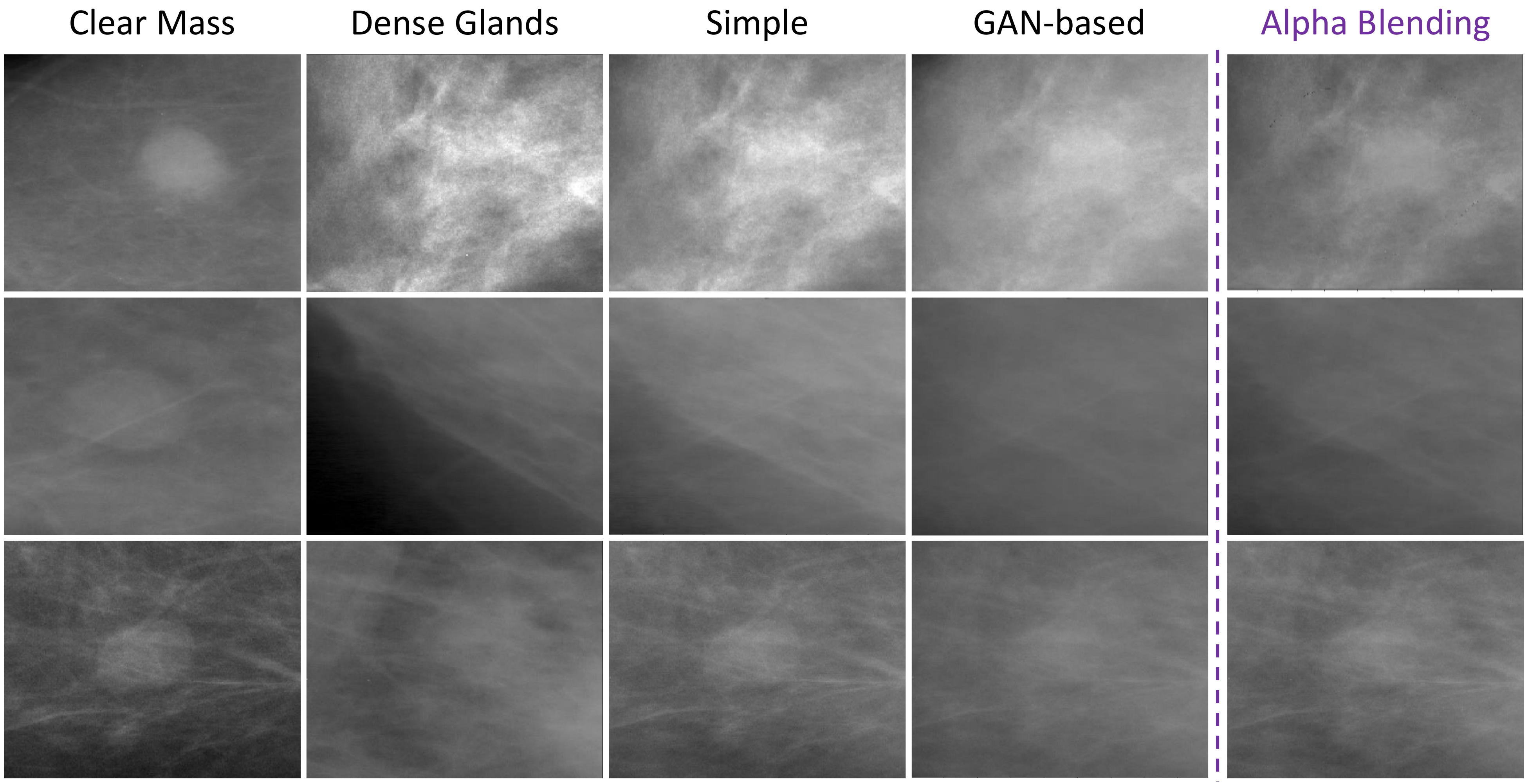
AUC Evaluation

Methodology	AUC				AUC only on *obscured cases*			
	Inh1	Inh2	Inh3	DDSM	Inh1	Inh2	Inh3	DDSM
ERM (He et al., 2016)	0.888	0.847	0.776	0.847	0.739	0.707	0.630	0.728
Chen *et al.* (Chen et al., 2019)	0.924	0.878	0.827	0.871	0.790	0.748	0.669	0.777
Guided-VAE (Ding et al., 2020)	0.921	0.867	0.809	0.869	0.782	0.751	0.673	0.782
DAE-GCN (Wang et al., 2021a)	0.963	0.901	0.857	0.919	0.871	0.837	0.783	0.880
Li *et al.* (Li et al., 2019)	0.908	0.859	0.828	0.875	0.767	0.726	0.648	0.771
ICADx (Kim et al., 2018)	0.911	0.871	0.816	0.879	0.801	0.793	0.665	0.782
NBNet (Cheng et al., 2021)	0.912	0.875	0.824	0.877	0.839	0.821	0.749	0.826
Uformer (Wang et al., 2021b)	0.923	0.879	0.832	0.872	0.845	0.813	0.757	0.834
Eformer (Luthra et al., 2021)	0.928	0.883	0.838	0.875	0.849	0.815	0.760	0.839
SPDNet (Yi et al., 2021)	0.908	0.862	0.814	0.866	0.823	0.791	0.739	0.816
AECRNet (Wu et al., 2021)	0.911	0.870	0.826	0.870	0.846	0.818	0.752	0.825
DAB-Net **(Ours)**	**0.956**	**0.907**	**0.849**	**0.913**	**0.910**	**0.878**	**0.826**	**0.924**
DAB-Net(**Ours**) + (Chen et al., 2019)	**0.964**	**0.913**	**0.861**	**0.920**	**0.916**	**0.883**	**0.835**	**0.934**
DAB-Net(**Ours**) + (Ding et al., 2020)	**0.959**	**0.903**	**0.855**	**0.918**	**0.913**	**0.882**	**0.829**	**0.932**
DAB-Net(**Ours**) + (Wang et al., 2021a)	**0.976**	**0.930**	**0.878**	**0.943**	**0.921**	**0.891**	**0.847**	**0.945**

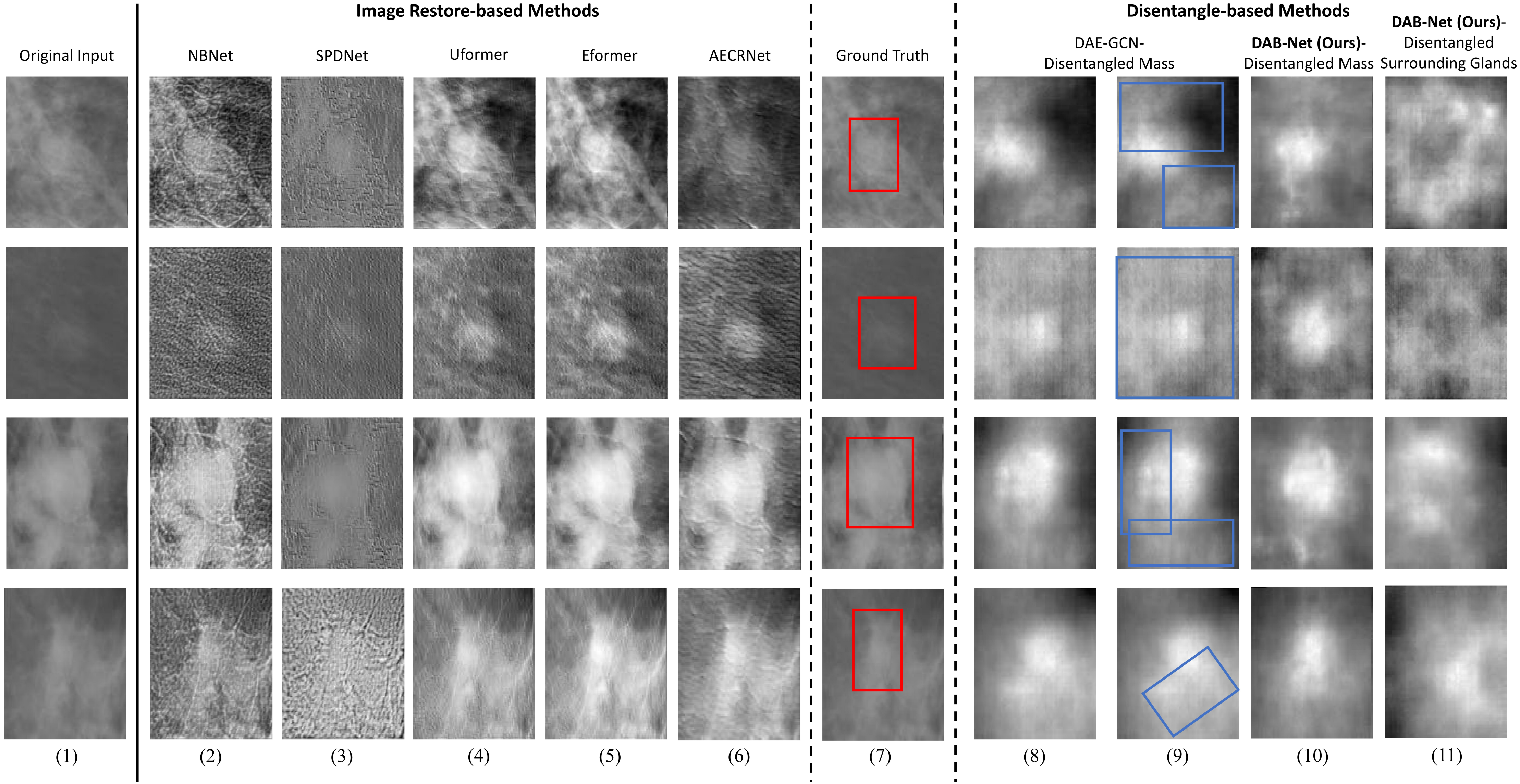
Ablation Study

Alpha Blending	Disentangle	DAE-GCN	Inh1	Inh2	Inh3	DDSM
×	×	×	0.888	0.847	0.776	0.847
AD	×	×	0.886	0.843	0.771	0.836
Simple	✓	×	0.936	0.882	0.839	0.893
GAN-based	✓	×	0.950	0.906	0.847	0.902
✓	*No Mass Decoder*	×	0.921	0.878	0.818	0.869
✓	*No Glands Decoder*	×	0.925	0.884	0.824	0.873
✓	*One branch*	×	0.939	0.887	0.831	0.889
✓	✓	×	**0.956**	**0.907**	**0.849**	**0.913**
✓	✓	✓	**0.976**	**0.930**	**0.878**	**0.943**

Visualization of Blending



Visualization of Disease-related Features



Thanks for your attention!