

*Added Prognostic Value of 3D Deep
Learning-Derived Features from
Preoperative MRI for Adult-type Diffuse
Gliomas*



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- 학력사항

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- 경력사항

現 서울대학교병원 영상의학과 AICON 연구원

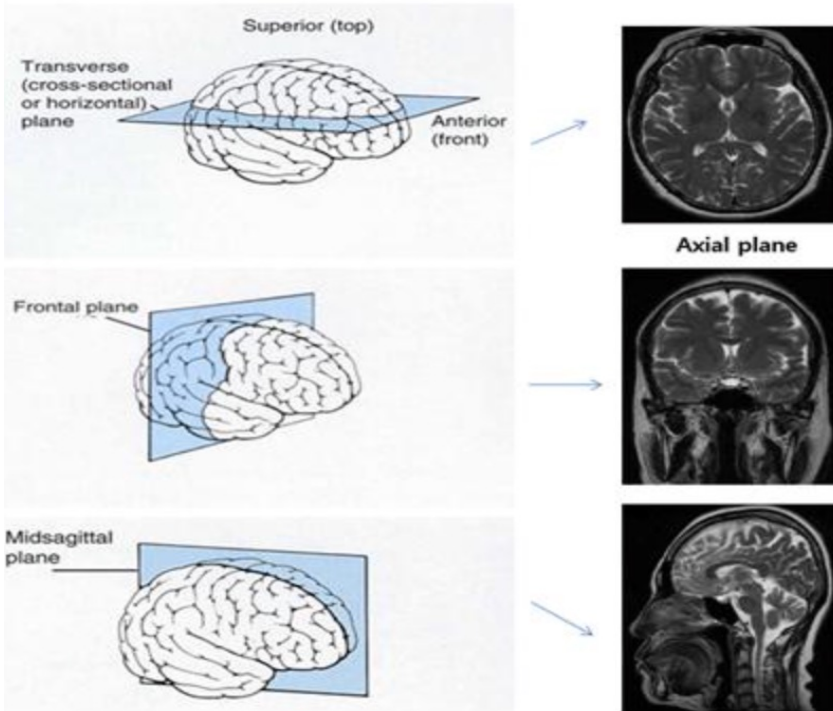
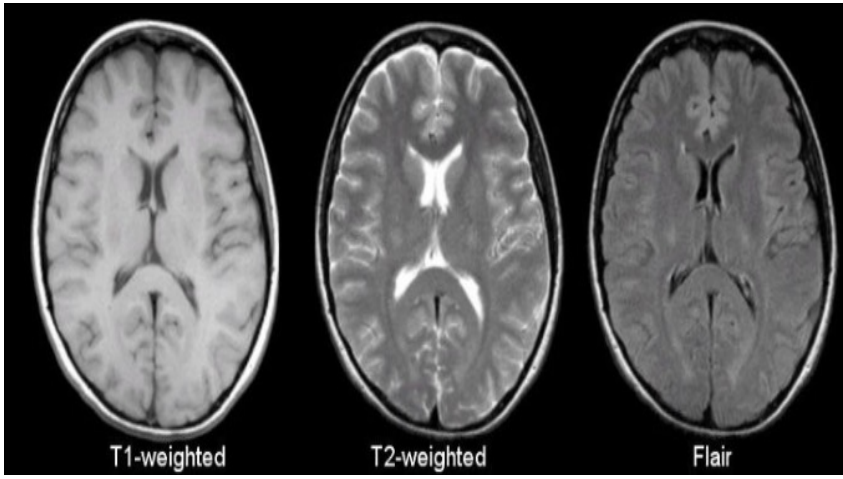
前 엔씨소프트 금융 AI R&D 시장이해팀

前 엔씨소프트 금융 AI R&D 투자전략팀

前 한국수자원기술원 인턴

주요 성과

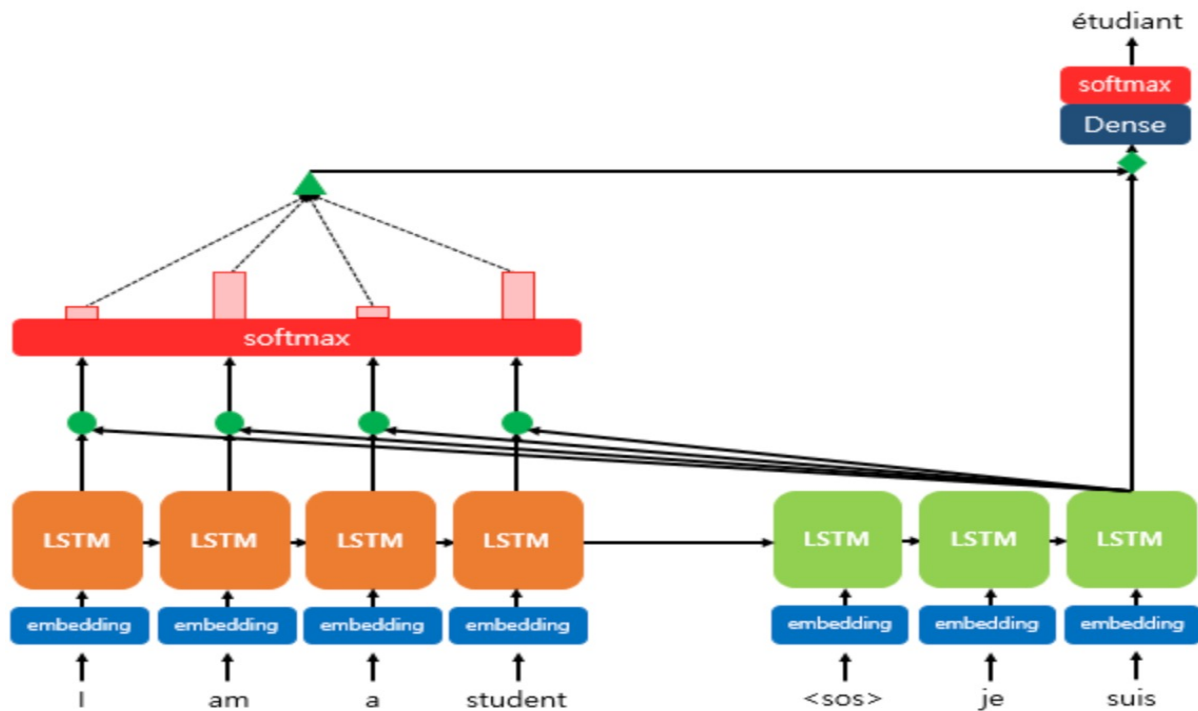
1. 교모세포종 환자 생존 분석 SCIE 논문 공동저자 (American Society of Neuroradiology)
2. 빅데이터 기반 KOSPI 200, KOSDAQ 150 증권시장 ETL 파이프라인 설계
3. 전기차 배터리 불량 유형 분류 및 예측 2D 이미지 딥러닝 모델 설계 및 최적화 논문 공동저자



Background

- **MRI (Magnetic Resonance Imaging)**
 - 강력한 자기장과 라디오 파동을 활용하여 수소 원자(Proton)에서 방출되는 신호를 수집하여 이미지로 변환
- **T1-weighted (T1-강조영상)**
 - 뇌의 해부학적 구조에 대해서 파악하기 용이함
 - (Fat : White, Water : Dark)
- **T2-weighted (T2-강조영상)**
 - 급성기 병변을 파악하기 용이함
 - (Fat : Dark, Water : White)
- **Flair**
 - CSF 신호를 억제시킨 영상, T2-강조영상보다 병변을 파악하기 더욱 용이함
 - (Fat : Dark, Water : Dark)

Attention Mechanism



RNN 기반 Seq2seq 모델 한계를 보완하고자 제시되었던 방법론

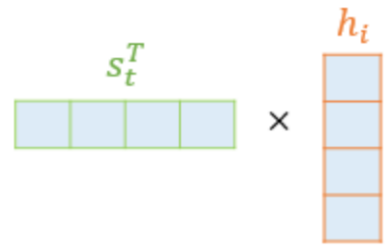
핵심 : 매 시점마다 현재 시점에서 예측해야 할 값과 연관이 있는 입력 부분을 좀 더 집중해서 봄 (입력 값에 대하여 전부 동일한 비율로 참고하는 것이 아님, 차별성을 두겠다는 것이 메인 포인트)

1. RNN의 고질적인 문제 기울기 소실 문제

-> RNN에서는 주로 활성화 함수로 Hypervolic tanh를 사용하기에 레이어가 많아질수록 오차 역전파 과정에서 문제가 생긴다.

2. Seq2Seq에서는 입력된 정보를 고정된 길이의 컨텍스트 벡터에 압축하다보니 정보손실이 발생하며, 시퀀스가 길어질수록 더욱 심해진다.

Attention Score

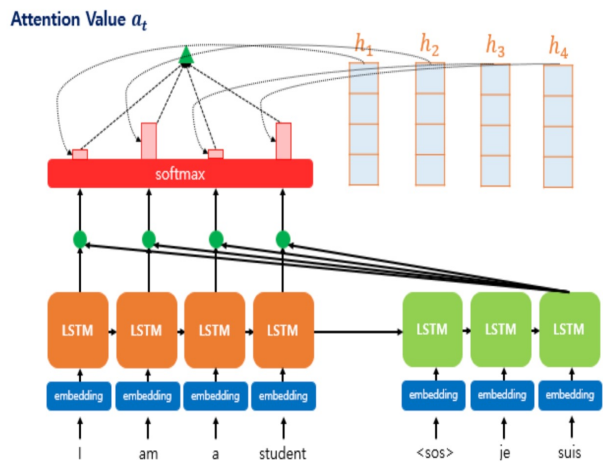


$$score(s_t, h_i) = s_t^T h_i$$

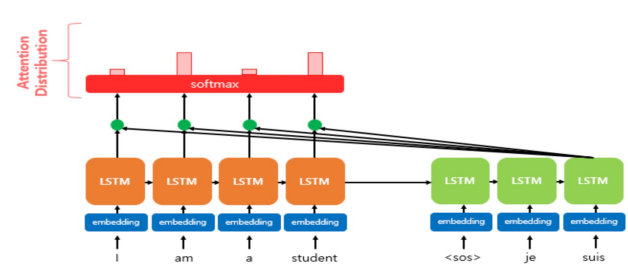
$$e^t = [s_t^T h_1, \dots, s_t^T h_N]$$

Attention Value

$$a_t = \sum_{i=1}^N \alpha_i^t h_i$$



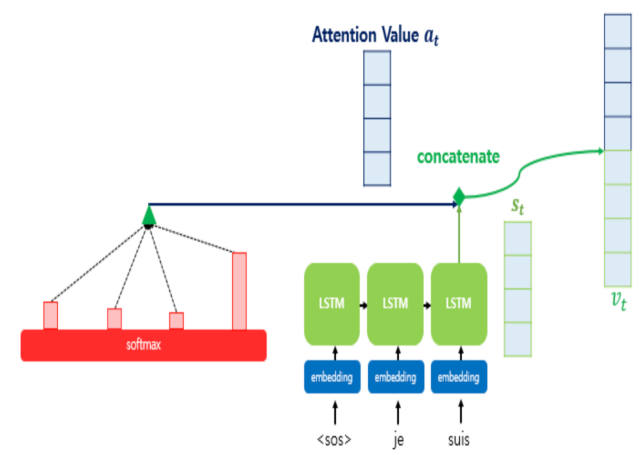
Attention Distribution



$$\alpha^t = softmax(e^t)$$

모든 값을 합하면 1이 되는 확률 분포 (각각의 값은 Attention Weights)

어텐션 값과 디코더의 t 시점의 은닉 상태를 연결한다.(Concatenate)



Preparation

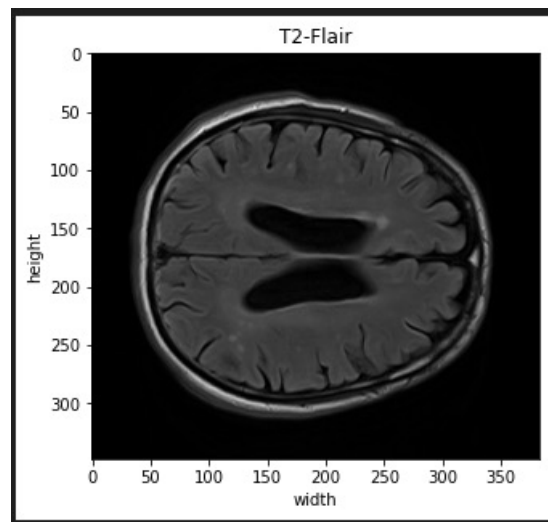
SNUH with Glioma Patients (N=1139)

Model : SE-RESNEXT50 (Internal:SNUH, External:TCGA)

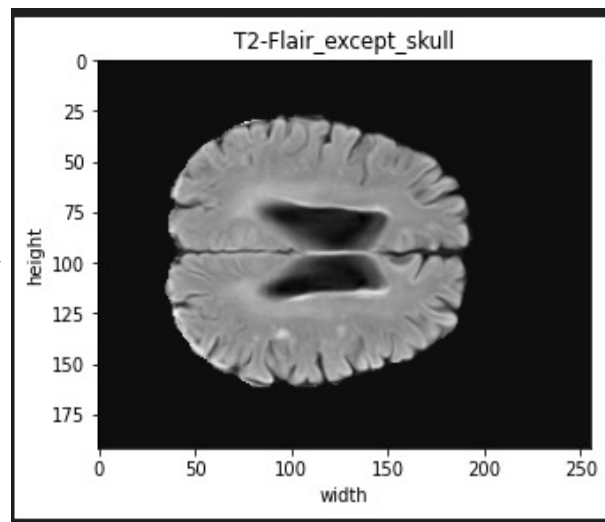
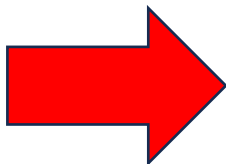
1. Duration:OS, Pathology:all (train=1025, valid=114, test=160)
2. Duration:OS, Pathology:GBL (train=586, valid=66, test=61)
3. Duration:1yr, Pathology:all (train=1025, valid=114, test=160)
4. Duration:1yr, Pathology:GBL (train=586, valid=66, test=61)

Model : ResNet50-CBAM (Internal:SNUH, External:TCGA)

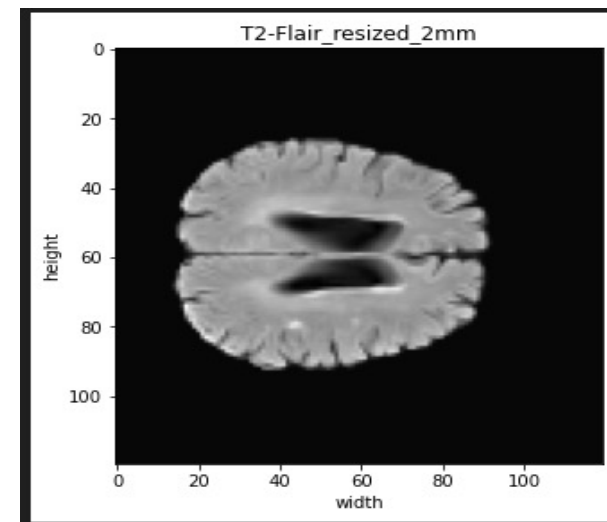
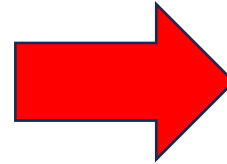
1. Duration:OS, Pathology:all (train=1025, valid=114, test=160)
2. Duration:OS, Pathology:GBL (train=586, valid=66, test=61)
3. Duration:1yr, Pathology:all (train=1025, valid=114, test=160)
4. Duration:1yr, Pathology:GBL (train=586, valid=66, test=61)



(348, 384, 26)



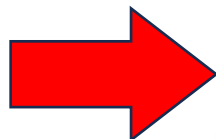
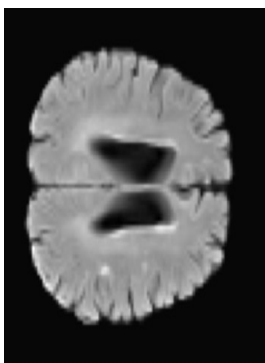
(192, 256, 256)



(120, 120, 78)

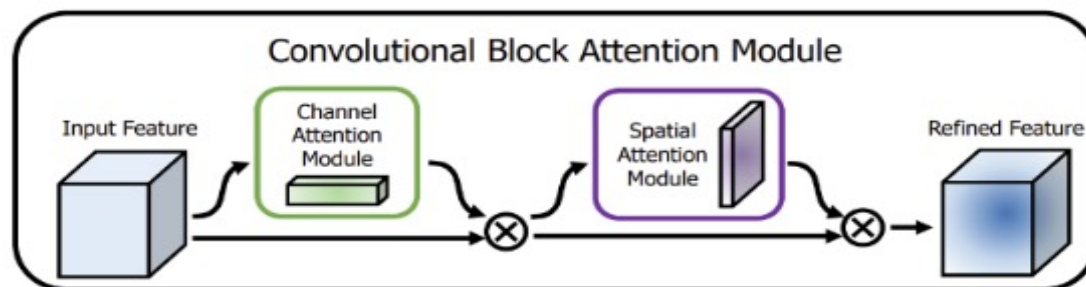
Architecture

Resnet50-CBAM



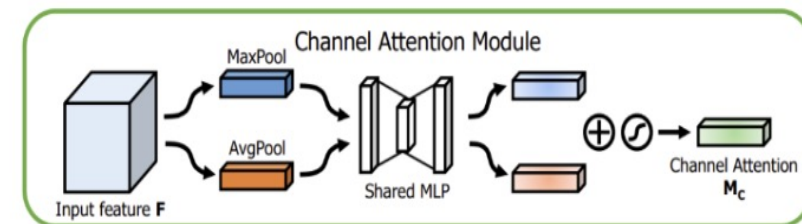
ILSVRC 2015

layer name	output size	18-layer	34-layer	50-layer	101-layer	152-layer
conv1	112×112	7×7, 64, stride 2				
conv2_x	56×56	3×3 max pool, stride 2				
		$\begin{bmatrix} 3 \times 3, 64 \\ 3 \times 3, 64 \end{bmatrix} \times 2$	$\begin{bmatrix} 3 \times 3, 64 \\ 3 \times 3, 64 \end{bmatrix} \times 3$	$\begin{bmatrix} 1 \times 1, 64 \\ 3 \times 3, 64 \\ 1 \times 1, 256 \end{bmatrix} \times 3$	$\begin{bmatrix} 1 \times 1, 64 \\ 3 \times 3, 64 \\ 1 \times 1, 256 \end{bmatrix} \times 3$	$\begin{bmatrix} 1 \times 1, 64 \\ 3 \times 3, 64 \\ 1 \times 1, 256 \end{bmatrix} \times 3$
conv3_x	28×28	$\begin{bmatrix} 3 \times 3, 128 \\ 3 \times 3, 128 \end{bmatrix} \times 2$	$\begin{bmatrix} 3 \times 3, 128 \\ 3 \times 3, 128 \end{bmatrix} \times 4$	$\begin{bmatrix} 1 \times 1, 128 \\ 3 \times 3, 128 \\ 1 \times 1, 512 \end{bmatrix} \times 4$	$\begin{bmatrix} 1 \times 1, 128 \\ 3 \times 3, 128 \\ 1 \times 1, 512 \end{bmatrix} \times 4$	$\begin{bmatrix} 1 \times 1, 128 \\ 3 \times 3, 128 \\ 1 \times 1, 512 \end{bmatrix} \times 8$
conv4_x	14×14	$\begin{bmatrix} 3 \times 3, 256 \\ 3 \times 3, 256 \end{bmatrix} \times 2$	$\begin{bmatrix} 3 \times 3, 256 \\ 3 \times 3, 256 \end{bmatrix} \times 6$	$\begin{bmatrix} 1 \times 1, 256 \\ 3 \times 3, 256 \\ 1 \times 1, 1024 \end{bmatrix} \times 6$	$\begin{bmatrix} 1 \times 1, 256 \\ 3 \times 3, 256 \\ 1 \times 1, 1024 \end{bmatrix} \times 23$	$\begin{bmatrix} 1 \times 1, 256 \\ 3 \times 3, 256 \\ 1 \times 1, 1024 \end{bmatrix} \times 36$
conv5_x	7×7	$\begin{bmatrix} 3 \times 3, 512 \\ 3 \times 3, 512 \end{bmatrix} \times 2$	$\begin{bmatrix} 3 \times 3, 512 \\ 3 \times 3, 512 \end{bmatrix} \times 3$	$\begin{bmatrix} 1 \times 1, 512 \\ 3 \times 3, 512 \\ 1 \times 1, 2048 \end{bmatrix} \times 3$	$\begin{bmatrix} 1 \times 1, 512 \\ 3 \times 3, 512 \\ 1 \times 1, 2048 \end{bmatrix} \times 3$	$\begin{bmatrix} 1 \times 1, 512 \\ 3 \times 3, 512 \\ 1 \times 1, 2048 \end{bmatrix} \times 3$
	1×1	average pool, 1000-d fc, softmax				
FLOPs		1.8×10^9	3.6×10^9	3.8×10^9	7.6×10^9	11.3×10^9



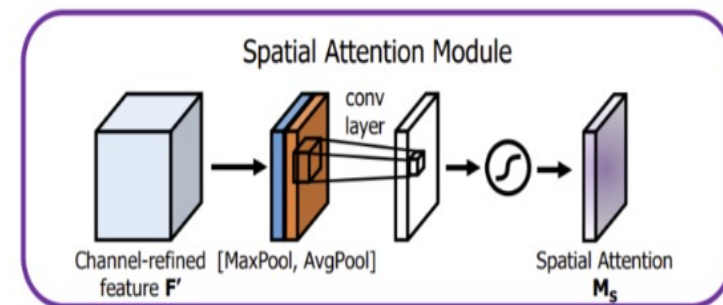
- 두가지 어텐션 모듈 추가 (Channel Attention, Spatial Attention)
 -> Intermediate Feature (중간특징)을 효과적으로 강조 및 억제

Channel Attention Module



$$\begin{aligned} \mathbf{M}_c(\mathbf{F}) &= \sigma(\text{MLP}(\text{AvgPool}(\mathbf{F})) + \text{MLP}(\text{MaxPool}(\mathbf{F}))) \\ &= \sigma(\mathbf{W}_1(\mathbf{W}_0(\mathbf{F}_{\text{avg}})) + \mathbf{W}_1(\mathbf{W}_0(\mathbf{F}_{\text{max}}))), \end{aligned} \quad (2)$$

where σ denotes the sigmoid function, $\mathbf{W}_0 \in \mathbb{R}^{C/r \times C}$, and $\mathbf{W}_1 \in \mathbb{R}^{C \times C/r}$. Note that the MLP weights, \mathbf{W}_0 and \mathbf{W}_1 , are shared for both inputs and the ReLU activation function is followed by \mathbf{W}_0 .



$$\begin{aligned} \mathbf{M}_s(\mathbf{F}) &= \sigma(f^{7 \times 7}([\text{AvgPool}(\mathbf{F}); \text{MaxPool}(\mathbf{F})])) \\ &= \sigma(f^{7 \times 7}([\mathbf{F}_{\text{avg}}^s; \mathbf{F}_{\text{max}}^s])), \end{aligned} \quad (3)$$

where σ denotes the sigmoid function and $f^{7 \times 7}$ represents a convolution operation with the filter size of 7×7 .

SE-RESNEXT50

ILSVRC 2017

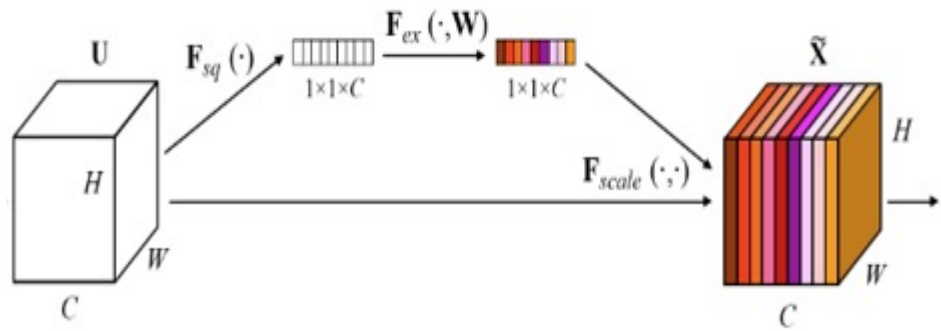
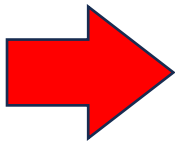
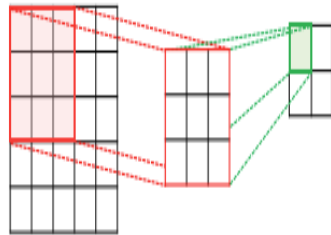
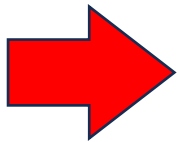
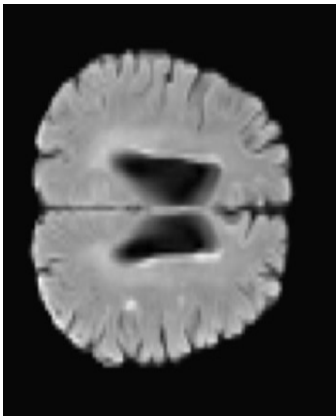
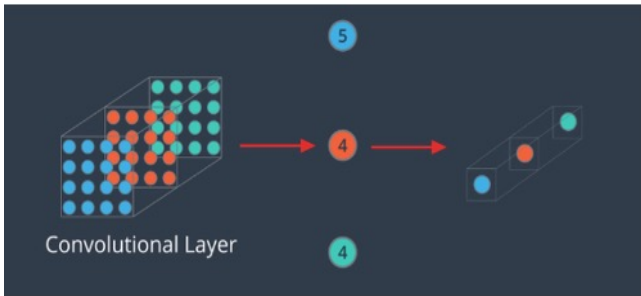


Figure 1: A Squeeze-and-Excitation block.

Squeeze

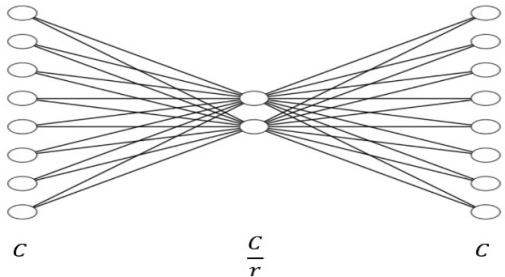
$$z_c = F_{sq}(u_c) = \frac{1}{H \times W} \sum_{i=1}^H \sum_{j=1}^W u_c(i, j)$$



각 채널들의 중요 정보 추출

Excitation

$$s = F_{ex}(z, W) = \sigma(W_2 \delta(W_1 z))$$



논문에서 저자들은
채널 간 관계성을 파악하기 위한 방법으로
의도적으로 채널을 r만큼 수축시킨 후
Relu를 활용하여 채널간의 관계를 살폈음

- 어느 네트워크에도 바로 부착가능
 - 연산량 증가 대비 모델 성능 향상도가 매우 큼
- 계산 복잡도 결과 (0.26% 증가) (SE-NET 논문 인용)
Resnet 50 : ~3.86 GFLOPs
SE-Resnet 50 : ~3.87 GFLOPs

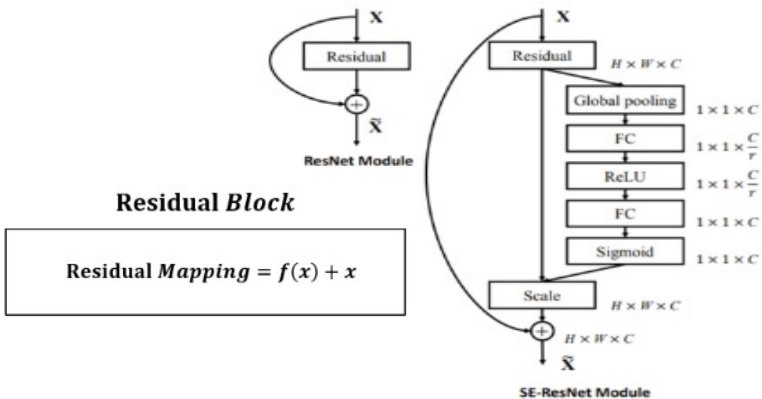


Figure 3: The schema of the original Residual module (left) and the SE-ResNet module (right).

DenseNet-121

Layers	Output Size	DenseNet-121	DenseNet-169	DenseNet-201	DenseNet-264
Convolution	112×112	7×7 conv, stride 2			
Pooling	56×56	3×3 max pool, stride 2			
Dense Block (1)	56×56	$\begin{bmatrix} 1 \times 1 \text{ conv} \\ 3 \times 3 \text{ conv} \end{bmatrix} \times 6$	$\begin{bmatrix} 1 \times 1 \text{ conv} \\ 3 \times 3 \text{ conv} \end{bmatrix} \times 6$	$\begin{bmatrix} 1 \times 1 \text{ conv} \\ 3 \times 3 \text{ conv} \end{bmatrix} \times 6$	$\begin{bmatrix} 1 \times 1 \text{ conv} \\ 3 \times 3 \text{ conv} \end{bmatrix} \times 6$
Transition Layer (1)	56×56	1×1 conv			
	28×28	2×2 average pool, stride 2			
Dense Block (2)	28×28	$\begin{bmatrix} 1 \times 1 \text{ conv} \\ 3 \times 3 \text{ conv} \end{bmatrix} \times 12$	$\begin{bmatrix} 1 \times 1 \text{ conv} \\ 3 \times 3 \text{ conv} \end{bmatrix} \times 12$	$\begin{bmatrix} 1 \times 1 \text{ conv} \\ 3 \times 3 \text{ conv} \end{bmatrix} \times 12$	$\begin{bmatrix} 1 \times 1 \text{ conv} \\ 3 \times 3 \text{ conv} \end{bmatrix} \times 12$
Transition Layer (2)	28×28	1×1 conv			
	14×14	2×2 average pool, stride 2			
Dense Block (3)	14×14	$\begin{bmatrix} 1 \times 1 \text{ conv} \\ 3 \times 3 \text{ conv} \end{bmatrix} \times 24$	$\begin{bmatrix} 1 \times 1 \text{ conv} \\ 3 \times 3 \text{ conv} \end{bmatrix} \times 32$	$\begin{bmatrix} 1 \times 1 \text{ conv} \\ 3 \times 3 \text{ conv} \end{bmatrix} \times 48$	$\begin{bmatrix} 1 \times 1 \text{ conv} \\ 3 \times 3 \text{ conv} \end{bmatrix} \times 64$
Transition Layer (3)	14×14	1×1 conv			
	7×7	2×2 average pool, stride 2			
Dense Block (4)	7×7	$\begin{bmatrix} 1 \times 1 \text{ conv} \\ 3 \times 3 \text{ conv} \end{bmatrix} \times 16$	$\begin{bmatrix} 1 \times 1 \text{ conv} \\ 3 \times 3 \text{ conv} \end{bmatrix} \times 32$	$\begin{bmatrix} 1 \times 1 \text{ conv} \\ 3 \times 3 \text{ conv} \end{bmatrix} \times 32$	$\begin{bmatrix} 1 \times 1 \text{ conv} \\ 3 \times 3 \text{ conv} \end{bmatrix} \times 48$
Classification Layer	1×1	7×7 global average pool			
		1000D fully-connected, softmax			

Table 1: DenseNet architectures for ImageNet. The growth rate for all the networks is $k = 32$. Note that each “conv” layer shown in the table corresponds the sequence BN-ReLU-Conv.

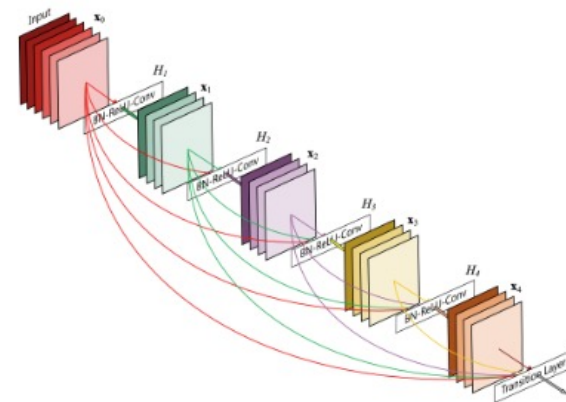


Figure 1: A 5-layer dense block with a growth rate of $k = 4$. Each layer takes all preceding feature-maps as input.

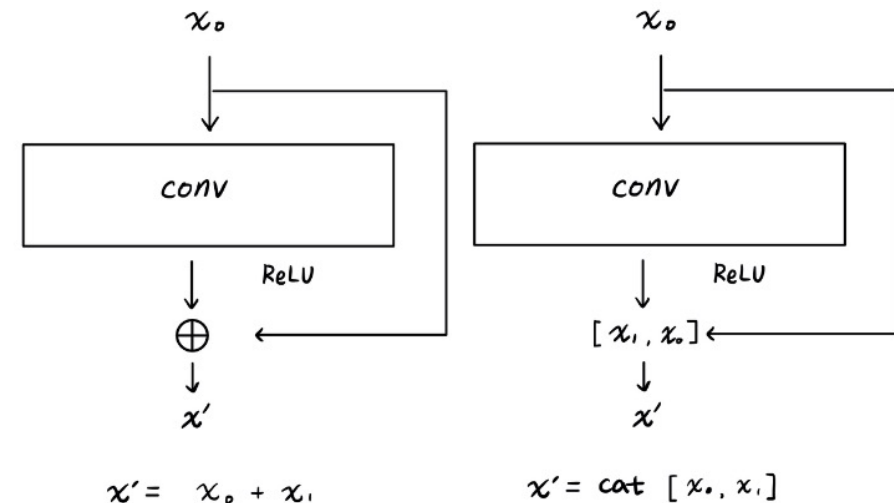
ResNet, DenseNet 차이점

Resnet

-> Summation (Feature) \rightarrow Axis=Channel

DenseNet

-> Concatenation (Feature) \rightarrow Axis = Channel



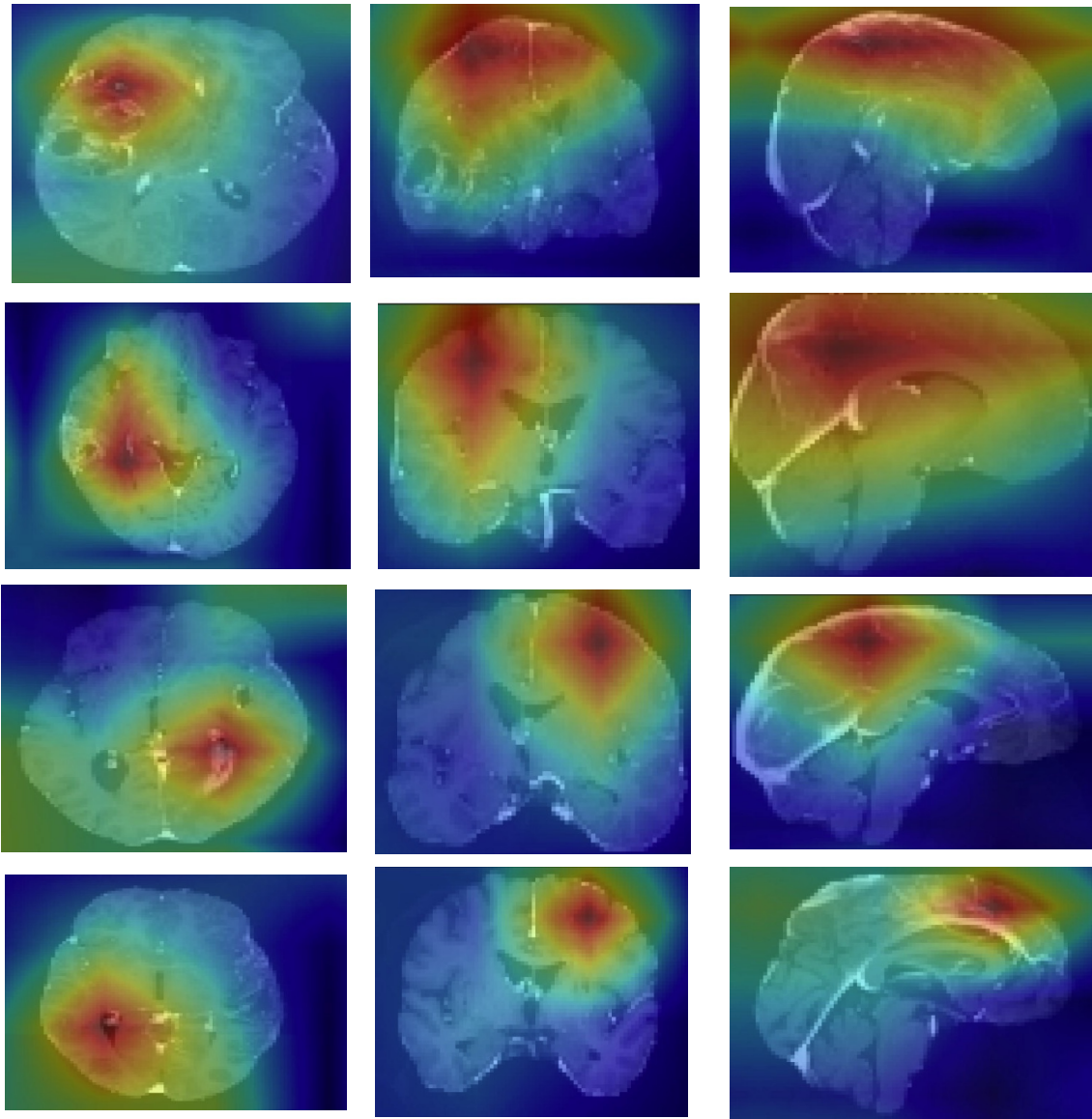
Performance

95% Confidence Interval for C-index
epochs=200, learning rate = 0.0001, weight_decay=1e-06, n_fold=10, batch_size = 64

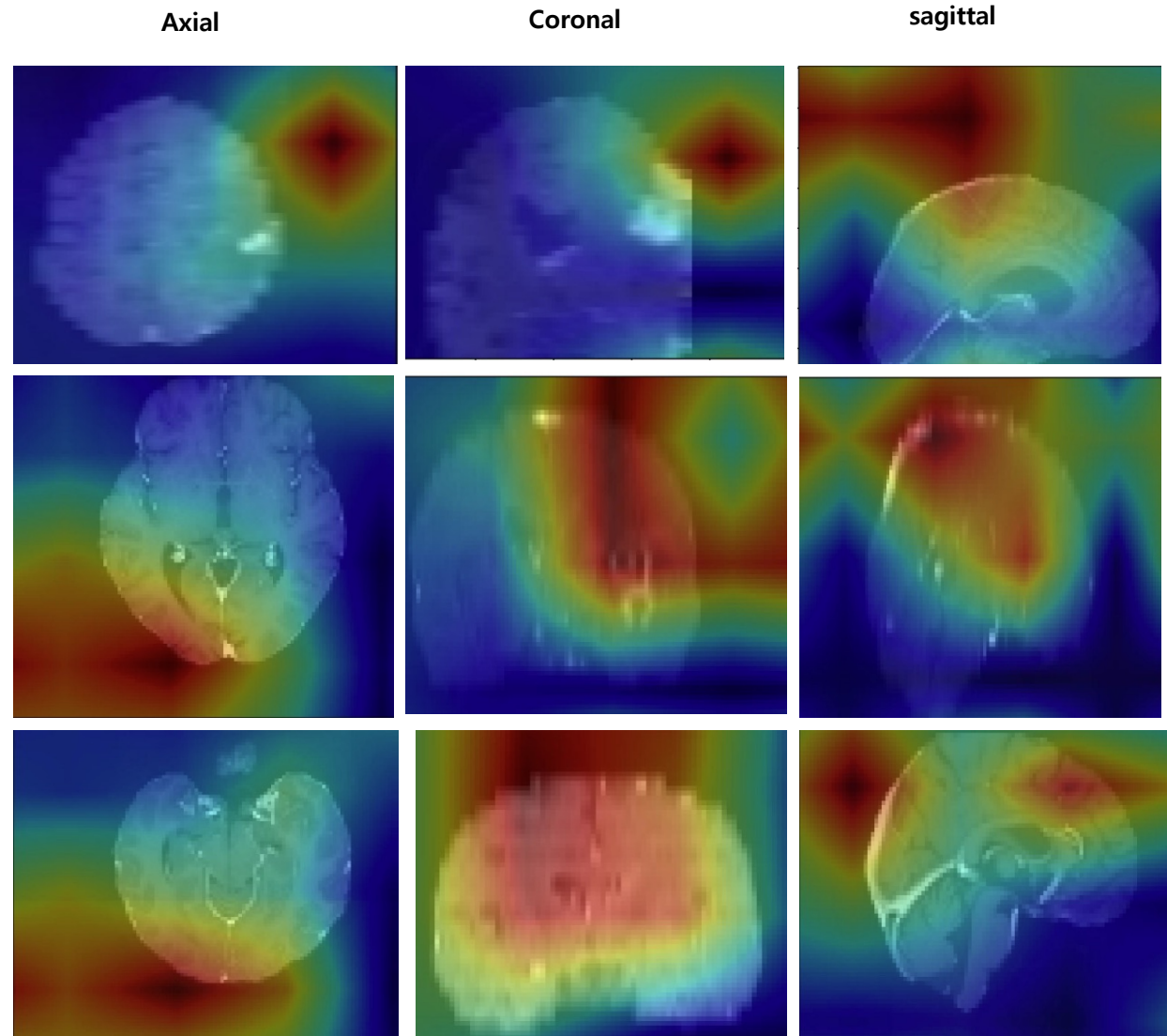
	SE-ResNext50				ResNet50-CBAM			
	OS,all	OS,GBL	1yr,all	1yr,GBL	OS,all	OS,GBL	1yr,all	1yr,GBL
C-index	0.733 [0.7124, 0.7540]	0.551 [0.5174, 0.5807]	0.606 [0.5665, 0.6459]	0.55 [0.5073, 0.5918]	0.763 [0.7430, 0.7818]	0.625 [0.5952, 0.6528]	0.7961 [0.7676, 0.8255]	0.65 [0.6066, 0.6909]
Brier Score	0.148	0.201	0.164	0.199	0.147	0.204	0.14	0.213

Results

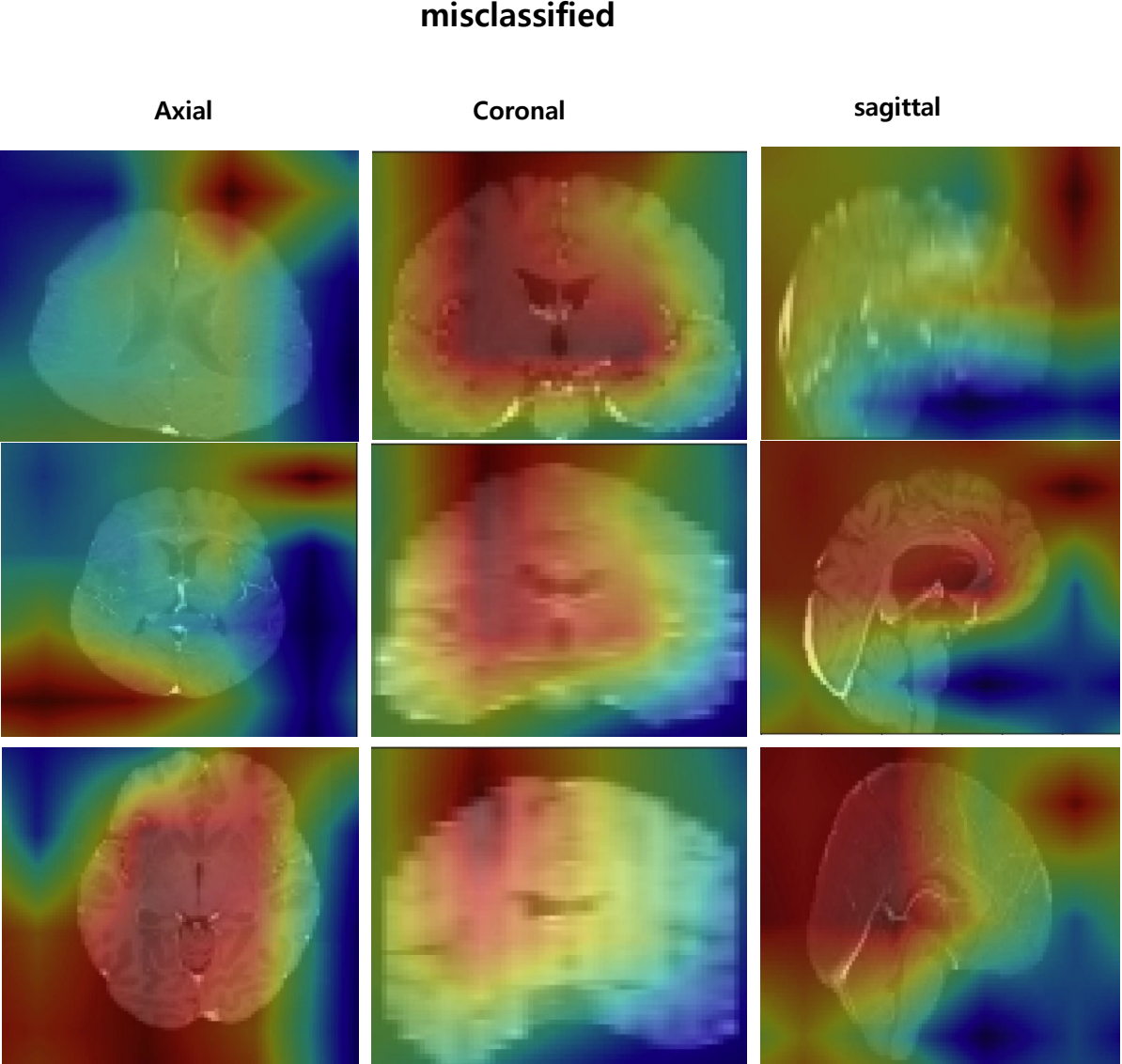
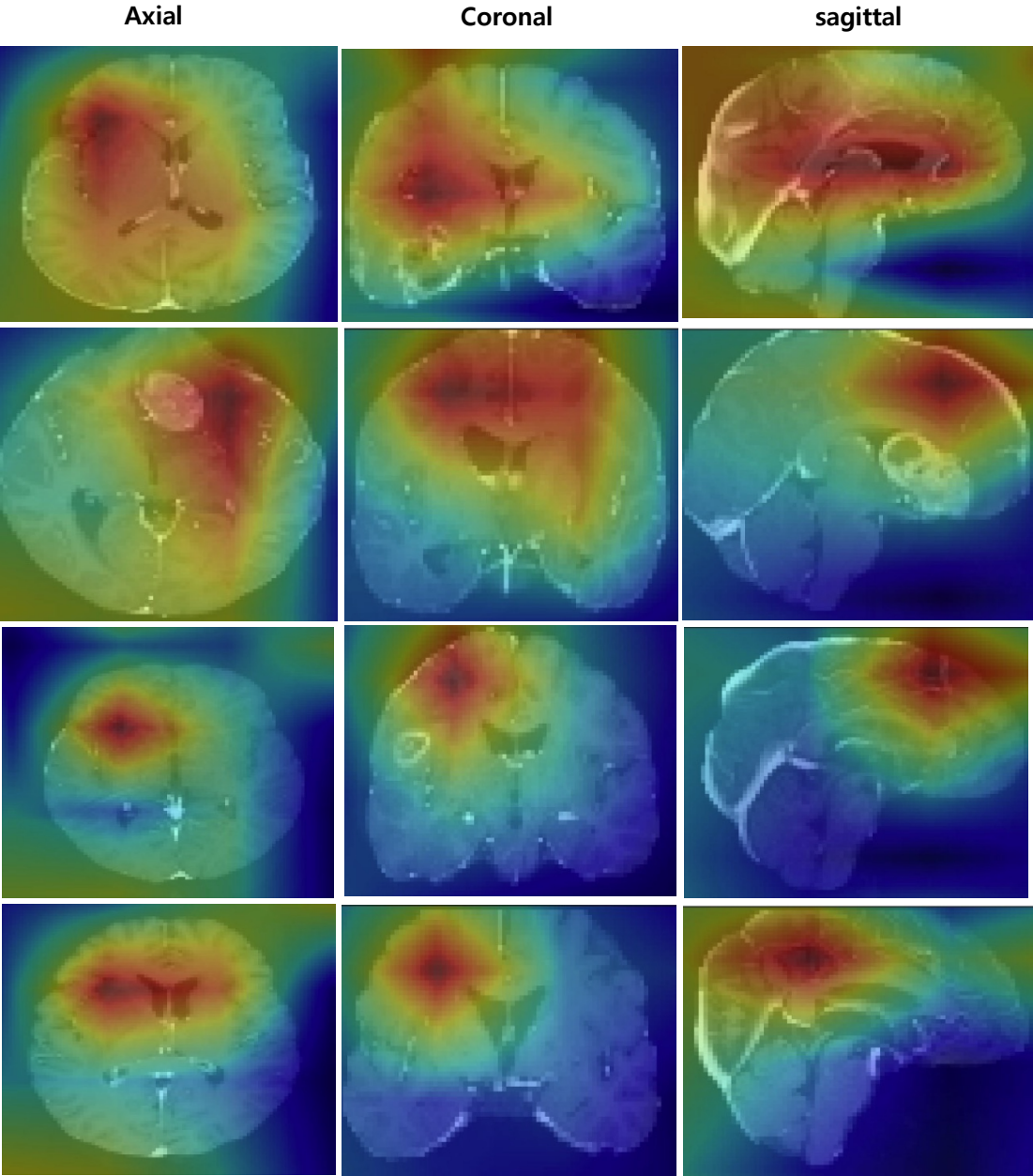
grad-CAM (ResNet-CBAM (OS,ALL), C-index = 0.704 [0.6302, 0.7716], Brier Score = 0.106



misclassified



grad-CAM (ResNet-CBAM (1yr,ALL), C-index = 0.72 [0.625, 0.8122], Brier Score = 0.148



Discussion

1. 환자 별 grad-CAM 2d-plot을 확인한 결과,

상대적으로 Axial (가로면)보다 **Coronal, Sagittal (관상면, 시상면)**에서 Tumor를 잘 인식하여 클래스를 잘 분류하는 것을 알 수 있었음.

2. 사용자 관점에서 초기에 사용할 때,

새로운 Dataset (SNUH 1100 Patients with gliomas)을 활용한 "CustomNet"의 Inference 성능이 좋지 못하였으나

각 전처리 파이프라인을 거친 이미지 Shape, Model Input으로 사용되는 labling 값과 같은 **중간값들을 지속적으로 확인 후 수정**하였고

모델 성능이 눈에 띄게 개선되었음. (1-year Survival and Overall Survival All pathology)

3. GBL (WHO Grade 4), High grade glioma (WHO Grade 3), Low grade glioma (WHO Grade 1,2) **정보가 모두 주어졌을 때** 성능이 Dramatic하게 높지만

Filtering을 거친 후, **GBL 데이터만 제공된 모델의 성능**은 상대적으로 좋지 않은 것을 확인할 수 있었음.

4. **향후 모델 성능 향상 방안으로**

IDH 유전자 변이 여부에 따른 **추가적인 뇌교종 타입 정보**를 제공할 예정임. (Diffuse glioma, Oligodendro glioma, Astrocytoma, OligoAstrocytoma, GBL)

5. 최적화 된 하이퍼파라미터를 찾기 위하여,

SE-RESNEXT를 활용한 Medical 분야 및 Glioma Classification Task에서 성능을 발휘한 해외 논문 및 레퍼런스에서 사용한 하이퍼파라미터 값들을 참고하여

우리 모델에 적용하여 각 하이퍼파라미터 별 모델 결과값을 비교할 예정임.