Scalable PathMNIST image classification with a Neural Cellular Automata

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Deep Generative Models

Intro

Neural cellular automata (NCA) are iterative, self-organizing systems inspired by biological growth and wound-healing processes. Unlike traditional convolutional neural networks, NCAs update each pixel ("cell") over time via a learned local update rule, enabling emergent computation and spatial flexibility. In this project, we apply NCA to the PathMNIST histopathology classification task: input patches evolve over a fixed number of time steps under learned dynamics, and a global average pooling of the final state is used for nine-way classification.

Neural Cellular Automata

A Neural Cellular Automaton (NCA) is a model where each pixel (or "cell") updates its state over time based on local rules learned by a neural network. Instead of passing an image through layers, the entire image evolves step-by-step, with each cell only interacting with its neighbors. Each cell has an internal state representation of 16 values where the first 3 are the RGB values. NCAs are inspired by natural processes like tissue growth and wound healing, making them ideal for modeling spatial patterns in image data.

PathMNIST

PathMNIST is a medical image classification dataset of H&E-stained colorectal tissue patches labeled into 9 classes (e.g., tumor, normal, background).

- Original size: 28×28 RGB
- Upsampled sizes: 64×64, 128×128, 224×224
- Commonly used to test model performance across resolutions.

Training and Evaluation

The NCA Model and CNN Model are trained on the 28x28 PathMNIST dataset. After that they are evaluated on the 28x28, 64x64, 128x128 and 224x224 PathMNIST dataset to check weathere the models are scaling.

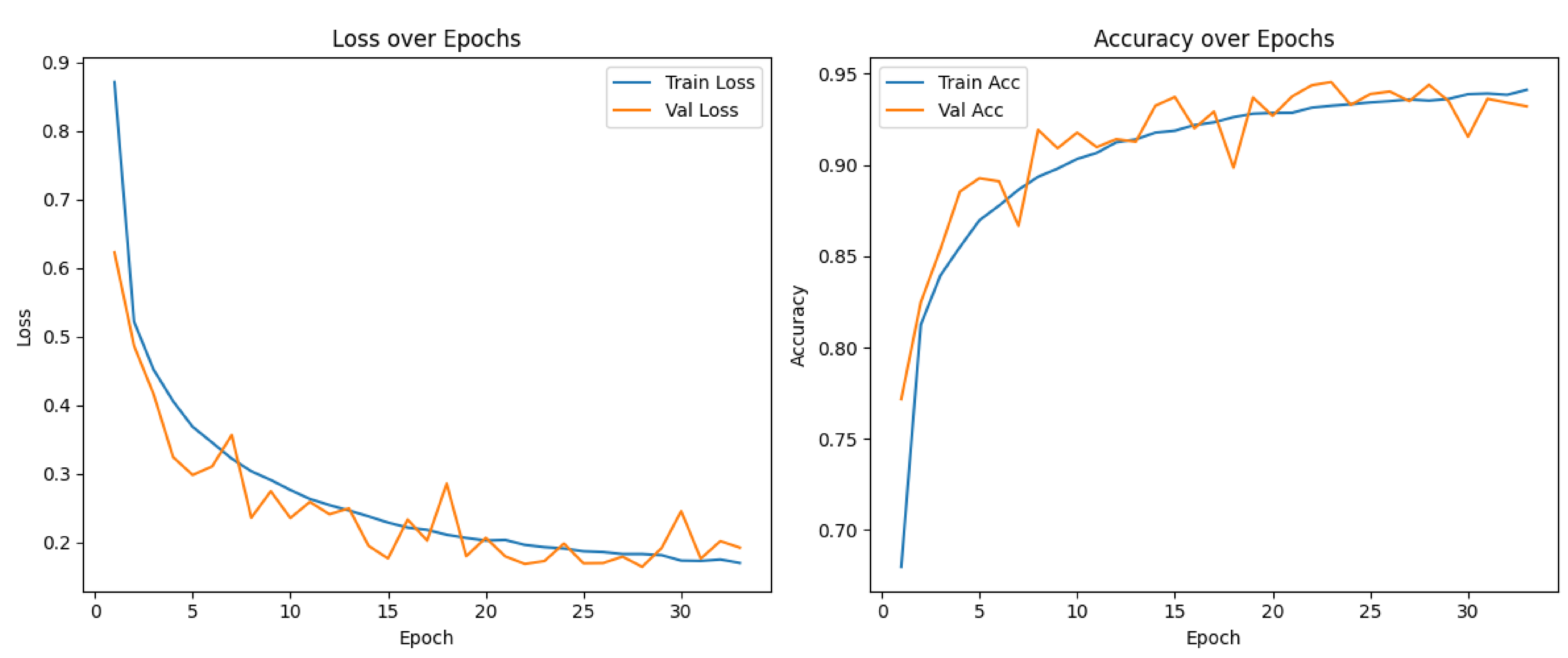

Fig. 1: NCA training and validation error and accuracy.

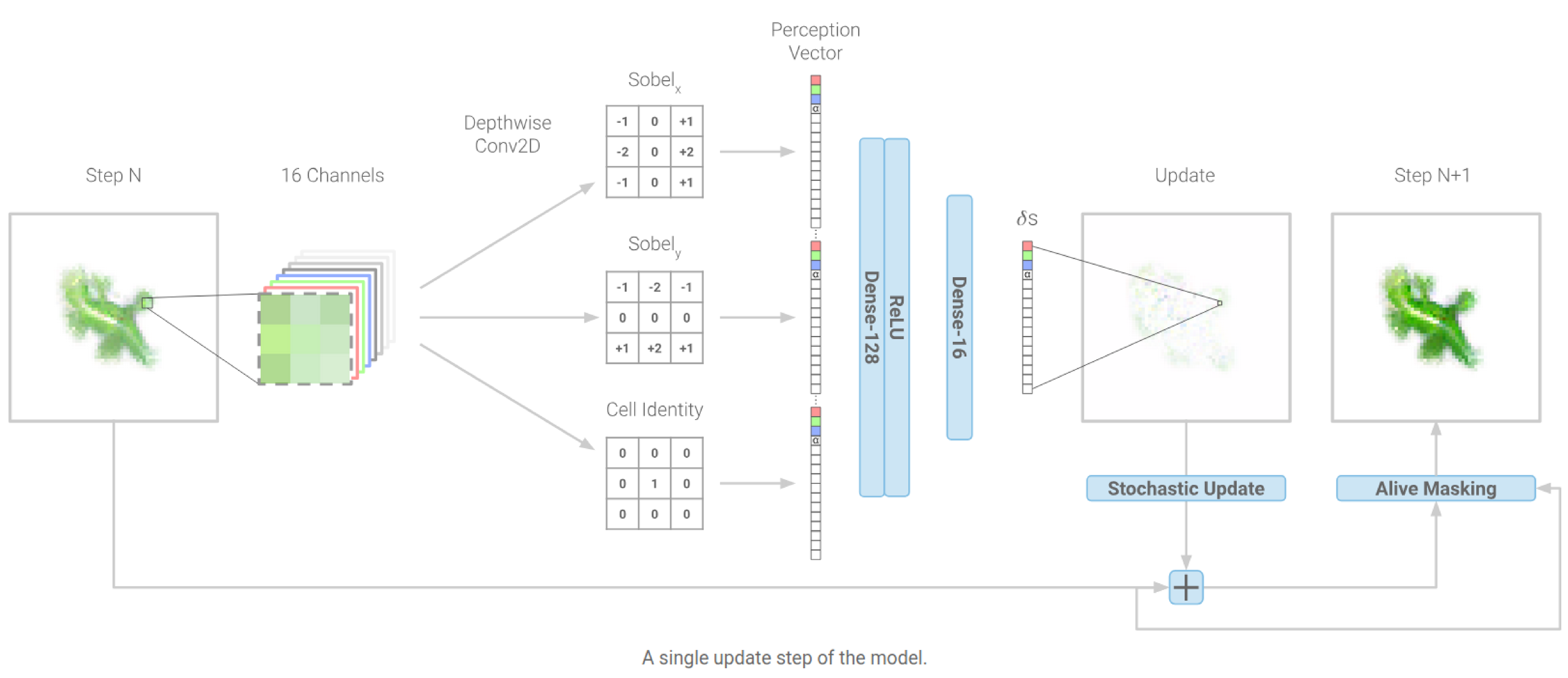

Fig. 2: A single update step of the model.

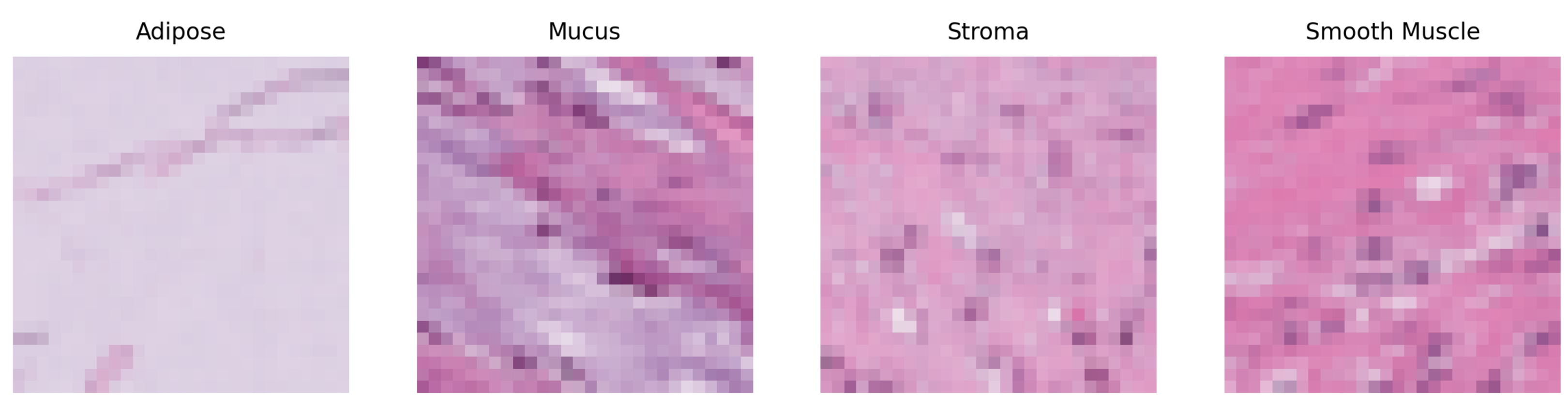

Fig. 3: PathMNIST images.

Results

Resolution	Model	Acc (↑)	BAC (↑)	MAE (↓)	Brier (↓)	NLL (↓)	MPE (↓)	ECE (↓)
28x28	CNN	0.8216	0.7853	0.5536	0.2595	0.7132	0.3278	0.0574
28x28	NCA	**0.8529**	**0.8126**	**0.4721**	**0.2273**	**0.5395**	**0.2724**	**0.0471**
64x64	CNN	0.6343	0.5874	1.0153	0.5183	1.3972	0.5596	0.1516
64x64	NCA	**0.7333**	**0.6788**	**0.8554**	**0.3859**	**0.9882**	**0.5331**	**0.0690**
128x128	CNN	0.3932	0.4095	1.6242	0.8864	2.8619	**0.5808**	0.3862
128x128	NCA	**0.4404**	**0.4520**	**1.3752**	**0.8136**	**2.6875**	0.7855	**0.2532**
224x224	CNN	**0.3294**	**0.3416**	**1.7976**	**1.0390**	**4.4632**	**0.5250**	**0.4737**
224x224	NCA	0.2492	0.3073	2.3504	1.1674	5.2557	0.7428	0.4782

Future Work

To improve the performance further the focus should lay on optimizing NCA hyperparameters such as state dimensionality, neighborhood radius, number of evolution steps and exploring multi-scale fusion architectures that jointly process low and high-resolution inputs.
We also aim to endow the model with an adaptive stopping criterion, allowing each patch to learn when to halt evolution for greater efficiency, and to validate performance across additional histopathology datasets.

Conclusion

NCA provide a compelling alternative to standard CNNs for histopathology patch classification. On average, NCA outperforms the CNN baseline by +3.5% points in balanced accuracy at 28×28 and 64×64, and reduces ECE by nearly 0.1 across low and medium resolutions.

NCA step: [**https://distill.pub/2020/growing-ca/**]