

1 Highlights

2 **STAMNet - A Spatiotemporal Attention Module and Network for** 3 **Upscaling Reactive Transport Simulations of the Hyporheic Zone**

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- 5 • STAMNet allows for rapid upscaling of reactive transport simulations
6 of bioremediation in the hyporheic zone.
- 7 • The spatiotemporal attention module (STAM) uses cross-dimensional
8 relationships to extract complex features and is shown to improve per-
9 formance more than efficient channel attention methods.
- 10 • STAMNet shows strong performance for upscaling of biomass, electron
11 donor, and chromium concentrations.
- 12 • STAMNet-Upsample uses the STAM architecture to rapidly increase
13 simulation resolution with high accuracy.

STAMNet - A Spatiotemporal Attention Module and Network for Upscaling Reactive Transport Simulations of the Hyporheic Zone

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Abstract

Reactive transport (RT) simulations are important tools for understanding and predicting phenomena in the subsurface. However, RT is computationally intensive and complex simulations can be numerically unstable. Here, we present STAMNet, a low-parameter attention-based suite of neural nets that can upscale and upsample reactive transport simulations, applied to example problem of bioremediation in the hyporheic zone. We show that a simple MLP offers 30x speedup over standard multiphysics RT simulations and can accurately ($\approx 90\%$ R^2) predict the output of multiple variables of a 1x20 meter RT simulation by using the output from a 1x2 meter simulation as input. We add efficient channel attention to our optimized MLP which significantly improves the mean average error but doesn't affect the R^2 . We further develop a novel spatiotemporal attention module (STAM), which results in improvements both in mean square error and R^2 (92.5%). Finally, we present a network architecture that utilizes STAM to accurately (99.9% R^2) upsample simulations in two dimensions. Specifically, our model allows for the 2x upsampling of simulations in the x and y dimensions to convert a coarse-grained input into a fine-grained output. These models have potential use for Monte-Carlo-style investigations of bioremediation and the work presented serves as a proof-of-concept for accurate prediction of large sets of spatiotemporal outputs.

Keywords: Reactive Transport, Deep Learning, Attention, Upscaling, Hyporheic Zone

1. Introduction

In the vast realm of environmental science, the hyporheic zone (HZ) stands out as a complex interface that has captured the attention of researchers for decades [1, 2, 3]. This subsurface region, generally defined as the interface between river water and groundwater, hosts a myriad of complex interactions [4], with biofilms serving as a central character influencing broader hydrological and geochemical cycles [5].

Multiphysics simulators that use analytical and numerical methods to solve systems of equations that describe hydro-biogeochemical interactions in the subsurface environments, also known as reactive transport (RT) simulators, such as PFLOTRAN [6], STOMP [7], and CrunchFlow [8], are generally considered the gold standard for simulations of phenomena in the HZ. However, large scale RT simulations, and Monte-Carlo-type investigations of RT simulations, have high computational complexity and cost which are sensitive to convergence criteria [9, 10] causing numerical instability and challenges in supporting hydro-biogeochemical research efforts.

Several recent studies in the field of computer science have shown that accurate multi-physics simulation emulation is possible with deep learning [11, 12, 13, 14, 15]. Thus, to alleviate the common shortcomings of RT simulators, some studies have attempted to apply these emulation frameworks to RT data [16, 17, 18, 19, 20, 21]. Laloy and Jacques presented some of the earliest studies that looked into RT emulation with deep learning. They found deep neural networks (DNNs) outperform polynomial chaos expansion networks for the prediction of a target RT variable given some input variables of the RT timeseries. Although emulation is still a popular topic, much of the current research in this domain also seeks to upscale micro and pore-scale models to the macro/continuum scale. Wang and Battiato (2024) provide a comprehensive framework to upscale RT in fracture-matrix systems. Their framework uses a combination of traditional RT algorithms with a recurrent neural network (RNN) to capture the impact of small-scale features, which they show results in improved accuracy compared to a pure macroscale model. You et al. (2024) used convolutional neural networks (CNNs) to upscale pore-scale simulations to continuum-scale simulations. They found that the effective surface area and effective diffusion coefficient could be predicted with high accuracy, but permeability is difficult to predict. These frameworks represent significant advances in the field of RT modeling, although they suffer from a lack of easy integration with current popular methods,

60 and are constrained in their scope. General models that can be easily im-
61 plemented would increase access of reactive transport simulation tools to a
62 larger community of researchers.

63 In this paper, we present STAMNet, a deep-learning-based method for
64 the upscaling and upsampling of RT simulations of biomass growth in the
65 HZ. We chose to model biomass growth in the hyporheic zone due to the
66 complexity of the simulations and its importance for many biogeochemical
67 functions they serve. Furthermore, simulations of biomass growth result in
68 outputs at large scales that could be very different than outputs at small
69 scales, which necessitates a more careful upscaling than a simple interpola-
70 tion or polynomial fit. Furthermore, we consider our simulations of biomass
71 growth in the hyporheic zone to be a proxy for general reactive transport
72 modeling, since the biomass growth simulations take advantage of most of
73 the modeling capabilities in PFLOTRAN. In addition to biomass growth, we
74 use STAMNet to upscale chromium and molasses, highlighting our frame-
75 work’s overall capabilities for the upscaling of bioremediation simulations.
76 We test the performance of an optimized MLP, the MLP + efficient chan-
77 nel attention, and the MLP + our spatiotemporal attention module, STAM,
78 which we find to generally outperform the other models. We test our upscal-
79 ing method to predict the spatiotemporal output for a 1x20 meter simulation
80 given a 1x2 meter simulation as input. This model allows for a 30x speedup
81 in the generation of large-scale simulations with an R^2 of the predicted mean
82 time series of 92.5%. We also devise an optimized linear architecture for the
83 task of upsampling, which takes a 1x2 meter simulation with a resolution of
84 100 voxels/m as input and outputs a 1x2 meter simulation with a resolution
85 of 400 voxels/m.

86 2. Methods

87 This study uses multiphysics simulations to explore biomass growth in the
88 HZ, and deep learning models to upscale and upsample these simulations. In
89 this section, we describe the boundary conditions and parameters used for
90 our simulations, and the model architectures and training/testing procedures
91 used for our upscaling and upsampling frameworks.

92 2.1. Simulations of the Hyporheic Zone

93 2.1.1. General Description of Simulations

94 Our simulations are based in PFLOTTRAN, a multi-physics reactive trans-
95 port simulator developed by multiple national laboratories [6]. PFLOTTRAN
96 represents a state-of-the-art computational framework for simulating cou-
97 pled subsurface flow and reactive transport processes across multiple spatial
98 and temporal scales. This massively parallel reactive transport code inte-
99 grates sophisticated numerical methods to resolve multi-phase and hydro-
100 biogeochemical interactions. The code’s architecture enables the simula-
101 tion of various subsurface processes, including density-dependent flow, vari-
102 able saturation conditions, and non-isothermal phenomena, alongside com-
103 prehensive biogeochemical reactions such as aqueous complexation, mineral
104 precipitation/dissolution kinetics, surface complexation, ion exchange, and
105 microbially-mediated transformations. As discussed in the introduction, we
106 seek to use this reactive transport simulator to model biomass growth in the
107 hyporheic zone. To this end, we have specifically adapted the Chrotran [22]
108 version of PFLOTTRAN to represent bioremediation in the hyporheic zone at
109 the Darcy scale. Chrotran defines biomass growth as a function of electron
110 donor (ED) concentration through simple Monod kinetics. It uses biotic and
111 abiotic reactions to model Cr(VI) reduction, defines a mobile-immobile mass
112 transfer system for biomass and ED, and allows for bioclogging modeling
113 capabilities via the dependence of porosity and permeability on biomass con-
114 centration. For a full description of the biomass growth model, please refer
115 to the original Chrotran paper.

116 The simulations described in this paper were created for the purpose of
117 modeling certain interactions in the hyporheic zone. We simulate different
118 flow conditions, permeability conditions, and concentration inputs to train
119 our models on general representation of bioremediation simulations in the
120 hyporheic zone. The simulations are not resource limited – simulations with
121 high concentration of nutrients allowed for relatively linear biomass growth
122 throughout the time frame of the simulations (up to 228 days) whereas
123 biomass growth leveled off more towards the end of the simulations for sce-
124 narios with low concentration of nutrients,. We chose to not investigate
125 nutrient-limited scenarios because we observed less differences between small
126 scale and large scale simulations in cases of nutrient limitation, meaning a
127 model that allows mapping between the two would be less useful. Further-
128 more, the primary purpose of our upscaling model (STAMNet) is to provide

129 a means for rapid generation of bioremediation simulations for a variety of
 130 input conditions. In most cases of bioremediation, biomass growth is stimu-
 131 lated through the injection of nutrients (i.e., an electron donor), so our focus
 132 on high-nutrient simulations enhances the model’s applicability to bioreme-
 133 diation.

134 2.1.2. Boundary Conditions

135 For the baseline, we simulate a 1 meter (in vertical, or direction of hy-
 136 porheic flow) by 2 meter longitudinal (in direction of river/groundwater flow)
 137 slice of a synthetic hyporheic zone represented by 100 by 200 voxels ($dx = dy$
 138 $= 0.01$ m). The top and bottom boundaries (1 m difference) respectively rep-
 139 resent the surface and bottom-HZ pressures (which controls the amount and
 140 direction of vertical flow), and the left and right boundaries (2m difference)
 141 represent the pressure gradient in the longitudinal direction, thus control-
 142 ling the vector of groundwater flow (also referred to here as the horizontal
 143 flow). The horizontal pressure gradient is constant over the duration of any
 144 given simulation, and the vertical pressure gradient for any given simulation
 145 is derived from three different sets of in-situ hyporheic flux data [23, 24, 25]
 146 (Fig. 1). The ”10x scale simulation” represents a 1 meter by 20 meter slice
 147 of the hyporheic zone with the same resolution as the baseline simulations.
 148 Importantly, we note here that the pressure boundary conditions are the
 149 same for each pair of baseline and 10x simulations. This means the pressure
 150 gradient changes between a baseline simulation and its respective 10x sim-
 151 ulation. This constant pressure boundary framework is useful for extending
 152 simulations of bioremediation in which a specified pressure is established due
 153 to stimulant injection, although we also recognize that an upscaling method
 154 for constant pressure gradient would be beneficial for general studies of the
 155 hyporheic zone.

156 As discussed in further sections of the methods, all simulation variables,
 157 including the horizontal and vertical pressure gradients, take on different
 158 values for different simulations. From these base time series, we introduce
 159 random variations (large variations for the ”high speed” time series and small
 160 variations for the other time series in Figure 1) to increase the variability in
 161 potential flow conditions for our models to be trained on. The base set of
 162 pressure gradients for the horizontal flow was determined a range of realistic
 163 groundwater flow rates. Both horizontal flow (V_y) and vertical flow (V_x), and
 164 transport, are regulated by Dirichlet boundary conditions.

165 The primary motivation of this study is to develop upscaling and upsam-

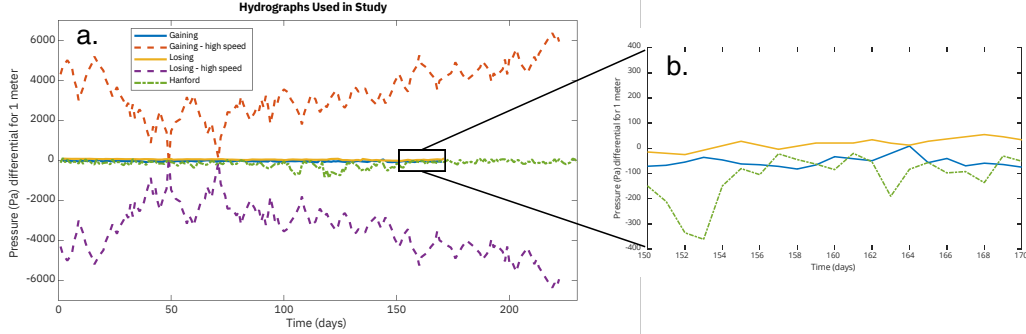


Figure 1: Different flow boundary conditions used in this study. Pressure time series were calculated from in-situ measurements of hyporheic flux ([23, 24, 25]). The gaining boundary conditions represent flux from the groundwater to the surface water, and losing boundary conditions represent flux from the surface water to the groundwater.

plung methods for RT simulations (specifically in the context of bioremedia-
tion) using deep learning (Fig. 2). Thus, we generated pairs of simulations
for training that are identical in every way except scale (for upscaling) or
resolution (for upsampling). As discussed above, the baseline simulations
represent a 1 meter by 2 meter slice of the HZ. For the upscaling task, all
models use the baseline 1x2 meter simulation as input to predict a 1x20
meter simulation. For the upsampling task, all models use the baseline 1x2
meter simulation with $dx = dy = 0.01$ m as input to generate a 1x2 meter
simulation with $dx = dy = 0.005$ m. All upscaling simulations ran for 228
days (114 timesteps) and all upsampling simulations ran for 86 days (43 time
steps). It should be noted that for the gaining and losing simulations the
in-situ hyporheic flux data (Fig. 1) only extended to 170 days. We therefore
applied constant flow boundary conditions to the last 58 days. The upscaling
simulations were also different from the upsampling simulations in that they
are based on heterogeneous permeability distributions whereas the upsam-
pling simulations contain homogeneous permeability distributions. Sample
permeability fields for the upscaling simulations are given in Figure 3.

2.1.3. Simulation Variables

To train and test our model on a large variety of simulations, we added
random variations to all variables of the simulations. The primary simulation
variables, as well as their voxel-specific min, max, and mean values across
all simulations, are given in Table 1. The average spatial distributions (in
time and across all simulations) of the output features of the 1x2 meter

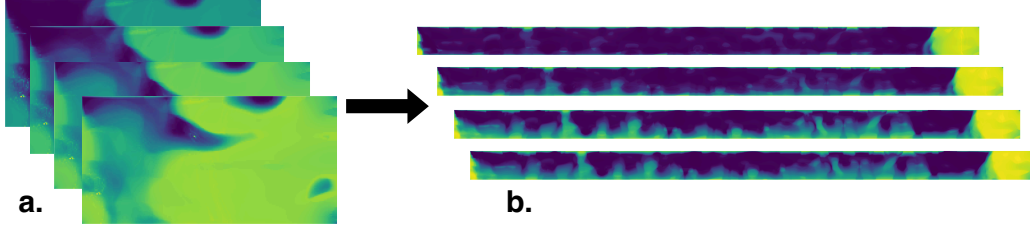


Figure 2: Sample ground truth snapshots of the 1x simulation (a) and 10x simulation (b) outputs. From top to bottom, the snapshots represent normalized biomass concentrations at $t = 40, 80, 120$, and 160 days. The primary motivation of this work is to provide a model that allows accurate mapping from 1x to 10x.

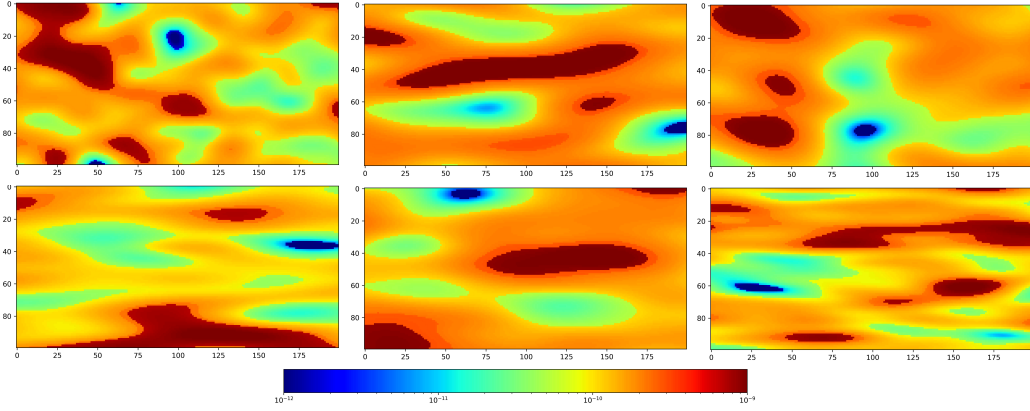


Figure 3: Sample heterogeneous permeability distributions (at $t=0$) used in simulations featured in this study. Heterogeneous permeability fields were used in the simulations generated to train and test our upscaling models, but for the case of our upsampling models, homogeneous permeability fields were used.

Table 1: Description of variables and their ranges of possible voxel-specific values used in the simulations. From left to right, these variables represent biomass, electron donor (molasses), and chromium concentrations, horizontal velocity, vertical velocity, pressure, temperature, porosity, permeability, biomass crowding parameter, and biomass growth parameter.

Var	B	ED	Cr(VI)	V_y	V_x	P	T	ϕ	k	α	λ_b
Units	$\frac{mol}{m^3}$	$\frac{mol}{L}$	$\frac{mol}{L}$	$\frac{m}{hr}$	$\frac{m}{hr}$	Pa	$^{\circ}C$	-	m^2	-	-
Min	1e-10	1e-20	1e-20	-632	-486	-1214	4.8	1e-4	1e-15	0.5	1e-5
Max	765	5.5e-3	7.6e-3	671	651	7099	24.9	0.6	1.1e-9	3.0	1e-4
Mean	58	8.1e-6	1.4e-5	-5.8e-2	-1.4e-2	786	11.5	0.13	2e-10	2.8	1e-5

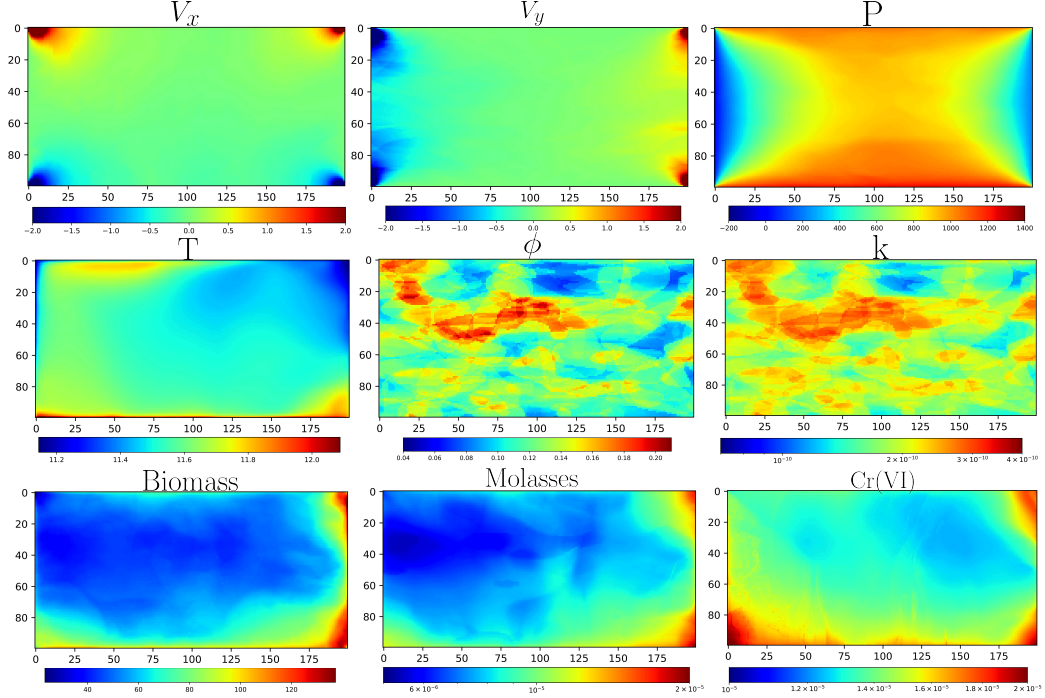


Figure 4: Mean spatial distributions for all simulations for (going from left to right and top to bottom) V_x (Darcy velocity in the vertical direction, measure in meters/hr), V_y (Darcy velocity in the direction of flow parallel to the river), pressure (Pa), temperature ($^{\circ}\text{C}$), porosity, permeability (m^2), biomass (mol/m^3), molasses (the electron donor, measured in mol/L), and Cr(VI) (mol/L).

189 upscaling simulations are shown in Figure 4. Molasses, biomass, and Cr(VI)
 190 all have similar distributions due to their coupling via chemical equilibria.
 191 In addition to the features listed in Table 1 and Figure 4, less consequential
 192 features that varied between simulations included S_c , S_d1 , and λ_c , which can
 193 all be classified as biomass growth parameters.

194 2.2. Deep-Learning-Based Upscaling

195 2.2.1. Model Architectures

196 Our initial model selection process was to look for published architectures
 197 that have been shown to be effective for spatiotemporal data [26, 27, 28].
 198 However, our input and output tensors have shape $[b, t, h, w]$, where b is
 199 batch size, t is the temporal dimension, and h and w are spatial dimensions.
 200 Given the irregular shape of our inputs ($[b, 114, 100, 200]$), and the large

shape of our outputs ([b, 114, 100, 2000]) for the upscaling task, we found that the available spatiotemporal models, which are often used for classification or object detection/tracking in video data, either were too large, or would not work well with our input shape. Thus, we moved to a smaller and simpler MLP-based structure of our own design (Fig. 5a). This architecture takes in a 4D input (including batch size) and passes it through a series of linear layers with nonlinear activation functions to progressively increase the size of the final dimension to the desired number. The best number and sizes of linear layers, and the best activation function, were determined via automated hyperparameter tuning with Optuna [29]. After optimizing the structure of the MLP, we used ablation experiments with different variations of the first layer to determine the best method for initial upscaling.

For both the upscaling and upsampling models, we also investigate the impact of attention on model performance. Specifically, we integrate efficient channel attention (ECA) [30], and a novel attention method (STAM), into the optimized MLP structure after the first layer (Figs. 5b & 5c). Our efficient channel attention method uses 1D convolution in the temporal dimension, allowing the model to focus on more relevant temporal features. STAM uses convolutions in multiple dimensions (fully described in section 2.2.2) to improve focus on task-relevant spatial and temporal features. The resulting architecture with the inclusion of STAM is called STAMNet. For the rest of the paper, we refer to the upscaling version of STAMNet as STAMNet-Upscale, and the upsampling version of STAMNet as STAMNet-Upsample. STAMNet-Upsample has a different architecture than STAMNet-Upscale because the task of upsampling requires a doubling in size for both of the spatial dimensions (Fig. 5c). At a basic level, STAMNet-Upscale increases the last spatial dimension by 10x, whereas STAMNet-Upsample increases both spatial dimensions by 2x.

2.2.2. Spatiotemporal Attention Module (STAM)

The STAM architecture (Fig 6) applies attention across multiple dimensions of the input tensor. It consists of four main branches (M1 - M4 from top to bottom) that process the input in different permutations, allowing the network to capture dependencies across various dimensions.

The four attention branches can be summarized as follows - M1 processes the input along the temporal dimension through convolutional layers and reduces the size of the width dimension through a linear layer, which results in an attention map of shape [b, t, h, 1]. M2 processes the input along

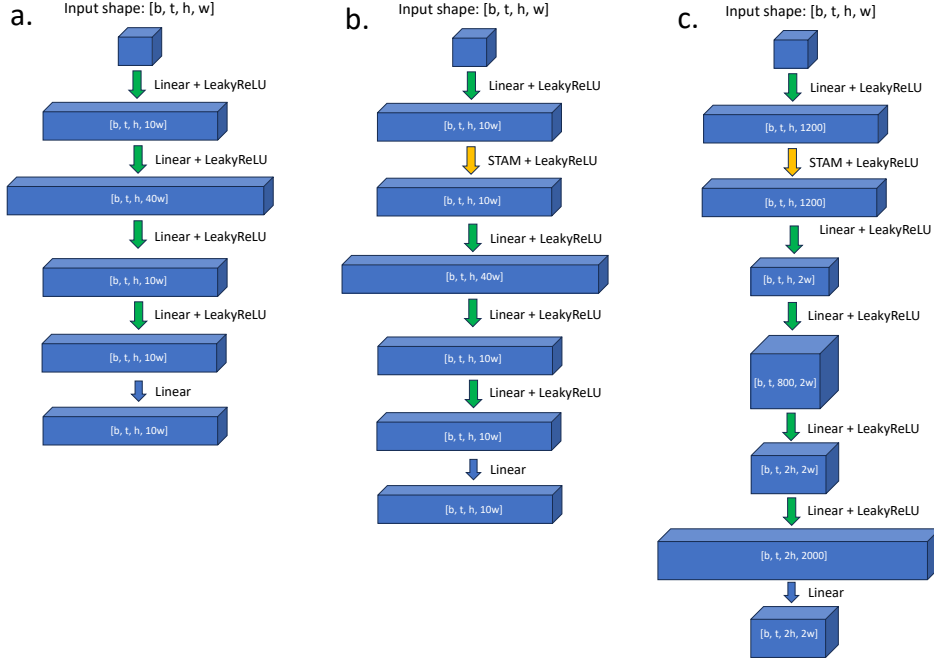


Figure 5: Model architectures for the optimal MLP (a), STAMNet-Upscale (b), and STAMNet-Upsample (c). Each block represents an intermediate output stage, and the arrows represent the layers of the model. The optimal MLP (a) and STAMNet-Upscale (b) take inputs of shape $[b, t, h, w]$ and return outputs of shape $[b, t, h, 10w]$. STAMNet-Upsample takes inputs of shape $[b, t, h, w]$ and returns outputs of shape $[b, t, 2h, 2w]$. STAM is a modular attention method that returns an output with the same shape as the input. The architecture of STAM is given in Figure 6. For STAMNet-Upsample (c), permutations are used after the 2nd and 4th linear layers to have the appropriate dimensions. This model takes an input of shape $[b, t, h, w]$ and gives an output of shape $[b, t, 2h, 2w]$.

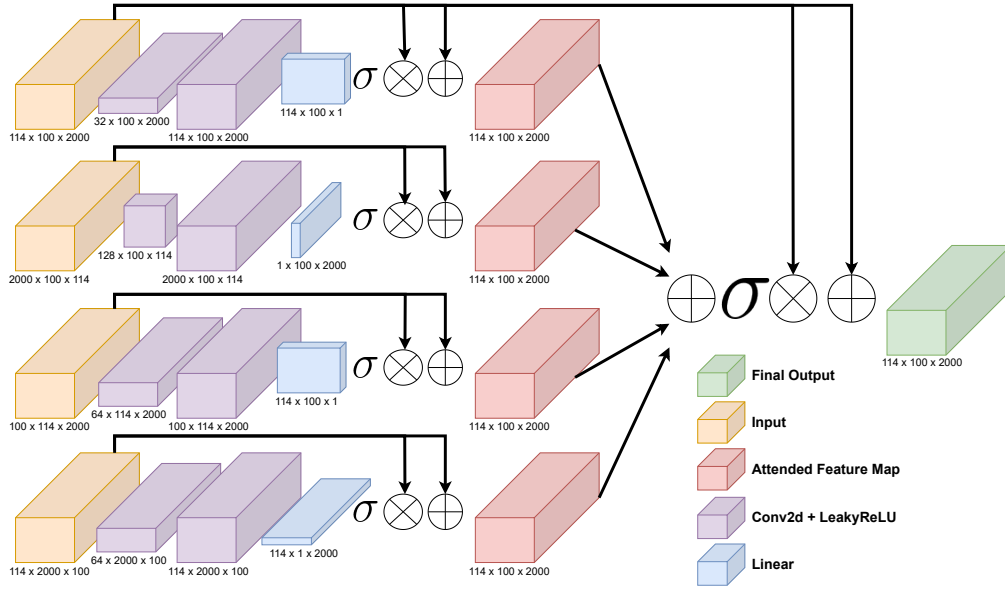


Figure 6: Architecture of the Spatiotemporal Attention Module (STAM). The model consists of four separate attention arms (M1-M4 from top to bottom). Each attention arm has two 2D convolutional layers and one linear layer followed by sigmoid activation, then multiplication and addition with the original input. The attention arms differ in their shapes, which results in feature maps that are able to capture complex cross-dimensional relationships. The attended feature maps from each attention arm are then averaged, passed through a sigmoid layer, multiplied by the input and finally added to the input to get the final output of the modular attention method.

the width dimension through convolutional layers and reduces the size of the time dimension (or the horizontal length being upscaled), which results in an attention map of shape $[b, 1, h, w]$. M3 processes the input along the height dimension and results in an attention map of shape $[b, t, h, 1]$, and M4 processes the input along the temporal dimension and results in an attention map of shape $[b, t, 1, w]$. M3 has a similar structure to M1 (and the same output shape) except it processes the height dimension through convolution instead of the weight dimension. Each branch follows a similar pattern: Conv2D (5x5) \rightarrow LeakyReLU \rightarrow Conv2D (1x1) \rightarrow LeakyReLU \rightarrow Linear \rightarrow Sigmoid. The output of each branch is multiplied with the input and the resulting product is added back to the input, creating two levels of residual connections. The outputs from all branches are then averaged and passed through a sigmoid activation function and multiplied and then added to the input to get the final attention map, thus creating additional residual connections.

STAM incorporates several architectural features that enhance its ability to map spatiotemporal relationships. By processing the input tensor along different dimensions, it captures complex spatial-temporal dependencies that simpler attention mechanisms or non-attentive models might overlook. The combination of 5x5 and 1x1 convolutions enables STAM to integrate both local and global context within each dimension [31, 32, 33]. Through residual connections and a final aggregation step, the model adaptively refines features, highlighting important patterns while attenuating less relevant information [34, 35]. The incorporation of LeakyReLU activations and dropout (in M2) introduces non-linearity and regularization, potentially enhancing the model’s generalization capabilities [36]. Furthermore, by processing the input through different permutations, STAM generates complementary attention maps, effectively capturing diverse data patterns [37]. Lastly, the addition of the input to the attention-weighted features preserves original information while facilitating the learning of cross-dimensional representations, thus providing a comprehensive approach to spatiotemporal feature extraction and refinement.

2.2.3. Training, Validation and Testing Process

Although the RT simulations contain multiple output features (Fig. 4), we chose to focus on upscaling biomass, Cr(VI), and molasses. All other variables either have little variation between 1x and 10x scale simulations (such as temperature and pressure) or can be easily upscaled through physics-

275 based methods (such as flow [38, 39, 40] and permeability [41]. With about
 276 48 GB of VRAM, models could be developed to upscale all three variable at
 277 once. However, we were restricted to 24 GB of VRAM, and at this amount
 278 of VRAM we weren’t able to effectively train multi-feature models. Thus, we
 279 trained a suite of models that separately upscale our three target variables.

280 For the upscaling task, 48 pairs of simulations were used for training, 8
 281 pairs of simulations were used for validation, and 13 pairs of simulations were
 282 used for testing. Validation scores were used to optimize hyperparameters
 283 and determine layer placement within STAMNet. Once the best model archi-
 284 tectures were determined through hyperparameter optimization and ablation
 285 studies, the validation data was also used for training, resulting in 56 pairs
 286 of training simulations and 13 pairs of testing simulations for the final cal-
 287 culation of scores. We used the AdamW optimizer, dropout of 0.2 after the
 288 first linear layer (or after the attention layer for models with attention), and
 289 a learning rate (lr) between $1.6e-4$ and $4.6e-4$ with a cosine annealing warm
 290 restarts scheduler. For biomass upscaling we used a lr of $1.6e-4$ and trained
 291 for 25 epochs, for biomass upsampling we used a lr of $4.6e-4$ and trained for
 292 900 epochs, and for ED and CR(VI) upscaling we used a lr of $3.0e-4$ and
 293 trained for 110 epochs. The number of epochs used for each feature was
 294 determined based on when the validation set stopped showing improvement.
 295 For all biomass upscaling experiments, we trained and tested each model type
 296 14 times and report the averages of each performance metric (MSE, MAE,
 297 and R^2). Each metric is calculated between all elements of the output tensor
 298 (x) and the ground truth (y). For example, the MAE is the sum of errors
 299 between each element of x and y divided by the number of elements in x and
 300 y. We also plot the mean time series and spatial distributions (over all sim-
 301 ulations) for each model to provide a visual understanding of the prediction
 302 errors. Specifically we use time series to investigate the average temporal
 303 distributions of the predictions of biomass, molasses (ED), and chromium
 304 for a simple interpolation model, an MLP+ECA model, and our STAMNet
 305 model. The spatial distributions are presented in two ways. The blue-green-
 306 yellow spatial distributions show the absolute concentrations of the feature
 307 in question, while the blue-white-red spatial distributions show the difference
 308 between the ground truth and the prediction for that particular model. For
 309 this visual analysis, we use a simple ensemble of the best-scoring variations
 310 of each model.

311 For the upsampling task, 40 pairs were used for training, 8 for validation,
 312 and 12 for testing. After optimal model structures were determined, the 8

simulation pairs used for validation were included in the training set, resulting in a final 48 simulation pairs for training and 12 simulation pairs for testing. All results for the upsampling task are a comparison of the average of 8 separately trained and tested models. For both upscaling and upsampling, the loss function used for training was $MSE + 0.6 \times MAE$, which was used over a standard MSE loss function as we found that only using MSE tends to result in a higher degree of overfitting. Furthermore, we found Huber loss to not weight the MAE strongly enough, which resulted in decreased MAE and R^2 scores.

3. Results and Discussion

3.1. Ablation Experiments

To determine the best simple method of upscaling, we experimented with three model variations (Table 2). The structure of the linear model is shown in Figure 5a. This structure was determined through optimization of validation scores via Optuna. In the linear model, the first layer is a linear layer that increases the size of the final dimension of the input by 10x. To reduce the number of parameters, or have roughly the same number of parameters with a deeper first layer, we tried to replace the first linear layer with a 10x interpolation layer and a 20x interpolation layer. Since simple interpolation often allows for reasonably accurate upscaling, the interpolation scheme implemented here is expected to be a parameter-efficient way to upscale the final dimension. The 10x interpolation layer takes the input of shape [b, t, h, w] and outputs a tensor of shape [b, t, h, 10w], while the 20x interpolation layer takes the same shape of input and outputs a tensor of shape [b, t, h, 20w]. Thus, the interpolation 10x model has the same structure as the linear model besides the 1st layer, which is instead a 10x repeat interleave layer. Similarly, the 20x interpolation model has an initial layer that interpolates the final dimension of the input to 20x size. Because the linear layer of the optimal MLP upscales the final dimension to 10x, the 20x model has a slightly different structure of second layer as it takes an input of [b, t, h, 20w]. The linear model performed best in the MAE and R^2 metrics. Thus, although interpolation allows for model parameter savings, it is not much, and the reduced accuracy is not worth these savings in most cases, so we developed STAMNet on top of this optimal linear architecture.

Table 2: Ablation experiments for biomass upscaling to determine the best method of increasing dimension size. MAE is given in $\frac{mol}{m^3}$ and MSE is given in $\frac{mol^2}{m^3}$.

	Linear	Interpolation (10x)	Interpolation (20x)
MSE	2508	2471	2471
MAE	21.62	22.25	22.02
R^2	0.897	0.880	0.875

3.2. STAMNet-Upscale Performance

3.2.1. Biomass Upscaling

The results of our upscaling models for the biomass prediction task are given in Table 3. The interpolation model here is different than the interpolation models used in the ablation experiments. In the ablation experiments, the interpolation was used as an initial layer of a model with multiple linear layers and an activation function after the interpolation. For the interpolation model in table 3, there are no linear layers after the interpolation. In other words, it is just a simple interpolation of the final dimension, which is the most simple and rapid way to generate reasonably accurate results for the task of upscaling as defined in this paper. This interpolation model can also be thought of as a simple reproduction of the baseline scale (but with extended dimensions), meaning that the errors for the interpolation model are a proxy for the differences between 1x and 10x scale. The simple MLP is a one-layer MLP that increases the size of the final dimension by 10x. The optimal MLP is the fully optimized MLP structure given in Figure 5a. The structure of STAMNet, our proposed best-performing model, can be seen in Figure 5c. The MLP+ECA model has the same structure as STAMNet, but with the ECA attention module instead of the STAM attention module.

For all models tested, STAMNet-Upscale shows the strongest performance by a statistically significant margin for the both MSE and R^2 metrics. Both models with attention modules outperform the optimal MLP, further indicating that attention is a useful tool for developing robust upscaling model architectures. STAMNet-Upscale performs better than the MLP+ECA model, indicating that cross-dimensional feature refinement offers performance benefits over single dimensional (temporal) feature refinement. All trained models perform better than simple interpolation, showing the general benefit to the approach of using deep learning for upscaling of reactive transport simulations.

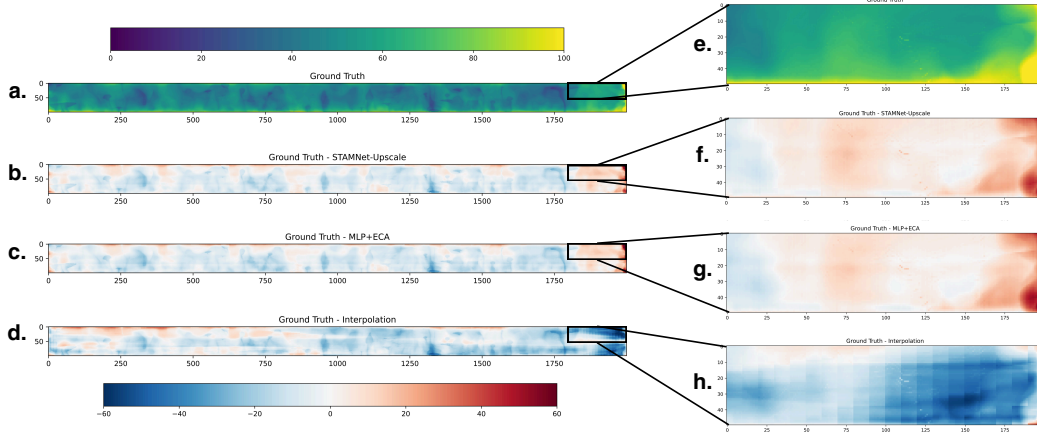


Figure 7: Spatial error distribution of biomass averaged over all test simulations and time steps. (a) Ground truth spatial distribution. (b) Ground truth minus output from STAMNet-Upscale. (c) Ground truth minus the MLP+ECA model. (d) Ground truth minus simple interpolation. (e-h) Zoomed in versions of a-d. These figures show that STAMNet has difficulty predicting fine spatial variations but is more accurate than a simple interpolation.

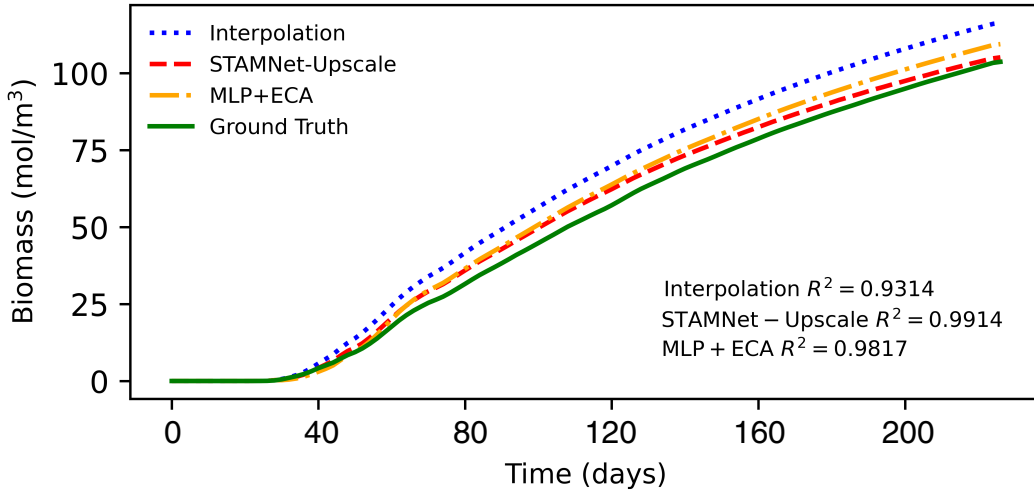


Figure 8: Biomass time series averaged over all upscaling test simulations and time steps. The blue dotted line corresponds to the time series for a simple interpolation of the input, the red dashed line corresponds to the output for STAMNet-Upscale, the yellow dash-dotted line corresponds to the output for the MLP+ECA model, and the green dash-dotted line corresponds to the ground truth (i.e., the time series of the 10x scale simulation output). This figure shows STAMNet outperforms simple interpolation and achieves a high level of accuracy in terms of time series prediction.

376 To further investigate the performance of our different models for the task
 377 of upscaling biomass, we plot the spatial error (Fig. 7) and the mean time se-
 378 ries error (Fig. 8). The spatial errors show that the simple interpolation (Fig.
 379 7d), the MLP+ECA (Fig. 7c), and STAMNet-Upscale (Fig. 7b) all fail to
 380 capture fine variations in the ground truth spatial distribution. Instead, they
 381 achieve a low MSE/MAE by averaging out the variabilities in space. This is
 382 to be expected, however. Without a method that specifically constrains the
 383 spatial distributions of biomass concentrations, the model lacks the ability
 384 to predict exactly what the upscaled version will look like, so the model just
 385 makes an average guess. In other words, the neural nets may learn to approx-
 386 imate the vertical variability in biomass well, since this doesn’t change much
 387 between small and large-scale simulations, but have no ability to predict the
 388 horizontal variability in biomass as this may change significantly based on
 389 scale and more strongly depends on the differences between the small and
 390 large-scale permeability fields. To compensate for this lack of knowledge, the
 391 neural nets make predictions that represent averages across many horizontal
 392 voxels. We experimented with loss functions to try to add this constraint to
 393 the spatial distribution of the outputs, but found it had too negative of an
 394 impact on the outputs of time series distributions and did not improve the
 395 accuracy of the spatial distributions (either in exact value or ”look”) enough
 396 to warrant further investigation. Thus, although there are some differences
 397 in the spatial error between different models, no model we tested provides an
 398 adequate representation of physically realistic spatial variations, and more
 399 robust techniques are needed to achieve high-fidelity spatial predictions.

400 In terms of comparison between the methods, STAMNet-Upscale and the
 401 MLP+ECA clearly outperform the interpolation, which can be better seen
 402 from the zoomed-in sections of the spatial error distributions (Figs. 7e-7h).
 403 There is a very slight difference between error for STAMNet-Upscale and the
 404 MLP+ECA, but it is essentially negligible with regards to the overall accu-
 405 racy of the predictions of spatial distributions. One big difference between
 406 the interpolation and the attention-based neural nets is that the interpola-
 407 tion model greatly overcalculates biomass concentrations, especially near the
 408 right boundary of the domain. The right boundary of the domain is often a
 409 source of nutrients and thus a location of dense biomass growth. In the 1x2
 410 meter simulation, these nutrients are able to reach into and cause biomass
 411 growth in about half of the domain, meaning a simple interpolation to the
 412 1x20 meter simulation leads to high biomass concentrations that extend too
 413 far into the domain. The primary reason for this significant error in the

414 simple interpolation model is that the 1x and 10x scale simulations have the
 415 same pressure boundary conditions, meaning they have different pressure
 416 gradients. Specifically, the 1x simulation has a pressure gradient 10 times
 417 greater than the 10x solution, meaning horizontal flow results in less biomass
 418 growth at 10x scale in terms of the percentage of the domain. The neural
 419 nets are able to provide more accurate mapping between the two scales, al-
 420 though they still show significant spatial errors at the right-hand boundary
 421 due to their tendency to average local variations in concentration.

422 In addition to our analysis of the spatial errors of the simple interpolation
 423 method and attention-based models, we also investigate their performance
 424 in terms of the average time series prediction (Fig. 8). Unlike the spa-
 425 tial distributions, all models perform quite well at the task of capturing the
 426 average upscaled time series. Both attention-based models clearly outper-
 427 form a simple interpolation, and STAMNet-Upscale slightly outperforms the
 428 MLP+ECA model.

429 3.2.2. *Low and High-Concentration Biomass Upscaling*

430 To further refine our general investigation of the upscaling potential of
 431 STAMNet for RT simulations, we split this analysis up to investigate per-
 432 formance on high-concentration and low-concentration simulations. Of the
 433 13 test simulations, 5 simulations can be categorized as high-concentration
 434 (mean biomass greater than $50 \text{ mol}/m^3$), and 5 simulations can be catego-
 435 rized as low-concentration (mean biomass less than $15 \text{ mol}/m^3$). The spatial
 436 errors for both the low and high concentrations (Fig. 9) show the same trends
 437 as the spatial errors for the full set of results (Fig. 7). For the low concentra-
 438 tions, STAMNet-Upscale (Fig. 9b) and the MLP+ECA model (Fig. 9c) are
 439 completely indistinguishable, and both clearly outperform the interpolation
 440 (Fig. 9d). For the high concentrations, there is similarly very little difference
 441 between the spatial errors for STAMNet (Fig. 9f) and the MLP+ECA model
 442 (Fig. 9g). Both attention-based neural nets outperform simple interpolation
 443 (Fig. 9h), although similar to the full set of results (Fig. 7) for biomass
 444 upscaling, these differences are negligible compared to the overall error of
 445 the spatial distributions.

446 The time series plots for the low and high-concentration upscaling (Fig.
 447 10) reveal slightly more interesting deviations from the analysis of all test
 448 simulations. The low-concentration time series (Fig. 10a) shows dramatically
 449 better performance for the attention-based neural nets when compared to the
 450 simple interpolation. The high-concentration time series (Fig. 10b), on the

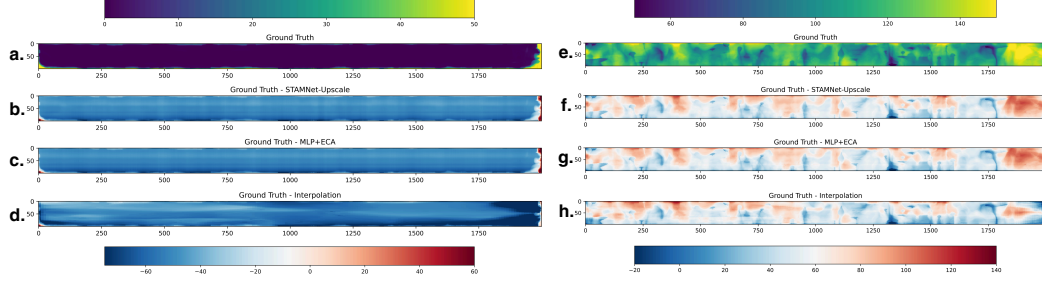


Figure 9: Spatial error distribution of biomass averaged over low and high-concentration test simulations. (a) Ground truth spatial distribution for low-concentration simulations. (b) Ground truth minus output from STAMNet-Upscale for low-concentration simulations. (c) Ground truth minus the MLP+ECA model for the low-concentration simulations. (d) Ground truth minus simple interpolation for low-concentration simulations. (e-h) High-concentration versions of a-d. These figures show greater difference between the spatial errors of the interpolation and our trained networks for low-concentration simulations than high-concentration simulations.

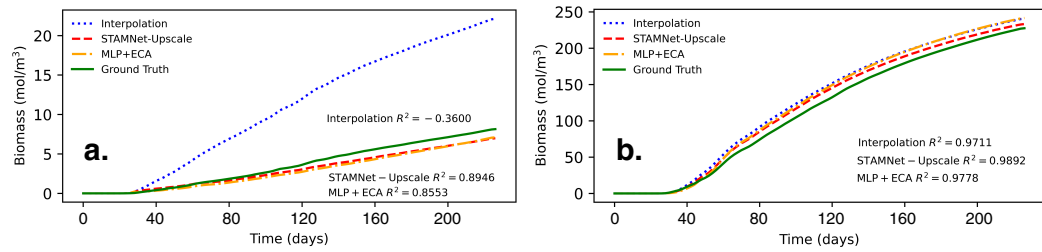


Figure 10: Biomass time series averaged over low (a) and high-concentration (b) upscaling test simulations. This figure shows STAMNet-Upscale outperforms simple interpolation and our MLP+ECA architecture, especially for low-concentration simulations.

Table 3: Results for biomass upscaling. Each model was trained and tested 14 times, and values here correspond to the average scores over all 14 model iterations. MAE of biomass is given in $\frac{mol}{m^3}$ and MSE is given in $\frac{mol^2}{m^3}$. Values in bold indicate statistically significantly better performance than all other models.

	Interpolation	Simple MLP	Optimal MLP	MLP + ECA	STAMNet-Upscale
MSE	4089	2691	2508	2525	2480
MAE	26.42	28.08	21.62	21.35	21.60
R^2	0.727	0.903	0.897	0.892	0.925

other hand, shows relatively small differences between each model. Thus, our results indicate that a simple interpolation is a generally accurate way to upscale high-concentration RT simulations of biomass growth, but not for low-concentration simulations as it results in a large amount of overprediction of biomass concentrations. As previously discussed, this overprediction is due to the differences in pressure gradients at low and high scales, which appear to be especially relevant in low-concentration simulations.

Across all biomass upscaling experiments, our results show that compared to models without attention, STAM can selectively focus on important features in the input, potentially leading to better performance on tasks that require understanding of complex spatial-temporal relationships. Compared to ECA, which focuses on attention in the temporal dimension, STAM provides a more comprehensive attention mechanism that considers both spatial and temporal dimensions. STAM generally performs better than ECA, which indicates the cross-dimensional attention, which improves feature mapping in both the spatial and temporal dimensions, is advantageous for the task of upscaling.

3.2.3. Molasses and Cr(VI) Upscaling

We further show the strong performance of STAMNet by upscaling RT simulations for the molasses (electron donor - ED) and Cr(VI) features. We find that STAMNet significantly outperforms the simple interpolation and MLP+ECA model for ED prediction in the MSE and R^2 metrics (Table 4). Furthermore, the MLP+ECA model also significantly outperforms the simple interpolation in all metrics, which once again shows the benefit of neural architectures, and especially those with attention, for the task of upscaling. Specifically, these results show that the benefits of our neural architectures for upscaling are not restricted to biomass, and can be extended to other features. The results for Cr(VI) similarly show high upscaling per-

Table 4: Results for upscaling experiments with molasses (ED) and Chromium. MAE is given in $\frac{mol}{L}$ and MSE is given in $\frac{mol^2}{L}$. Values in bold indicate statistically significantly better performance than all other models.

ED	Interpolation	MLP + ECA	STAMNet-Upscale
MSE	1.20×10^{-4}	2.77×10^{-5}	2.62×10^{-5}
MAE	2.72×10^{-3}	1.81×10^{-3}	1.80×10^{-3}
R^2	0.2937	0.888	0.913
Cr(VI)	Interpolation	MLP + ECA	STAMNet-Upscale
MSE	5.32×10^{-4}	1.02×10^{-4}	8.92×10^{-5}
MAE	3.31×10^{-3}	2.45×10^{-3}	2.23×10^{-3}
R^2	0.9093	0.9508	0.9227

479 formance for both STAMNet-Upscale and the MLP+ECA model. Also, in
 480 this case, the MLP+ECA model outperforms STAMNet-Upscale in the R^2
 481 metric, but performs worse than STAMNet-Upscale for the MSE and MAE
 482 metrics (although none of these differences are significant), indicating that
 483 the differences in performance between STAM and ECA may depend on the
 484 particular task. Thus, in addition to providing trained models for biomass,
 485 ED, and Cr(VI) upscaling, we provide multiple frameworks with which fu-
 486 ture researchers can train their own upscaling models for specific features
 487 they may be interested in. Although we find STAMNet to outperform our
 488 optimized MLP+ECA model, we encourage researchers to run their own ex-
 489 periments with their data to determine which model works best for their
 490 task.

491 Similar to our results for the biomass upscaling, we also present spa-
 492 tial and time series errors for chromium and molasses (Fig. 11). Like
 493 all the spatial errors for biomass, we find that STAMNet-Upscale and the
 494 MLP+ECA model outperform the simple interpolation but are not able to
 495 capture the fine-grained details of the spatial distributions for molasses (Fig.
 496 11c) and chromium (Fig. 11d). For the mean time series comparison, we
 497 see STAMNet-Upscale and the MLP+ECA model perform equally well at
 498 molasses upscaling (Fig. 11a). Surprisingly, although the MLP+ECA model
 499 gives a higher R^2 for Cr(VI) when the metric is calculated as the mean over
 500 the set of R^2 values for each time series, when the R^2 is calculated from the
 501 mean time series (i.e. the time series is averaged over all simulations then R^2
 502 is calculated), we see STAMNet-Upscale has a slightly higher R^2 (Fig. 11b).
 503 This indicates that MLP+ECA is more accurate for the Cr(VI) upscaling

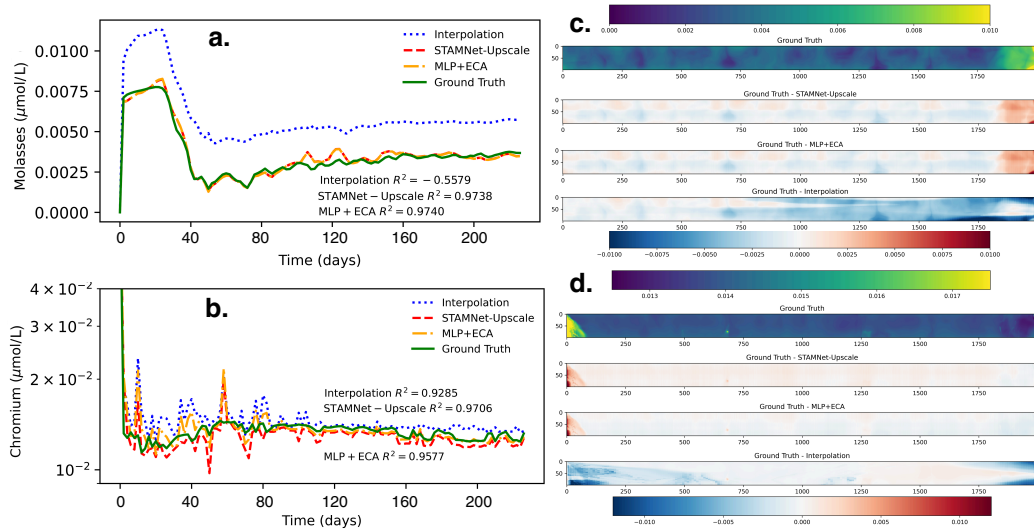


Figure 11: STAMNet-Upscale, MLP+ECA, and interpolation performance for (a) molasses time series, (b) chromium time series, (c) molasses spatial error distributions, and (d) chromium spatial error distributions. STAMNet outperforms interpolation in the molasses time series and spatial distribution and the chromium spatial distribution, but it is nearly indistinguishable from the interpolation for the chromium time series.

of any given simulation, but that STAMNet-Upscale will be more accurate when considering the mean value of a variety of simulations. The simple interpolation performs well for Cr(VI), but not for molasses, further showing its inconsistent performance compared to that of the attention-based neural nets.

3.3. STAMNet-Upsample Performance

In addition to our investigation of upscaling in the sense of increasing the lateral domain of the simulation output, we also use another variant of the STAMNet architecture (Fig. 5c) to increase the resolution of the simulation

Table 5: Results for upsampling experiments. MAE is given in $\frac{\text{mol}}{\text{m}^3}$ and MSE is given in $\frac{\text{mol}^2}{\text{m}^3}$.

	Interpolation	Simple MLP	Optimal MLP	MLP+ECA	STAMNet-Upsample
MSE	73.50	54.45	28.58	29.76	26.22
MAE	1.443	1.557	1.263	1.268	1.238
R^2	0.9997	0.9987	0.9984	0.9987	0.9986

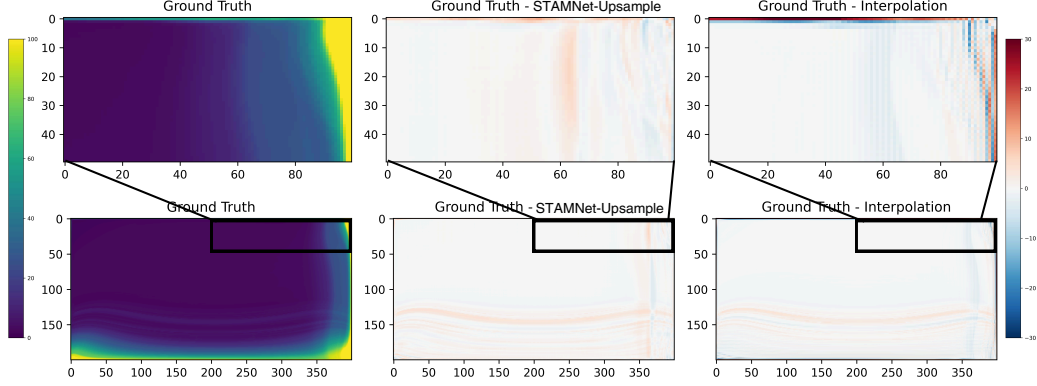


Figure 12: Spatial error distribution of biomass averaged over all test simulations and time steps for the upsampling task. (a) Ground truth spatial distribution. (b) Ground truth minus output from STAMNet-Upsample. (c) Ground truth minus simple interpolation. (d-f) Zoomed in versions of a-c. These figures show the superior spatial performance of STAMNet over interpolation for the task of upsampling, especially near the boundaries of the domain.

output, which we refer to as the task of upsampling. We find that STAMNet-Upsample shows significantly better performance than all other models for the upsampling task in MSE and MAE, although a simple interpolation gives the best performance for R^2 (Table 5). Considering we trained and tested on a smaller number of simulations for the task of upsampling compared to the task of upsampling, and that we only used homogeneous permeability fields for the upsampling simulations, it is likely that the upsampling task was not difficult enough to result in large performance differences between models. Furthermore, some degree of overfitting on the MSE and MAE during training may have resulted in a model that focuses more on the spatial aspects of the upsampling task than the average temporal ones. Looking at the spatial distributions for STAMNet-Upsample and the interpolation (Fig. 12), we can see that STAMNet-Upsample does indeed have more accurate spatial approximations (especially at the domain boundaries). Thus, while it could be argued the simple interpolation may be more appropriate for tasks that don't care about the accuracy of the spatial distribution, for tasks where spatial accuracy is important, STAMNet-Upsample is clearly advantageous to simple interpolation. We also find that the addition of STAM to the optimized MLP improves performance, but the addition of ECA to the optimized MLP generally decreases performance. These results contrast those of the

533 upscaling task, where both ECA and STAM were found to improve MLP per-
 534 formance. As seen by the high R^2 of all models for the average time series,
 535 the task of upsampling does not result in large differences in the average tem-
 536 poral trends. Thus, ECA, which uses 1D convolution to improve temporal
 537 feature extraction, results in a tiny improvement in R^2 (relative to the opti-
 538 mal MLP), but causes a decrease in MAE and MSE due to the extra focus on
 539 temporal features. This trend is not observed in the upscaling results (Table
 540 3), however, as ECA shows significant improvements to MAE for biomass
 541 upscaling. Given the significant differences in task and input tensors, these
 542 differences are likely a result of differences in the task-specific performances
 543 of each architecture and imperfect training hyperparameters. Thus, although
 544 ECA generally doesn't perform as well as STAMNet-Upsample for the task of
 545 upsampling, it is possible these results would be different if hyperparameters
 546 were individually tuned for each model, which strengthens our suggestion for
 547 future researchers to experiment with both the STAMNet and MLP+ECA
 548 architectures.

549 4. Conclusions

550 This study presents STAMNet, a novel deep learning architecture for up-
 551 scaling and upsampling reactive transport simulations in the hyporheic zone
 552 with specific applications to Monte-Carlo-style investigations of bioremedia-
 553 tion. Our results demonstrate that STAMNet outperforms traditional inter-
 554 polation methods and simpler neural network architectures across multiple
 555 tasks and metrics. STAMNet-Upscale significantly improved upon simple in-
 556 terpolation and optimized MLP models for biomass upscaling, achieving the
 557 highest R^2 (0.925) and lowest MSE among tested models. Furthermore, the
 558 spatiotemporal attention module (STAM) consistently outperformed efficient
 559 channel attention (ECA), indicating the benefits of cross-dimensional feature
 560 refinement for reactive transport modeling. Notably, STAMNet showed ro-
 561 bust performance across different concentration regimes, with particularly
 562 strong improvements over interpolation for low-concentration simulations.
 563 The architecture performed well with other reactive transport variables,
 564 showing significant improvements for molasses (electron donor) upscaling and
 565 competitive performance for chromium upscaling. Furthermore, STAMNet-
 566 Upsample demonstrated superior performance in increasing simulation reso-
 567 lution, particularly in capturing spatial details more accurately than simple
 568 interpolation. By enabling rapid upscaling and upsampling of simulations,

569 this approach has the potential to accelerate research in hyporheic zone pro-
570 cesses and enhance our ability to quickly design bioremediation approaches
571 at large scales. As the field continues to evolve, the integration of advanced
572 deep learning architectures like STAMNet with domain-specific knowledge
573 promises to unlock new possibilities in environmental modeling and decision-
574 making.

575 While STAMNet shows promise for accelerating and enhancing reactive
576 transport simulations, some limitations should be noted. The current imple-
577 mentation struggles to capture fine-grained spatial variations in upscaled sim-
578 ulations, instead producing averaged distributions. Additionally, the model’s
579 performance may vary depending on the specific reactive transport variable
580 being predicted, as seen in the differences between biomass, molasses, and
581 chromium results. It’s also important to acknowledge that the study focused
582 on a specific bioremediation scenario, and further testing is needed to con-
583 firm generalizability to other subsurface environments and reactive transport
584 systems.

585 Future research directions should address these limitations and expand
586 upon the current work. Investigators should explore methods to incorporate
587 physical constraints or multi-scale approaches to improve the spatial fidelity
588 of upscaled predictions. Extending the model to handle a wider range of
589 reactive transport variables and scenarios, including more complex biogeo-
590 chemical reactions, constant pressure gradients, and heterogeneous subsur-
591 face environments, would further enhance its applicability. The integration
592 of STAMNet with physics-based models to create hybrid approaches that
593 leverage both data-driven and mechanistic insights is also an exciting avenue
594 for development. Finally, investigating the potential of STAMNet for other
595 spatiotemporal prediction tasks beyond reactive transport, such as climate
596 modeling or ecosystem dynamics, could open up new applications for this
597 innovative architecture.

598 **CRediT authorship contribution statement**

599 Marc Berghouse: Data curation, Formal analysis, Investigation, Software,
600 Conceptualization, Visualization, Writing – original draft, Writing – review
601 & editing, Methodology. Rishi Parashar: Supervision, Writing - review &
602 editing, Project administration.

603 Declaration of Competing Interests

604 The authors declare no competing interests.

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610 Data Availability

611 Data used for training and testing are available upon request. The source
612 codes are available for downloading at the link: <https://github.com/mberghouse/STAMNet>

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