Application Text / Cover Letter Cum Research Background
January 29th, 2024

Dear prof,

I am Sanyam, currently an MSc student at Østfold University College (tentative finish date in May 2024) and a Research Asst. at OsloMet University. I am fulfilling both the roles under the supervision of my professor Stefano Nichele. Previously I was Research Fellow at Indian Institute of Technology, Jodhpur from 2020-22. Some of my responsibilities also included Teaching Asst. for Machine Learning class. While I finished my BTech Computer Science Engineering from UPES Dehradun in 2019, I wrote GATE and secured 94.16 percentile (All India Rank of 5692) in the year 2020. My current field of interest is driven by computational biology of complex systems in Alife, and some of my previous research also shows my interest in Deep Learning for Computer Vision [14-16]. I have been always part of Interdisciplinary research, be it related to Machine Learning or Complexity in ALife! Most of my work from MSc and Research Asst. is related to capture, measure and quantifying emerging complexity in *in-silico* substrates (for example Discrete Cellular Automata (CA), Game of Life, Lenia, and Neural CA). We developed statistical tools like frequency histogram coarse graining to eliminate noise in the evolved behavior of the CA as substrate [1,10], variation over time measures using auto-encoders with the idea that chaotic behavior produces higher loss in reconstruction, while order shows small loss as it is easier to reconstruct for. With that idea, we developed fitness function for the evolutionary algorithms that could result emerging patters in the substrate, for example, ring forming bacteria in Lenia [2,11]. For most of my research I also studied potential applications of Lenia in particle systems [3], physical systems [4] and biological systems [5] and with multi-specie simulations [6,7]. Some of our proposed and published research from the *living technology lab* in this line of work is provided in [8-12]. While I am focused on the publication of research work, I also try to take most out of such opportunities in the form of conference reports [13] which works as summary of co-researchers work.

Earlier, I have demonstrated exceptional hands-on proficiency in the deep learning stack. As outlined in the project description and to align with my pertinent experience, the following project summaries illustrate the diversity of my completed projects.

1. Reproducing Results of StyleGAN 2 (NVIDIA LABS) on five different dataset ("Grade A" as part of Advanced Machine Learning course at IITJ): As part of independent project, I completed it in 15 days including training from scratch, evaluating and building a pipeline that uses trained GAN models. Part of it was released as GitHub repo here [20]. The project explored reproducing the results of StyleGAN 2 on Clothing Dataset and Helen Face dataset while pretrained models were fine-tuned on Flower, Painting faces, wiki art, Obama and CIFAR100 datasets. This project was completed in 2021.
2. DeepSeaNet (Part of Advanced ML course at Østfold University College, Grade "A"): Developing a novel object detection architecture for deep sea underwater dataset to analyze and classify key marine species. Marine animals and deep underwater objects are difficult to recognize and monitor for safety of aquatic life. There is an increasing challenge when the water is saline with granular particles and impurities. In such natural adversarial environment, traditional approaches like CNN start to fail and are expensive to compute. This project involves implementing and evaluating various object detection models, including EfficientDet, YOLOv5, YOLOv8, and Detectron2, on an existing annotated underwater dataset, called the Brackish-Dataset. The dataset comprises

annotated image sequences of fish, crabs, starfish, and other aquatic animals captured in Limfjorden water with limited visibility. The aim of this research project is to study the efficiency of newer models on the same dataset and contrast them with the previous results based on accuracy and inference time. Firstly, I compare the results of YOLOv3 (31.10% mean Average Precision (mAP)), YOLOv4 (83.72% mAP), YOLOv5 (97.6%), YOLOv8 (98.20%), EfficientDet (98.56% mAP) and Detectron2 (95.20% mAP) on the same dataset. Secondly, I provide a modified BiSkFPN mechanism (BiFPN neck with skip connections) to perform complex feature fusion in adversarial noise which makes modified EfficientDet robust to perturbations. Third, analyzed the effect on accuracy of EfficientDet (98.63% mAP) and YOLOv5 by adversarial learning (98.04% mAP). Last, I provide class activation map based explanations (CAM) for the two models to promote Explainability in black box models. Overall, the results indicate that modified EfficientDet achieved higher accuracy with five-fold cross validation than the other models with 88.54% IoU of feature maps. The preprint is available at [15]. This project was completed in 2023.

3. There are two other mini projects related computer vision including "ADVERSARIAL ATTACK ON YOLOV5 FOR TRAFFIC AND ROAD SIGN DETECTION" and "ADDSL: Hand Gesture Detection and Sign Language Recognition on Annotated Danish Sign Language" in [14, 16]. Both the projects were finished in 2023.

My MSc thesis is on the title AI generating Algorithms using self-organizing neural cellular automata which is very much inspired from building an open-ended substrate that could evolve complex dynamics as marked in [17]. Moreover, for the research I also studied morphogenesis in Alife (for example, planarian re-generation [18] or biome [19]) The mid-term progress so far covers building such environment where cellular agents (each equipped with an ANN) could evolve and interact to produce different behaviors (for example Phenotypes). For now, we implement it using connected lattice like CA where each pixel corresponds to an agent containing livelihood layer and composition layer (which could be energy, chemical properties, or enzymes!). Information from both the layers are passed to an agent which then decides what needs to be done in the next generation that could benefit its survival. Therefore, the only way that agents could thrive in the environment is using self-replication with inheritance and mutation. Since we seed some agents pre-dominating in the substrate, they are the *founders* of the community that can evolve in later generations. The data collected from this synthetic biological process is then processed to perform analysis, for example, in Phenotypic level we analyze the diversity of cells and species using entropy, mean and variance-based measures. Specifically, we call those proposed methods as global entropy, local variance, global variance, and local-global variances that compares local neighborhoods with expected neighborhoods. Further, in genotypic level analysis, we track genealogies of certain genetic traits, cell clustering, and hash mapping of the gene-sequence. This helps in understanding which specific genetic trait has prolonged in the evolution, which agents have build their communities and others have diverged too far after generations that they have changed their genotype. We also verify in our experiments, multiple genotypes having similar phenotype and one genotype having multiple phenotype (phenotypic plasticity). However the major research questions include asking (1) What are the key species that emerge, survive, reproduce and becomes extinct (dead) in the evolved substrate model, (2) How does the genotypic diversity evolve over successive generations, (3) What is the impact of the self-replication and self-maintenance processes, characteristic of autopoiesis, on the genetic makeup, (4) How do phenotypic variations (observable differences) manifest within the model, and what are the underlying factors contributing to this diversity. In our system, we expect the major contributions towards the phenotype diversity is led by intra-cellular communications, evolutionary pressures driving

the selection of specific genetic traits, leading to the emergence of phenotypic variations that confer advantages in terms of survival and reproduction, (5) To what extent do the cellular activities within the substrate exhibit sensitivity to initial conditions (for example number of generations). While these are some of the research questions, we implement above mentioned methods to find out answers to such questions. Glimpse of the results (till mid-term thesis) is shown in Figure 1 below.

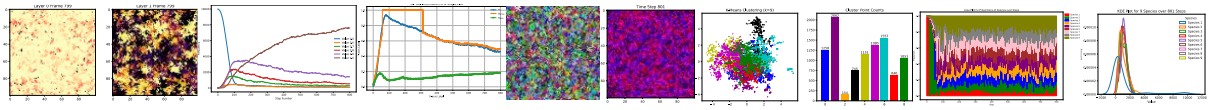

Figure 1 In the row, evolved substrate(alpha layer and chemical layer), frequency of species, entropy and variance plots, genetic diversity plots (showing heterogeneity in multi-gene spectrum and homogeneity in three-gene picked trait spectrum), cell clustering plot, speciation plots (High resolution image at https://s4nyam.github.io/fig1.pdf)

We also plan to build a more realistic substrate such that its not restricted within the lattice model (for example CA) but provides flexibility to connect random nodes as a connected graph (as gene regulatory network) as part of the next semester progression of the thesis.

I also find this PhD Project very feasible logistically, reason being moving from Norway to rest of the Europe looks super easy considering my single status. Additionally, I am flexible when it comes to environment, resources, and mentor supervision. I have also equipped a good hands on with using high performance commuting and community GPU clusters (for example Simula eX3 in Norway). I find myself fit on all the qualifications mentioned in the project advertisement, to be specific, my education background is in Computer Science, Research Experience have demonstrated in Deep Learning for CV, GANs, Autoencoders, and other architectures. I have been using torch and TF with Python for last 4 years now for all of my projects along with JAX for high parallelization of CUDA usage. And my publication record also includes work in YOLOv5, EfficientDet, Adversarial Learning, and FedML.

Thanks for considering my application!

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