

# Project Selection Task: Protein Reconstruction

## **Deadline for the Task: 7th May 2021 11:59PM**

In this task, you are supposed to build a simple image classification model. ([Reference](#))

You are provided with the iNaturalist12k Dataset containing 12,000 images split into 10,000 train and 2,000 validation samples. The images from the dataset belong to 10 classes. You can **download the dataset from here:**

[https://storage.googleapis.com/wandb\\_datasets/nature\\_12K.zip](https://storage.googleapis.com/wandb_datasets/nature_12K.zip)

Further to make your task simpler, we provide a starter code (obviously with portions missing from it). There are indicators for the areas where you need to fill code at the **TOP** of each script. Reference links are also provided at the corresponding locations.

### **Link to code:**

<https://drive.google.com/drive/folders/1j2cTZIQFXGdQPDm8TZceqCleRstelZOG?usp=sharing>

Once again, we reiterate, there are **no prerequisites** for this project. All the learning happens after you get selected into the project team.

**Note:** We are **NOT** going to evaluate you based on the accuracy or performance of the model. Hence, it's completely fine if you are unable to train the model (due to compute reasons, or whatever it be). We are specifically looking to gauge your understanding and willingness to learn/explore.

Apart from the above classification task, we expect you to explore and **answer the following questions**. Once again there is no right or wrong answer to these questions and it's basically to understand your thought process.

1. After training our model, suppose we figure out that it learns to focus specifically only on a single view. For example: it preferred to reconstruct entirely based on the top view. Is this desirable or not and justify your answer. (Brownie points: Describe how we can either make this happen or prevent it)
2. Suppose we train a Generative Adversarial Network to synthesize 3D protein structures from a protein image(s) and we notice that the model generates the same output irrespective of the input provided. What are the possible measures to solve this?
3. AlphaFold2 is a model which can generate a protein structure given its sequence ([Reference](#)). Now does it make sense to use such a model for our particular task (i.e) somehow transfer knowledge from an Alpha Fold-like model to a model which can map images to a 3D structure? Also suggest ways in which this can be done.(A technical answer is not necessarily required)

**TIP**

Deep Learning was invented to mimic how a neuron / human learns (to a certain degree). Keep this in mind while answering the questions above. Your answers need not be technically accurate (but it would be appreciated) and can be loosely worded, but they **MUST** have some intuition backing them.

In case of any doubts feel free to contact any of the Group Admins in the **3D Reconstruction** whatsapp group.

HAPPY SOLVING!!!