

Setup process for using RibbonFold:

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Note: All the codes are to be written in Linux terminal or Ubuntu for Windows.

Github: <https://github.com/Mingchenchen/RibbonFold>

1. Update and upgrade existing packages:

- `~$ sudo apt update && sudo apt upgrade -y`

2. Installing packages:

- `~$ sudo apt install -y python3 python3-pip python3-venv git wget`
python3 and python3-pip are needed to install further dependencies. Python3-venv is needed for created isolated environments.

3. Clone the RibbonFold repository from Github:

- `~$ ls`
- `~$ cd #directory of choice`
- `~$ git clone https://github.com/Mingchenchen/RibbonFold.git`
- `~$ cd RibbonFold`

4. Creating a virtual environment for RibbonFold:

- `~$ conda create -n ribbon_env python=3.9`
This is a conda based setup that requires NVIDIA GPU support.
If running only on CPU, change the following:
`~$ pip install torch torchvision torchaudio --index-url https://download.pytorch.org/whl/cpu`
`~$ pip install tensorflow-cpu==2.6.0`
Then, modify inference.py - device = torch.device("cpu")
- `~$ conda activate ribbon_env`
- `~$ conda deactivate` *## if you want to deactivate the env*

5. Installing CUDA and Python dependencies:

- `~$ conda install -y cudatoolkit=11.8 -c nvidia`
- `~$ pip install torch==2.1.0+cu118 torchvision==0.16.0+cu118 torchaudio==2.1.0+cu118 -f https://download.pytorch.org/whl/torch_stable.html`
- `~$ ls`
- `~$ pip install torchtyping==0.1.4 funtorch tensorflow-cpu==2.6.0 tensorflow-estimator==2.14.0`
- `~$ pip install pandas==1.3.5 scipy==1.5.4 biopython dm-tree treelib tqdm ml_collections pytz python-dateutil contextlib2 PyYAML --no-deps`
- `~$ pip install protobuf==3.19.6`

6. Download the model weights:

- `~$ wget https://zenodo.org/records/15128410/files/model_checkpoints.tar.gz?download=1`
Rename the file to "model_checkpoints.tar.gz"
- `~$ mkdir -p ./ckpt`
- `~$ tar -xvzf model_checkpoints.tar.gz -C ./ckpt`

7. Running RibbonFold:

Prepare the MSA feature file:

- You'll have to make your own MSA file in A3M format (.a3m) from AlphaFold2. You also have to clean and process the MSA file for process_msa_file.py to run. Here's a detailed instruction on how to do so:
 - a. **Generate the structure module using AlphaFold2. Parameters used:**
 - num_relax: 5
 - template_mode: pdb100
 - msa_mode: mmseqs2_uniref_env
 - pair_mode: unpaired_paired
 - num_recycles: 48 (can lower as well)
 - dpi: 600 (if you want to save the structures)
 - b. **Download the results**
 - c. **Extract the msa file (.A3M) file and run a custom python code, "clean_msa.py"**
 - This code trims the msa file to a accessible file for RibbonFold. You can find this code in my Signals LNB or Github (<https://github.com/APaul26>).
- Once done, run these commands. Here, I'm using the example provided (5oqv – Aß(1-42))
- `~$ python process_msa_file.py --input_fasta ./examples/5oqv.fasta --msa_file ./examples/5oqv_msa.a3m --output ./examples/5oqv_msa.pkl.gz`

this preprocess the MSA features from an AlphaFold2 msa file. A pkl.gz file will be generated, and this file should be passed through the following inference script.

update the locations of the fasta file and alignment file based on your preference

Run inference.py:

- **Sample code, modify the script and run:**

```
~$ CHECKPOINT_PATH="./ckpt/model_ckpt_001.pt"
INPUT_PKL_FILE="./examples/5oqv_msa.pkl.gz"
OUTPUT_DIR="./results/"
ROUNDS=10
python inference.py \
--checkpoint ${CHECKPOINT_PATH} \
--input_pkl ${INPUT_PKL_FILE} \
--ribbon_name 5oqv \
--output_dir ${OUTPUT_DIR} \
--rounds ${ROUNDS} \
--use_dropout true \
--use_init_structure true
```
- **Test code for alpha_synuclein: ### changed the no. of chains to 3 to account for memory**

```
~$ CHECKPOINT_PATH="./ckpt/model_ckpt_001.pt"
INPUT_PKL_FILE="./test/SYUA_msa.pkl.gz"
OUTPUT_DIR="./test/"
ROUNDS=3
python inference_test.py \ ### Custom modified code
--checkpoint ${CHECKPOINT_PATH} \
--input_pkl ${INPUT_PKL_FILE} \
--ribbon_name SYUA \
--output_dir ${OUTPUT_DIR} \
--rounds ${ROUNDS} \
--use_dropout true \
--use_init_structure true
```