AlphaFold 3

`/fs00/software/alphafold/3.0.0/AlphaFold-v3.0.0.sif`

0. ????

alphafold3 Google DeepMind json

- data pipeline:

  (multi-sequence alginment, msa) (templates)

  json
- inference: msa templates json mmcif

  confidence score

github apptainer alphafold3

——

term of use

Google DeepMind

1. ????

```
path_to_af3db="/fsb/data/alphafold/3"
path_to_af3container="/fs00/software/alphafold/3.0.0/AlphaFold-v3.0.0.sif "

io_dir=</path/to/your/input/and/output>
weights_dir=<path/to/directory/containing/your/af3-weights>

RUN_ALPHAFOLD="apptainer run --nv --bind
```

```
${path_to_af3db}:/databases,${io_dir}:/host_iopath,${weights_dir}:/af3_weights
${path_to_af3container} python run_alphafold.py"
```

□□ `${path_to_af3db}`□□□□ alphafold3□□□□□□ `${io_dir}`
□□□□□□□□□□□□□□□□□□□□ `${weights_dir}`□□□□□□ alphafold3□□□□□□□□□
`run_alphafold.py`□ □□ github□ □□□□□□□□□□□□□□□□□□□□□□□□□□□□□□

□□□□□□ (□□□□□□)

```
${RUN_ALPHAFOLD} --help
```

□□□□□ `input.json`□□ `${io_dir}`□□□□□□□□□□ alphafold3□□□□□□□□□□□□

```
${RUN_ALPHAFOLD} --db_dir=/databases/ --model_dir=/af3_weights/ \
  --json_path=/host_iopath/input.json --output_dir=/host_iopath/
```

□□□□□ `input.json`□□ name□□□□□ `${io_dir}`□□□□□□□□□ data pipeline□□□□□□ json
□□□□□□□□□□ confidence score□□□□□□□□□□□□□□□□ log□□□□ stderr□□ (□□
python logging□□□□□)□□□□□□□□□□□□□□□□□□□□□□ input documentation□ output
documentation□

2. ????data pipeline?inference

□□□□□□□□□□□□□ data pipeline□ inference□□□□□□ data pipeline□□□ cpu
□□□□□□□□□□□ gpu□□□□□□□□ gpu□□□□□□□□□□□□□□□□□ gpu□□□□□□□□
□□□□ **cpu**□□□□□ **data pipeline**□□□□□□□ **(**□□□□□□ **json)** □□□□□□□ **gpu**
□□□□□□□□□ □

□□□□□□□□□□□ bool□□□□□□ `--run_data_pipeline`□ `--run_inference`
□□□□□□□□□□□□□□□□□□□□ True.

□□□□□□□□ :

- data pipeline (cpu job)

```
${RUN_ALPHAFOLD} --db_dir=/databases/ --model_dir=/af3_weights/ \
  --json_path=/host_iopath/input.json --output_dir=/host_iopath/ \
  --run_inference=False
```

- inference (gpu job)

```
${RUN_ALPHAFOLD} --db_dir=/databases/ --model_dir=/af3_weights/ \
  --json_path=/host_iopath/input.json --output_dir=/host_iopath/ \
  --run_data_pipeline=False
```

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3. ?????????

□□□□□□□□□□□□□□□□□□□□□□□□□□□□ `${RUN_ALPHAFOLD} --help`□□□□□□ `run_alphafold.py`□□□□□□□□ 3□□□□□□

- `--input_dir`□ `--json_path`□□□□□□□□□□□□□□□□□□□□□□□□□□□□ input_dir □□□□□□ input_dir□□□□□ json□□□□□□□□□□□□
- `--jackhmmer_n_cpu`□ `--nhmmer_n_cpu`□□□□□□□□□□ cpu cores□□□□□
- □□□□□□□□□□□□□ random seed□□□□□□□□□□□□ alphafold3□ random seed □□□□□□□□□□□□□□□ input.json□

4. ?????????????

data pipeline□□□□□□□□ inference□□□□ gpu□□□□□□□□□□□□□□□□

- 2PV7□□□□□□ homomer□□□□□ 298
- 1AKE□□□□□□ homomer□□□□□ 214

□□□ 83a100ib□ 734090d□□□□□□□□□□□□□□□□ A100□ (memory 40 G) □□□ 4090d (memory 24 G) □□□□□ inference. □□□ 722080tiib□ 72rtxib□□□□□□□□ . □□ GPU □□□□□□□□□□□□ performance documentation□□□□□□□□□□ alphafold3□ A100(80G), A100(40 G)□ H100□□□□□□□□□□□□□□□□ 4090□□□□□□□□□□□□□□□□□□□□□□□□

□□□ data pipeline□ inference□□□□□□□□□

- □□ 8 cpu cores□□□□□ 300□□□□□□□ msa□ templates□□□□□ 1.5-2 h□ □□ □□□ msa□□□□□□□□□□□□□□□□ templates□□□ 10 s□□□□□□□□□□□□□□
- □□□□□□□□ alphafold3□□□ 5□□□□□□□□□□□□□□□□□□□□□□□□□□□□ 100 s□□□ inference□□□□□□□□□□□□□□

□□ performance□□□□□□□ performance documentation□

5. ?????????

□□ 2PV7□□□□□□□□□□□□□□ RMSD=4.410 (□□ : Angstrom□□□)□ □□□□□□□□□□□□□□□□ A:B□ -□□ A:B□□ RMSD□ 4□ RMSD□□□□ 3.012, 2.759, 2.971, 2.740. □□□□□ alphafold3□□□□□□□ alphafold2. □□□ 2□ subunits□□□□□□□□□□ DockQ □□□ 0.499>0.23□□□□□ docking□□□

1AKE□□□□□□□□□□□□□□□□□ 1AKE□□□□ RMSD=18.176□□ 4AKE□□□□ RMSD=26.791 □□□□□□□ alphafold2-multimer□ subunits□ DockQ=0.019<<0.23 □□□□□□□□□□□□□□□□□□□□ Alphafold3□□□□□□□□□□□□□□□□□□□□ 4090d□ A100□□□□□□□□□□

> “ dockQ (Mirabello & Wallner, 2024, Bioinformatics) □□□□□□□□□ subunits □□□□□□□□□□□□□□□□□□□□ 0-1□□□ <0.23□□□□□ >0.8□□□□□

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