GEFormerV1.0 usermannual.pdf

1. Download the source code and sample data of GEFormer engineering project:

git clone https://github.com/Deep-Breeding/GEFormer

Or download from Baidu Netdisk:

Link: https://pan.baidu.com/s/1HrJSrV_tPrsqmllEHEmYqA

Extraction code: 1234

2. GEFormer Environment configuration

```
First, install: Anaconda (https://www.anaconda.com/)
```

Install environment command:

conda create -n GEFormer python=3.8 // Create GEFormer virtual environment conda activate GEFormer // Create GEFormer virtual environment

cd GEFomer

pip install -r requirements.txt // The dependency packages required for installing

GEformer

3. Input data file

(1) Genotype file: geno.csv

(2) Phenotype file: phe.csv

(3) Environment file: env.csv

(4) Data partitioning: CVF.csv

4. The model training of GEFormer

Parameters:

```
--geno_path // Genotype file path--pheno_path // Phenotype file path--pheno_name // Phenotype name--env path // Environment file path
```

--CVF path // Set up training and validation sets

--model path // Output file path

--device //Runing device (CPU or GPU)-- optuna // hyperparameter optimization

The following are optional parameters:

```
-- optuna epoch // Number of tuning
```

--batch //batch size
--lr // learn reating
--drop_out //drop put
--depth //feature depth
--neurons1 // neurons number 1
--neurons2 // neurons number 2

The example of training model:

python run_train.py --geno_path ./data/geno.csv --pheno_path ./data/phe.csv --pheno_name PH --env_path ./data/env.csv --CVF_path ./data/CVF.csv --model_path ./model --device cpu --optuna True

python run_train.py --geno_path ./data/geno.csv --pheno_path ./data/phe.csv --pheno_name PH --env_path ./data/env.csv --CVF_path ./data/CVF.csv --model_path ./model --device cpu --optuna False

Output:

After training, the Pearson correlation coefficient between the predicted values and the true values is written in the log file, as shown as the following:

Pearson = (0.71, 0.0030)

The value is the Pearson correlation coefficient (0.71) and the second number is the P-value (0.0030).