DNNGP User Manual

# DNNGP, a deep neural network-based method for genomic prediction using multi-omics data in plants

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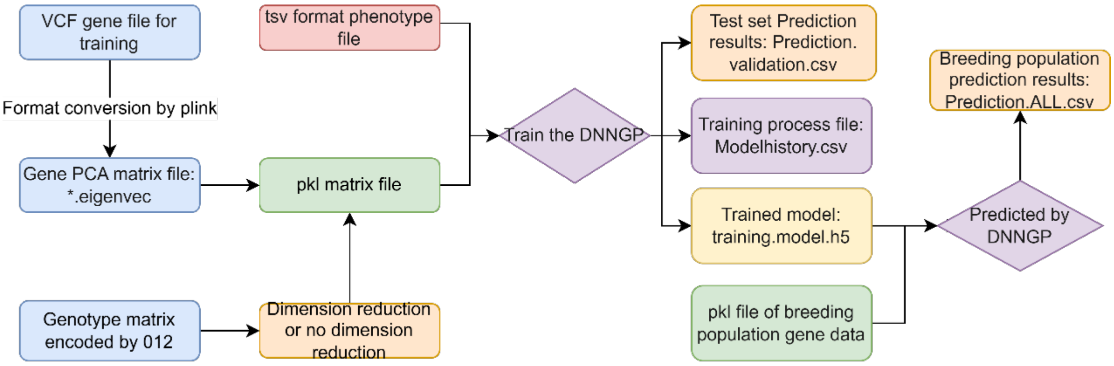
# Contents

## 1. Overview of the DNNGP project

DNNGP is a genome-wide prediction model based on deep learning theory, which aims to predict plant and animal phenotypes using genome-wide markers. In addition, DNNGP can be used for multiomics data prediction in plants and animals. This model mainly uses Python 3.9.16 and TensorFlow 2.6.0 writes. The training and prediction process of DNNGP is as follows:



### 1.1 Project address: https://github.com/AIBreeding/DNNGP

### 1.2 File directory structure

```
DNNGP:
│  double_click_me_first.bat
│  Tsv2Pkl.exe
│  Start_DNNGP.bat
│  CN 使用说明.pdf
│  EN usermanual.pdf
│  requirements.txt
│
├─Input_files
│      wheat1.tsv
│      wheat599_pc95.pkl
│      wheat599_pc95.tsv
│
├─Output_files
│      Modelhistory.csv
│      Prediction.ALL.csv
│      Prediction.validation.csv
│      training.model.h5
│
└─Scripts
        config_dnngp.cp39-win_amd64.pyd
        D.ico
```

dnngp.cp39-win_amd64.pyd
DNNGP.exe
dnngp_runner.py
environment.yaml
Pre-Batch_run.py
Pre_config_dnngp.cp39-win_amd64.pyd
Pre_dnngp.cp39-win_amd64.pyd
Pre_runner.py
Train-Batch_run.py

The file mainly contains the following five parts:

**(1) GUI file**

This part of the document mainly includes three files, namely: double_click_me_first.bat, Tsv2Pkl.exe, Start_DNNGP.bat. Under Windows Platform, double-click double_click_me_first.bat to build the environment. Double-click tsv2pkl.exe can convert tsv files to pkl files according to GUI prompts. Then double-click Start_DNNGP.bat can train and predict the model.

**(2) requirements.txt / environment.yaml**

For environment construction, environment configuration required packages and their versions.

**(3) Input_files**

In this directory are sample files for input data.

**(4) Scripts**

This directory contains the scripts needed to train the model and predict the scripts.

Train the model: After completion, the terminal displays the model prediction results to evaluate the training effect. Three files are output at the same time: the trained model (training.model.h5) and the validation set prediction (Prediction.validation.csv), as well as the values of each epoch in the training process (Modelhistory.csv） .

Model prediction: By reading the model trained in the previous step, the phenotype of the breeding population is predicted and the predicted value of all individuals is output (Prediction.ALL.csv).

**(5) Output_files**

This directory contains the output files after the DNNGP method executes the input sample files.

The use of models should follow the following order: (1) set up the running environment (2) prepare data, (3) train the model, and (4) use the trained model to make predictions

## 2. Data preparation

### Genotypic data processing based on Plink2 software

```
./plink2 --threads 30 --vcf *.vcf --pca 10 --out PCA10
```

**--threads 30** uses 30 threads

**--vcf** *.vcf read vcf files

**--pca 10** takes PC1-PC10 (number of samples ≤ can be set≤8000).

**--out pca10** output file name is pca10

If a non-numeric chromosome number is present, the --allow-extra-chr parameter needs to be added

```
./plink2 --allow-extra-chr --threads 30 --vcf *.vcf --pca 10 --out PCA10
```

The result is two files with the suffixes .eigenval and .eigenvec, which show the weight of each PC, the weight/gravity of each PC, and the degree of interpretation for each PC. eigenval is the PCA matrix we need to use.

**Tips:**

(1) The above commands apply to Powershell terminals under Windows platform and Linux and Mac terminals. If you use the cmd terminal under the Windows platform, please replace ./plink2 with plink2.

(2) If PCA is used to convert genetic data, it is necessary to first combine the data of the breeding population and the training population and then perform PCA analysis, and then separate the two after obtaining the PCA matrix.

## 3. DNNGP environment setup

(1) Download project address: https://github.com/AIBreeding/DNNGP

(2) To run DNNGP, you first need to set up the operating environment:

Install Miniconda (https://docs.conda.io/en/latest/miniconda.html) first and add it to the system environment. (Miniconda can be checked when installing it, which is required to use the GUI.)

Under the Windows platform, you can directly double-click **Double_click_me_first.bat** file to build an environment with one click.

If the one-click environment failure to build, use the following command to build the running environment:

- `conda create -n DNNGP3 python=3.9.16`
- `conda activates DNNGP3`
- `cd DNNGP`
- `conda installation --yes --file requirements .txt`
- `conda Install -c nvidia cuda-nvcc`
- `pip installation framework reproducibility==0.4.0`

**4. Enter the data file**

After the environment is set up, you need to prepare various data files according to the sample data format, which is located in the following directory:

`.. /DNNGP/input_file/`

It contains the following four files:

- **wheat1.tsv:** A tab-delimited phenotypic data file.
- **wheat599_pc95.tsv:** A tab-delimited principal component matrix file.
- **wheat599_pc95.pkl:** A principal component matrix file that the model can read.
- **tsv2pkl.py:** Convert the script from TSV to PKL file**.**

Among them, wheat599_pc95.pkl files can be run by **wheat599_pc95.tsv** files by **running tsv2pkl.py (tsv2pkl.exe)** converted. Eigenval files generated by plink2 can also be directly converted via tsv2pkl.py. The conversion method is as follows

After opening the tsv2pkl.py, modify the file path in the fifth line of inpath and the sixth line of outpath to your own file path. Then run tsv2pkl.py in DNNGP3 environment which was created by conda.

```
python tsv2pkl.py
```

Under the Windows platform, you can double-click the tsv2Pkl.exe program in the DNNGP directory to use the GUI to complete the file format conversion.

The phenotypic data text file formats are as follows:

| ID | env1 |
|---|---|
| M1 | 1.67162948 |
| M2 | -0.25270276 |
| M3 | 0.341815127 |
| M4 | 0.785439489 |
| M5 | 0.998317613 |
| M6 | 2.336096876 |
| M7 | 0.617410817 |

The principal component matrix TSV file format is as follows:

| ID | PC1 | PC2 | PC3 | … |
|---|---|---|---|---|
| M1 | 7.0408269 | 2.053877771 | -6.161150675 | … |
| M2 | 5.924749016 | 1.137903031 | 1.132296531 | … |
| M3 | 5.953045926 | 1.082444715 | 1.139961515 | … |

### 5. DNNGP model training

This section requires two inputs, the principal component matrix file prepared in the previous step and the phenotypic data file. For the specific format, please refer to the previous section.

**Parameter description:**

**--batch_size** the sample size called to train the model

**--lr** initial learning rate

**--epoch** number of iterations

**--dropout1** first feature discard (to prevent overfitting).

**--dropout2** second feature discard (to prevent overfitting).

**--patience** no improvement reduces the learning rate threshold (when the model reaches the threshold without improvement, it automatically decreases the learning rate).

**--seed** random seed

**--cv** sets the number of cross-validation folds

**--part** Select a piece of cross-validation data as the validation set

**--earlystopping** if the training effect does not improve, the training threshold will be stopped (when the model reaches the threshold without improving the number of times, the training will be automatically stopped and the best parameter will be saved)

**--snp** principal component matrix file path

**--pheno** phenotypic data file path

**--output** output directory

The above parameters, except --snp、-- pheno, and --output, are numeric.

**Example command to go into the Scripts directory:**

```
cd Scripts
```

**Train model example command:**

```
python dnngp_runner.py --batch_size 28 --lr 0.001 --epoch 100 --dropout1 0.5 --dropout2 0.3 --patience 5 --seed 123 --cv10 --part 1 --earlystopping 10 --snp "../input_files/wheat599_pc95.pkl" --pheno "../input_files/wheat1.tsv" --output "/Your_path/"
```

Under the Windows platform, you can directly double-click the Start_DNNGP.bat in the DNNGP directory to start the GUI and follow the GUI prompts. The right side of the GUI outputs standard commands and the training process.

## Train the model output file

After the training is completed, three output files will be generated in the specified output directory, namely:

**Prediction.validation.csv**: The prediction result of the DNNGP model on the validation set (the ordinal number of the first column represents the name of the predicted value individual in the original data set).

**training.model.h5**: The trained model file is used for the next step of phenotypic trait prediction in the breeding population.

**Modelhistory.csv**: records the changes in various values during the training process.

After the training is complete, the terminal displays the Pearson correlation coefficient between the predicted and true values, as shown below:

```
'Corrobs vs pred =',(0.582, 0.001)
```

The first number is the correlation coefficient (0.582) and the second number is the *p*-value (0.001).

### 6. Use the trained model to make predictions on the test data

After getting the trained model file, we want to predict the phenotypic traits of the test data set (i.e., the breeding population). This part requires two input files, one is the model file generated by the previous training step, that is, training.model.h5, and the second is the breeding population principal component matrix file (*.pkl). The format is the same as the one used to train the model in the previous step.

**Predict the breeding population phenotypic traits example command:**

```
python Pre_runner.py --Model "/Your_path/training.model.h5" --SNP "/Your_path/wheat599_pc95.pkl" --output "/Your_path/"
```

**Description of DNNGP prediction parameters:**

**--Model:** the path to the .h5 model file generated when training the model

**--SNP:** the genetic data file path of the dataset to be predicted

**--output:** the directory where the prediction result file is generated

Under the Windows platform, you can double-click the Start_DNNGP.bat in the DNNGP directory to launch the GUI interface, and then follow the GUI prompts.

## Model prediction output file

After the DNNGP model completes the prediction, the result file **Prediction.ALL.csv** is generated in the specified directory, which is the phenotypic trait prediction results of all individuals in the breeding population.

### 7. Special Instructions:

The Script directory contains the name Train-Batch_run.py and Pre-Batch_run.py's Python script can be tested in batches, where the former is a batch script for training a model, and the latter is a batch script for model prediction.

**Run the example command:**

`Python training Batch_run. py` or `python pre-Batch_run: py`