Tutorial of the OmniGS-R (v1.0)

Genomic Selection Pipeline Using R Packages

This tutorial provides step-by-step instructions for running three different use cases of OmniGS-R: Cross-Validation, prediction with test phenotype and prediction without test phenotype. It assumes you have installed the pipeline and its dependencies correctly.

Pipeline Setup and example Data

1. Ensure R and all required packages are installed as listed in the README.

2. Clone the repository and enter the example folder:

```
zhengc@biocomp-0-1.local:CZ_project>git clone https://github.com/ORDC-Crop-Bioinformatics/OmniGS-R.git
Cloning into 'OmniGS-R'...
remote: Enumerating objects: 178, done.
remote: Counting objects: 100% (178/178), done.
remote: Compressing objects: 100% (159/159), done.
remote: Total 178 (delta 62), reused 109 (delta 18), pack-reused 0 (from 0)
Receiving objects: 100% (178/178), 15.31 MiB | 11.86 MiB/s, done.
Resolving deltas: 100% (62/62), done.
zhengc@biocomp-0-1.local:CZ_project>cd OmniGS-R/example/
```

3. Review the example genotype, phenotype, and configuration files.

Cross-Validation

1. Input data: example/inputFile/train_genotype.vcf and example/inputFile/train_phenotype.txt
2. Configure Cross-Validation
   Edit the configuration file (e.g., gs_parameters_example_CV.config) to define cross-validation parameters. Specify the GS_Mode, number of replicates, input genotype and phenotype file, and output directory.

   As the first step, you can keep the same parameters as the file gs_example_CV.config. **But you MUST change the RScriptPath to point to your own Rscript in the configuration file.**

   # R path
   RScriptPath = your/Rscript

3. Run Cross-Validation
   Run the pipeline script using the example configuration:

   ./OmniGS-R_run_example_CV.sh

```
zhengc@biocomp-0-1.local:example>cat OmniGS-R_run_example_CV.sh
java -version
R --version

java -Xmx2000g -jar ../pipeline/OmniGS-R/OmniGS-R.jar  gs_parameters_example_CV.config
zhengc@biocomp-0-1.local:example>
zhengc@biocomp-0-1.local:example>./OmniGS-R_run_example_CV.sh
openjdk version "24.0.2-internal" 2025-07-15
OpenJDK Runtime Environment (build 24.0.2-internal-adhoc.conda.src)
OpenJDK 64-Bit Server VM (build 24.0.2-internal-adhoc.conda.src, mixed mode, sharing)
R version 3.5.1 (2018-07-02) -- "Feather Spray"
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Platform: x86_64-pc-linux-gnu (64-bit)

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Check configuration...
✓ All configuration parameters validated successfully

[Log] Writing console output to: outputFile_CV/gs_68687466975805498.log
```

4. Results and output Figures

-- The output folder (outputFile_CV) contains detailed cross validation results (all_CV_results.txt) and summary statistics (CV_summary_statistics.csv) for all the replications and folds.

```
zhengc@biocomp-0-1.local:example>ls -l outputFile_CV/
total 344
-rwxrwxr-x 1 zhengc domain users 21315 Oct 24 12:01 all_CV_results.txt
-rwxrwxr-x 1 zhengc domain users   479 Oct 24 12:01 CV_summary_statistics.csv
-rwxrwxr-x 1 zhengc domain users 14760 Oct 24 12:01 gs_68687466975805498.log
drwxrwxr-x 2 zhengc domain users   389 Oct 24 11:00 intermediate_data
drwxrwxr-x 2 zhengc domain users    94 Oct 24 11:00 pheno_data
drwxrwxr-x 2 zhengc domain users    48 Oct 24 12:01 plots
drwxrwxr-x 2 zhengc domain users     0 Oct 24 11:00 trait_predictions
```

-- The distribution of the phenotypic values (pheno_data/YLD_hist.png)

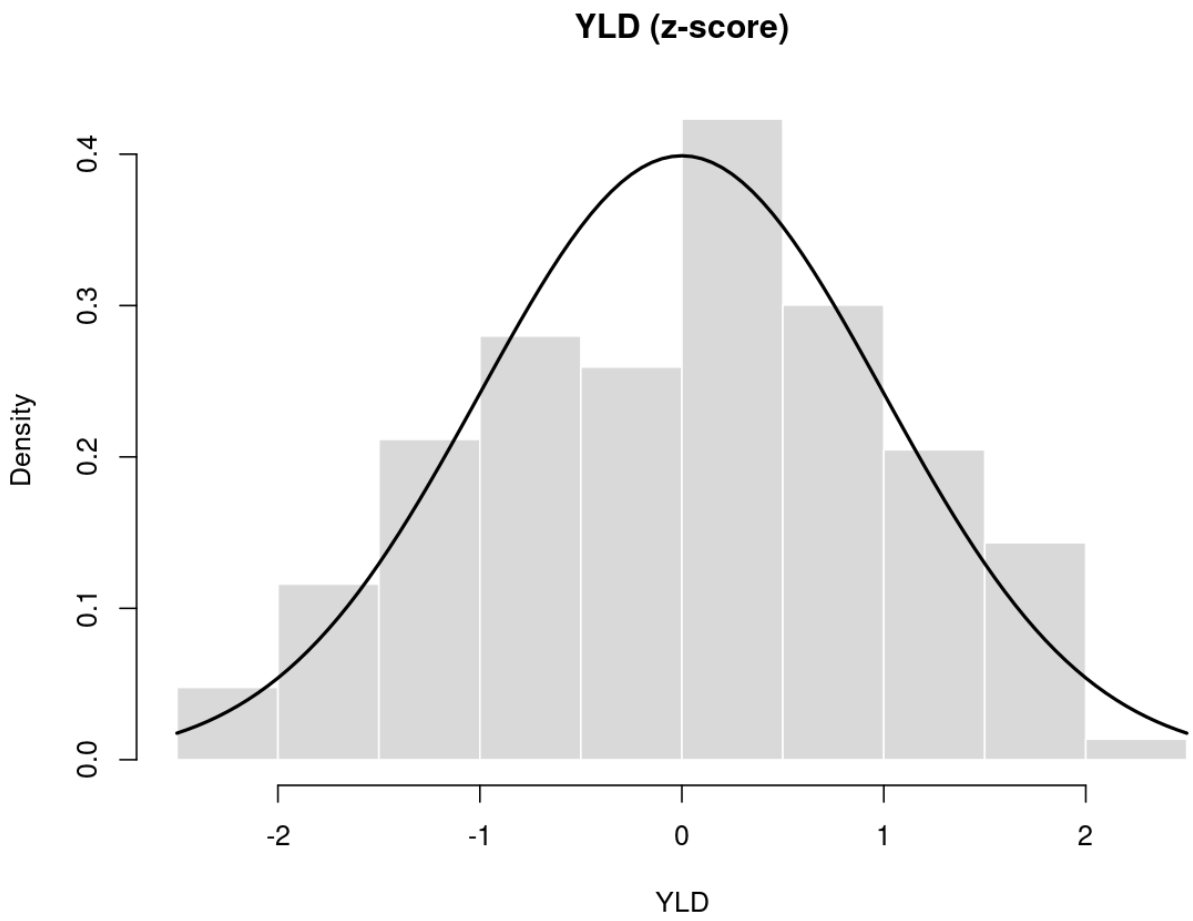

Figure 1: Distribution of the phenotypic (YLD) value

-- Summary of the cross validation results for each model (plots/SNP_model_trait_box_r_plot.png)

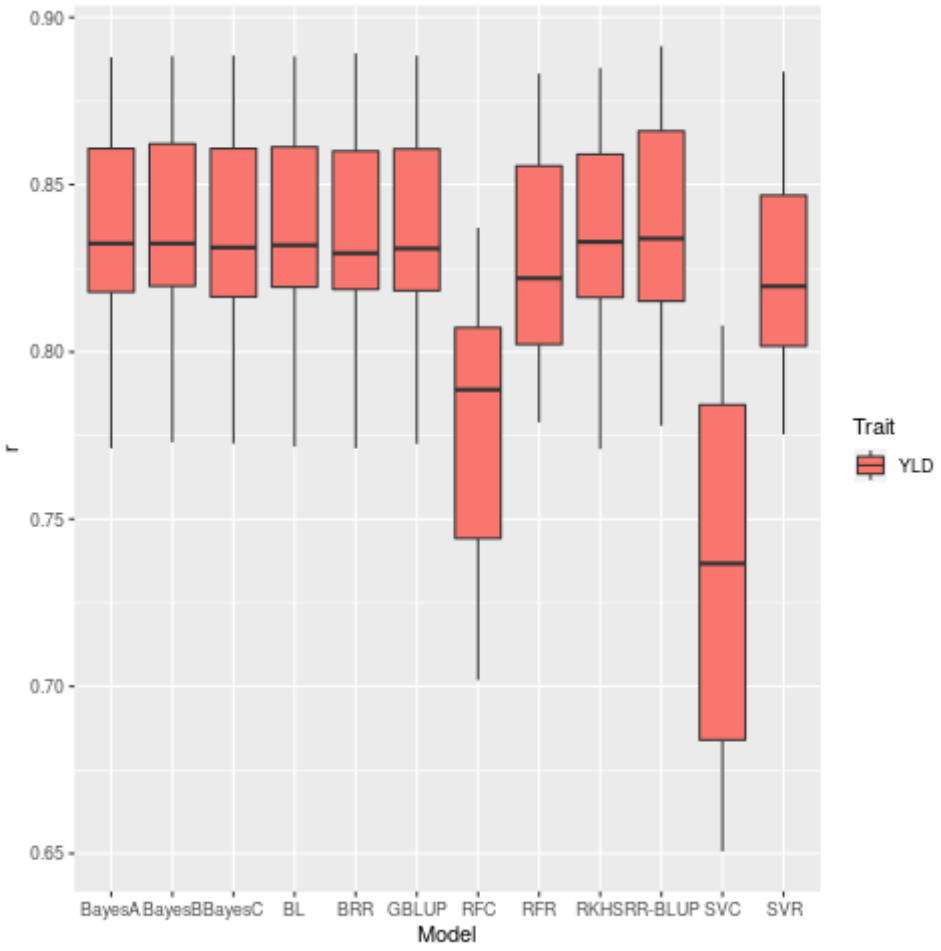

Figure 2: Summary of the cross validation results for each model.

Prediction with test phenotype data

1. Input data:

   example/inputFile/train_genotype.vcf and example/inputFile/train_phenotype.txt

   example/inputFile/test_genotype.vcf and example/inputFile/test_phenotype.txt

2. Configure prediction with known test Phenotype data
   Edit the configuration file (e.g., gs_parameters_example_prediction1.config) to define cross-validation parameters. Specify the GS_Mode, number of replicates, input genotype and phenotype file, and output directory.

   As the first step, you can keep the same parameters as the file gs_parameters_example_prediction1.config. **But you MUST change the RScriptPath to point to your own Rscript.**

   # R path

RScriptPath = your/Rscript

3. Run the pipeline script using the example configuration:

```
zhengc@biocomp-0-1.local:example>cat OmniGS-R_run_example_prediction1.sh
java -version
R --version

java -Xmx2000g -jar ../pipeline/OmniGS-R/OmniGS-R.jar  gs_parameters_example_prediction1.confi
zhengc@biocomp-0-1.local:example>
zhengc@biocomp-0-1.local:example>./OmniGS-R_run_example_prediction1.sh
openjdk version "24.0.2-internal" 2025-07-15
OpenJDK Runtime Environment (build 24.0.2-internal-adhoc.conda.src)
OpenJDK 64-Bit Server VM (build 24.0.2-internal-adhoc.conda.src, mixed mode, sharing)
R version 3.5.1 (2018-07-02) -- "Feather Spray"
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Platform: x86_64-pc-linux-gnu (64-bit)

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Check configuration...
✓ All configuration parameters validated successfully

[Log] Writing console output to: outputFile_prediction_with_test_pheno/gs_68692401536040151.lo

================================================================
OmniGS-R (1.0): GENOMIC SELECTION PIPELINE USING R PACKAGES
================================================================
```

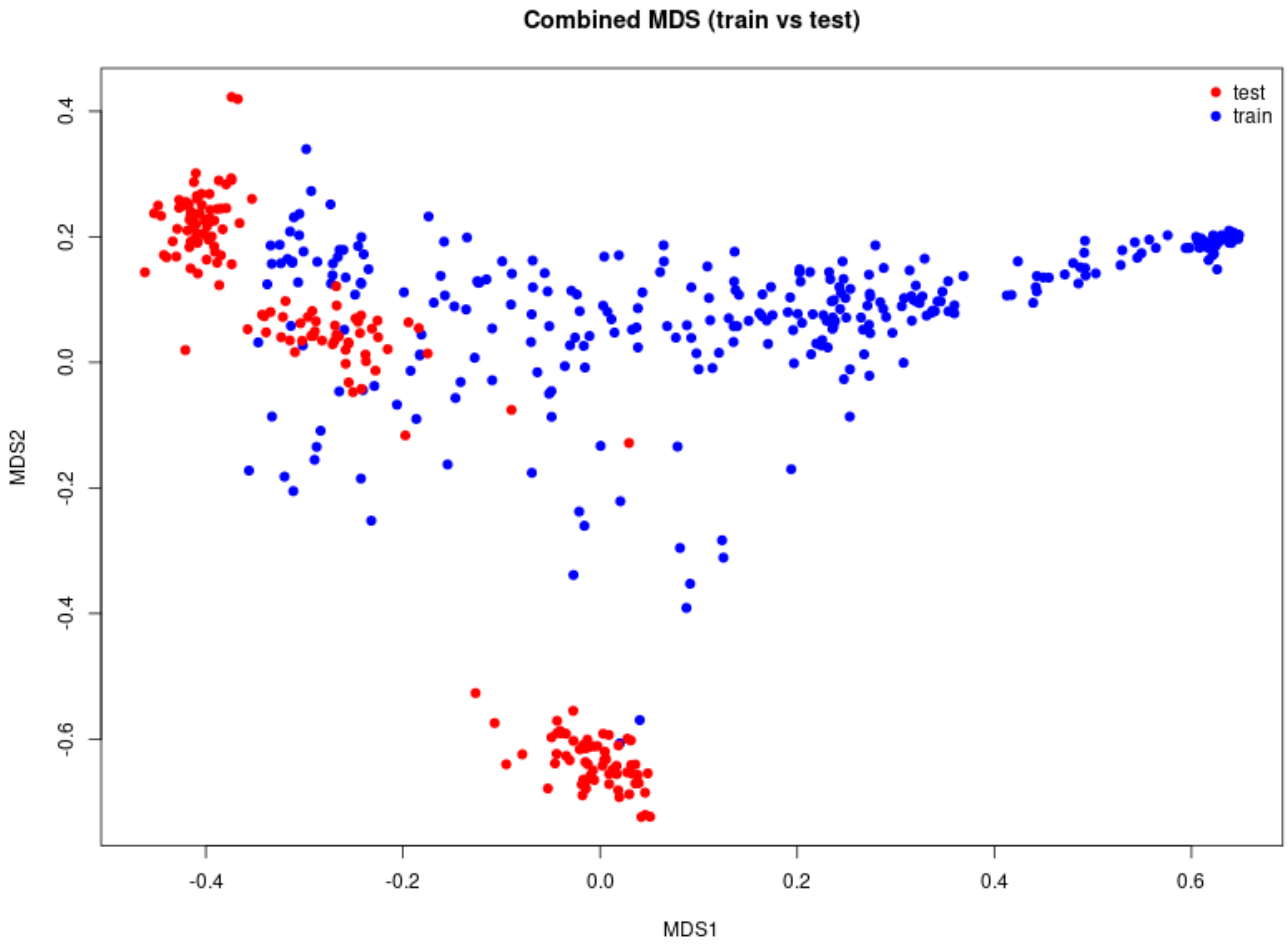
4. Results and output Figures.

   --The output folder (outputFile_prediction_with_test_pheno) contains detailed prediction results (prediction_detailed_results.txt)

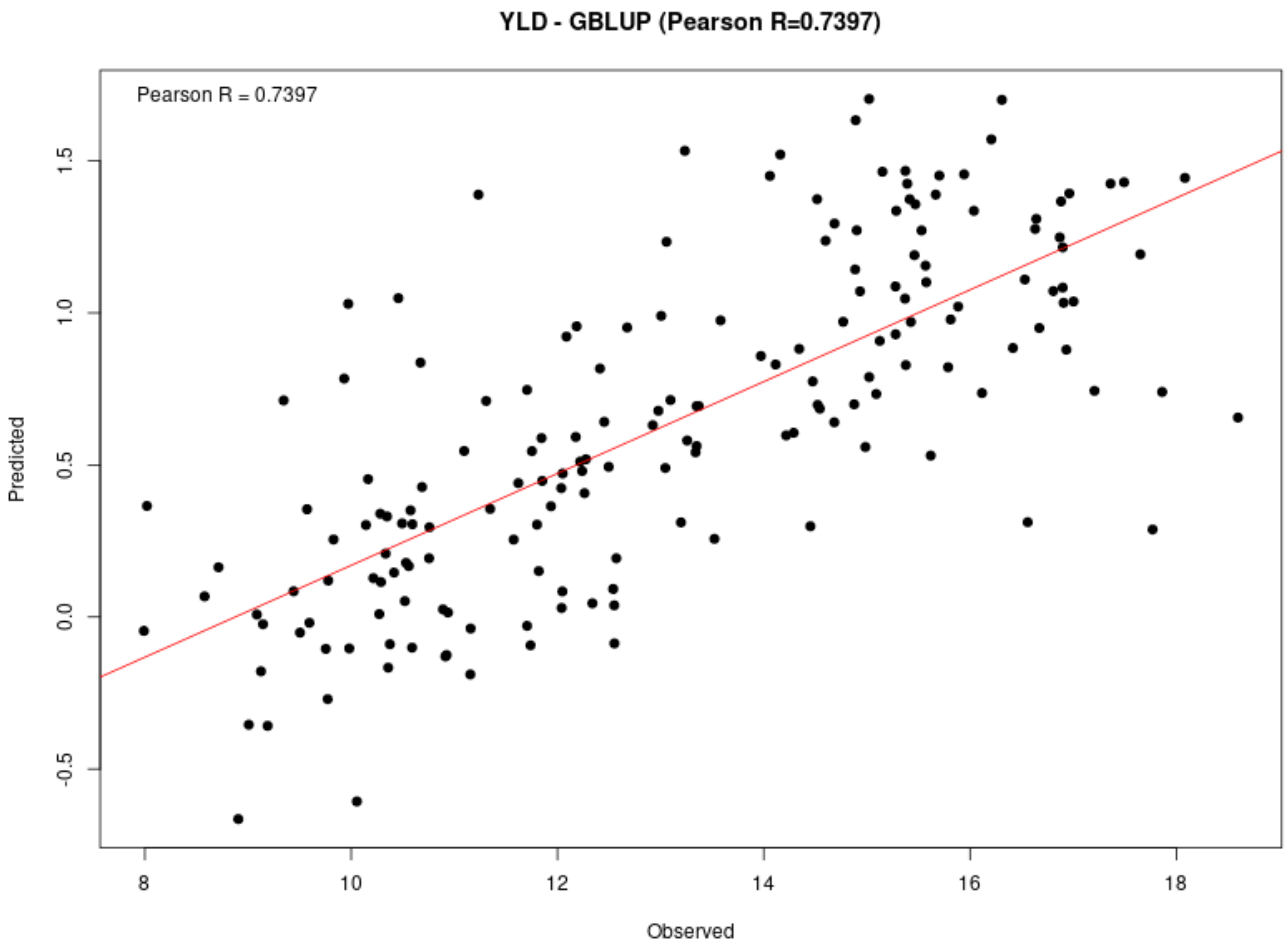
```
zhengc@biocomp-0-1.local:example>ls -l outputFile_prediction_with_test_pheno/
total 248
-rwxrwxr-x 1 zhengc domain users 8242 Oct 24 12:45 gs_68692401536040151.log
drwxrwxr-x 2 zhengc domain users  827 Oct 24 12:41 intermediate_data
drwxrwxr-x 2 zhengc domain users   94 Oct 24 12:41 pheno_data
drwxrwxr-x 2 zhengc domain users 1528 Oct 24 12:45 plots
-rwxrwxr-x 1 zhengc domain users  306 Oct 24 12:45 prediction_detailed_results.txt
drwxrwxr-x 2 zhengc domain users  632 Oct 24 12:45 trait_predictions
```

   - The predict values for phenotype value for test population are stored in the folder trait_predictions

   - Combined_mds.png



- Scattered plot between observed and predicted phenotypic values for test populations.



Prediction without test phenotype data

1. Input data:

   example/inputFile/train_genotype.vcf and example/inputFile/train_phenotype.txt

   example/inputFile/test_genotype.vcf

2. Configure prediction with known test Phenotype data
   Edit the configuration file (e.g., gs_parameters_example_prediction1.config) to define cross-validation parameters. Specify the GS_Mode, number of replicates, input genotype and phenotype file, and output directory.

   As the first step, you can keep the same parameters as the file gs_parameters_example_prediction1.config. **But you MUST change the RScriptPath to point to your own Rscript.**

   # R path
   RScriptPath = your/Rscript

3. Run the pipeline script using the example configuration:

```
zhengc@biocomp-0-1.local:example>cat OmniGS-R_run_example_prediction2.sh
java -version
R --version

java -Xmx2000g -jar ../pipeline/OmniGS-R/OmniGS-R.jar  gs_parameters_example_prediction2.config
zhengc@biocomp-0-1.local:example>./OmniGS-R_run_example_prediction2.sh
openjdk version "24.0.2-internal" 2025-07-15
OpenJDK Runtime Environment (build 24.0.2-internal-adhoc.conda.src)
OpenJDK 64-Bit Server VM (build 24.0.2-internal-adhoc.conda.src, mixed mode, sharing)
R version 3.5.1 (2018-07-02) -- "Feather Spray"
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For more information about these matters see
http://www.gnu.org/licenses/.


Check configuration...
✓ All configuration parameters validated successfully
```

4. results and output figures

all the result files are stored in the folder outputFile_prediction_no_test_pheno

```
zhengc@biocomp-0-1.local:example>ls -l outputFile_prediction_no_test_pheno/
total 224
-rwxrwxr-x 1 zhengc domain users 5605 Oct 24 13:12 gs_68693585733433887.log
drwxrwxr-x 2 zhengc domain users  827 Oct 24 13:01 intermediate_data
drwxrwxr-x 2 zhengc domain users   94 Oct 24 13:01 pheno_data
drwxrwxr-x 2 zhengc domain users  139 Oct 24 13:01 plots
-rwxrwxr-x 1 zhengc domain users  233 Oct 24 13:12 prediction_detailed_results.txt
drwxrwxr-x 2 zhengc domain users  632 Oct 24 13:12 trait_predictions
zhengc@biocomp-0-1.local:example>
```

The predict values for phenotype value for test population are stored in the folder trait_predictions