Random Forest Pipeline — [run_model.py] (Tutorial)

This guide explains what the script does, in what order, and why, and shows how to run it from the CLI for training and evaluation.

1) What this script is for

Train and/or evaluate **Random Forest** models on pre-made CSV folds, supporting:

- Model types: regression (reg), binary classification (bin), multi-class classification (mclass)
- Repeated K-fold cross-validation (e.g., 5 folds × 5 repeats)
- Multiple datasets indexed by scramble fraction (e.g., $\begin{bmatrix} 0.00 \end{bmatrix}$, $\begin{bmatrix} 0.25 \end{bmatrix}$, $\begin{bmatrix} 1.00 \end{bmatrix}$)

Note: The script **does not create folds**. It expects CSVs already split and named in a specific pattern (see §4).

2) Input data expectations

Each CSV must include:

- An ID column (default sequence , settable via --ref_id_col)
- A label column (default label, settable via --ref_label_col)
- Feature columns: all remaining columns are treated as numeric features.

The loader casts features to float32. Labels are cast to int for bin/mclass, else kept numeric for reg.

3) Directory & filename conventions

- --data_dir: where CSVs live (default: Data/)
 --model dir: where models are saved/loaded (default: Model/)
- --prefix : dataset prefix in filenames (default: gbsa)
- --model_type : reg | bin | mclass
- --scramble_fractions : one or more floats; used only in filenames

A scramble fraction f is formatted as $scr\{frac_str\}$ where $frac_str = f''\{f:.2f\}''.replace('.', 'p')$.

Expected CSV names:

- Training fold: {prefix}_{model_type}_scr{frac_str}_trn_{repeat}_{fold}.csv
- •Validation fold: {prefix}_{model_type}_scr{frac_str}_val_{repeat}_{fold}.csv
- Final test set: {prefix}_{model_type}_scr{frac_str}_tst_final.csv

Saved models:

```
• Model/rf_fold_{repeat}_{fold}_{model_type}_scr{frac_str}.pkl
```

Per-fold predictions (training mode):

```
• {output_file}_{model_type}_scr{frac_str}_rep{repeat}_fold{fold}.csv
```

Aggregated predictions (training mode):

```
• {output_file}_{model_type}_final_avg_scr{frac_str}.csv
```

Average metrics CSVs:

- Training: final_metrics_{model_type}_trn_scr{frac_str}.csv
- Test: final_metrics_{model_type}_tst_scr{frac_str}.csv

Prediction CSV schema:

```
Label,Predicted,True
<ID>,<model_output>,<ground_truth>
```

4) Script flow — step by step (what & why)

4.1 Parse CLI args

Reads all hyperparameters, file/directory settings, CV layout, and mode selection (--mode 0 train, --mode 1 evaluate).

4.2 Mode selection

- **Mode 0: training** → iterate fractions → repeats → folds; for each fold: load train/val, train RF, save model, evaluate on val, log metrics, write fold predictions. Aggregate all folds/repeats and write average metrics + averaged predictions.
- Mode 1: evaluation → iterate fractions; for each fraction: load final test CSV; for every saved model (repeat×fold), evaluate on the test set; save all predictions and average metrics.

4.3 Data loading (load_csv_data)

- Verifies that the file exists and contains --ref_id_col and --ref_label_col.
- Extracts **X** (feature matrix), **y** (targets), and **ids** (ID list). Feature dtypes are coerced to float32 for compactness and speed.

Why: Standardizes inputs for scikit-learn and keeps memory usage reasonable.

4.4 Build the Random Forest (build_random_forest)

Creates or with:

Why: Encapsulates hyperparameter handling and model type selection.

4.5 Fit & save (training mode)

For each fold:

- 1. Type cast labels to int for bin / mclass.
- 2. Fit the RF on training features/labels.
- 3. **Save** model to model_dir via joblib.dump.

Why: Store per-fold models so they can be reused for test-time evaluation or ensembling.

4.6 Evaluate (evaluate_model)

Computes metrics and emits row-level predictions. Evaluation differs by model type:

- Regression (``)
- Predict continuous values.
- Per-ID aggregation: average predictions and targets across duplicate IDs.
- Metrics: MSE, R², Pearson r.
- Also derives binary metrics (MCC, Accuracy) by thresholding at $\begin{bmatrix} 0.0 \end{bmatrix}$ if $\begin{bmatrix} --data_scale \ log \end{bmatrix}$, else $\begin{bmatrix} 1.0 \end{bmatrix}$.
- Binary (``)
- Predict class labels (0/1).
- Per-ID aggregation: majority vote of predictions and of targets.
- Metrics: MCC, Accuracy.
- Multi-class (``)
- Predict class probabilities.
- **Per-ID aggregation**: sum probabilities across rows per ID, take argmax for final class; target by majority vote.
- Metrics: MCC, Accuracy.

Row-level output is a list of tuples (ID, predicted, true) used to write per-fold CSVs.

Why per-ID aggregation? Some datasets provide multiple rows per ID (e.g., multiple windows/features). Aggregation yields a single label/prediction per unique entity.

4.7 Aggregate across folds & repeats (training mode)

- Metrics: average available metrics over all folds and repeats (NaNs ignored).
- **Predictions**: group per ID and **average or majority-vote** depending on task; save to {output_file}_{model_type}_final_avg_scr{frac_str}.csv }.

Why: Produces a stable estimate across CV runs and a single consolidated prediction per ID.

4.8 Evaluate all models on test (evaluation mode)

```
    For each fraction, load ..._tst_final.csv once.
    For every saved fold model, predict on the test set and log metrics.
    Save all per-model predictions to {output_file}_test_{model_type}
    _scr{frac_str}.csv and write averaged test metrics to final_metrics_{model_type}
    _tst_scr{frac_str}.csv.
```

Why: Ensures test results reflect all trained models, not just one fold.

5) CLI usage — common recipes

5.1 Quick start: regression, 5×5 CV, no scrambling

```
python run_model.py \
    --mode 0 \
    --model_type reg \
    --prefix gbsa \
    --data_dir Data \
    --model_dir Model \
    --output_file preds \
    --kfold 5 \
    --num_repeats 5 \
    --scramble_fractions 0.0
```

Then evaluate on test:

```
python run_model.py \
    --mode 1 \
    --model_type reg \
    --prefix gbsa \
    --data_dir Data \
    --model_dir Model \
    --output_file preds \
    --kfold 5 \
```

```
--num_repeats 5 \
--scramble_fractions 0.0
```

5.2 Binary classification with custom RF hyperparams

```
python run_model.py \
  --mode 0 \
  --model_type bin \
  --prefix gbsa \
  --data_dir Data \
  --model_dir Model \
  --output_file preds_bin \
  --kfold 5 \
  --num_repeats 3 \
  --scramble_fractions 0.0 0.25 1.0 \
  --n_estimators 500 \
  --max_depth 12 \
  --max_features 0.5 \
  --min_samples_split 4 \
  --min_samples_leaf 2 \
  --random_state 1337
```

5.3 Multi-class with non-log scale (affects reg threshold only)

```
python run_model.py \
    --mode 1 \
    --model_type mclass \
    --prefix gbsa \
    --data_dir Data \
    --model_dir Model \
    --output_file preds_mclass \
    --kfold 5 \
    --num_repeats 5 \
    --scramble_fractions 0.0
```

Note: --data_scale only alters the regression binary threshold (0.0 for log), 1.0 for nonlog). It has no effect for bin mclass.

6) Preparing your CSVs (naming checklist)

For each **scramble fraction** f and for **each** repeat and fold:

```
Training: {prefix}_{model_type}_scr{f}_trn_{repeat}_{fold}.csvValidation: {prefix}_{model_type}_scr{f}_val_{repeat}_{fold}.csv
```

For each **scramble fraction** f:

```
• Test: {prefix}_{model_type}_scr{f}_tst_final.csv}

Each CSV must include --ref_id_col and --ref_label_col. All other columns are features.
```

Scramble fraction is used **only** to select among multiple dataset variants. The script assumes these files were created upstream (e.g., label shuffling or feature scrambling).

7) Outputs you'll get

- Per-fold prediction CSVs (training mode) with Label, Predicted, True.
- Aggregated predictions across all folds/repeats (training mode).
- Average metrics CSV summarizing MSE/R²/Pearson (reg) or MCC/Accuracy (bin/mclass).
- Test-time predictions & metrics (evaluation mode) across all saved models.

8) Tips, tuning & pitfalls

- max_features: Accepts strings (auto), sqrt, log2) or numbers. Numeric ∈ (0,1] means a fraction of features per split; integer means an absolute count.
- Class balance: For bin / mclass , ensure folds are stratified upstream; RF handles imbalance but metrics can be misleading without good splits.
- **Random state:** Controls tree-wise randomness; for repeated K-fold, the **data splits** are determined by your CSVs, not by this seed.
- NaNs / Inf: Ensure no NaNs in features; scikit-learn RF does not support NaNs.
- Large feature sets: Consider reducing max_features and limiting max_depth to avoid overfitting and speed up training.

9) Reference: CLI arguments

```
--mode \{0,1\}
                                # 0=train, 1=evaluate
--model_type {reg,bin,mclass}
--model_obj MODEL_OBJ
                                # descriptor (not used in filenames)
--data_scale {log,nonlog}
                                # affects reg thresholding of binary metrics
--kfold K
                                # folds per repeat
--num_repeats R
                                # repeated K-fold count
--model_dir DIR
                                # where .pkl models go
--data_dir DIR
                                # where CSVs live
                                # prefix for prediction/metric outputs
--output_file PREFIX
--ref_id_col COL
                                # ID column in CSV (default: sequence)
                                # label column in CSV (default: label)
--ref_label_col COL
--n estimators N
--max_depth DEPTH|None
--max_features AUTO|SQRT|LOG2|FLOAT|INT
--min_samples_split N
--min samples leaf N
```

```
--random_state SEED
--prefix DATA_PREFIX  # dataset name stem in CSV filenames
--scramble_fractions F1 [F2 ...]
```

10) End-to-end example (train then evaluate)

```
# Train 5x5 CV regression models on three dataset variants
python run_model.py \
    --mode 0 --model_type reg --prefix gbsa \
    --data_dir Data --model_dir Model --output_file preds_reg \
    --kfold 5 --num_repeats 5 --scramble_fractions 0.0 0.25 1.0 \
    --n_estimators 300 --max_depth 20 --max_features 0.7 --random_state 42

# Evaluate all saved models on the corresponding test sets
python run_model.py \
    --mode 1 --model_type reg --prefix gbsa \
    --data_dir Data --model_dir Model --output_file preds_reg \
    --kfold 5 --num_repeats 5 --scramble_fractions 0.0 0.25 1.0
```

TL;DR

- Mode 0 (train): loads each train/val fold → trains RF → saves model → evaluates on val → aggregates metrics/predictions.
- Mode 1 (eval): loads test set → runs every saved model → aggregates predictions/metrics across folds and repeats.

You now have a reproducible RF pipeline with clear inputs/outputs and CLI recipes.