

# Package: spFW (via r-universe)

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**Type** Package

**Title** Hierarchical Spatial Finlay-Wilkinson Model

**Version** 0.1.0

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**Description** Estimation and Prediction Functions Using Bayesian Hierarchical Spatial Finlay-Wilkinson Model for Analysis of Multi-Environment Field Trials.

**License** GPL-3

**Encoding** UTF-8

**LazyData** true

**RoxygenNote** 6.1.1

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HFWM\_est

*Estimation Function for Hierarchical Finlay-Wilkinson Model***Description**

This function ignores spatial effects.

**Usage**

```
HFWM_est(Y, VAR, ENV, kin_info = FALSE, A = NULL, env_info = FALSE,
         Z = NULL, inits = NULL, hyper_para = NULL, M_iter = 5000,
         burn_in = 3000, thin = 5, save_chain = FALSE, seed = NULL)
```

**Arguments**

Y	A length-N numerical response vector
VAR	A length-N factor/character vector indicating the genotype information of Y
ENV	A length-N factor/character vector indicating the field information of Y
kin_info	A logical parameter controlling if to use kinship matrix
A	kinship matrix, give value only if kin_info = TRUE
env_info	A logical parameter controlling whether to use environmental covariates
Z	environmental covariates matrix with rownames = field names, give value only if env_info = TRUE
inits	initial values, default is given
hyper_para	hyper-parameter values, default is given
M_iter	Total iteration number
burn_in	Burn in number
thin	Thinning value
save_chain	A logical parameter controlling whether to save MCMC chain: 'Chains.rds' in current working directory
seed	Random seed value

**Value**

Mean estimates and RMSE value

**Examples**

```
library(spFW)

# load data
data(spFW_example_data)
Y <- spFW_example_data$yield
VAR <- spFW_example_data$geno
```

```

ENV <- spFW_example_data$loc
COOR <- spFW_example_data[,c(4,5)]

# run model
fit0 <- HFWM_est(Y, VAR, ENV, M_iter = 1000, burn_in = 500, thin = 5)

# plot estimated Y
plot(Y, fit0$yhat)

```

---

HFWM\_pred

*Prediction Function for Hierarchical Finlay-Wilkinson Model*


---

### Description

This function ignores spatial effects.

### Usage

```

HFWM_pred(Y, VAR, ENV, VAR2, ENV2, save_int = FALSE, kin_info = FALSE,
  A = NULL, inits = NULL, hyper_para = NULL, M_iter = 5000,
  burn_in = 3000, thin = 5, seed = NULL)

```

### Arguments

Y	A length-N1 numerical response vector from training set
VAR	A length-N1 factor/character vector indicating the genotype information of Y
ENV	A length-N1 factor/character vector indicating the field information of Y
VAR2	A length-N2 factor/character vector indicating the genotype information of testing set
ENV2	A length-N2 factor/character vector indicating the field information of testing set
save_int	A logical parameter controlling whether to save prediction credible intervals
kin_info	A logical parameter controlling if to use kinship matrix
A	kinship matrix, give value only if kin_info = TRUE
inits	initial values, default is given
hyper_para	hyper-parameter values, default is given
M_iter	Total iteration number
burn_in	Burn in number
thin	Thinning value
seed	Random seed value

### Value

Mean prediction values and/or prediction intervals

**Examples**

```

library(spFW)

# load and split data
data(spFW_example_data)
idx_pred <- sample(125, 25)

Y0 <- spFW_example_data$yield
VAR0 <- spFW_example_data$geno
ENV0 <- spFW_example_data$loc

Y1 <- Y0[-idx_pred]
Y2 <- Y0[idx_pred]
VAR1 <- VAR0[-idx_pred]
VAR2 <- VAR0[idx_pred]
ENV1 <- ENV0[-idx_pred]
ENV2 <- ENV0[idx_pred]
order_y <- order(Y2)

# run model
pred0 <- HFWM_pred(Y1, VAR1, ENV1, VAR2, ENV2, save_int = TRUE,
                  M_iter = 1000, burn_in = 500, thin = 5)

# visualize prediction results
plot(1:25, pred0$PY[order_y], ylim = c(50, 250), pch = 15, col = "red",
     xlab = "Plant ID for Prediction", ylab = "Yield",
     main = "95% Prediction Intervals with Predicted Mean (Red) Versus True Yield (Blue)")
points(1:25, Y2[order_y], col = "blue")
for (i in 1:25){
  lines(x = c(i,i), y = c(pred0$PY_CI[,order_y][1,i], pred0$PY_CI[,order_y][4,i]))
}

```

---

HSFWM\_est

*Estimation Function for Hierarchical Spatial Finlay-Wilkinson Model*


---

**Description**

This function considers spatial adjustments.

**Usage**

```

HSFWM_est(Y, VAR, ENV, COOR, kin_info = FALSE, A = NULL,
          env_info = FALSE, Z = NULL, inits = NULL, hyper_para = NULL,
          M_iter = 5000, burn_in = 3000, thin = 5, save_chain = FALSE,
          seed = NULL)

```

**Arguments**

Y	A length-N numerical response vector
VAR	A length-N factor/character vector indicating the genotype information of Y
ENV	A length-N factor/character vector indicating the field information of Y
COOR	A N by 2 numerical matrix indicating the spatial locations of Y
kin_info	A logical parameter controlling if to use kinship matrix
A	kinship matrix, give value only if kin_info = TRUE
env_info	A logical parameter controlling whether to use environmental covariates
Z	environmental covariates matrix with rownames = field names, give value only if env_info = TRUE
inits	initial values, default is given
hyper_para	hyper-parameter values, default is given
M_iter	Total iteration number
burn_in	Burn in number
thin	Thinning value
save_chain	A logical parameter controlling whether to save MCMC chain: 'Chains.rds' in current working directory
seed	Random seed value

**Value**

Mean estimates and RMSE value

**Examples**

```
library(spFW)

# load data
data(spFW_example_data)
Y <- spFW_example_data$yield
VAR <- spFW_example_data$geno
ENV <- spFW_example_data$loc
COOR <- spFW_example_data[,c(4,5)]

# run model
fit1 <- HSFWM_est(Y, VAR, ENV, COOR,
                 M_iter = 1000, burn_in = 500, thin = 5)

# plot estimated Y
plot(Y, fit1$yhat)
```

---

HSFWM\_pred

*Prediction Function for Hierarchical Spatial Finlay-Wilkinson Model*


---

### Description

This function considers spatial adjustments.

### Usage

```
HSFWM_pred(Y, VAR, ENV, COOR, VAR2, ENV2, COOR2, save_int = FALSE,
  kin_info = FALSE, A = NULL, inits = NULL, hyper_para = NULL,
  M_iter = 5000, burn_in = 3000, thin = 5, seed = NULL)
```

### Arguments

Y	A length-N1 numerical response vector from training set
VAR	A length-N1 factor/character vector indicating the genotype information of Y
ENV	A length-N1 factor/character vector indicating the field information of Y
COOR	A N1 by 2 numerical matrix indicating the spatial locations of Y
VAR2	A length-N2 factor/character vector indicating the genotype information of testing set
ENV2	A length-N2 factor/character vector indicating the field information of testing set
COOR2	A N2 by 2 numerical matrix indicating the spatial locations of testing set
save_int	A logical parameter controlling whether to save prediction credible intervals
kin_info	A logical parameter controlling if to use kinship matrix
A	kinship matrix, give value only if kin_info = TRUE
inits	initial values, default is given
hyper_para	hyper-parameter values, default is given
M_iter	Total iteration number
burn_in	Burn in number
thin	Thinning value
seed	Random seed value

### Value

Mean prediction values and/or prediction intervals

**Examples**

```

library(spFW)

# load and split data
data(spFW_example_data)
idx_pred <- sample(125, 25)

Y0 <- spFW_example_data$yield
VAR0 <- spFW_example_data$geno
ENV0 <- spFW_example_data$loc
COOR0 <- spFW_example_data[,c(4,5)]

Y1 <- Y0[-idx_pred]
Y2 <- Y0[idx_pred]
VAR1 <- VAR0[-idx_pred]
VAR2 <- VAR0[idx_pred]
ENV1 <- ENV0[-idx_pred]
ENV2 <- ENV0[idx_pred]
COOR1 <- COOR0[-idx_pred,]
COOR2 <- COOR0[idx_pred,]
order_y <- order(Y2)

# run model
pred1 <- HSFWM_pred(Y1, VAR1, ENV1, COOR1, VAR2, ENV2, COOR2, save_int = TRUE,
                   M_iter = 1000, burn_in = 500, thin = 5)

# visualize prediction results
plot(1:25, pred1$PY[order_y], ylim = c(50, 250), pch = 15, col = "red",
     xlab = "Plant ID for Prediction", ylab = "Yield",
     main = "95% Prediction Intervals with Predicted Mean (Red) Versus True Yield (Blue)")
points(1:25, Y2[order_y], col = "blue")
for (i in 1:25){
  lines(x = c(i,i), y = c(pred1$PY_CI[,order_y][1,i], pred1$PY_CI[,order_y][4,i]))
}

```

---

spFW\_example\_data

*Example Data for Analysis*


---

**Description**

A data frame containing the plant yield, genotypes, environments, and within-field positions.

**Usage**

```
spFW_example_data
```

**Format**

A data frame with 5 elements, which are:

**yield** Plant yield

**geno** Plant genotype ID

**loc** Plant environment ID

**range** Plant x-coordinate at a given environment

**pass** Plant y-coordinate at a given environment

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