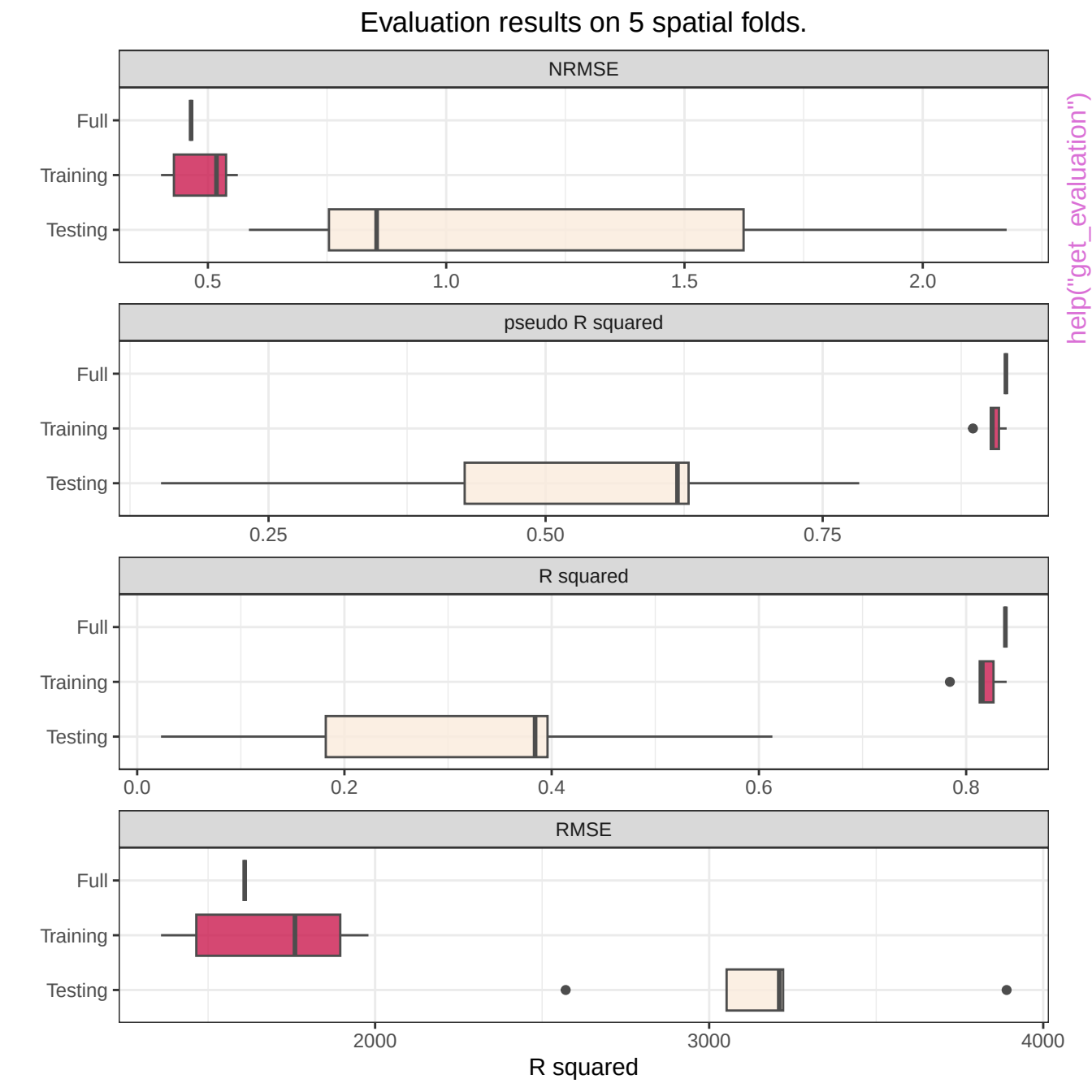
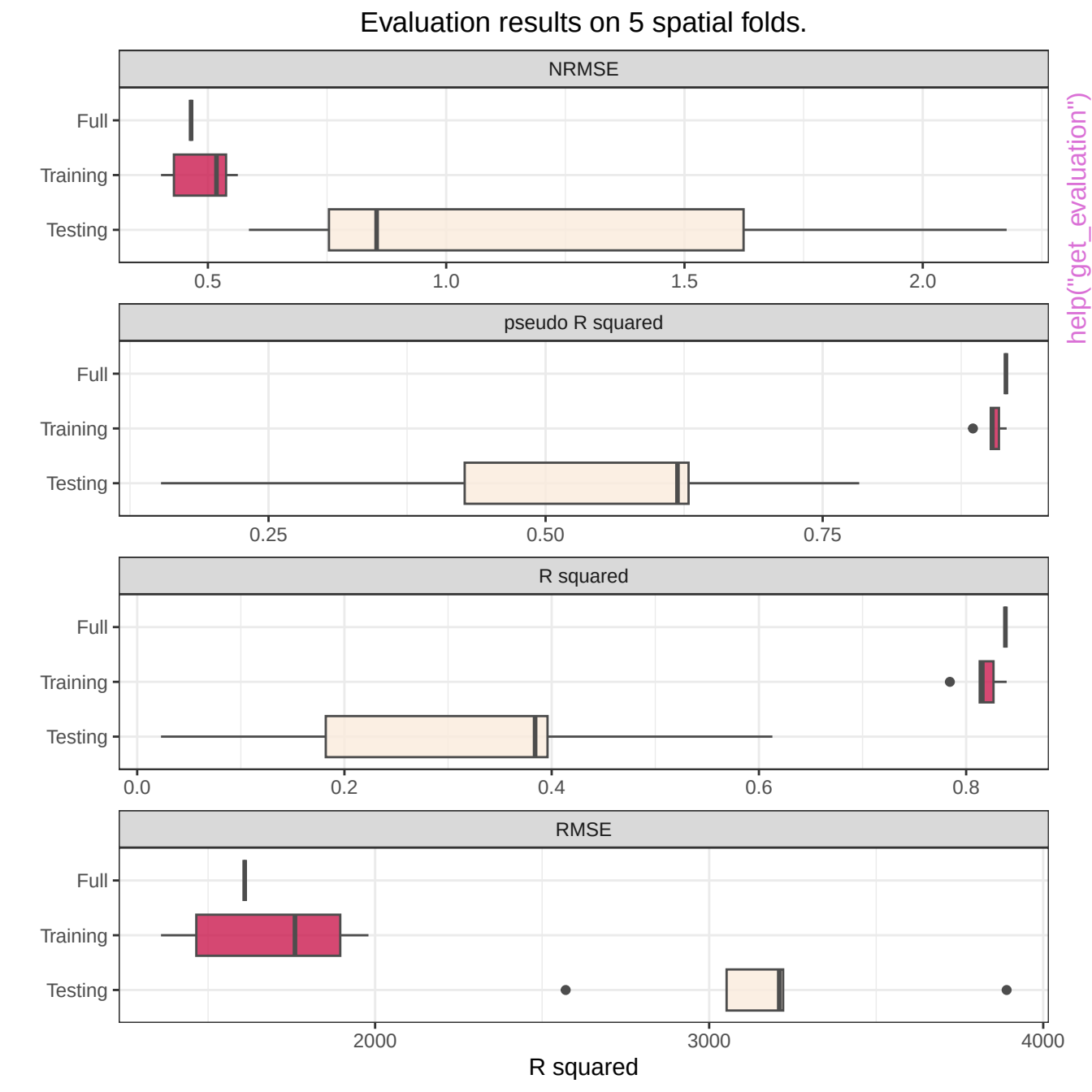
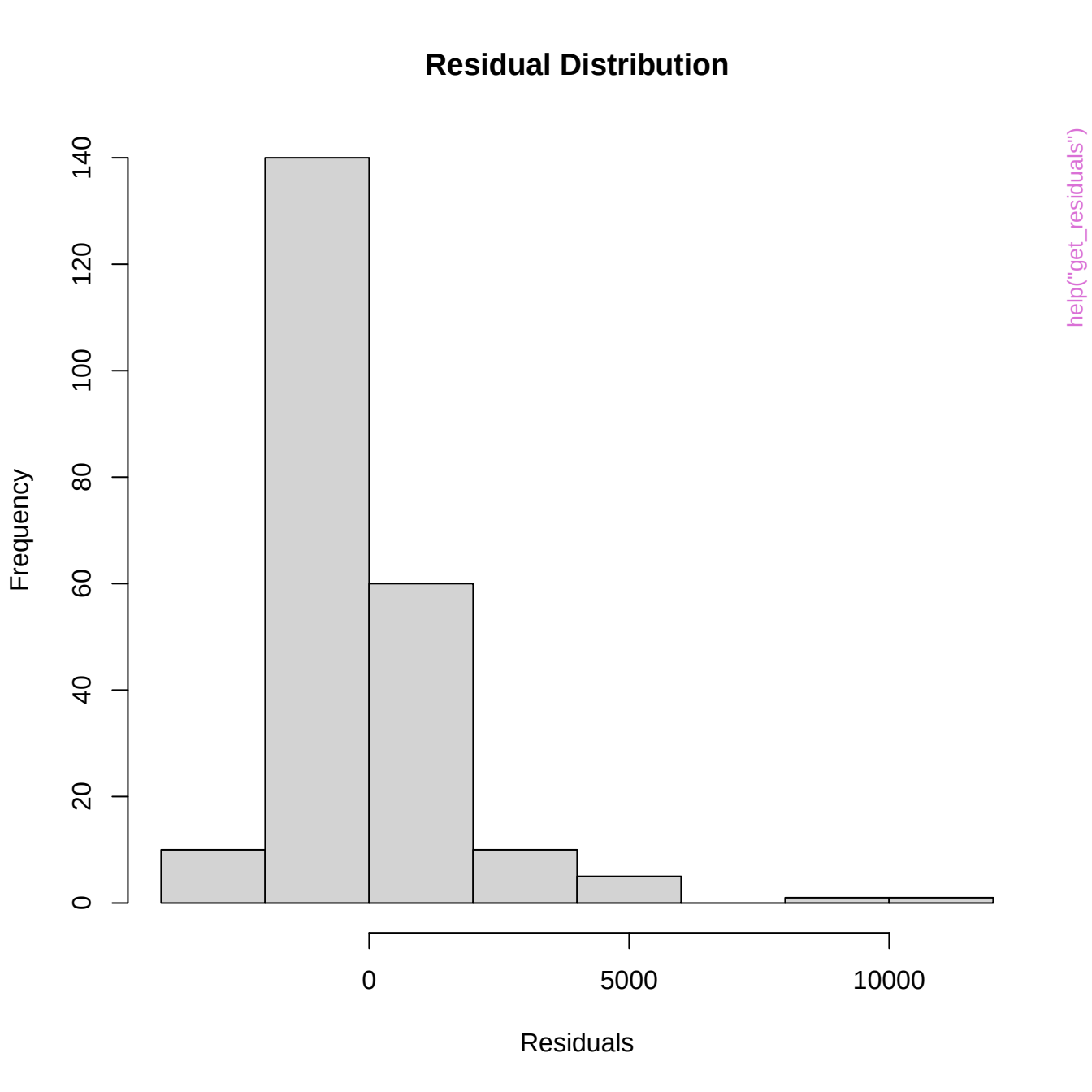
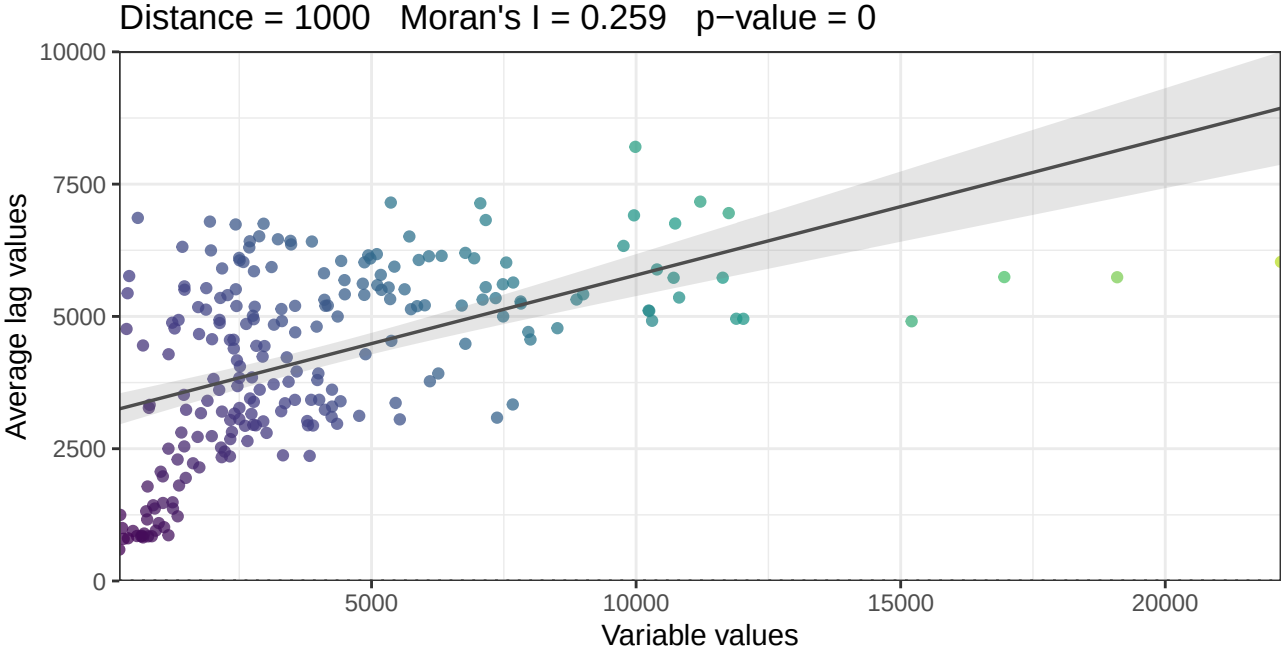
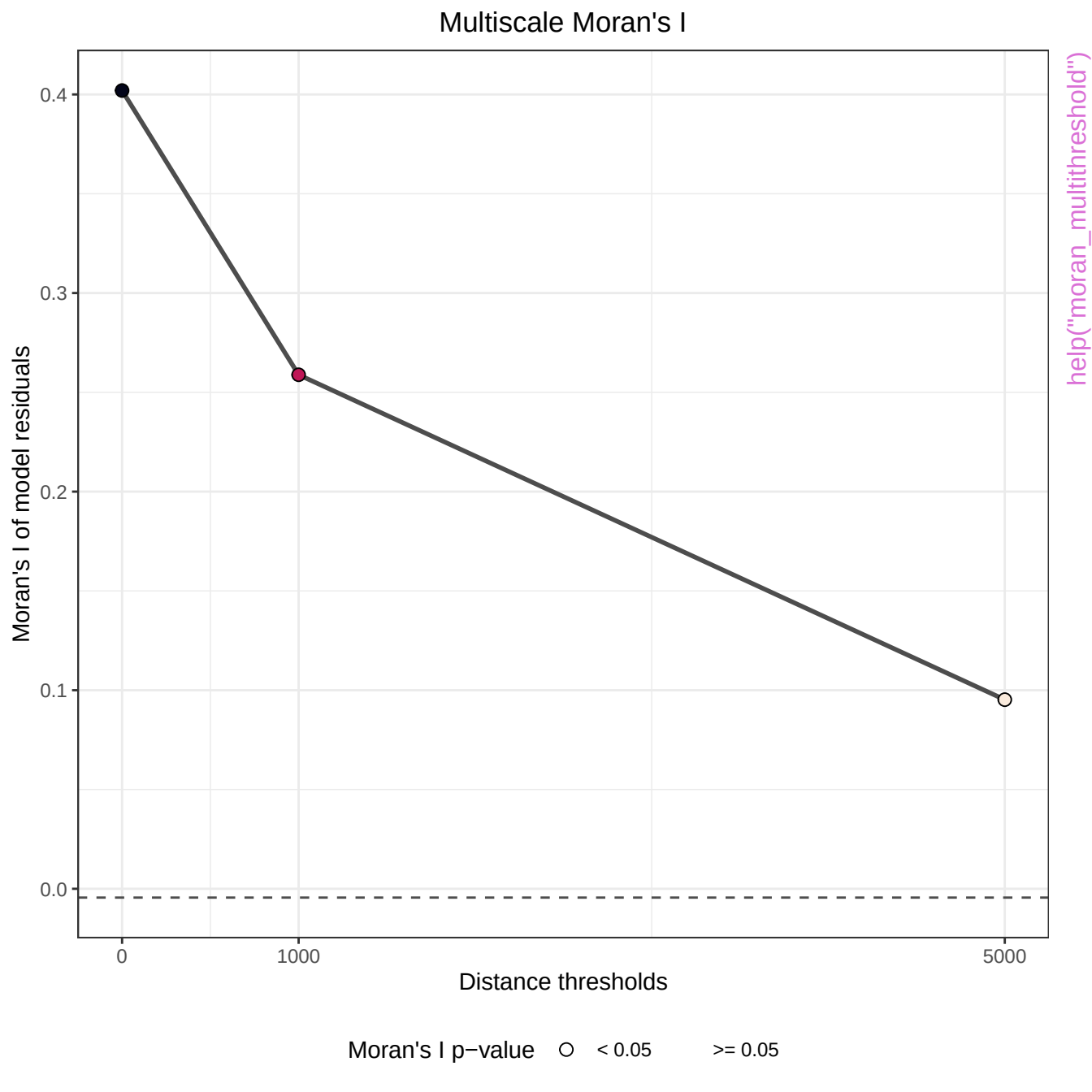

Evaluation results on 5 spatial folds.
NRMSE
Full
Training
Testing
0.5
1.0
1.5
2.0
pseudo R squared
Full
Training
Testing
0.25
0.50
0.75
R squared
Full
Training
Testing
0.0
0.2
0.4
0.6
0.8
RMSE
Full
Training
Testing
2000
3000
4000
R squared
help("get_evaluation")

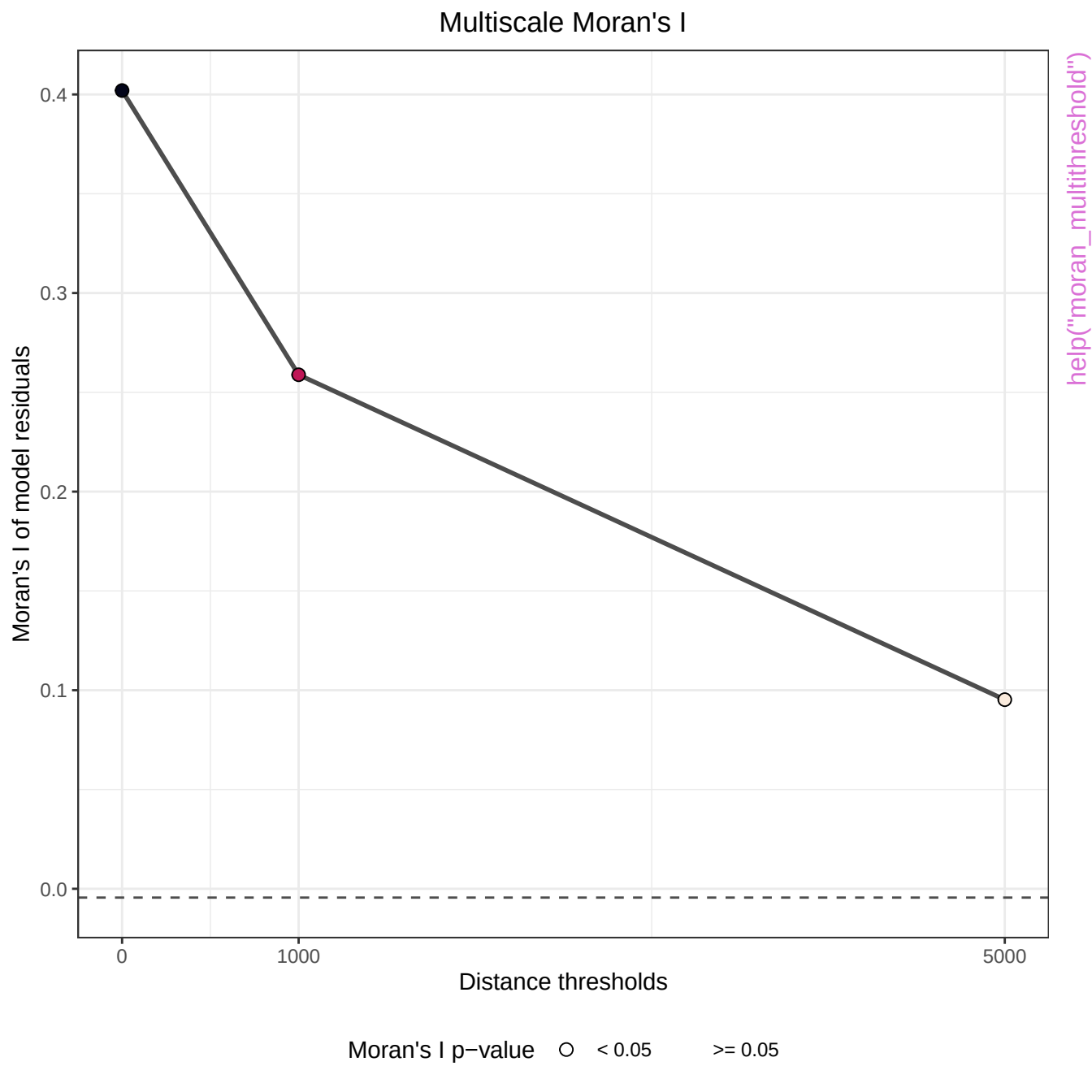

Evaluation results on 5 spatial folds.
NRMSE
Full
Training
Testing
0.5
1.0
1.5
2.0
pseudo R squared
Full
Training
Testing
0.25
0.50
0.75
R squared
Full
Training
Testing
0.0
0.2
0.4
0.6
0.8
RMSE
Full
Training
Testing
2000
3000
4000
R squared
help("get_evaluation")

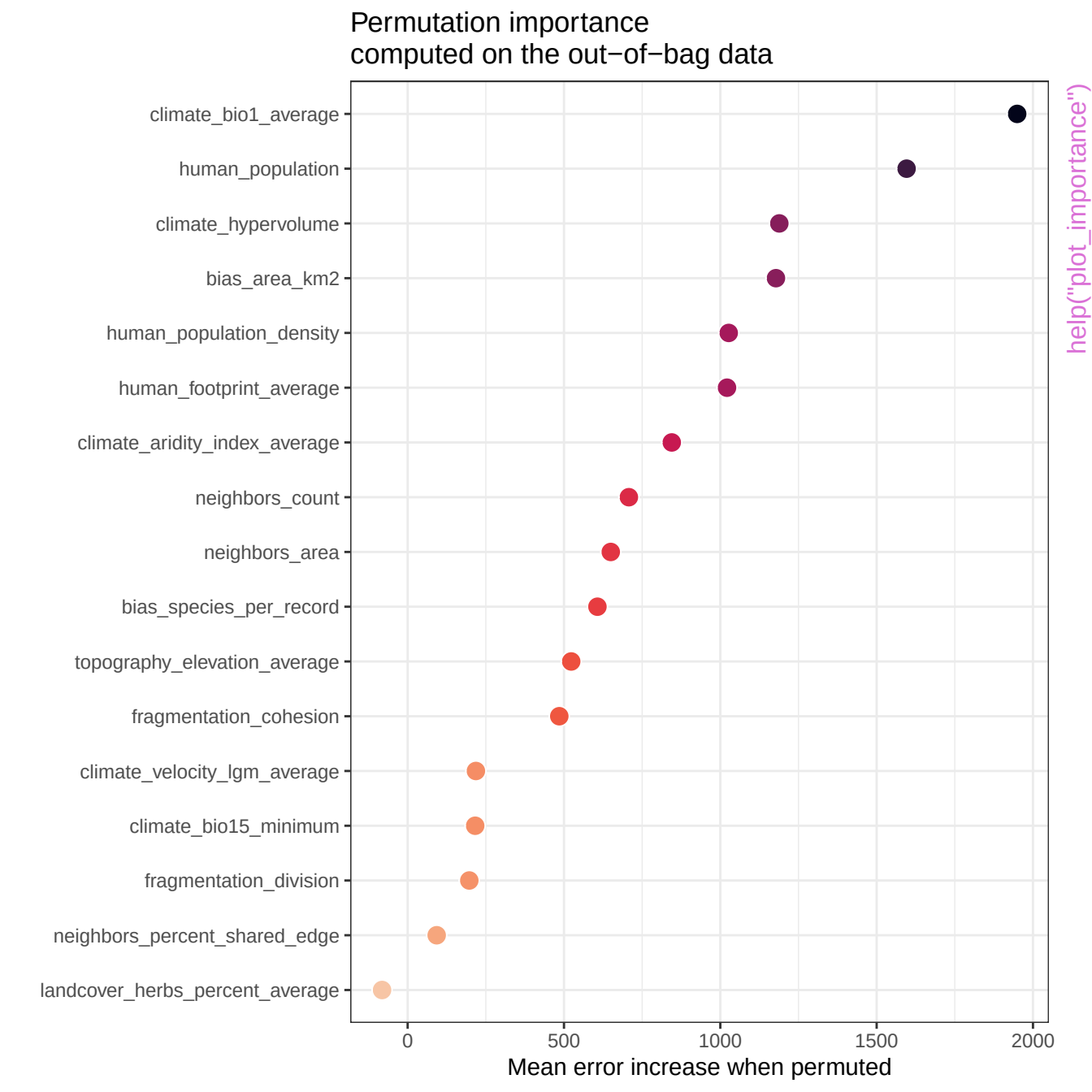

Residual Distribution
Frequency
0
20
40
60
80
100
120
140
0
5000
10000
Residuals
help("get_residuals")

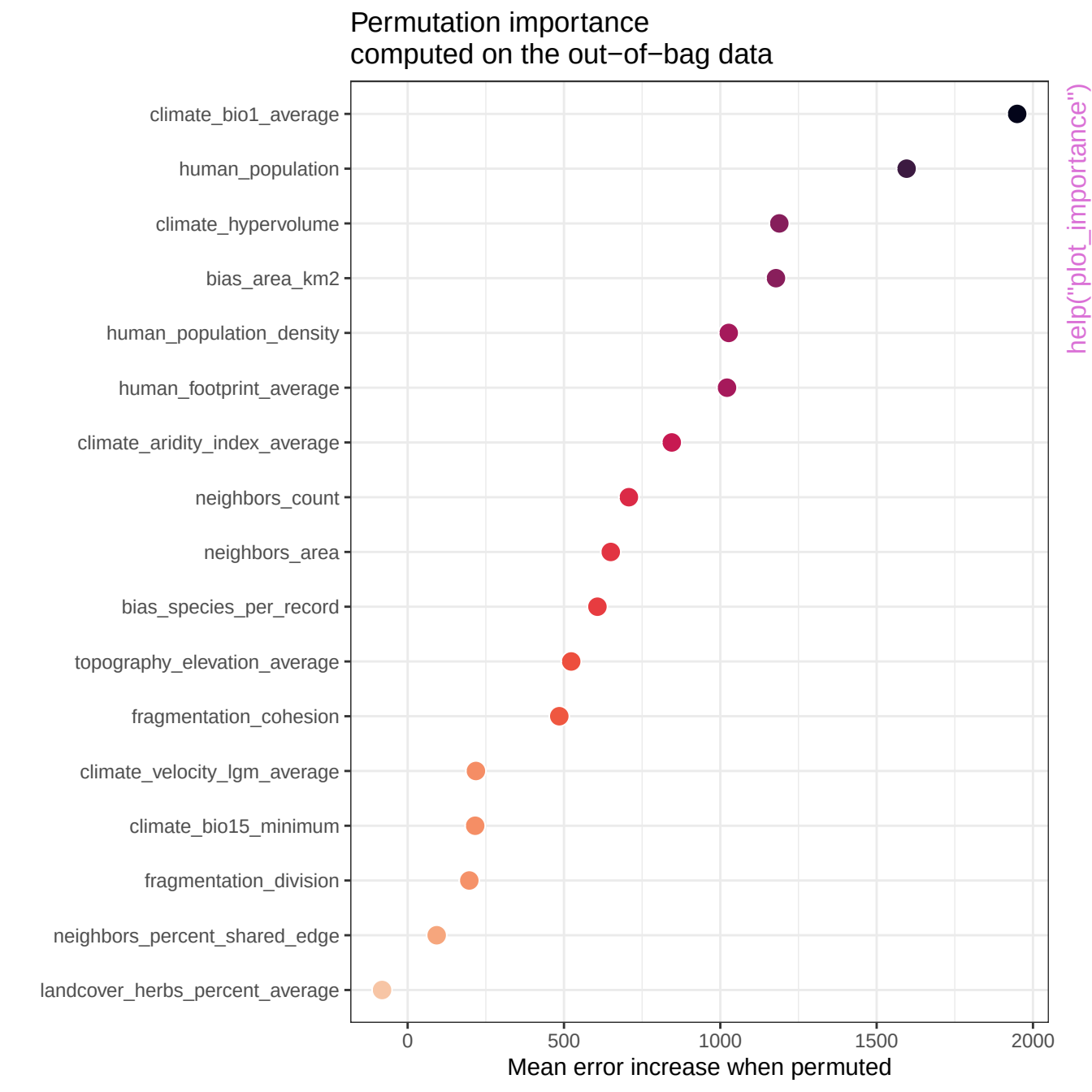
help("moran")

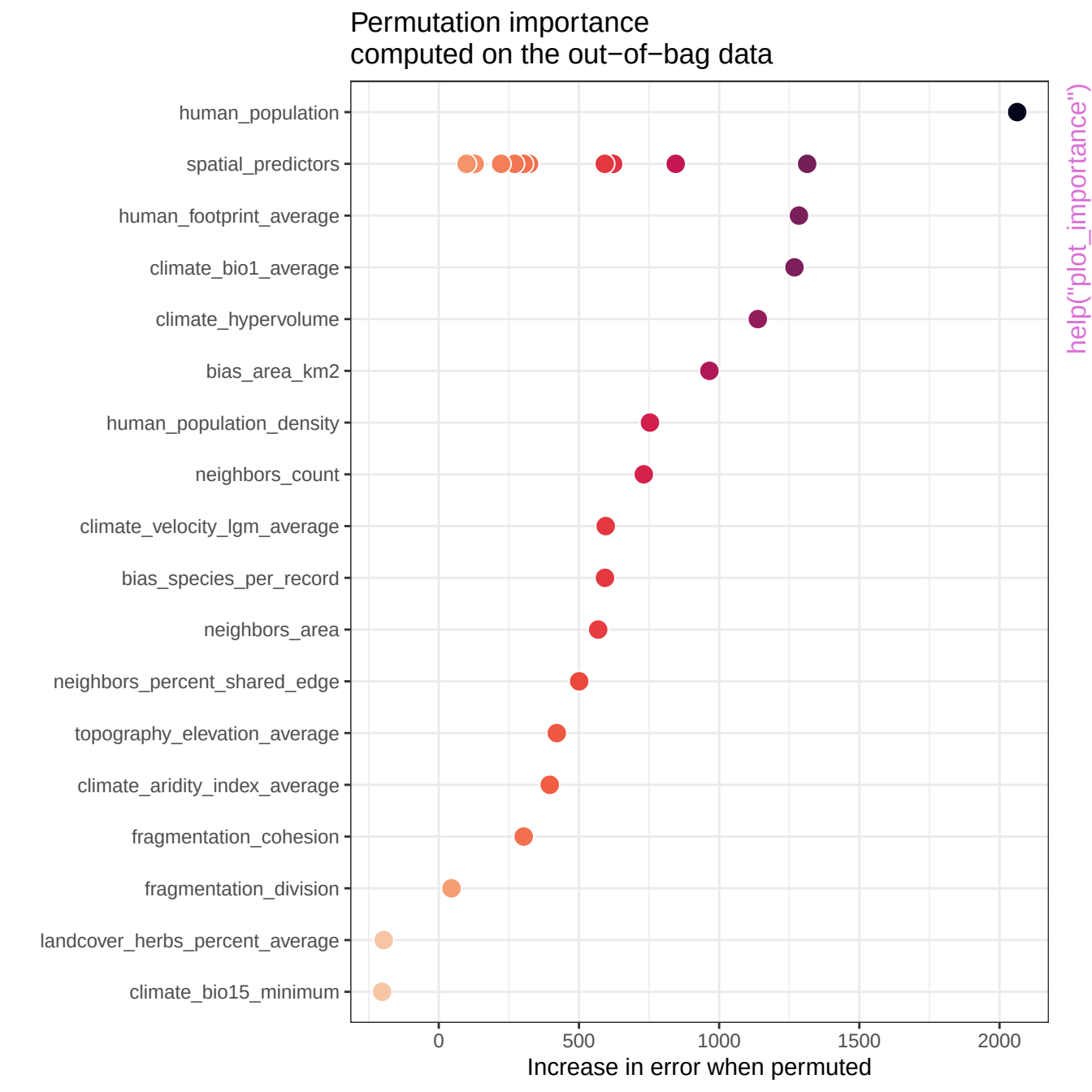

Distance = 1000 Moran's I = 0.259 p−value = 0
Average lag values
Variable values
0
2500
5000
7500
10000
5000
10000
15000
20000

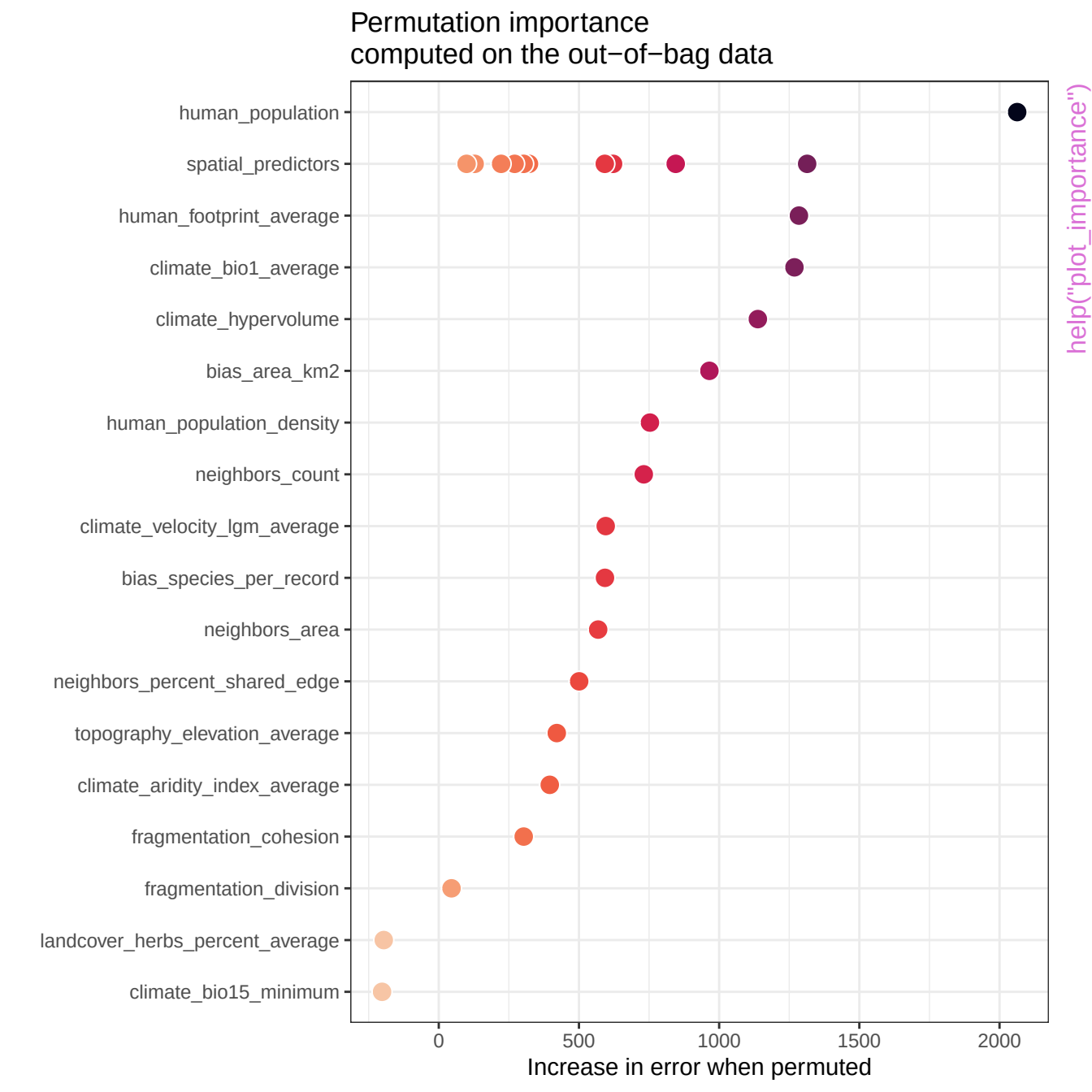

Multiscale Moran's I
Moran's I of model residuals
0.4
0.3
0.2
0.1
0.0
0
1000
5000
Distance thresholds
Moran's I p−value
< 0.05
>= 0.05
help("moran_multithreshold")

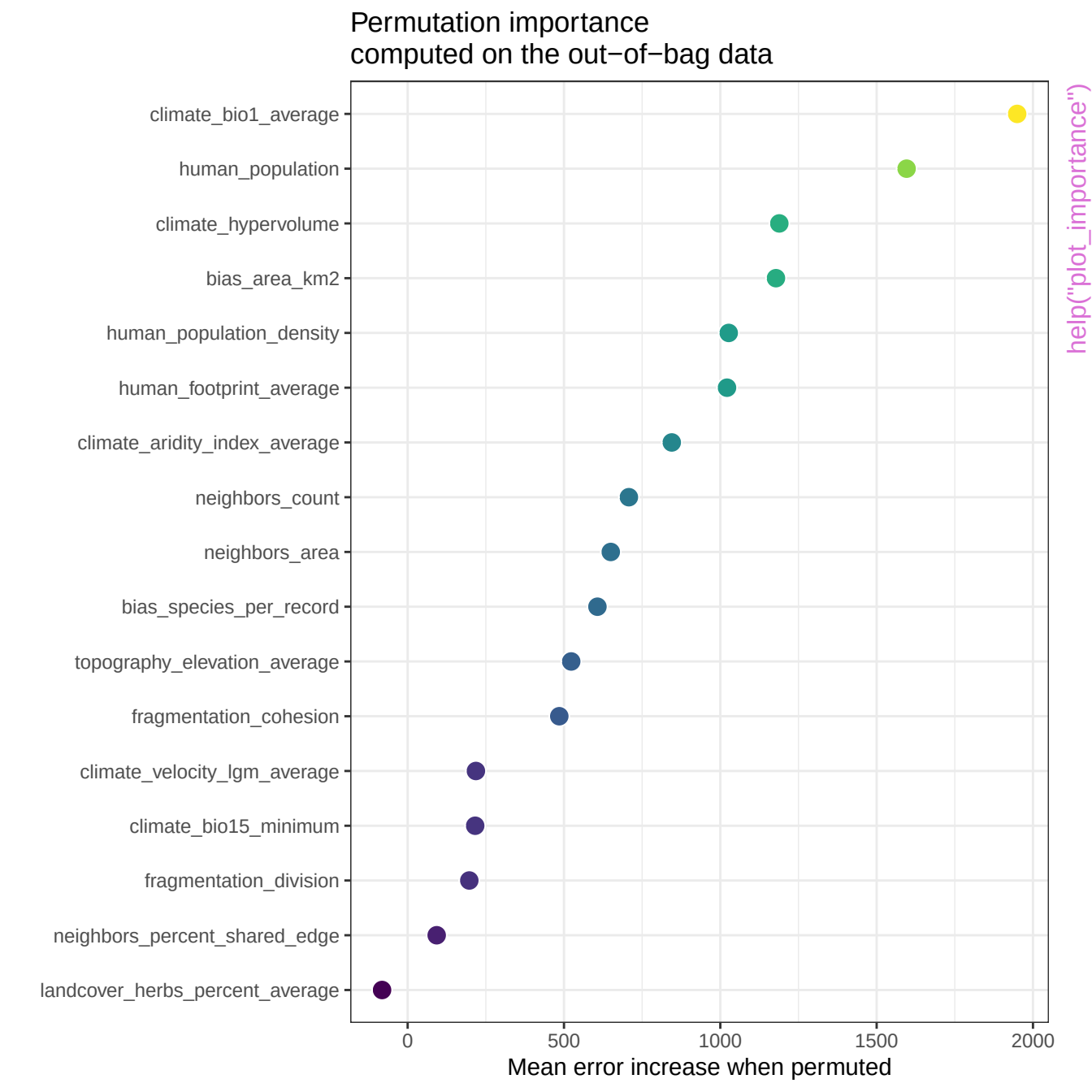

Multiscale Moran's I
Moran's I of model residuals
0.4
0.3
0.2
0.1
0.0
0
1000
5000
Distance thresholds
Moran's I p−value
< 0.05
>= 0.05
help("moran_multithreshold")

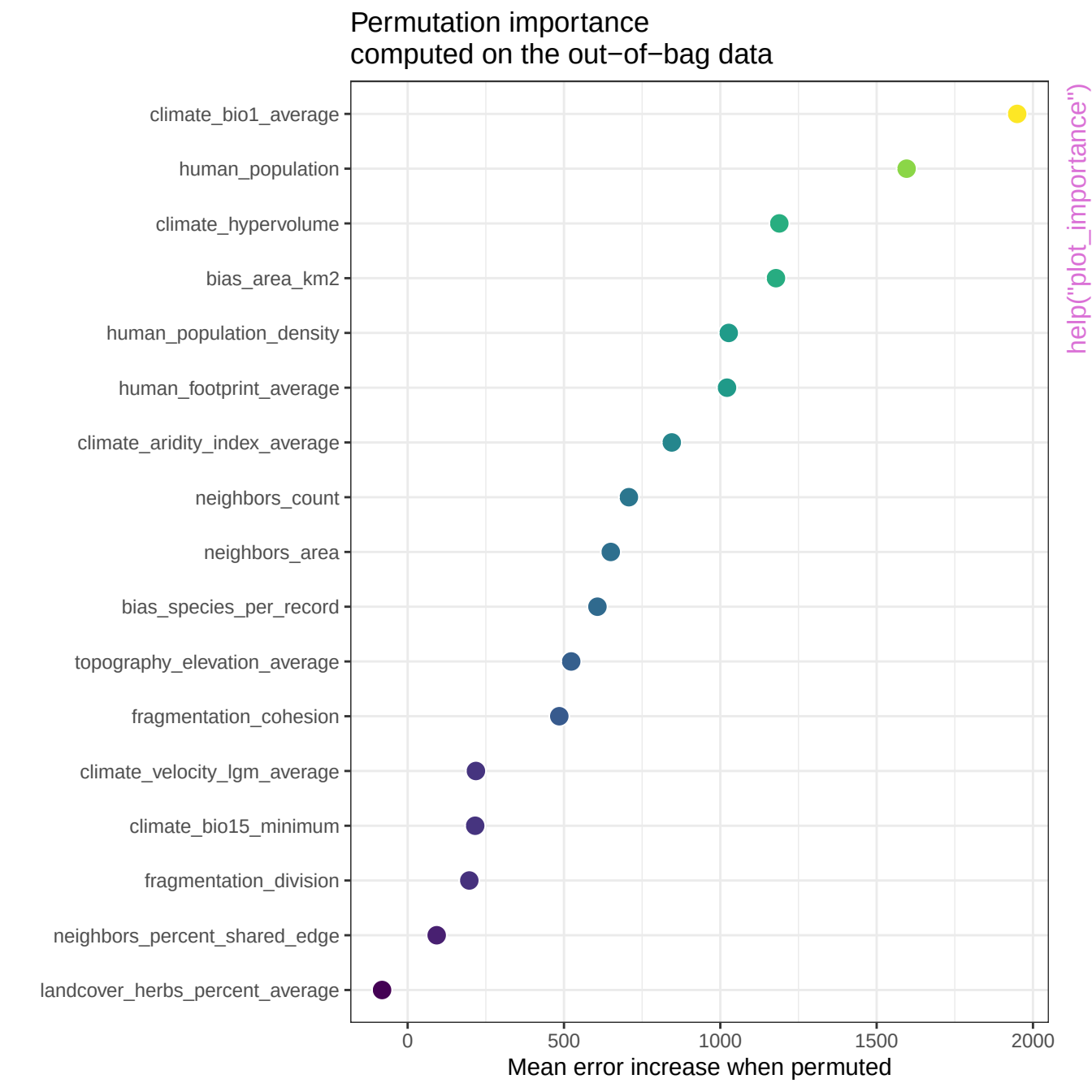

Permutation importance
computed on the out−of−bag data
climate_bio1_average
human_population
climate_hypervolume
bias_area_km2
human_population_density
human_footprint_average
climate_aridity_index_average
neighbors_count
neighbors_area
bias_species_per_record
topography_elevation_average
fragmentation_cohesion
climate_velocity_lgm_average
climate_bio15_minimum
fragmentation_division
neighbors_percent_shared_edge
landcover_herbs_percent_average
0
500
1000
1500
2000
Mean error increase when permuted
help("plot_importance")

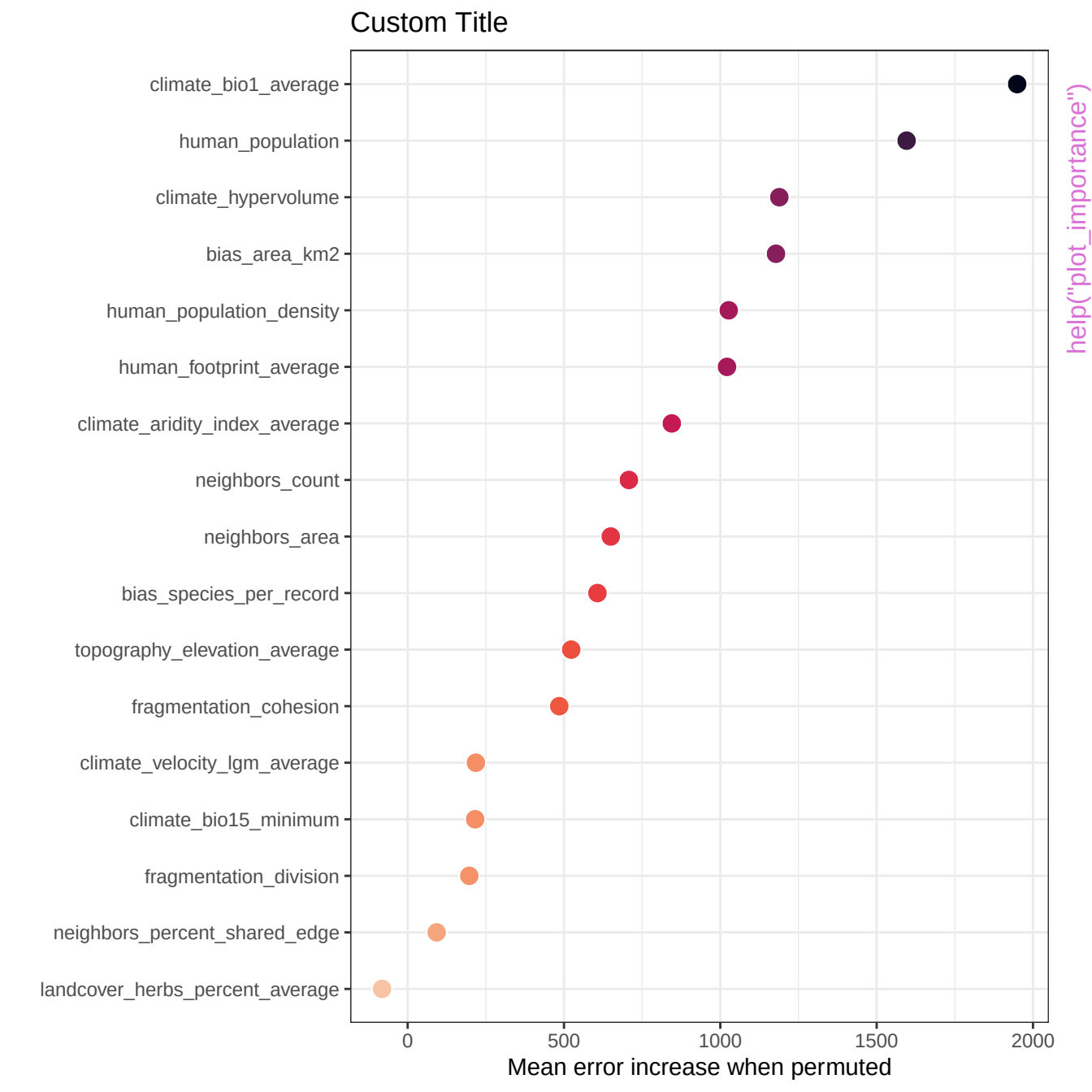

Permutation importance
computed on the out−of−bag data
climate_bio1_average
human_population
climate_hypervolume
bias_area_km2
human_population_density
human_footprint_average
climate_aridity_index_average
neighbors_count
neighbors_area
bias_species_per_record
topography_elevation_average
fragmentation_cohesion
climate_velocity_lgm_average
climate_bio15_minimum
fragmentation_division
neighbors_percent_shared_edge
landcover_herbs_percent_average
0
500
1000
1500
2000
Mean error increase when permuted
help("plot_importance")

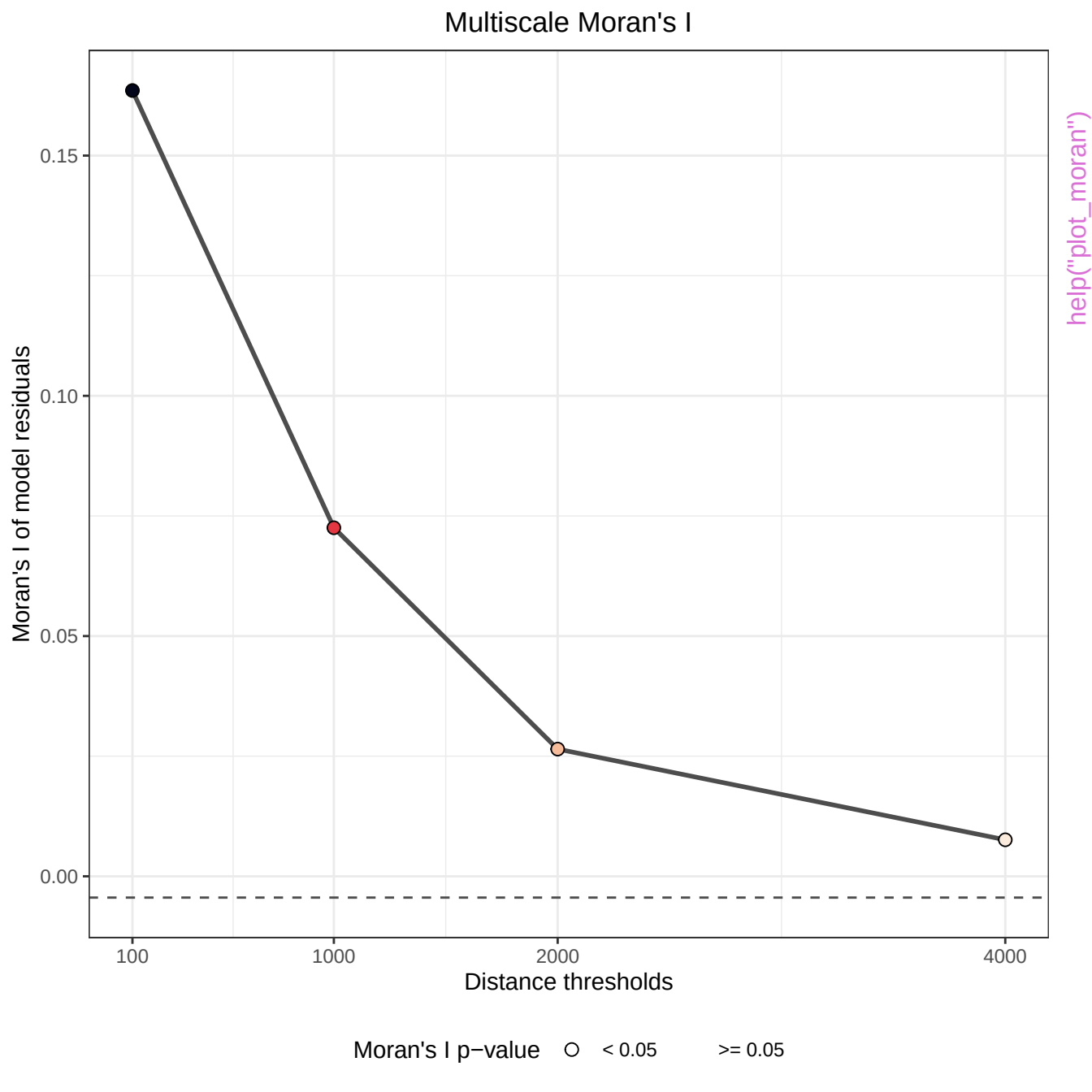

Permutation importance
computed on the out−of−bag data
human_population
spatial_predictors
human_footprint_average
climate_bio1_average
climate_hypervolume
bias_area_km2
human_population_density
neighbors_count
climate_velocity_lgm_average
bias_species_per_record
neighbors_area
neighbors_percent_shared_edge
topography_elevation_average
climate_aridity_index_average
fragmentation_cohesion
fragmentation_division
landcover_herbs_percent_average
climate_bio15_minimum
0
500
1000
1500
2000
Increase in error when permuted
help("plot_importance")

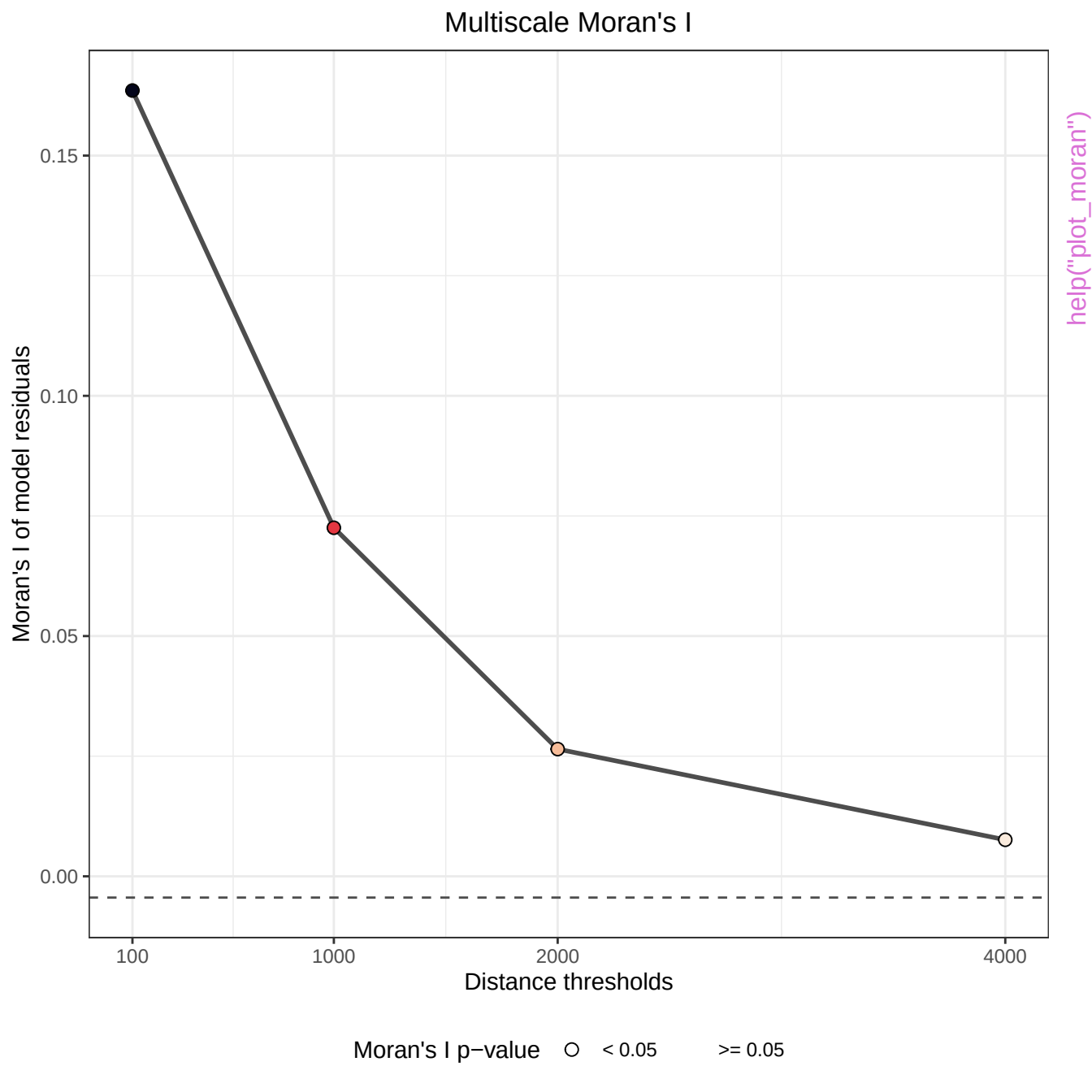

Permutation importance
computed on the out−of−bag data
human_population
spatial_predictors
human_footprint_average
climate_bio1_average
climate_hypervolume
bias_area_km2
human_population_density
neighbors_count
climate_velocity_lgm_average
bias_species_per_record
neighbors_area
neighbors_percent_shared_edge
topography_elevation_average
climate_aridity_index_average
fragmentation_cohesion
fragmentation_division
landcover_herbs_percent_average
climate_bio15_minimum
0
500
1000
1500
2000
Increase in error when permuted
help("plot_importance")

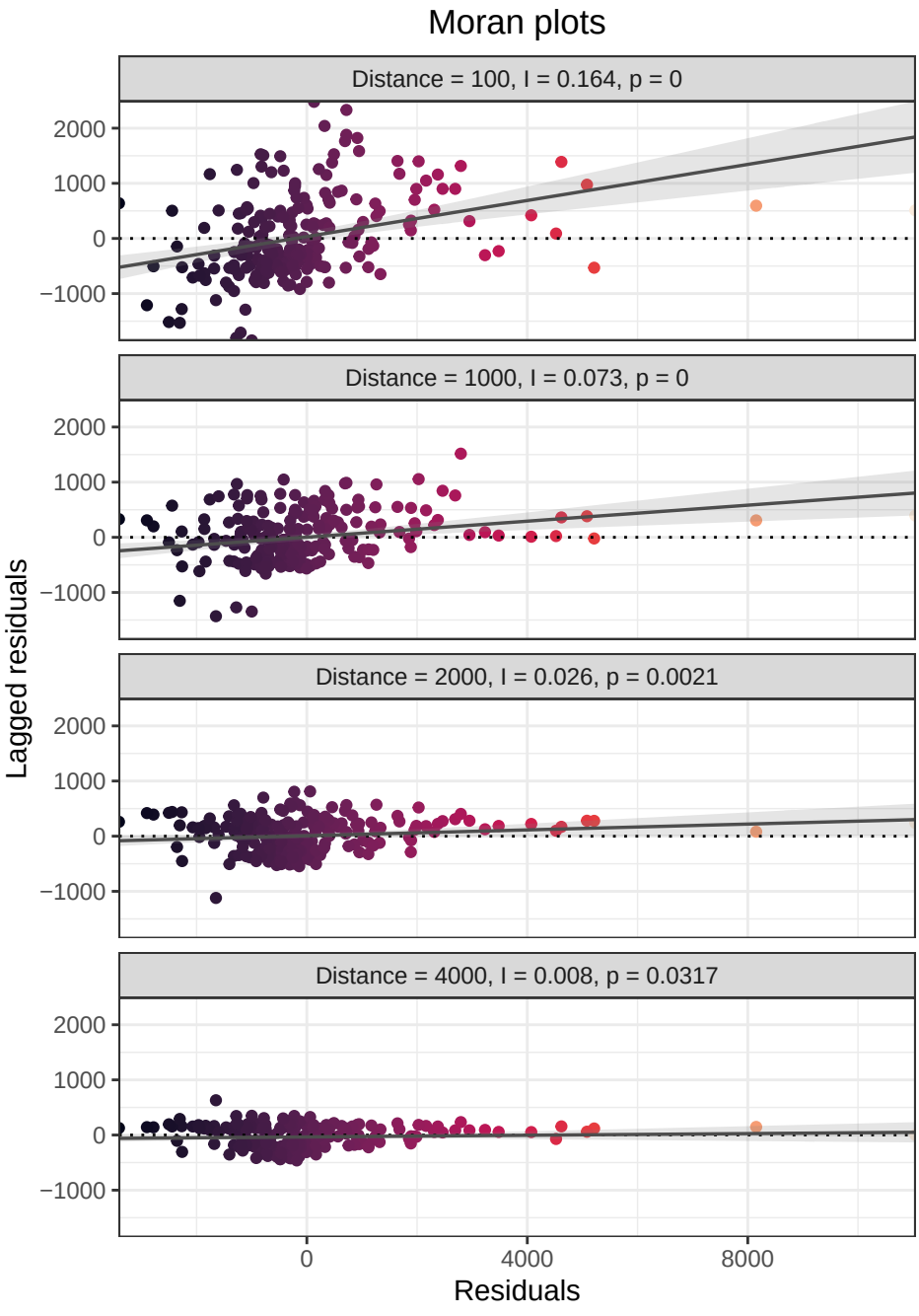

Permutation importance
computed on the out−of−bag data
climate_bio1_average
human_population
climate_hypervolume
bias_area_km2
human_population_density
human_footprint_average
climate_aridity_index_average
neighbors_count
neighbors_area
bias_species_per_record
topography_elevation_average
fragmentation_cohesion
climate_velocity_lgm_average
climate_bio15_minimum
fragmentation_division
neighbors_percent_shared_edge
landcover_herbs_percent_average
0
500
1000
1500
2000
Mean error increase when permuted
help("plot_importance")


Permutation importance
computed on the out−of−bag data
climate_bio1_average
human_population
climate_hypervolume
bias_area_km2
human_population_density
human_footprint_average
climate_aridity_index_average
neighbors_count
neighbors_area
bias_species_per_record
topography_elevation_average
fragmentation_cohesion
climate_velocity_lgm_average
climate_bio15_minimum
fragmentation_division
neighbors_percent_shared_edge
landcover_herbs_percent_average
0
500
1000
1500
2000
Mean error increase when permuted
help("plot_importance")

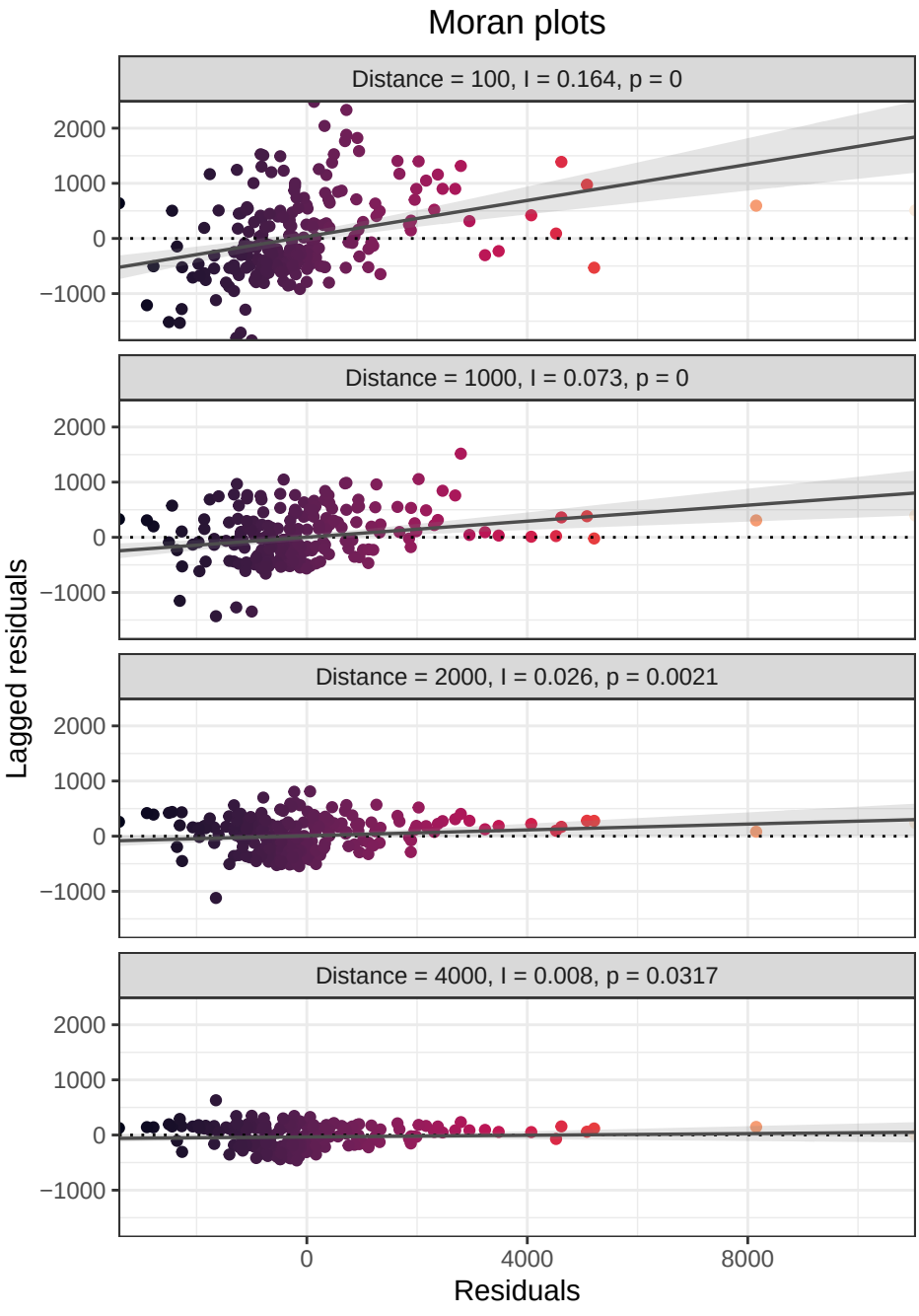

Custom Title
climate_bio1_average
human_population
climate_hypervolume
bias_area_km2
human_population_density
human_footprint_average
climate_aridity_index_average
neighbors_count
neighbors_area
bias_species_per_record
topography_elevation_average
fragmentation_cohesion
climate_velocity_lgm_average
climate_bio15_minimum
fragmentation_division
neighbors_percent_shared_edge
landcover_herbs_percent_average
0
500
1000
1500
2000
Mean error increase when permuted
help("plot_importance")


Multiscale Moran's I
Moran's I of model residuals
0.15
0.10
0.05
0.00
100
1000
2000
4000
Distance thresholds
help("plot_moran")
Moran's I p−value
< 0.05
>= 0.05

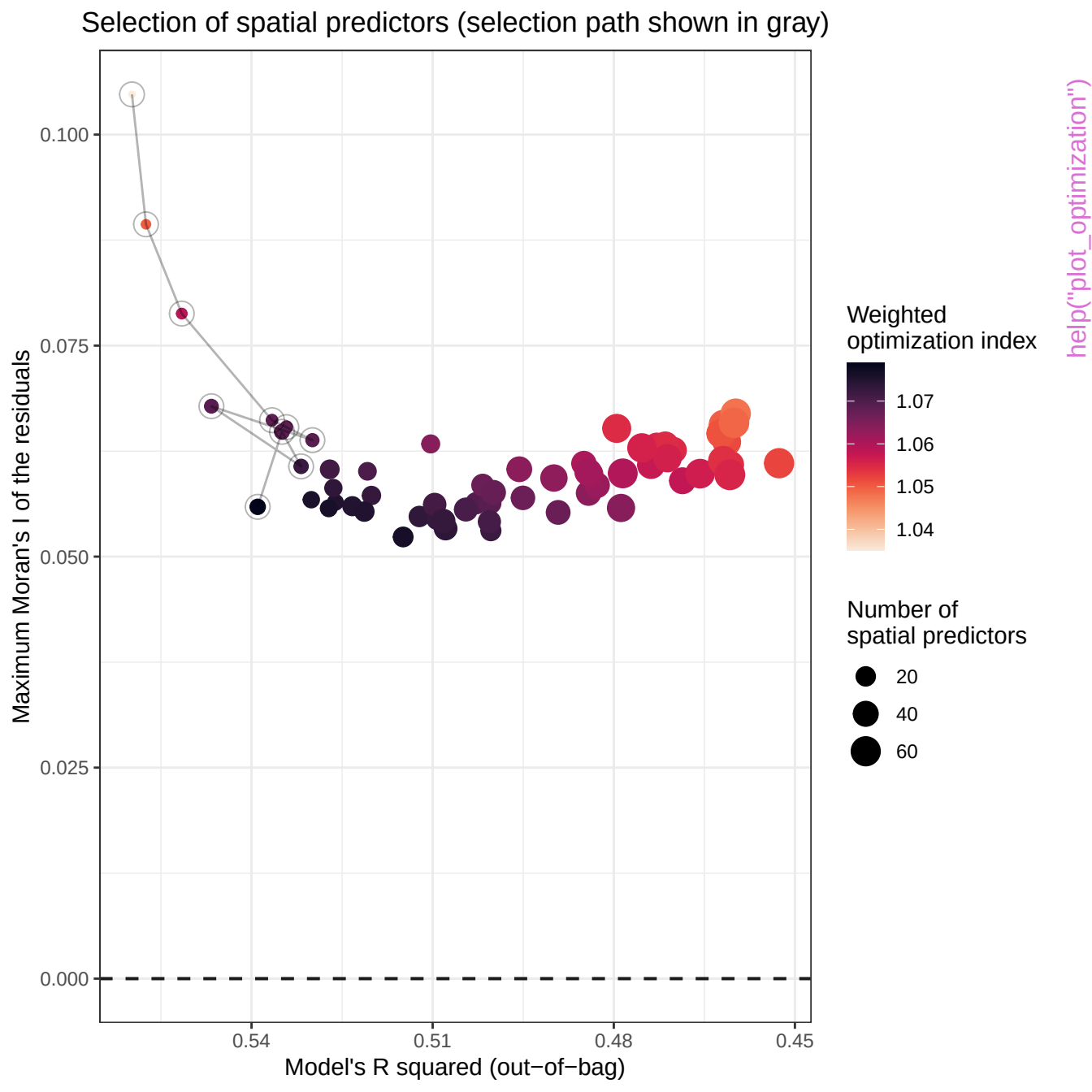

Multiscale Moran's I
Moran's I of model residuals
0.15
0.10
0.05
0.00
100
1000
2000
4000
Distance thresholds
help("plot_moran")
Moran's I p−value
< 0.05
>= 0.05

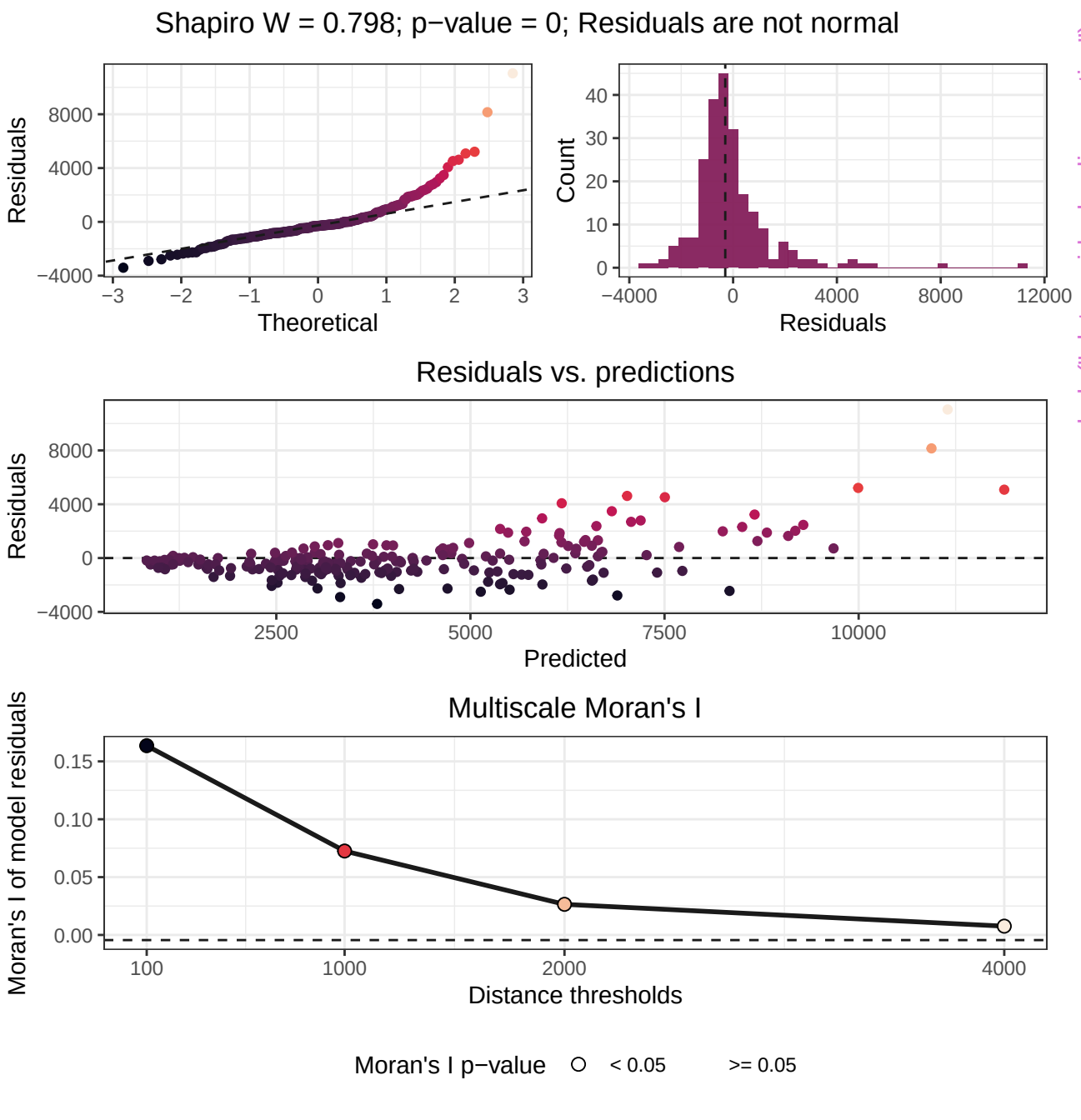


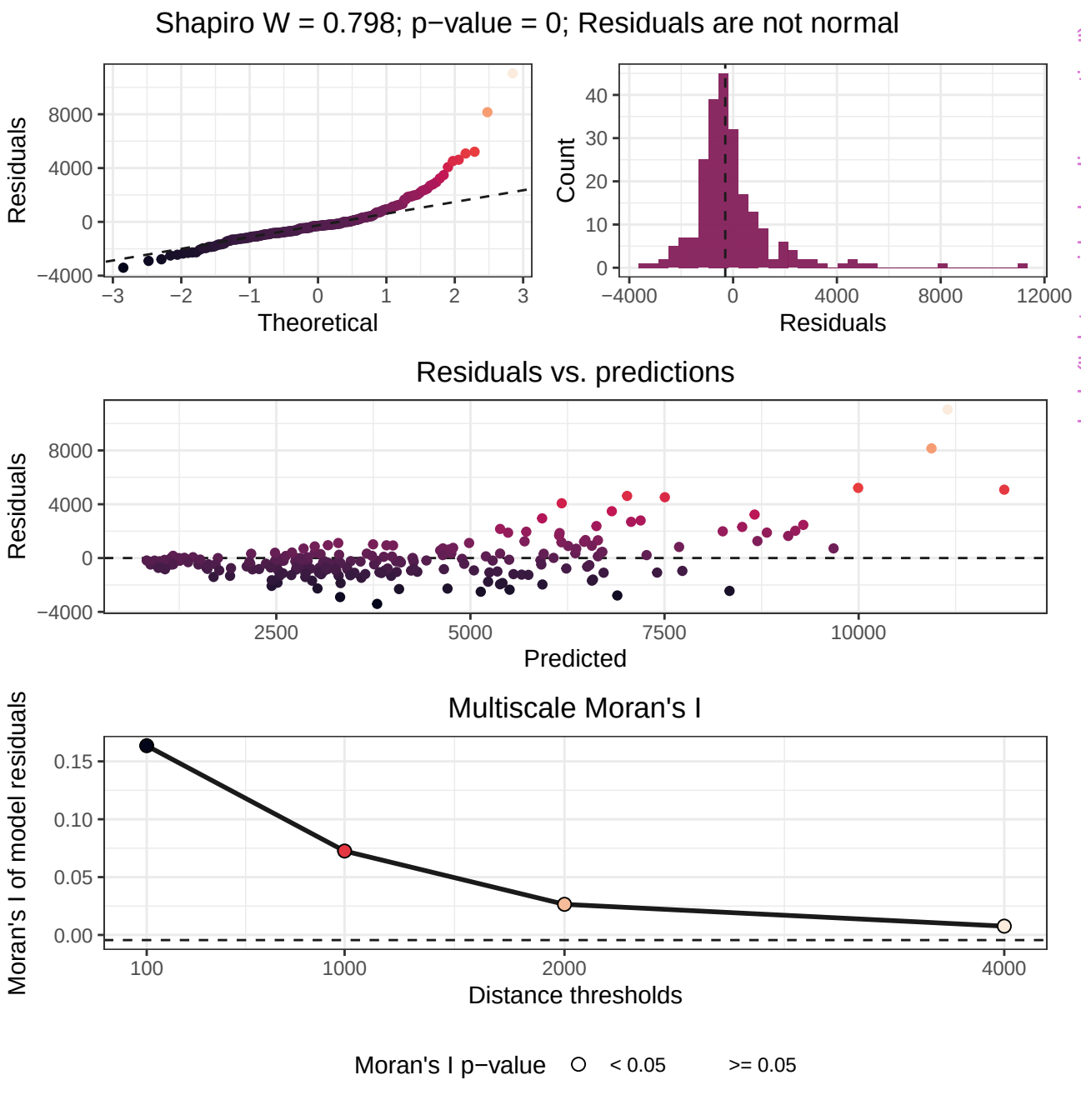
help("plot_moran")

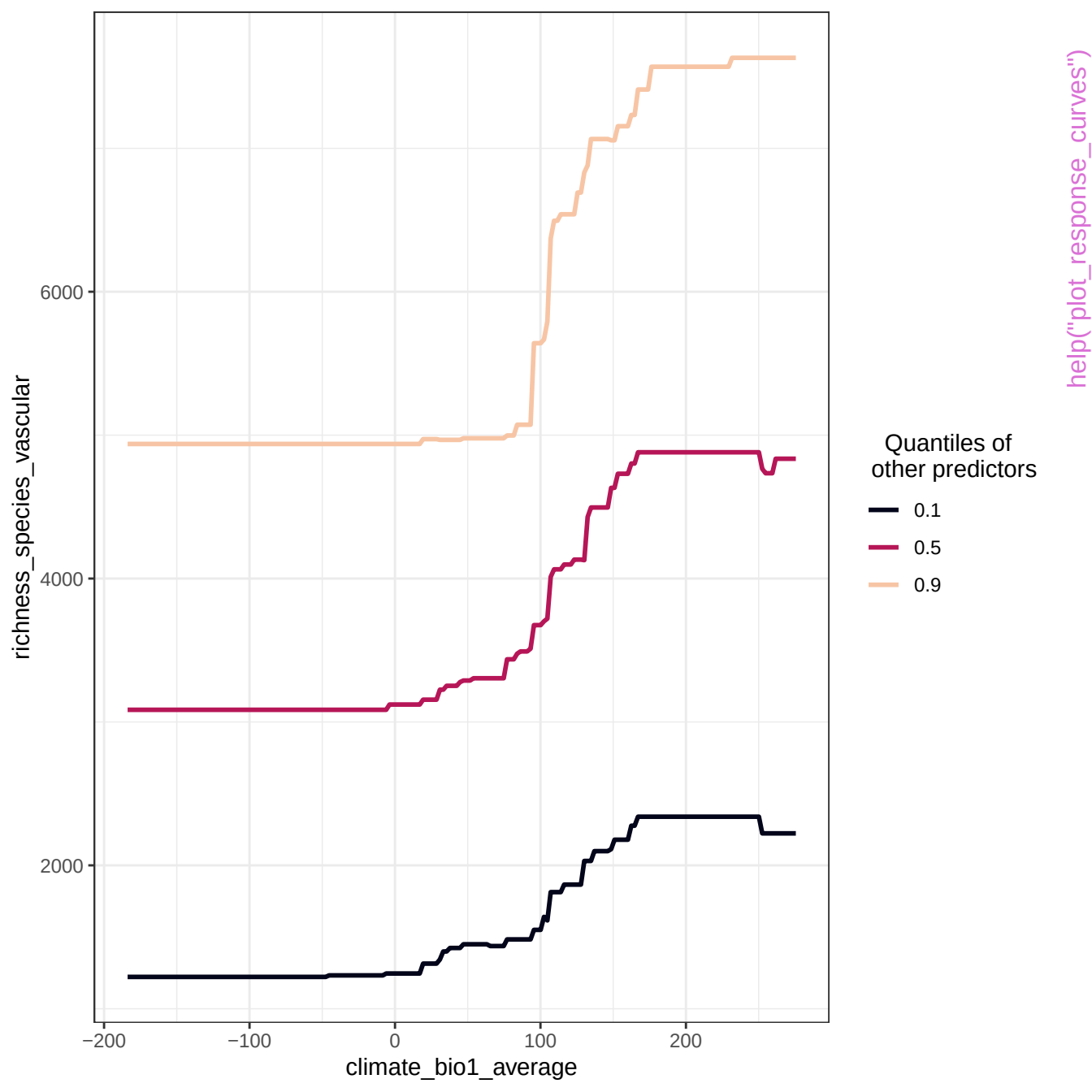


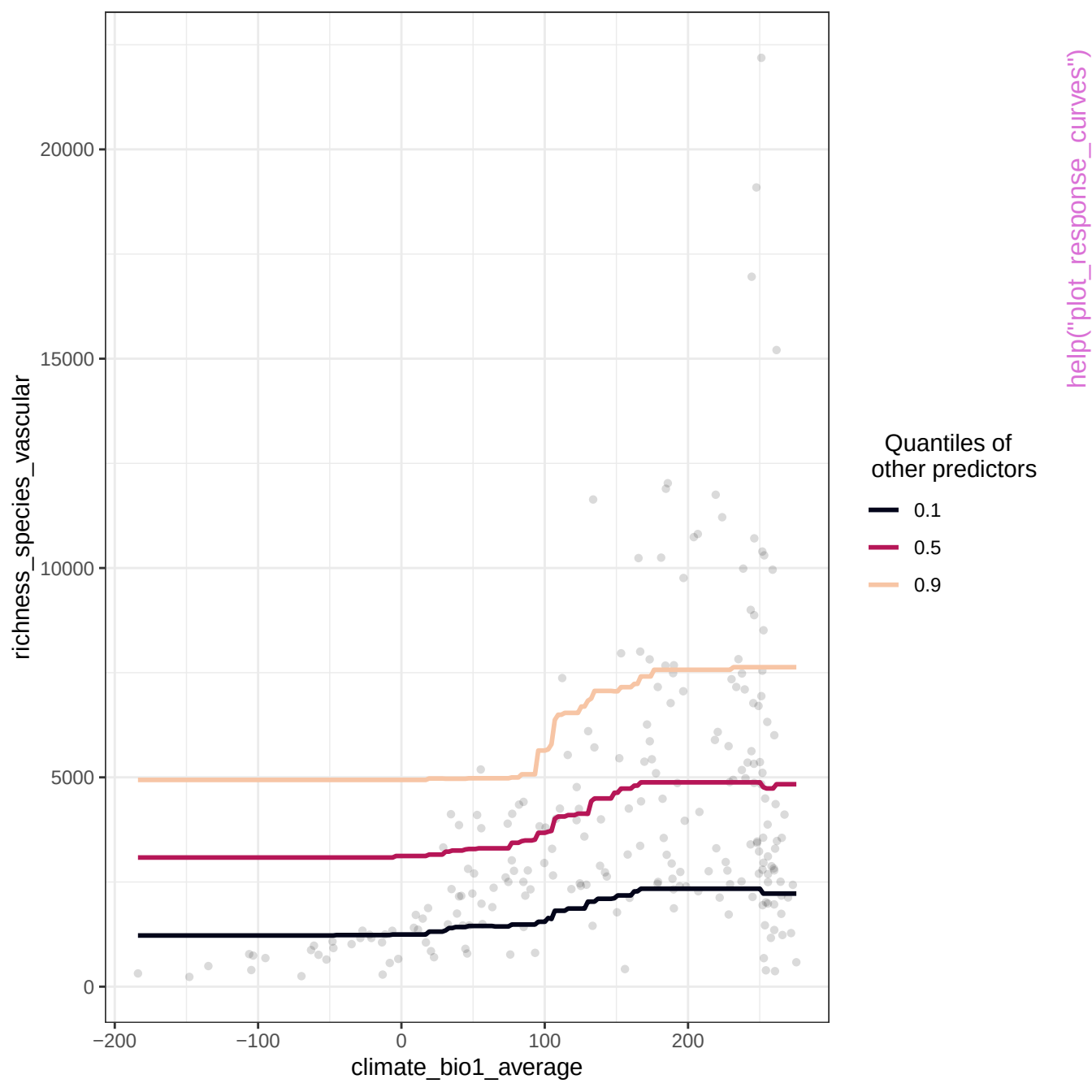
help("plot_moran")

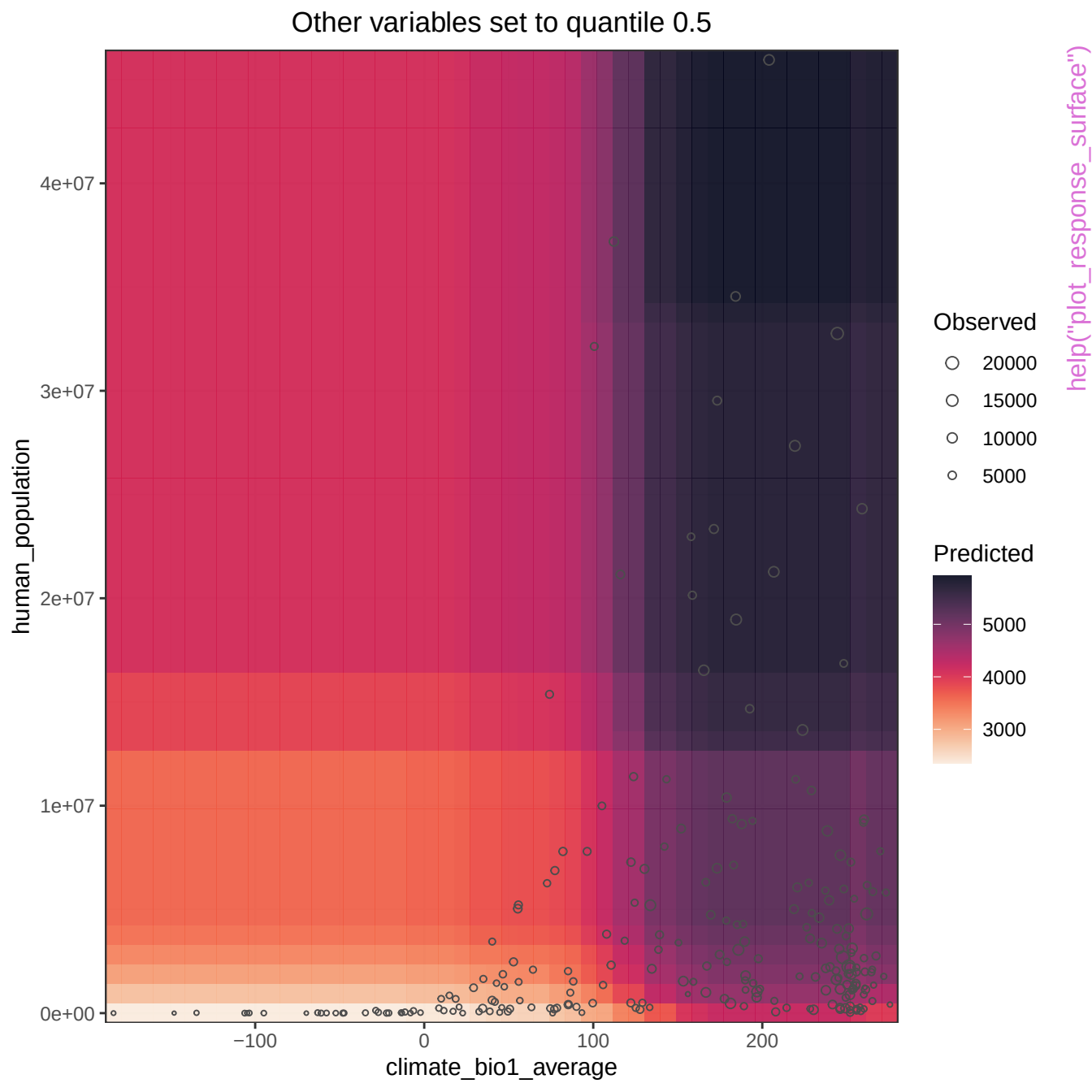

Selection of spatial predictors (selection path shown in gray)
Maximum Moran's I of the residuals
0.100
0.075
0.050
0.025
0.000
0.54
0.51
0.48
0.45
Model's R squared (out−of−bag)
Weighted optimization index
1.07
1.06
1.05
1.04
Number of spatial predictors
20
40
60
help("plot_optimization")

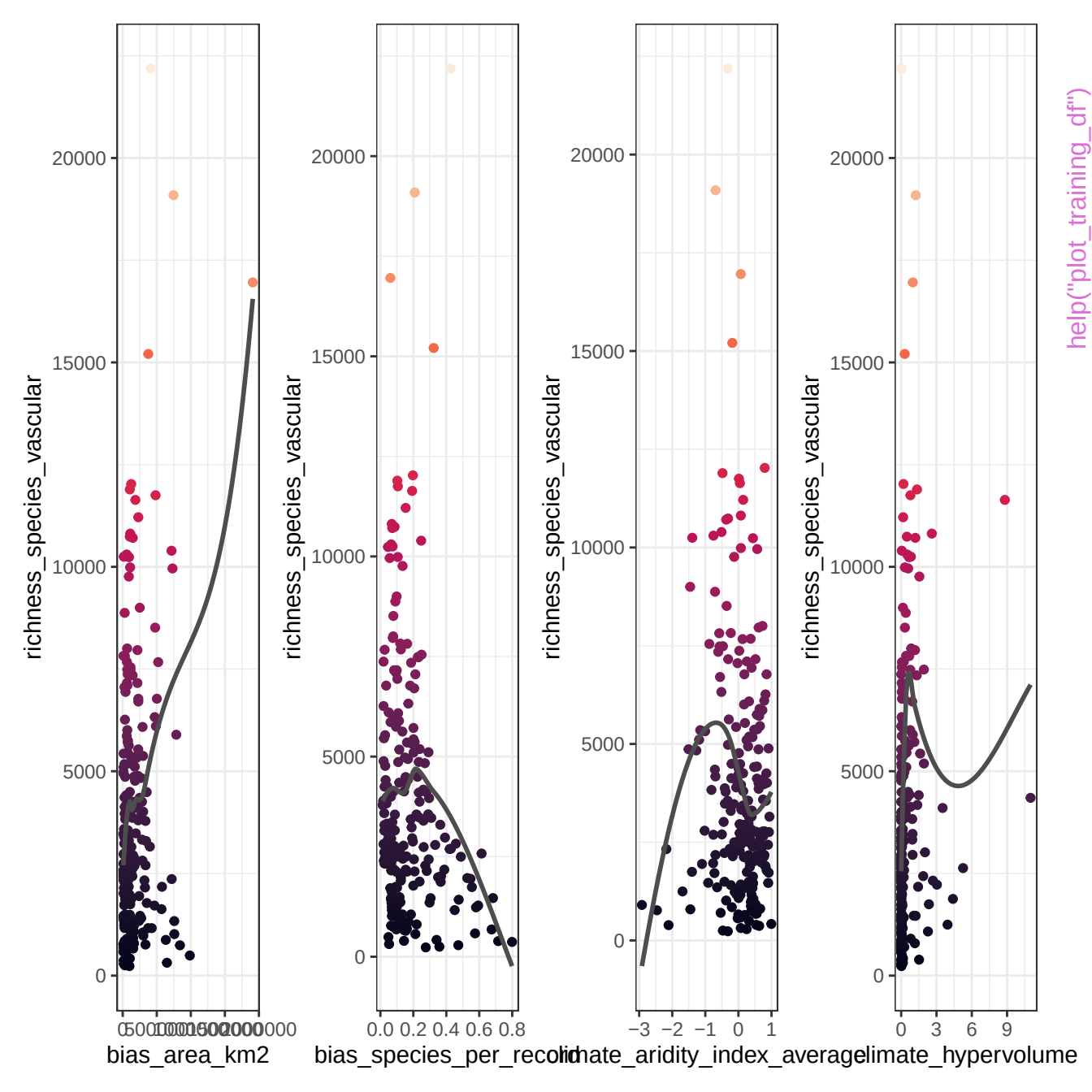

Shapiro W = 0.798; p−value = 0; Residuals are not normal
Residuals
Theoretical
Count
Residuals
Residuals vs. predictions
Residuals
Predicted
Multiscale Moran's I
Moran's I of model residuals
Distance thresholds
Moran's I p−value
< 0.05
>= 0.05
help("plot_residuals_diagnostics")

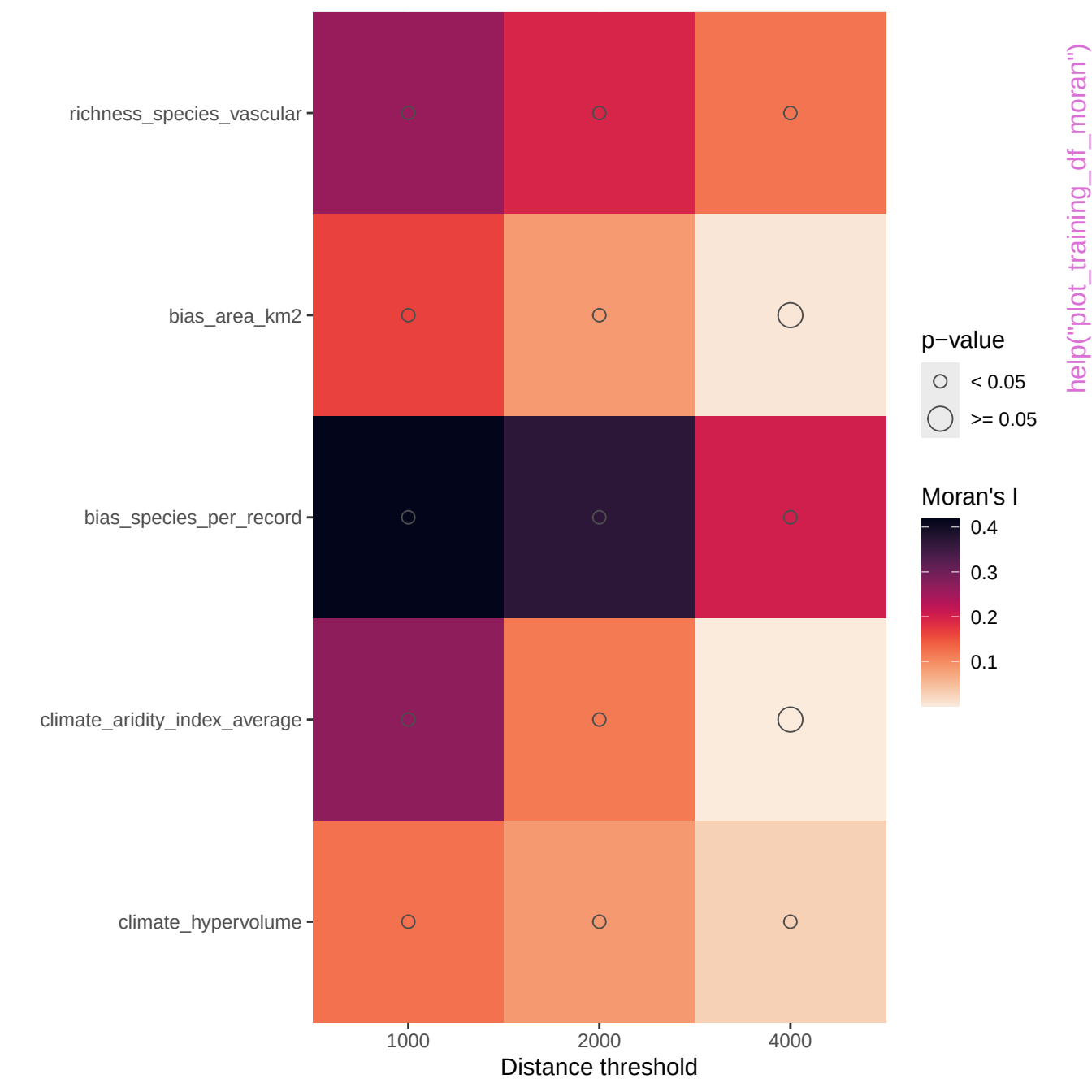

Shapiro W = 0.798; p−value = 0; Residuals are not normal
Residuals
Theoretical
Count
Residuals
Residuals vs. predictions
Residuals
Predicted
Multiscale Moran's I
Moran's I of model residuals
Distance thresholds
Moran's I p−value
< 0.05
>= 0.05
help("plot_residuals_diagnostics")

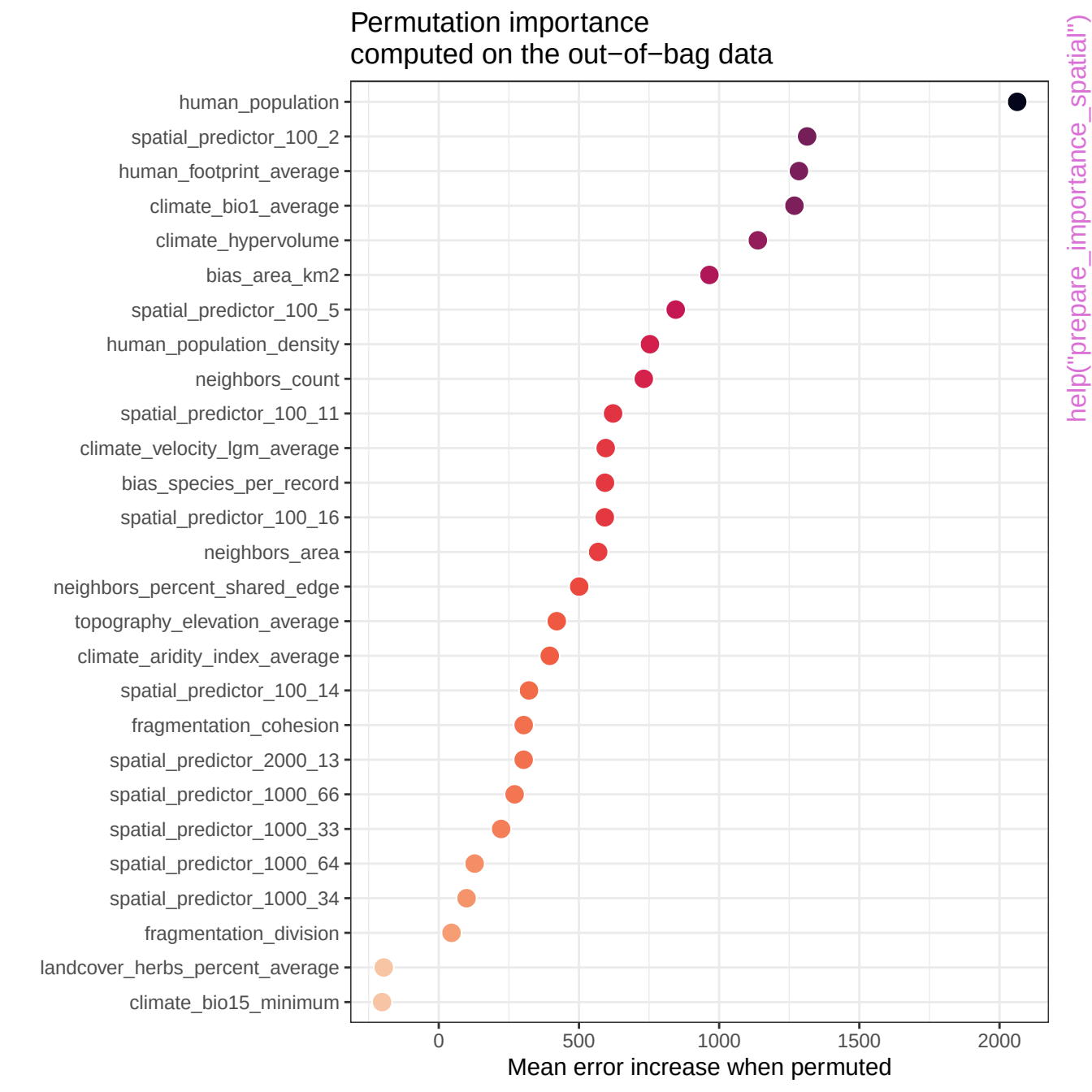

richness_species_vascular
6000
4000
2000
−200
−100
0
100
200
climate_bio1_average
Quantiles of other predictors
0.1
0.5
0.9
help("plot_response_curves")

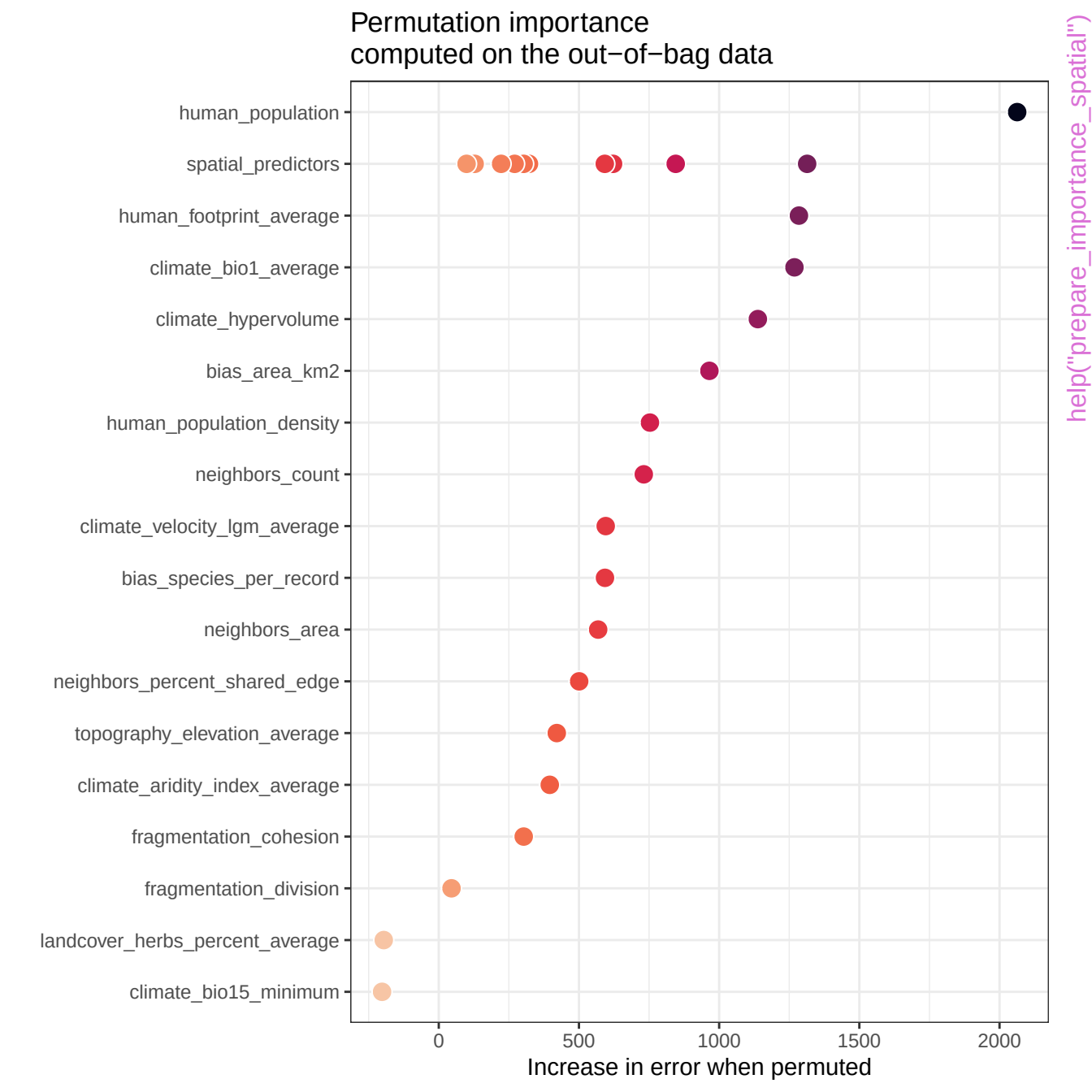

richness_species_vascular
20000
15000
10000
5000
0
−200
−100
0
100
200
climate_bio1_average
Quantiles of other predictors
0.1
0.5
0.9
help("plot_response_curves")

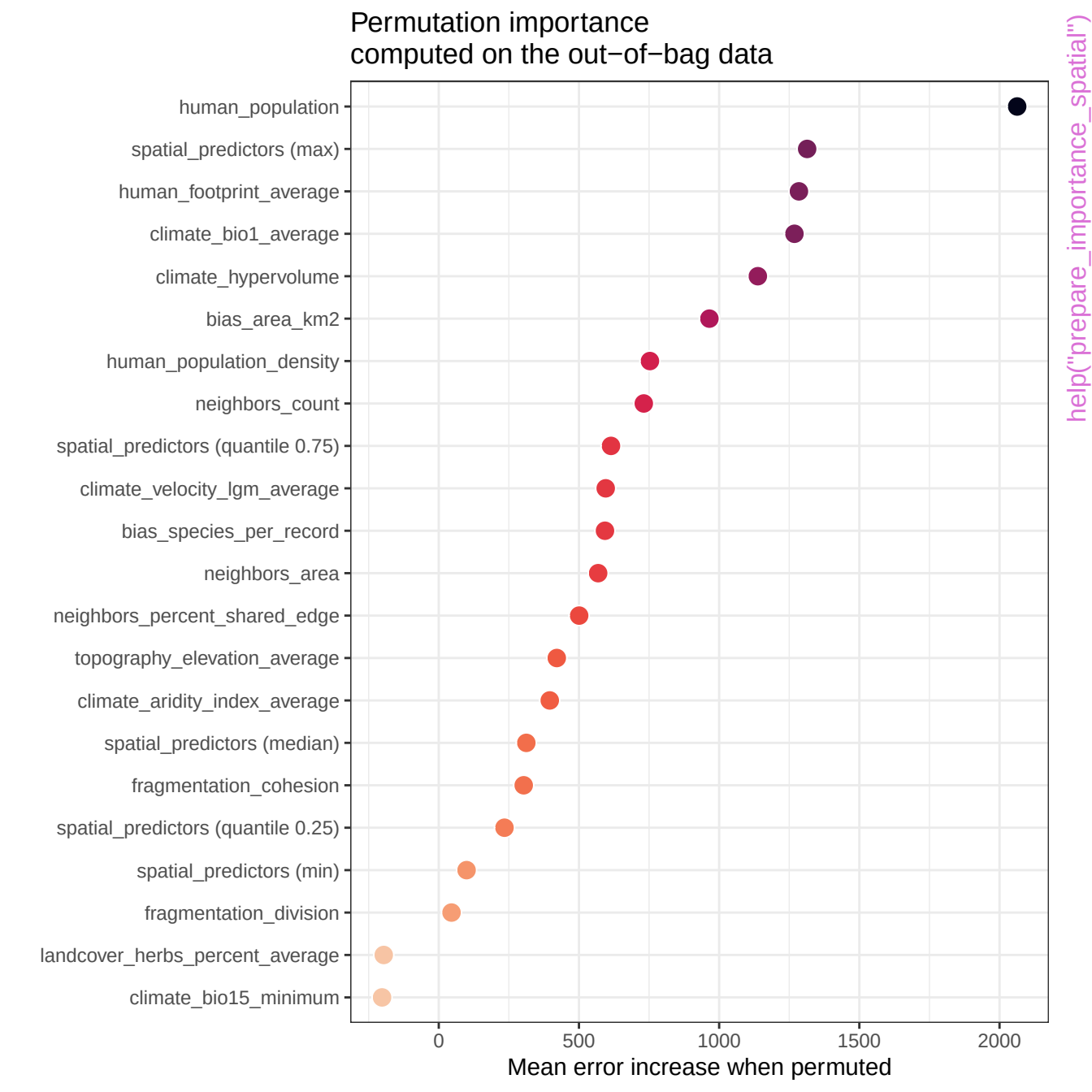

Other variables set to quantile 0.5
human_population
4e+07
3e+07
2e+07
1e+07
0e+00
−100
0
100
200
climate_bio1_average
Observed
20000
15000
10000
5000
Predicted
5000
4000
3000
help("plot_response_surface")

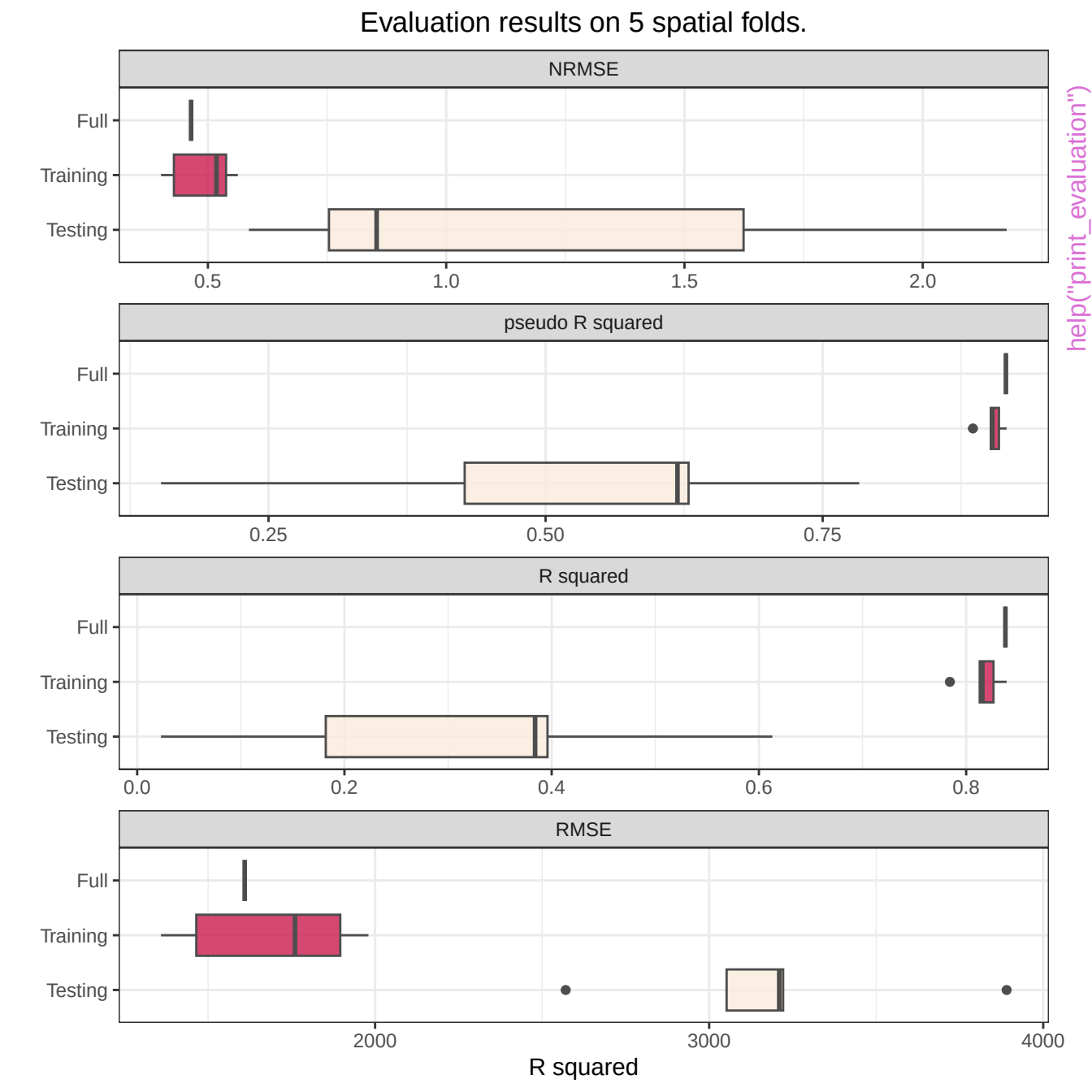

richness_species_vascular
20000
15000
10000
5000
0
bias_area_km2
bias_species_per_record
0.0 0.2 0.4 0.6 0.8
climate_aridity_index_average
−3 −2 −1 0 1
climate_hypervolume
0 3 6 9
help("plot_training_df")

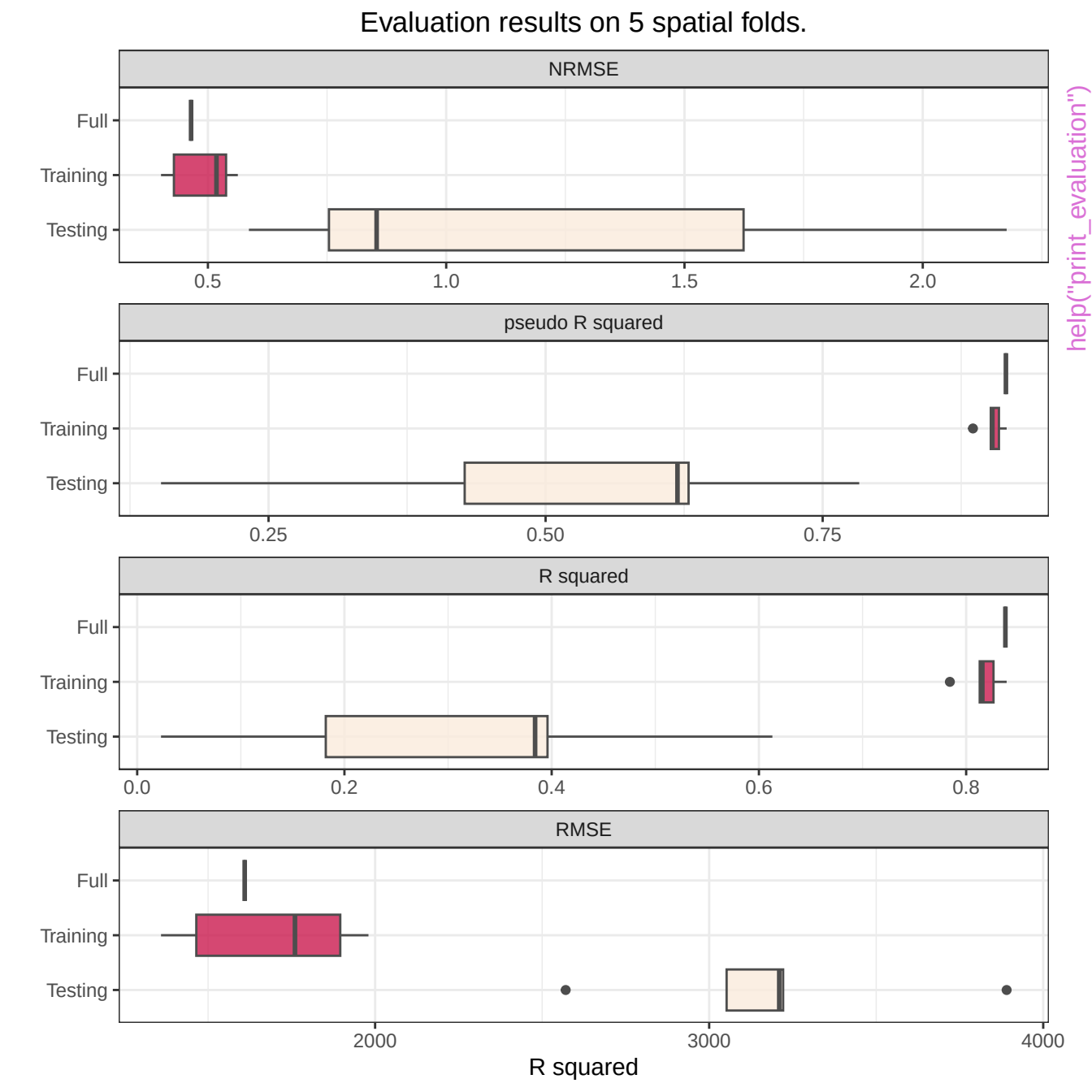

richness_species_vascular
bias_area_km2
bias_species_per_record
climate_aridity_index_average
climate_hypervolume
1000
2000
4000
Distance threshold
p−value
< 0.05
>= 0.05
Moran's I
0.4
0.3
0.2
0.1
help("plot_training_df_moran")

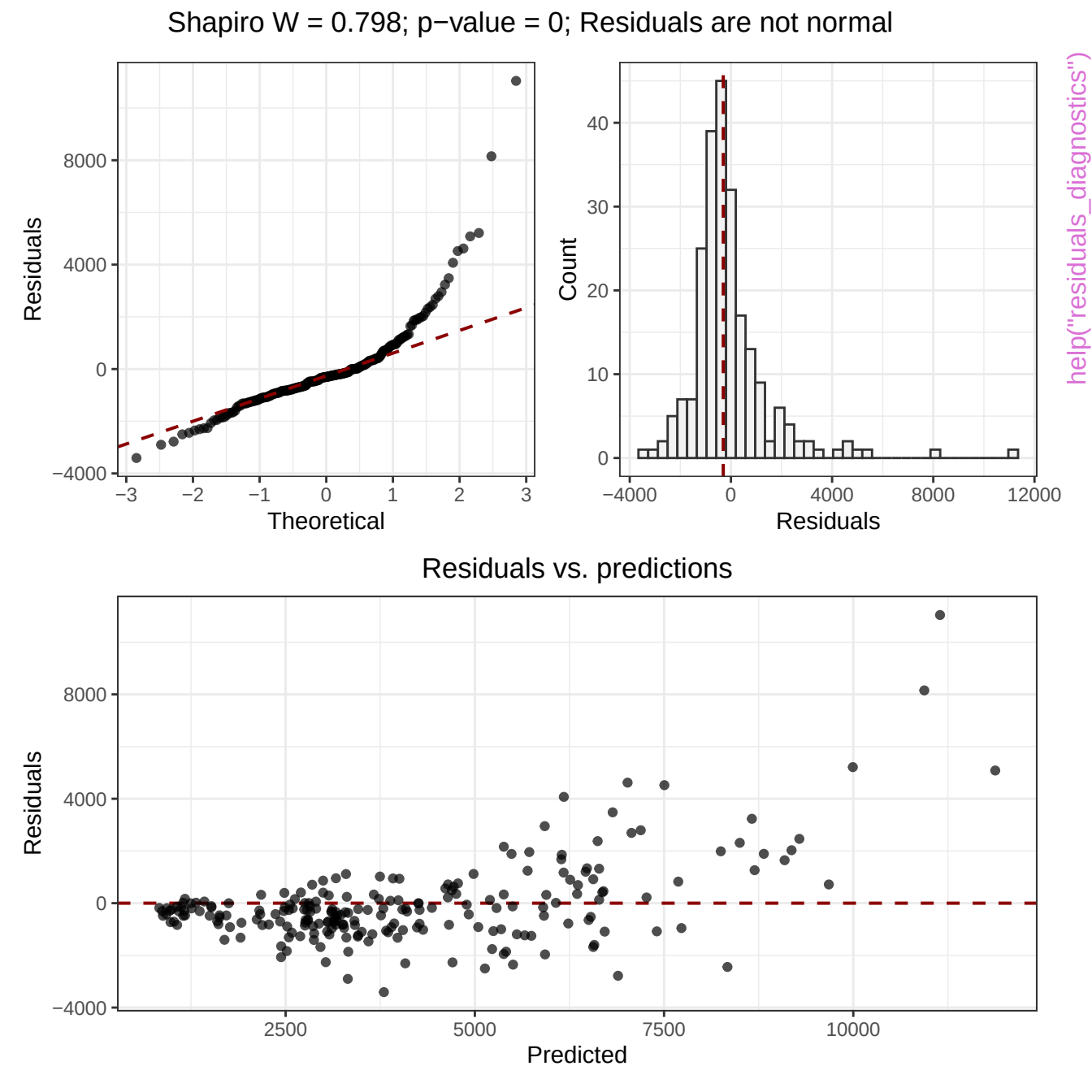

Permutation importance
computed on the out−of−bag data
human_population
spatial_predictor_100_2
human_footprint_average
climate_bio1_average
climate_hypervolume
bias_area_km2
spatial_predictor_100_5
human_population_density
neighbors_count
spatial_predictor_100_11
climate_velocity_lgm_average
bias_species_per_record
spatial_predictor_100_16
neighbors_area
neighbors_percent_shared_edge
topography_elevation_average
climate_aridity_index_average
spatial_predictor_100_14
fragmentation_cohesion
spatial_predictor_2000_13
spatial_predictor_1000_66
spatial_predictor_1000_33
spatial_predictor_1000_64
spatial_predictor_1000_34
fragmentation_division
landcover_herbs_percent_average
climate_bio15_minimum
0
500
1000
1500
2000
Mean error increase when permuted
help("prepare_importance_spatial")

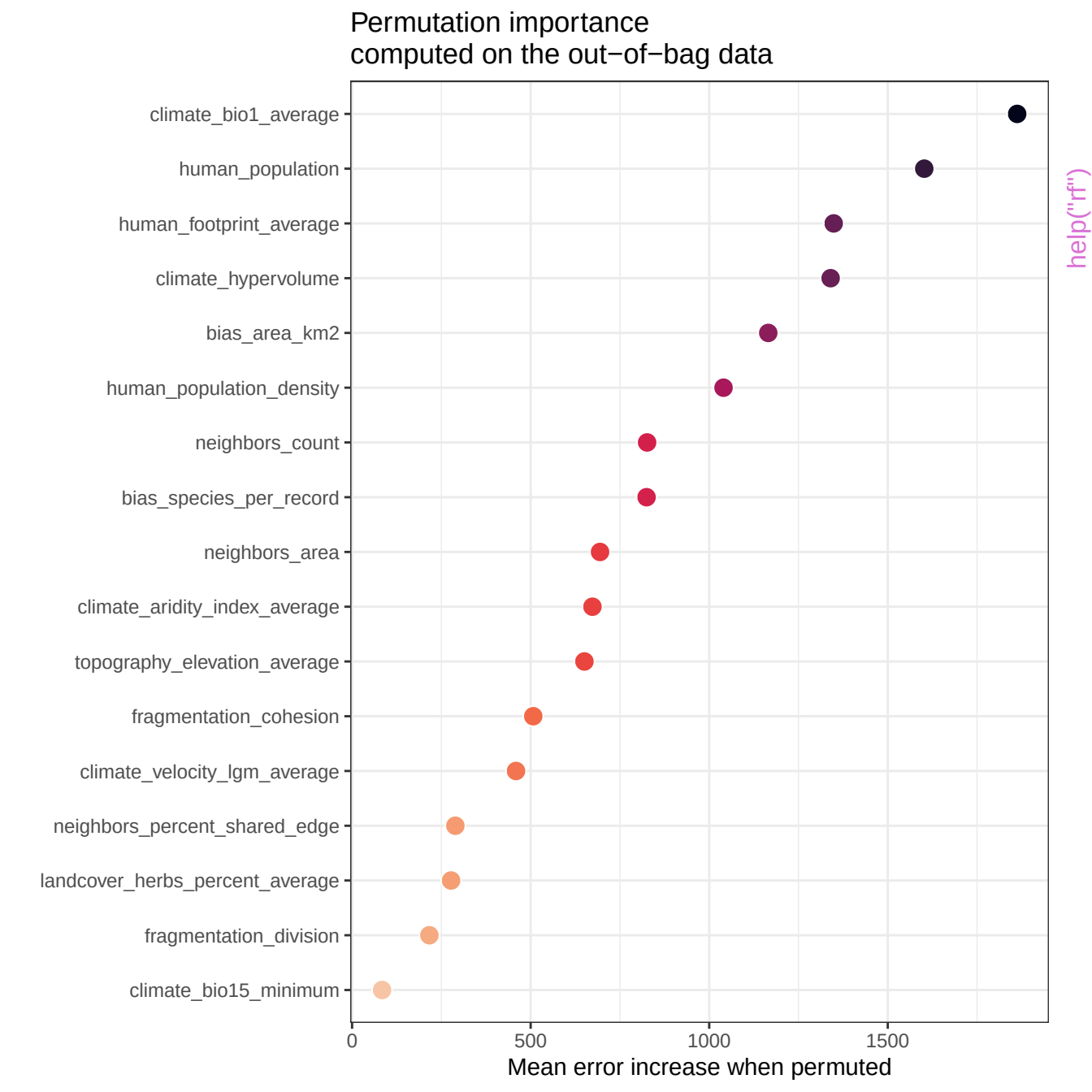

Permutation importance
computed on the out−of−bag data
human_population
spatial_predictors
human_footprint_average
climate_bio1_average
climate_hypervolume
bias_area_km2
human_population_density
neighbors_count
climate_velocity_lgm_average
bias_species_per_record
neighbors_area
neighbors_percent_shared_edge
topography_elevation_average
climate_aridity_index_average
fragmentation_cohesion
fragmentation_division
landcover_herbs_percent_average
climate_bio15_minimum
0
500
1000
1500
2000
Increase in error when permuted
help("prepare_importance_spatial")

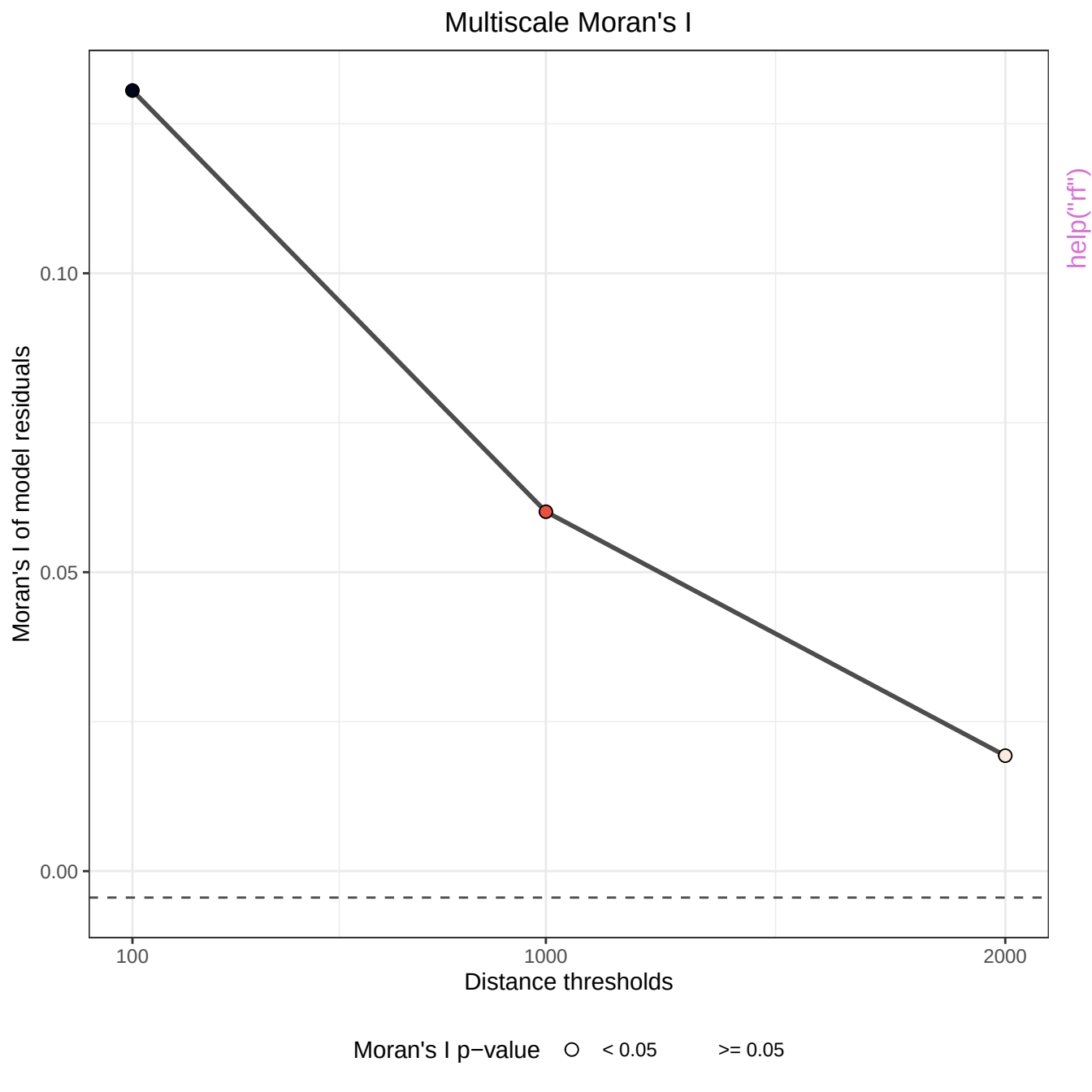

Permutation importance
computed on the out−of−bag data
human_population
spatial_predictors (max)
human_footprint_average
climate_bio1_average
climate_hypervolume
bias_area_km2
human_population_density
neighbors_count
spatial_predictors (quantile 0.75)
climate_velocity_lgm_average
bias_species_per_record
neighbors_area
neighbors_percent_shared_edge
topography_elevation_average
climate_aridity_index_average
spatial_predictors (median)
fragmentation_cohesion
spatial_predictors (quantile 0.25)
spatial_predictors (min)
fragmentation_division
landcover_herbs_percent_average
climate_bio15_minimum
0
500
1000
1500
2000
Mean error increase when permuted
help("prepare_importance_spatial")

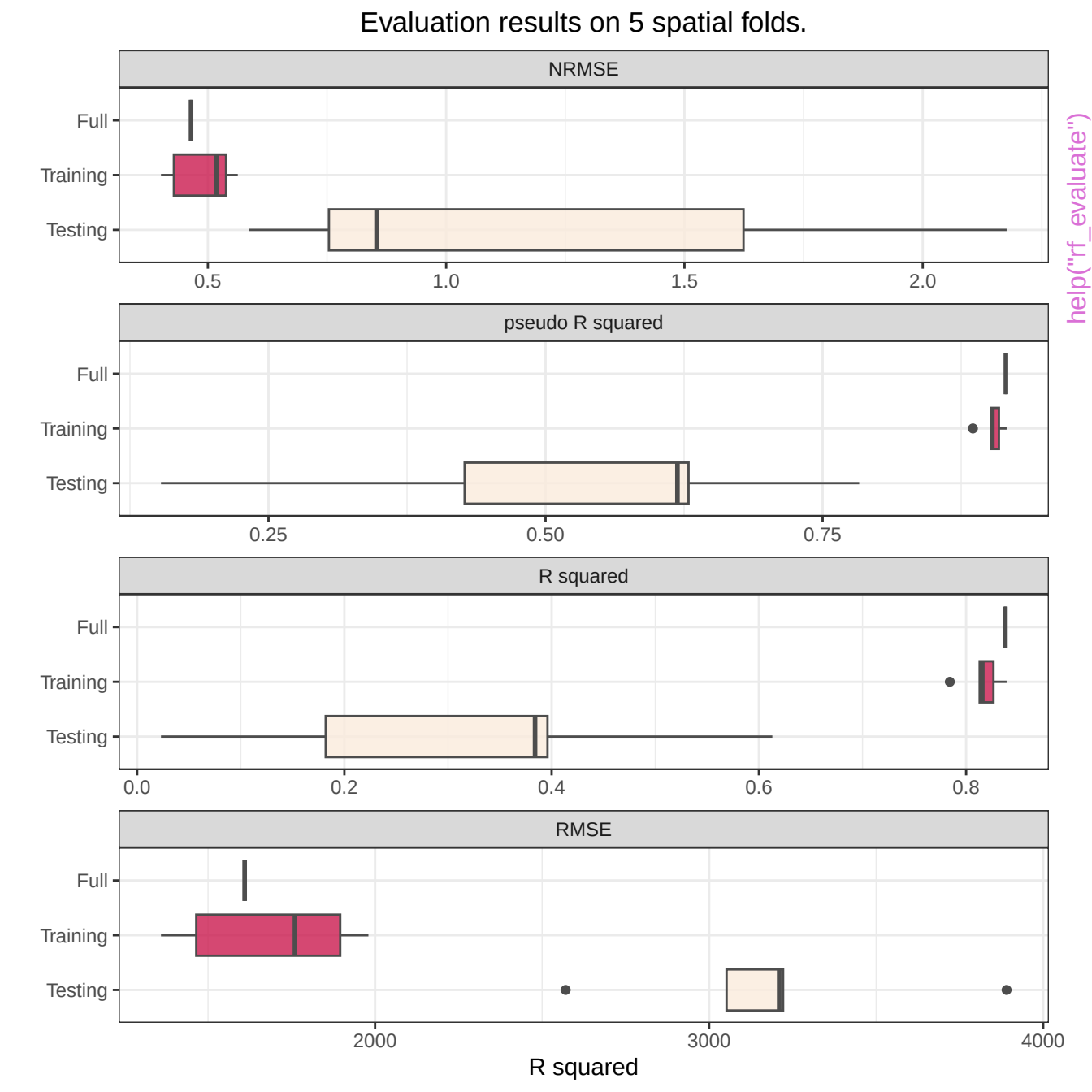

Evaluation results on 5 spatial folds.
NRMSE
Full
Training
Testing
0.5
1.0
1.5
2.0
pseudo R squared
Full
Training
Testing
0.25
0.50
0.75
R squared
Full
Training
Testing
0.0
0.2
0.4
0.6
0.8
RMSE
Full
Training
Testing
2000
3000
4000
R squared
help("print_evaluation")

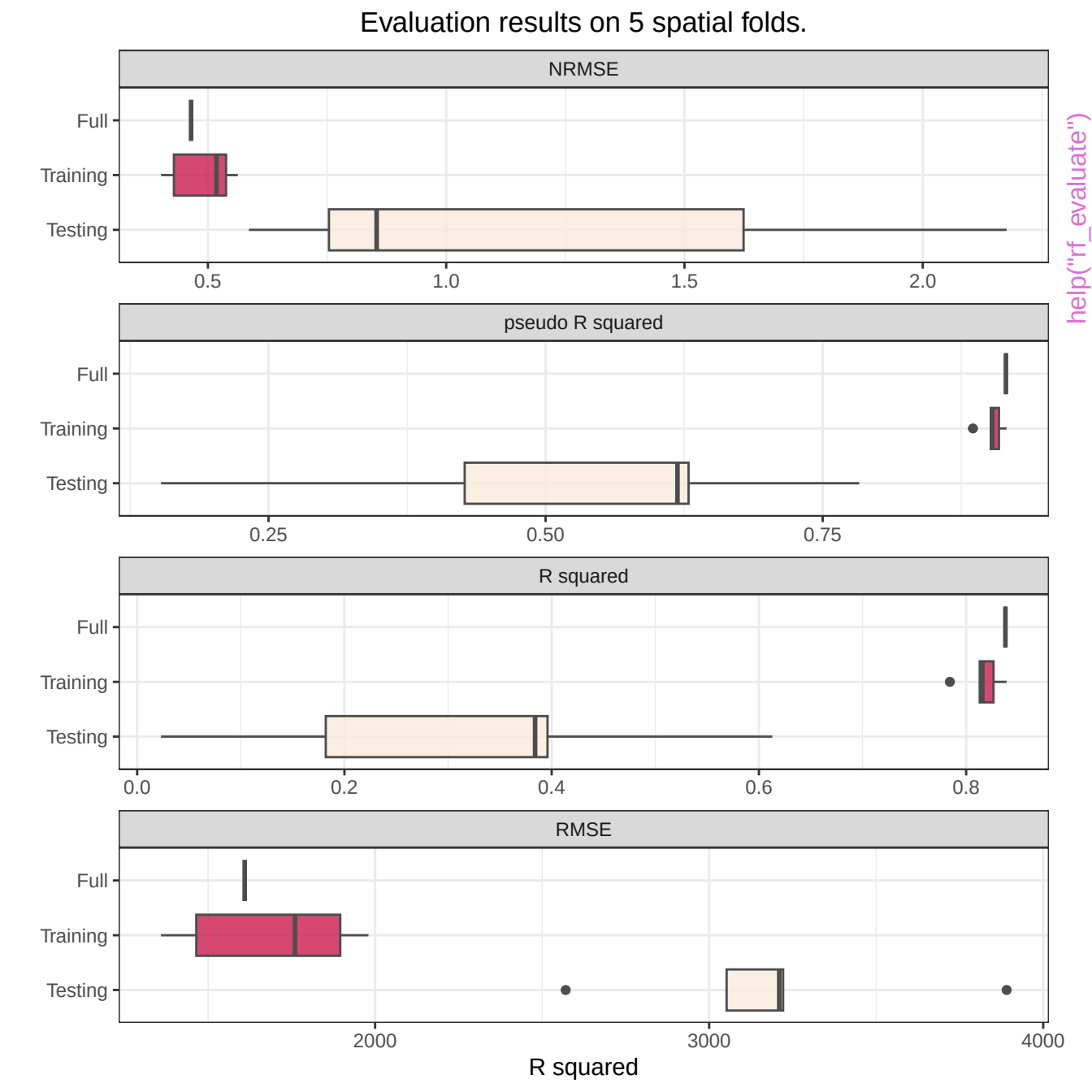

Evaluation results on 5 spatial folds.
NRMSE
Full
Training
Testing
0.5
1.0
1.5
2.0
pseudo R squared
Full
Training
Testing
0.25
0.50
0.75
R squared
Full
Training
Testing
0.0
0.2
0.4
0.6
0.8
RMSE
Full
Training
Testing
2000
3000
4000
R squared
help("print_evaluation")

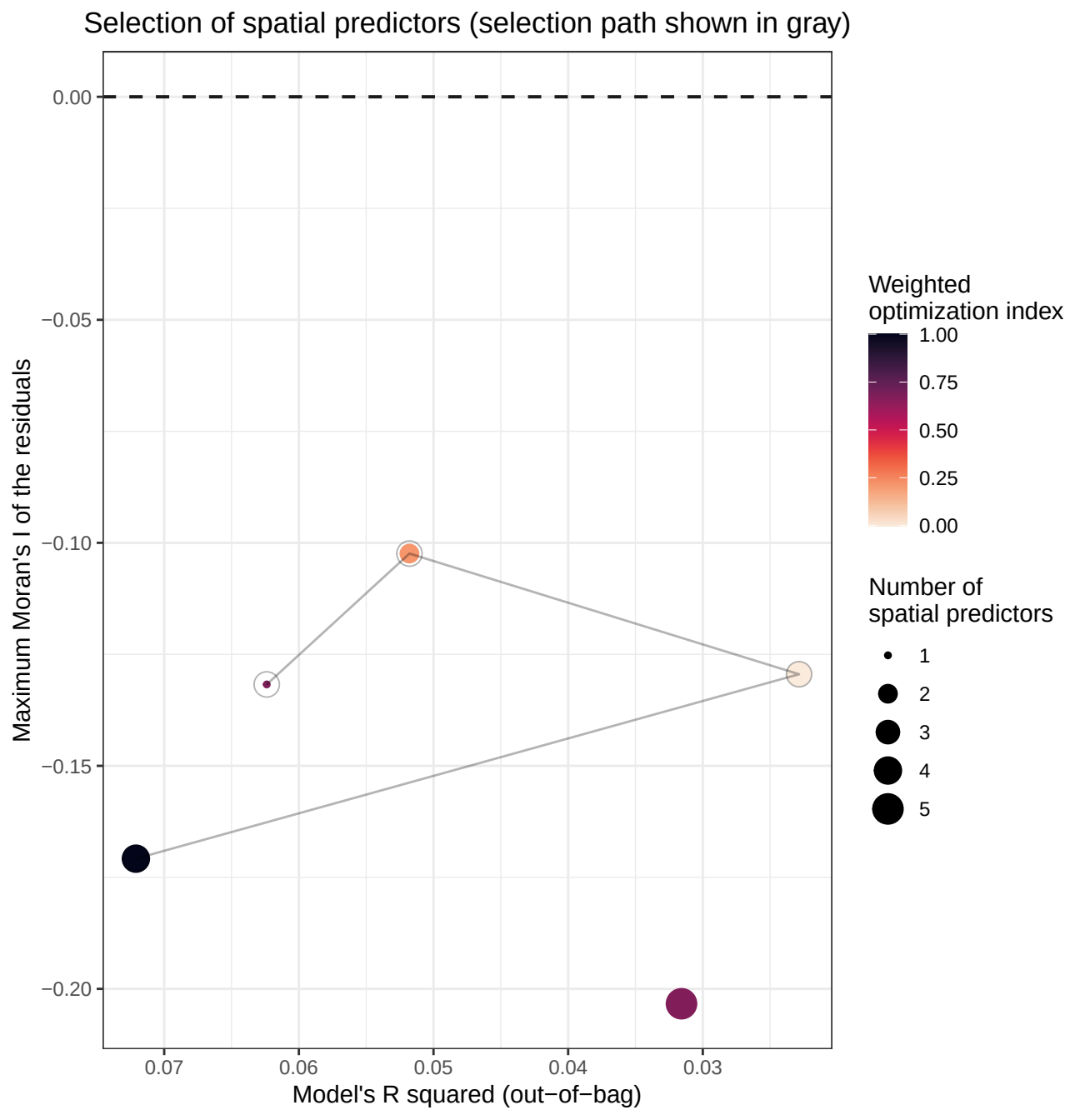

Shapiro W = 0.798; p−value = 0; Residuals are not normal
Residuals
Theoretical
Count
Residuals
help("residuals_diagnostics")
Residuals vs. predictions
Residuals
Predicted


Permutation importance
computed on the out−of−bag data
climate_bio1_average
human_population
human_footprint_average
climate_hypervolume
bias_area_km2
human_population_density
neighbors_count
bias_species_per_record
neighbors_area
climate_aridity_index_average
topography_elevation_average
fragmentation_cohesion
climate_velocity_lgm_average
neighbors_percent_shared_edge
landcover_herbs_percent_average
fragmentation_division
climate_bio15_minimum
0
500
1000
1500
Mean error increase when permuted
help("rf")


Multiscale Moran's I
help("rf")
Moran's I of model residuals
0.10
0.05
0.00
100
1000
2000
Distance thresholds
Moran's I p−value
< 0.05
>= 0.05


Evaluation results on 5 spatial folds.
NRMSE
Full
Training
Testing
0.5
1.0
1.5
2.0
pseudo R squared
Full
Training
Testing
0.25
0.50
0.75
R squared
Full
Training
Testing
0.0
0.2
0.4
0.6
0.8
RMSE
Full
Training
Testing
2000
3000
4000
R squared
help("rf_evaluate")


Evaluation results on 5 spatial folds.
NRMSE
Full
Training
Testing
0.5
1.0
1.5
2.0
pseudo R squared
Full
Training
Testing
0.25
0.50
0.75
R squared
Full
Training
Testing
0.0
0.2
0.4
0.6
0.8
RMSE
Full
Training
Testing
2000
3000
4000
R squared
help("rf_evaluate")


Selection of spatial predictors (selection path shown in gray)
0.00
−0.05
−0.10
−0.15
−0.20
Maximum Moran's I of the residuals
0.07
0.06
0.05
0.04
0.03
Model's R squared (out−of−bag)
Weighted optimization index
1.00
0.75
0.50
0.25
0.00
Number of spatial predictors
1
2
3
4
5
help("select_spatial_predictors_sequentia