TRhizo-localAdaptation

Local Adaptation by Urbanization

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Contents

Load Packages & Data

```
## Load the tidyverse
library(tidyverse)

## Load packages for data analysis
library(broom)
library(easystats)

## Read in data
# Urbanization data
urbanization.data <- read_rds(file = "data/full_urbanization_data.rds")
# Local adaptation indices
load("data_analysis/4-local_adaptation_indices/local_adaptation_indices.RData")

## Set function for scaling variables
center_and_scale <- function(x) {
  (x - mean(x, na.rm = TRUE)) / sd(x, na.rm = TRUE)
}
```

Data Management

```
## Aboveground biomass
# Global index
aboveground.biomass.LA.global.combined.data <- aboveground.biomass.LA.global.data %>%
  left_join(urbanization.data, by = "Population") %>%
  drop_na() %>%
  type_convert(col_types = c("ffnnnnnfnin")) %>%
  mutate(
    Distance_Scaled = center_and_scale(Distance),
    Human_Influence_Index_Scaled = center_and_scale(Human_Influence_Index),
    Mean_ISC_Scaled = center_and_scale(Mean_ISC)
  )
# Rural index
aboveground.biomass.LA.rural.combined.data <- aboveground.biomass.LA.rural.data %>%
  left_join(urbanization.data, by = "Population") %>%
  drop_na() %>%
  type_convert(col_types = c("ffnnnnnfnin")) %>%
  mutate(
    Distance_Scaled = center_and_scale(Distance),
    Human_Influence_Index_Scaled = center_and_scale(Human_Influence_Index),
    Mean_ISC_Scaled = center_and_scale(Mean_ISC)
  )
# Urban index
aboveground.biomass.LA.urban.combined.data <- aboveground.biomass.LA.urban.data %>%
  left_join(urbanization.data, by = "Population") %>%
  drop_na() %>%
  type_convert(col_types = c("ffnnnnnfnin")) %>%
  mutate(
    Distance_Scaled = center_and_scale(Distance),
    Human_Influence_Index_Scaled = center_and_scale(Human_Influence_Index),
    Mean_ISC_Scaled = center_and_scale(Mean_ISC)
  )

## Belowground biomass
# Global index
belowground.biomass.LA.global.combined.data <- belowground.biomass.LA.global.data %>%
  left_join(urbanization.data, by = "Population") %>%
  drop_na() %>%
  type_convert(col_types = c("ffnnnnnfnin")) %>%
  mutate(
    Distance_Scaled = center_and_scale(Distance),
    Human_Influence_Index_Scaled = center_and_scale(Human_Influence_Index),
    Mean_ISC_Scaled = center_and_scale(Mean_ISC)
  )
# Rural index
belowground.biomass.LA.rural.combined.data <- belowground.biomass.LA.rural.data %>%
  left_join(urbanization.data, by = "Population") %>%
  drop_na() %>%
  type_convert(col_types = c("ffnnnnnfnin")) %>%
  mutate(
    Distance_Scaled = center_and_scale(Distance),
    Human_Influence_Index_Scaled = center_and_scale(Human_Influence_Index),
    Mean_ISC_Scaled = center_and_scale(Mean_ISC)
```

```
  )
# Urban index
belowground.biomass.LA.urban.combined.data <- belowground.biomass.LA.urban.data %>%
  left_join(urbanization.data, by = "Population") %>%
  drop_na() %>%
  type_convert(col_types = c("ffnnnnnfnin")) %>%
  mutate(
    Distance_Scaled = center_and_scale(Distance),
    Human_Influence_Index_Scaled = center_and_scale(Human_Influence_Index),
    Mean_ISC_Scaled = center_and_scale(Mean_ISC)
  )

## Nodule density
# Global index
nodule.density.LA.global.combined.data <- nodule.density.LA.global.data %>%
  left_join(urbanization.data, by = "Population") %>%
  drop_na() %>%
  type_convert(col_types = c("ffnnnnnfnin")) %>%
  mutate(
    Distance_Scaled = center_and_scale(Distance),
    Human_Influence_Index_Scaled = center_and_scale(Human_Influence_Index),
    Mean_ISC_Scaled = center_and_scale(Mean_ISC)
  )
# Rural index
nodule.density.LA.rural.combined.data <- nodule.density.LA.rural.data %>%
  left_join(urbanization.data, by = "Population") %>%
  drop_na() %>%
  type_convert(col_types = c("ffnnnnnfnin")) %>%
  mutate(
    Distance_Scaled = center_and_scale(Distance),
    Human_Influence_Index_Scaled = center_and_scale(Human_Influence_Index),
    Mean_ISC_Scaled = center_and_scale(Mean_ISC)
  )
# Urban index
nodule.density.LA.urban.combined.data <- nodule.density.LA.urban.data %>%
  left_join(urbanization.data, by = "Population") %>%
  drop_na() %>%
  type_convert(col_types = c("ffnnnnnfnin")) %>%
  mutate(
    Distance_Scaled = center_and_scale(Distance),
    Human_Influence_Index_Scaled = center_and_scale(Human_Influence_Index),
    Mean_ISC_Scaled = center_and_scale(Mean_ISC)
  )

## Fixing nodule density
fixing.nodule.density.LA.global.combined.data <- fixing.nodule.density.LA.global.data %>%
  left_join(urbanization.data, by = "Population") %>%
  drop_na() %>%
  type_convert(col_types = c("ffnnnnnfnin")) %>%
  mutate(
    Distance_Scaled = center_and_scale(Distance),
    Human_Influence_Index_Scaled = center_and_scale(Human_Influence_Index),
    Mean_ISC_Scaled = center_and_scale(Mean_ISC)
```

```
  )
# Rural index
fixing.nodule.density.LA.rural.combined.data <- fixing.nodule.density.LA.rural.data %>%
  left_join(urbanization.data, by = "Population") %>%
  drop_na() %>%
  type_convert(col_types = c("ffnnnnnfnin")) %>%
  mutate(
    Distance_Scaled = center_and_scale(Distance),
    Human_Influence_Index_Scaled = center_and_scale(Human_Influence_Index),
    Mean_ISC_Scaled = center_and_scale(Mean_ISC)
  )
# Urban index
fixing.nodule.density.LA.urban.combined.data <- fixing.nodule.density.LA.urban.data %>%
  left_join(urbanization.data, by = "Population") %>%
  drop_na() %>%
  type_convert(col_types = c("ffnnnnnfnin")) %>%
  mutate(
    Distance_Scaled = center_and_scale(Distance),
    Human_Influence_Index_Scaled = center_and_scale(Human_Influence_Index),
    Mean_ISC_Scaled = center_and_scale(Mean_ISC)
  )
```

Aboveground Biomass Regressions

Global Index

Fit the Regressions

```
## Distance
aboveground.biomass.by.distance.global.LM <- lm(
  AG_Biomass_LA_Global ~ Distance_Scaled,
  data = aboveground.biomass.LA.global.combined.data
)

## Human influence index
aboveground.biomass.by.HII.global.LM <- lm(
  AG_Biomass_LA_Global ~ Human_Influence_Index_Scaled,
  data = aboveground.biomass.LA.global.combined.data
)

## Impervious surface cover
aboveground.biomass.by.ISC.global.LM <- lm(
  AG_Biomass_LA_Global ~ Mean_ISC_Scaled,
  data = aboveground.biomass.LA.global.combined.data
)
```

Check Model Assumptions

```
## Distance
check_model(aboveground.biomass.by.distance.global.LM)
# Linear assumption met
# Homogeneity of variance
# Residuals approximately follow a normal distribution

## Human influence index
check_model(aboveground.biomass.by.HII.global.LM)
# Linear assumption met
# Homogeneity of variance
# Residuals approximately follow a normal distribution

## Impervious surface cover
check_model(aboveground.biomass.by.ISC.global.LM)
# Linear assumption met
# Homogeneity of variance
# Residuals approximately follow a normal distribution
```

Model Summaries

Table 1: Summary of the aboveground biomass global local adaptation index by distance model. Adjusted R-squared = 0.

Term	Estimate	SE	t	P-value
(Intercept)	0	0.002	-0.044	0.965
Distance_Scaled	0	0.002	-0.090	0.929

Table 2: Summary of the aboveground biomass global local adaptation index by HII model. Adjusted R-squared = 0.031.

Term	Estimate	SE	t	P-value
(Intercept)	0.000	0.002	-0.045	0.964
Human_Influence_Index_Scaled	-0.003	0.002	-1.687	0.097

Table 3: Summary of the aboveground biomass global local adaptation index by ISC model. Adjusted R-squared = 0.

Term	Estimate	SE	t	P-value
(Intercept)	0.000	0.002	-0.044	0.965
Mean_ISC_Scaled	0.001	0.002	0.652	0.517

Rural Index

Fit the Regressions

```
## Distance
aboveground.biomass.by.distance.rural.LM <- lm(
  AG_Biomass_LA_Rural ~ Distance_Scaled,
  data = aboveground.biomass.LA.rural.combined.data
)

## Human influence index
aboveground.biomass.by.HII.rural.LM <- lm(
  AG_Biomass_LA_Rural ~ Human_Influence_Index_Scaled,
  data = aboveground.biomass.LA.rural.combined.data
)

## Impervious surface cover
aboveground.biomass.by.ISC.rural.LM <- lm(
  AG_Biomass_LA_Rural ~ Mean_ISC_Scaled,
  data = aboveground.biomass.LA.rural.combined.data
)
```

Check Model Assumptions

```
## Distance
check_model(aboveground.biomass.by.distance.rural.LM)
# Linear assumption met
# Homogeneity of variance
# Residuals approximately follow a normal distribution

## Human influence index
check_model(aboveground.biomass.by.HII.rural.LM)
# Linear assumption met
# Homogeneity of variance
# Residuals approximately follow a normal distribution

## Impervious surface cover
check_model(aboveground.biomass.by.ISC.rural.LM)
# Linear assumption met
# Homogeneity of variance
# Residuals approximately follow a normal distribution
```

Model Summaries

Table 4: Summary of the aboveground biomass rural local adaptation index by distance model. Adjusted R-squared = 0.

Term	Estimate	SE	t	P-value
(Intercept)	0.000	0.002	0.00	1.000
Distance_Scaled	0.001	0.002	0.33	0.743

Table 5: Summary of the aboveground biomass rural local adaptation index by HII model. Adjusted R-squared = 0.012.

Term	Estimate	SE	t	P-value
(Intercept)	0.000	0.002	0.000	1.000
Human_Influence_Index_Scaled	-0.003	0.002	-1.307	0.196

Table 6: Summary of the aboveground biomass rural local adaptation index by ISC model. Adjusted R-squared = 0.

Term	Estimate	SE	t	P-value
(Intercept)	0	0.002	0.00	1.000
Mean_ISC_Scaled	0	0.002	0.22	0.827

Urban Index

Fit the Regressions

```
## Distance
aboveground.biomass.by.distance.urban.LM <- lm(
  AG_Biomass_LA_Urban ~ Distance_Scaled,
  data = aboveground.biomass.LA.urban.combined.data
)

## Human influence index
aboveground.biomass.by.HII.urban.LM <- lm(
  AG_Biomass_LA_Urban ~ Human_Influence_Index_Scaled,
  data = aboveground.biomass.LA.urban.combined.data
)

## Impervious surface cover
aboveground.biomass.by.ISC.urban.LM <- lm(
  AG_Biomass_LA_Urban ~ Mean_ISC_Scaled,
  data = aboveground.biomass.LA.urban.combined.data
)
```

Check Model Assumptions

```
## Distance
check_model(aboveground.biomass.by.distance.urban.LM)
# Linear assumption met
# Homogeneity of variance
# Residuals approximately follow a normal distribution

## Human influence index
check_model(aboveground.biomass.by.HII.urban.LM)
# Linear assumption met
# Slight (+ non-concerning) heterogeneity of variance
# Residuals approximately follow a normal distribution

## Impervious surface cover
check_model(aboveground.biomass.by.ISC.urban.LM)
# Linear assumption met
# Homogeneity of variance
# Residuals approximately follow a normal distribution
```

Model Summaries

Table 7: Summary of the aboveground biomass urban local adaptation index by distance model. Adjusted R-squared = 0.

Term	Estimate	SE	t	P-value
(Intercept)	0.000	0.002	-0.144	0.886
Distance_Scaled	-0.001	0.002	-0.469	0.641

Table 8: Summary of the aboveground biomass urban local adaptation index by HII model. Adjusted R-squared = 0.022.

Term	Estimate	SE	t	P-value
(Intercept)	0.000	0.002	-0.146	0.884
Human_Influence_Index_Scaled	-0.003	0.002	-1.516	0.135

Table 9: Summary of the aboveground biomass urban local adaptation index by ISC model. Adjusted R-squared = 0.

Term	Estimate	SE	t	P-value
(Intercept)	0.000	0.002	-0.144	0.886
Mean_ISC_Scaled	0.002	0.002	0.865	0.391

Belowground Biomass Regressions

Global Index

Fit the Regressions

```
## Distance
belowground.biomass.by.distance.global.LM <- lm(
  BG_Biomass_LA_Global ~ Distance_Scaled,
  data = belowground.biomass.LA.global.combined.data
)

## Human influence index
belowground.biomass.by.HII.global.LM <- lm(
  BG_Biomass_LA_Global ~ Human_Influence_Index_Scaled,
  data = belowground.biomass.LA.global.combined.data
)

## Impervious surface cover
belowground.biomass.by.ISC.global.LM <- lm(
  BG_Biomass_LA_Global ~ Mean_ISC_Scaled,
  data = belowground.biomass.LA.global.combined.data
)
```

Check Model Assumptions

```
## Distance
check_model(belowground.biomass.by.distance.global.LM)
# Linear assumption met
# Homogeneity of variance
# Residuals approximately follow a normal distribution

## Human influence index
check_model(belowground.biomass.by.HII.global.LM)
# Linear assumption met
# Homogeneity of variance
# Residuals approximately follow a normal distribution

## Impervious surface cover
check_model(belowground.biomass.by.ISC.global.LM)
# Linear assumption met
# Homogeneity of variance
# Residuals approximately follow a normal distribution
```

Model Summaries

Table 10: Summary of the belowground biomass global local adaptation index by distance model. Adjusted R-squared = 0.

Term	Estimate	SE	t	P-value
(Intercept)	0.000	0.001	-0.022	0.983
Distance_Scaled	-0.001	0.001	-0.695	0.490

Table 11: Summary of the belowground biomass global local adaptation index by HII model. Adjusted R-squared = 0.012.

Term	Estimate	SE	t	P-value
(Intercept)	0.000	0.001	-0.022	0.983
Human_Influence_Index_Scaled	-0.001	0.001	-1.304	0.198

Table 12: Summary of the belowground biomass global local adaptation index by ISC model. Adjusted R-squared = 0.

Term	Estimate	SE	t	P-value
(Intercept)	0.000	0.001	-0.022	0.983
Mean_ISC_Scaled	0.001	0.001	0.999	0.322

Rural Index

Fit the Regressions

```
## Distance
belowground.biomass.by.distance.rural.LM <- lm(
  BG_Biomass_LA_Rural ~ Distance_Scaled,
  data = belowground.biomass.LA.rural.combined.data
)

## Human influence index
belowground.biomass.by.HII.rural.LM <- lm(
  BG_Biomass_LA_Rural ~ Human_Influence_Index_Scaled,
  data = belowground.biomass.LA.rural.combined.data
)

## Impervious surface cover
belowground.biomass.by.ISC.rural.LM <- lm(
  BG_Biomass_LA_Rural ~ Mean_ISC_Scaled,
  data = belowground.biomass.LA.rural.combined.data
)
```

Check Model Assumptions

```
## Distance
check_model(belowground.biomass.by.distance.rural.LM)
# Linear assumption met
# Homogeneity of variance
# Residuals approximately follow a normal distribution

## Human influence index
check_model(belowground.biomass.by.HII.rural.LM)
# Linear assumption met
# Homogeneity of variance
# Residuals approximately follow a normal distribution

## Impervious surface cover
check_model(belowground.biomass.by.ISC.rural.LM)
# Linear assumption met
# Homogeneity of variance
# Residuals approximately follow a normal distribution
```

Model Summaries

Table 13: Summary of the belowground biomass rural local adaptation index by distance model. Adjusted R-squared = 0.

Term	Estimate	SE	t	P-value
(Intercept)	0	0.001	0.000	1.000
Distance_Scaled	0	0.001	-0.065	0.948

Table 14: Summary of the belowground biomass rural local adaptation index by HII model. Adjusted R-squared = 0.024.

Term	Estimate	SE	t	P-value
(Intercept)	0.000	0.001	0.000	1.000
Human_Influence_Index_Scaled	-0.001	0.001	-1.551	0.126

Table 15: Summary of the belowground biomass rural local adaptation index by ISC model. Adjusted R-squared = 0.

Term	Estimate	SE	t	P-value
(Intercept)	0	0.001	0.000	1.000
Mean_ISC_Scaled	0	0.001	0.033	0.974

Urban Index

Fit the Regressions

```
## Distance
belowground.biomass.by.distance.urban.LM <- lm(
  BG_Biomass_LA_Urban ~ Distance_Scaled,
  data = belowground.biomass.LA.urban.combined.data
)

## Human influence index
belowground.biomass.by.HII.urban.LM <- lm(
  BG_Biomass_LA_Urban ~ Human_Influence_Index_Scaled,
  data = belowground.biomass.LA.urban.combined.data
)

## Impervious surface cover
belowground.biomass.by.ISC.urban.LM <- lm(
  BG_Biomass_LA_Urban ~ Mean_ISC_Scaled,
  data = belowground.biomass.LA.urban.combined.data
)
```

Check Model Assumptions

```
## Distance
check_model(belowground.biomass.by.distance.urban.LM)
# Linear assumption met
# Homogeneity of variance
# Residuals approximately follow a normal distribution

## Human influence index
check_model(belowground.biomass.by.HII.urban.LM)
# Linear assumption met
# Slight (+ non-concerning) heterogeneity of variance
# Residuals approximately follow a normal distribution

## Impervious surface cover
check_model(belowground.biomass.by.ISC.urban.LM)
# Linear assumption met
# Homogeneity of variance
# Residuals approximately follow a normal distribution
```

Model Summaries

Table 16: Summary of the belowground biomass urban local adaptation index by distance model. Adjusted R-squared = 0.001.

Term	Estimate	SE	t	P-value
(Intercept)	0.000	0.001	-0.113	0.911
Distance_Scaled	-0.001	0.001	-1.025	0.310

Table 17: Summary of the belowground biomass urban local adaptation index by HII model. Adjusted R-squared = 0.

Term	Estimate	SE	t	P-value
(Intercept)	0.000	0.001	-0.112	0.911
Human_Influence_Index_Scaled	-0.001	0.001	-0.722	0.473

Table 18: Summary of the belowground biomass urban local adaptation index by ISC model. Adjusted R-squared = 0.022.

Term	Estimate	SE	t	P-value
(Intercept)	0.000	0.001	-0.114	0.910
Mean_ISC_Scaled	0.001	0.001	1.505	0.138

Nodule Density Regressions

Global Index

Fit the Regressions

```
## Distance
nodule.density.by.distance.global.LM <- lm(
  Nod_Density_LA_Global ~ Distance_Scaled,
  data = nodule.density.LA.global.combined.data
)

## Human influence index
nodule.density.by.HII.global.LM <- lm(
  Nod_Density_LA_Global ~ Human_Influence_Index_Scaled,
  data = nodule.density.LA.global.combined.data
)

## Impervious surface cover
nodule.density.by.ISC.global.LM <- lm(
  Nod_Density_LA_Global ~ Mean_ISC_Scaled,
  data = nodule.density.LA.global.combined.data
)
```

Check Model Assumptions

```
## Distance
check_model(nodule.density.by.distance.global.LM)
# Linear assumption met
# Homogeneity of variance
# Residuals approximately follow a normal distribution

## Human influence index
check_model(nodule.density.by.HII.global.LM)
# Linear assumption met
# Homogeneity of variance
# Residuals approximately follow a normal distribution

## Impervious surface cover
check_model(nodule.density.by.ISC.global.LM)
# Linear assumption met
# Slight (+ non-concerning) heterogeneity of variance
# Residuals approximately follow a normal distribution
```

Model Summaries

Table 19: Summary of the nodule density global local adaptation index by distance model. Adjusted R-squared = 0.

Term	Estimate	SE	t	P-value
(Intercept)	0.000	0.006	0.072	0.943
Distance_Scaled	0.001	0.006	0.132	0.895

Table 20: Summary of the nodule density global local adaptation index by HII model. Adjusted R-squared = 0.

Term	Estimate	SE	t	P-value
(Intercept)	0.000	0.006	0.072	0.943
Human_Influence_Index_Scaled	0.003	0.006	0.624	0.535

Table 21: Summary of the nodule density global local adaptation index by ISC model. Adjusted R-squared = 0.

Term	Estimate	SE	t	P-value
(Intercept)	0.000	0.006	0.072	0.943
Mean_ISC_Scaled	-0.002	0.006	-0.400	0.691

Rural Index

Fit the Regressions

```
## Distance
nodule.density.by.distance.rural.LM <- lm(
  Nod_Density_LA_Rural ~ Distance_Scaled,
  data = nodule.density.LA.rural.combined.data
)

## Human influence index
nodule.density.by.HII.rural.LM <- lm(
  Nod_Density_LA_Rural ~ Human_Influence_Index_Scaled,
  data = nodule.density.LA.rural.combined.data
)

## Impervious surface cover
nodule.density.by.ISC.rural.LM <- lm(
  Nod_Density_LA_Rural ~ Mean_ISC_Scaled,
  data = nodule.density.LA.rural.combined.data
)
```

Check Model Assumptions

```
## Distance
check_model(nodule.density.by.distance.rural.LM)
# Linear assumption met
# Homogeneity of variance
# Residuals approximately follow a normal distribution

## Human influence index
check_model(nodule.density.by.HII.rural.LM)
# Linear assumption met
# Homogeneity of variance
# Residuals approximately follow a normal distribution

## Impervious surface cover
check_model(nodule.density.by.ISC.rural.LM)
# Linear assumption met
# Homogeneity of variance
# Residuals approximately follow a normal distribution
```

Model Summaries

Table 22: Summary of the nodule density rural local adaptation index by distance model. Adjusted R-squared = 0.006.

Term	Estimate	SE	t	P-value
(Intercept)	0.000	0.006	0.079	0.937
Distance_Scaled	0.007	0.006	1.174	0.245

Table 23: Summary of the nodule density rural local adaptation index by HII model. Adjusted R-squared = 0.014.

Term	Estimate	SE	t	P-value
(Intercept)	0.000	0.006	0.080	0.937
Human_Influence_Index_Scaled	0.008	0.006	1.356	0.180

Table 24: Summary of the nodule density rural local adaptation index by ISC model. Adjusted R-squared = 0.

Term	Estimate	SE	t	P-value
(Intercept)	0.000	0.006	0.078	0.938
Mean_ISC_Scaled	-0.003	0.006	-0.488	0.627

Urban Index

Fit the Regressions

```
## Distance
nodule.density.by.distance.urban.LM <- lm(
  Nod_Density_LA_Urban ~ Distance_Scaled,
  data = nodule.density.LA.urban.combined.data
)

## Human influence index
nodule.density.by.HII.urban.LM <- lm(
  Nod_Density_LA_Urban ~ Human_Influence_Index_Scaled,
  data = nodule.density.LA.urban.combined.data
)

## Impervious surface cover
nodule.density.by.ISC.urban.LM <- lm(
  Nod_Density_LA_Urban ~ Mean_ISC_Scaled,
  data = nodule.density.LA.urban.combined.data
)
```

Check Model Assumptions

```
## Distance
check_model(nodule.density.by.distance.urban.LM)
# Linear assumption met
# Homogeneity of variance
# Residuals approximately follow a normal distribution

## Human influence index
check_model(nodule.density.by.HII.urban.LM)
# Linear assumption met
# Slight (+ non-concerning) heterogeneity of variance
# Residuals approximately follow a normal distribution

## Impervious surface cover
check_model(nodule.density.by.ISC.urban.LM)
# Linear assumption met
# Homogeneity of variance
# Residuals approximately follow a normal distribution
```

Model Summaries

Table 25: Summary of the nodule density urban local adaptation index by distance model. Adjusted R-squared = 0.

Term	Estimate	SE	t	P-value
(Intercept)	-0.001	0.008	-0.105	0.917
Distance_Scaled	-0.006	0.008	-0.747	0.458

Table 26: Summary of the nodule density urban local adaptation index by HII model. Adjusted R-squared = 0.

Term	Estimate	SE	t	P-value
(Intercept)	-0.001	0.008	-0.104	0.917
Human_Influence_Index_Scaled	0.000	0.008	-0.060	0.952

Table 27: Summary of the nodule density urban local adaptation index by ISC model. Adjusted R-squared = 0.

Term	Estimate	SE	t	P-value
(Intercept)	-0.001	0.008	-0.104	0.917
Mean_ISC_Scaled	-0.002	0.008	-0.218	0.828

Fixing Nodule Density Regressions

Global Index

Fit the Regressions

```
## Distance
fixing.nodule.density.by.distance.global.LM <- lm(
  Fix_Nod_Density_LA_Global ~ Distance_Scaled,
  data = fixing.nodule.density.LA.global.combined.data
)

## Human influence index
fixing.nodule.density.by.HII.global.LM <- lm(
  Fix_Nod_Density_LA_Global ~ Human_Influence_Index_Scaled,
  data = fixing.nodule.density.LA.global.combined.data
)

## Impervious surface cover
fixing.nodule.density.by.ISC.global.LM <- lm(
  Fix_Nod_Density_LA_Global ~ Mean_ISC_Scaled,
  data = fixing.nodule.density.LA.global.combined.data
)
```

Check Model Assumptions

```
## Distance
check_model(fixing.nodule.density.by.distance.global.LM)
# Linear assumption met
# Homogeneity of variance
# Residuals approximately follow a normal distribution

## Human influence index
check_model(fixing.nodule.density.by.HII.global.LM)
# Linear assumption met
# Homogeneity of variance
# Residuals approximately follow a normal distribution

## Impervious surface cover
check_model(fixing.nodule.density.by.ISC.global.LM)
# Linear assumption met
# Slight (+ non-concerning) heterogeneity of variance
# Residuals approximately follow a normal distribution
```

Model Summaries

Table 28: Summary of the fixing nodule density global local adaptation index by distance model. Adjusted R-squared = 0.

Term	Estimate	SE	t	P-value
(Intercept)	0.000	0.001	0.027	0.978
Distance_Scaled	-0.001	0.001	-0.721	0.474

Table 29: Summary of the fixing nodule density global local adaptation index by HII model. Adjusted R-squared = 0.

Term	Estimate	SE	t	P-value
(Intercept)	0	0.001	0.027	0.978
Human_Influence_Index_Scaled	0	0.001	0.176	0.861

Table 30: Summary of the fixing nodule density global local adaptation index by ISC model. Adjusted R-squared = 0.

Term	Estimate	SE	t	P-value
(Intercept)	0.000	0.001	0.028	0.978
Mean_ISC_Scaled	-0.001	0.001	-0.749	0.457

Rural Index

Fit the Regressions

```
## Distance
fixing.nodule.density.by.distance.rural.LM <- lm(
  Fix_Nod_Density_LA_Rural ~ Distance_Scaled,
  data = fixing.nodule.density.LA.rural.combined.data
)

## Human influence index
fixing.nodule.density.by.HII.rural.LM <- lm(
  Fix_Nod_Density_LA_Rural ~ Human_Influence_Index_Scaled,
  data = fixing.nodule.density.LA.rural.combined.data
)

## Impervious surface cover
fixing.nodule.density.by.ISC.rural.LM <- lm(
  Fix_Nod_Density_LA_Rural ~ Mean_ISC_Scaled,
  data = fixing.nodule.density.LA.rural.combined.data
)
```

Check Model Assumptions

```
## Distance
check_model(fixing.nodule.density.by.distance.rural.LM)
# Linear assumption met
# Homogeneity of variance
# Residuals approximately follow a normal distribution

## Human influence index
check_model(fixing.nodule.density.by.HII.rural.LM)
# Linear assumption met
# Homogeneity of variance
# Residuals approximately follow a normal distribution

## Impervious surface cover
check_model(fixing.nodule.density.by.ISC.rural.LM)
# Linear assumption met
# Homogeneity of variance
# Residuals approximately follow a normal distribution
```

Model Summaries

Table 31: Summary of the fixing nodule density rural local adaptation index by distance model. Adjusted R-squared = 0.

Term	Estimate	SE	t	P-value
(Intercept)	0	0.001	0.054	0.957
Distance_Scaled	0	0.001	-0.151	0.880

Table 32: Summary of the fixing nodule density rural local adaptation index by HII model. Adjusted R-squared = 0.

Term	Estimate	SE	t	P-value
(Intercept)	0	0.001	0.054	0.957
Human_Influence_Index_Scaled	0	0.001	0.284	0.778

Table 33: Summary of the fixing nodule density rural local adaptation index by ISC model. Adjusted R-squared = 0.

Term	Estimate	SE	t	P-value
(Intercept)	0.000	0.001	0.054	0.957
Mean_ISC_Scaled	-0.001	0.001	-0.475	0.637

Urban Index

Fit the Regressions

```
## Distance
fixing.nodule.density.by.distance.urban.LM <- lm(
  Fix_Nod_Density_LA_Urban ~ Distance_Scaled,
  data = fixing.nodule.density.LA.urban.combined.data
)

## Human influence index
fixing.nodule.density.by.HII.urban.LM <- lm(
  Fix_Nod_Density_LA_Urban ~ Human_Influence_Index_Scaled,
  data = fixing.nodule.density.LA.urban.combined.data
)

## Impervious surface cover
fixing.nodule.density.by.ISC.urban.LM <- lm(
  Fix_Nod_Density_LA_Urban ~ Mean_ISC_Scaled,
  data = fixing.nodule.density.LA.urban.combined.data
)
```

Check Model Assumptions

```
## Distance
check_model(fixing.nodule.density.by.distance.urban.LM)
# Linear assumption met
# Homogeneity of variance
# Residuals approximately follow a normal distribution

## Human influence index
check_model(fixing.nodule.density.by.HII.urban.LM)
# Linear assumption met
# Homogeneity of variance
# Residuals approximately follow a normal distribution

## Impervious surface cover
check_model(fixing.nodule.density.by.ISC.urban.LM)
# Linear assumption met
# Homogeneity of variance
# Residuals approximately follow a normal distribution
```

Model Summaries

Table 34: Summary of the fixing nodule density urban local adaptation index by distance model. Adjusted R-squared = 0.

Term	Estimate	SE	t	P-value
(Intercept)	0.000	0.002	-0.07	0.944
Distance_Scaled	-0.001	0.002	-0.95	0.346

Table 35: Summary of the fixing nodule density urban local adaptation index by HII model. Adjusted R-squared = 0.

Term	Estimate	SE	t	P-value
(Intercept)	0	0.002	-0.070	0.945
Human_Influence_Index_Scaled	0	0.002	0.091	0.928

Table 36: Summary of the fixing nodule density urban local adaptation index by ISC model. Adjusted R-squared = 0.

Term	Estimate	SE	t	P-value
(Intercept)	0.000	0.002	-0.070	0.945
Mean_ISC_Scaled	-0.001	0.002	-0.758	0.451

R Session Information

Table 37: Packages required for data management and analysis.

Package	Loaded Version	Date
bayestestR	0.13.1	2023-04-07
broom	1.0.5	2023-06-09
correlation	0.8.4	2023-04-06
datawizard	0.8.0	2023-06-16
dplyr	1.1.2	2023-04-20
easystats	0.6.0	2022-11-29
effectsize	0.8.3	2023-01-28
forcats	1.0.0	2023-01-29
ggplot2	3.4.2	2023-04-03
insight	0.19.3	2023-06-29
kableExtra	1.3.4	2021-02-20
knitr	1.43	2023-05-25
lubridate	1.9.2	2023-02-10
modelbased	0.8.6	2023-01-13
parameters	0.21.1	2023-05-26
performance	0.10.4	2023-06-02
purrr	1.0.1	2023-01-10
readr	2.1.4	2023-02-10
report	0.5.7	2023-03-22
see	0.8.0	2023-06-05
stringr	1.5.0	2022-12-02
tibble	3.2.1	2023-03-20
tidyr	1.3.0	2023-01-24
tidyverse	2.0.0	2023-02-22