

TRhizo-localAdaptation

Local Adaptation by Urbanization

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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("ffnnnnnnfnin")) %>%
  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("ffnnnnnnfnin")) %>%
  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("ffnnnnnnfnin")) %>%
  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("ffnnnnnnfnin")) %>%
  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("ffnnnnnnfnin")) %>%
  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("ffnnnnnnfnin")) %>%
  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("ffnnnnnnfnin")) %>%
  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("ffnnnnnnfnin")) %>%
  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("ffnnnnnnfnin")) %>%
  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("ffnnnnnnfnin")) %>%
  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 | -0.044 | 0.965 |
| Human_Influence_Index_Scaled | 0.001 | 0.002 | 0.528 | 0.599 |

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 | -0.001 | 0.002 | -0.434 | 0.666 |

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 | 0.885 |
| Human_Influence_Index_Scaled | 0.003 | 0.002 | 1.312 | 0.195 |

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 | 1.165 | 0.249 |

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 | 0.001 | 0.000 | 1.000 |
| Human_Influence_Index_Scaled | 0 | 0.001 | -0.049 | 0.961 |

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 | -0.115 | 0.909 |
| Human_Influence_Index_Scaled | 0.002 | 0.001 | 1.858 | 0.068 |

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 | 0.006 | 0.072 | 0.943 |
| Human_Influence_Index_Scaled | 0 | 0.006 | -0.024 | 0.981 |

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 | 0.079 | 0.937 |
| Human_Influence_Index_Scaled | -0.008 | 0.006 | -1.319 | 0.192 |

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 | -0.105 | 0.916 |
| Human_Influence_Index_Scaled | 0.008 | 0.008 | 1.000 | 0.321 |

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) | 0.000 | 0.001 | 0.027 | 0.978 |
| Human_Influence_Index_Scaled | 0.001 | 0.001 | 0.473 | 0.638 |

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 | -0.268 | 0.790 |

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) | 0.000 | 0.002 | -0.070 | 0.944 |
| Human_Influence_Index_Scaled | 0.001 | 0.002 | 0.897 | 0.374 |

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 | 0.13.2 | 2024-02-12 |
| broom | 1.0.5 | 2023-06-09 |
| correlation | 0.8.4 | 2023-04-06 |
| datawizard | 0.10.0 | 2024-03-26 |
| dplyr | 1.1.4 | 2023-11-17 |
| easystats | 0.7.1 | 2024-03-28 |
| effectsize | 0.8.6 | 2023-09-14 |
| forcats | 1.0.0 | 2023-01-29 |
| ggplot2 | 3.5.0 | 2024-02-23 |
| insight | 0.19.10 | 2024-03-22 |
| kableExtra | 1.4.0 | 2024-01-24 |
| knitr | 1.45 | 2023-10-30 |
| lubridate | 1.9.3 | 2023-09-27 |
| modelbased | 0.8.7 | 2024-02-15 |
| parameters | 0.21.6 | 2024-03-18 |
| performance | 0.11.0 | 2024-03-22 |
| purrr | 1.0.2 | 2023-08-10 |
| readr | 2.1.5 | 2024-01-10 |
| report | 0.5.8 | 2023-12-07 |
| see | 0.8.3 | 2024-03-24 |
| stringr | 1.5.1 | 2023-11-14 |
| tibble | 3.2.1 | 2023-03-20 |
| tidyr | 1.3.1 | 2024-01-24 |
| tidyverse | 2.0.0 | 2023-02-22 |