Geographic overlap from SDM and Ace2 results

Norah Saarman

2025-04-18

1. Load and Process Species Distribution Models (SDMs)

```r
# Load MaxEnt SDMs
sdm_pipiens <- raster("../gis/culex_pipiens_meansuitability.nc")
sdm_quinque <- raster("../gis/culex_quinquefasciatus_meansuitability.nc")

# Threshold to binary
threshold <- 0.5
sdm_pipiens_bin <- sdm_pipiens >= threshold
sdm_quinque_bin <- sdm_quinque >= threshold
```

2. Convert SDMs to Polygons

```r
# Raster to terra
sdm_pipiens_v <- terra::rast(sdm_pipiens_bin)
sdm_quinque_v <- terra::rast(sdm_quinque_bin)

# Raster to polygons
poly_pipiens <- terra::as.polygons(sdm_pipiens_v, dissolve = TRUE)
poly_quinque <- terra::as.polygons(sdm_quinque_v, dissolve = TRUE)

# Terra to sf
poly_pipiens_sf <- st_as_sf(poly_pipiens)
poly_quinque_sf <- st_as_sf(poly_quinque)

# Filter to presence only
names(poly_pipiens_sf)[1] <- "presence"
names(poly_quinque_sf)[1] <- "presence"
poly_pipiens_sf <- poly_pipiens_sf %>% filter(presence == 1)
poly_quinque_sf <- poly_quinque_sf %>% filter(presence == 1)
```

3. Project to Albers Equal Area and Calculate Overlap

```r
# Define CRS
aea_crs <- st_crs("+proj=aea +lat_1=29.5 +lat_2=45.5 +lat_0=23 +lon_0=-96")

# Project
poly_pipiens_sf <- st_transform(poly_pipiens_sf, aea_crs)
poly_quinque_sf <- st_transform(poly_quinque_sf, aea_crs)
```

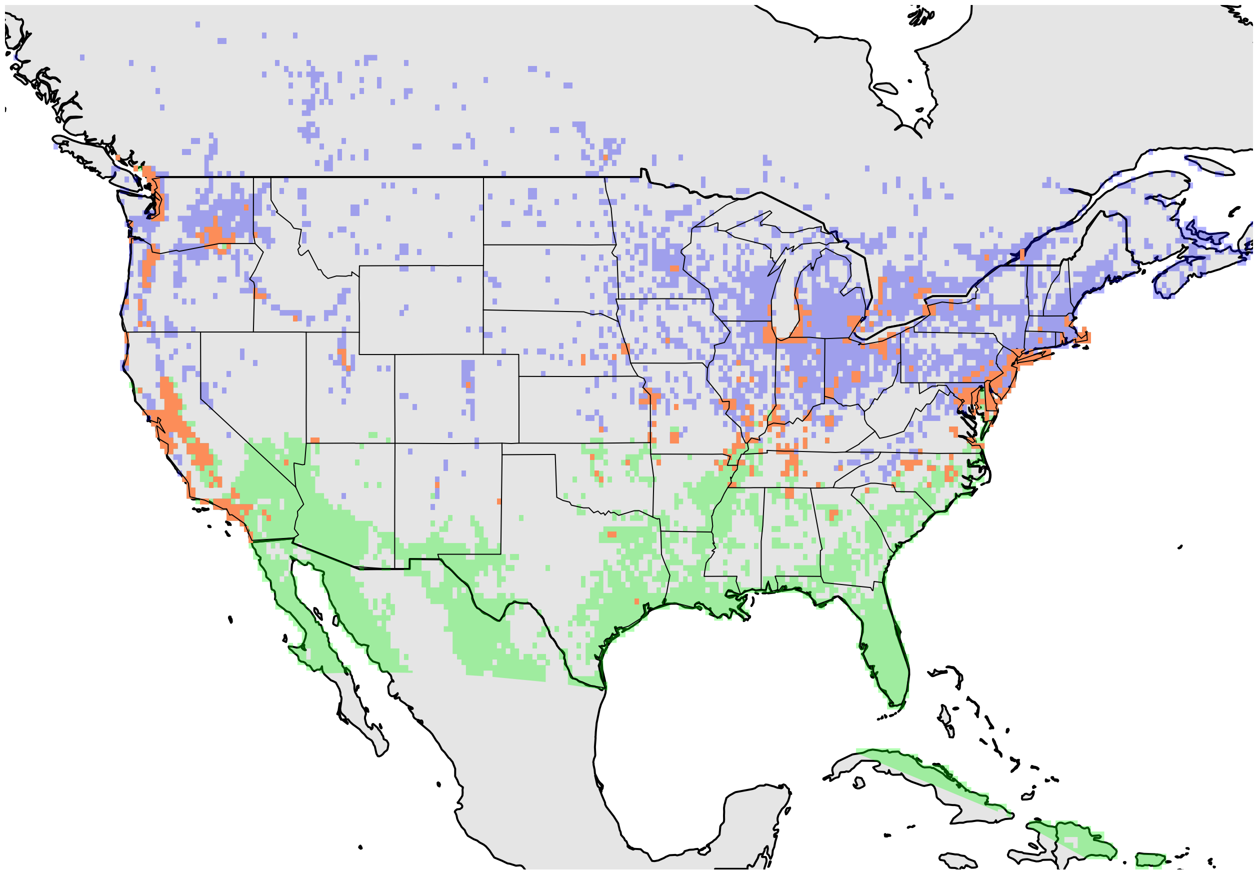
```r
# Overlap
overlap_sf <- st_intersection(poly_pipiens_sf, poly_quinque_sf)

# Calculate areas (km²)
area_pipiens_km2 <- sum(st_area(poly_pipiens_sf)) / 1e6
area_quinque_km2 <- sum(st_area(poly_quinque_sf)) / 1e6
area_overlap_km2 <- sum(st_area(overlap_sf)) / 1e6
```

4. Clip to North America and Reproject to WGS84

```r
# US base map
us_states <- st_as_sf(map("usa", plot = FALSE, fill = TRUE))
us_states <- st_transform(us_states, crs = aea_crs)

# Clip extent
bbox_na <- st_as_sfc(st_bbox(c(xmin = -170, xmax = -50, ymin = 5, ymax = 85), crs = st_crs(4326)))
bbox_na_sf <- st_transform(bbox_na, crs = aea_crs)

# Clip
poly_pipiens_sf <- st_intersection(st_make_valid(poly_pipiens_sf), bbox_na_sf)
poly_quinque_sf <- st_intersection(st_make_valid(poly_quinque_sf), bbox_na_sf)
overlap_sf <- st_intersection(st_make_valid(overlap_sf), bbox_na_sf)

# Reproject to WGS84
poly_pipiens_ll <- st_transform(poly_pipiens_sf, 4326)
poly_quinque_ll <- st_transform(poly_quinque_sf, 4326)
overlap_ll <- st_transform(overlap_sf, 4326)
```

5. Visualize SDMs and Overlap

```r
par(xpd = NA)
map("usa")
map(add = TRUE, col = "grey90", fill = TRUE)

plot(st_geometry(poly_pipiens_ll), col = rgb(0, 0, 1, 0.3), border = NA, add = TRUE)
plot(st_geometry(poly_quinque_ll), col = rgb(0, 1, 0, 0.3), border = NA, add = TRUE)
plot(st_geometry(overlap_ll), col = adjustcolor("#fc8d59", alpha.f = 1), border = NA, add = TRUE)

map("state", add = TRUE, col = "black", lwd = 0.5)
```

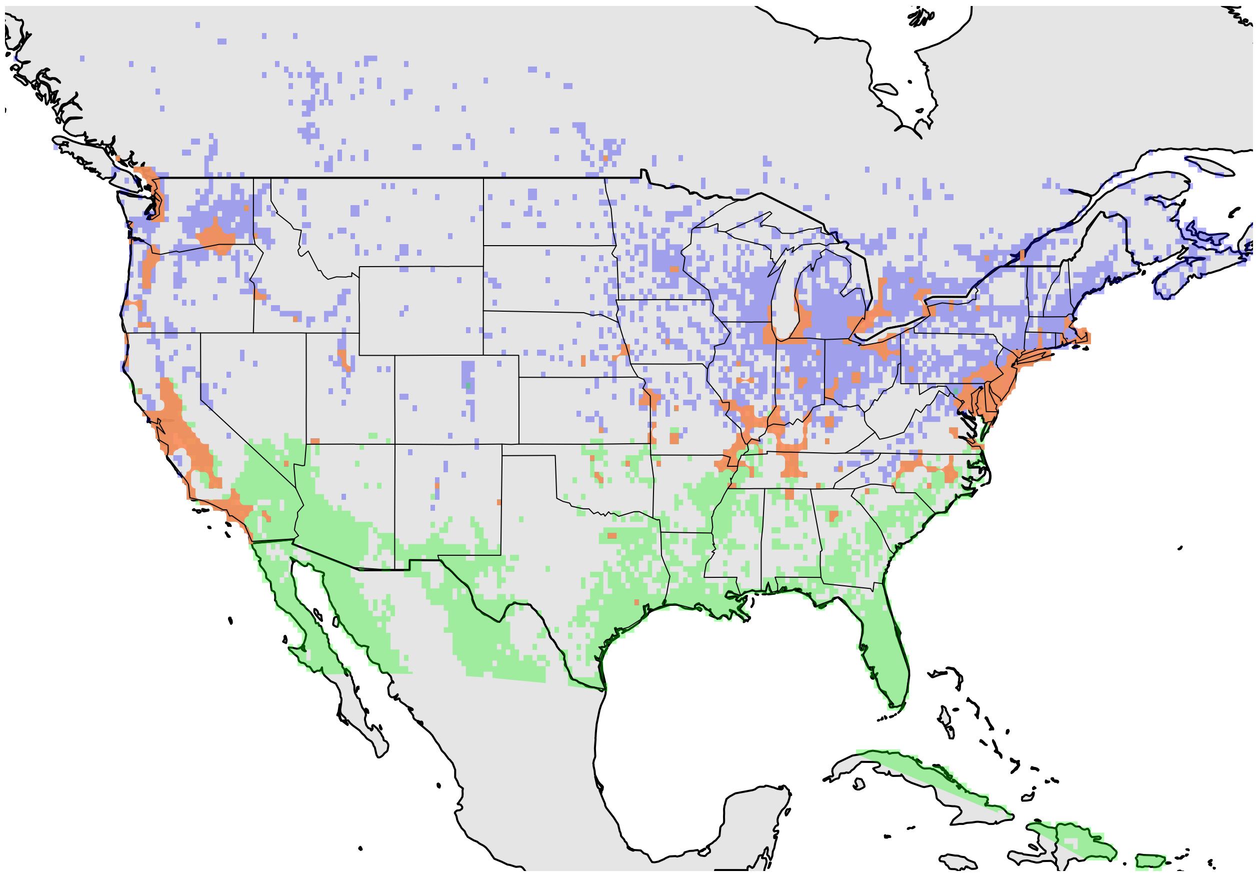


6. Merge Nearby Overlapping Regions

```r
# Reproject overlap
overlap_ll_proj <- st_transform(overlap_ll, aea_crs)

# Make valid and extract polygons
overlap_valid <- st_make_valid(overlap_ll_proj)
overlap_polygons <- st_collection_extract(overlap_valid, "POLYGON")
overlap_parts <- st_cast(overlap_polygons, "POLYGON")

# Buffer outward
buffer_dist_meters <- 25000
overlap_buffered <- st_buffer(overlap_parts, dist = buffer_dist_meters)
overlap_buffered <- st_make_valid(overlap_buffered)

# Merge touching patches
overlap_combined <- st_union(overlap_buffered)
overlap_combined <- st_make_valid(overlap_combined)

# Buffer inward
overlap_combined <- st_buffer(overlap_combined, dist = -buffer_dist_meters)
overlap_combined <- st_make_valid(overlap_combined)

# Finalize
overlap_combined <- st_cast(overlap_combined, "MULTIPOLYGON")
overlap_combined <- st_transform(overlap_combined, 4326)
```

7. Visualize Combined Overlap Regions

```
#pdf("../figs/overlap_SDM.pdf", width = 8, height = 6)
par(xpd = NA)
map("usa")
map(add = TRUE, col = "grey90", fill = TRUE)

plot(st_geometry(poly_pipiens_ll), col = rgb(0, 0, 1, 0.3), border = NA, add = TRUE)
plot(st_geometry(poly_quinque_ll), col = rgb(0, 1, 0, 0.3), border = NA, add = TRUE)
plot(st_geometry(overlap_combined), col = adjustcolor("#fc8d59", alpha.f = 0.9), border = NA, add = TRUI

map("state", add = TRUE, col = "black", lwd = 0.5)
```

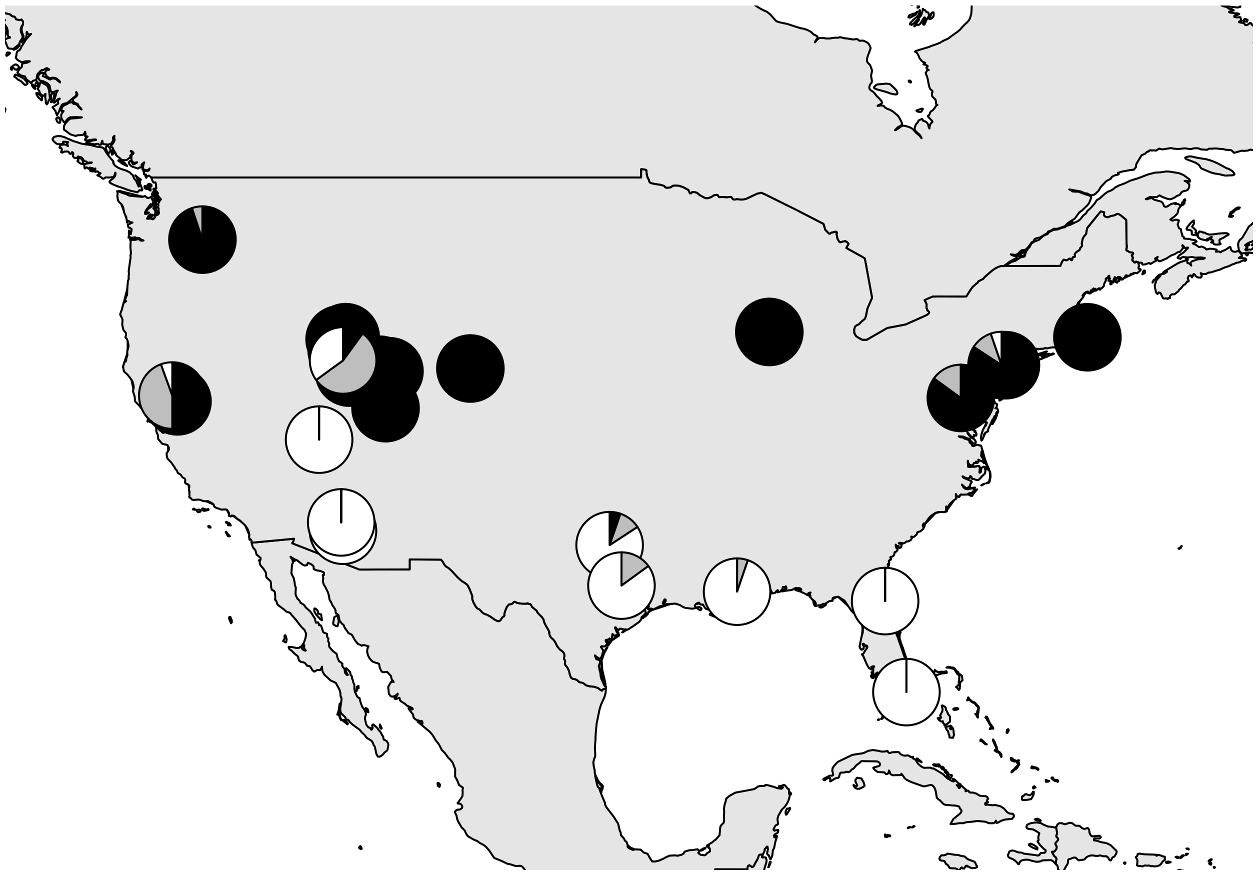


```
#dev.off()
```

8. Add Sampling Points and Population Structure (Pie Charts)

```
# Load counts
counts <- read.csv("../data/ThisStudy_v9.txt", sep = "\t")
coord <- as.data.frame(counts[,c("long","lat")])
```

```r
# Prepare
countsDf <- as.data.frame(counts[,c(2,1,4,5,6,9,10,7,8)])
names(countsDf) <- c("locality","site","pp","pq","qq","latitude","longitude","year","h_index")
rownames(countsDf) <- countsDf$site

# Frequencies
freqsDf <- t(apply(countsDf[,c("pp","pq","qq")], 1, function(row) row / sum(row)))
freqsDf <- as.matrix(freqsDf)

# Plot pies
par(xpd = NA)
plot_order <- rev(order(countsDf$h_index))

map("usa")
map(add = TRUE, col = "grey90", fill = TRUE)

for (i in plot_order) {
  add.pie(z = freqsDf[i,],
          x = coord[i,1],
          y = coord[i,2],
          clockwise = TRUE,
          labels = "",
          col = c("black", "grey", "white"),
          cex = 1.5, radius = 1.5)
}
```



Some jitter, added by hand:

Create a jitter data frame by hand:

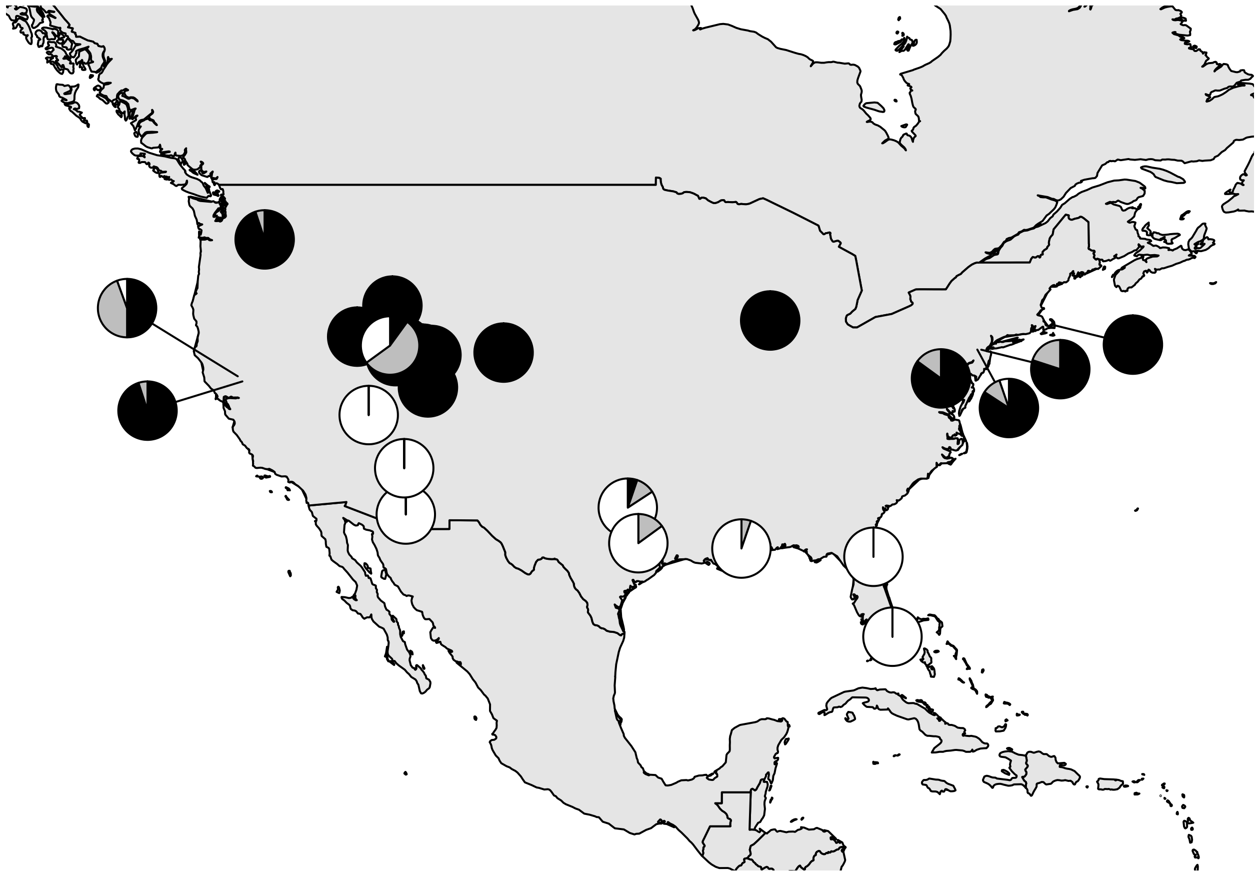
```r
# Create a jitter df
jitterDf <- data.frame(x_jitter = rep(0,25), y_jitter = rep(0,25))
rownames(jitterDf) <- rownames(countsDf)
jitterDf[3,] <- c(0,1)
jitterDf[4,] <- c(5,-1)
jitterDf[5,] <- c(1,-1)
jitterDf[6,] <- c(-2,0)
jitterDf[8,] <- c(2,-3)
jitterDf[9,] <- c(5,-1)
jitterDf[14,] <- c(-7,3.5)
jitterDf[16,] <- c(-6,-1.5)
jitterDf[19,] <- c(1,1)
jitterDf[20,] <- c(1,-1)
```

Calculate bounds of map based on coordinates + jitter:

```r
# Expand x/y limits by a small margin (e.g., 2 degrees)
x_range <- range(coord[, 1] + jitterDf[, 1], na.rm = TRUE)
y_range <- range(coord[, 2] + jitterDf[, 2], na.rm = TRUE)

x_margin <- 2
y_margin <- 2

x_lim <- c(x_range[1] - x_margin, x_range[2] + x_margin)
y_lim <- c(y_range[1] - y_margin, y_range[2] + y_margin)
```

Add jitter with a line from true origin:

```r
# Open PDF device
#pdf("../figs/ace2_pies_ThisStudy.pdf", width = 8, height = 6)

# Set xpd to NA to allow for plotting in the margins
par(xpd = NA)

# Plot map with expanded margins
map("usa", xlim = x_lim, ylim = y_lim)
map(add = TRUE, col = "grey90", fill = TRUE)

for (i in plot_order) {
  # Jittered coordinates
  jittered_x <- coord[i, 1] + (jitterDf[i, 1])
  jittered_y <- coord[i, 2] + (jitterDf[i, 2])

  # Draw line from true location to jittered pie
  segments(x0 = coord[i, 1],
           y0 = coord[i, 2],
           x1 = jittered_x,
           y1 = jittered_y,
           col = "black", lty = 1, lwd = 1)

  # Plot pie chart at jittered location
  add.pie(z = freqsDf[i,],
          x = jittered_x,
          y = jittered_y,
          clockwise = TRUE,
          labels = "",
          col = c("black", "grey", "white"),
          cex = 1.5, radius = 1.5)
}
```



```
#dev.off()
```

Predicted level of overlapping suitable habitat?

```
# ----------------------------------------------
# Quantify predicted overlap around each sample point
# ----------------------------------------------

# Step 1: Make sample points an sf object
samples_sf <- st_as_sf(countsDf, coords = c("longitude", "latitude"), crs = 4326)

# Step 2: Reproject sample points to Albers Equal Area CRS
samples_sf <- st_transform(samples_sf, crs = aea_crs)

# Step 3: Buffer each point by 30 km (30,000 meters)
sample_buffers <- st_buffer(samples_sf, dist = 30000)

# Step 4: Prepare overlap_combined layer in same CRS
overlap_combined_proj <- st_transform(overlap_combined, crs = aea_crs)

# Step 5: Calculate proportion of buffer area that overlaps
```

```
predicted_overlap_prop <- sapply(1:nrow(sample_buffers), function(i) {
  buf <- sample_buffers[i,]
  intersection <- st_intersection(buf, overlap_combined_proj)

  if (nrow(intersection) == 0) {
    # No overlap
    overlap_area <- 0
  } else {
    # Sum all overlapping parts
    overlap_area <- sum(st_area(intersection))
  }

  buffer_area <- st_area(buf)

  # Return proportion
  as.numeric(overlap_area) / as.numeric(buffer_area)
})

# Step 6: Add predicted overlap to countsDf
countsDf$predicted_overlap <- predicted_overlap_prop

# Step 7: Quick check
head(countsDf[, c("site", "h_index", "predicted_overlap")])
```

```
##                             site h_index predicted_overlap
## 001.ByroWA.2023 001.ByroWA.2023    0.97         0.8411216
## 007.CookIL.2023 007.CookIL.2023    1.00         0.9993222
## 008.CachUT.2023 008.CachUT.2023    1.00         0.0000000
## 009.BarnMA.2023 009.BarnMA.2023    1.00         0.8248844
## 011.BoxEUT.2024 011.BoxEUT.2024    1.00         0.0000000
## 012.OgdeUT.2024 012.OgdeUT.2024    1.00         0.4750927
```

Now, add directionality with 0 = quinq, 1 = pip, to estimate “predicted_h_index”

```
# ---------------------------------------------
# New: Predict directional hybrid index from habitat around each sampling site
# ---------------------------------------------

# Step 1: Prepare the pipiens-only and quinque-only polygons
# (We already have poly_pipiens_ll and poly_quinque_ll, but need to transform)
poly_pipiens_proj <- st_transform(poly_pipiens_ll, crs = aea_crs)
poly_quinque_proj <- st_transform(poly_quinque_ll, crs = aea_crs)
overlap_combined_proj <- st_transform(overlap_combined, crs = aea_crs)  # already done above

# Step 2: Create pip-only and quinque-only polygons (remove overlap area)
pip_only <- st_difference(poly_pipiens_proj, overlap_combined_proj)
quinque_only <- st_difference(poly_quinque_proj, overlap_combined_proj)

# Step 3: Calculate areas for each sample buffer
library(units)  # make sure units package is loaded

predicted_h_index <- sapply(1:nrow(sample_buffers), function(i) {
  buf <- sample_buffers[i, ]

  pip_intersect <- st_intersection(buf, pip_only)
```

```r
  quinque_intersect <- st_intersection(buf, quinque_only)
  overlap_intersect <- st_intersection(buf, overlap_combined_proj)

  pip_area <- if (nrow(pip_intersect) == 0) units::set_units(0, "m^2") else sum(st_area(pip_intersect))
  quinque_area <- if (nrow(quinque_intersect) == 0) units::set_units(0, "m^2") else sum(st_area(quinque_
  overlap_area <- if (nrow(overlap_intersect) == 0) units::set_units(0, "m^2") else sum(st_area(overlap_

  total_area <- pip_area + quinque_area + overlap_area

  if (as.numeric(total_area) == 0) {
    return(NA)  # no habitat found
  } else {
    pred_h <- (pip_area + 0.5 * overlap_area) / total_area
    return(as.numeric(pred_h))  # strip units at the end
  }
})
# Step 4: Add predicted_h_index to countsDf
countsDf$predicted_h_index <- predicted_h_index

# Step 5: Quick check and save
(summary_table <- countsDf[, c("site", "latitude", "longitude", "h_index", "predicted_overlap", "predic
```

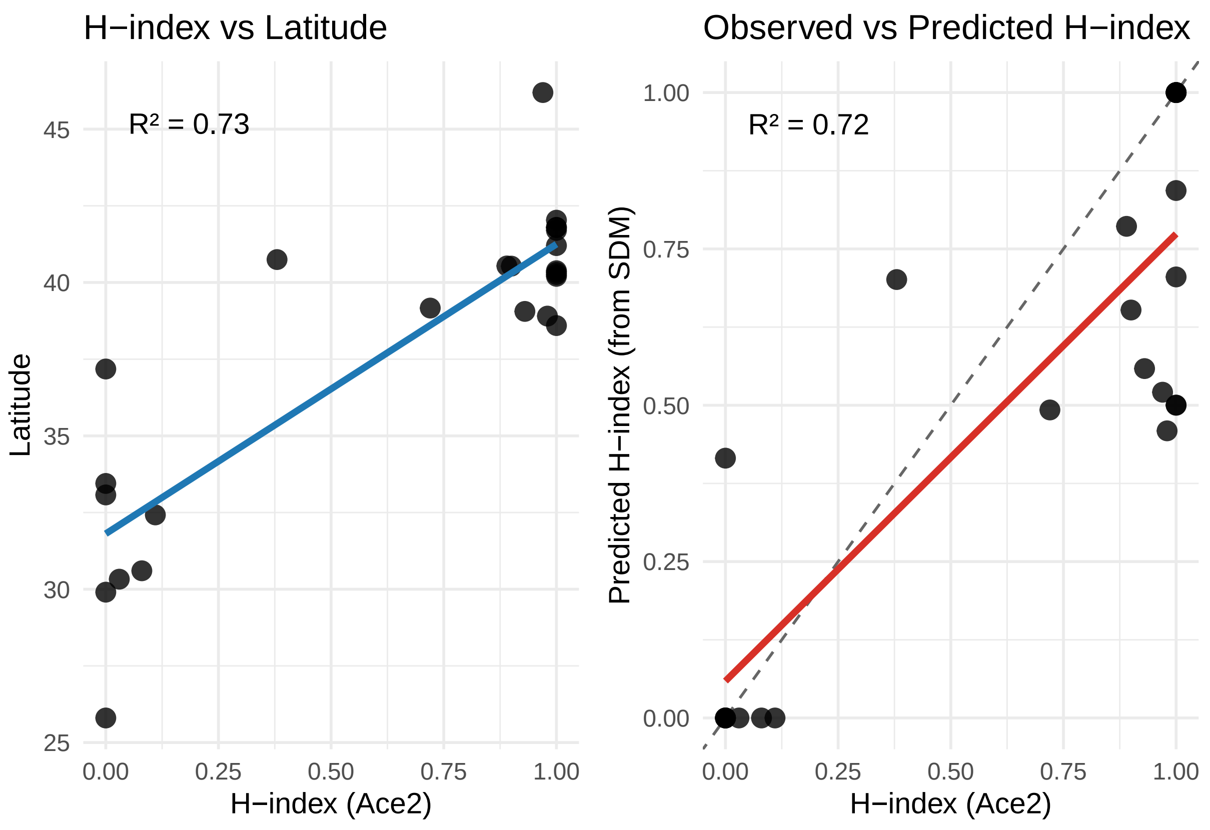
```
##                             site latitude  longitude h_index predicted_overlap
## 001.ByroWA.2023 001.ByroWA.2023 46.19300 -119.89900    0.97         0.8411216
## 007.CookIL.2023 007.CookIL.2023 42.03176  -87.93087    1.00         0.9993222
## 008.CachUT.2023 008.CachUT.2023 41.79696 -111.82005    1.00         0.0000000
## 009.BarnMA.2023 009.BarnMA.2023 41.79362  -69.99427    1.00         0.8248844
## 011.BoxEUT.2024 011.BoxEUT.2024 41.69945 -112.16386    1.00         0.0000000
## 012.OgdeUT.2024 012.OgdeUT.2024 41.20359 -112.04803    1.00         0.4750927
## 015.SaltUT.2023 015.SaltUT.2023 40.74805 -111.96788    0.38         0.4850847
## 022.HuntNJ.2023 022.HuntNJ.2023 40.53959  -74.83462    0.89         0.4277893
## 023.SomeNJ.2023 023.SomeNJ.2023 40.53358  -74.58610    0.90         0.6953889
## 024.FortCO.2023 024.FortCO.2023 40.38428 -104.78940    1.00         0.0000000
## 025.UteTUT.2024 025.UteTUT.2024 40.32890 -109.89110    1.00         0.0000000
## 026.VernUT.2024 026.VernUT.2024 40.26180 -109.35110    1.00         0.0000000
## 028.ProvUT.2024 028.ProvUT.2024 40.20065 -111.62731    1.00         0.1866844
## 035.SuttCA.2023 035.SuttCA.2023 39.16647 -121.59845    0.72         0.9144982
## 038.RockMD.2023 038.RockMD.2023 39.05775  -77.13055    0.93         0.8748454
## 041.LincCA.2023 041.LincCA.2023 38.90447 -121.30633    0.98         0.8557477
## 054.MoabUT.2024 054.MoabUT.2024 38.59597 -109.57376    1.00         0.0000000
## 072.StGeUT.2023 072.StGeUT.2023 37.17900 -113.32000    0.00         0.3040211
## 119.PhoeAZ.2024 119.PhoeAZ.2024 33.44844 -112.07414    0.00         0.0000000
## 123.MariAZ.2023 123.MariAZ.2023 33.07362 -111.97377    0.00         0.0000000
## 124.DalFTX.2024 124.DalFTX.2024 32.42235  -96.93698    0.11         0.0000000
## 130.CollTX.2023 130.CollTX.2023 30.60044  -96.26893    0.08         0.0000000
## 131.SlidLA.2024 131.SlidLA.2024 30.32700  -89.74900    0.03         0.0000000
## 133.AnasFL.2023 133.AnasFL.2023 29.90311  -81.40074    0.00         0.0000000
## 137.MiDaFL.2023 137.MiDaFL.2023 25.80141  -80.19909    0.00         0.0000000
##                 predicted_h_index
## 001.ByroWA.2023         0.5208546
## 007.CookIL.2023         0.5003389
## 008.CachUT.2023         1.0000000
## 009.BarnMA.2023         0.5000000
## 011.BoxEUT.2024         1.0000000
## 012.OgdeUT.2024         0.7051935
## 015.SaltUT.2023         0.7010426
## 022.HuntNJ.2023         0.7861053
## 023.SomeNJ.2023         0.6523055
## 024.FortCO.2023         1.0000000
## 025.UteTUT.2024         1.0000000
## 026.VernUT.2024         1.0000000
## 028.ProvUT.2024         0.8433459
## 035.SuttCA.2023         0.4925275
## 038.RockMD.2023         0.5586669
## 041.LincCA.2023         0.4591174
## 054.MoabUT.2024                NA
## 072.StGeUT.2023         0.4154164
## 119.PhoeAZ.2024         0.0000000
## 123.MariAZ.2023         0.0000000
## 124.DalFTX.2024         0.0000000
## 130.CollTX.2023         0.0000000
## 131.SlidLA.2024         0.0000000
## 133.AnasFL.2023         0.0000000
## 137.MiDaFL.2023         0.0000000
```

```r
# Save as CSV
write.csv(summary_table, file = "../data/summary_hindex_prediction.csv", row.names = FALSE)
```

Plot h_index versus latitude, and h_index versus predicted h_index based on SDM habitat MaxEnt models:

```r
library(ggplot2)
library(patchwork)

# ----------------------------------
# First plot: H-index vs Latitude
# ----------------------------------

# Fit linear model for H-index vs Latitude
lm_lat <- lm(latitude ~ h_index, data = countsDf)
r_squared_lat <- summary(lm_lat)$r.squared
r_squared_lat_text <- paste0("R² = ", round(r_squared_lat, 2))

p1 <- ggplot(countsDf, aes(x = h_index, y = latitude)) +
  geom_point(size = 3, alpha = 0.8, color = "black") +
  geom_smooth(method = "lm", formula = y ~ x, se = FALSE, color = "#1f78b4", linewidth = 1.2) +
  annotate("text", x = 0.05, y = max(countsDf$latitude, na.rm = TRUE) - 1, label = r_squared_lat_text,
  theme_minimal() +
  labs(x = "H-index (Ace2)", y = "Latitude", title = "H-index vs Latitude") +
  xlim(0, 1)

# ----------------------------------
# Second plot: H-index vs Predicted H-index
# ----------------------------------

# Fit linear model for H-index vs Predicted H-index
lm_pred <- lm(predicted_h_index ~ h_index, data = countsDf)
r_squared_pred <- summary(lm_pred)$r.squared
r_squared_pred_text <- paste0("R² = ", round(r_squared_pred, 2))
```

```
p2 <- ggplot(countsDf, aes(x = h_index, y = predicted_h_index)) +
  geom_abline(slope = 1, intercept = 0, linetype = "dashed", color = "grey40") +
  geom_point(size = 3, alpha = 0.8, color = "black") +
  geom_smooth(method = "lm", formula = y ~ x, se = FALSE, color = "#d73027", linewidth = 1.2) +
  annotate("text", x = 0.05, y = 0.95, label = r_squared_pred_text, hjust = 0, size = 4) +
  theme_minimal() +
  labs(x = "H-index (Ace2)", y = "Predicted H-index (from SDM)",
       title = "Observed vs Predicted H-index") +
  xlim(0, 1) +
  ylim(0, 1)

# ---------------------------------
# Combine side-by-side
# ---------------------------------

(p1 | p2) +
  plot_layout(guides = 'collect')
```


H−index vs Latitude
R² = 0.73
Latitude
H−index (Ace2)
Observed vs Predicted H−index
R² = 0.72
Predicted H−index (from SDM)
H−index (Ace2)