

ICCB Species distribution modelling and validation

Scott Forrest and Charlotte Patterson

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In this script we are fitting species distribution models to the data of koalas (*Phascolarctos cinereus*) in the South-East Queensland (SEQ) region under current environmental conditions, which we will predict into future environmental conditions.

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We wrote this script drawing on some of the following resources:

- Ecocommons Notebooks <https://www.ecocommons.org.au/notebooks/>
- Damaris Zurell's SDM Intro <https://damarisurell.github.io/SDM-Intro/>
- https://damarisurell.github.io/EEC-MGC/b4_SDM_eval.html

Import packages

```
library(dplyr)
```

Attaching package: 'dplyr'

The following objects are masked from 'package:stats':

filter, lag

The following objects are masked from 'package:base':

intersect, setdiff, setequal, union

```
library(purrr)
library(ggplot2)
library(terra)
```

terra 1.8.50

```
library(sf)
```

Linking to GEOS 3.13.0, GDAL 3.8.5, PROJ 9.5.1; sf_use_s2() is TRUE

```
library(predicts)
library(blockCV)
```

blockCV 3.1.5

```
library(ecospat)
library(usdm)
library(randomForest)
```

randomForest 4.7-1.2

Type rfNews() to see new features/changes/bug fixes.

Attaching package: 'randomForest'

The following object is masked from 'package:ggplot2':

margin

The following object is masked from 'package:dplyr':

combine

```
library(precrec)
library(corrplot)
```

corrplot 0.95 loaded

```
# Install the mecofun package, used in the materials at https://damarisurell.github.io/SDM-
library(devtools)
```

Loading required package: usethis

```
devtools::install_git("https://gitup.uni-potsdam.de/macroecology/mecofun.git")
```

Skipping install of 'mecofun' from a xgit remote, the SHA1 (feb82c4a) has not changed since
Use `force = TRUE` to force installation

```
# Load the mecofun package
library(mecofun)
```

Load koala presences and background points

They are loaded as spatvectors, but we also want them as dataframes for model input requirements.

```
koala_occ <- vect("Data/Biological_records/SEQ_koala_occurrences.shp")
background <- vect("Data/Biological_records/background_points_2.5k_random.shp")

# Make a dataframe of just x, y and presence
koala_occ_df <- koala_occ %>%
  as.data.frame(geom = "XY") %>%
```

```
dplyr::select(x,y) %>%
mutate(Presence = 1)

head(koala_occ_df)
```

	x	y	Presence
1	1868673	-3265806	1
2	1851054	-3232106	1
3	1846917	-3231913	1
4	1874167	-3262365	1
5	1857487	-3259935	1
6	1874262	-3262395	1

```
background_df <- background %>%
  as.data.frame(geom = "XY") %>%
  dplyr::select(x,y) %>%
  mutate(Presence = 0)

head(background_df)
```

	x	y	Presence
1	1854692	-3111330	0
2	1859816	-3111330	0
3	1864940	-3111330	0
4	1870064	-3111330	0
5	1875188	-3111330	0
6	1880312	-3111330	0

```
# Combine to one
pr_bg <- rbind(koala_occ_df, background_df)
```

Load environmental covariates

Loading current covariate rasters. We formatted these rasters in the same way as the Koala data, so that they are all in the same projection and extent. We did this in the script: 'ICCB_Environmental_data.qmd'

```
covs_current <- rast("Data/Environmental_variables/current_bioclim.tif")

# Define the BIOCLIM names for the raster layers
layer_names <- c(
```

```

"BI01_Annual_Mean_Temp",
"BI02_Mean_Diurnal_Temp_Range",
"BI03_Isothermality",
"BI04_Temperature_Seasonality",
"BI05_Max_Temp_Warmest_Month",
"BI06_Min_Temp_Coldest_Month",
"BI07_Temperature_Annual_Range",
"BI08_Mean_Temp_Wettest_Quarter",
"BI09_Mean_Temp_Driest_Quarter",
"BI010_Mean_Temp_Warmest_Quarter",
"BI011_Mean_Temp_Coldest_Quarter",
"BI012_Annual_Precipitation",
"BI013_Precip_Wettest_Month",
"BI014_Precip_Driest_Month",
"BI015_Precip_Seasonality",
"BI016_Precip_Wettest_Quarter",
"BI017_Precip_Driest_Quarter",
"BI018_Precip_Warmest_Quarter",
"BI019_Precip_Coldest_Quarter")

```

```
names(covs_current) <- layer_names
```

Covariate selection

Option 1. Narrow down potential covariates based on ecological knowledge

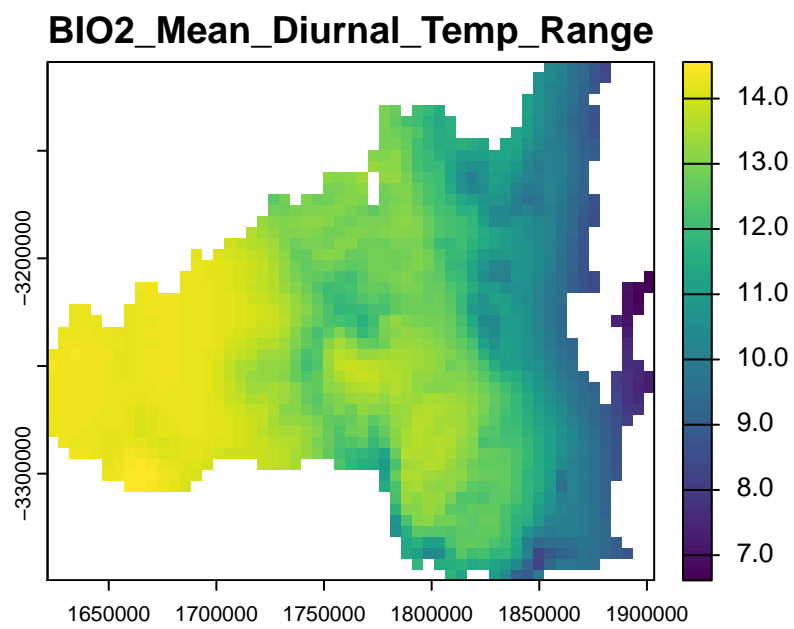
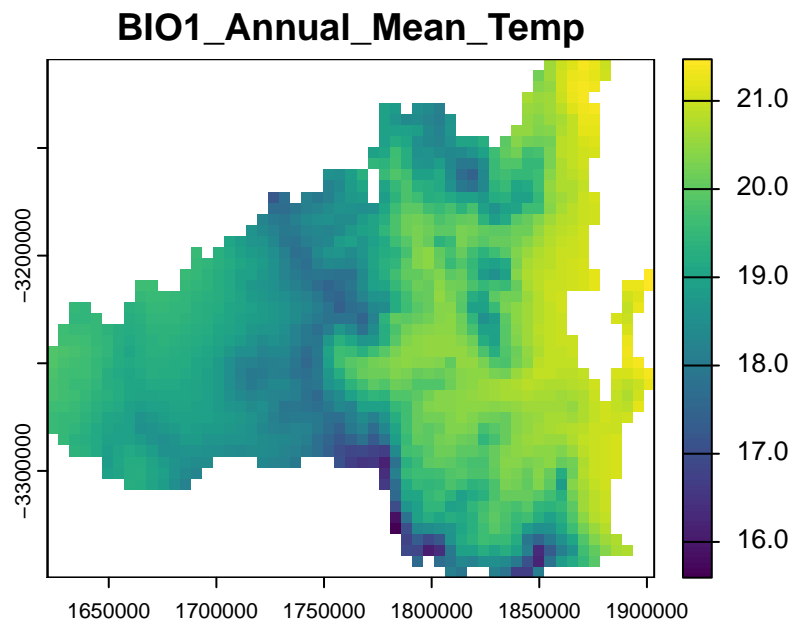
For this example, we had advice from CSIRO scientists who conducted an expert elicitation to gather a set of potential covariates that are likely to be important for koalas. We use this knowledge to filter out the key bioclim variables.

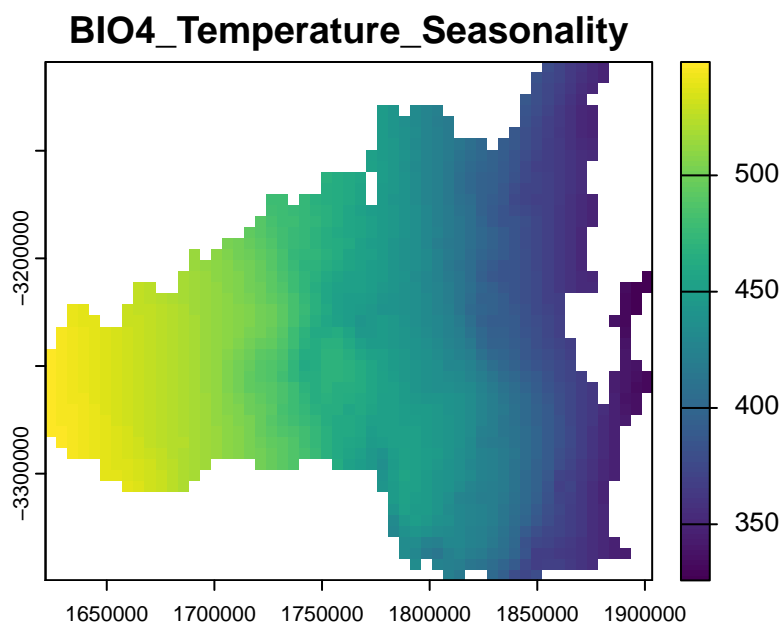
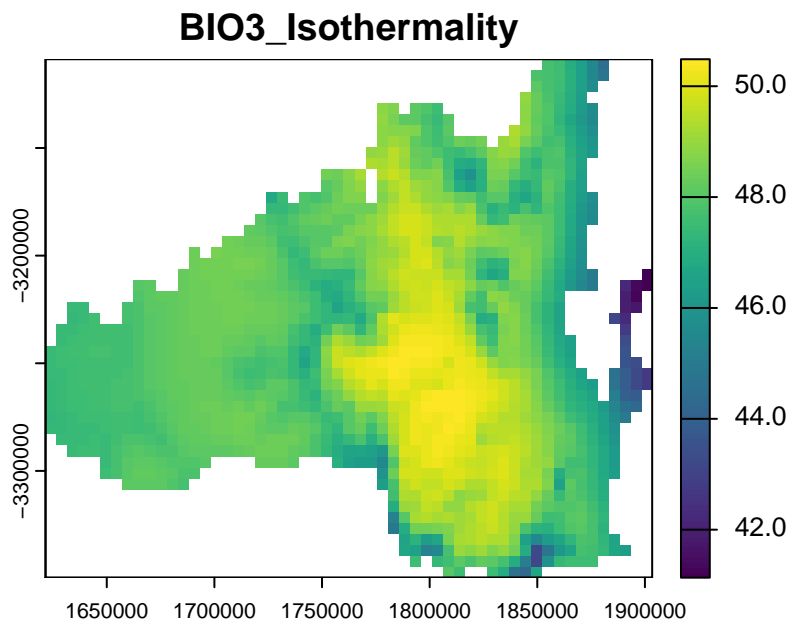
We select the following: Bio5 : Max temp of the warmest month (mainly for the northern populations) Bio6 : Min temp of the coldest month (mainly for southern populations, which essentially excludes alpine regions) Bio12 : Annual Precipitation Bio15 : Precipitation seasonality (coefficient of variation)

```

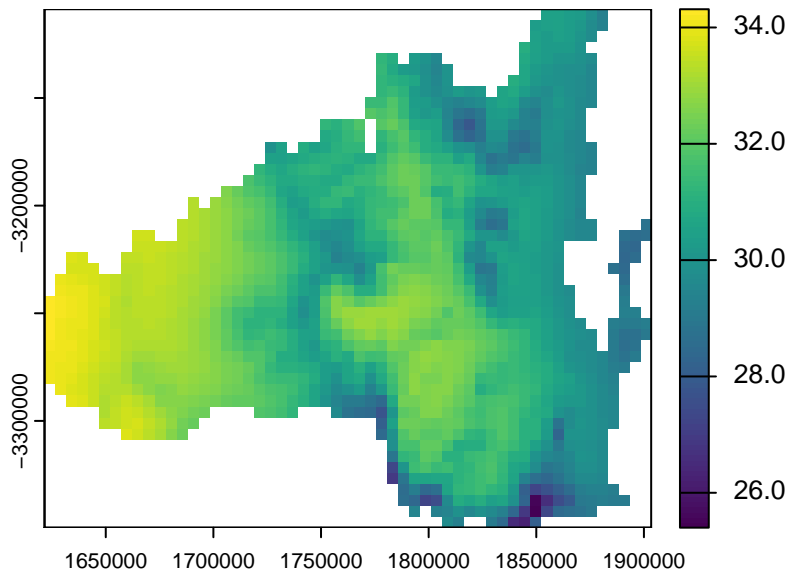
for(i in 1:nlyr(covs_current)) {
  terra::plot(covs_current[[i]], main = names(covs_current)[[i]])
}

```

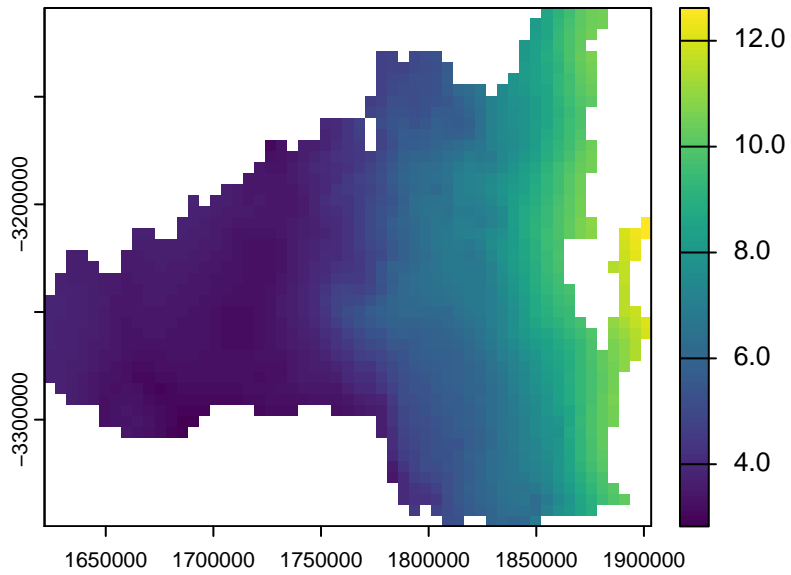




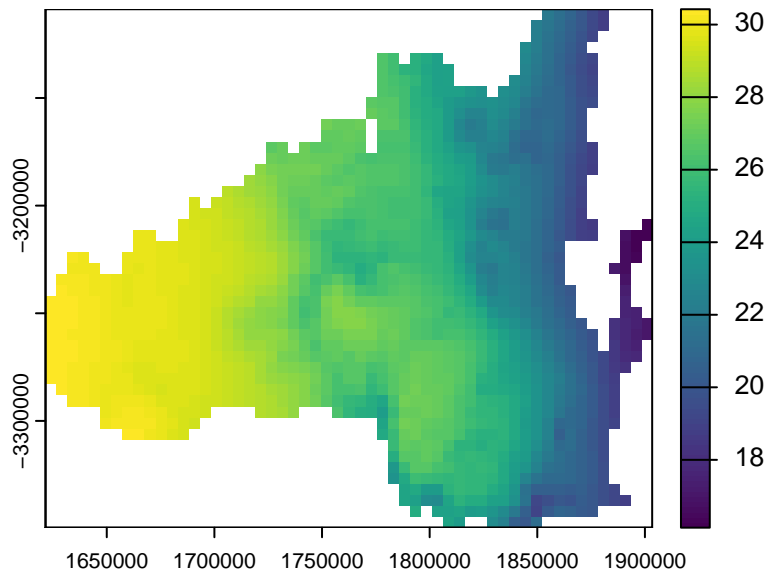
BIO5_Max_Temp_Warmest_Month



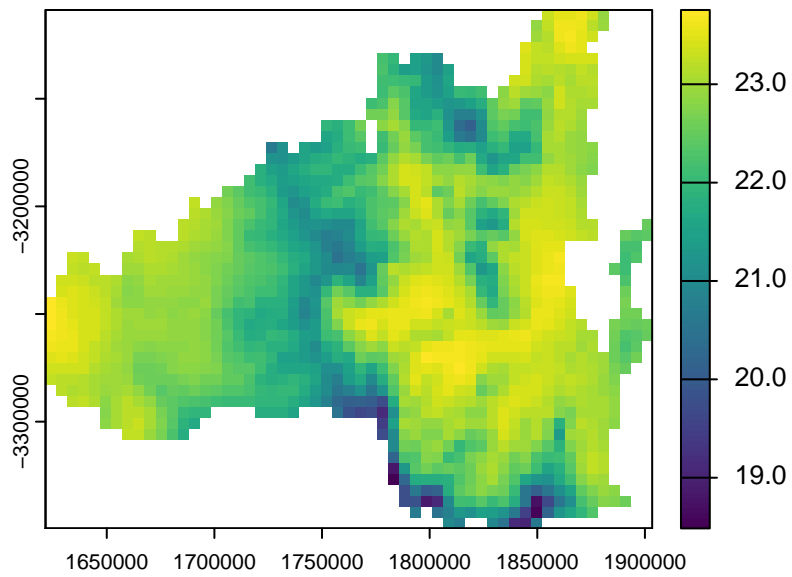
BIO6_Min_Temp_Coldest_Month



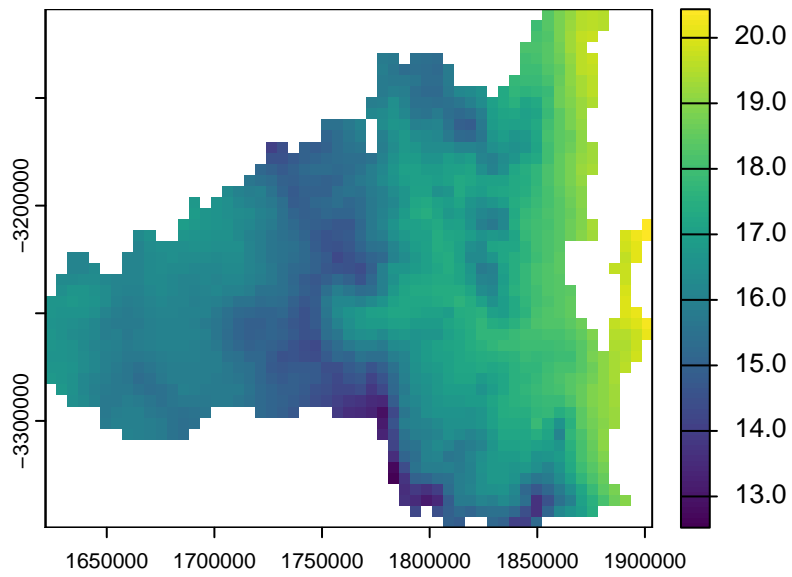
BIO7_Temperature_Annual_Range



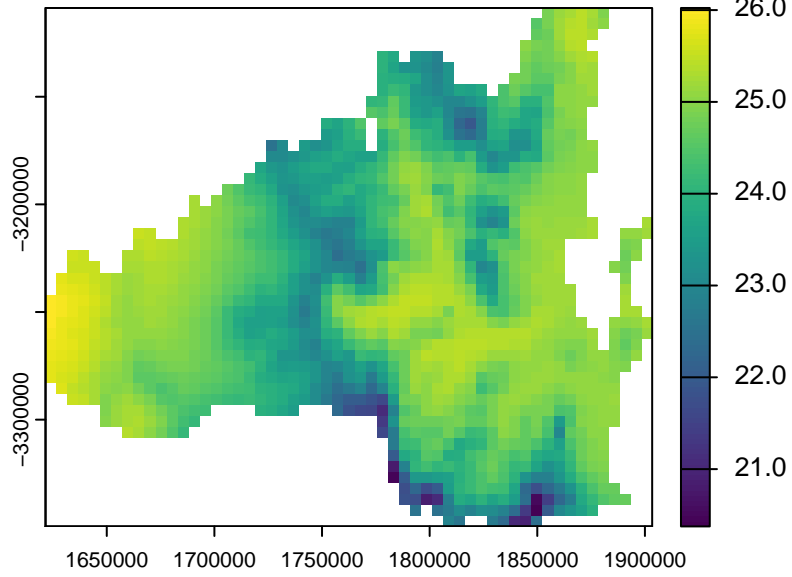
BIO8_Mean_Temp_Wettest_Quarter



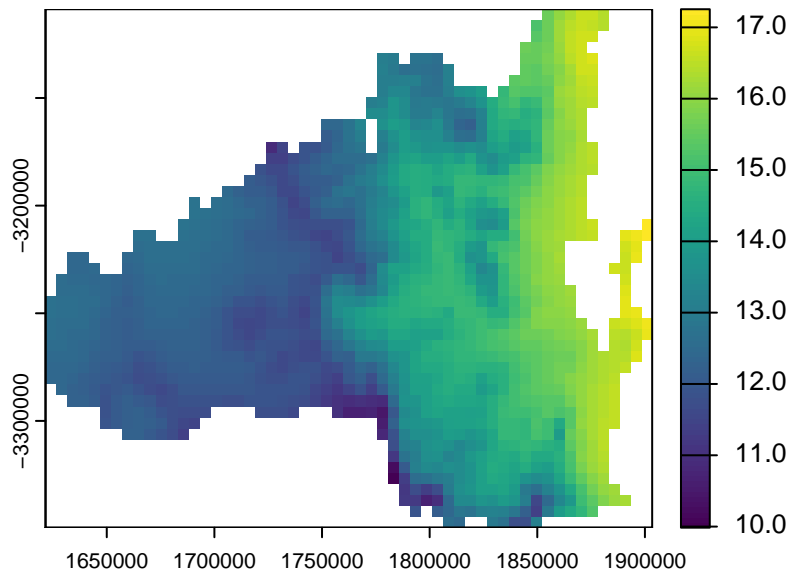
BIO9_Mean_Temp_Driest_Quarter



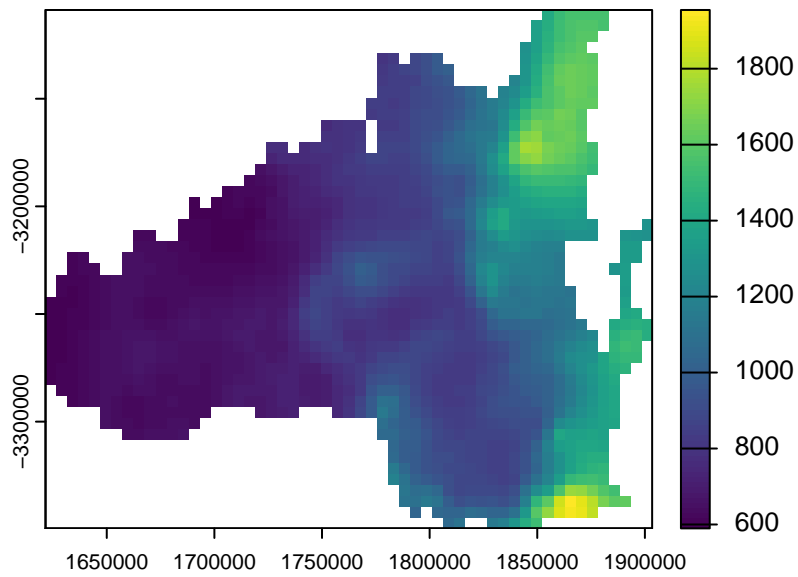
BIO10_Mean_Temp_Warmest_Quarter

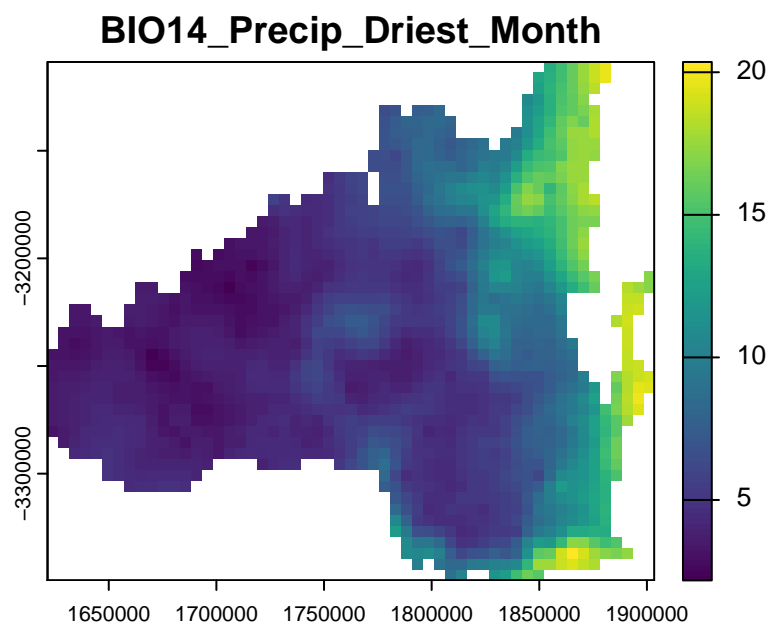
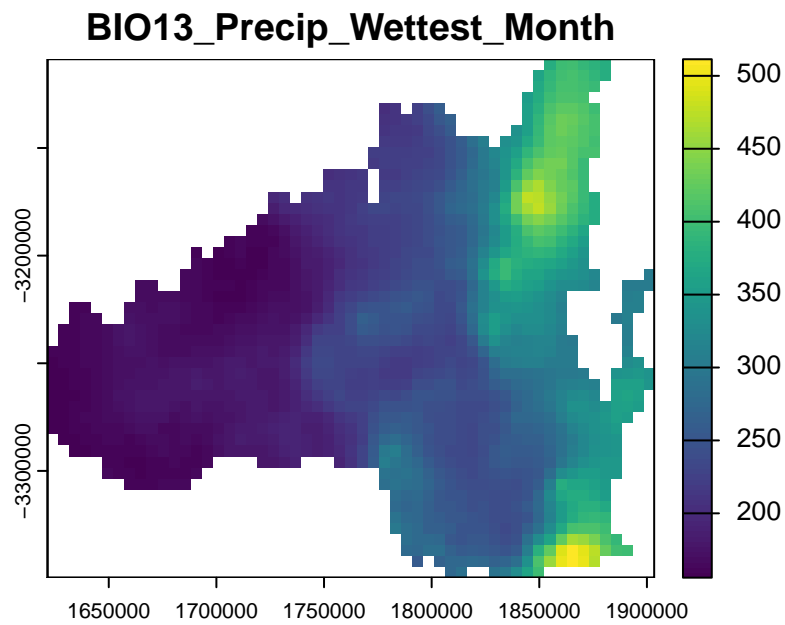


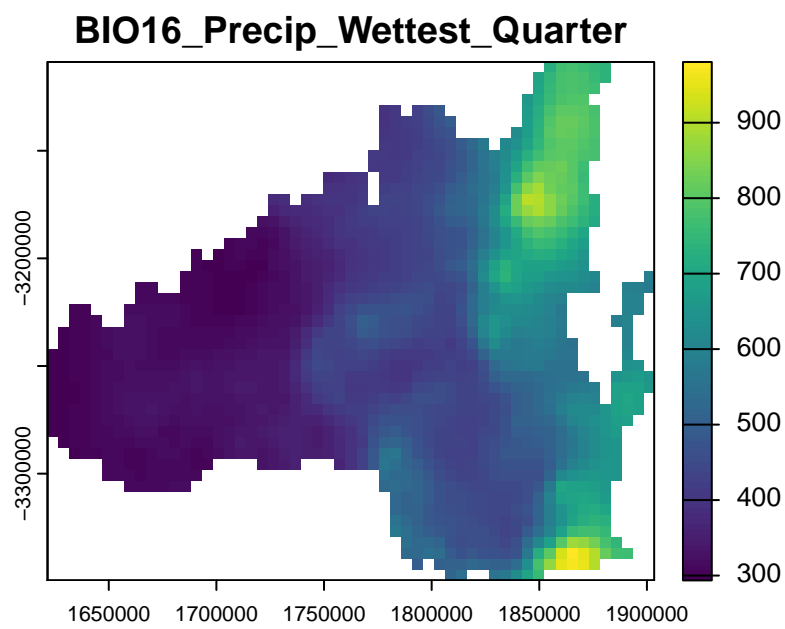
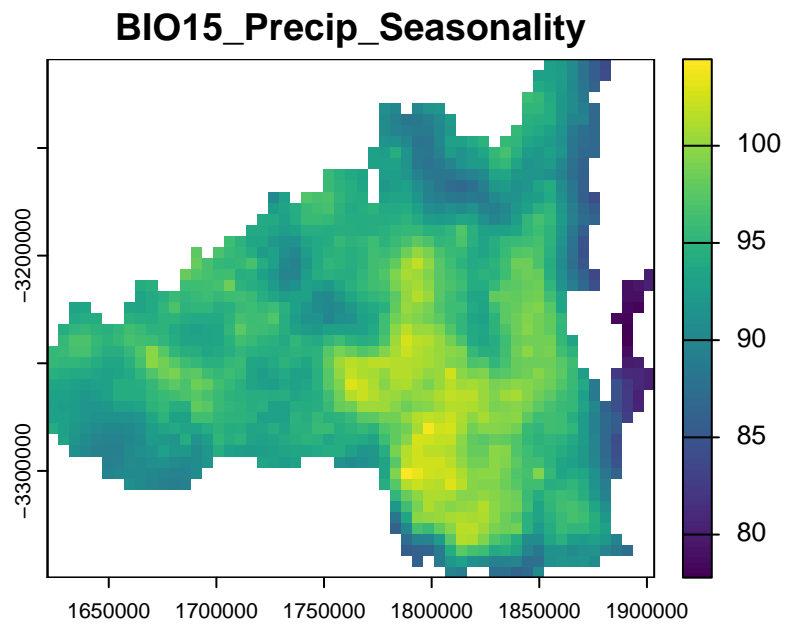
BIO11_Mean_Temp_Coldest_Quarter

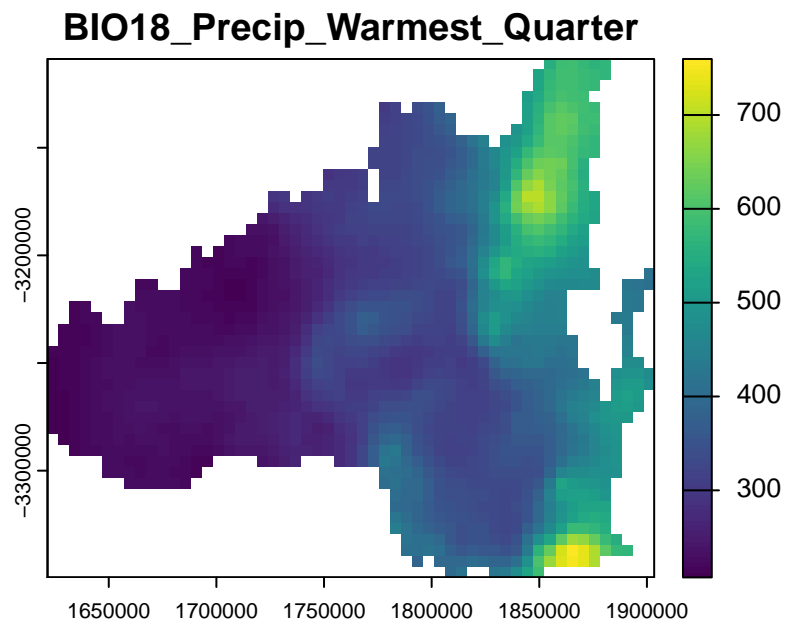
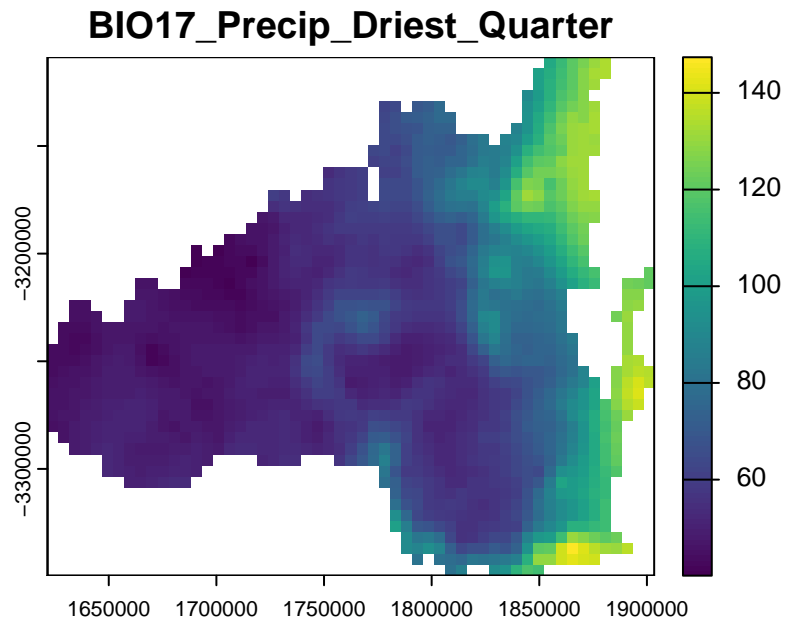


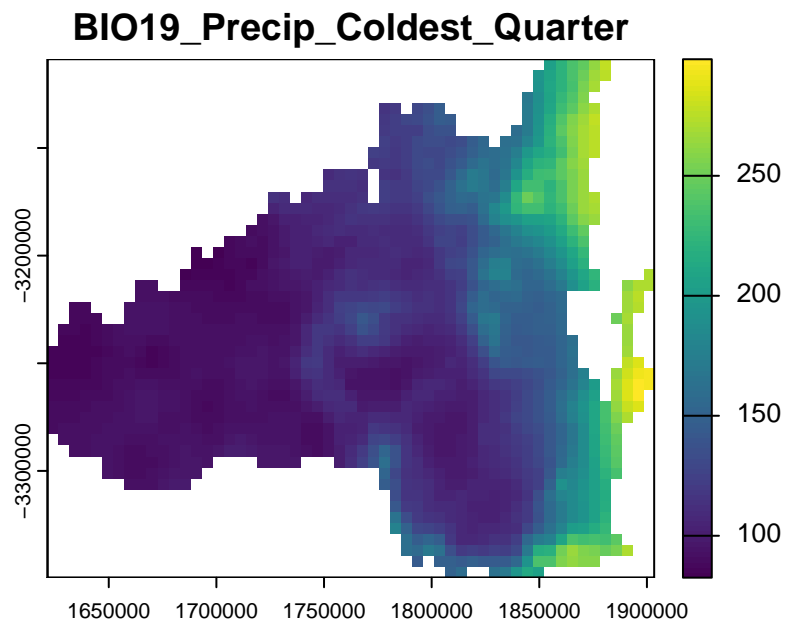
BIO12_Annual_Precipitation









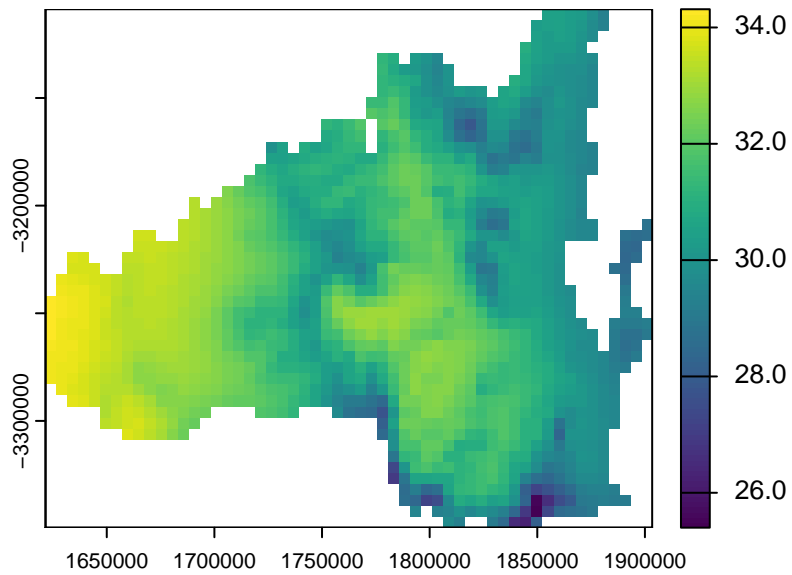


Show the four from expert elicitation the layers

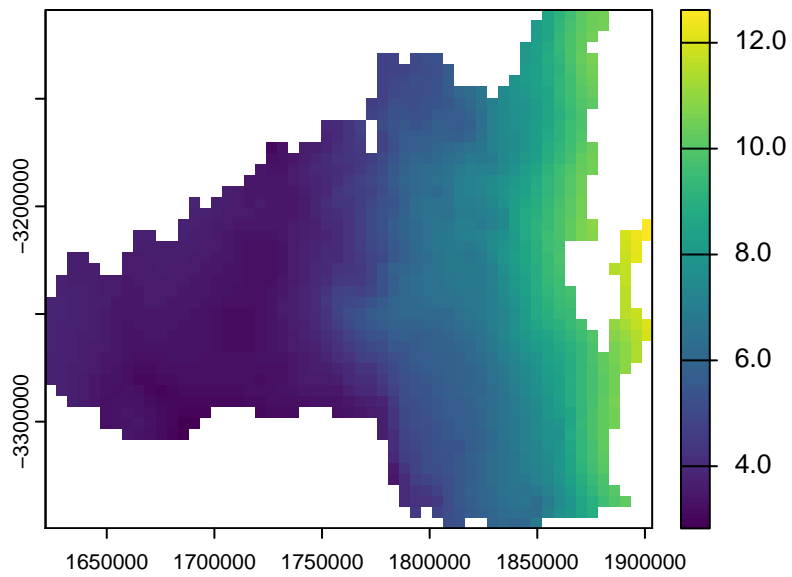
```
covs_current_expert <- subset(covs_current, names(covs_current) %in% c("BI05_Max_Temp_Warmes",
  "BI06_Min_Temp_Coldes",
  "BI012_Annual_Precipi",
  "BI015_Precip_Seasona"))

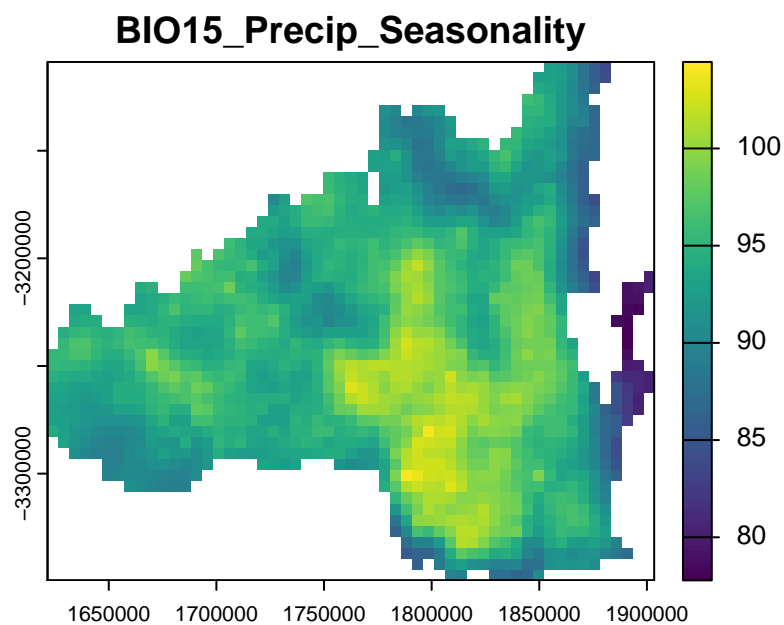
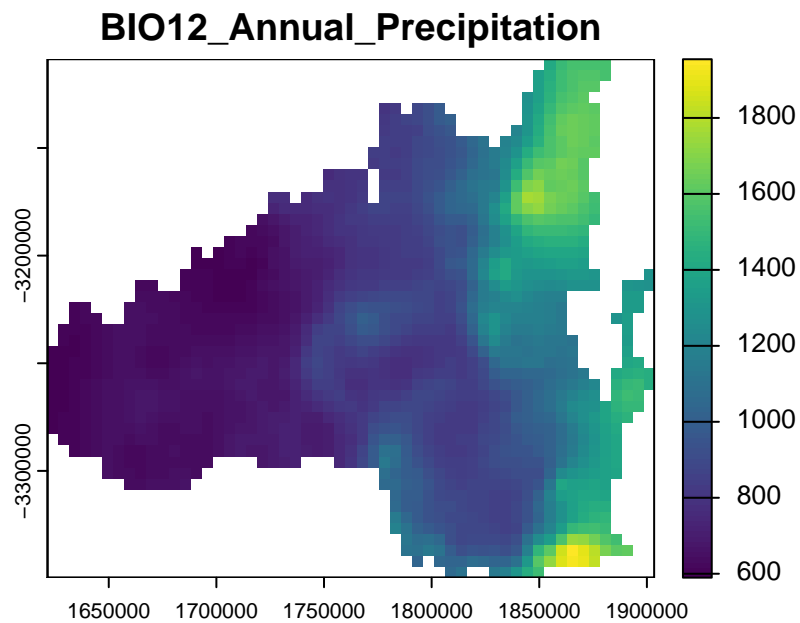
for(i in 1:nlyr(covs_current_expert)) {
  terra::plot(covs_current_expert[[i]], main = names(covs_current_expert)[[i]])
}
```


BIO5_Max_Temp_Warmest_Month



BIO6_Min_Temp_Coldest_Month





Extract environmental covariate values from presence and background locations (training locations)

```
train_PB_covs <- terra::extract(covs_current, pr_bg[,c("x", "y")], xy = T)
train_PB_covs <- cbind(train_PB_covs, pr_bg["Presence"])

# Remove rows where there's values missing from at least one covariate
print(paste0("RECORDS FROM ", nrow(train_PB_covs) - sum(complete.cases(train_PB_covs)), " R0"))
```

[1] "RECORDS FROM 68 ROWS IN TRAINING DATA REMOVED DUE TO MISSING COVARIATE VALUES"

```
train_PB_covs <- train_PB_covs[complete.cases(train_PB_covs), ]
train_PB_covs <- dplyr::select(train_PB_covs, -ID)

head(train_PB_covs)
```

	BI01_Annual_Mean_Temp	BI02_Mean_Diurnal_Temp_Range	BI03_Isothermality
1	20.73219	9.515615	46.85551
2	20.85025	10.291359	47.88751
3	20.61474	10.648253	48.39870
4	21.00405	9.129249	46.28033
5	20.75752	10.070734	47.49575
6	21.00405	9.129249	46.28033

	BI04_Temperature_Seasonality	BI05_Max_Temp_Warmest_Month
1	367.6388	29.73501
2	379.8710	30.47122
3	384.8382	30.53297
4	363.1416	29.72843
5	378.2968	30.20078
6	363.1416	29.72843

	BI06_Min_Temp_Coldest_Month	BI07_Temperature_Annual_Range
1	9.386996	20.34801
2	8.940289	21.53093
3	8.487451	22.04552
4	9.958574	19.76986
5	8.959633	21.24114
6	9.958574	19.76986

	BI08_Mean_Temp_Wettest_Quarter	BI09_Mean_Temp_Driest_Quarter
1	22.98827	18.36451
2	23.55152	18.09120
3	23.31077	17.78633
4	23.01914	18.89500
5	23.32381	18.13480
6	23.01914	18.89500

	BI010_Mean_Temp_Warmest_Quarter	BI011_Mean_Temp_Coldest_Quarter
1	24.94183	15.92675
2	25.18869	15.87509
3	24.99932	15.57214
4	25.18043	16.27002
5	25.08320	15.80299
6	25.18043	16.27002

	BI012_Annual_Precipitation	BI013_Precip_Wettest_Month
1	1238.362	327.7901

2	1165.235	327.1804		
3	1161.138	327.4446		
4	1222.618	311.3793		
5	1109.354	305.5583		
6	1222.618	311.3793		
BI014_Precip_Driest_Month BI015_Precip_Seasonality				
1	10.800349	92.89355		
2	8.330686	98.80420		
3	8.048150	99.45329		
4	11.913177	88.93709		
5	8.327950	97.22968		
6	11.913177	88.93709		
BI016_Precip_Wettest_Quarter BI017_Precip_Driest_Quarter				
1	606.3058	94.95189		
2	598.7009	77.30684		
3	598.9535	75.86132		
4	583.3614	100.51526		
5	558.9021	77.90620		
6	583.3614	100.51526		
BI018_Precip_Warmest_Quarter BI019_Precip_Coldest_Quarter				
1	449.8074	189.9305	1870064	-3265048
2	444.0957	147.6409	1849568	-3234305
3	445.4260	145.7036	1844444	-3234305
4	448.1904	200.5528	1875188	-3259924
5	408.9403	153.3001	1859816	-3259924
6	448.1904	200.5528	1875188	-3259924
Presence				
1	1			
2	1			
3	1			
4	1			
5	1			
6	1			

Thin the koala presence points (for tutorial only)

We now thin the presences to reduce the number of points to a manageable size for plotting and modelling. This is not a recommended step for real data, but is done here to make the tutorial run faster and to make the plots clearer.

```
train_PB_covs_pres <- train_PB_covs %>% filter(Presence == 1)
train_PB_covs_bg <- train_PB_covs %>% filter(Presence == 0)

# Thin the presences for plotting
```

```
train_PB_covs_pres_thin <- train_PB_covs_pres[sample(nrow(train_PB_covs_pres), 10000), ]

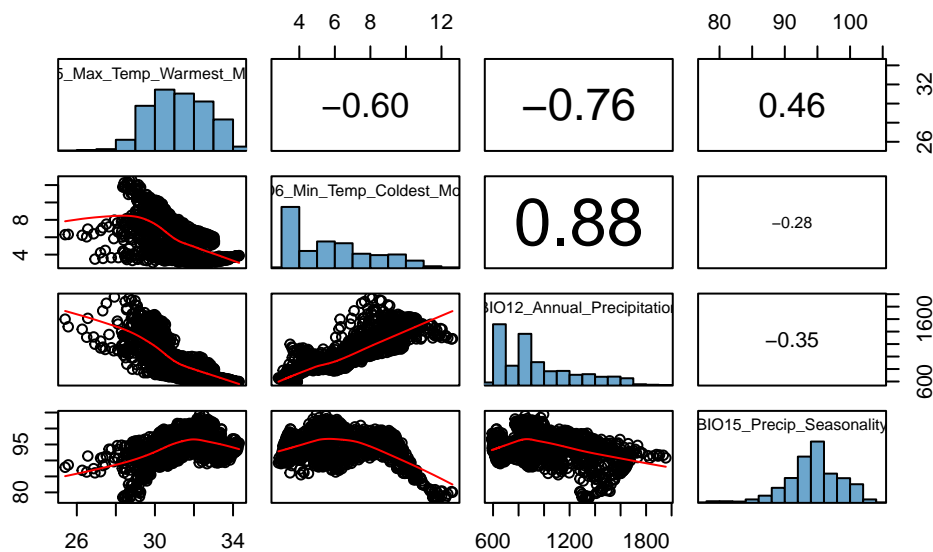
# Combine back into both presence and background
train_PB_covs_thinned <- rbind(train_PB_covs_pres_thin, train_PB_covs_bg)
```

Check correlation and multicollinearity of covariates

Correlation plot

There are several different methods for creating correlation plots.

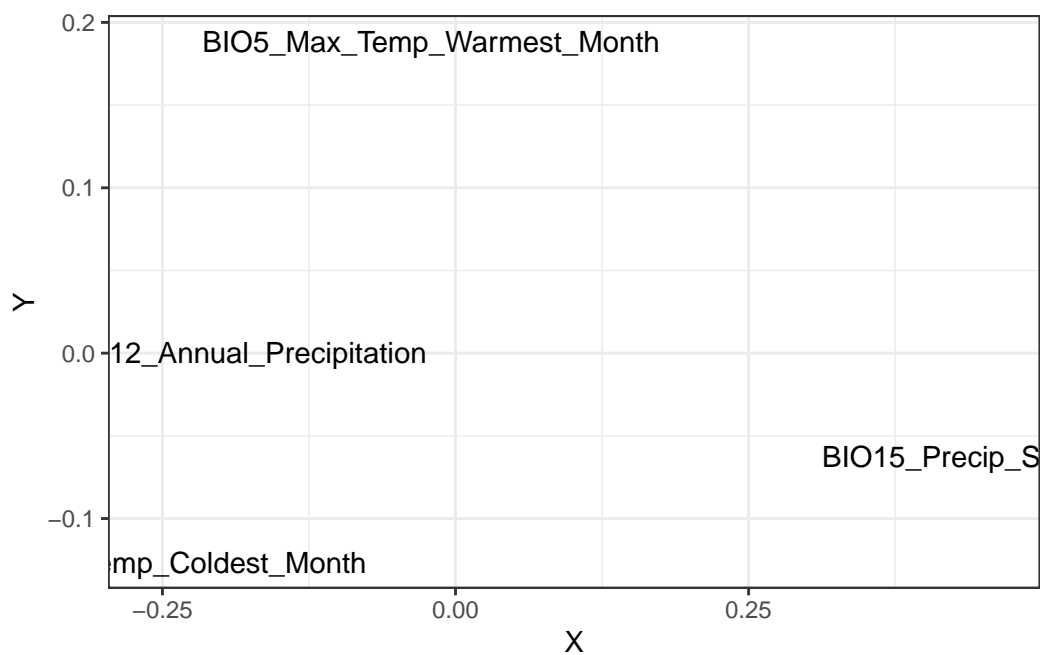
```
ecospat.cor.plot(covs_current_expert)
```



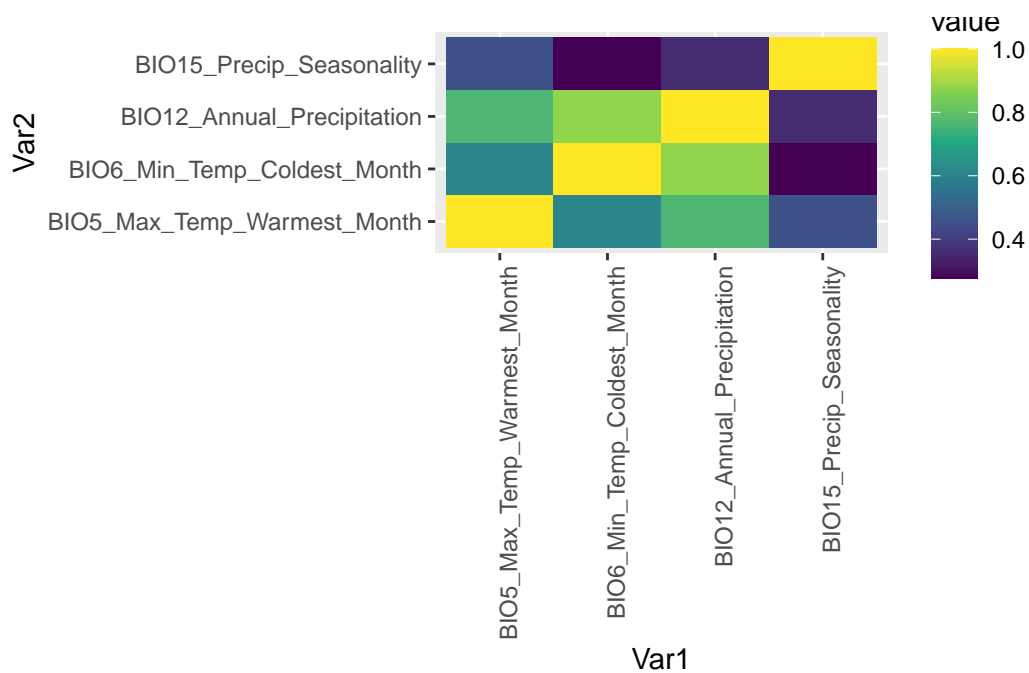
Using the corplots package

For a simple and quick plot.

```
corplots <- ENMTools::raster.cor.plot(covs_current_expert)
corplots$cor.mds.plot
```



```
corplots$cor.heatmap
```



Here, we use the `corrplot` package to create a correlation plot of the selected covariates (this is taken from an EcoCommons Australia notebook).

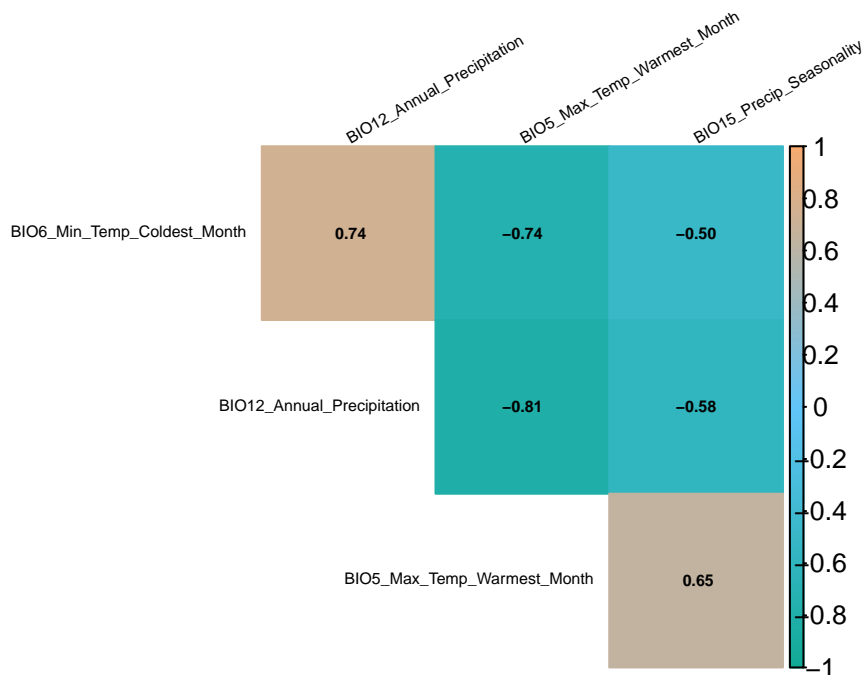
```
# Select columns by their names
cor_data <- train_PB_covs[, names(train_PB_covs) %in% c("BI05_Max_Temp_Warmest_Month",
"BI06_Min_Temp_Coldest_Month",
"BI012_Annual_Precipitation",
"BI015_Precip_Seasonality")]

# Check the structure of the numeric data
str(cor_data)
```

```
'data.frame':  88136 obs. of  4 variables:
 $ BI05_Max_Temp_Warmest_Month: num  29.7 30.5 30.5 29.7 30.2 ...
 $ BI06_Min_Temp_Coldest_Month: num  9.39 8.94 8.49 9.96 8.96 ...
 $ BI012_Annual_Precipitation : num  1238 1165 1161 1223 1109 ...
 $ BI015_Precip_Seasonality   : num  92.9 98.8 99.5 88.9 97.2 ...
```

```
# Calculate the correlation matrix for the numeric columns
cor_matrix <- cor(cor_data, use = "complete.obs", method = "pearson")

corrplot(cor_matrix,
  method = "color",           # Use colored squares for correlation
  type = "upper",             # Show upper triangle only
  order = "hclust",           # Reorder variables hierarchically
  addCoef.col = "black",      # Show correlation coefficients in black
  number.cex = 0.5,           # Reduce the size of correlation labels
  tl.col = "black",           # Text label color
  tl.srt = 30,                # Rotate labels slightly for readability
  tl.cex = 0.5,               # Reduce text size of variable labels (set smaller val
  cl.cex = 0.8,               # Reduce text size of color legend
  diag = FALSE,               # Hide diagonal
  col = colorRampPalette(c("#11aa96", "#61c6fa", "#f6aa70"))(200),
  sig.level = 0.01, insig = "blank")
```



Variance Inflation Factor (VIF)

If you find corplot is hard for you to make decisions, we can use Variance Inflation Factor (VIF). VIF is another statistical measure used to detect multicollinearity in a set of explanatory (independent) variables in a regression model.

Interpretation:

- VIF = 1: No correlation
- VIF > 1 and <= 5: Moderate correlation; may not require corrective action.
- VIF > 5: Indicates high correlation. Multicollinearity may be problematic, and further investigation is recommended.
- VIF > 10: Strong multicollinearity. The variable is highly collinear with others, and steps should be taken to address this.

```
# usdm::vif(covs_current_expert) # just VIF for all covariates
usdm::vifstep(covs_current_expert) # Variance Inflation Factor and test for multicollinearity
```

No variable from the 4 input variables has collinearity problem.

The linear correlation coefficients ranges between:

```
min correlation ( BIO15_Precip_Seasonality ~ BIO6_Min_Temp_Coldest_Month ): -0.2756697
max correlation ( BIO12_Annual_Precipitation ~ BIO6_Min_Temp_Coldest_Month ): 0.8769718
```

----- VIFs of the remained variables -----

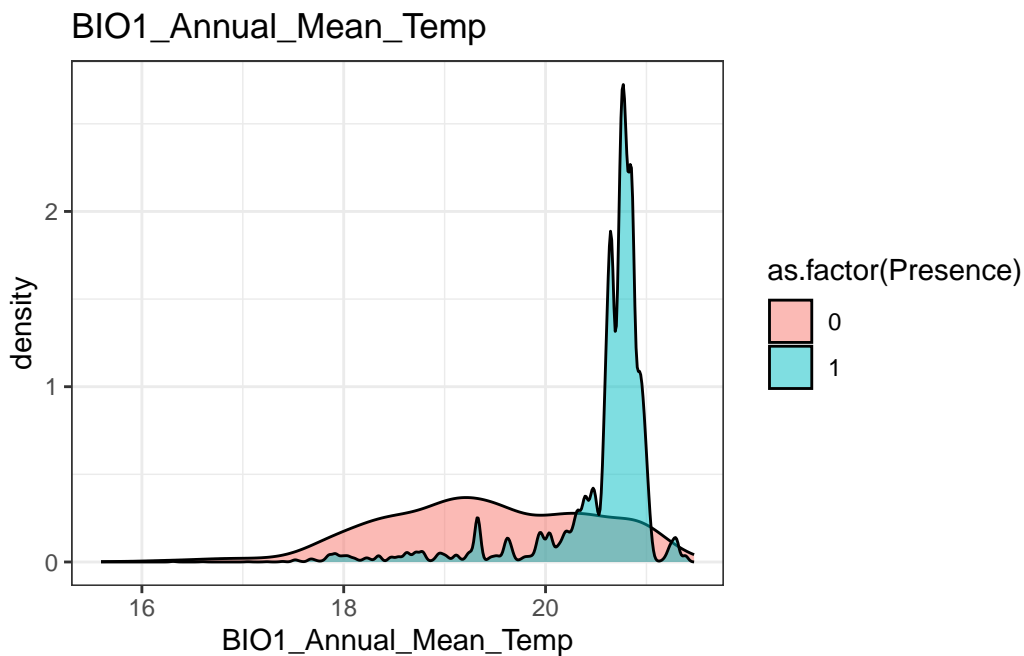
	Variables	VIF
1	BI05_Max_Temp_Warmest_Month	2.751370
2	BI06_Min_Temp_Coldest_Month	4.528719
3	BI012_Annual_Precipitation	6.888077
4	BI015_Precip_Seasonality	1.263385

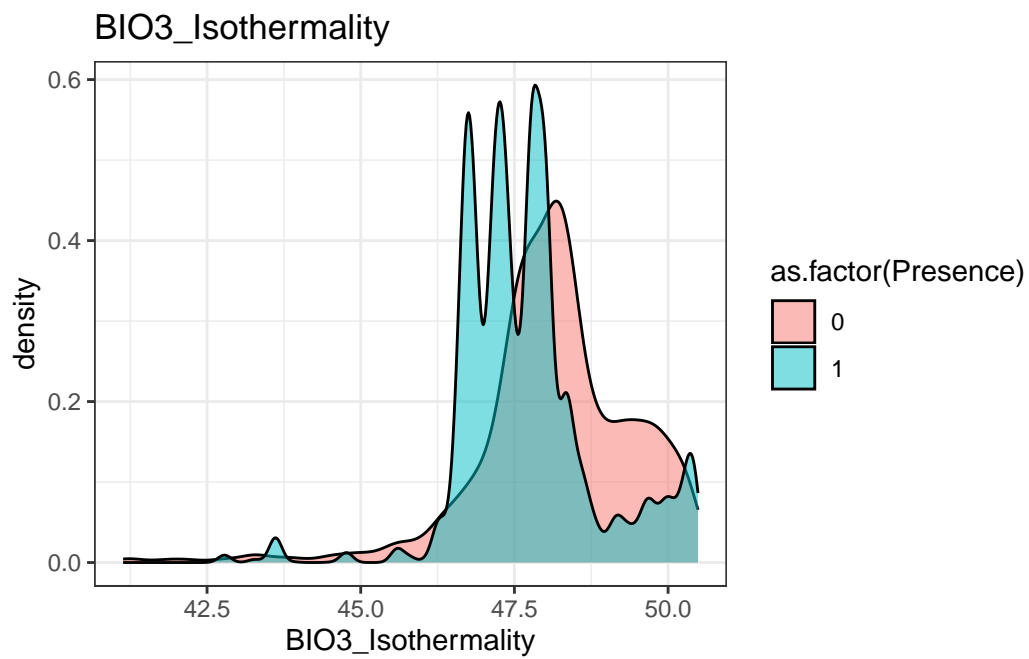
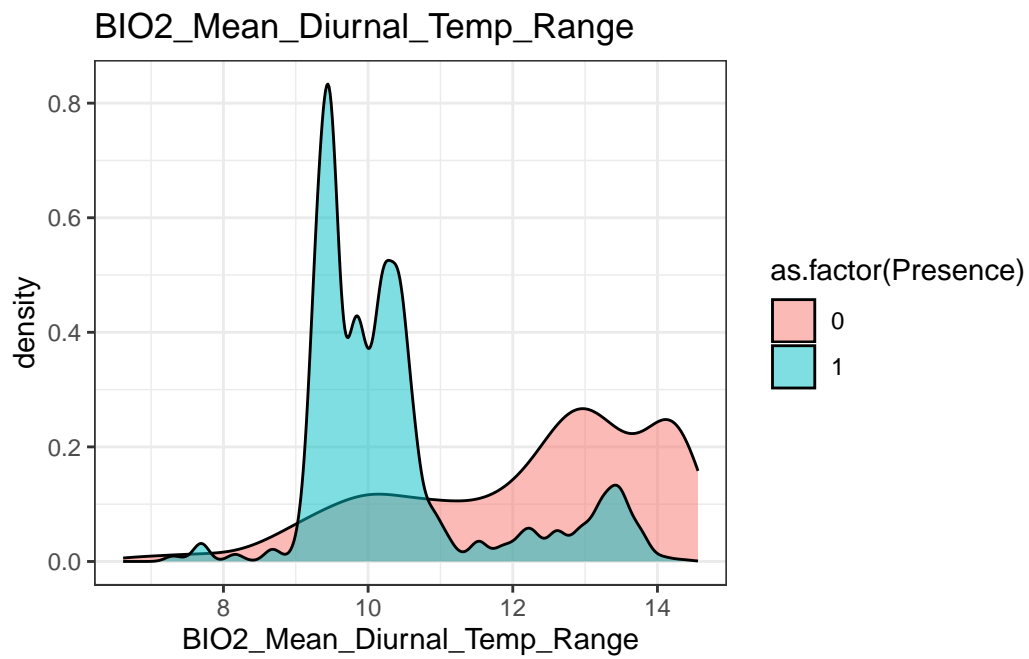
Exploration of the koala presence and background data

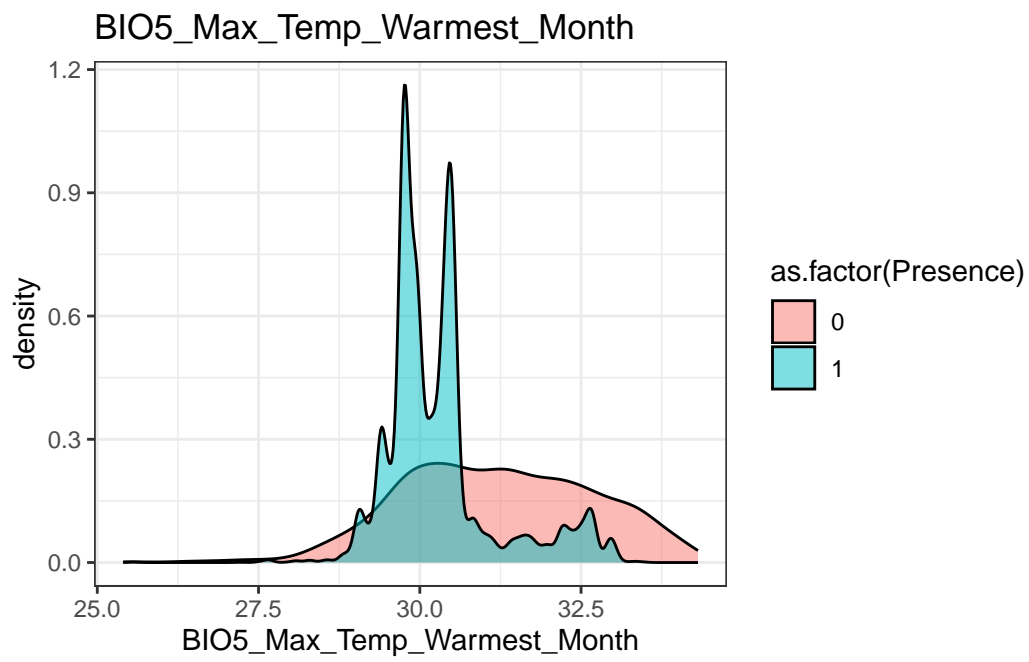
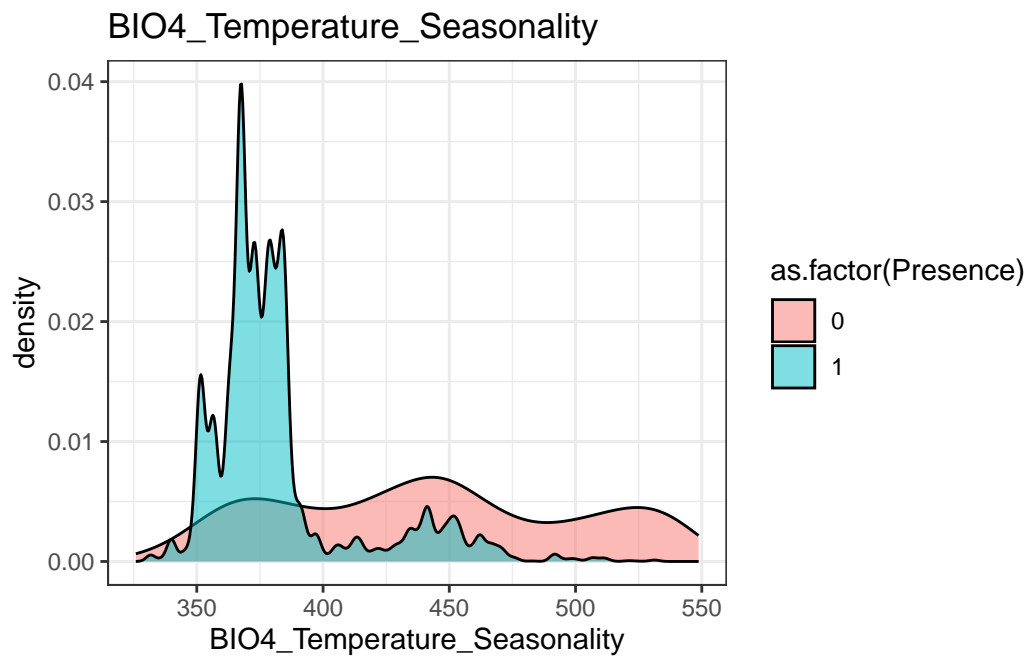
It is good practice to assess where in the environmental space the presence and background points are located. This can help to identify if there are any potential issues with the data, such as a lack of background points in certain areas of environmental space, and should show any patterns in the data that the model should pick up.

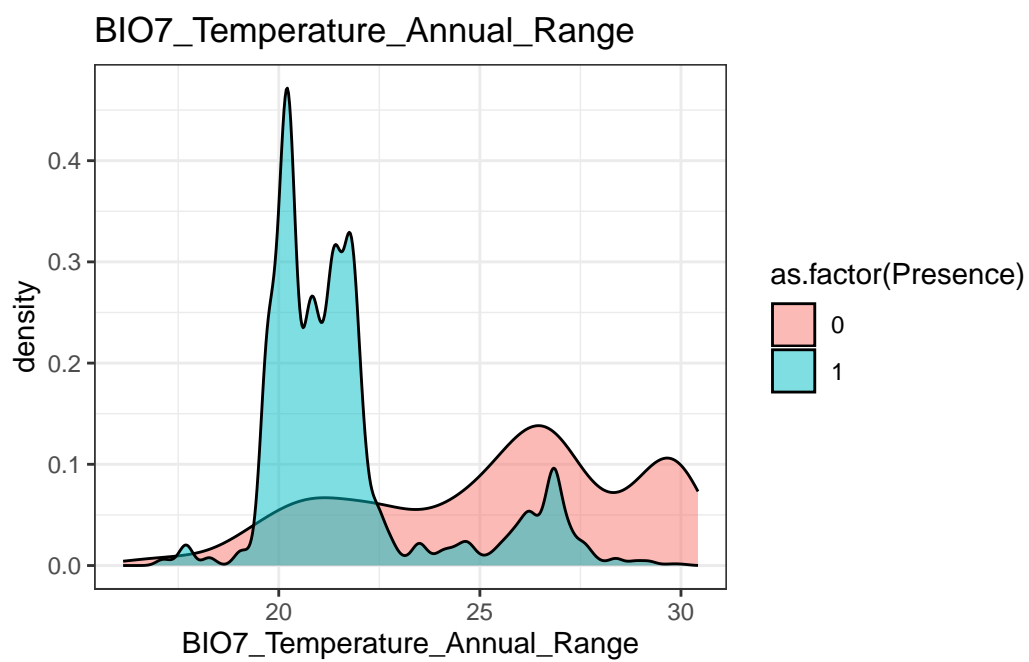
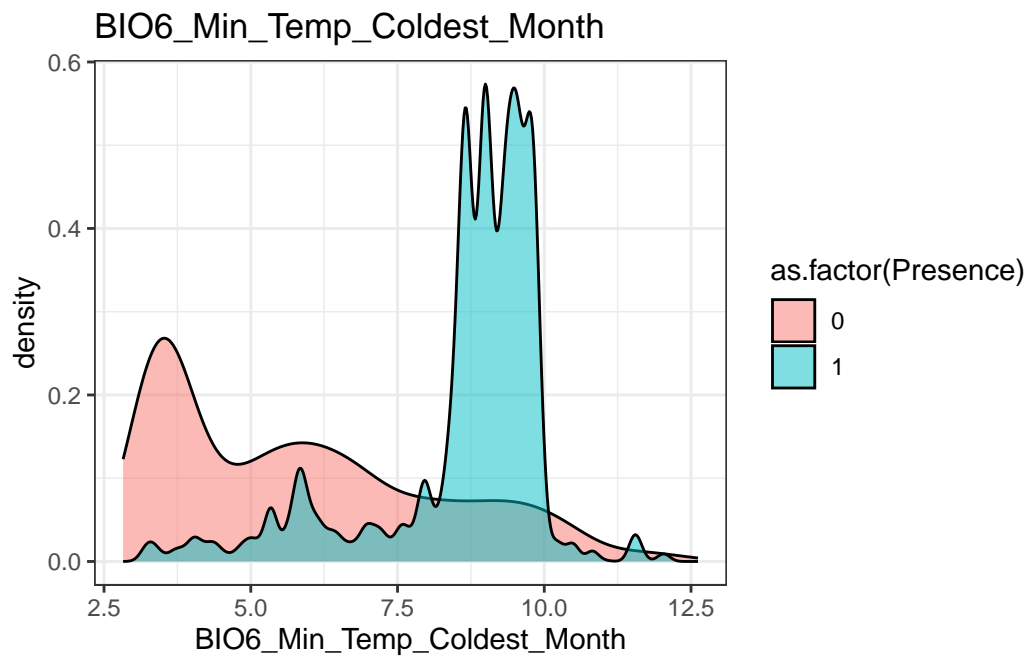
```
# Iterate over all of the variables to create density plots of the background and presence d
for(i in 1:ncol(train_PB_covs_thinned)) {

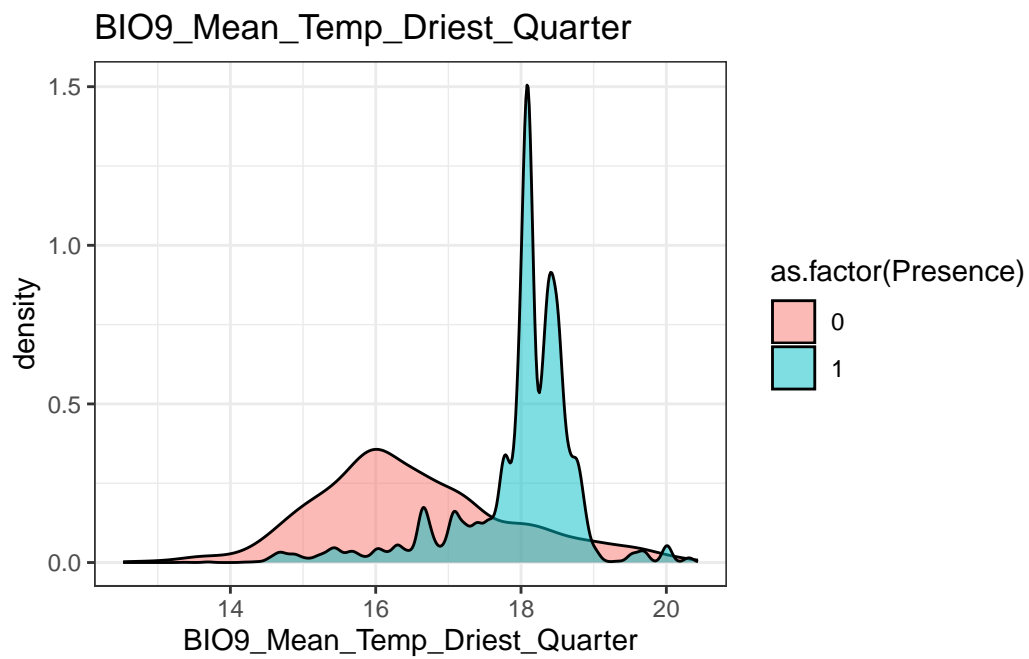
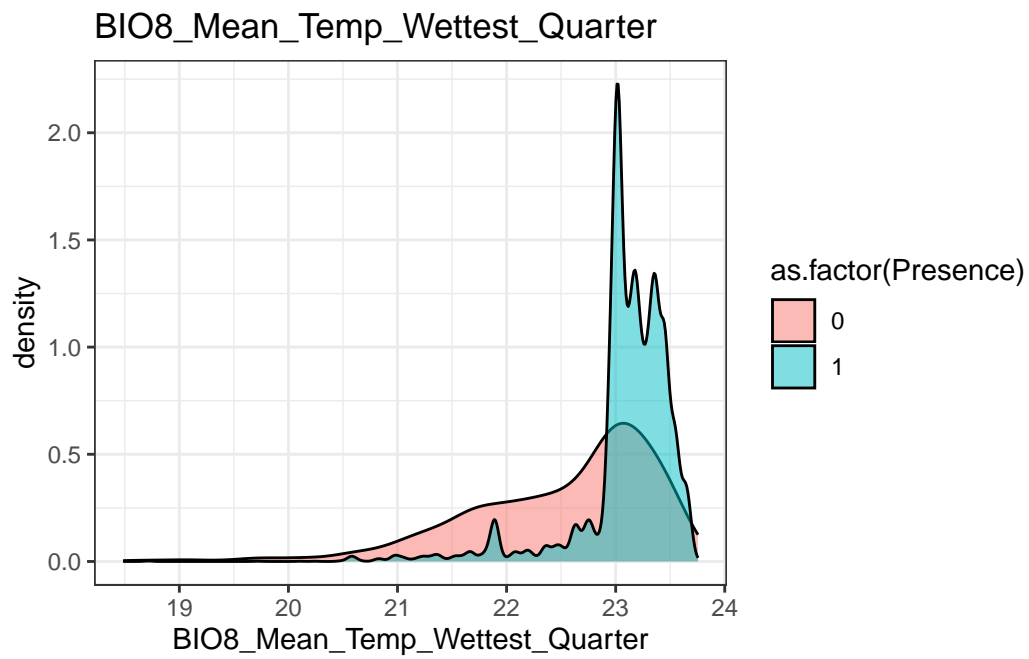
  print(ggplot() +
        geom_density(data = train_PB_covs_thinned,
                     aes(x = .data[[names(train_PB_covs_thinned)[i]]], fill = as.factor(Pr
                     alpha = 0.5) +
        theme_bw() +
        labs(title = names(train_PB_covs_thinned)[i]))
}
```

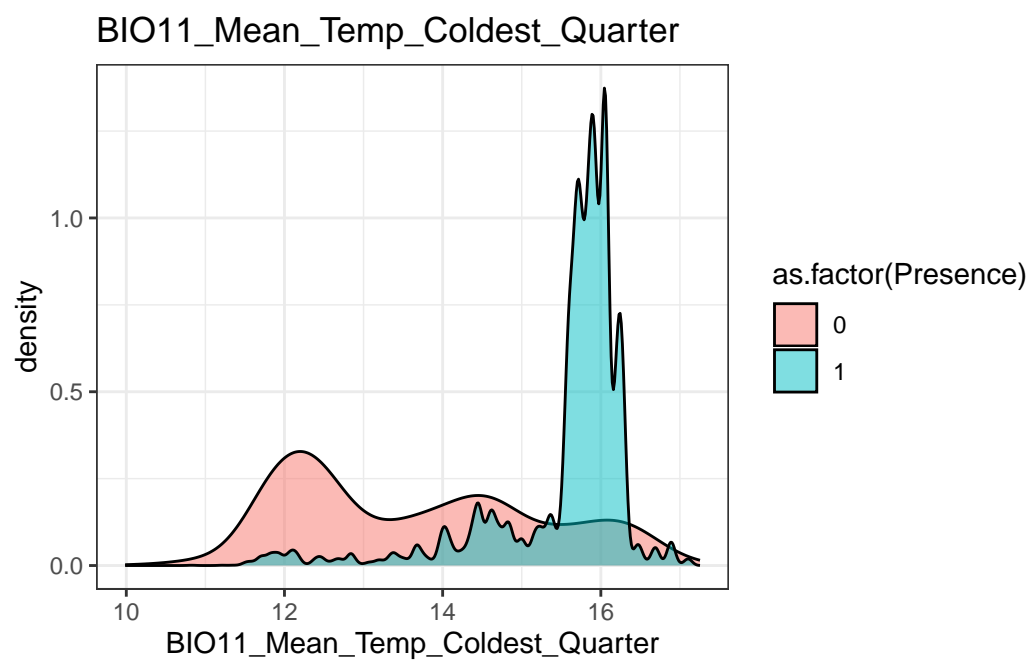
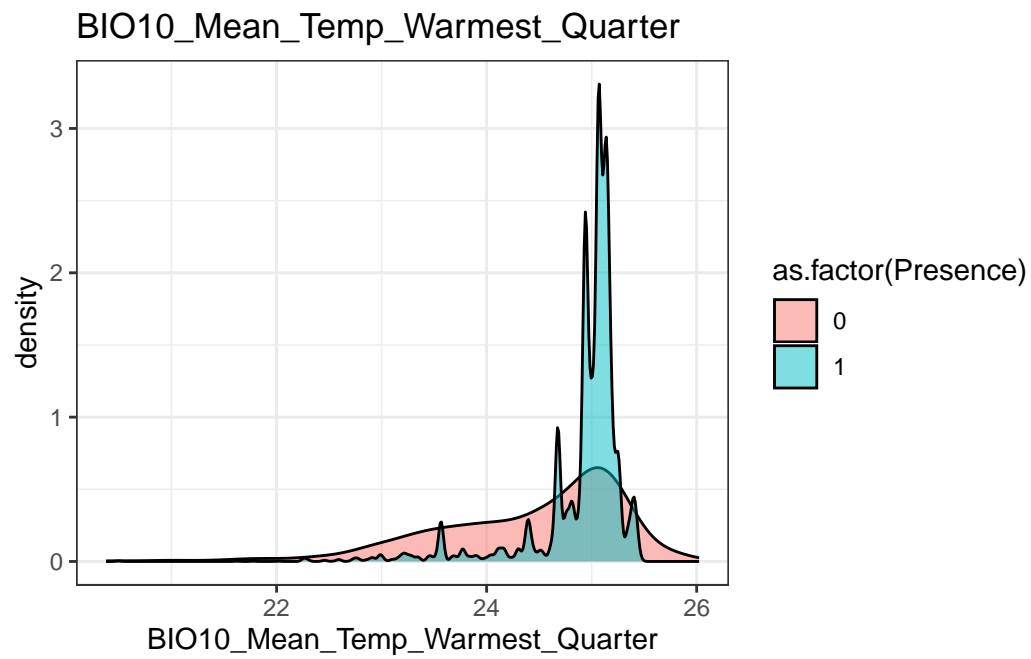


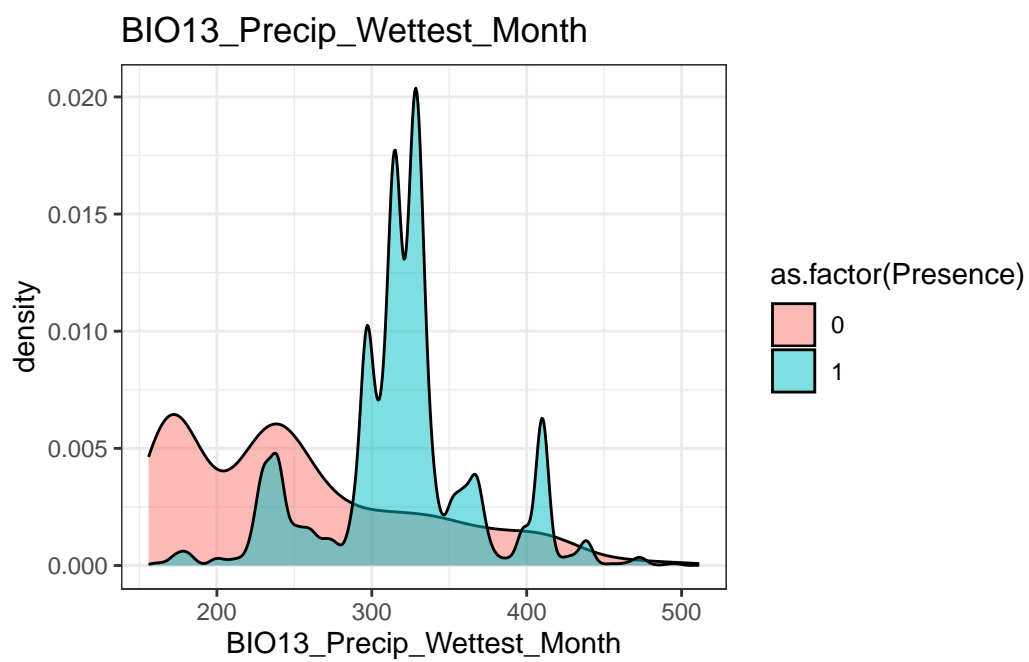
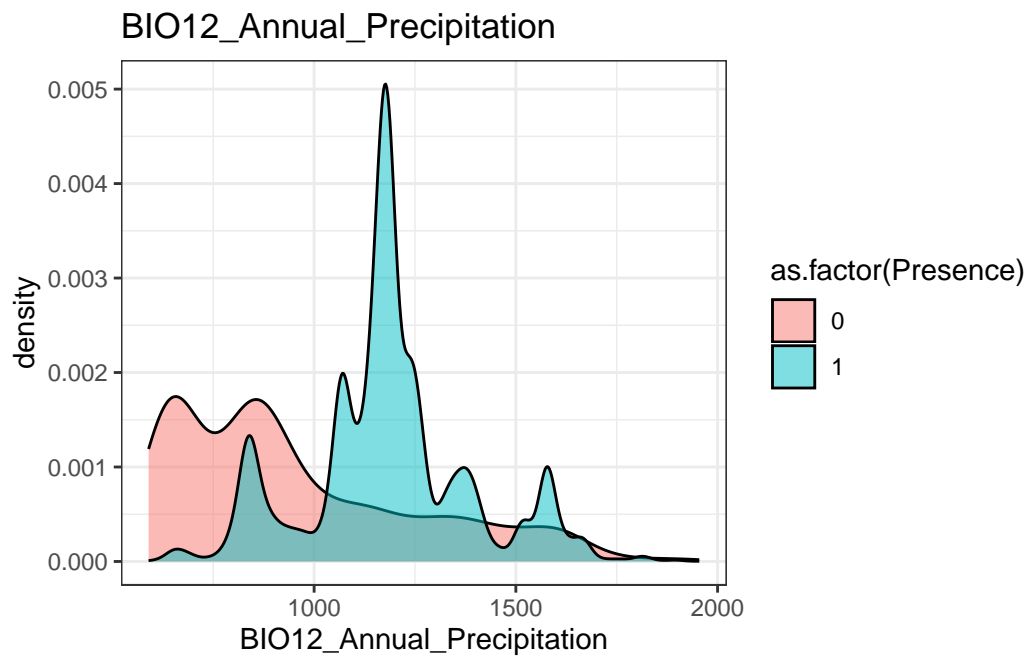


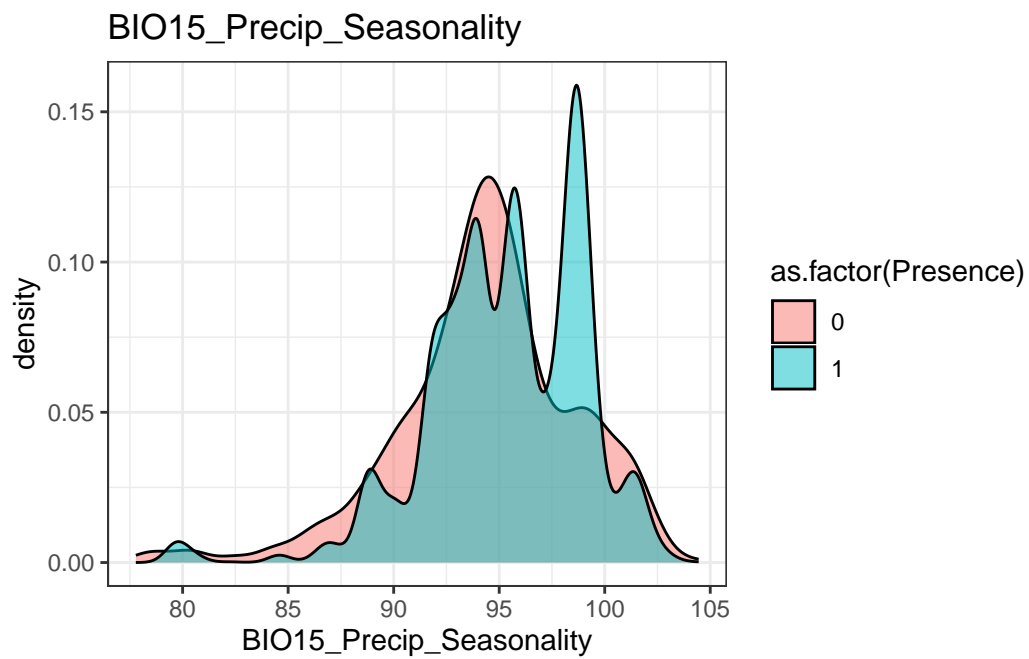
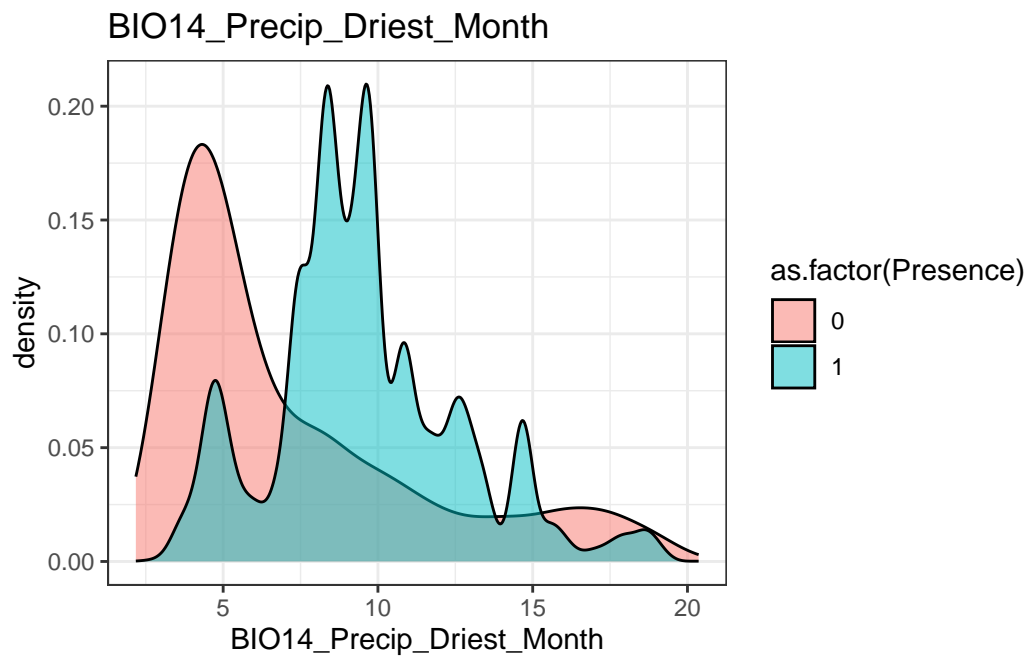


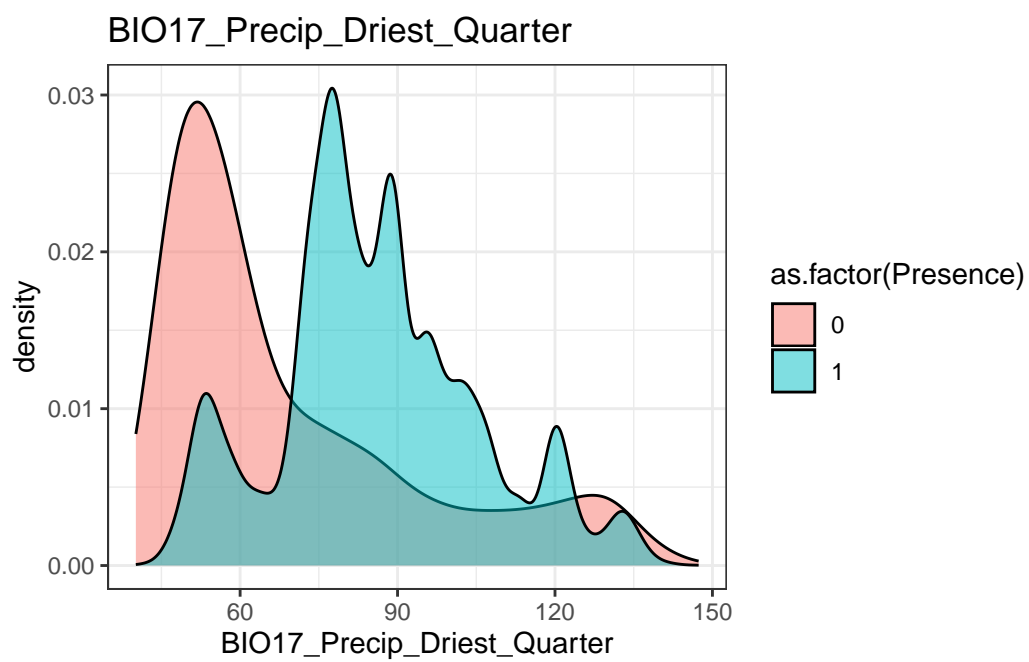
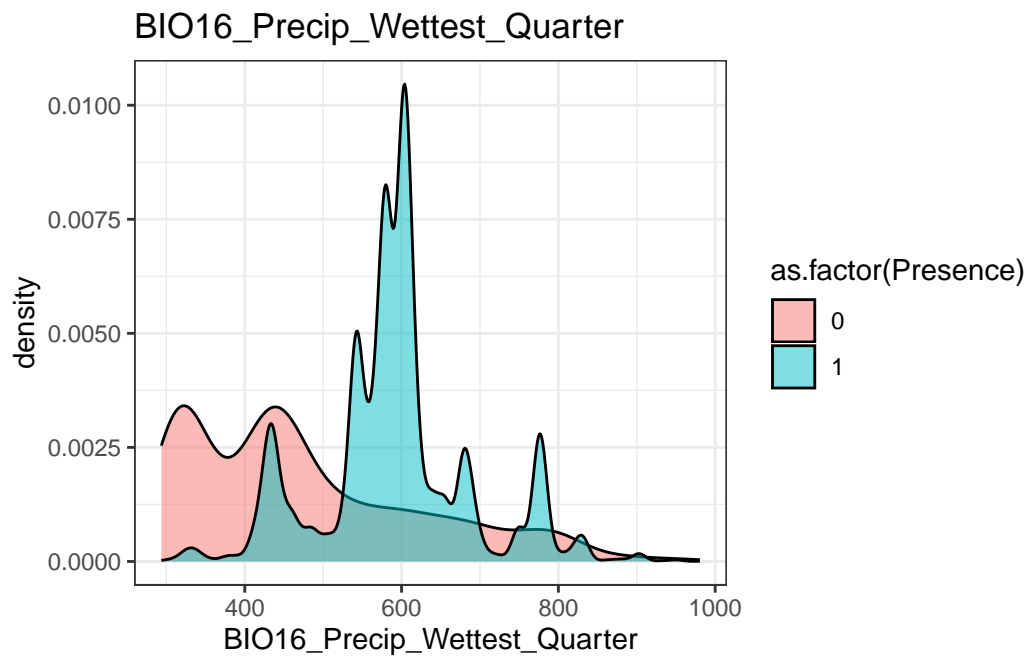


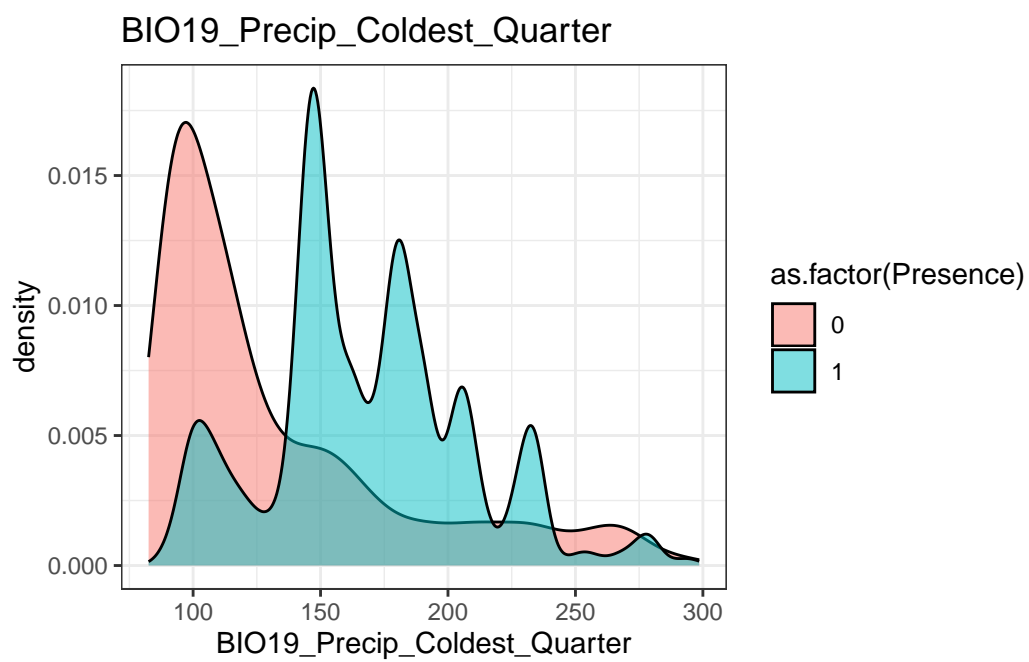
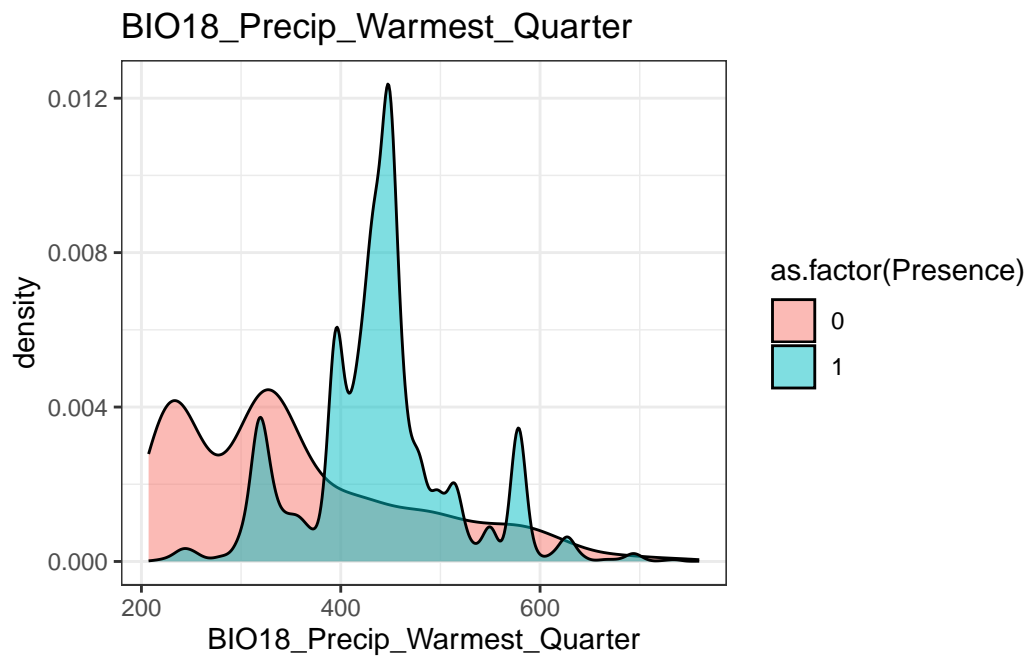


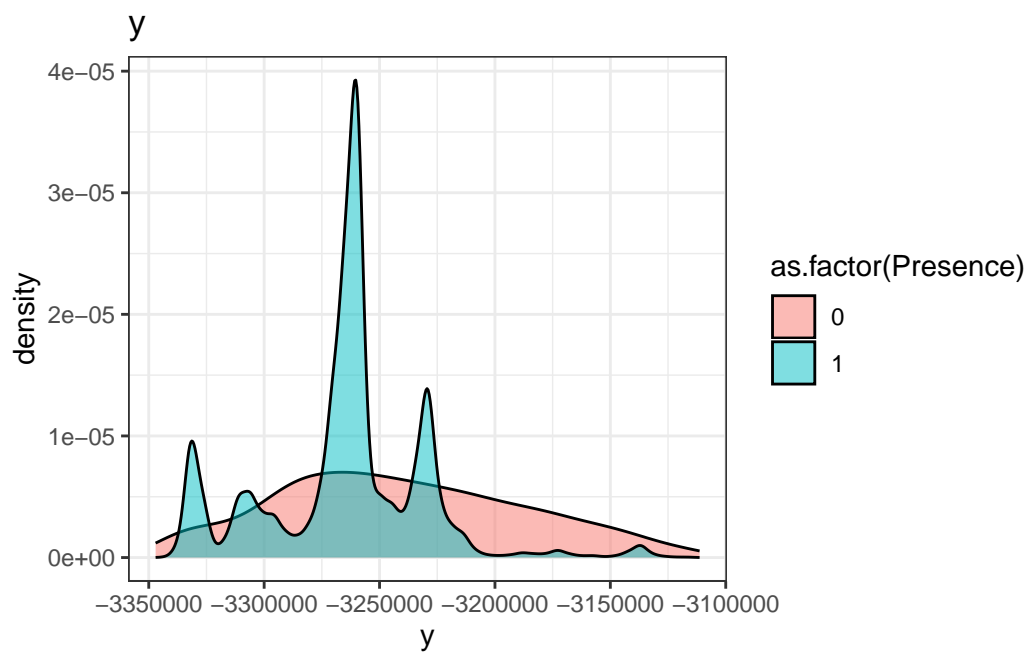
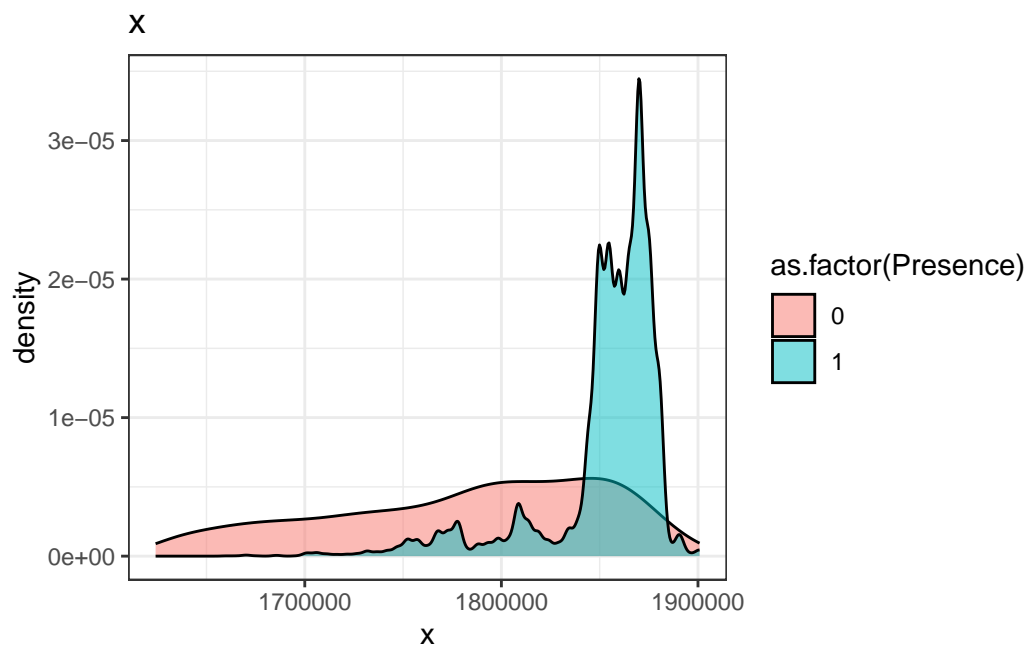


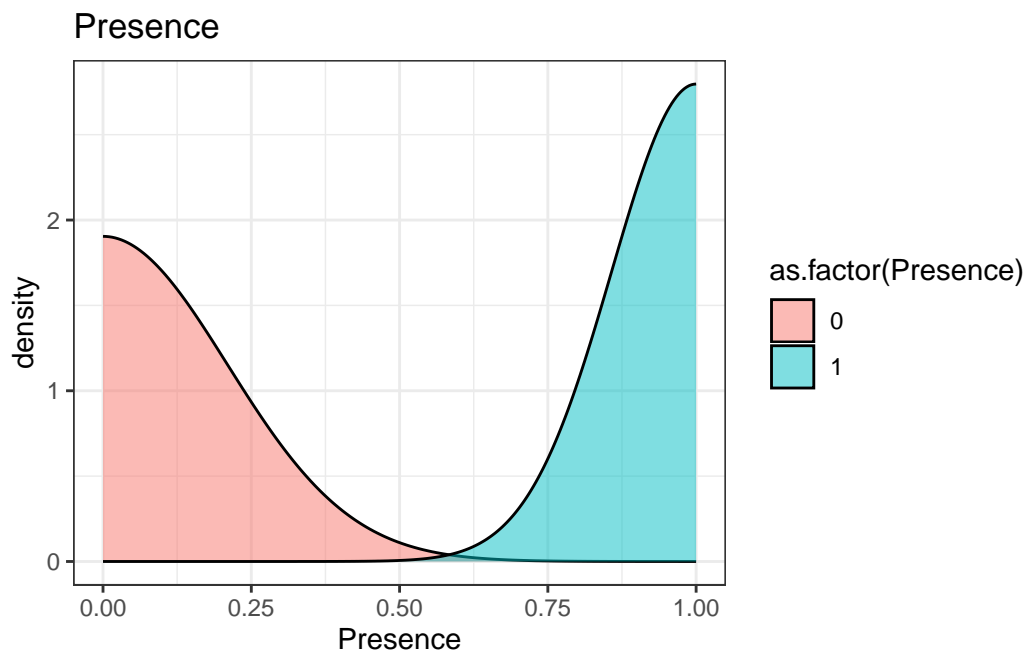












First Model: GLM model fitting

```
# Make a folder to save outputs
dir.create("outputs/GLM_outputs", showWarnings = F)
```

Null model

Null model: no explanatory variables or predictors are included.

It is always helpful to create a null model as a benchmark to assess how the inclusion of explanatory variables improves the model.

```
# Fit a null model with only the intercept
null_model <- glm(Presence ~ 1,
                  data = train_PB_covs,
                  family = binomial(link = "logit"))

# Check the model results
summary(null_model)
```

Call:

```
glm(formula = Presence ~ 1, family = binomial(link = "logit"),
```

```

data = train_PB_covs)

Coefficients:
              Estimate Std. Error z value Pr(>|z|)
(Intercept)  4.08096    0.02636   154.8   <2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for binomial family taken to be 1)

Null deviance: 14902  on 88135  degrees of freedom
Residual deviance: 14902  on 88135  degrees of freedom
AIC: 14904

Number of Fisher Scoring iterations: 7

```

GLM Model 1 - expert variables

```

glm_model_1 <- glm(Presence ~
  BI05_Max_Temp_Warmest_Month +
  BI06_Min_Temp_Coldest_Month +
  BI012_Annual_Precipitation +
  BI015_Precip_Seasonality,
  data=train_PB_covs_thinned,
  family = binomial(link = "logit"))

# Check the model results
summary(glm_model_1)

```

```

Call:
glm(formula = Presence ~ BI05_Max_Temp_Warmest_Month + BI06_Min_Temp_Coldest_Month +
  BI012_Annual_Precipitation + BI015_Precip_Seasonality, family = binomial(link = "logit")
  data = train_PB_covs_thinned)

```

```

Coefficients:
              Estimate Std. Error z value Pr(>|z|)
(Intercept)  -6.651059    1.562034  -4.258 2.06e-05 ***
BI05_Max_Temp_Warmest_Month -0.596618    0.051512 -11.582 < 2e-16 ***
BI06_Min_Temp_Coldest_Month  0.880896    0.028613  30.786 < 2e-16 ***
BI012_Annual_Precipitation  -0.002949    0.000275 -10.724 < 2e-16 ***
BI015_Precip_Seasonality    0.247330    0.010880  22.733 < 2e-16 ***
---

```

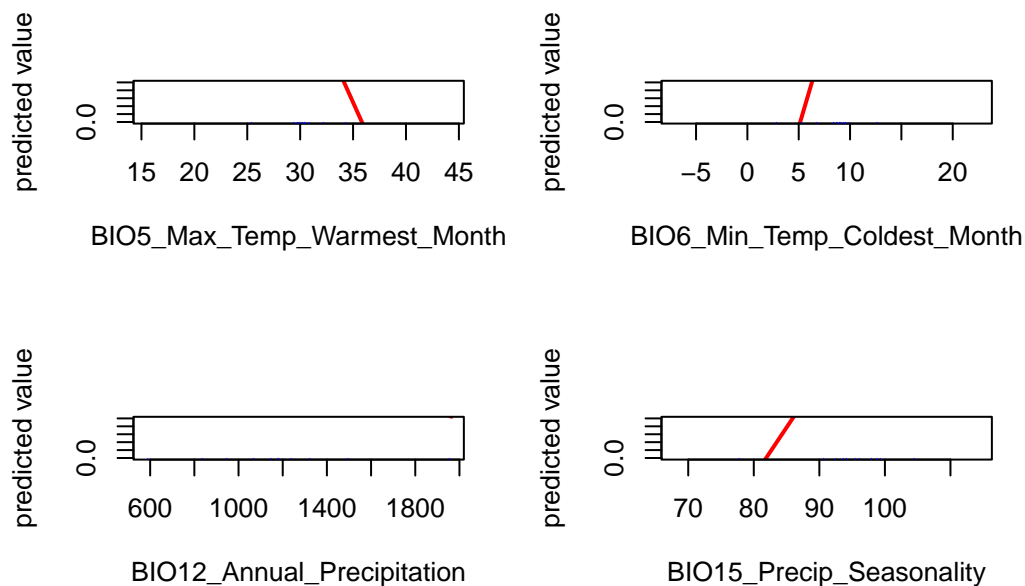
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for binomial family taken to be 1)

Null deviance: 8758.5 on 11463 degrees of freedom
Residual deviance: 5710.0 on 11459 degrees of freedom
AIC: 5720

Number of Fisher Scoring iterations: 6

```
# These response curves don't look very helpful  
dismo::response(glm_model_1)
```



GLM Model 2 - expert variables with quadratics

In this model, we include quadratic terms for the covariates. This is a common approach in species distribution modelling to account for non-linear relationships between the predictors and the response variable. This increases the complexity of the model and allows for more flexibility in fitting the data.

```
glm_model_2 <- glm(Presence ~  
  BIO5_Max_Temp_Warmest_Month + I(BIO5_Max_Temp_Warmest_Month^2) +  
  BIO6_Min_Temp_Coldest_Month + I(BIO6_Min_Temp_Coldest_Month^2) +  
  BIO12_Annual_Precipitation + I(BIO12_Annual_Precipitation^2) +  
  BIO15_Precip_Seasonality + I(BIO15_Precip_Seasonality^2),  
  data=train_PB_covs_thinned,  
  family = binomial(link = "logit"))
```

```
# Check the model results
summary(glm_model_2)
```

Call:

```
glm(formula = Presence ~ BI05_Max_Temp_Warmest_Month + I(BI05_Max_Temp_Warmest_Month^2) +
    BI06_Min_Temp_Coldest_Month + I(BI06_Min_Temp_Coldest_Month^2) +
    BI012_Annual_Precipitation + I(BI012_Annual_Precipitation^2) +
    BI015_Precip_Seasonality + I(BI015_Precip_Seasonality^2),
    family = binomial(link = "logit"), data = train_PB_covs_thinned)
```

Coefficients:

	Estimate	Std. Error	z value	Pr(> z)	
(Intercept)	-8.396e+01	1.828e+01	-4.593	4.37e-06	***
BI05_Max_Temp_Warmest_Month	-1.334e+00	1.180e+00	-1.130	0.2585	
I(BI05_Max_Temp_Warmest_Month^2)	1.292e-02	1.910e-02	0.676	0.4988	
BI06_Min_Temp_Coldest_Month	-1.096e+00	1.914e-01	-5.728	1.02e-08	***
I(BI06_Min_Temp_Coldest_Month^2)	1.456e-01	1.293e-02	11.260	< 2e-16	***
BI012_Annual_Precipitation	7.378e-04	1.941e-03	0.380	0.7039	
I(BI012_Annual_Precipitation^2)	-1.266e-06	6.923e-07	-1.828	0.0675	.
BI015_Precip_Seasonality	2.084e+00	2.380e-01	8.758	< 2e-16	***
I(BI015_Precip_Seasonality^2)	-9.202e-03	1.269e-03	-7.253	4.09e-13	***

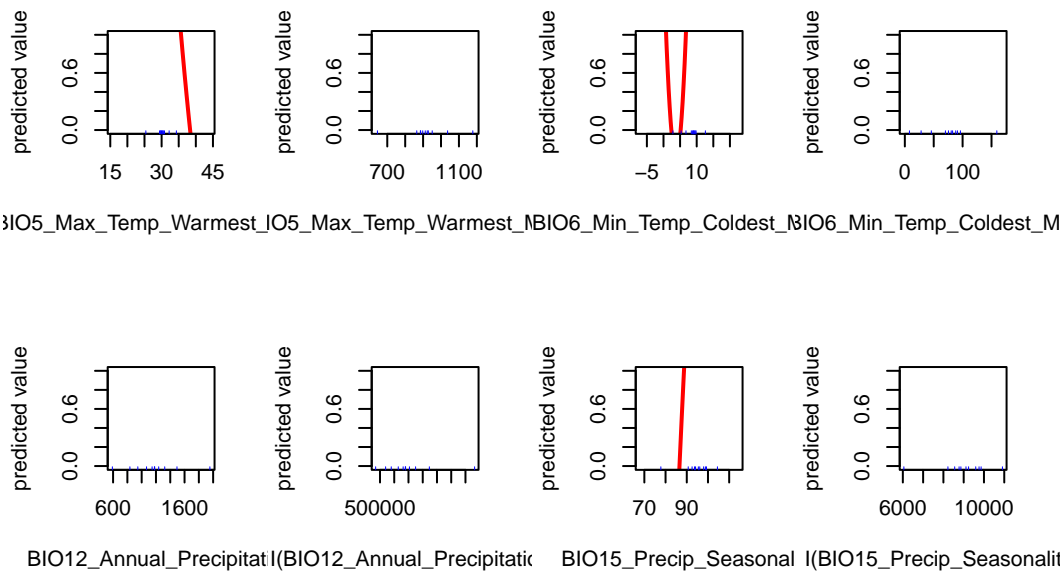
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for binomial family taken to be 1)

Null deviance: 8758.5 on 11463 degrees of freedom
 Residual deviance: 5546.0 on 11455 degrees of freedom
 AIC: 5564

Number of Fisher Scoring iterations: 6

```
# These response curves don't look very helpful
dismo::response(glm_model_2)
```



Model effect evaluation

Here we use a function presented in an EcoCommons Australia notebook to evaluate the model performance. The notebook can be found on their GitHub: <https://github.com/EcoCommonsAustralia/n>

```
# Function to plot effect size graph
plot_effect_size <- function(glm_model) {
  # Check if required libraries are installed
  if (!requireNamespace("ggplot2", quietly = TRUE)) {
    stop("Please install the 'ggplot2' package to use this function.")
  }
  library(ggplot2)

  # Extract effect sizes (coefficients) from the model
  coefs <- summary(glm_model)$coefficients
  effect_sizes <- data.frame(
    Variable = rownames(coefs)[-1], # Exclude the intercept
    Effect_Size = coefs[-1, "Estimate"],
    Std_Error = coefs[-1, "Std. Error"]
  )

  # Sort by effect size
  effect_sizes <- effect_sizes[order(-abs(effect_sizes$Effect_Size)), ]

  # Plot the effect sizes with error bars
  ggplot(effect_sizes, aes(x = reorder(Variable, Effect_Size), y = Effect_Size)) +
    geom_bar(stat = "identity", fill = "#11aa96") +
```



```

geom_errorbar(aes(ymin = Effect_Size - Std_Error, ymax = Effect_Size + Std_Error), width
coord_flip() +
labs(
  title = "Effect Sizes of Variables",
  x = "Variable",
  y = "Effect Size (Coefficient Estimate)"
) +
theme_minimal()
}

```

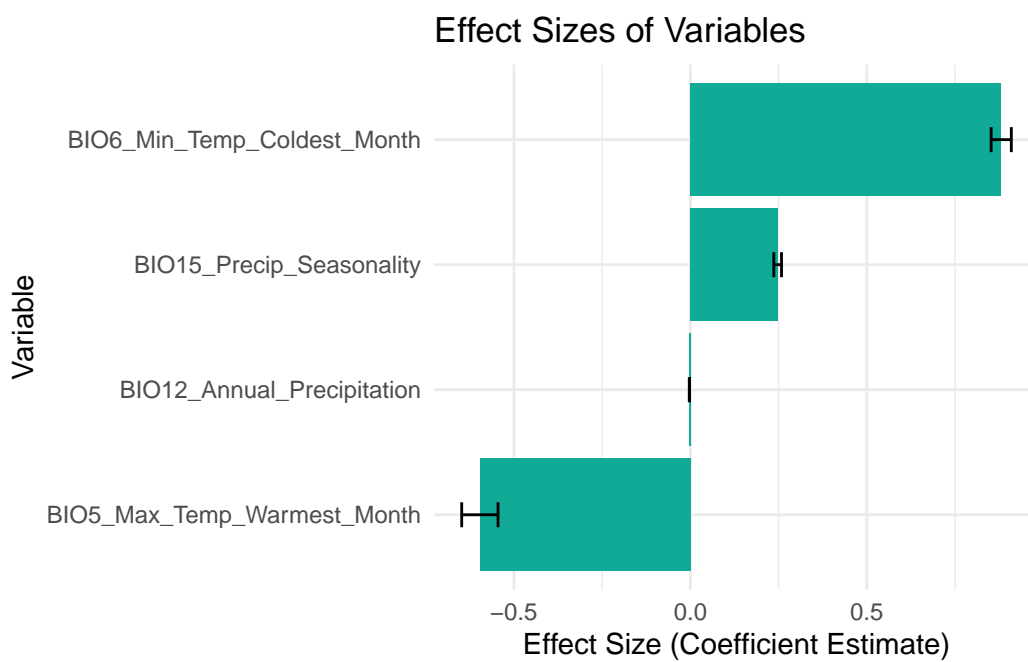
Use the function to check the effect sizes

We need to be careful when interpreting the effect sizes of models with quadratic terms however, as the response curve depends on the linear and the quadratic term.

```

# Example usage of effect size plot
plot_effect_size(glm_model_1)

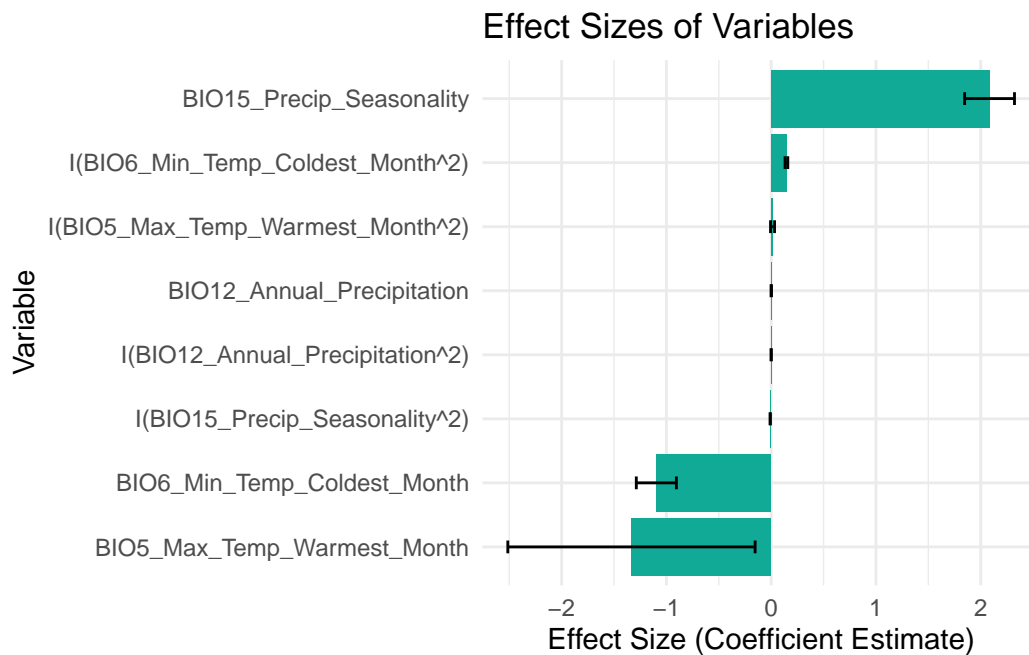
```



```

plot_effect_size(glm_model_2)

```



Response curves

Again, we can use a function from the EcoCommons notebook to plot the response curves from the model, although for quadratics we need to adjust the function or use something else.

```
plot_species_response <- function(glm_model, predictors, data) {
  # Check if required libraries are installed
  if (!requireNamespace("ggplot2", quietly = TRUE) || !requireNamespace("gridExtra", quietly = TRUE)) {
    stop("Please install the 'ggplot2' and 'gridExtra' packages to use this function.")
  }
  library(ggplot2)
  library(gridExtra)

  # Create empty list to store response plots
  response_plots <- list()

  # Loop through each predictor variable
  for (predictor in predictors) {
    # Create new data frame to vary predictor while keeping others constant
    pred_range <- seq(
      min(data[[predictor]], na.rm = TRUE),
      max(data[[predictor]], na.rm = TRUE),
      length.out = 100
    )
  }
}
```

```

const_data <- data[1, , drop = FALSE] # Use first row to keep other predictors constant
response_data <- const_data[rep(1, 100), ] # Duplicate the row
response_data[[predictor]] <- pred_range

# Predict probabilities
predicted_response <- predict(glm_model, newdata = response_data, type = "response")

# Create data frame for plotting
plot_data <- data.frame(
  Predictor_Value = pred_range,
  Predicted_Probability = predicted_response
)

# Add presence and absence data
presence_absence_data <- data.frame(
  Predictor_Value = data[[predictor]],
  Presence_Absence = data$Presence
)

# Generate the response plot
p <- ggplot() +

  geom_line(data = plot_data,
    aes(x = Predictor_Value, y = Predicted_Probability),
    color = "#61c6fa", linewidth = 1) +

  geom_point(data = presence_absence_data[presence_absence_data$Presence_Absence == 1, ],
    aes(x = Predictor_Value, y = Presence_Absence),
    color = "#11aa96", alpha = 0.6) +

  geom_point(data = presence_absence_data[presence_absence_data$Presence_Absence == 0, ],
    aes(x = Predictor_Value, y = Presence_Absence),
    color = "#f6aa70", alpha = 0.6) +

  labs(x = predictor, y = NULL) +
  theme_minimal() +
  theme(axis.title.y = element_blank())

# Store the plot in the list
response_plots[[predictor]] <- p
}

# Arrange all plots in one combined plot with a single shared y-axis label
grid.arrange(

```

```

    grobs = response_plots,
    ncol = 3,
    left = "Predicted Probability / Presence-Absence"
  )
}

```

Use the response curve function

```

predictors <- c("BI05_Max_Temp_Warmest_Month",
               "BI06_Min_Temp_Coldest_Month",
               "BI012_Annual_Precipitation",
               "BI015_Precip_Seasonality")

plot_species_response(glm_model_1, predictors, train_PB_covs_thinned)

```

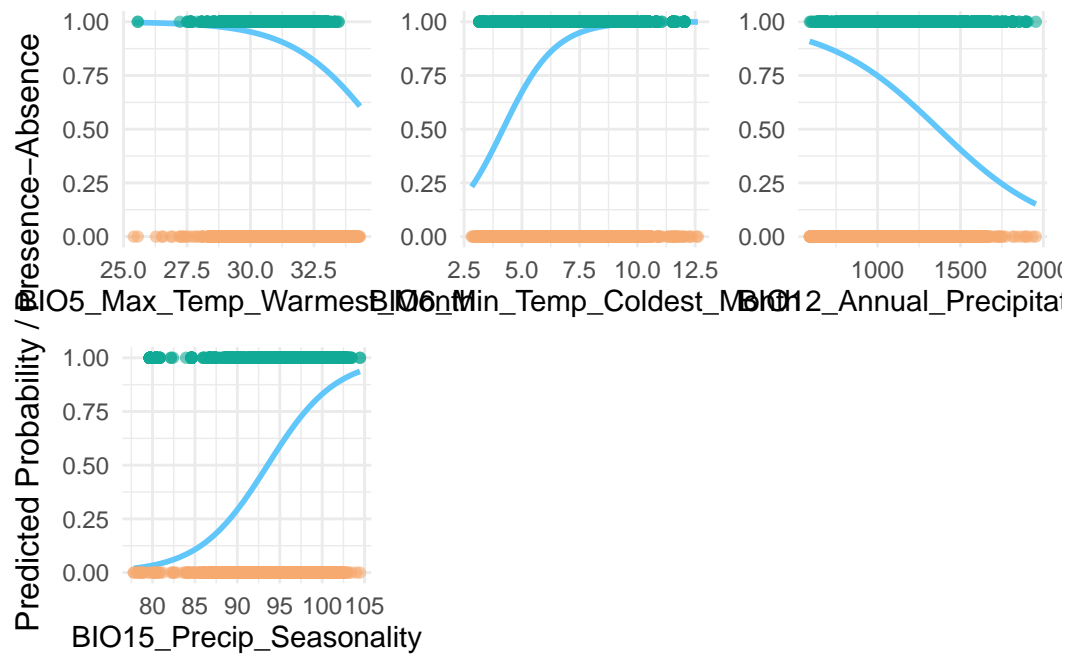
Attaching package: 'gridExtra'

The following object is masked from 'package:randomForest':

combine

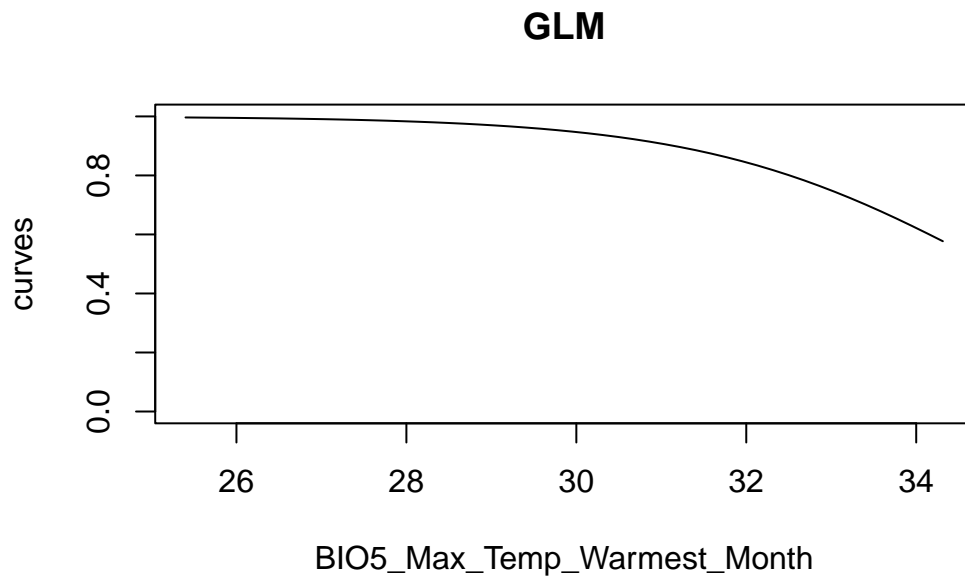
The following object is masked from 'package:dplyr':

combine

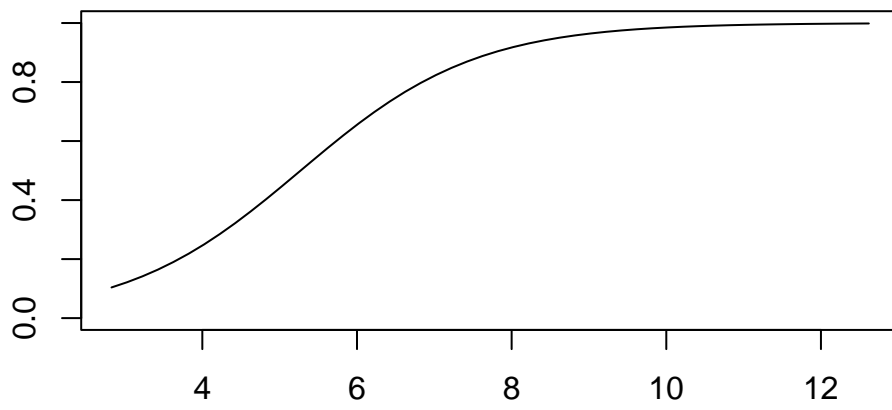


Model 1 partial responses

```
# Plot the partial responses
partial_response(glm_model_1, predictors = train_PB_covs_thinned[,predictors], main='GLM')
```

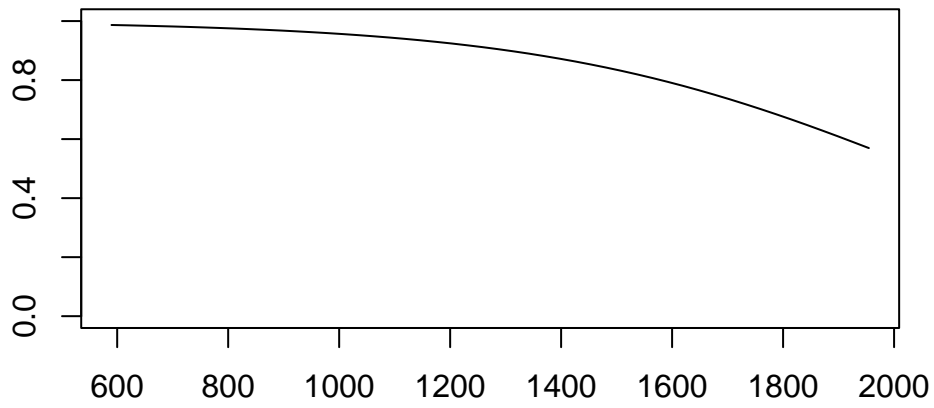


GLM

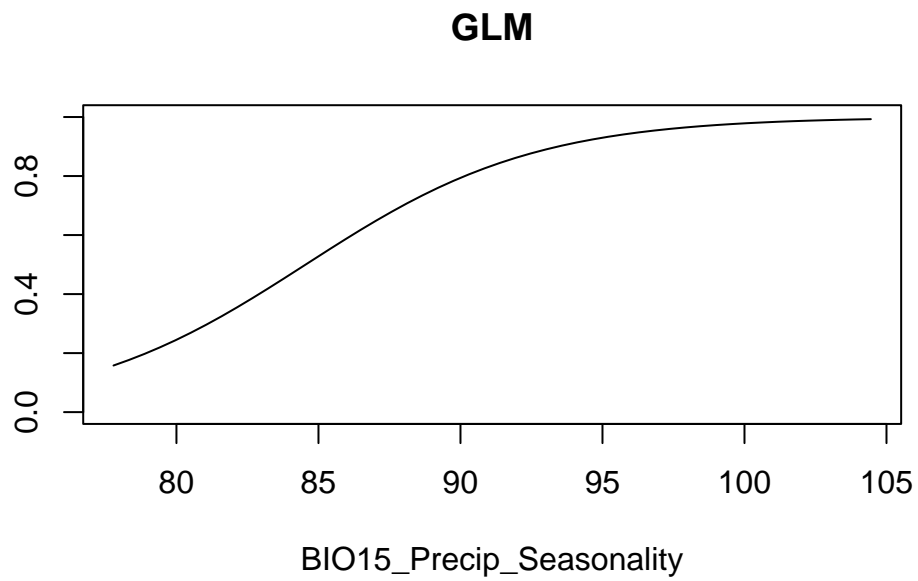


BIO6_Min_Temp_Coldest_Month

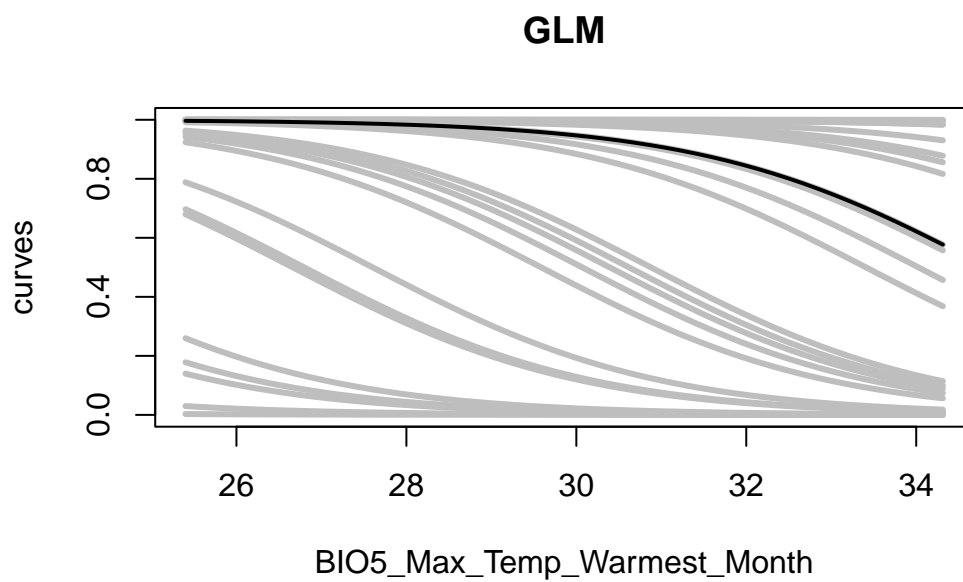
GLM



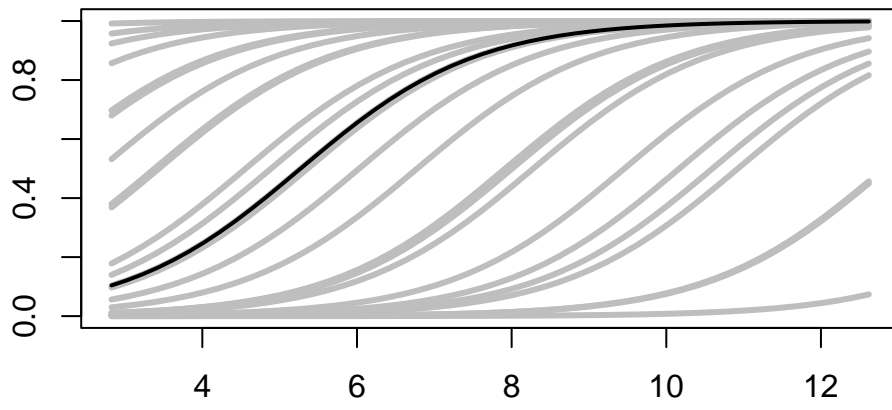
BIO12_Annual_Precipitation



```
# Plot inflated response curves:  
inflated_response(glm_model_1, predictors = train_PB_covs_thinned[,predictors], method = "st
```

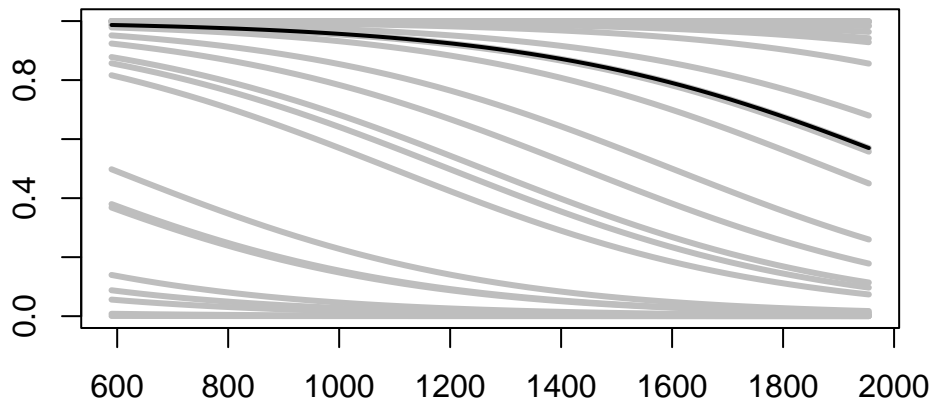


GLM

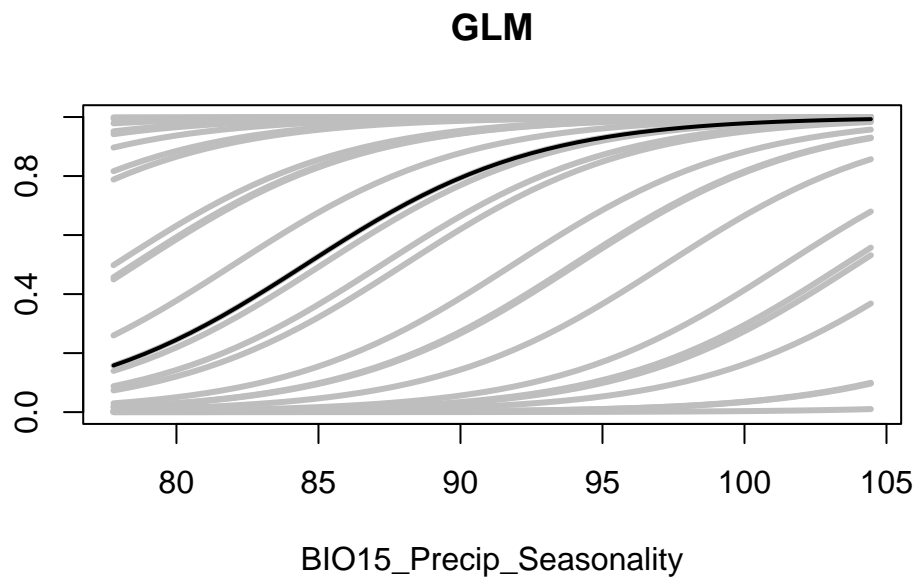


BIO6_Min_Temp_Coldest_Month

GLM

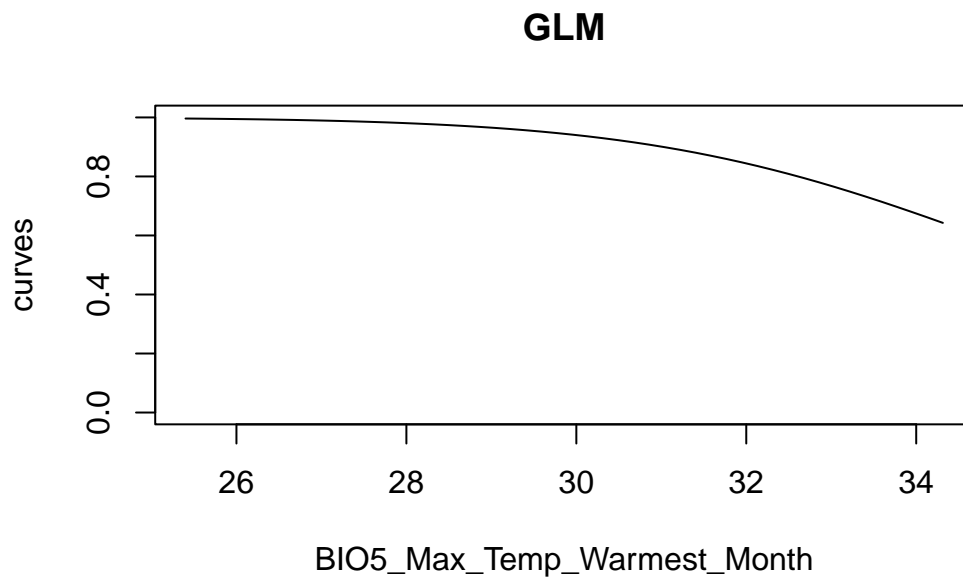


BIO12_Annual_Precipitation

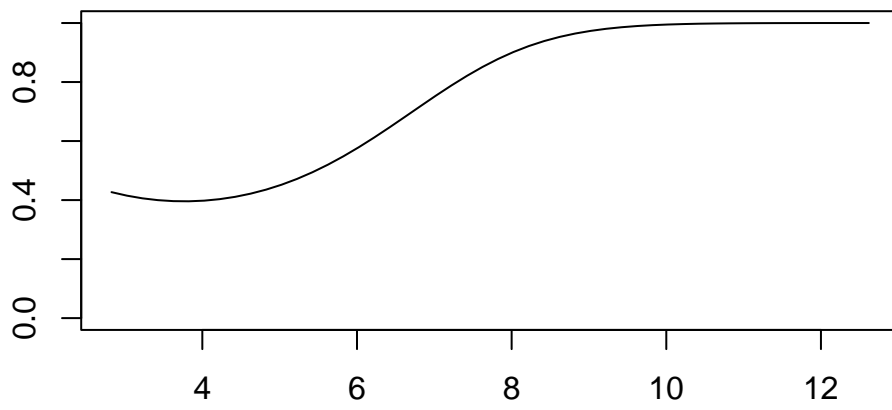


Model 2 partial responses

```
# Plot the partial responses
partial_response(glm_model_2, predictors = train_PB_covs_thinned[,predictors], main='GLM')
```

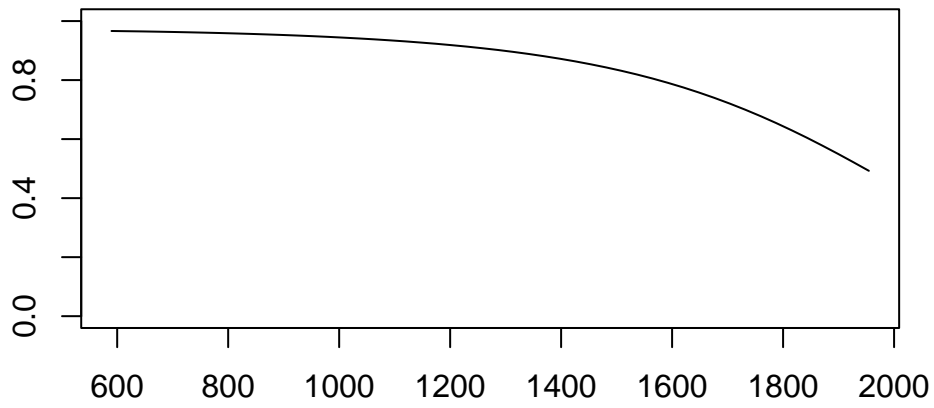


GLM

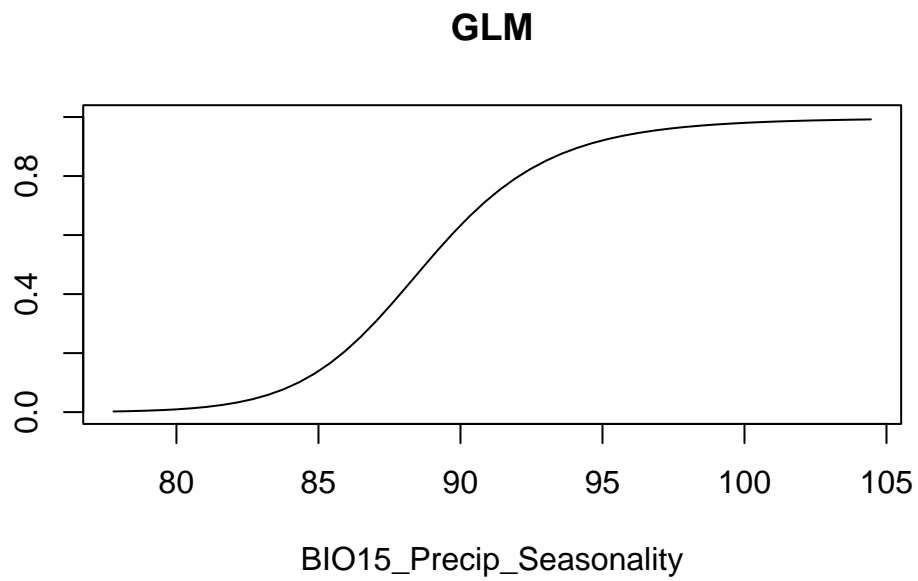


BIO6_Min_Temp_Coldest_Month

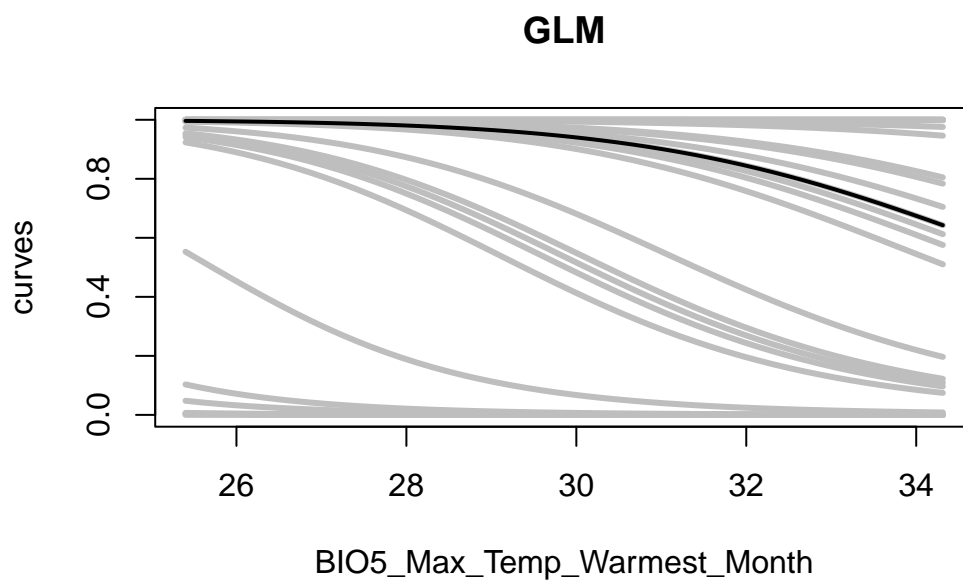
GLM



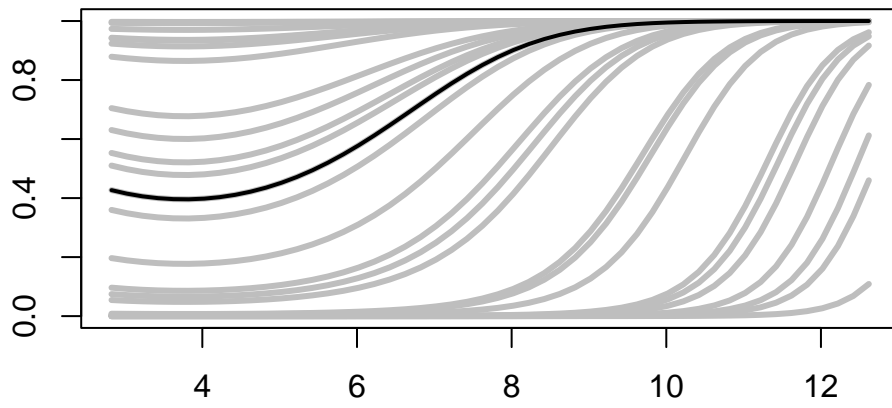
BIO12_Annual_Precipitation



```
# Plot inflated response curves:  
inflated_response(glm_model_2, predictors = train_PB_covs_thinned[,predictors], method = "st
```

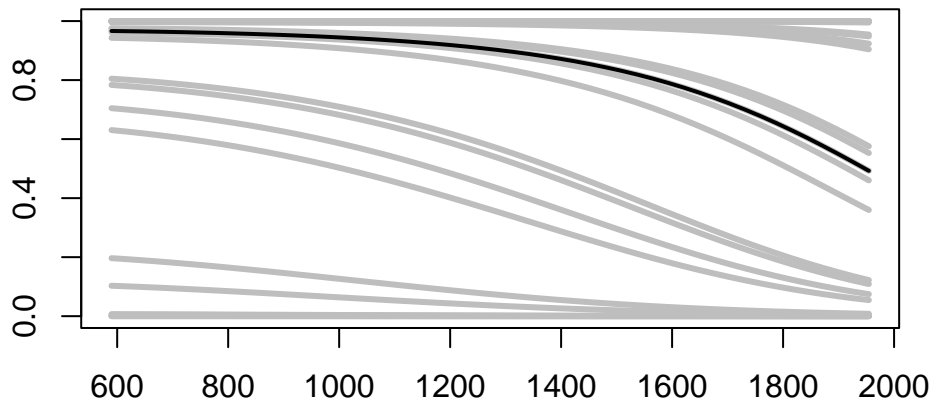


GLM

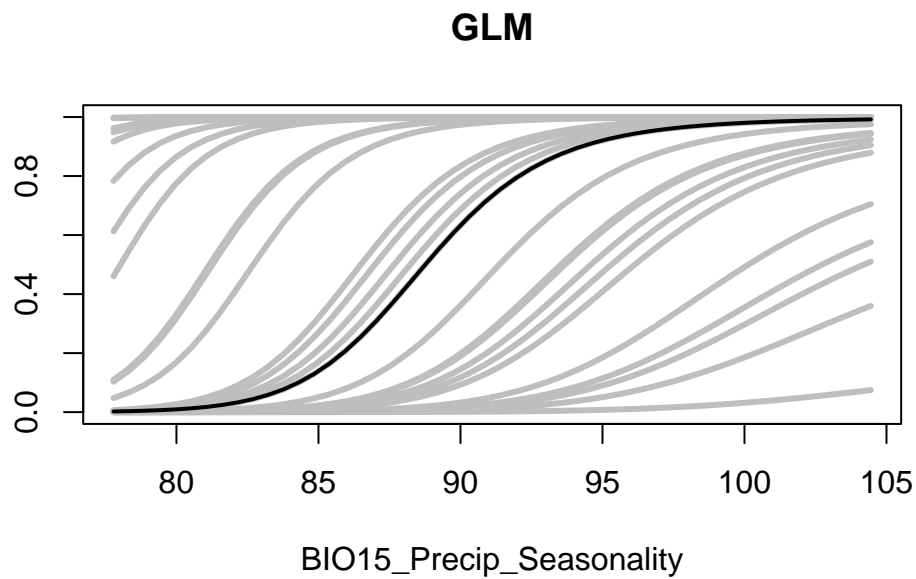


BIO6_Min_Temp_Coldest_Month

GLM



BIO12_Annual_Precipitation



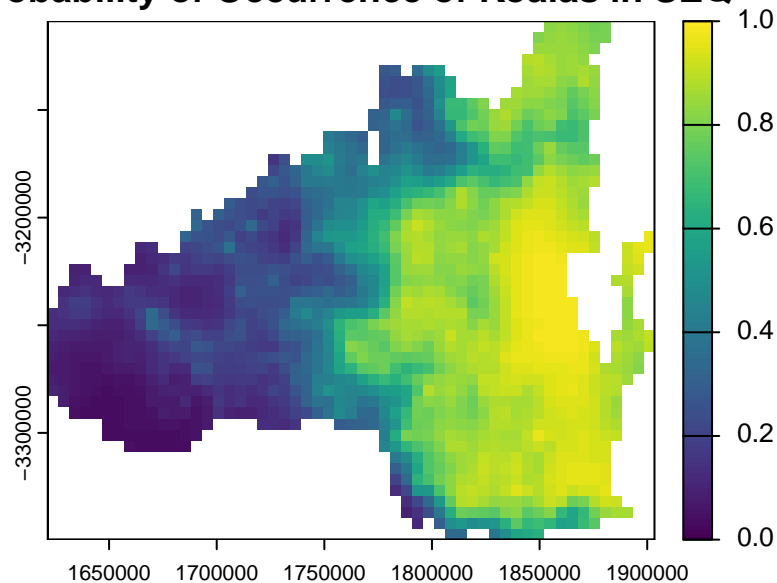
GLM predictions to current environment

Model 1

```
# Predict the presence probability across the entire raster extent
predicted_raster_model_1 <- predicts::predict(covs_current_expert, glm_model_1, type = "response")

# Plot the species distribution raster
plot(
  predicted_raster_model_1,
  range = c(0, 1), # Set min and max values for the color scale
  main = "Relative Probability of Occurrence of Koalas in SEQ - GLM 1"
)
```

Relative Probability of Occurrence of Koalas in SEQ – GLM 1

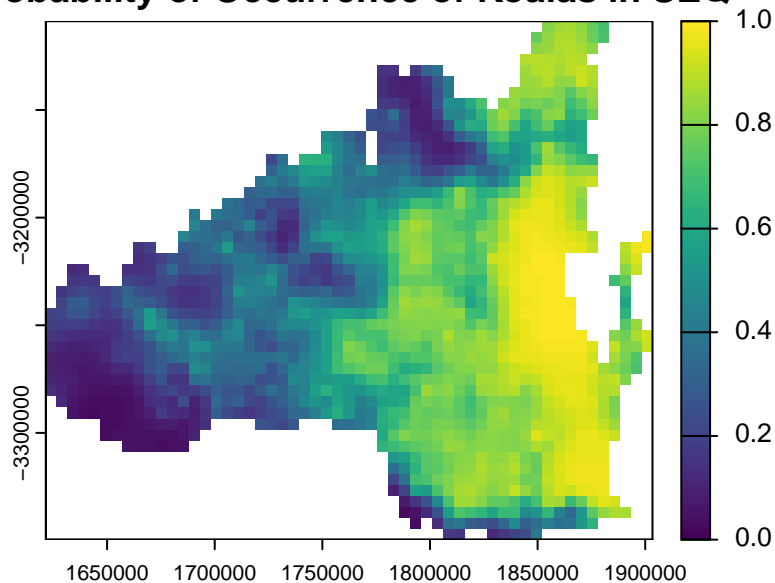


Model 2

```
# Predict the presence probability across the entire raster extent
predicted_raster_model_2 <- predicts::predict(covs_current_expert, glm_model_2, type = "response")

# Plot the species distribution raster
plot(
  predicted_raster_model_2,
  range = c(0, 1), # Set min and max values for the color scale
  main = "Relative Probability of Occurrence of Koalas in SEQ - GLM 2"
)
```

Relative Probability of Occurrence of Koalas in SEQ – GLM 2



Random forest

```
# Make a folder to save outputs

dir.create("outputs/RF_outputs", showWarnings = F)
```

Data preparation

Calculate the case weights (down/up-weighting)

Because we have a ‘class imbalance’ (uneven number of presences and background points), we are making their ‘weight’ in the model equal.

```
presNum <- as.numeric(table(train_PB_covs_thinned$Presence)["1"]) # number of presences
bgNum <- as.numeric(table(train_PB_covs_thinned$Presence)["0"]) # number of backgrounds
weight <- ifelse(train_PB_covs_thinned$Presence == 1, 1, presNum / bgNum) # down-weighting
```

Prepare for fitting the RF model(s)

```
# If wanting to fit a classification model
# Convert the response to factor for producing class relative likelihood
train_PB_covs_thinned$Presence_Factor <- as.factor(train_PB_covs_thinned$Presence)

# For down-sampling, the number of background (0s) in each bootstrap sample should be the same
# (1s). For this, we use sampsize argument to do this.
# We need to choose the SMALLER number out of the two classes
sample_size <- c("0" = bgNum, "1" = bgNum)
sample_size <- c(bgNum)
```

Random Forest Model - expert covariates

Classification or regression model?

```
# # Specify the model formula - classification
# model_formula <- as.formula(Presence_Factor ~
#                               BIO5_Max_Temp_Warmest_Month +
#                               BIO6_Min_Temp_Coldest_Month +
#                               BIO12_Annual_Precipitation +
#                               BIO15_Precip_Seasonality)

# Specify the model formula - regression
model_formula <- as.formula(Presence ~
                             BIO5_Max_Temp_Warmest_Month +
                             BIO6_Min_Temp_Coldest_Month +
                             BIO12_Annual_Precipitation +
                             BIO15_Precip_Seasonality)
```

Fit the random forest model

This will throw a warning as we only have two unique values (0s and 1s), but in our case that is fine, and you can ignore the warning.

```
rf_1 <- randomForest::randomForest(formula = model_formula,
                                   data = train_PB_covs_thinned,
                                   weights = weight,
                                   ntree = 1000,
                                   sampsize = sample_size,
                                   replace = T,
                                   importance=TRUE)
```


Warning in randomForest.default(m, y, ...): The response has five or fewer unique values. Are you sure you want to do regression?

Check the model results

```
# Model summary  
rf_1
```

Call:

```
randomForest(formula = model_formula, data = train_PB_covs_thinned, weights = weight,  
              Type of random forest: regression  
              Number of trees: 1000
```

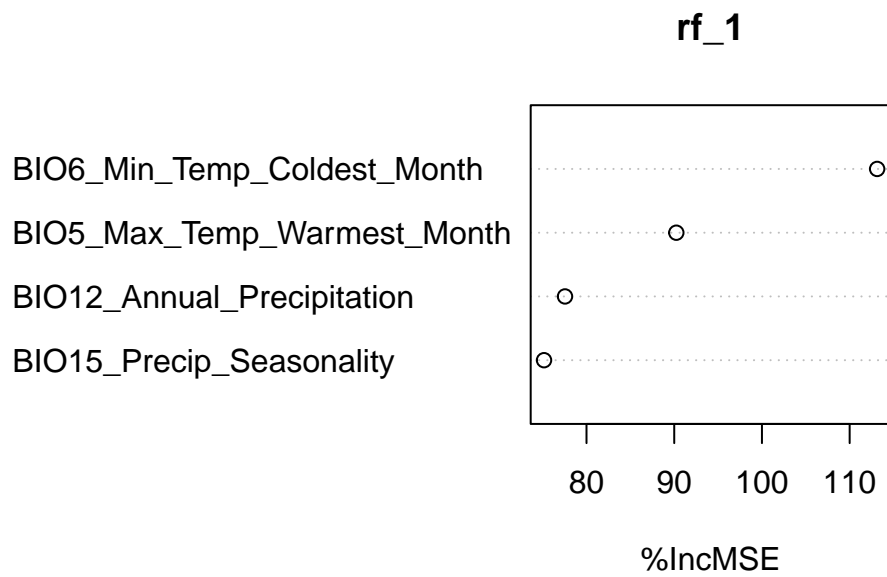
No. of variables tried at each split: 1

```
      Mean of squared residuals: 0.08568366  
      % Var explained: 23.08
```

```
# Variable importance:  
importance(rf_1)
```

	%IncMSE	IncNodePurity
BI05_Max_Temp_Warmest_Month	90.23977	69.47576
BI06_Min_Temp_Coldest_Month	113.13609	102.85306
BI012_Annual_Precipitation	77.54665	82.91868
BI015_Precip_Seasonality	75.15556	47.28076

```
# Plot variable importance  
varImpPlot(rf_1, type = 1)
```



```
# Look at single trees:
head(getTree(rf_1,1,T))
```

	left daughter	right daughter	split var	split point	status
1	2	3	BIO6_Min_Temp_Coldest_Month	8.319836	-3
2	4	5	BIO15_Precip_Seasonality	96.030197	-3
3	6	7	BIO6_Min_Temp_Coldest_Month	9.960938	-3
4	8	9	BIO6_Min_Temp_Coldest_Month	6.763289	-3
5	10	11	BIO12_Annual_Precipitation	1342.408508	-3
6	12	13	BIO6_Min_Temp_Coldest_Month	8.922107	-3

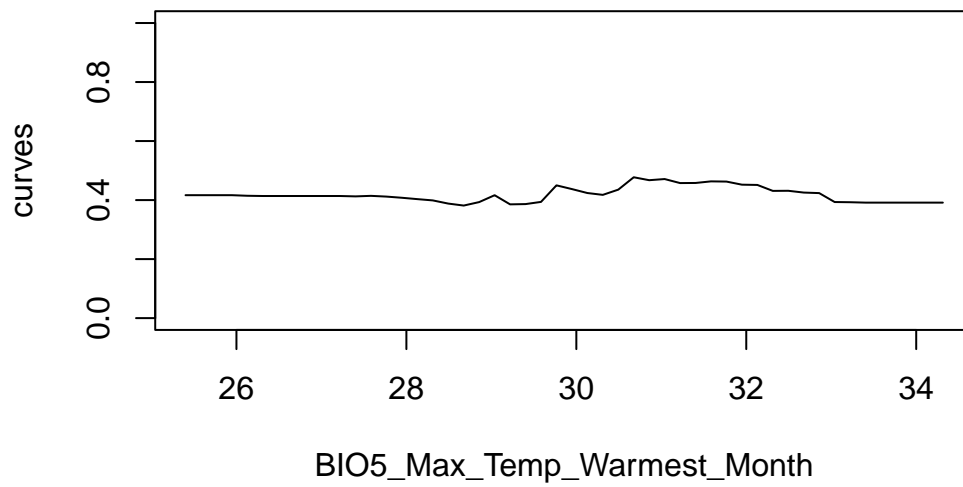
prediction

1	0.4965847
2	0.1905405
3	0.8093923
4	0.1025057
5	0.3189369
6	0.8502269

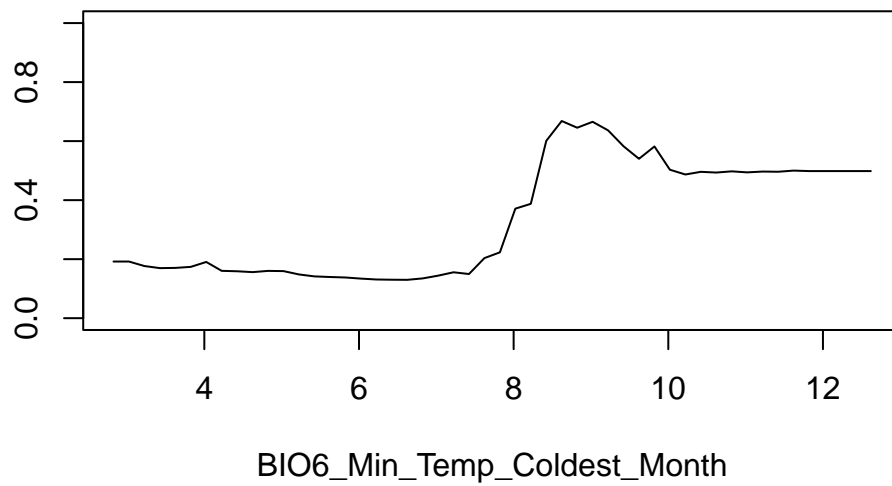
Partial dependence plots

```
# Now, we plot response curves in the same way as we did for GLMs above:
partial_response(rf_1, predictors = train_PB_covs_thinned[,predictors], main='Random Forest')
```

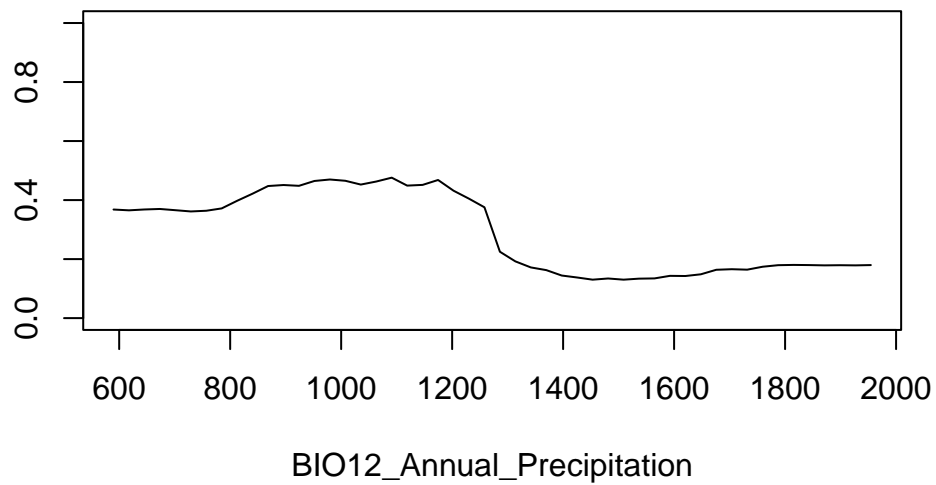
Random Forest



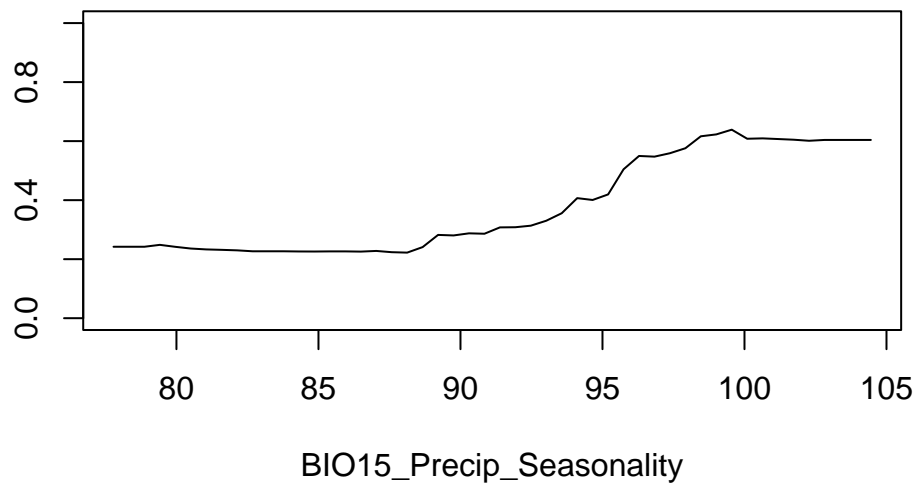
Random Forest



Random Forest

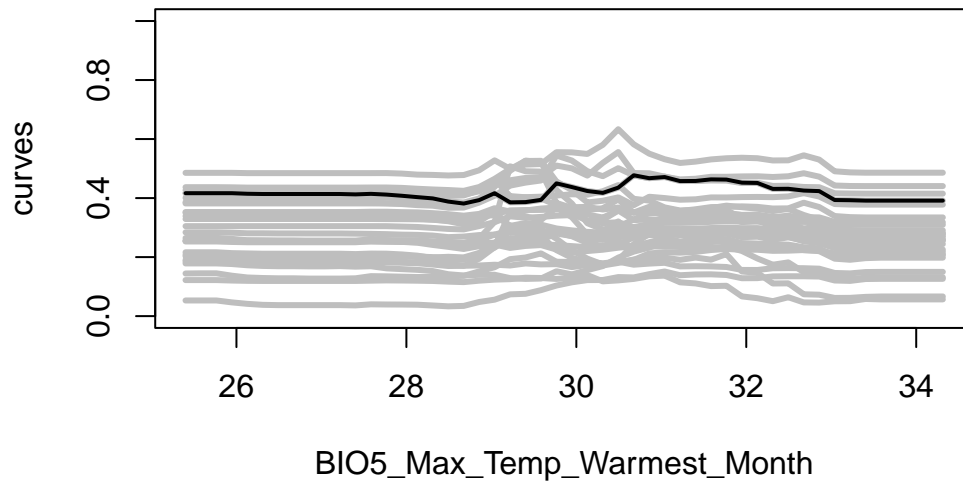


Random Forest

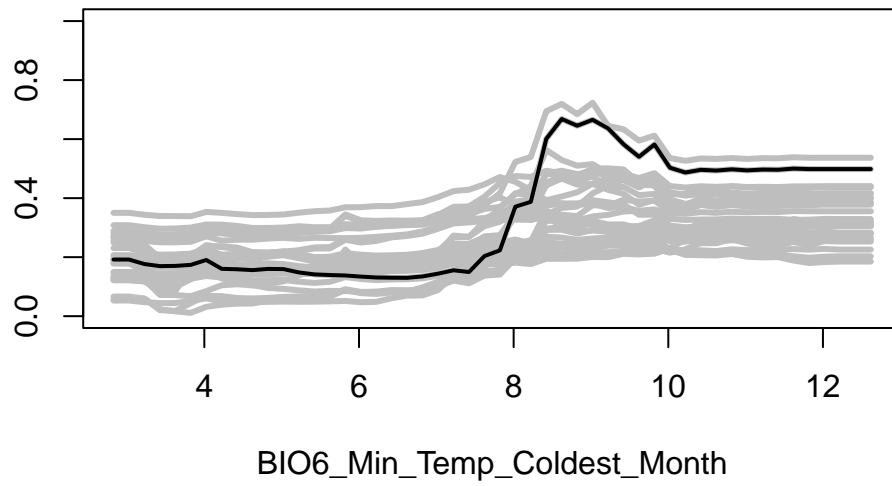


```
# Plot inflated response curves:  
inflated_response(rf_1, predictors = train_PB_covs_thinned[,predictors], method = "stat3", l
```

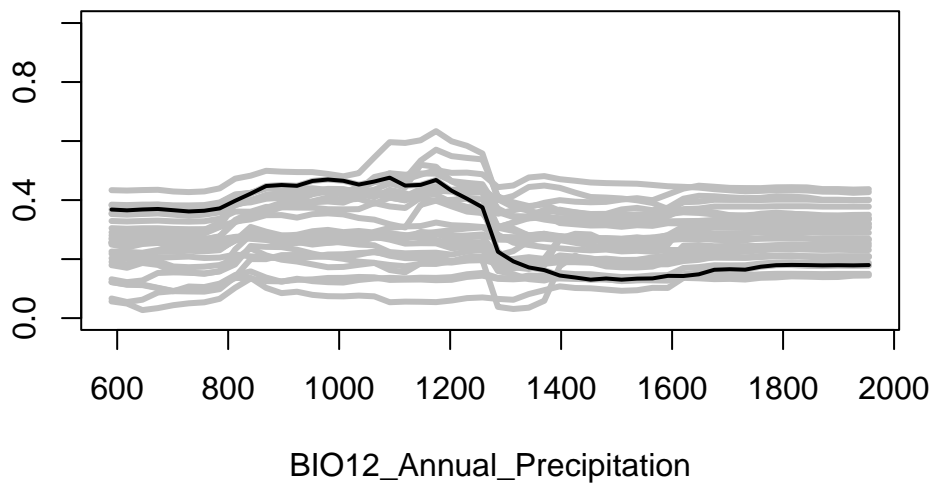
Random Forest



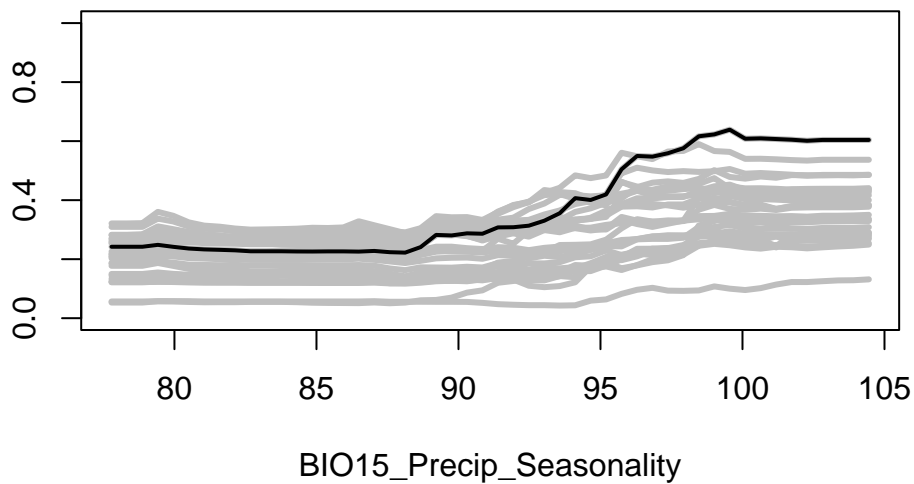
Random Forest



Random Forest



Random Forest



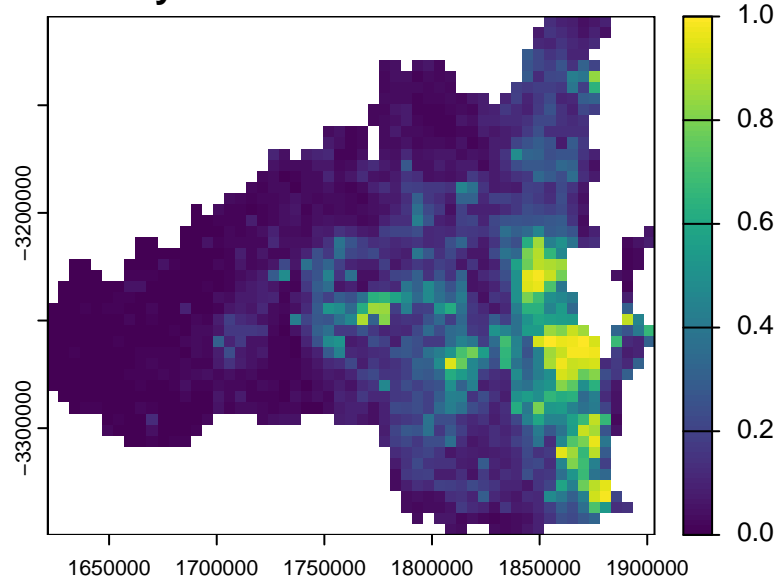
Random Forest predictions

```
# Predict the presence probability across the entire raster extent
predicted_raster_RF_1 <- predicts::predict(covs_current_expert, rf_1, type = "response")

# Plot the species distribution raster
plot(
  predicted_raster_RF_1,
  range = c(0, 1), # Set min and max values for the color scale
```

```
main = "Relative Probability of Occurrence of Koalas in SEQ - RF 1"
)
```

Relative Probability of Occurrence of Koalas in SEQ – RF 1



```
writeRaster(predicted_raster_RF_1,
            filename = "outputs/current_distribution_RF_1.tif",
            overwrite = TRUE)
```

Model evaluation with spatial block cross-validation

```
# Convert training data to sf
train_PB_covs_thinned_sf <- st_as_sf(train_PB_covs_thinned[, c("x", "y", "Presence")], coord

# Generate spatial blocks
spblock <- cv_spatial(x = train_PB_covs_thinned_sf,
                      column = "Presence",
                      r = NULL,
                      size = 50000, # Size of the blocks in metres
                      k = 5,
                      hexagon = TRUE,
                      selection = "random",
                      iteration = 100, # to find evenly-dispersed folds
                      biomod2 = FALSE)
```

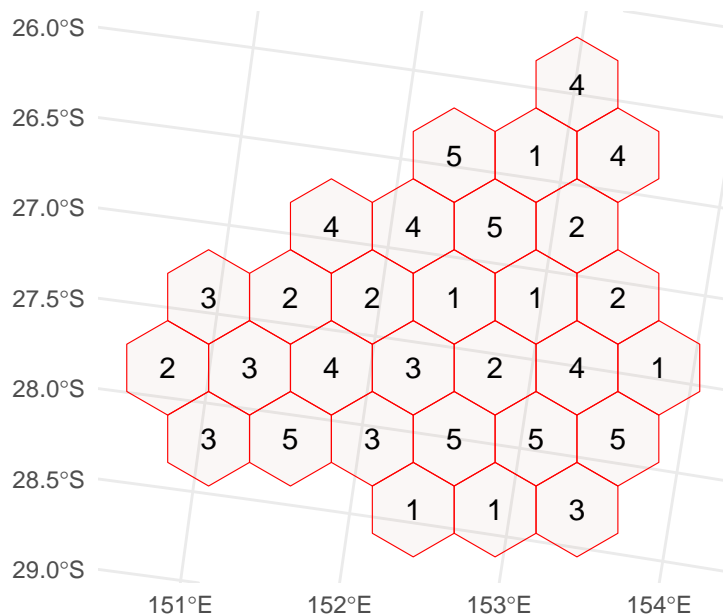
	0%
	1%
=	
	2%
=	
	3%
==	
	4%
===	
	5%
====	
	6%
=====	
	7%
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=====	38%
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=====	42%
=====	43%
=====	44%

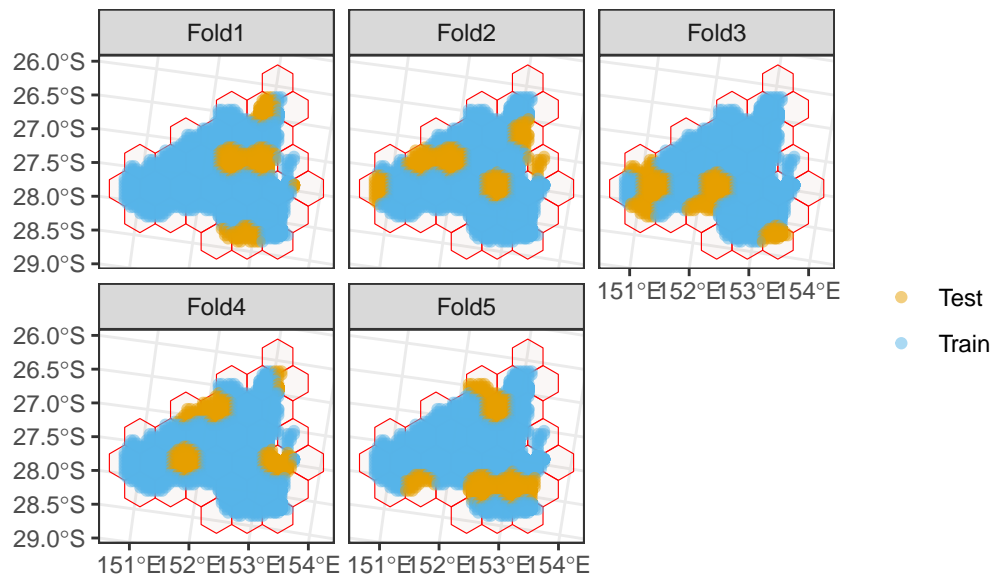
=====		45%
=====		46%
=====		47%
=====		48%
=====		49%
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=====	81%
=====	82%
=====	83%
=====	84%
=====	85%
=====	86%
=====	87%
=====	88%
=====	89%

	train_0	train_1	test_0	test_1
1	1206	8207	258	1793
2	1129	9274	335	726
3	1176	8653	288	1347
4	1202	5192	262	4808
5	1143	8674	321	1326



```
cv_plot(cv = spblock,
        x = train_PB_covs_thinned_sf,
        points_alpha = 0.5,
        nrow = 2)
```



```
# Extract the folds to save
spfolds <- spblock$folds_list
```

```
# We now have a list of 5 folds, where the first object is the training data, and the second
str(spfolds)
```

List of 5

```
$ :List of 2
..$ : int [1:9413] 10859 10860 10965 11019 11020 10706 10656 10707 10657 11021 ...
..$ : int [1:2051] 11421 11423 11382 6511 11442 11422 11402 11381 11401 10738 ...
$ :List of 2
..$ : int [1:10403] 11022 11264 11223 11265 11263 11074 4920 11075 11180 11224 ...
..$ : int [1:1061] 10859 10860 10965 11019 11020 10706 10656 10707 10657 11021 ...
$ :List of 2
..$ : int [1:9829] 10859 10860 10965 11019 11020 10706 10656 10707 10657 11021 ...
..$ : int [1:1635] 11022 11264 11223 11265 11263 11074 4920 11075 11180 11224 ...
$ :List of 2
..$ : int [1:6394] 10859 10860 10965 11019 11020 10706 10656 10707 10657 11021 ...
..$ : int [1:5070] 10982 11140 3731 9771 3978 5636 294 10774 10981 3251 ...
$ :List of 2
..$ : int [1:9817] 10859 10860 10965 11019 11020 10706 10656 10707 10657 11021 ...
..$ : int [1:1647] 11230 11271 11229 11231 11270 11137 11269 11233 11136 11228 ...
```

Run the model for every fold and evaluate

Model evaluation - metrics

Typically, it helps to evaluate your model with several metrics that describe different features of model performance and prediction. Here, we define a function to feed in a model prediction and calculate several evaluation metrics.

The metrics are:

-Area under the receiver operating characteristic curve (AUC ROC)

Higher values of this (closer to 1) suggest a model is good at distinguishing presence points from the background.

-Continuous boyce index

Higher values of this (closer to 1) suggest a model is good at predicting higher suitability at spots where there were presences.

```
# Start a dataframe to save results
eval_df <- data.frame(fold = numeric(),
                      ROC = numeric(),
                      boyce = numeric())

for(f in seq_along(sp folds)) {

  # Subset the training and testing data (spatial cross validation) (for the fth fold)

  train_PB_covs_scv <- train_PB_covs_thinned[sp folds[[f]][[1]], ]
```

```

test_PB_covs_scv <- train_PB_covs_thinned[spfolds[[f]][[2]], ]

glm_model_1 <- glm(Presence ~
  BI05_Max_Temp_Warmest_Month +
  BI06_Min_Temp_Coldest_Month +
  BI012_Annual_Precipitation +
  BI015_Precip_Seasonality,
  data=train_PB_covs_scv,
  family = binomial(link = "logit"))

# Predict to the testing data of fold f
test_PB_covs_scv$pred <- predict(glm_model_1, newdata = test_PB_covs_scv, type = "response")

# Evaluate prediction on test set
ROC = precrec::auc(precrec::evalmod(scores = test_PB_covs_scv$pred, labels = test_PB_covs_scv$Presence))

boyce = ecospat::ecospat.boyce(fit = test_PB_covs_scv$pred,
  obs = test_PB_covs_scv$pred[which(test_PB_covs_scv$Presence == 1)],
  nclass = 0, # Calculate continuous index
  method = "pearson",
  PEplot = F)[["cor"]]

# Add results to dataframe
eval_df <- eval_df %>% add_row(fold = f, ROC = ROC, boyce = boyce)

}

```

Summarise the evaluation metrics

```

# Mean AUC & boyce
eval_df %>%
  summarise(mean_AUC = mean(ROC),
    mean_boyce = mean(boyce),
    sd_AUC = sd(ROC),
    sd_boyce = sd(boyce))

```

	mean_AUC	mean_boyce	sd_AUC	sd_boyce
1	0.8470138	0.7584	0.08467198	0.1327057

Model evaluation for Random Forest with spatial block cross-validation

We're going to use the same spatial folds as before.

Run the RF model for every fold and evaluate

```
# Start a dataframe to save results
eval_df.RF <- data.frame(fold = numeric(),
                        ROC = numeric(),
                        boyce = numeric())

for(f in seq_along(sp folds)) {

  # Subset the training and testing data (spatial cross validation) (for the fth fold)

  train_PB_covs_scv <- train_PB_covs_thinned[sp folds[[f]][[1]], ]
  test_PB_covs_scv <- train_PB_covs_thinned[sp folds[[f]][[2]], ]

  presNum <- as.numeric(table(train_PB_covs_scv$Presence)[1]) # number of presences
  bgNum <- as.numeric(table(train_PB_covs_scv$Presence)[0]) # number of backgrounds
  weight <- ifelse(train_PB_covs_scv$Presence == 1, 1, presNum / bgNum) # down-weighting

  sample_size <- c("0" = bgNum, "1" = presNum)
  sample_size <- c(bgNum)

  rf_1 <- randomForest::randomForest(formula = model_formula,
                                    data = train_PB_covs_scv,
                                    weights = weight,
                                    ntree = 1000,
                                    sampsize = sample_size,
                                    replace = T,
                                    importance=TRUE)

  # Predict to the testing data of fold f
  test_PB_covs_scv$pred <- predict(rf_1, newdata = test_PB_covs_scv, type = "response")

  # Evaluate prediction on test set
  ROC = precrec::auc(precrec::evalmod(scores = test_PB_covs_scv$pred, labels = test_PB_covs_

  boyce = ecospat::ecospat.boyce(fit = test_PB_covs_scv$pred,
```



```

        obs = test_PB_covs_scv$pred[which(test_PB_covs_scv$Presence
        nclass = 0, # Calculate continuous index
        method = "pearson",
        PEplot = F)[["cor"]]

# Add results to dataframe
eval_df.RF <- eval_df.RF %>% add_row(fold = f, ROC = ROC, boyce = boyce)

}

```

Warning in randomForest.default(m, y, ...): The response has five or fewer unique values. Are you sure you want to do regression?

Warning in randomForest.default(m, y, ...): The response has five or fewer unique values. Are you sure you want to do regression?

Warning in randomForest.default(m, y, ...): The response has five or fewer unique values. Are you sure you want to do regression?

Warning in randomForest.default(m, y, ...): The response has five or fewer unique values. Are you sure you want to do regression?

Warning in randomForest.default(m, y, ...): The response has five or fewer unique values. Are you sure you want to do regression?

Warning in randomForest.default(m, y, ...): The response has five or fewer unique values. Are you sure you want to do regression?

Summarise the evaluation metrics

```

# Mean AUC & boyce
eval_df.RF %>%
  summarise(mean_AUC = mean(ROC),
            mean_boyce = mean(boyce),
            sd_AUC = sd(ROC),
            sd_boyce = sd(boyce))

```

	mean_AUC	mean_boyce	sd_AUC	sd_boyce
1	0.8121285	0.64	0.08989678	0.2091853

Make predictions to future climates

Load future environmental data

```
covs_future <- rast("Data/Environmental_variables/future_bioclim.2090.SSP370.tif")
names(covs_future) <- layer_names
covs_future
```

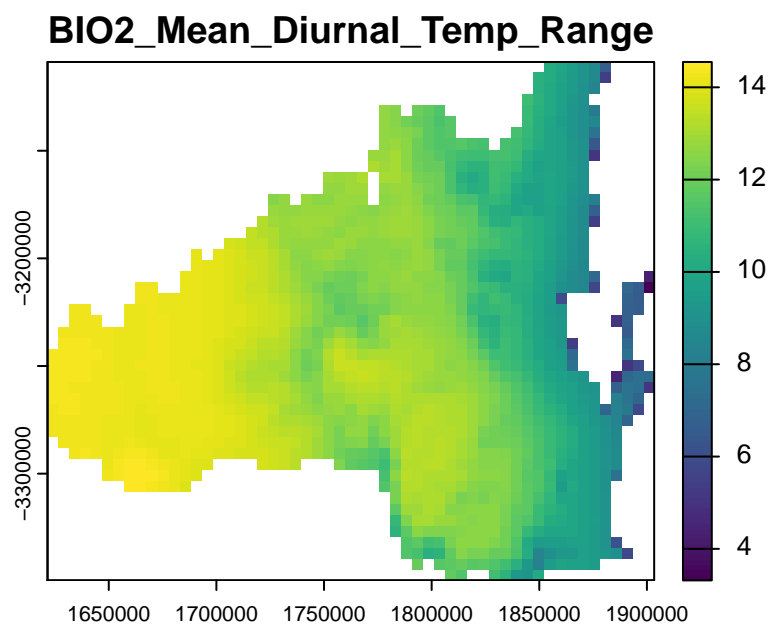
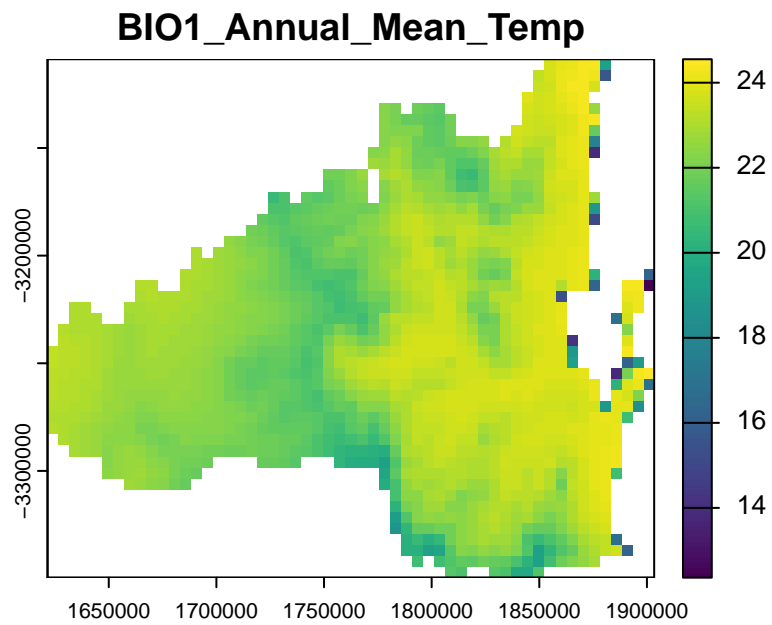
```
class      : SpatRaster
dimensions : 47, 55, 19  (nrow, ncol, nlyr)
resolution : 5123.954, 5123.954  (x, y)
extent      : 1621552, 1903370, -3349594, -3108768  (xmin, xmax, ymin, ymax)
coord. ref. : GDA94 / Geoscience Australia Lambert (EPSG:3112)
source      : future_bioclim.2090.SSP370.tif
names       : BI01_~_Temp, BI02_~Range, BI03_~ality, BI04_~ality, BI05_~Month, BI06_~Month,
min values  : 0.8177757, 0.3121004, 1.564732, 12.43535, 1.130271, 0.4521889,
max values  : 24.5521488, 14.5486765, 50.989292, 528.63293, 37.389927, 15.7586107,
```

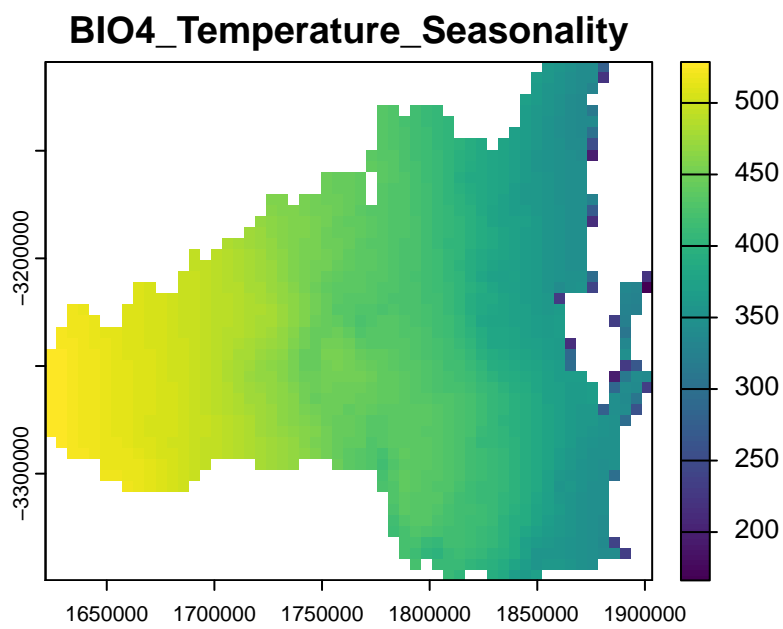
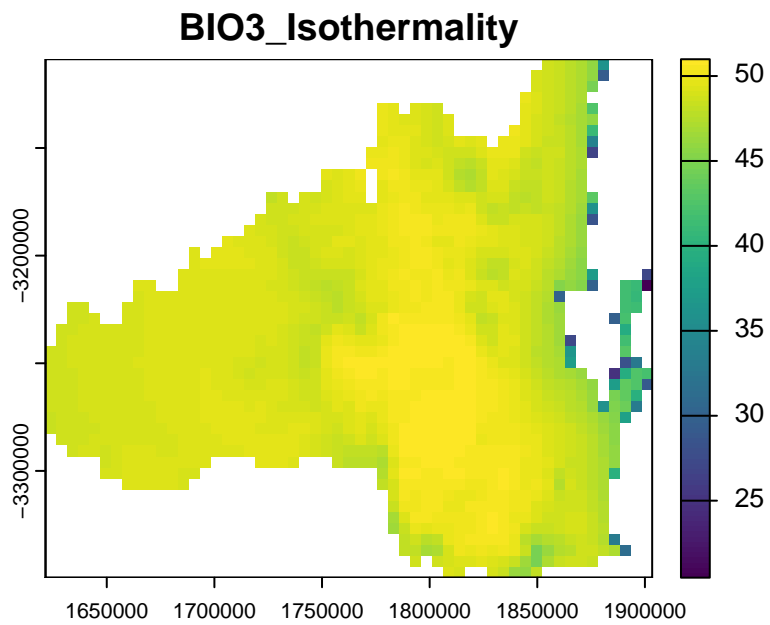
```
covs_future <- terra::mask(covs_future, covs_current) # Crop to SEQ extent
```

```
covs_future_expert <- subset(covs_future, names(covs_future) %in% c("BI05_Max_Temp_Warmest_M
"BI06_Min_Temp_Coldest_M
"BI012_Annual_Precipitat
"BI015_Precip_Seasonalit
```

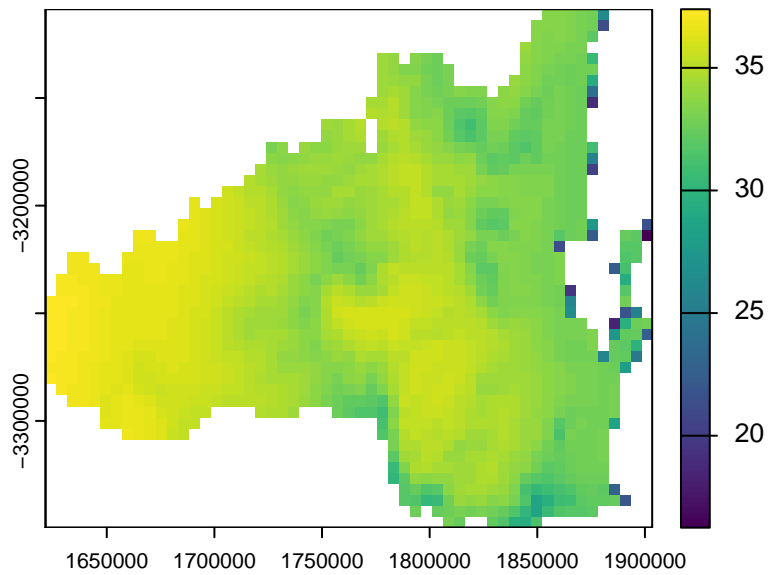
Plot the future rasters

```
for(i in 1:nlyr(covs_future)) {
  terra::plot(covs_future[[i]], main = names(covs_future)[[i]])
}
```

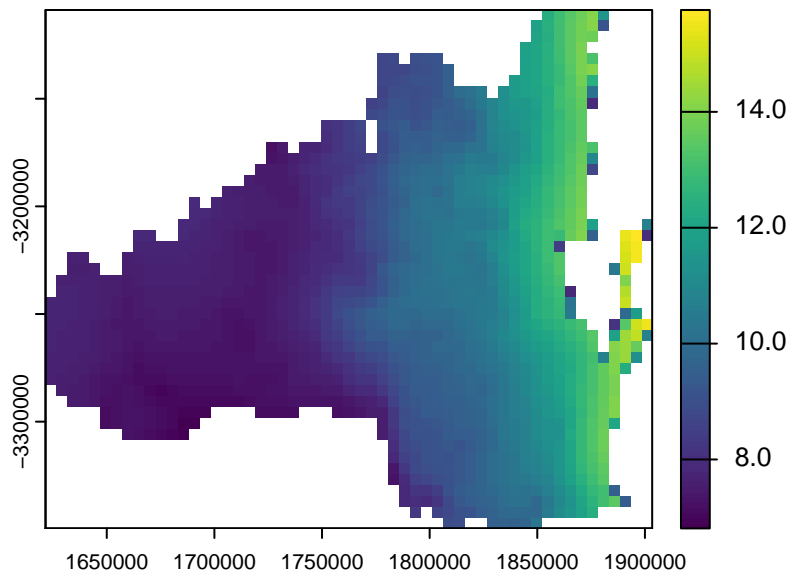




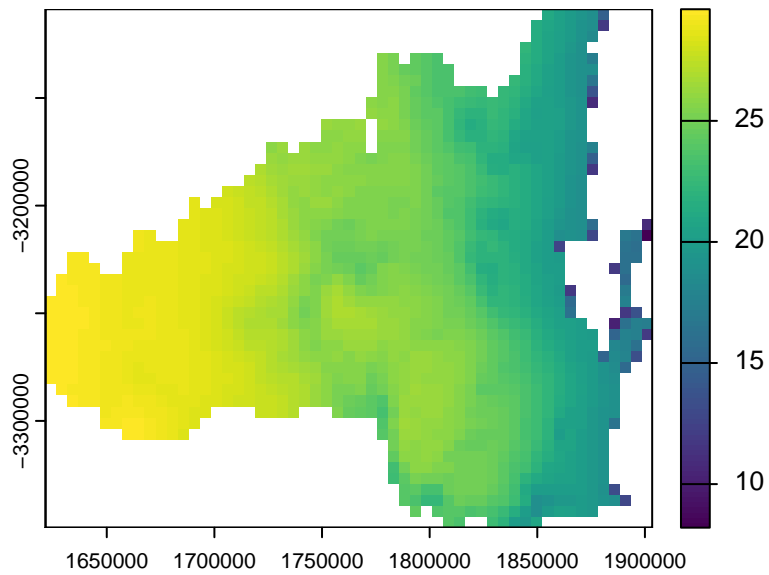
BIO5_Max_Temp_Warmest_Month



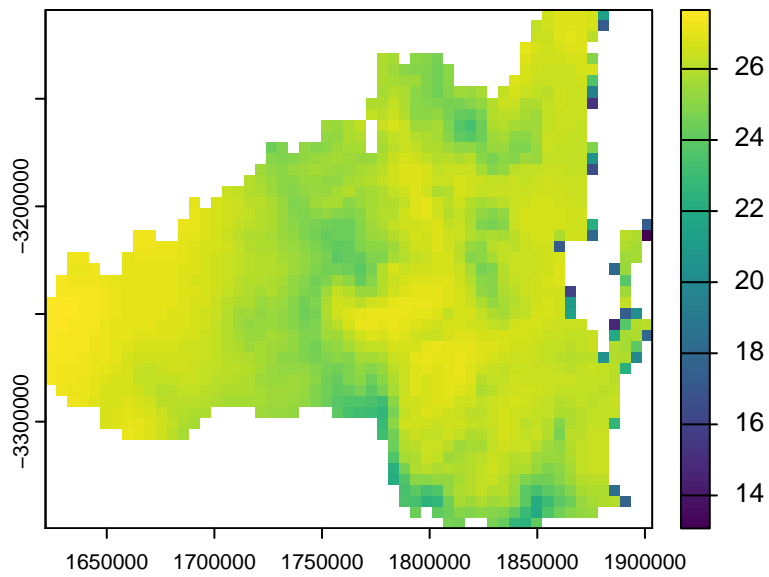
BIO6_Min_Temp_Coldest_Month



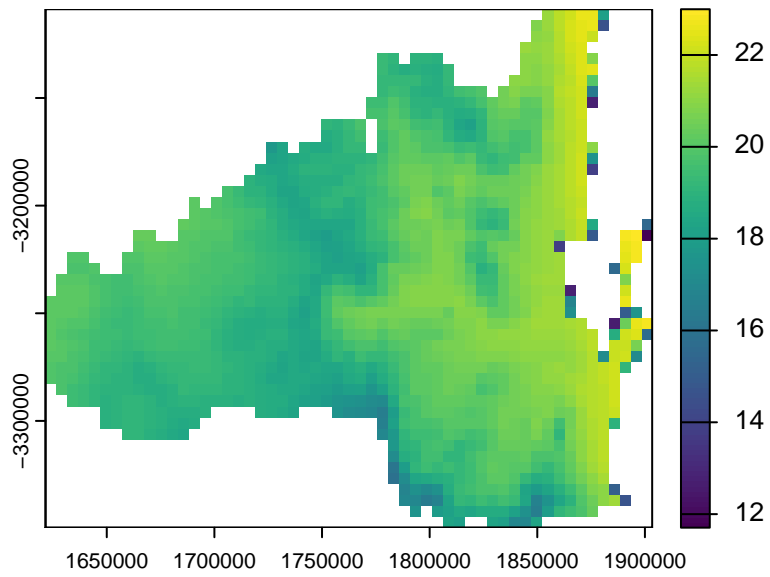
BIO7_Temperature_Annual_Range



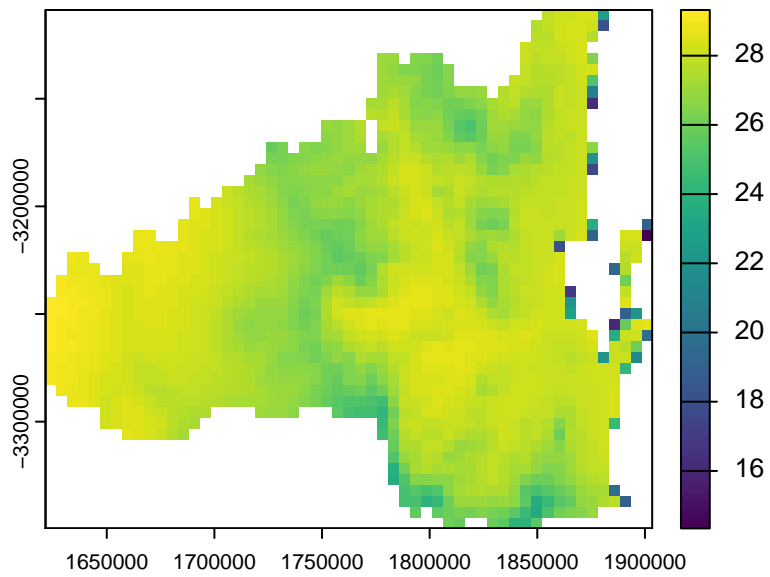
BIO8_Mean_Temp_Wettest_Quarter



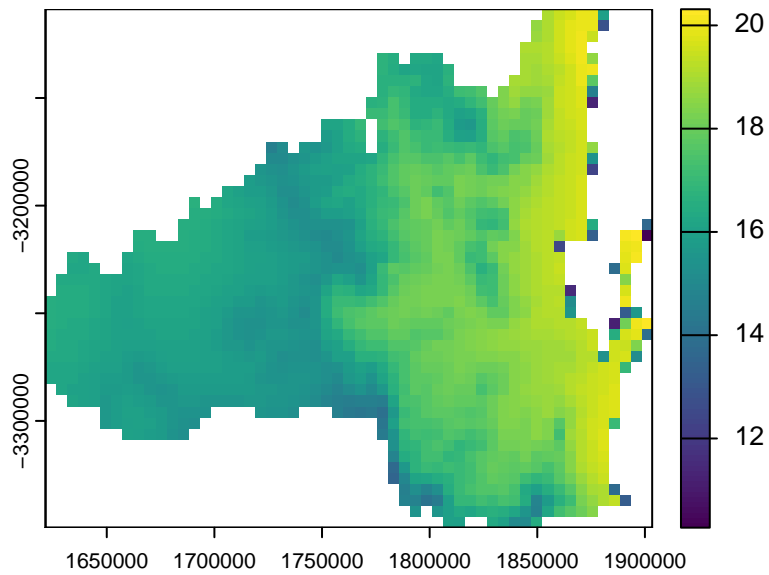
BIO9_Mean_Temp_Driest_Quarter



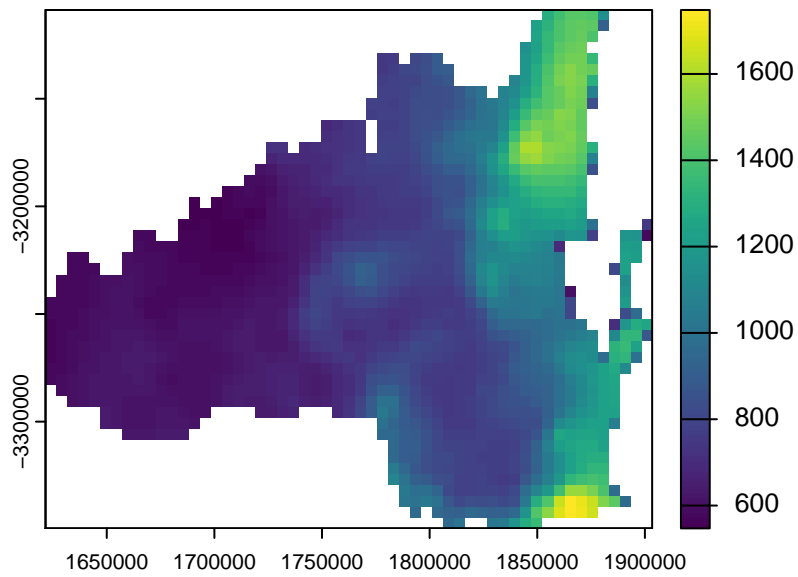
BIO10_Mean_Temp_Warmest_Quarter



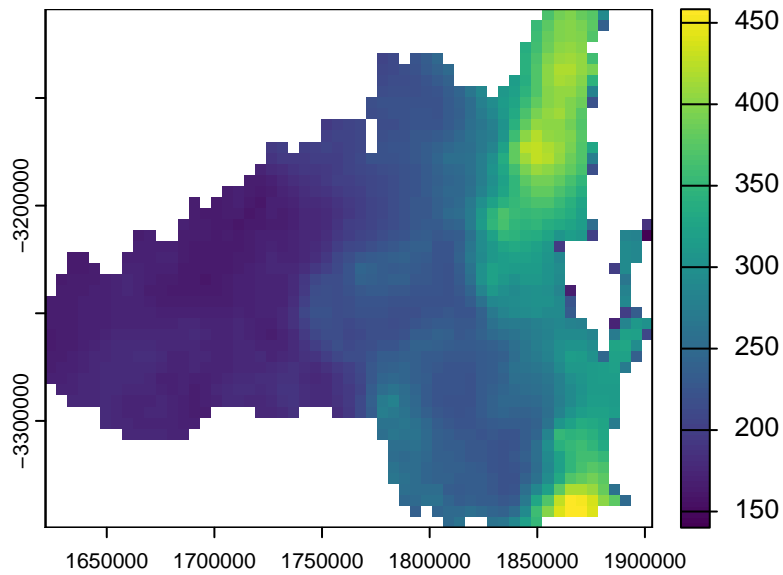
BIO11_Mean_Temp_Coldest_Quarter



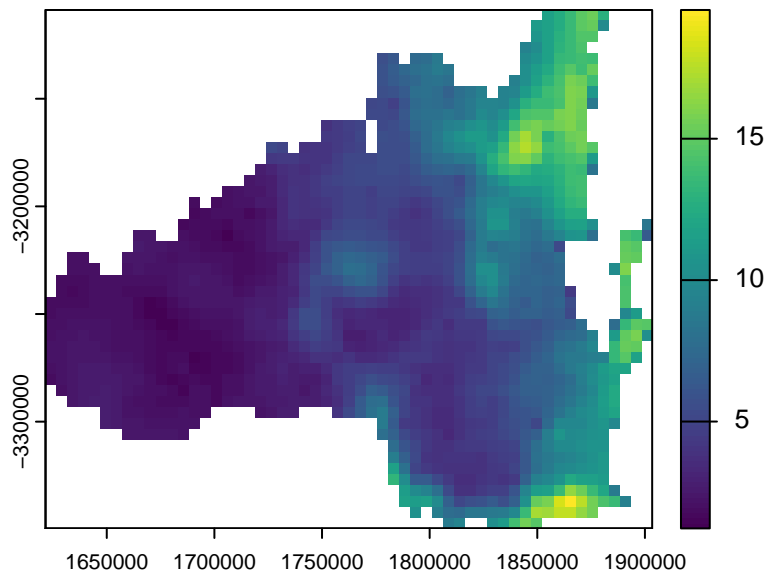
BIO12_Annual_Precipitation

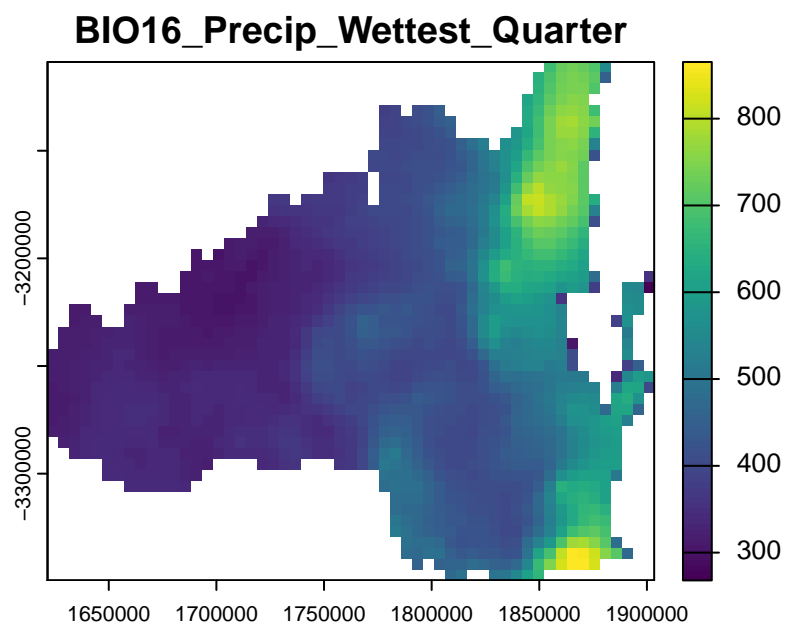
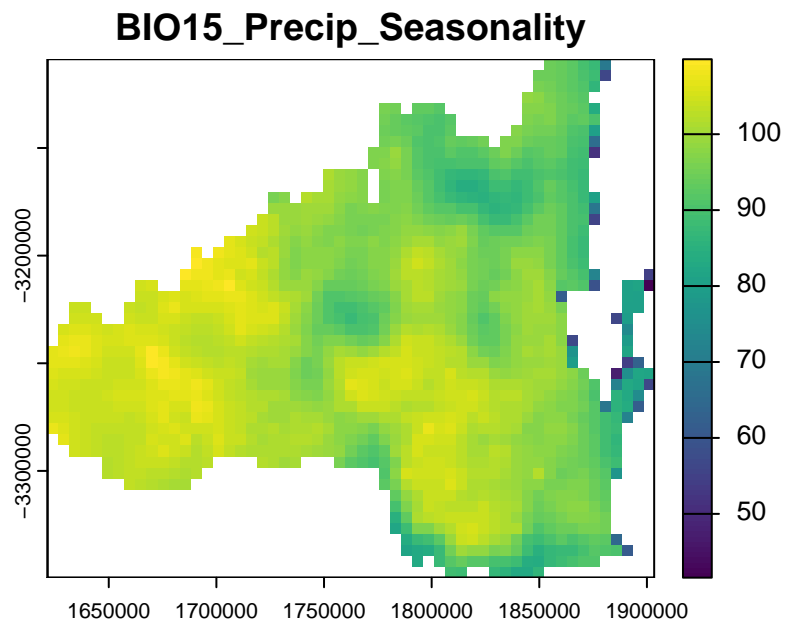


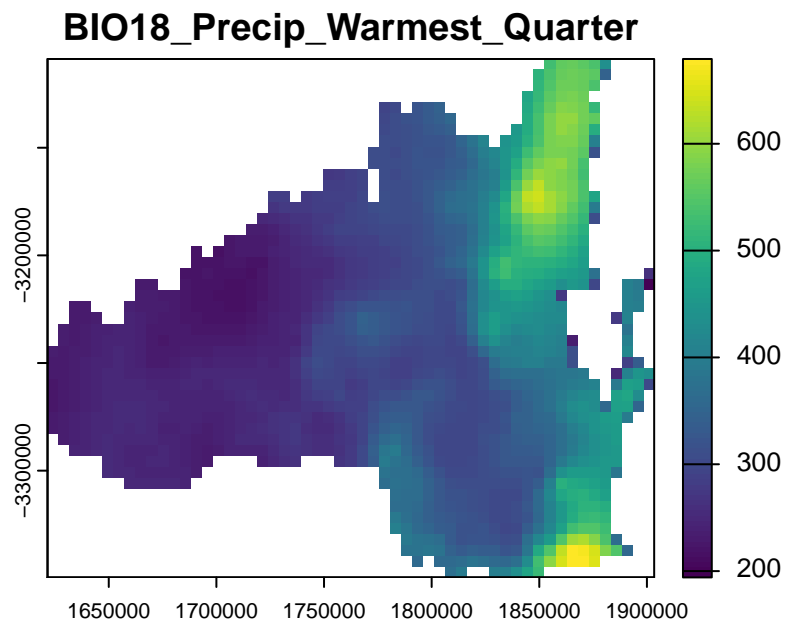
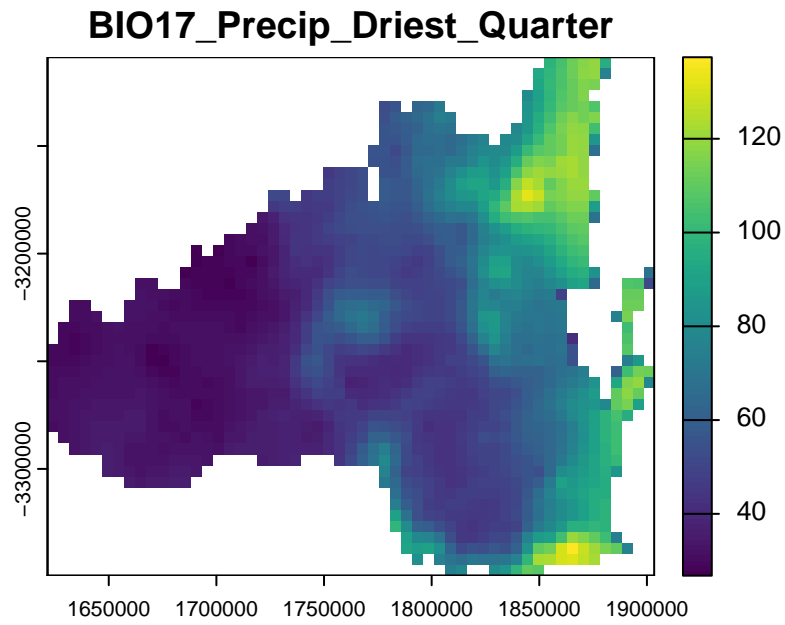
BIO13_Precip_Wettest_Month

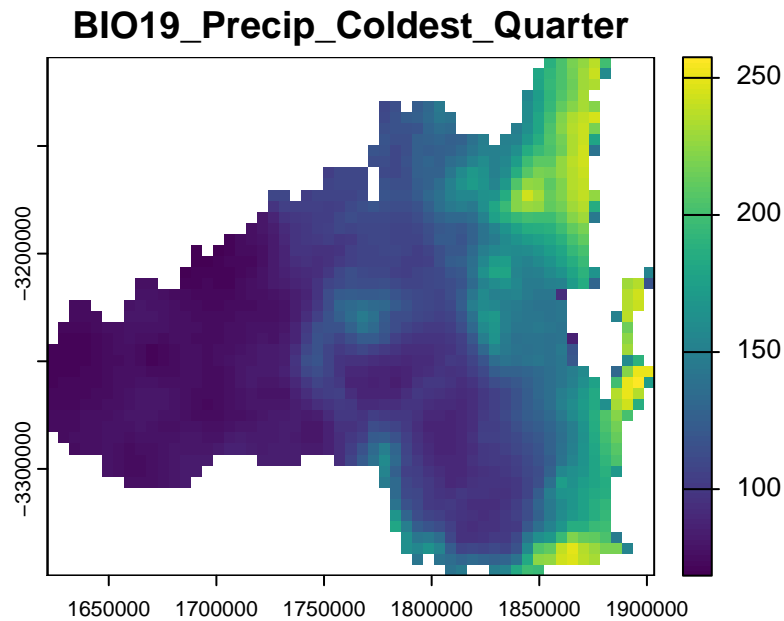


BIO14_Precip_Driest_Month

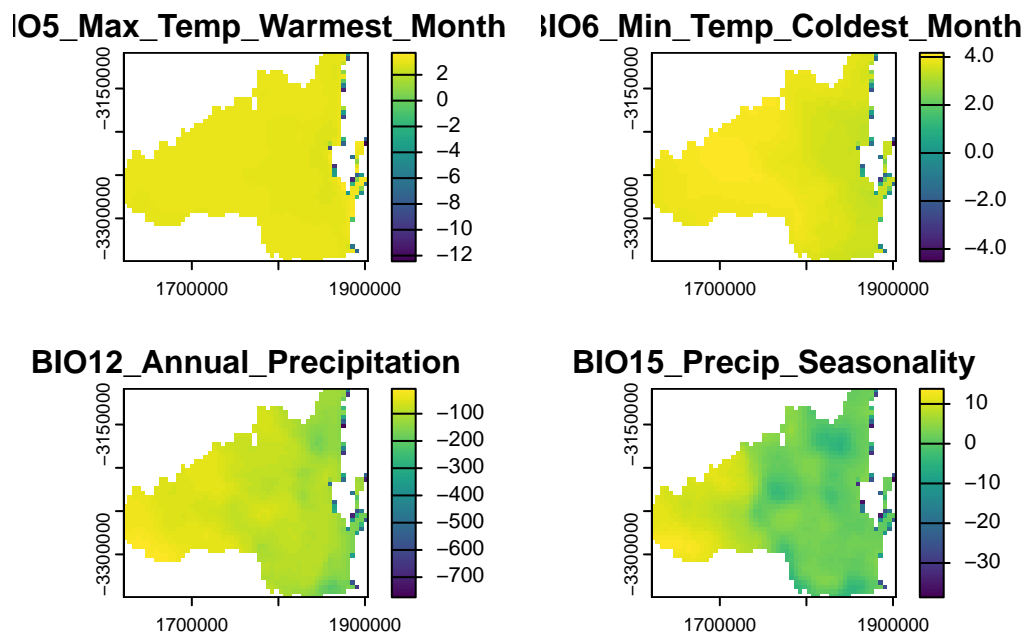








```
# Plot to compare the difference between the current and future rasters
plot(covs_future_expert - covs_current_expert)
```



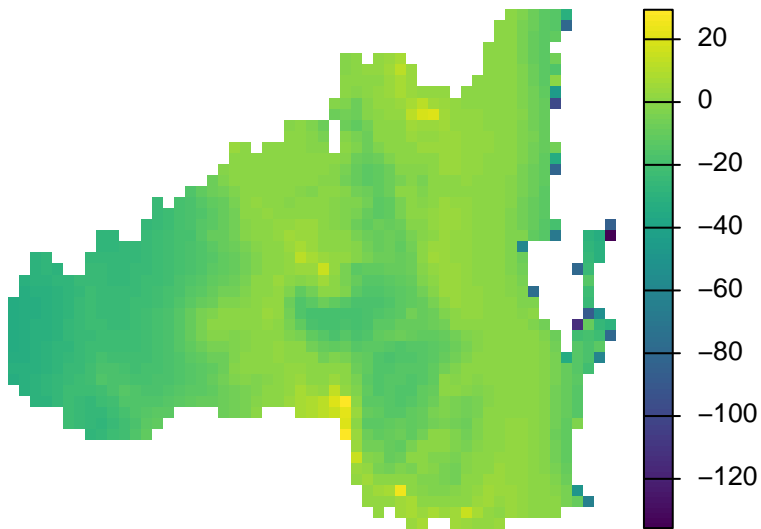
Test the environmental distance between current data and future conditions

```

mess <- predicts::mess(covs_future_expert,
                      train_PB_covs_thinned[, c("BI05_Max_Temp_Warmest_Month",
                                                "BI06_Min_Temp_Coldest_Month",
                                                "BI012_Annual_Precipitation",
                                                "BI015_Precip_Seasonality")])

plot(mess, axes = F)

```



```

r_mess_mask <- mess < 0
plot(r_mess_mask, axes=F)

```



Test which areas you might mask out because they are ‘novel’ in environmental space and therefore require model extrapolation.

```

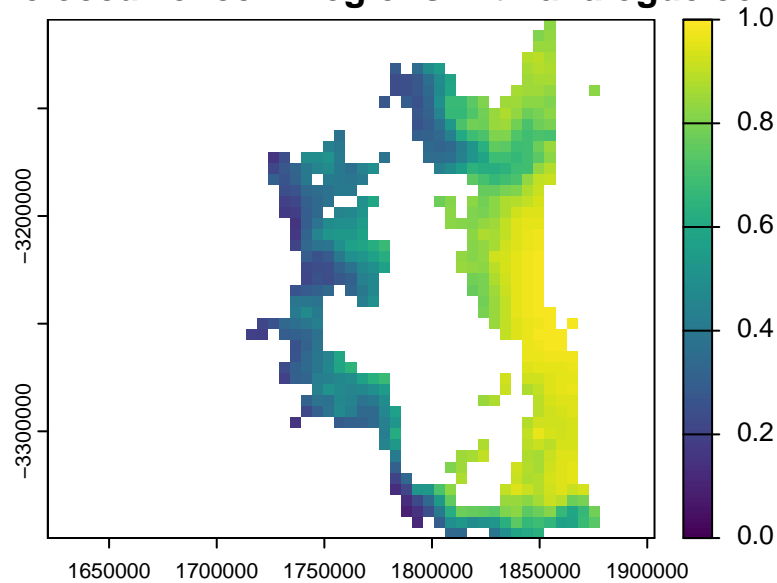
analog_fut <- predicted_raster_model_1

values(analog_fut)[values(mess)<0] <- NA

plot(analog_fut,
     range = c(0, 1), # Set min and max values for the color scale
     main = "Koala relative occurrence in regions with analogue conditions")

```

a relative occurrence in regions with analogue conditions



```

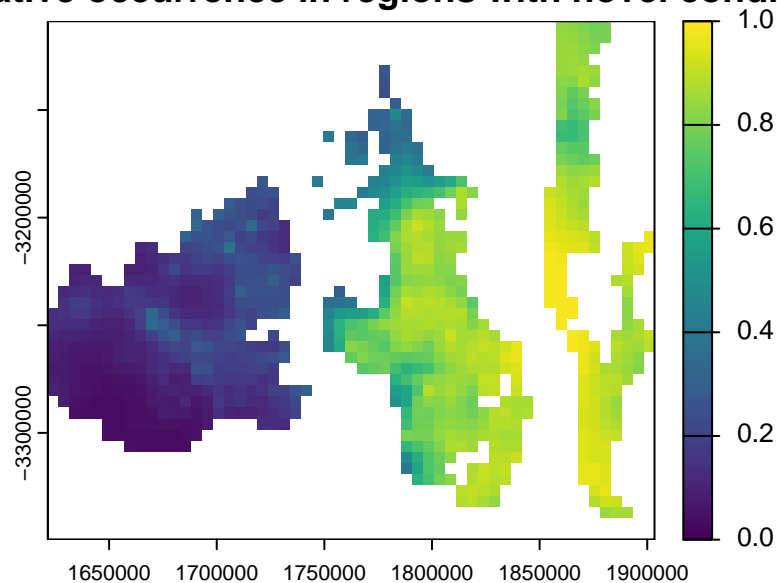
novel_fut <- predicted_raster_model_1

values(novel_fut)[values(mess)>0] <- NA

plot(novel_fut,
     range = c(0, 1), # Set min and max values for the color scale
     main = "Koala relative occurrence in regions with novel conditions")

```

ala relative occurrence in regions with novel conditions



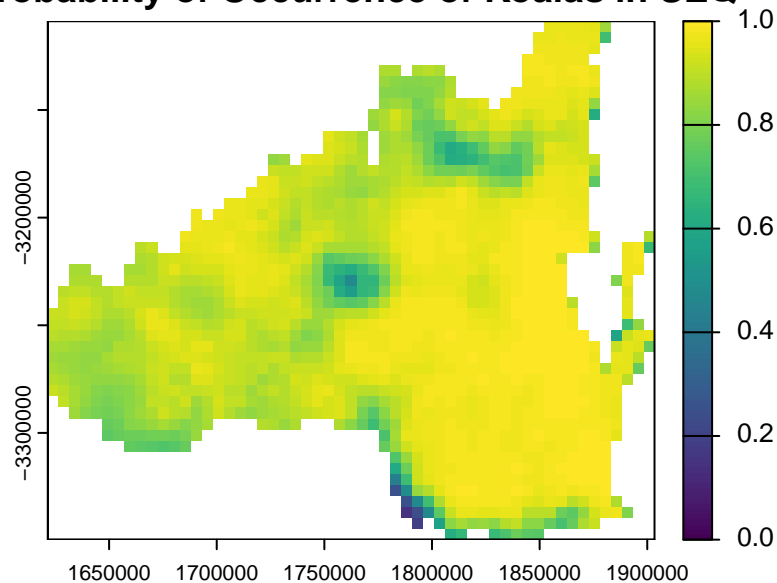
GLM future predictions

Model 1

```
# Predict the presence probability across the entire raster extent
predicted_raster_model_1 <- predict(covs_future_expert, glm_model_1, type = "response")

# Plot the species distribution raster
plot(
  predicted_raster_model_1,
  range = c(0, 1), # Set min and max values for the color scale
  main = "Relative Probability of Occurrence of Koalas in SEQ - GLM1"
)
```

Relative Probability of Occurrence of Koalas in SEQ – GLM1

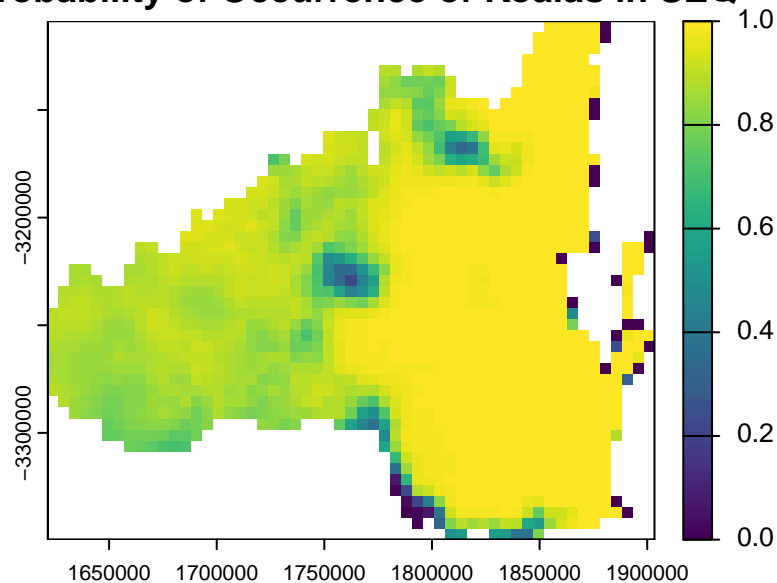


Model 2

```
# Predict the presence probability across the entire raster extent
predicted_raster_model_2 <- predict(covs_future_expert, glm_model_2, type = "response")

# Plot the species distribution raster
plot(
  predicted_raster_model_2,
  range = c(0, 1), # Set min and max values for the color scale
  main = "Relative Probability of Occurrence of Koalas in SEQ - GLM2"
)
```


Relative Probability of Occurrence of Koalas in SEQ – GLM2



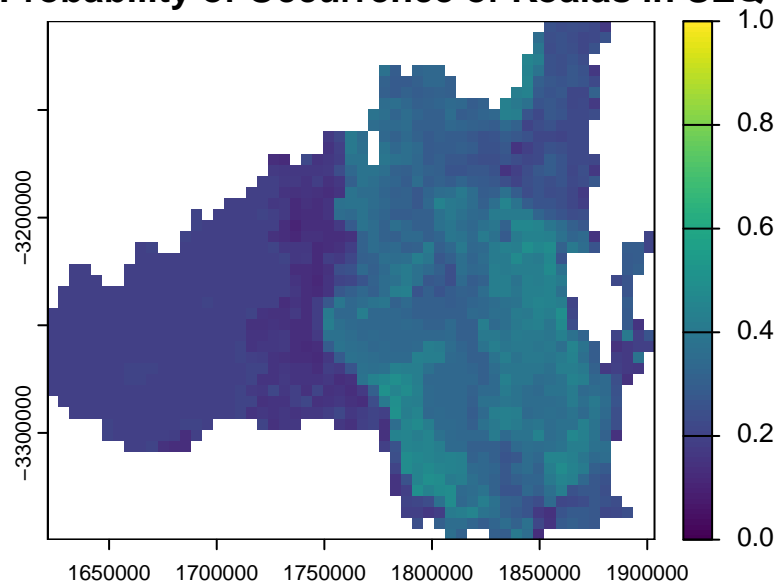
Random Forest future predictions

Model 1

```
# Predict the presence probability across the entire raster extent
predicted_raster_RF_1 <- predicts::predict(covs_future_expert, rf_1, type = "response", na.rm = TRUE)

# Plot the species distribution raster
plot(
  predicted_raster_RF_1,
  range = c(0, 1), # Set min and max values for the color scale
  main = "Relative Probability of Occurrence of Koalas in SEQ - RF"
)
```

Relative Probability of Occurrence of Koalas in SEQ – RF



Presenting predictions with uncertainty

There are many sources of model uncertainty that should be explored and ideally, presented alongside model predictions.

One that we'll focus on here is climate scenario uncertainty. We do so by fitting a second model to future climate data from a lower emission shared socioeconomic path scenario (SSP 1.26).

Load future environmental data (SSP 1.26)

```
covs_future_SSP126 <- rast("Data/Environmental_variables/future_bioclim.2090.SSP126.tif")
names(covs_future_SSP126) <- layer_names
covs_future_SSP126
```

```
class      : SpatRaster
dimensions : 47, 55, 19  (nrow, ncol, nlyr)
resolution : 5123.954, 5123.954  (x, y)
extent     : 1621552, 1903370, -3349594, -3108768  (xmin, xmax, ymin, ymax)
coord. ref.: GDA94 / Geoscience Australia Lambert (EPSG:3112)
source     : future_bioclim.2090.SSP126.tif
names      : BI01_~_Temp, BI02_~_Range, BI03_~_ality, BI04_~_ality, BI05_~_Month, BI06_~_Month,
min values : 0.7471204, 0.3128485, 1.585051, 12.19436, 1.046093, 0.3754203,
max values : 22.4384842, 14.8543510, 51.254021, 544.83429, 35.546104, 13.5217409,
```

```

covs_future_SSP126_expert <- subset(covs_future_SSP126, names(covs_future_SSP126) %in% c("BI
"B
"B
"B

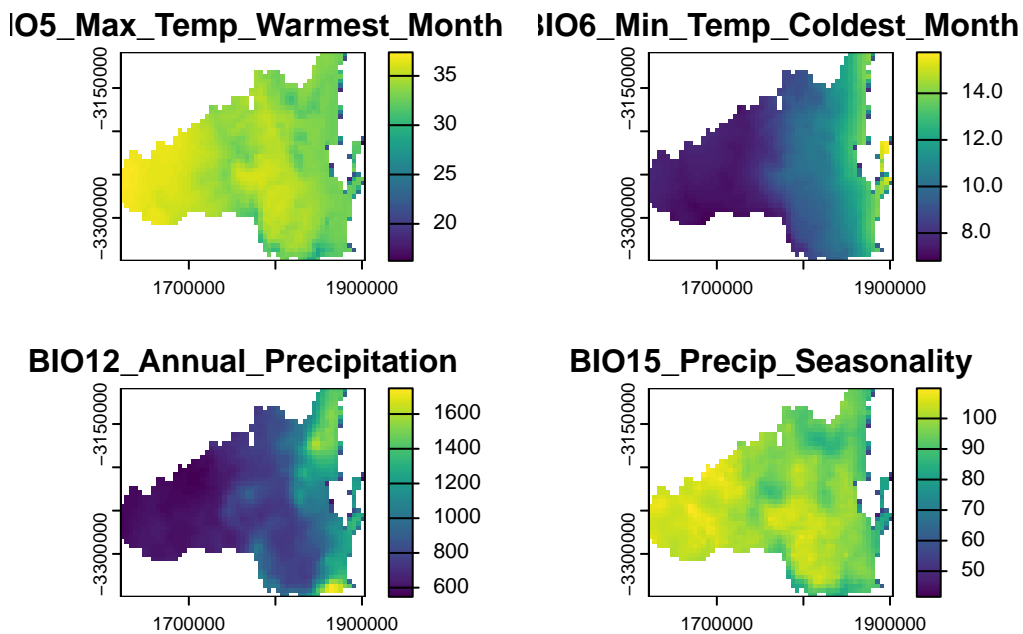
```

Plot to compare the variables across the two scenarios

```

plot(covs_future_expert)

```

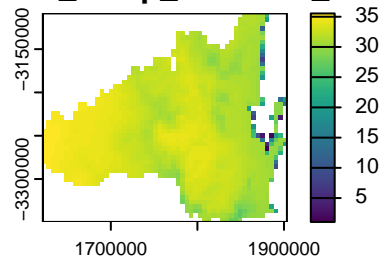


```

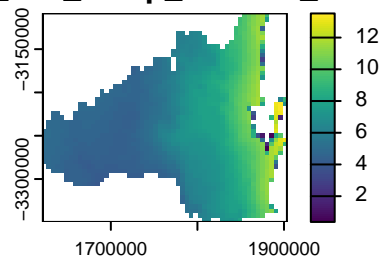
plot(covs_future_SSP126_expert)

```

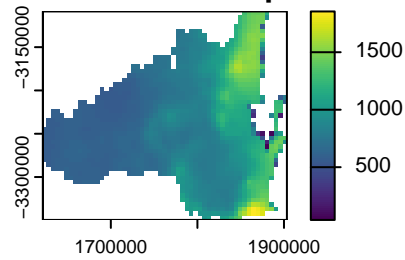
IO5_Max_Temp_Warmest_Month



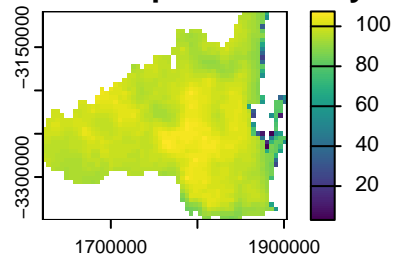
IO6_Min_Temp_Coldest_Month



BIO12_Annual_Precipitation



BIO15_Precip_Seasonality

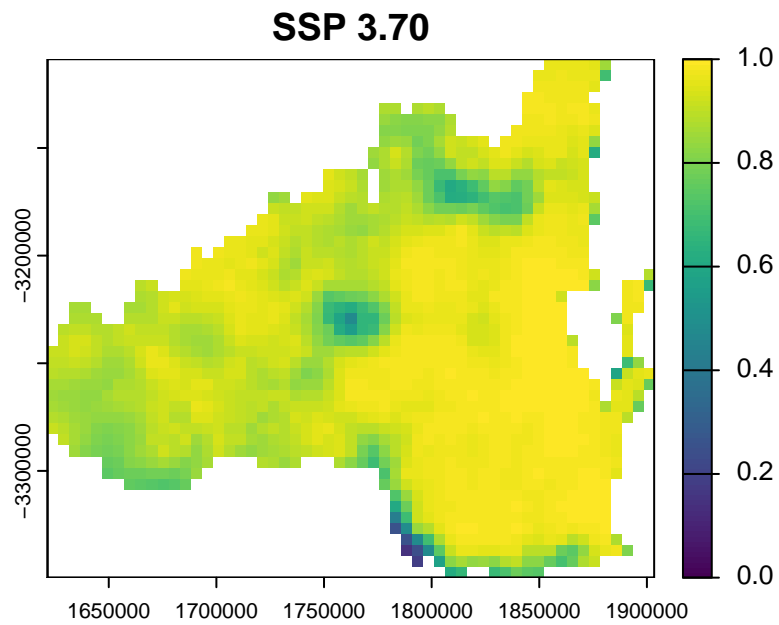


GLM future predictions (SSP 1.26)

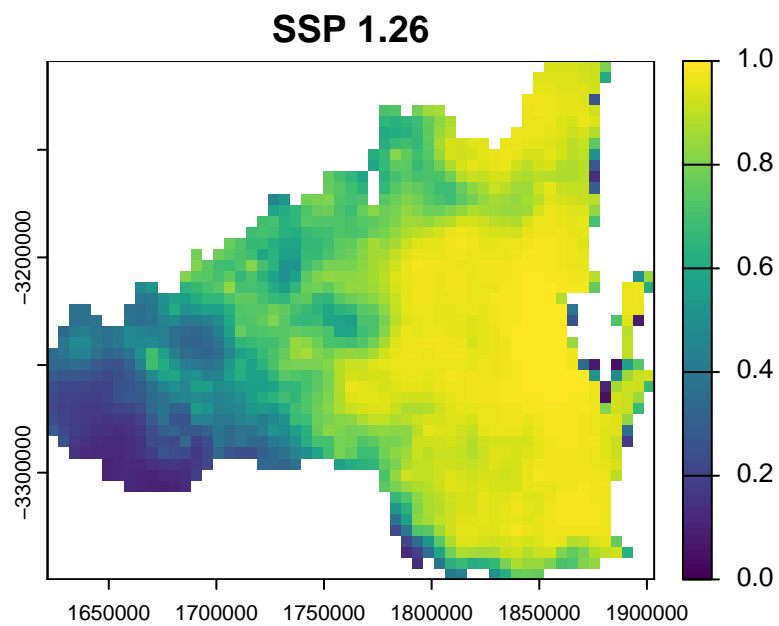
Model 1

```
# Predict the presence probability across the entire raster extent
predicted_raster_model_1_SSP126 <- predict(covs_future_SSP126_expert, glm_model_1, type = "r")

# Plot the species distribution raster
plot(
  predicted_raster_model_1,
  range = c(0,1),
  main = "SSP 3.70"
)
```



```
plot(
  predicted_raster_model_1_SSP126,
  range = c(0,1),
  main = "SSP 1.26"
)
```



Model uncertainty

Another element of uncertainty that can be represented is model uncertainty, or the standard error around the coefficient estimates.

```
# Extract standard errors of coefficients
```

```
coef_se <- summary(glm_model_1)$coefficients[, "Std. Error"]
```

```
print(coef_se)
```

```
              (Intercept) BI05_Max_Temp_Warmest_Month  
              1.7073577601                0.0565765829  
BI06_Min_Temp_Coldest_Month BI012_Annual_Precipitation  
              0.0320840066                0.0003021583  
BI015_Precip_Seasonality  
              0.0118936628
```

```
covs_df <- as.data.frame(covs_future_expert, na.rm = FALSE)
```

```
pred_link <- predict(glm_model_1, newdata = covs_df, type = "link", se.fit = TRUE)
```

```
# Linear predictor (eta)
```

```
eta <- pred_link$fit
```

```
se_eta <- pred_link$se.fit
```

```
# Confidence intervals (95%)
```

```
z <- 1.96
```

```
eta_lower <- eta - z * se_eta
```

```
eta_upper <- eta + z * se_eta
```

```
# Transform back to response scale
```

```
linkinv <- glm_model_1$family$linkinv
```

```
predicted <- linkinv(eta)
```

```
lower_ci <- linkinv(eta_lower)
```

```
upper_ci <- linkinv(eta_upper)
```

```
# Add to covs_df
```

```
covs_df$predicted <- predicted
```

```
covs_df$lower_ci <- lower_ci
```

```
covs_df$upper_ci <- upper_ci
```

```

predicted_r <- setValues(rast(covs_future_expert, nlyr = 1), predicted)
lower_ci_r <- setValues(rast(covs_future_expert, nlyr = 1), lower_ci)
upper_ci_r <- setValues(rast(covs_future_expert, nlyr = 1), upper_ci)

# Step 2: Name the layers
names(predicted_r) <- "predicted"
names(lower_ci_r) <- "lower_CI"
names(upper_ci_r) <- "upper_CI"

prediction_w_uncertainty <- c(predicted_r, lower_ci_r, upper_ci_r)

plot(prediction_w_uncertainty, range = c(0, 1))

```

