

Home range analysis of kākā at Orokonui Ecosanctuary

Scott Forrest

2025-05-19

In this script we are fitting home range models to GPS data of kākā (*Nestor meridionalis*) at Orokonui Ecosanctuary, New Zealand. We are fitting data across the whole tracking period to estimate their long-term space use.

Load packages and set working directory.

```
library(tidyverse)

## -- Attaching core tidyverse packages ----- tidyverse 2.0.0 --
## v dplyr      1.1.4      v readr      2.1.5
## v forcats    1.0.0      v stringr   1.5.1
## v ggplot2    3.5.2      v tibble    3.2.1
## v lubridate  1.9.4      v tidyr     1.3.1
## v purrr      1.0.4
## -- Conflicts ----- tidyverse_conflicts() --
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()     masks stats::lag()
## i Use the conflicted package (<http://conflicted.r-lib.org/>) to force all conflicts to become errors

packages <- c("move", "lattice", "purrr", "here", "raster", "sf", "ggpubr",
              "patchwork", "jtools", "MuMIn", "statmod", "ctmm", "terra")

walk(packages, require, character.only = T)

## Loading required package: move
## Loading required package: geosphere
## Loading required package: sp
## Loading required package: raster
##
## Attaching package: 'raster'
##
## The following object is masked from 'package:dplyr':
##
##     select
##
## Loading required package: lattice
## Loading required package: here
## here() starts at /Users/scottforrest/Library/CloudStorage/OneDrive-QueenslandUniversityofTechnology/1
## Loading required package: sf
## Linking to GEOS 3.13.0, GDAL 3.8.5, PROJ 9.5.1; sf_use_s2() is TRUE
## Loading required package: ggpubr
##
## Attaching package: 'ggpubr'
```

```

##
## The following object is masked from 'package:raster':
##
##     rotate
##
## Loading required package: patchwork
##
## Attaching package: 'patchwork'
##
## The following object is masked from 'package:raster':
##
##     area
##
## Loading required package: jtools
## Loading required package: MuMIn
## Registered S3 methods overwritten by 'MuMIn':
##   method      from
##   nobs.multinom broom
##   nobs.fitdistr broom
## Loading required package: statmod
## Loading required package: ctmm
##
## Attaching package: 'ctmm'
##
## The following objects are masked from 'package:move':
##
##     distance, plot, speed
##
## The following objects are masked from 'package:raster':
##
##     distance, head, plot, predict, tail
##
## The following object is masked from 'package:sp':
##
##     plot
##
## The following object is masked from 'package:ggplot2':
##
##     annotate
##
## Loading required package: terra
## terra 1.8.42
##
## Attaching package: 'terra'
##
## The following objects are masked from 'package:ctmm':
##
##     distance, meta
##
## The following object is masked from 'package:patchwork':
##
##     area
##
## The following object is masked from 'package:ggpubr':

```

```
##
## rotate
##
## The following object is masked from 'package:tidyr':
##
## extract
##
## The following object is masked from 'package:knitr':
##
## spin
```

Import data.

```
# create vector of GPS date filenames
GPSfiles <- list.files("CSV input data - dd_speed_6")

# create a vector for the tag numbers indicating different kākā
id <- 45505:45514

# import data
all_tags_list <- vector(mode = "list", length = length(GPSfiles))

for(i in 1:length(GPSfiles)){
  all_tags_list[[i]] <- read.csv(paste("CSV input data - dd_speed_6/",
                                       GPSfiles[[i]],
                                       sep = ""))

  all_tags_list[[i]]$id <- id[i]
}
```

Create an extent raster to be used for each individual. It is important to keep these the same size for the dynamic space use incremental analysis, so it is important that the raster covers the extent of each individual's locations.

```
ext_object <- as(extent(1390000, 1435000, 4910000, 4950000), 'SpatialPolygons')
crs(ext_object) <- "EPSG:2193"
ext_raster <- raster::raster(ext_object, res = 25) # resolution in m
```

Fit home range models

Using the `ctmm` package to fit continuous-time movement models to the data.

We are mostly following the step-by-step approach presented by Silva et al. (2022), Supplementary Materials 2.

To determine the best model for **each individual**, we start by using the `ctmm.guess` function. This gets starting values for the `ctmm.select` function, which is used for model selection. We then fit the best model for each individual using the `akde` function. We do this for each individual by looping over each one. We leave commented out code here to show the diagnostic and model checking steps that we took to ensure that the model fits were suitable for each individual's data, such as trying to fit models with the **pHREML** method, and using the **ML** method. We also check the variogram of the data for each individual.

```
tag_ctmm_list <- vector(mode = "list", length = 10)
# FIT1_ML_list <- vector(mode = "list", length = 10)
FIT1_pHREML_list <- vector(mode = "list", length = 10)
# UD1w_ML_list <- vector(mode = "list", length = 10)
```

```

UD1w_pHREML_list <- vector(mode = "list", length = 10)

for(i in 1:10) {

  # create data frames of only necessary information
  tag <- all_tags_list[[i]] %>% mutate(ID = id,
                                       timestamp = DateTime,
                                       longitude = lon,
                                       latitude = lat,
                                       .keep = "none")

  # reproject
  tag_ctmm_list[[i]] <- as.telemetry(tag, timezone = "GMT",
                                     projection = paste0("+proj=tmerc +lat_0=0 +lon_0=173 ",
                                                         "+k=0.9996 +x_0=1600000 +y_0=10000000 ",
                                                         "+ellps=GRS80 +towgs84=0,0,0,0,0,0,0 ",
                                                         "+units=m +no_defs +type=crs"))

  # plot(tag_ctmm_list[[i]])

  level <- 0.95 # we want to display 95% confidence intervals
  SVF <- variogram(tag_ctmm_list[[i]])
  # plot(SVF, fraction = 1, level = level,
  #       main = paste0("id ", tag_ctmm_list[[i]]@info$identity))

  # Estimating the ctmm that is most appropriate for the data

  # Calculate an automated model guesstimate:
  # ctmm.guess(tag_ctmm_list[[i]], interactive = TRUE)
  # using interactive starting estimates
  # FIT1_ML_list[[i]] <- ctmm.select(tag_ctmm_list[[i]], GUESS,
  #                                method = 'ML', IC = "AIC",
  #                                verbose = TRUE)

  # Calculate an automated model guesstimate:
  GUESS1 <- ctmm.guess(tag_ctmm_list[[i]], interactive = FALSE)

  # Automated model selection, starting from GUESS:
  ## reminder: it will default to pHREML if no method is specified.
  # FIT1_ML_list[[i]] <- ctmm.select(tag_ctmm_list[[i]], GUESS1,
  #                                method = 'ML', IC = "AIC",
  #                                verbose = TRUE)

  # print(summary(FIT1_ML_list[[i]]))

  # plot(SVF, CTMM = FIT1_ML_list[[i]][[1]],
  #       main = paste0("ML - ", rownames(summary(FIT1_ML_list[[i]]))[1],
  #                     " - ID ", tag_ctmm_list[[i]]@info$identity))
  #
  # plot(SVF, CTMM = FIT1_ML_list[[i]][[1]], fraction = 0.02,
  #       main = paste0("ML - ", rownames(summary(FIT1_ML_list[[i]]))[1],
  #                     " - ID ", tag_ctmm_list[[i]]@info$identity))

```

```

# using pHREML
FIT1_pHREML_list[[i]] <- ctmselect(tag_ctmm_list[[i]], GUESS1,
                                method = 'pHREML', IC = "AIC",
                                verbose = TRUE)

print(summary(FIT1_pHREML_list[[i]]))
# OUa_pHREML <- FIT1_pHREML_list[[i]][[1]]

plot(SVF, CTMM = FIT1_pHREML_list[[i]][[1]], fraction = 1,
     main = paste0("pHREML - ", rownames(summary(FIT1_pHREML_list[[i]]))[1],
                  " - ID ", tag_ctmm_list[[i]]@info$identity))

# to view zoomed in plot to assess fit
# plot(SVF, CTMM = FIT1_pHREML_list[[i]][[1]], fraction = 0.02,
#      main = paste0("pHREML - ", rownames(summary(FIT1_pHREML_list[[i]]))[1],
#                   " - ID ", tag_ctmm_list[[i]]@info$identity))

# Fitting home range model

# Run an area-corrected AKDE with weights:
# UD1w_ML_list[[i]] <- akde(tag_ctmm_list[[i]], FIT1_ML_list[[i]],
#                          weights = TRUE, grid = ext_raster)
# summary(UD1w_ML_list[[i]])
# summary(UD1_ML)$CI # home range area estimation
# plot(UD1w_ML_list[[i]])
# print(summary(UD1w_ML_list[[i]])$DOF["area"]) # effective sample size of animal1
# print(nrow(tag_ctmm_list[[i]])) # absolute sample size

# Run an area-corrected AKDE with weights using the pHREML estimated model:
UD1w_pHREML_list[[i]] <- akde(tag_ctmm_list[[i]], FIT1_pHREML_list[[i]],
                             weights = TRUE, grid = ext_raster)

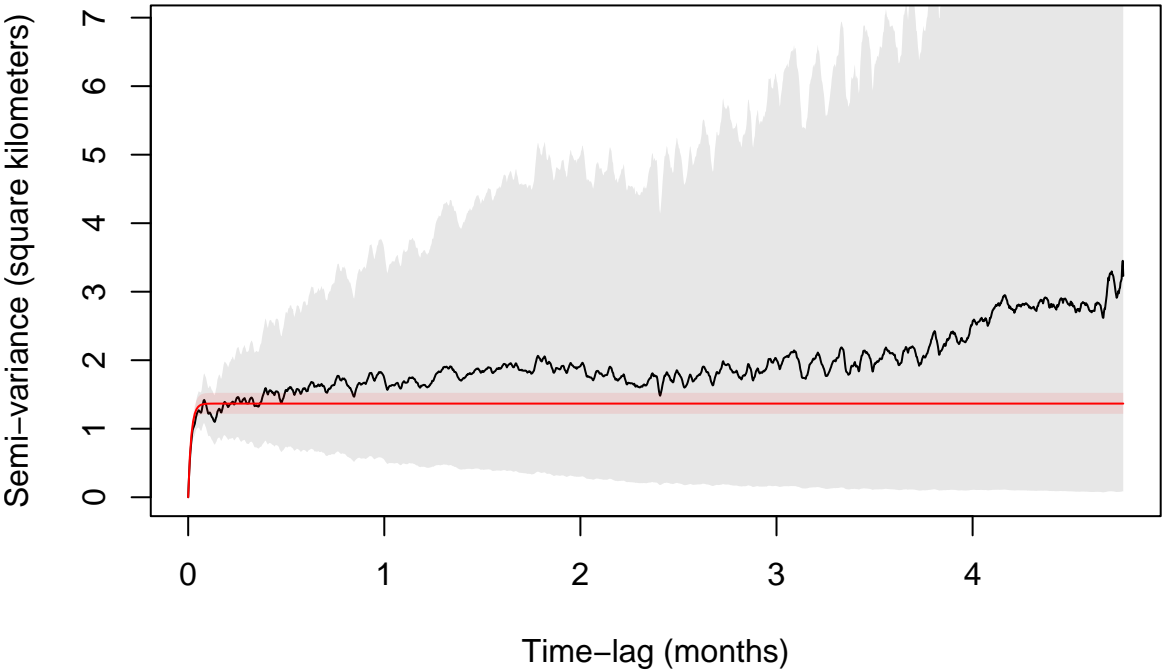
summary(UD1w_pHREML_list[[i]])
plot(UD1w_pHREML_list[[i]])
print(summary(UD1w_pHREML_list[[i]])$DOF["area"]) # effective sample size of animal1
print(nrow(tag_ctmm_list[[i]])) # absolute sample size
}

```

```
## Minimum sampling interval of 14.9 minutes in 45505
```

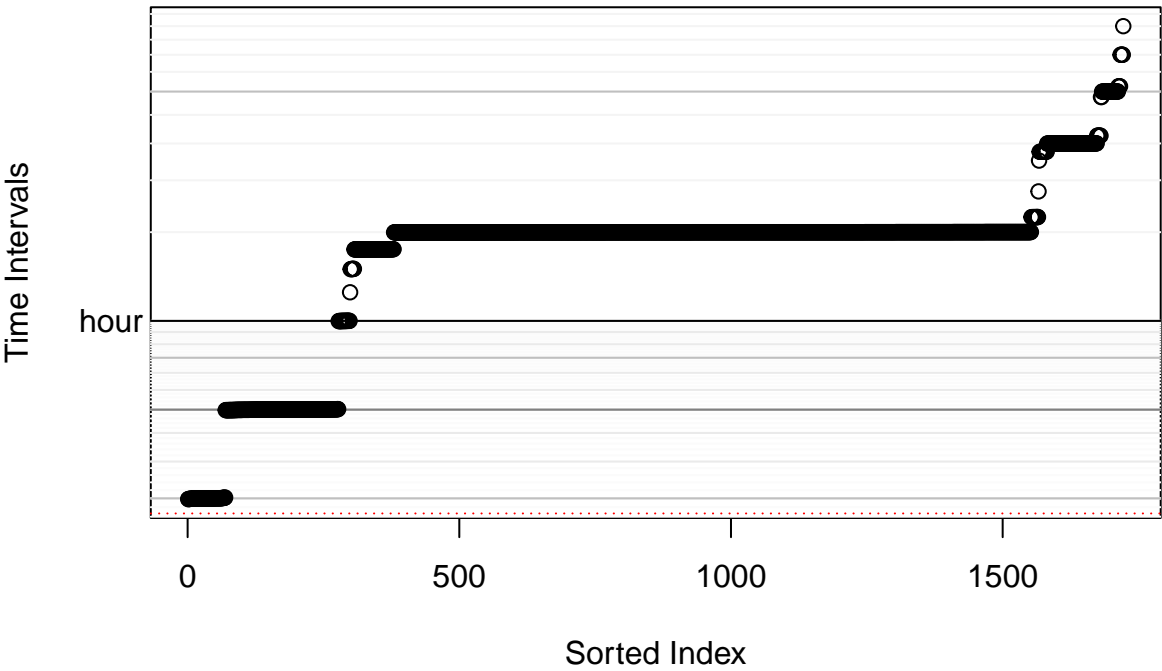
##		ΔAIC	$\Delta RMSPE$ (m)	$DOF[area]$
##	OU anisotropic	0.000000	107.2540	286.8548
##	OUF anisotropic	1.986637	102.4139	293.9135
##	OU	465.438629	331.8688	227.5025
##	OUF	467.422086	324.4040	234.9283
##	Ouf anisotropic	1290.708487	0.0000	978.8073
##	IID anisotropic	3711.231921	303.6194	1722.0000

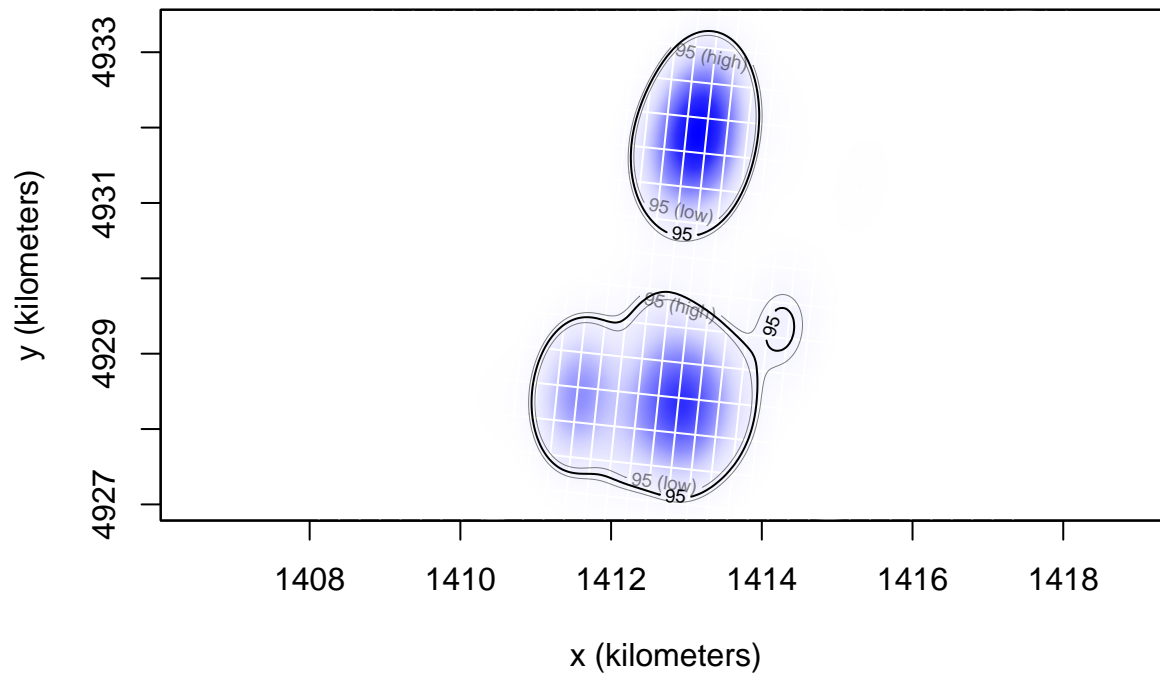
pHREML – OU anisotropic – ID 45505



Default grid size of 13.3314814814815 minutes chosen for bandwidth(...,fast=TRUE).

45505



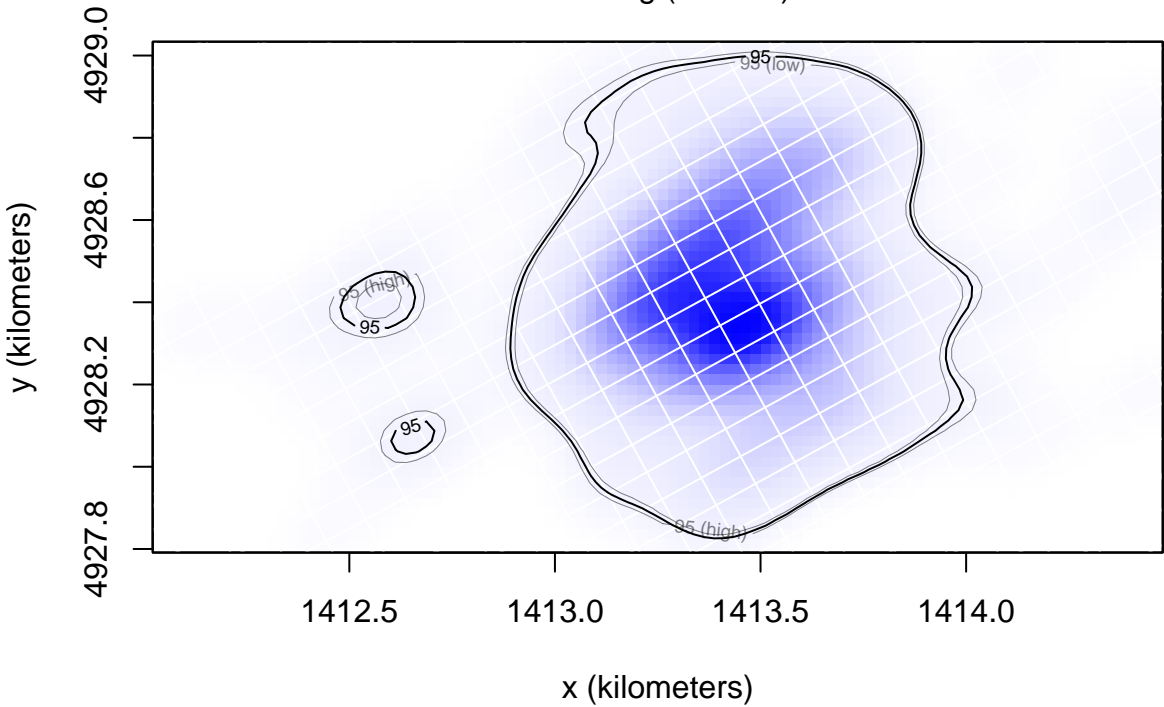
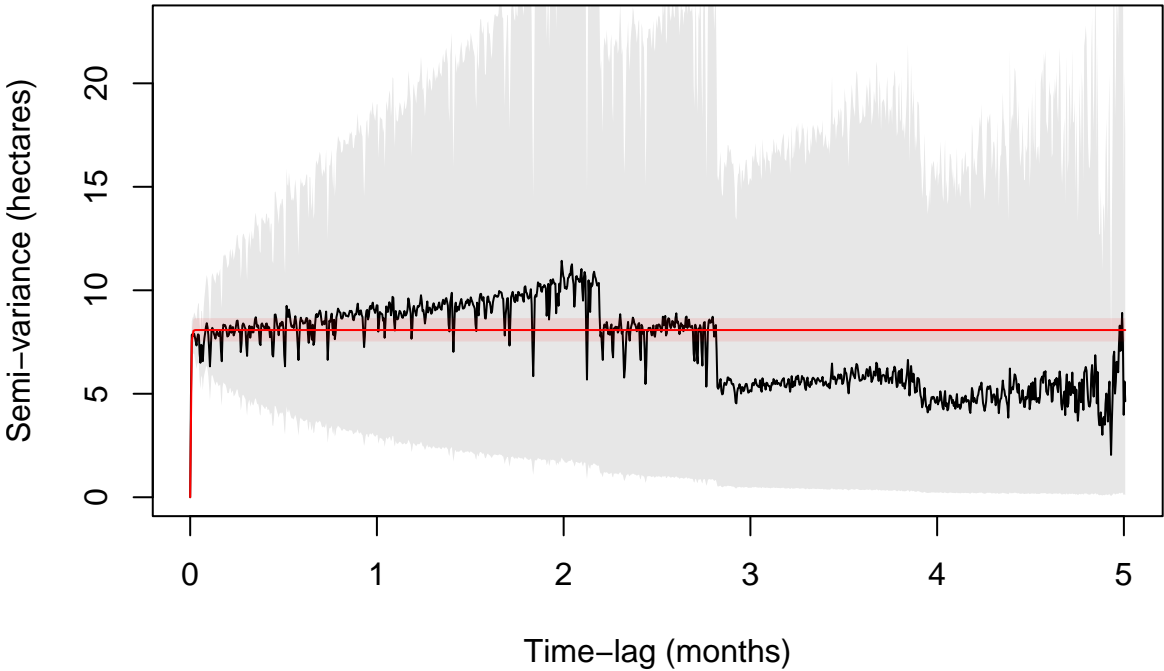


```
##      area
## 286.8548
## [1] 1723

## Minimum sampling interval of 59.9 minutes in 45506

##           ΔAIC ΔRMSPE (m) DOF[area]
## OU anisotropic    0.0000000 0.0000000 846.9103
## OUF anisotropic   0.8208396 0.4442276 842.8596
## OUf anisotropic  23.4689080 1.1613180 891.1219
## OUF              120.7719872 4.7694035 827.8475
## OU              122.6437241 3.6203542 830.1620
## IID anisotropic 150.4756940 0.3683857 985.0000
```

pHREML – OU anisotropic – ID 45506



```
##      area
## 846.9103
## [1] 986

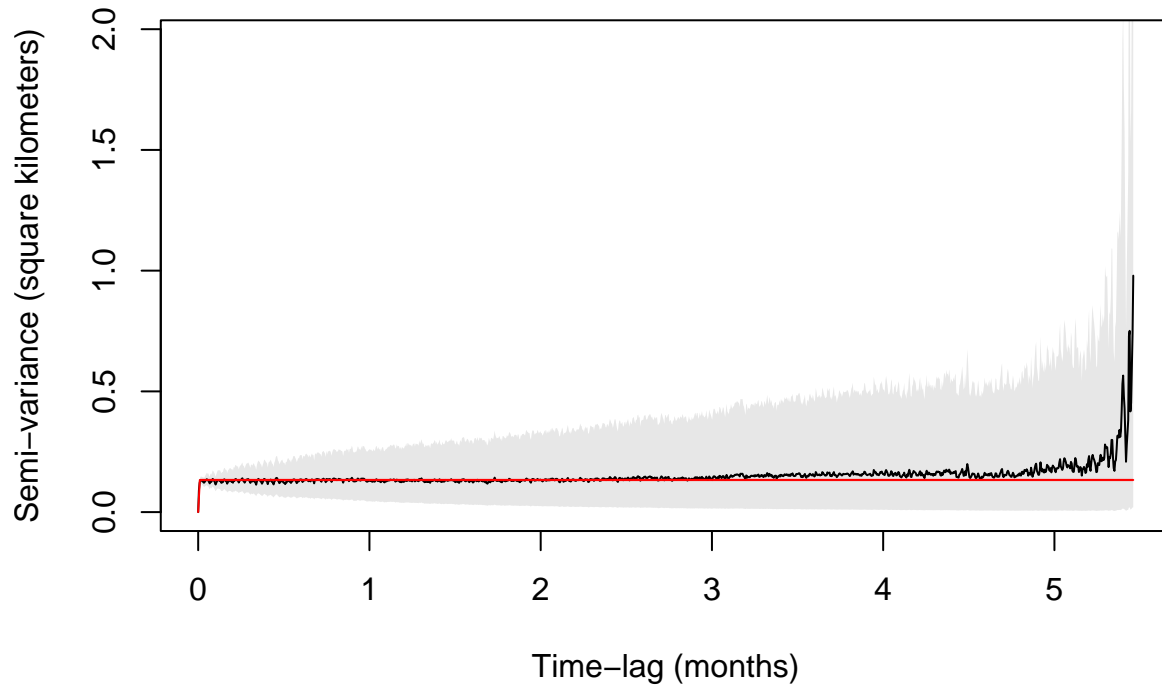
## Minimum sampling interval of 59.9 minutes in 45507

##              ΔAIC ΔRMSPE (m) DOF[area]
## 0Uf anisotropic 0.00000 8.900758 1011.298
```



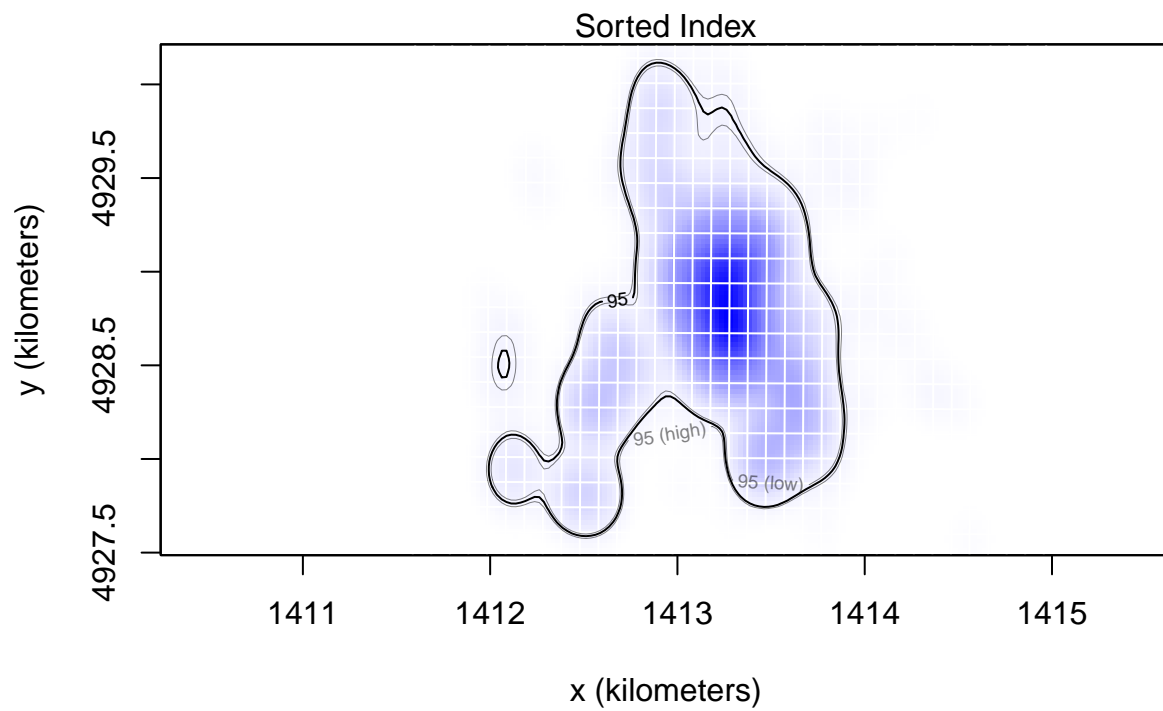
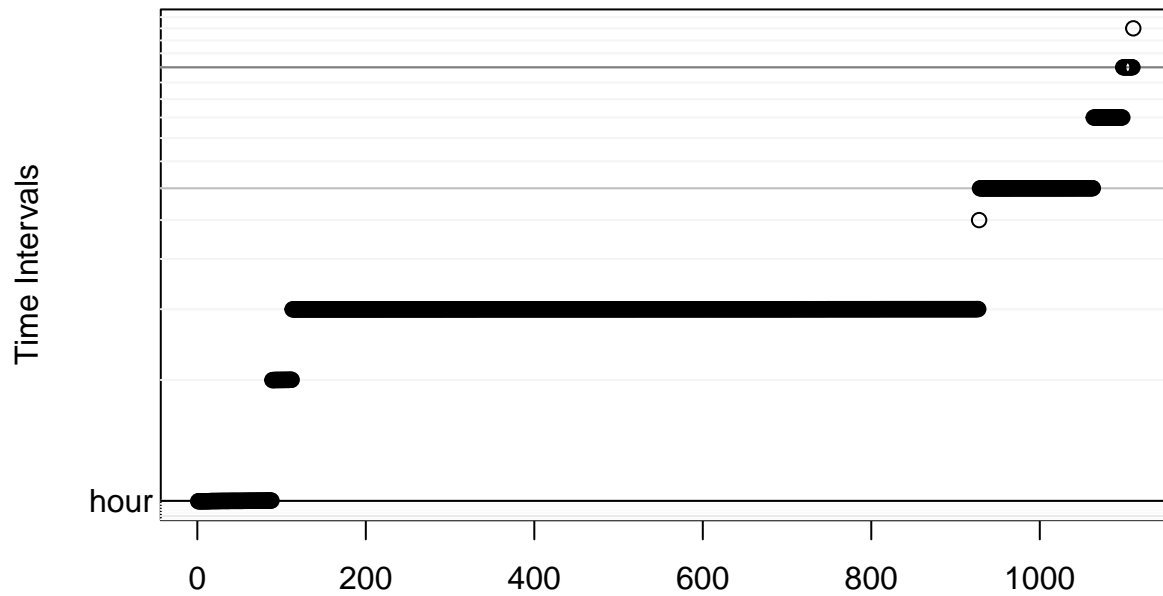
```
## OUΩ anisotropic 2.00000 8.900758 1000.172
## OUF anisotropic 2.00000 8.900758 1011.298
## OU anisotropic 24.04701 5.590181 1015.459
## IID anisotropic 86.69121 0.000000 1111.000
## OUf 92.34493 8.332524 1015.071
## OUF 94.34493 8.332524 1015.071
```

pHREML – OUf anisotropic – ID 45507



```
## Default grid size of 45 minutes chosen for bandwidth(...,fast=TRUE).
```

45507



```
##      area
## 1011.298
## [1] 1112

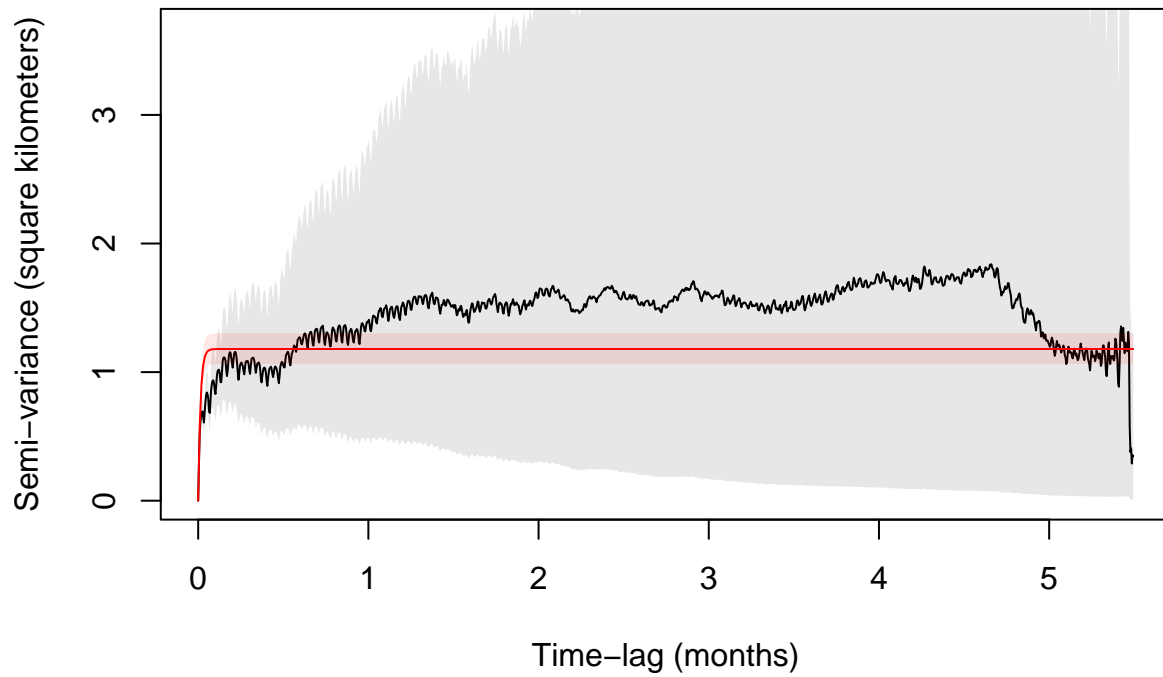
## Minimum sampling interval of 59.9 minutes in 45508

##              ΔAIC ΔRMSPE (m) DOF[area]
## OUF anisotropic  0.0000000    70.7448  369.4021
## OU anisotropic   0.4458837    71.0737  357.2924
## OUf anisotropic 315.8271248     0.0000  695.0203
```

OUF

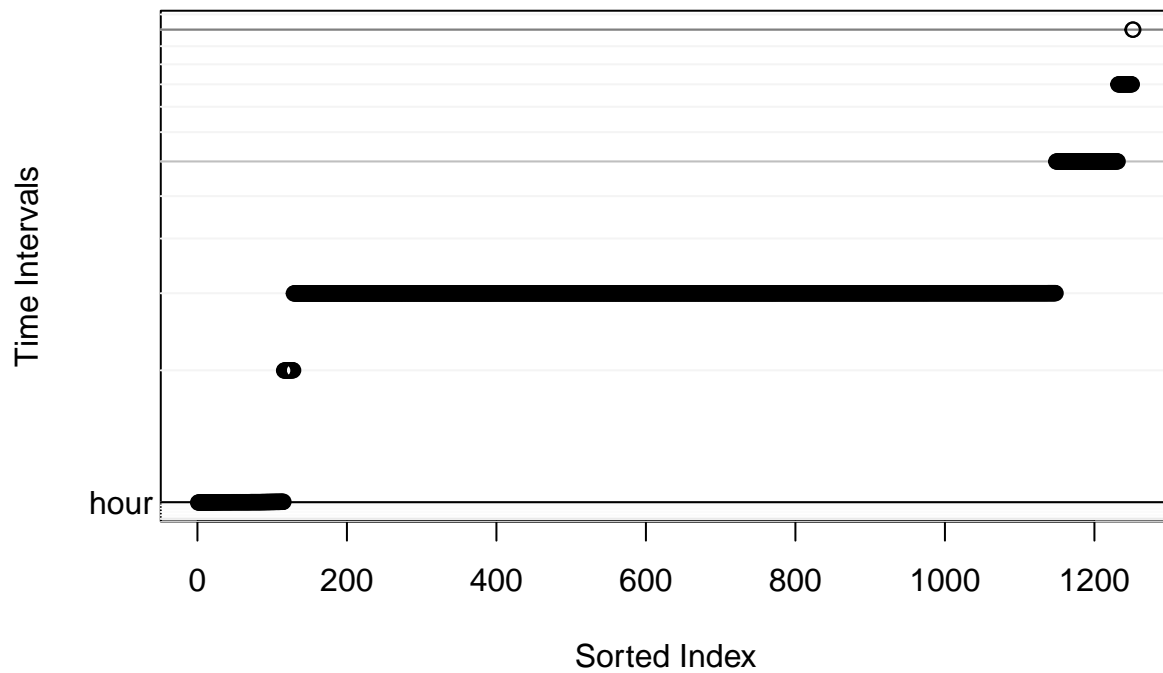
534.8997393 225.9840 321.7635

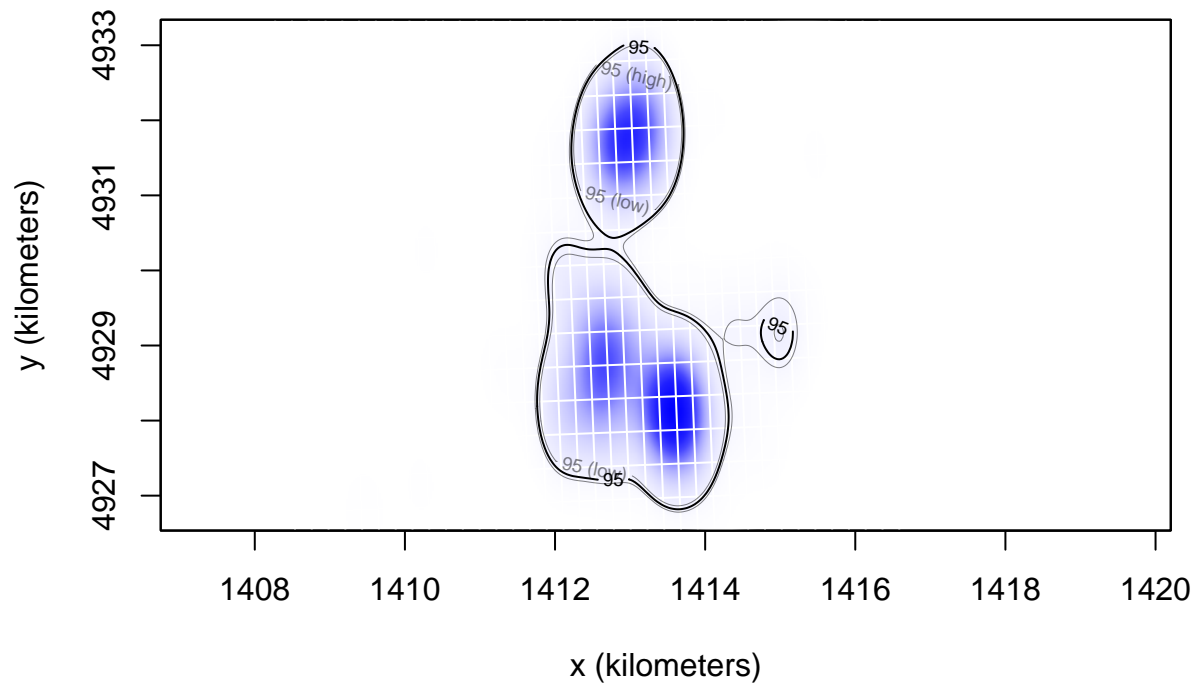
pHREML – OUF anisotropic – ID 45508



Default grid size of 45 minutes chosen for bandwidth(...,fast=TRUE).

45508



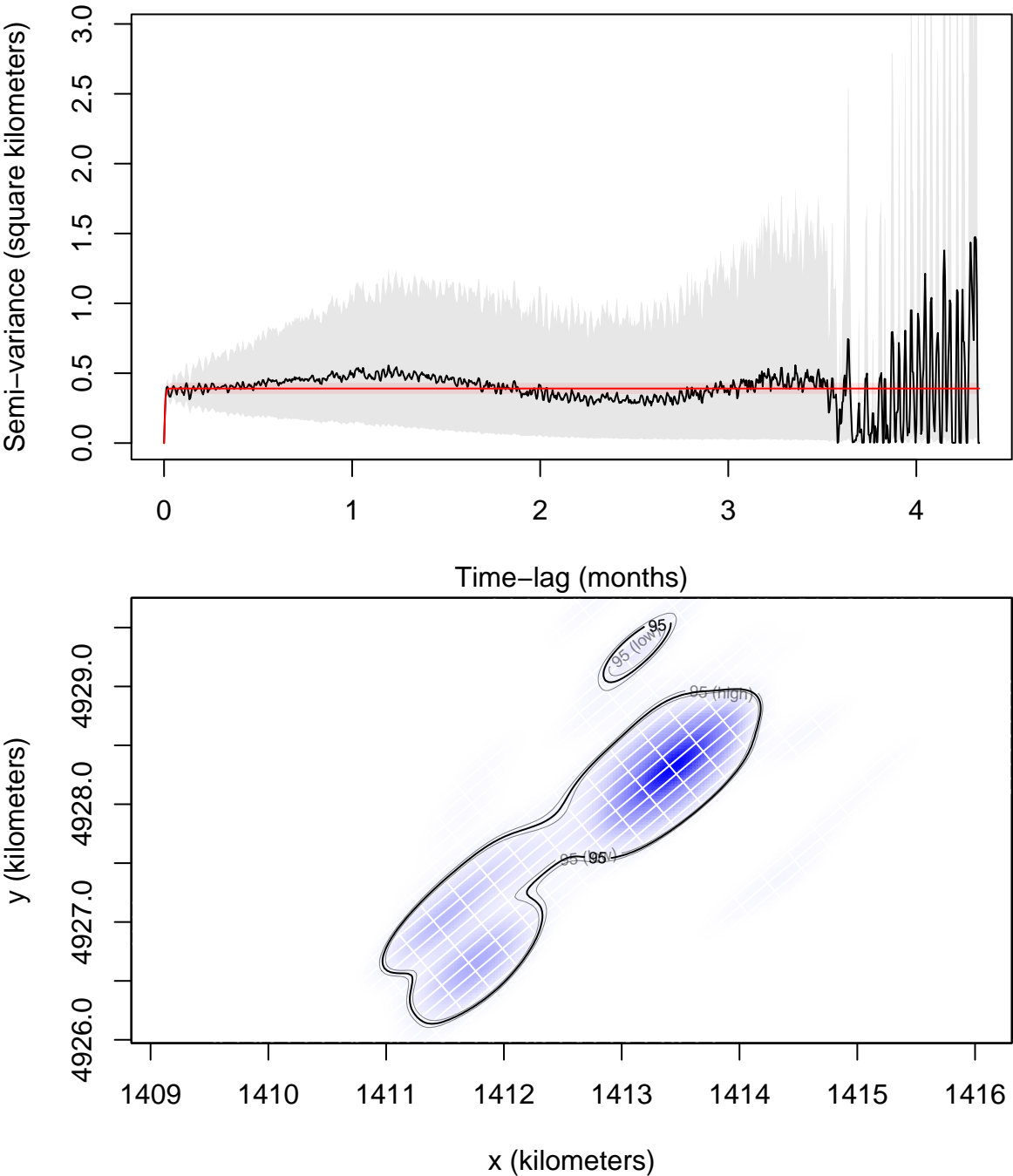


```
##      area
## 369.4021
## [1] 1253

## Minimum sampling interval of 59.9 minutes in 45509

##              ΔAIC ΔRMSPE (m) DOF[area]
## OU anisotropic   0.000000   9.153379  513.3899
## OUF anisotropic   1.950689   9.088046  510.7531
## OUf anisotropic  67.582592   0.000000  611.0610
## IID anisotropic 324.424055  33.217677  720.0000
## OUF              770.090095  55.208573  483.0277
## OU               797.168288  48.119598  457.0585
```

pHREML – OU anisotropic – ID 45509



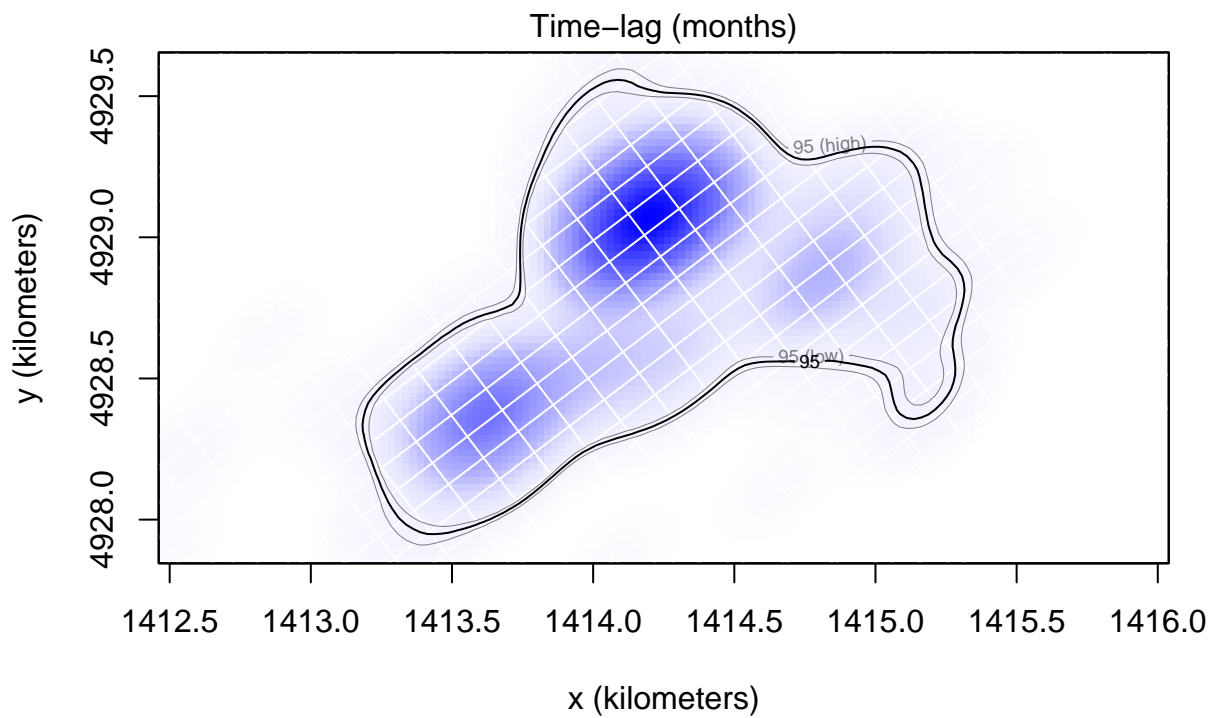
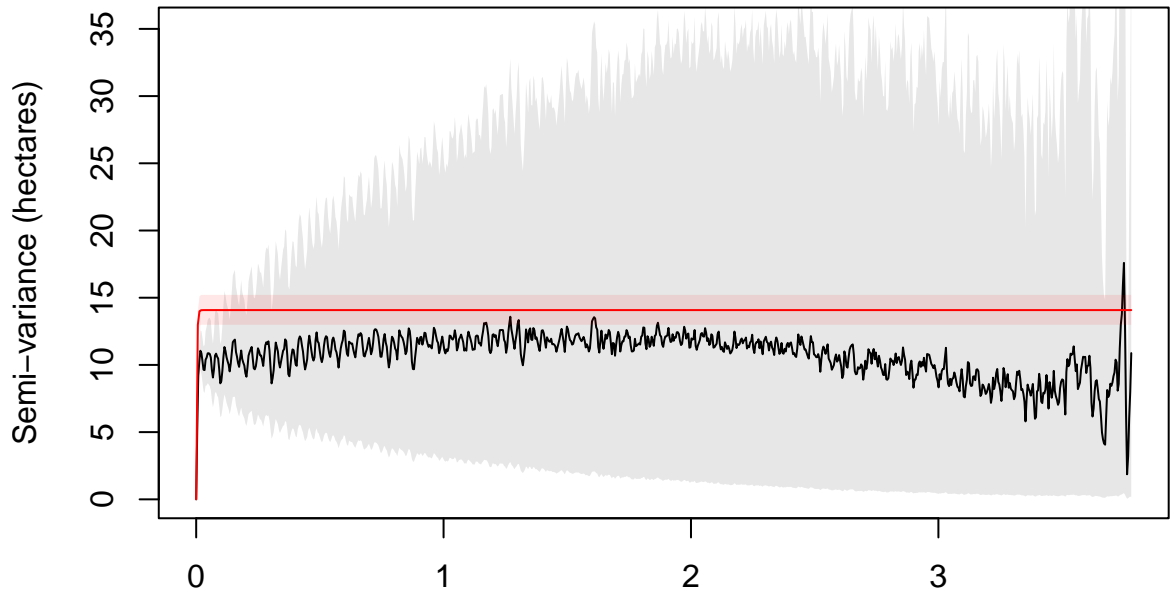
```
##      area
## 513.3899
## [1] 721

## Minimum sampling interval of 59.9 minutes in 45510

##              ΔAIC ΔRMSPE (m) DOF[area]
## OU anisotropic  0.000000  0.1841355  685.6219
## OUF anisotropic  1.996786  0.0000000  687.7744
```

```
## OUf anisotropic 41.376353 2.0059506 724.7845
## IID anisotropic 170.746204 7.4402083 817.0000
## OU 182.431389 9.7269138 655.5609
## OUF 184.427858 9.4481709 658.0421
```

pHREML – OU anisotropic – ID 45510

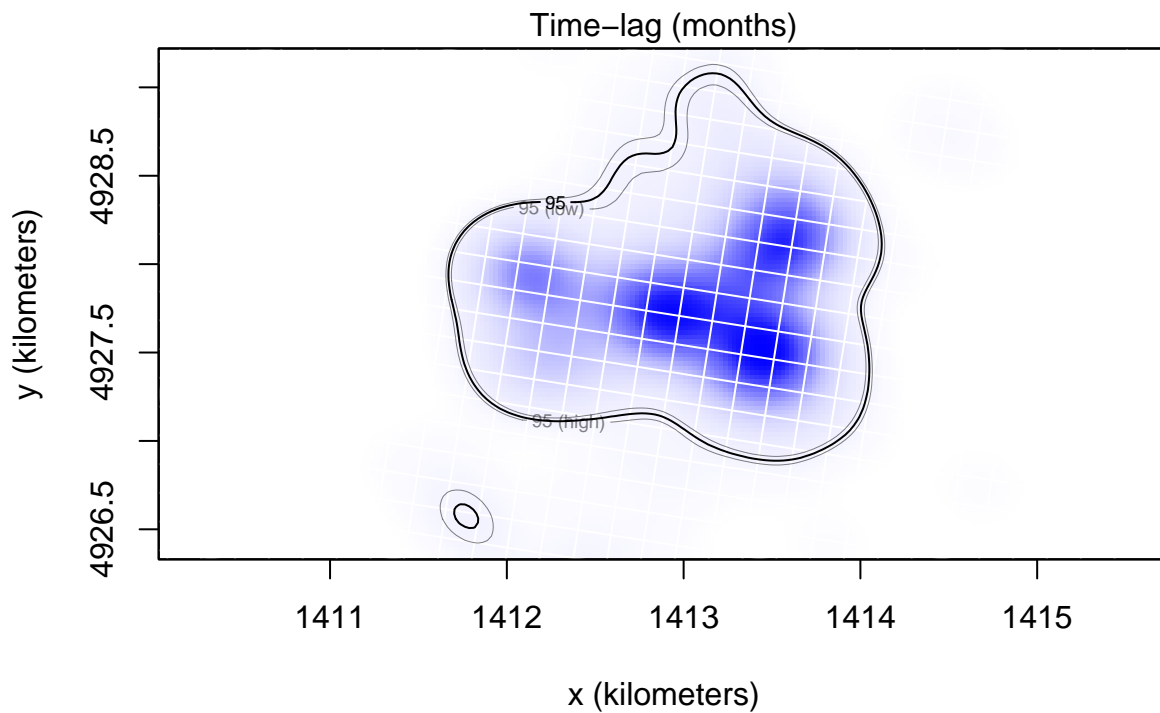
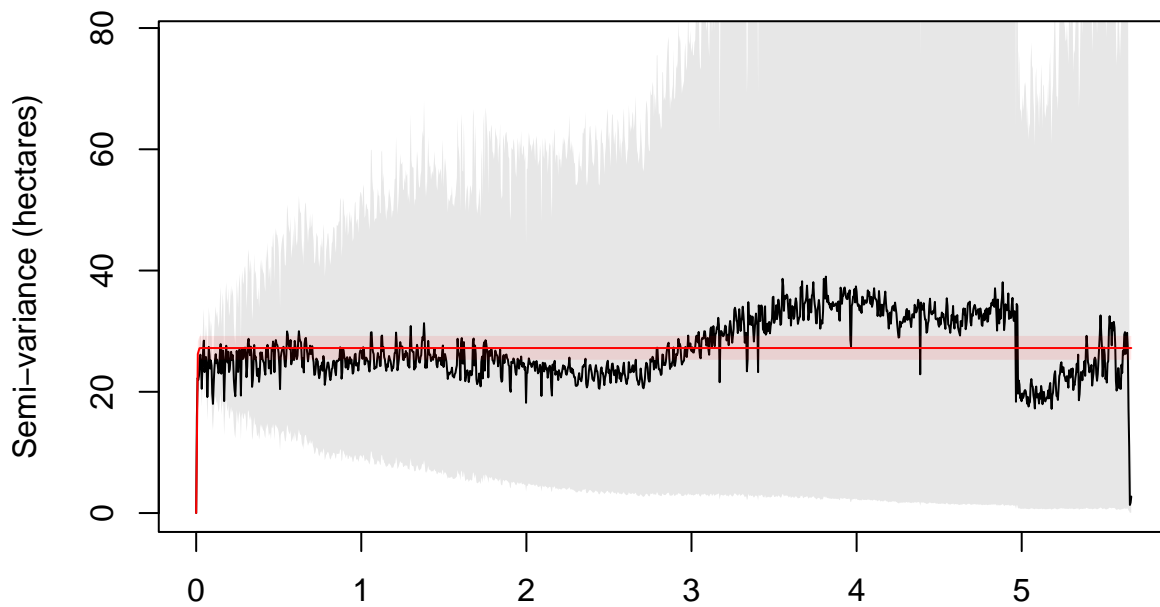


```
## area
## 685.6219
## [1] 818
```

```
## Minimum sampling interval of 59.9 minutes in 45511
```

```
##          ΔAIC ΔRMSPE (m) DOF[area]
## OUF anisotropic 0.000000 1.967446 733.7471
## OU anisotropic  7.389306 0.000000 717.7578
## OUF anisotropic 13.300706 0.661853 794.1486
## OUF          19.242447 6.925795 720.5158
```

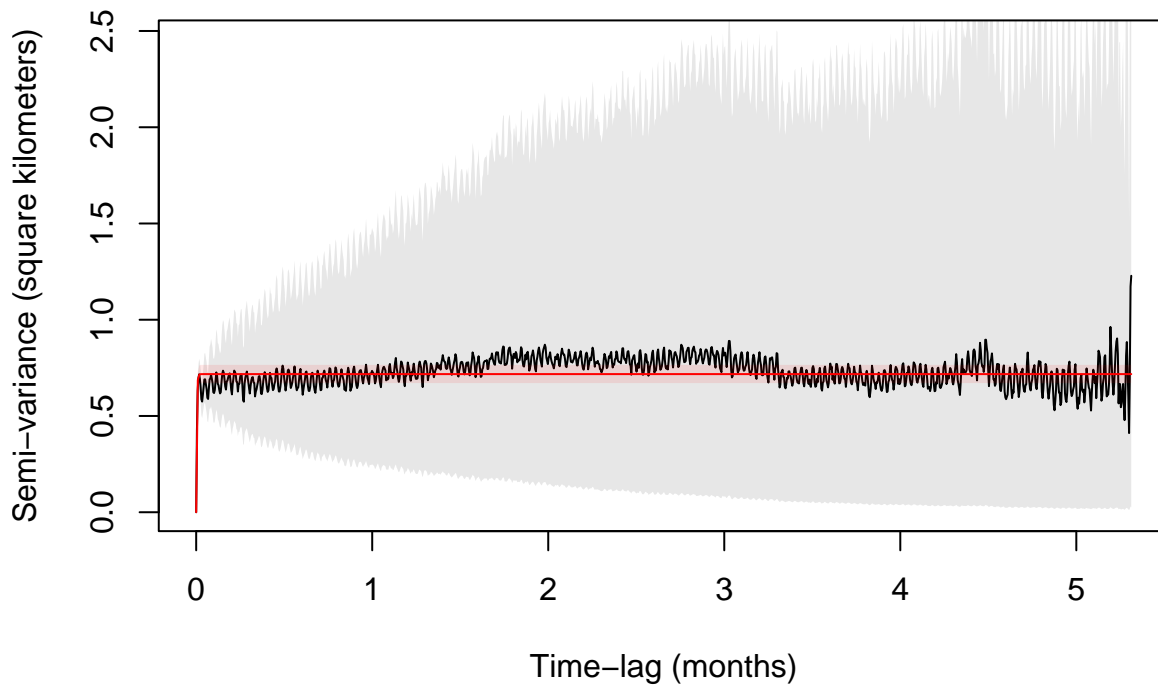
pHREML – OUF anisotropic – ID 45511



```
## area
## 733.7471
```

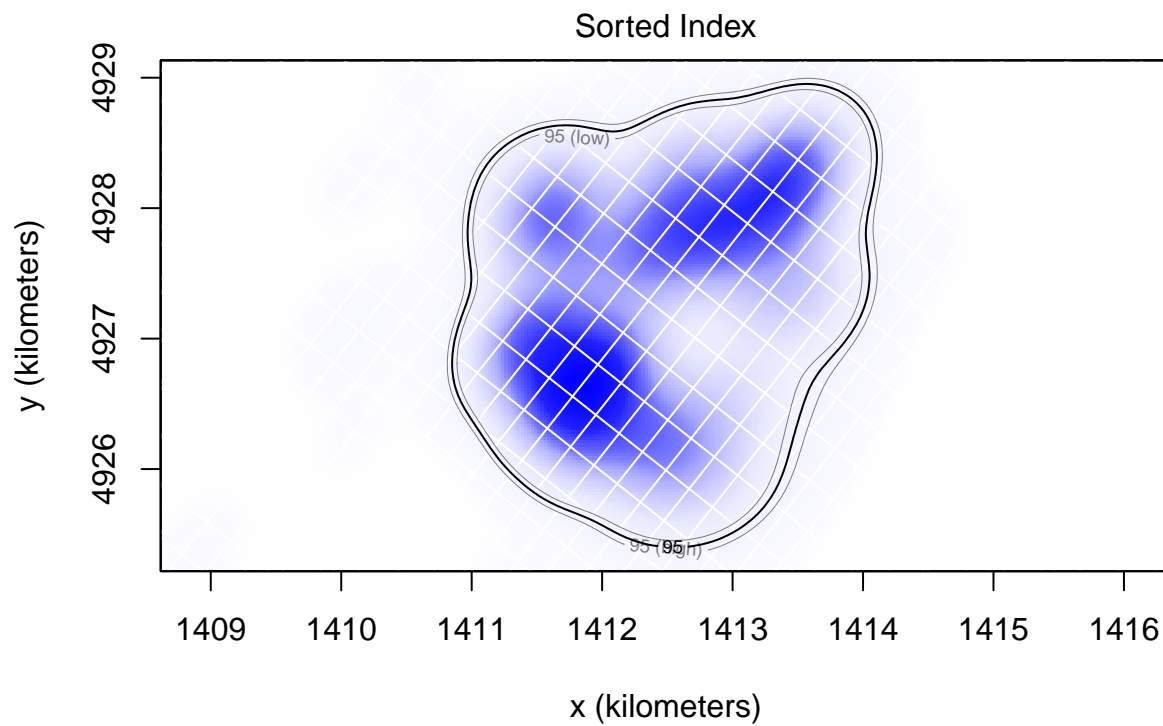
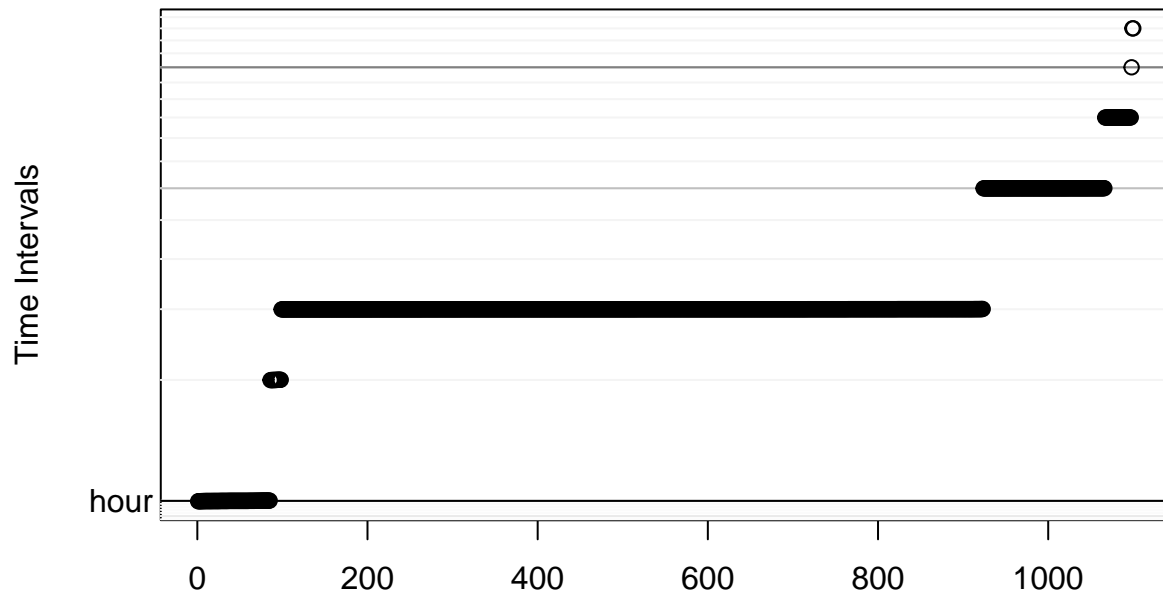
```
## [1] 912
## Minimum sampling interval of 59.9 minutes in 45512
##
##          ΔAIC ΔRMSPE (m) DOF[area]
## OU anisotropic    0.000000  11.301191  941.5755
## OUF anisotropic    1.997032  10.911905  944.1140
## OUf anisotropic   57.401865   7.375213 1041.0132
## OU               102.398751  14.997668  927.6605
## OUF              104.395637  14.561947  930.3576
## IID anisotropic  143.321028   0.000000 1100.0000
```

pHREML – OU anisotropic – ID 45512



```
## Default grid size of 45 minutes chosen for bandwidth(...,fast=TRUE).
```


45512



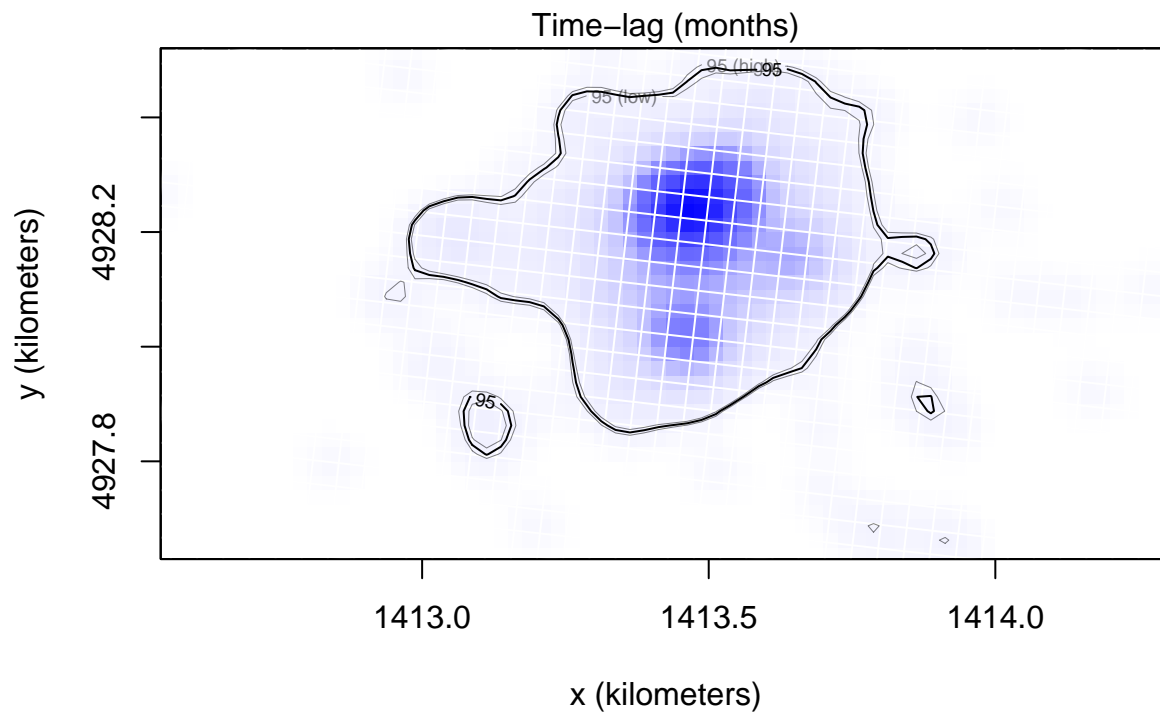
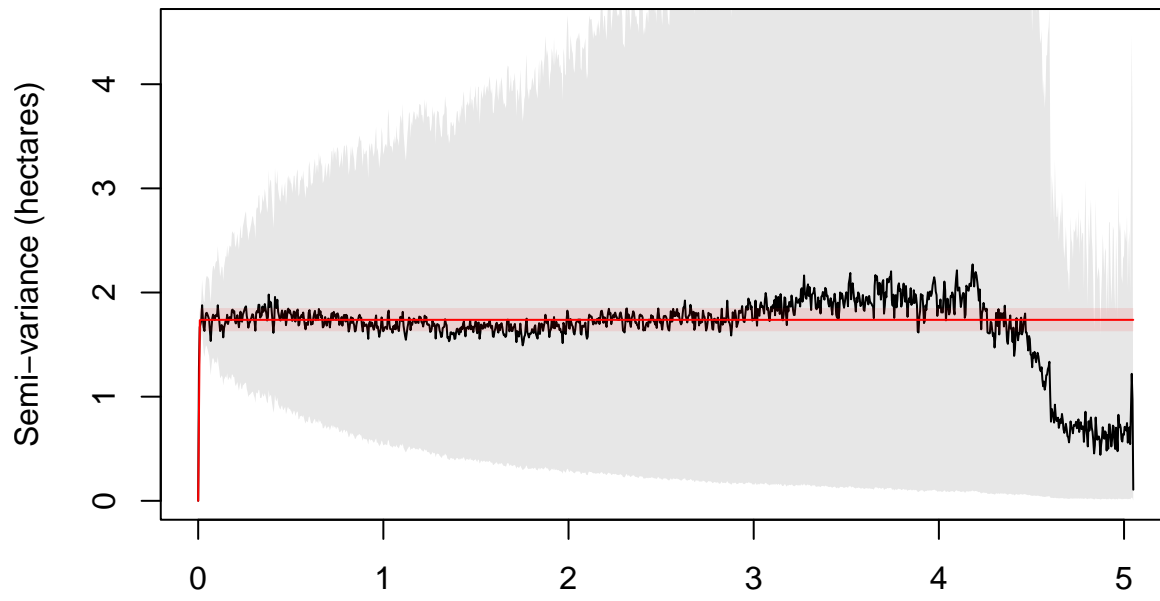
```
##      area
## 941.5755
## [1] 1101

## Minimum sampling interval of 59.9 minutes in 45513

##              ΔAIC ΔRMSPE (m) DOF[area]
## OUf anisotropic  0.000000   1.907064  936.4161
## OUΩ anisotropic  2.000000   1.907064  906.3812
```

```
## OUF anisotropic 2.000000 1.907064 936.4161
## OUf 5.692126 1.997073 934.4467
## OUF 7.692126 1.997073 934.4467
## OU anisotropic 15.527871 1.068795 944.9249
## IID anisotropic 54.242845 0.000000 999.0000
```

pHREML – OUf anisotropic – ID 45513

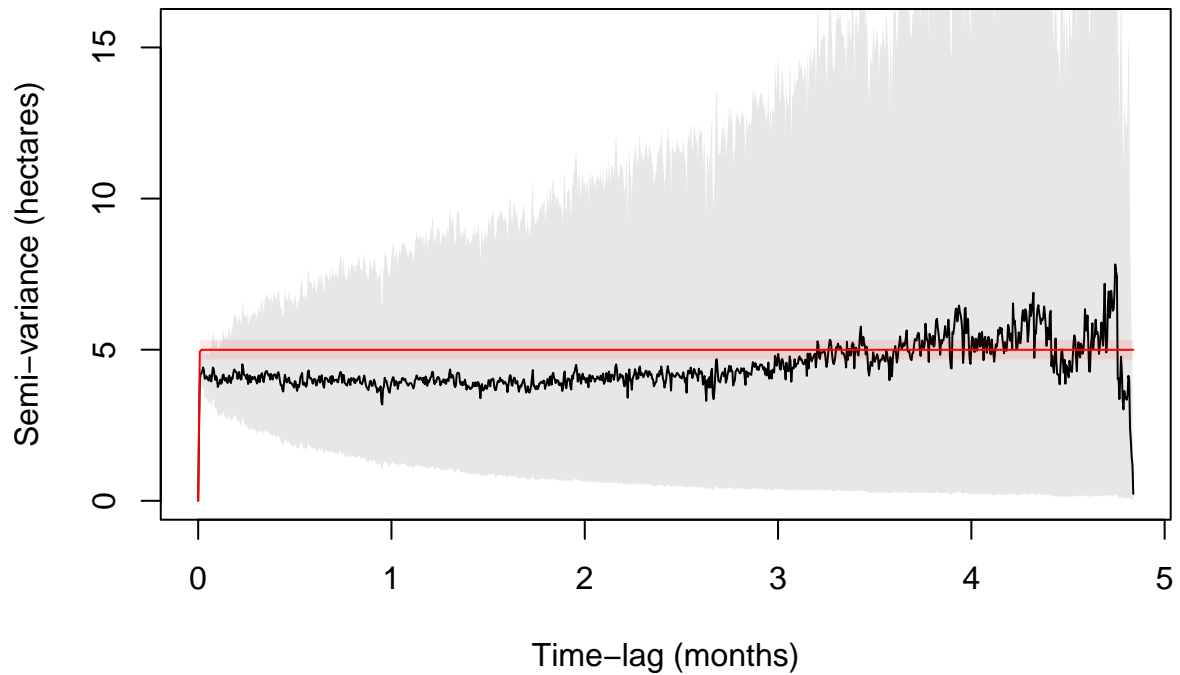


```
## area
## 936.4161
## [1] 1000
```

```
## Minimum sampling interval of 59.9 minutes in 45514
```

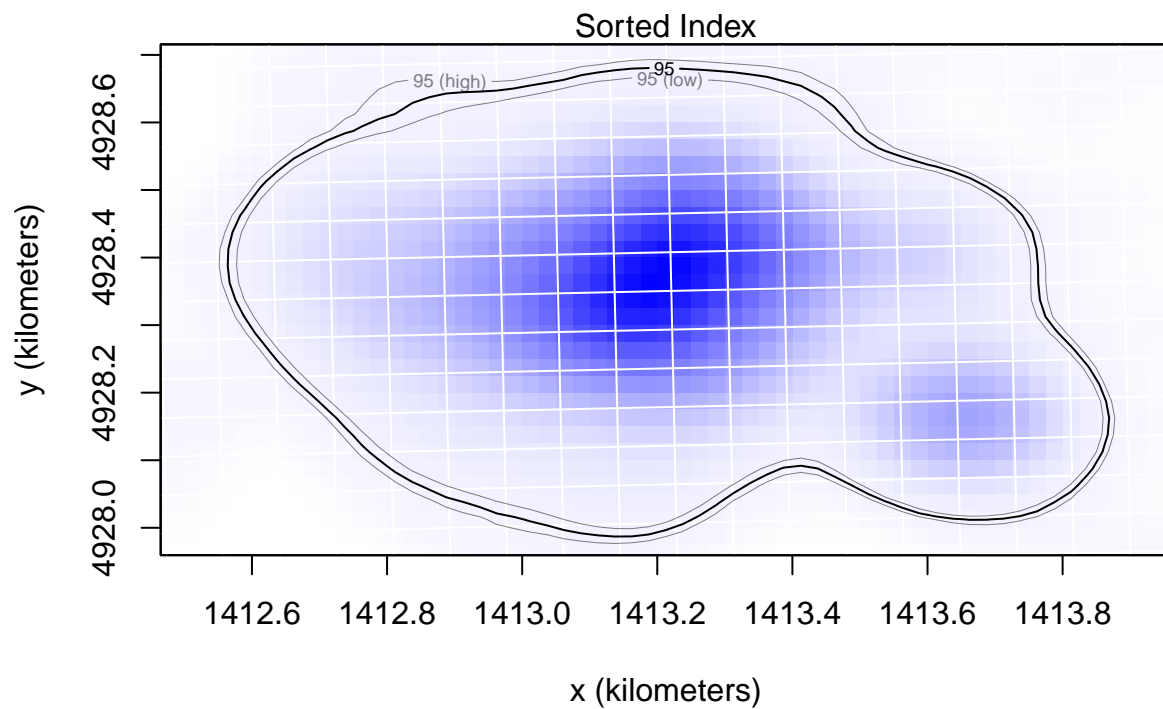
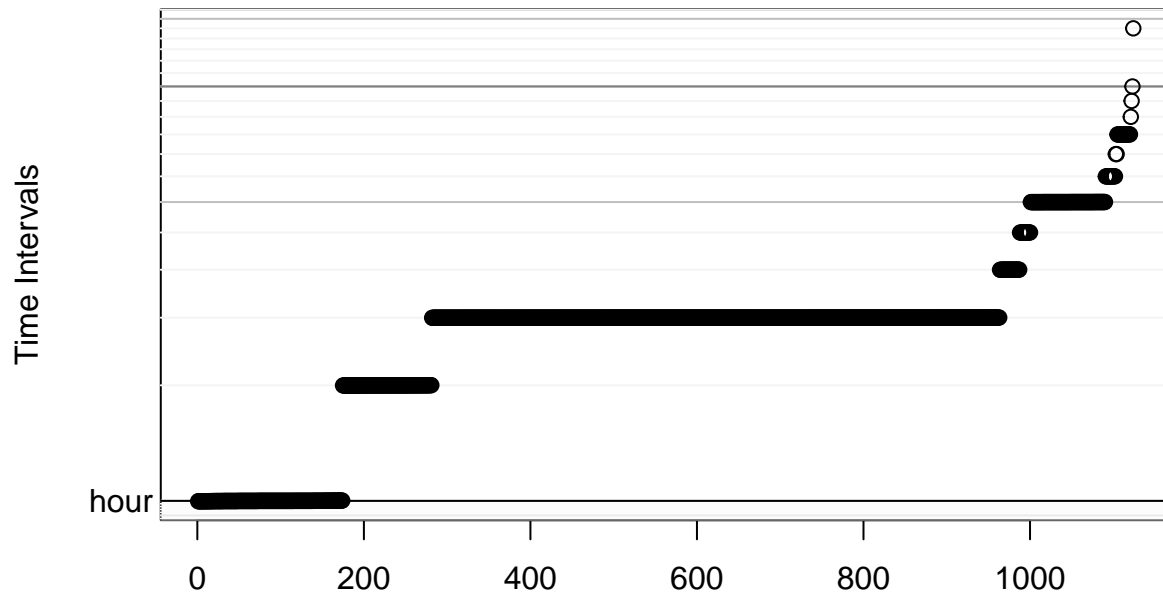
```
##           ΔAIC ΔRMSPE (m) DOF[area]
## OU anisotropic    0.000000    4.027020  1001.722
## OUF anisotropic    1.997307    3.942493  1003.638
## OUf anisotropic   15.378231    4.118174  1013.689
## IID anisotropic   55.374160    0.000000   1124.000
## OU                156.194320    4.234378  1002.376
## OUF                158.191681    4.149972  1004.292
```

pHREML – OU anisotropic – ID 45514



```
## Default grid size of 44.9958333333333 minutes chosen for bandwidth(...,fast=TRUE).
```

45514



```
##      area
## 1001.722
## [1] 1125
```

To print any specific outputs.

These are commented out but uncomment to view results (if the objects have been created).

```
for(i in 1:10) {
  # print(summary(UD1w_pHREML_list[[i]]))
}
```

```
# print(summary(UD1w_pHREML_list[[i]])$CI)
# plot(UD1w_pHREML_list[[i]], level.UD = c(0.5, 0.95))
# plot(UD1w_pHREML_list[[i]], level.UD = c(0.5, 0.95))
}
```

Import a spatial object of the Orokonui Ecosanctuary fence.

```
OrokonuiFence <- st_read("mapping/OrokonuiFence.shp")
```

```
## Reading layer `OrokonuiFence' from data source
##   `/Users/scottforrest/Library/CloudStorage/OneDrive-QueenslandUniversityofTechnology/MSc - Scott For
##   using driver `ESRI Shapefile'
## Simple feature collection with 2 features and 1 field
## Geometry type: POLYGON
## Dimension:      XY
## Bounding box:   xmin: 1412176 ymin: 4927554 xmax: 1413950 ymax: 4930746
## Projected CRS: NZGD2000 / New Zealand Transverse Mercator 2000
```

```
# check map
ggplot(OrokonuiFence) +
  geom_sf() +
  theme_classic()
```



Extract contours for further analysis.

```
# use the ML estimated UD
# UD_ctmm_contour_list <- map(UD1w_ML_list, SpatialPolygonsDataFrame.UD,
#                               level.UD = c(0.5, 0.95),
#                               level = 0.95)
```

```

# use the perturbative Hybrid REML (pHREML) estimated UD
UD_ctmm_contour_list <- map(UD1w_pHREML_list, SpatialPolygonsDataFrame.UD,
                             level.UD = c(0.5, 0.95),
                             level = 0.95)

# create a df with the spatial objects
UD_ctmm_sf <- map(UD_ctmm_contour_list, st_as_sf, crs = 4326) %>%
  map(., st_transform, crs = 4326) %>%
  bind_rows() %>% mutate(id = substr(name, start = 1, stop = 5),
                          age = rep(c(1, 10, 5, 1, 3, 2, 2, 3, 10, 8), each = 6),
                          contour = substr(name, start = 7, stop = 8),
                          interval = substr(name, start = 11, stop = 13),
                          age_group = ifelse(age < 4,
                                              "3 years or younger (n = 6)",
                                              "5 years or older (n = 4)"))

UD_ctmm_sf

## Simple feature collection with 60 features and 6 fields
## Geometry type: GEOMETRY
## Dimension: XY
## Bounding box: xmin: 170.5661 ymin: -45.79998 xmax: 170.6251 ymax: -45.72836
## Geodetic CRS: WGS 84
## First 10 features:
##
##          name          geometry      id age contour
## 45505 50% low 45505 50% low MULTIPOLYGON (((170.5884 -4... 45505 1 50
## 45505 50% est 45505 50% est MULTIPOLYGON (((170.5878 -4... 45505 1 50
## 45505 50% high 45505 50% high MULTIPOLYGON (((170.5874 -4... 45505 1 50
## 45505 95% low 45505 95% low MULTIPOLYGON (((170.5691 -4... 45505 1 95
## 45505 95% est 45505 95% est MULTIPOLYGON (((170.5685 -4... 45505 1 95
## 45505 95% high 45505 95% high MULTIPOLYGON (((170.5679 -4... 45505 1 95
## 45506 50% low 45506 50% low MULTIPOLYGON (((170.5972 -4... 45506 10 50
## 45506 50% est 45506 50% est MULTIPOLYGON (((170.5969 -4... 45506 10 50
## 45506 50% high 45506 50% high MULTIPOLYGON (((170.5969 -4... 45506 10 50
## 45506 95% low 45506 95% low MULTIPOLYGON (((170.5886 -4... 45506 10 95
##
##          interval      age_group
## 45505 50% low      low 3 years or younger (n = 6)
## 45505 50% est      est 3 years or younger (n = 6)
## 45505 50% high     hig 3 years or younger (n = 6)
## 45505 95% low      low 3 years or younger (n = 6)
## 45505 95% est      est 3 years or younger (n = 6)
## 45505 95% high     hig 3 years or younger (n = 6)
## 45506 50% low      low 5 years or older (n = 4)
## 45506 50% est      est 5 years or older (n = 4)
## 45506 50% high     hig 5 years or older (n = 4)
## 45506 95% low      low 5 years or older (n = 4)

```

Plotting for manuscript

```

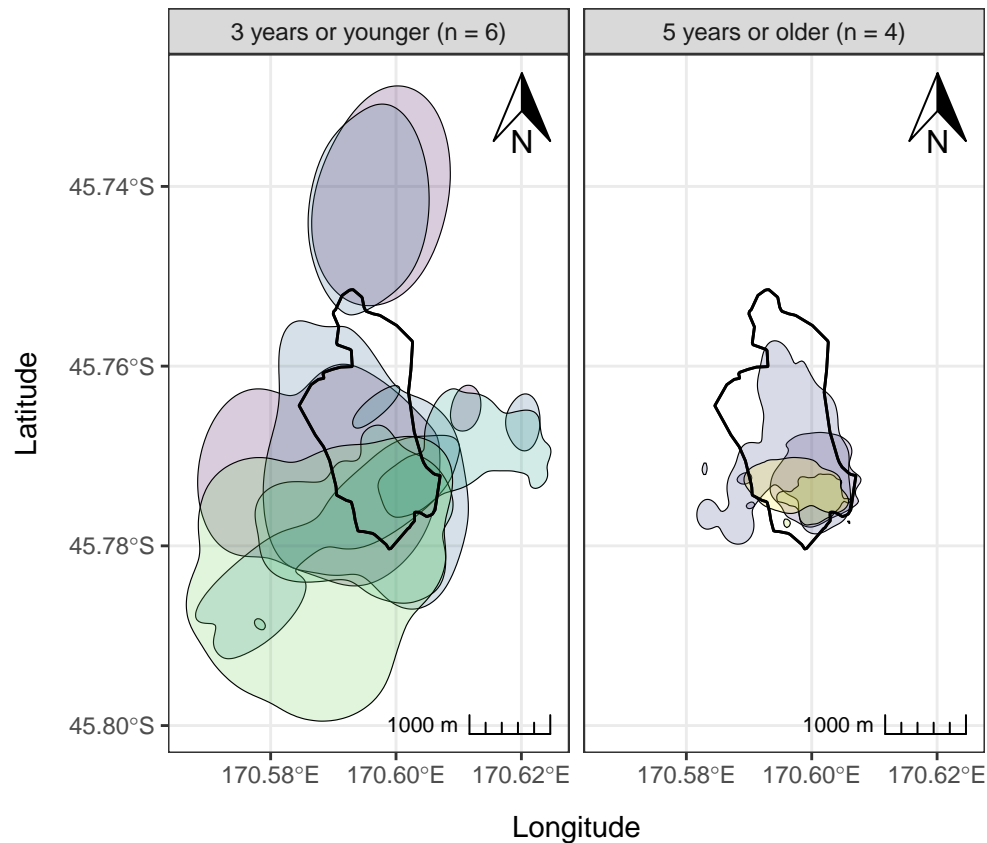
ggplot() +
  geom_sf(data = UD_ctmm_sf %>% dplyr::filter(contour == 95 & interval == "est"),
          aes(fill = factor(id)),
          alpha = 0.2,

```

```

        colour = "black",
        size = 0.25) +
# to also add the 50% contours - makes it a bit messy in this case
# geom_sf(data = UD_ctmm_sf %>% dplyr::filter(contour == 50 & interval == "est"),
#         # aes(fill = factor(id)),
#         alpha = 0,
#         colour = "black",
#         size = 0.25,
#         linetype = "dashed") +
geom_sf(data = OrokonuiFence, colour = "black", fill = NA, lwd = 0.5) +
coord_sf() +
scale_y_continuous("Latitude", breaks = seq(-45.74, -45.80, by = -0.02)) +
scale_x_continuous("Longitude", breaks = seq(170.56, 170.62, by = 0.02)) +
scale_fill_viridis_d(name = "ID") +
facet_wrap(vars(age_group)) +
theme_bw() +
theme(legend.position = "none",
      axis.title.y = element_text(margin = margin(t = 0, r = 10, b = 0, l = 0)),
      axis.title.x = element_text(margin = margin(t = 10, r = 0, b = 0, l = 0))) +
ggspatial::annotation_north_arrow(location = "tr",
                                   which_north = "true",
                                   height = unit(1, "cm"),
                                   width = unit(.75, "cm")) +
ggspatial::annotation_scale(location = "br",
                             style = "ticks",
                             bar_cols = c("grey60", "white"),
                             height = unit(0.25, "cm"))

```



```
filetypes <- c("pdf", "tiff", "jpeg", "png")

for(i in 1:length(filetypes)) {
  ggsave(filename = paste0("Graphical outputs/",
    "all_home_ranges_wAKDE_young_old_", Sys.Date(), ".",
    filetypes[i]),
    width = 180,
    height = 150,
    units = "mm",
    dpi = 800)
}
```

Determine the area contained within the isopleths

```
UD_ctmm_area_50 <- vector(mode = "numeric", length = 10)
UD_ctmm_area_95 <- vector(mode = "numeric", length = 10)

for(i in 1:10) {
  # estimated 50% contour
  UD_ctmm_area_50[[i]] <- UD_ctmm_contour_list[[i]]@polygons[[2]]@area
  # estimated 95% contour
  UD_ctmm_area_95[[i]] <- UD_ctmm_contour_list[[i]]@polygons[[5]]@area
}
```


Add additional information about each kākā and create data frame

Familiarity is the number of years that a kākā had been in Orokonui Ecosanctuary, as we were trying to determine whether the kākā's age was leading to small home ranges, or whether it was how long each kākā had been in Orokonui, as we thought that individuals which had been recently released in Orokonui might have been more exploratory, even though they were older. For most individuals their age is the same as their familiarity, as they fledged in Orokonui or were released as juveniles, but there is one 10 year old individual that was released as an adult. This individual had a very small home range, which gave more weight to the 'age' hypothesis rather than 'familiarity'.

```
id <- 45505:45514
age <- c(1, 10, 5, 1, 3, 2, 2, 3, 10, 8)
familiarity <- c(1, 10, 5, 1, 3, 2, 2, 3, 1, 8)
sex <- c("M", "M", "M", "F", "F", "F", "F", "M", "M", "F")
origin <- c("Orokonui", "Orokonui", "Captive", "Orokonui", "Orokonui", "Orokonui",
           "Orokonui", "Captive", "Captive", "Orokonui")

all_contours_95_df <- data.frame("ID" = id,
                                "Age" = age,
                                "Familiarity" = familiarity,
                                "Sex" = sex,
                                "Origin" = origin,
                                "UD50_area" = UD_ctmm_area_50,
                                "UD95_area" = UD_ctmm_area_95,
                                "UD50_area_km2" = UD_ctmm_area_50/1e6,
                                "UD95_area_km2" = UD_ctmm_area_95/1e6) %>%
  mutate(age_group = ifelse(Age < 4, "3 years or younger (n = 6)",
                             "5 years or older (n = 4)"))

head(all_contours_95_df)
```

```
##      ID Age Familiarity Sex   Origin UD50_area UD95_area UD50_area_km2
## 1 45505   1           1   M Orokonui 1860836.7 9924325.7    1.8608367
## 2 45506  10           10   M Orokonui 145453.7  987249.6    0.1454537
## 3 45507   5           5   M  Captive 251523.8 2377871.7    0.2515238
## 4 45508   1           1   F Orokonui 1902419.0 9705908.9    1.9024190
## 5 45509   3           3   F Orokonui 241209.0 3044136.8    0.2412090
## 6 45510   2           2   F Orokonui 190743.3 1823074.1    0.1907433
##      UD95_area_km2      age_group
## 1      9.9243257 3 years or younger (n = 6)
## 2      0.9872496  5 years or older (n = 4)
## 3      2.3778717  5 years or older (n = 4)
## 4      9.7059089 3 years or younger (n = 6)
## 5      3.0441368 3 years or younger (n = 6)
## 6      1.8230741 3 years or younger (n = 6)
```

```
max(all_contours_95_df$UD95_area_km2) / min(all_contours_95_df$UD95_area_km2)
```

```
## [1] 29.16754
```

```
# size difference between largest and smallest UD's = 29 fold-difference
```

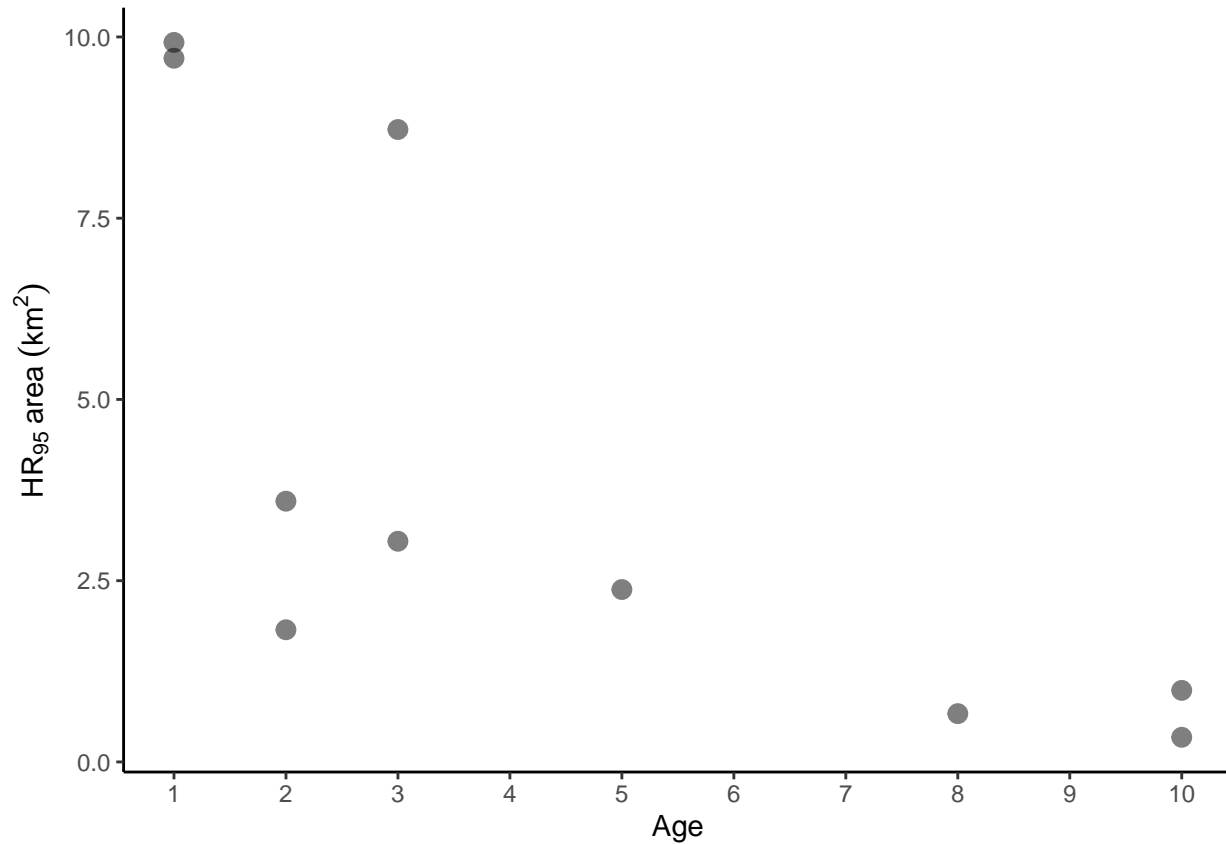
Convert to utilisation distributions (continuous probability surfaces).

Calculating the area contained within UD isopleths, which will be in m^2 .

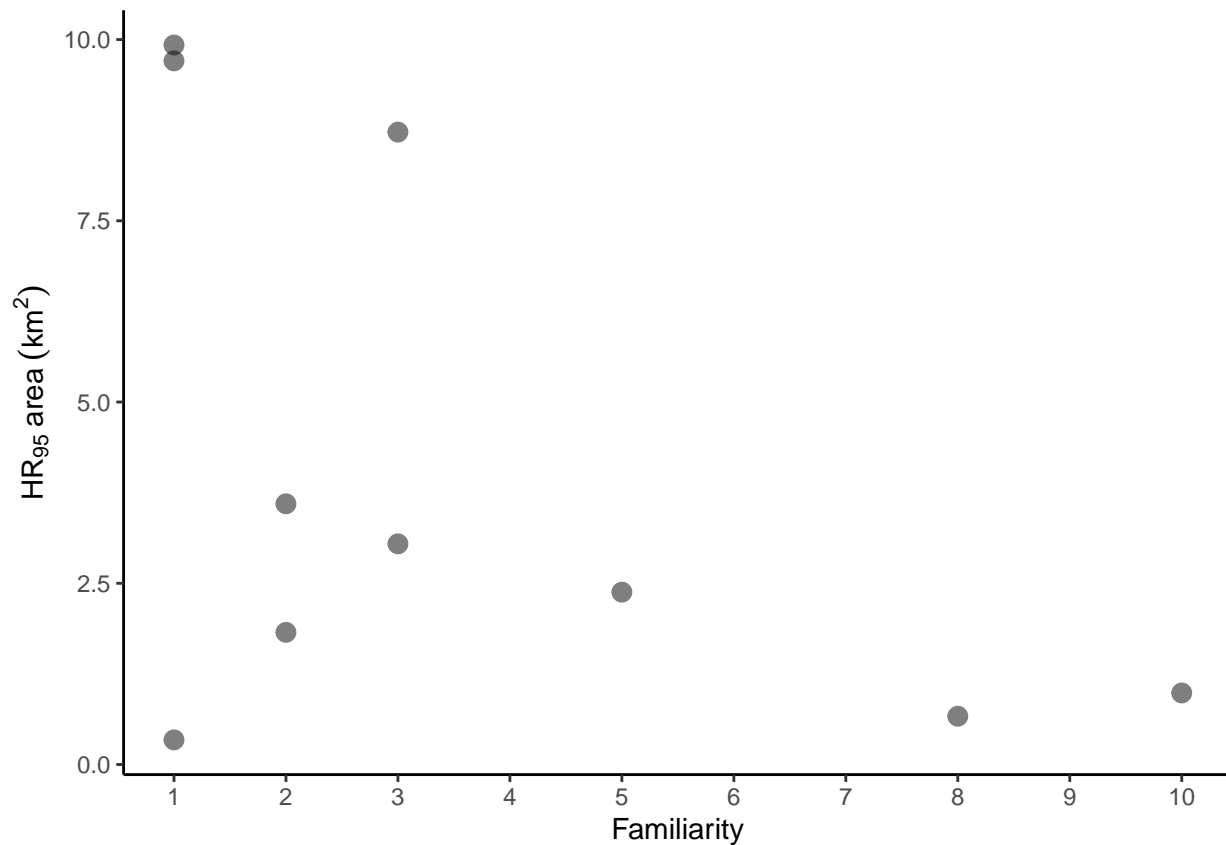
Add in individual-level covariates and create a data frame.

Plot

```
all_contours_95_df %>% ggplot(aes(Age, UD95_area_km2)) +  
  geom_point(alpha = 0.5, size = 3) +  
  scale_x_continuous(breaks = c(1:10)) +  
  labs(y = expression(HR[95]~area~(km^2))) +  
  theme_classic()
```



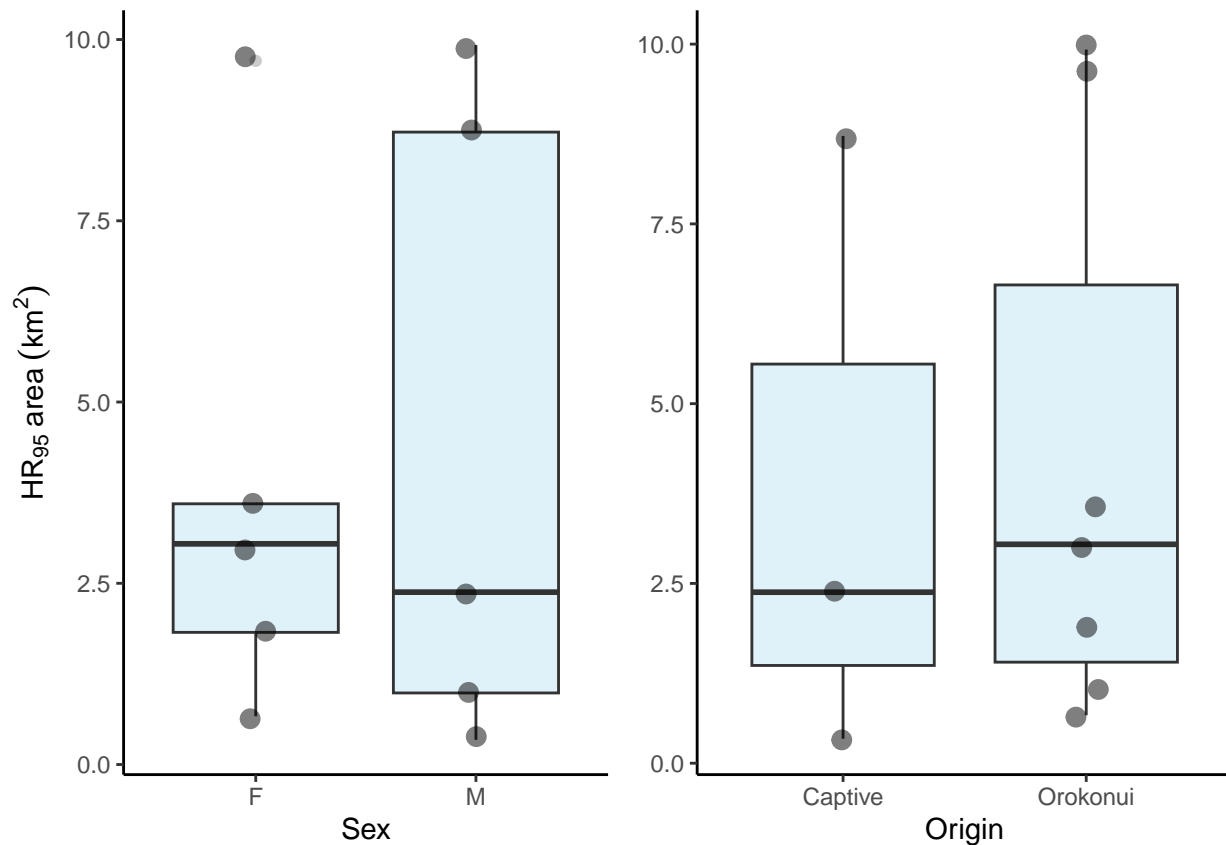
```
all_contours_95_df %>% ggplot(aes(Familiarity, UD95_area_km2)) +  
  geom_point(alpha = 0.5, size = 3) +  
  scale_x_continuous(breaks = c(1:10)) +  
  labs(y = expression(HR[95]~area~(km^2))) +  
  theme_classic()
```



```
sexplot <- all_contours_95_df %>% ggplot(aes(Sex, UD95_area_km2)) +
  geom_boxplot(alpha = 0.25, fill = "skyblue") +
  # geom_violin(alpha = 0.25, fill = "skyblue") +
  geom_jitter(width = 0.05, size = 3, alpha = 0.5) +
  labs(y = expression(HR[95]~area~(km^2))) +
  theme_classic()

originplot <- all_contours_95_df %>% ggplot(aes(Origin, UD95_area_km2)) +
  geom_boxplot(alpha = 0.25, fill = "skyblue") +
  # geom_violin(alpha = 0.25, fill = "skyblue") +
  geom_jitter(width = 0.05, size = 3, alpha = 0.5) +
  theme_classic()

ggarrange(sexplot, originplot + rremove("ylab"))
```



```
# save objects in multiple filetypes
for(i in 1:length(filetypes)){
  ggsave(filename = paste0("Graphical outputs/",
    "sex_age_plots_", Sys.Date(), ".",
    filetypes[i]),
    width = 160,
    height = 100,
    units = "mm",
    dpi = 800)
}
```

Statistical analysis of home range area

Now that we have extracted the area from the contours, we can use those values in statistical models such as GLMs, to assess whether there are any significant differences in home range area due to factors such as age and sex.

Fit the models

```
# four models used for model selection
area_age_glm <- glm(UD95_area_km2 ~ Age,
  data = all_contours_95_df,
  family = Gamma(link = "log"))

area_familiarity_glm <- glm(UD95_area_km2 ~ Familiarity,
  data = all_contours_95_df,
```

```

        family = Gamma(link = "log"))

area_sex_glm <- glm(UD95_area_km2 ~ Sex,
                  data = all_contours_95_df,
                  family = Gamma(link = "log"))

area_origin_glm <- glm(UD95_area_km2 ~ Origin,
                     data = all_contours_95_df,
                     family = Gamma(link = "log"))

area_null_glm <- glm(UD95_area_km2 ~ 1,
                   data = all_contours_95_df,
                   family = Gamma(link = "log"))

```

Model summaries of age model

```

# model with age
summary(area_age_glm)

##
## Call:
## glm(formula = UD95_area_km2 ~ Age, family = Gamma(link = "log"),
##      data = all_contours_95_df)
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  2.33979    0.30026   7.792 5.27e-05 ***
## Age         -0.28734    0.05333  -5.388 0.000655 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Gamma family taken to be 0.3256456)
##
##      Null deviance: 10.1179  on 9  degrees of freedom
## Residual deviance:  2.7417  on 8  degrees of freedom
## AIC: 40.088
##
## Number of Fisher Scoring iterations: 5
AIC(area_age_glm)

## [1] 40.08817
anova(area_age_glm, test="F")

## Analysis of Deviance Table
##
## Model: Gamma, link: log
##
## Response: UD95_area_km2
##
## Terms added sequentially (first to last)
##
##
##      Df Deviance Resid. Df Resid. Dev      F    Pr(>F)

```

```
## NULL          9      10.1179
## Age   1    7.3762      8      2.7417 22.651 0.001428 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
r.squaredLR(area_age_glm)
```

```
## [1] 0.7592754
## attr("adj.r.squared")
## [1] 0.7653702
```

```
confint(area_age_glm)
```

```
## Waiting for profiling to be done...
```

```
##           2.5 %      97.5 %
## (Intercept) 1.7917699 2.9596986
## Age        -0.3867466 -0.1798822
```

Model summaries of familiarity model

```
# model with age
```

```
summary(area_familiarity_glm)
```

```
##
## Call:
## glm(formula = UD95_area_km2 ~ Familiarity, family = Gamma(link = "log"),
##      data = all_contours_95_df)
##
## Coefficients:
##           Estimate Std. Error t value Pr(>|t|)
## (Intercept)  2.06945    0.34236   6.045 0.000308 ***
## Familiarity -0.23166    0.07333  -3.159 0.013408 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Gamma family taken to be 0.4752928)
##
## Null deviance: 10.1179 on 9 degrees of freedom
## Residual deviance: 6.5156 on 8 degrees of freedom
## AIC: 49.361
##
## Number of Fisher Scoring iterations: 5
```

```
AIC(area_familiarity_glm)
```

```
## [1] 49.3608
```

```
anova(area_familiarity_glm, test="F")
```

```
## Analysis of Deviance Table
##
## Model: Gamma, link: log
##
## Response: UD95_area_km2
##
## Terms added sequentially (first to last)
```

```
##
##
##           Df Deviance Resid. Df Resid. Dev      F Pr(>F)
## NULL                      9      10.1179
## Familiarity 1    3.6023          8      6.5156 7.579 0.02494 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
r.squaredLR(area_familiarity_glm)
```

```
## [1] 0.3915488
## attr("adj.r.squared")
## [1] 0.3946919
```

```
confint(area_familiarity_glm)
```

```
## Waiting for profiling to be done...
```

```
##           2.5 %      97.5 %
## (Intercept) 1.4365759 2.78387860
## Familiarity -0.3647995 -0.07404951
```

Model summaries of sex model

```
# model with sex
summary(area_sex_glm)
```

```
##
## Call:
## glm(formula = UD95_area_km2 ~ Sex, family = Gamma(link = "log"),
##      data = all_contours_95_df)
##
## Coefficients:
##           Estimate Std. Error t value Pr(>|t|)
## (Intercept)  1.3263      0.4342   3.055  0.0157 *
## SexM         0.1712      0.6140   0.279  0.7875
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Gamma family taken to be 0.9425835)
##
## Null deviance: 10.118  on 9  degrees of freedom
## Residual deviance: 10.045  on 8  degrees of freedom
## AIC: 54.245
##
## Number of Fisher Scoring iterations: 6
```

```
AIC(area_sex_glm)
```

```
## [1] 54.24532
```

```
anova(area_sex_glm, test="F")
```

```
## Analysis of Deviance Table
##
## Model: Gamma, link: log
##
```

```
## Response: UD95_area_km2
##
## Terms added sequentially (first to last)
##
##
##      Df Deviance Resid. Df Resid. Dev      F Pr(>F)
## NULL                9      10.118
## Sex   1 0.073168      8      10.045 0.0776 0.7876
```

```
r.squaredLR(area_sex_glm)
```

```
## [1] 0.008351581
## attr("adj.r.squared")
## [1] 0.008418621
```

```
confint(area_sex_glm)
```

```
## Waiting for profiling to be done...
##              2.5 %    97.5 %
## (Intercept)  0.5810799 2.317249
## SexM        -1.0689425 1.411305
```

Model summaries of origin model

```
# model with kākā origin
summary(area_origin_glm)
```

```
##
## Call:
## glm(formula = UD95_area_km2 ~ Origin, family = Gamma(link = "log"),
##      data = all_contours_95_df)
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    1.3386     0.5697   2.350  0.0467 *
## OriginOrokonui  0.1082     0.6810   0.159  0.8777
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Gamma family taken to be 0.9737961)
##
##      Null deviance: 10.118  on 9  degrees of freedom
## Residual deviance: 10.094  on 8  degrees of freedom
## AIC: 54.301
##
## Number of Fisher Scoring iterations: 6
```

```
AIC(area_origin_glm)
```

```
## [1] 54.30147
```

```
anova(area_origin_glm, test="F")
```

```
## Analysis of Deviance Table
##
## Model: Gamma, link: log
```



```
##
## Response: UD95_area_km2
##
## Terms added sequentially (first to last)
##
##
##      Df Deviance Resid. Df Resid. Dev      F Pr(>F)
## NULL                9      10.118
## Origin  1 0.024235      8      10.094 0.0249 0.8786
```

```
r.squaredLR(area_origin_glm)
```

```
## [1] 0.002768081
## attr("adj.r.squared")
## [1] 0.002790301
```

```
confint(area_origin_glm)
```

```
## Waiting for profiling to be done...
##
##              2.5 %   97.5 %
## (Intercept)   0.3970024 2.708181
## OriginOrokonui -1.4032936 1.371822
```

Model summaries of null model

```
# null model (intercept only)
summary(area_null_glm)
```

```
##
## Call:
## glm(formula = UD95_area_km2 ~ 1, family = Gamma(link = "log"),
##      data = all_contours_95_df)
##
## Coefficients:
##      Estimate Std. Error t value Pr(>|t|)
## (Intercept)   1.4156      0.2939   4.817 0.000951 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Gamma family taken to be 0.8635406)
##
##      Null deviance: 10.118  on 9  degrees of freedom
## Residual deviance: 10.118  on 9  degrees of freedom
## AIC: 52.329
##
## Number of Fisher Scoring iterations: 5
```

```
AIC(area_null_glm)
```

```
## [1] 52.32919
```

```
anova(area_null_glm, test="F")
```

```
## Analysis of Deviance Table
##
## Model: Gamma, link: log
```

```
##
## Response: UD95_area_km2
##
## Terms added sequentially (first to last)
##
##
##      Df Deviance Resid. Df Resid. Dev F Pr(>F)
## NULL                9      10.118
```

```
r.squaredLR(area_null_glm)
```

```
## [1] 0
## attr("adj.r.squared")
## [1] 0
```

```
confint(area_null_glm)
```

```
## Waiting for profiling to be done...
```

```
##      2.5 %      97.5 %
## 0.8901078 2.0525576
```

Model diagnostics

Only the age and familiarity models were significant, but as they were competing hypotheses we chose one, which was the age model, as it explains the data better (the older individual that was released into Orokonui had a small home range), and has a higher R-squared. We therefore check model diagnostics and produce a plot with fitted model.

```
dfun <- function(object) {
  with(object, sum((weights * residuals^2)[weights > 0]) / df.residual)
}
```

```
dfun(area_age_glm)
```

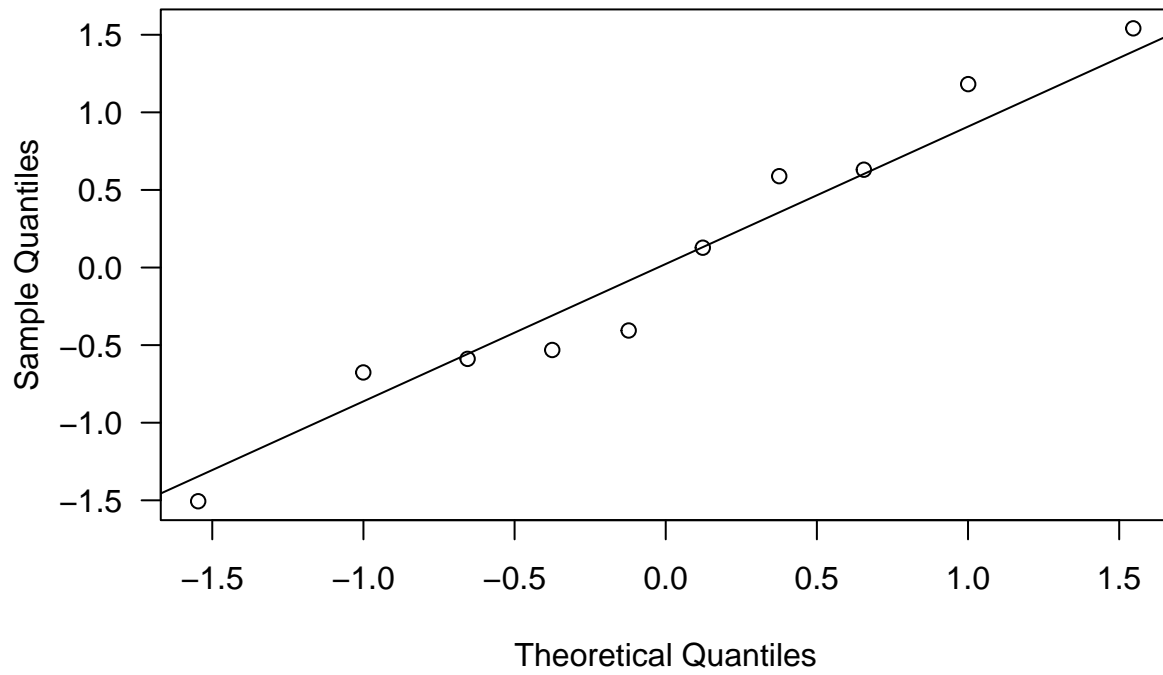
```
## [1] 0.3256456
```

```
pseudoR2 <- 1 - (area_age_glm$deviance / area_age_glm$null.deviance)
pseudoR2
```

```
## [1] 0.7290285
```

```
qr.area_age_glm <- qresid(area_age_glm)
qqnorm(qr.area_age_glm, las = 1)
qqline(qr.area_age_glm)
```

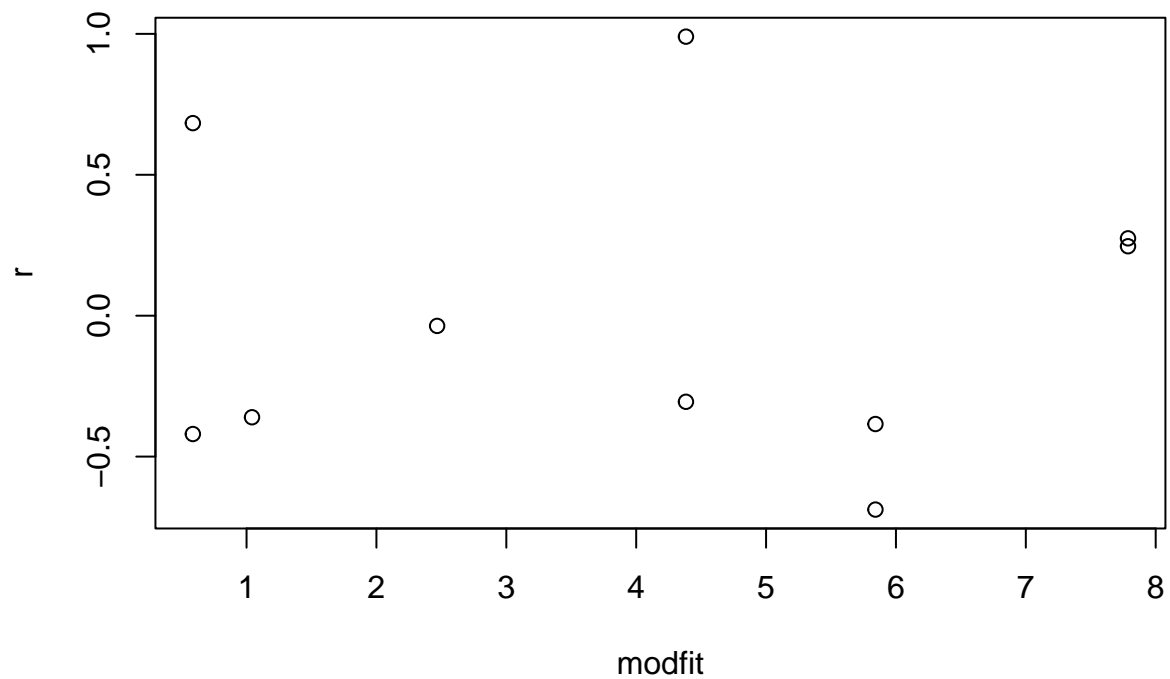
Normal Q-Q Plot



```
r<-residuals(area_age_glm,type="pearson")
modfit<-fitted(area_age_glm)

plot(r-modfit, main = "Pearson's Residuals")
```

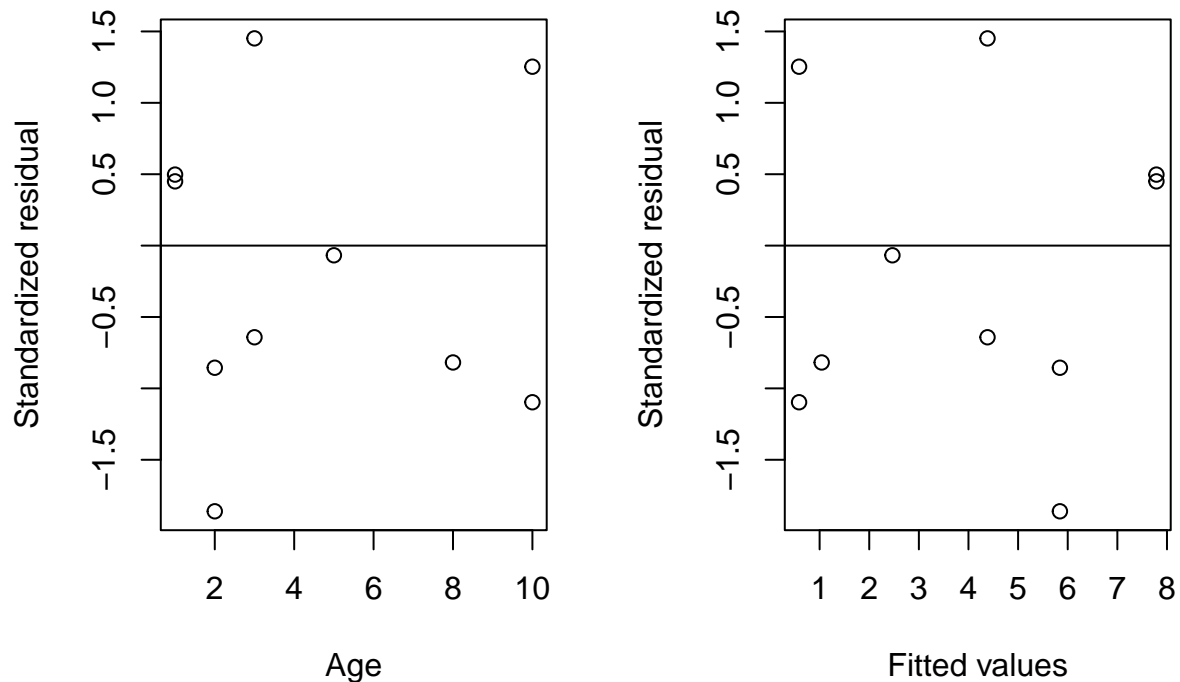
Pearson's Residuals



```
par(mfrow=c(1,2)) # change plot window to accommodate 2 plots
```

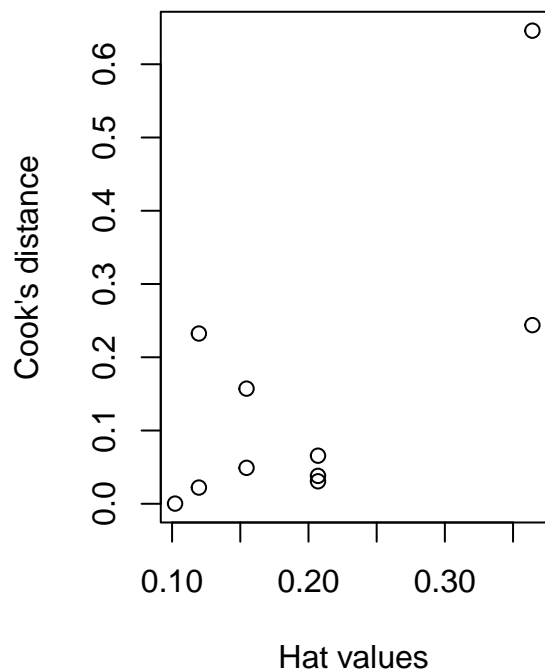
```
r = rstandard(area_age_glm)
lf <- fitted(area_age_glm)
plot(all_contours_95_df$Age, r,xlab="Age",
     ylab="Standardized residual")
abline(h=0)
```

```
plot(lf, r,xlab="Fitted values",ylab="Standardized residual")
abline(h=0)
```



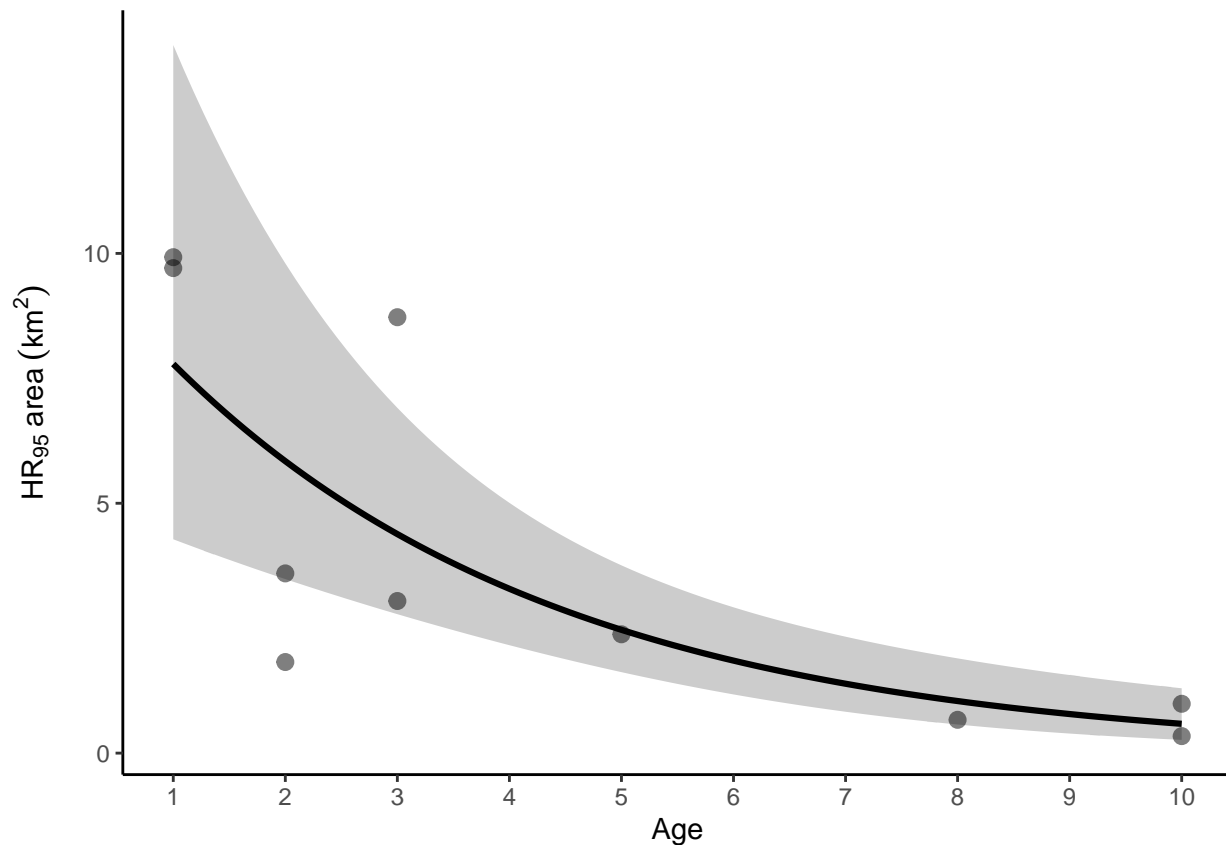
```
h <- hatvalues(area_age_glm)
cd <- cooks.distance(area_age_glm)
plot(h,cd,xlab="Hat values",ylab="Cook's distance")

par(mfrow=c(1,1)) # return to single plotting
```



```
area_age_glm_plot <- effect_plot(area_age_glm,
                                pred = Age,
                                plot.points = T,
                                interval = T,
                                point.size = 2.5,
                                point.alpha = 0.5) +
  scale_x_continuous("Age", breaks = c(1:10)) +
  ylab(expression(HR[95]~area~(km^2))) +
  theme_classic() +
  theme(axis.title.y = element_text(margin = margin(r = 10)))

area_age_glm_plot
```



```
for(i in 1:length(filetypes)){
  ggsave(filename = paste0("Graphical outputs/",
                           "age_area_glm_", Sys.Date(), ".",
                           filetypes[i]),
        width = 160,
        height = 100,
        units = "mm",
        dpi = 800)
}
```

We also check the diagnostics and create a plot for the familiarity model.

```
dfun <- function(object) {
  with(object, sum((weights * residuals^2)[weights > 0])/df.residual)
}
```

```
dfun(area_familiarity_glm)
```

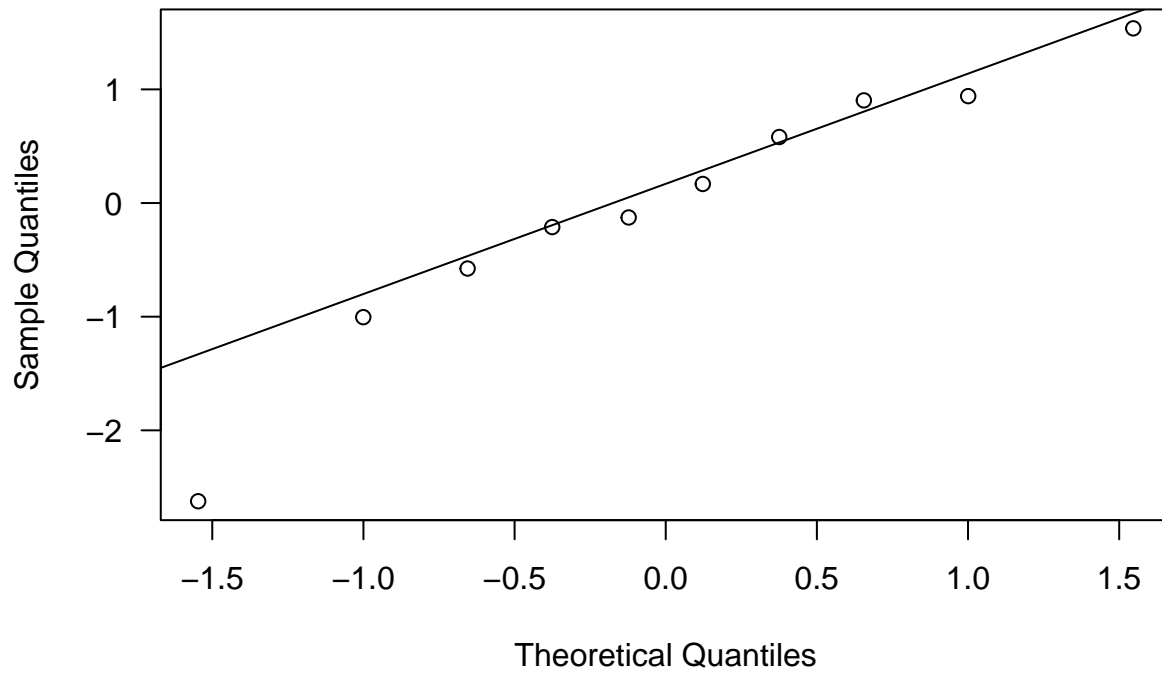
```
## [1] 0.4752928
```

```
pseudoR2 <- 1 - (area_familiarity_glm$deviance / area_familiarity_glm$null.deviance)
pseudoR2
```

```
## [1] 0.3560283
```

```
qr.area_familiarity_glm <- qresid(area_familiarity_glm)
qqnorm(qr.area_familiarity_glm, las = 1)
qqline(qr.area_familiarity_glm)
```

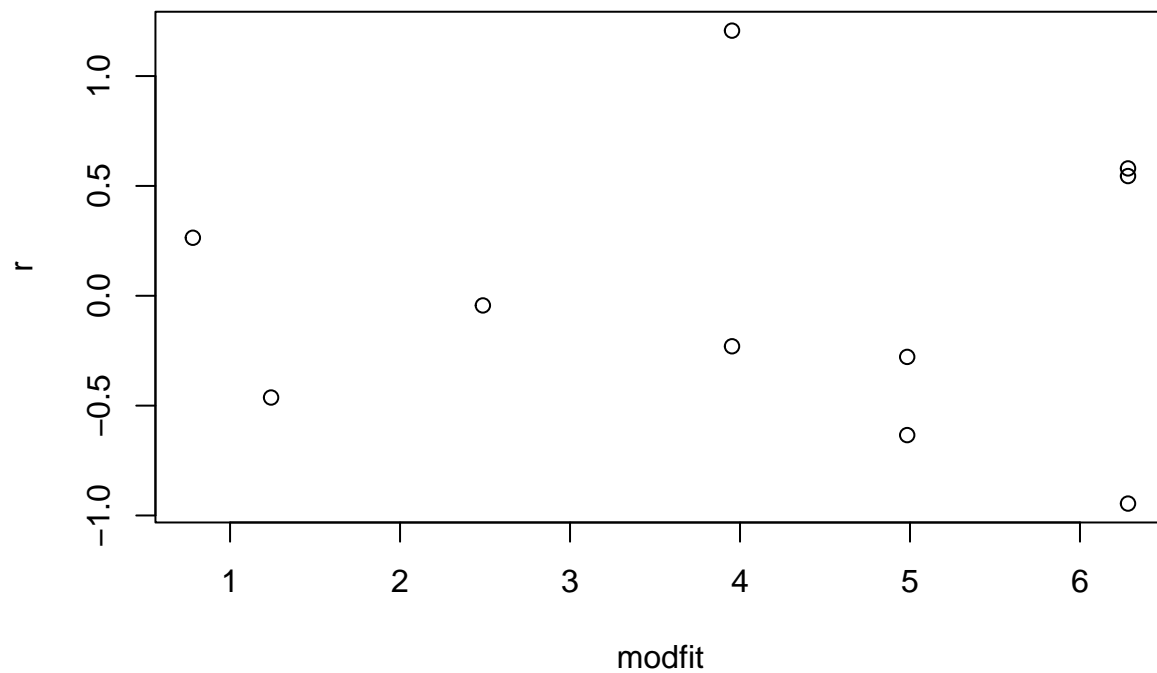
Normal Q-Q Plot



```
r<-residuals(area_familiarity_glm,type="pearson")
modfit<-fitted(area_familiarity_glm)

plot(r~modfit, main = "Pearson's Residuals")
```

Pearson's Residuals



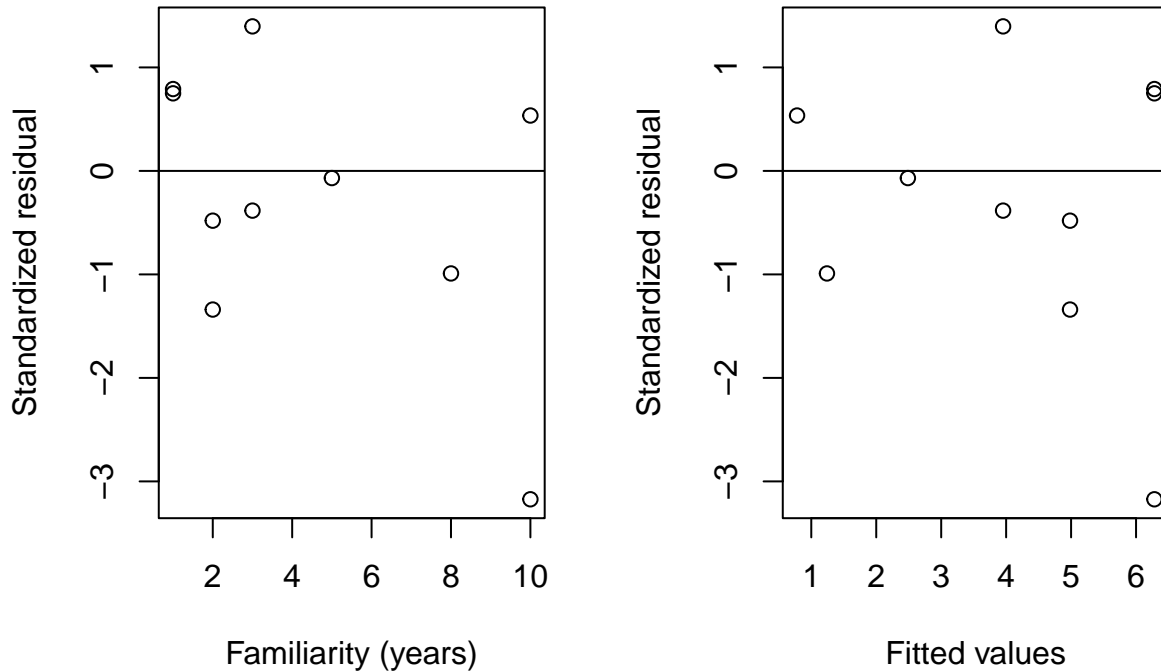
```

par(mfrow=c(1,2)) # change plot window to accommodate 2 plots

r = rstandard(area_familiarity_glm)
lf <- fitted(area_familiarity_glm)
plot(all_contours_95_df$Age, r,xlab="Familiarity (years)",
      ylab="Standardized residual")
abline(h=0)

plot(lf, r,xlab="Fitted values",ylab="Standardized residual")
abline(h=0)

```

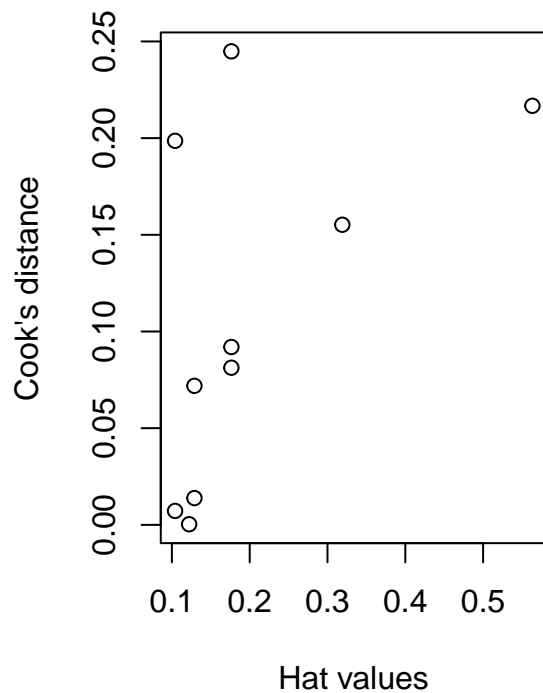


```

h <- hatvalues(area_familiarity_glm)
cd <- cooks.distance(area_familiarity_glm)
plot(h,cd,xlab="Hat values",ylab="Cook's distance")

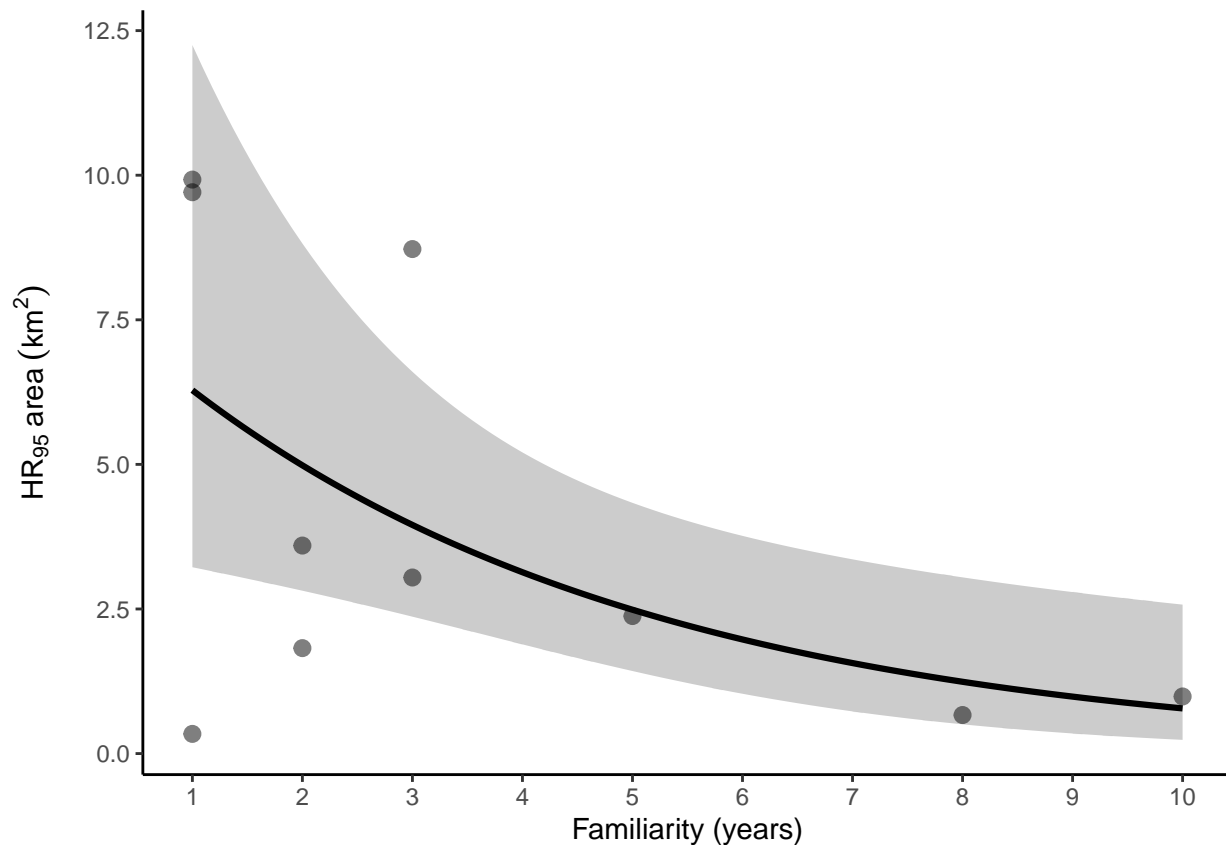
par(mfrow=c(1,1)) # return to single plotting

```

```
area_familiarity_glm_plot <- effect_plot(area_familiarity_glm,
                                         pred = Familiarity,
                                         plot.points = T,
                                         interval = T,
                                         point.size = 2.5,
                                         point.alpha = 0.5) +
  scale_x_continuous("Familiarity (years)", breaks = c(1:10)) +
  ylab(expression(HR[95] ~ area ~ (km^2))) +
  theme_classic() +
  theme(axis.title.y = element_text(margin = margin(r = 10)))

area_familiarity_glm_plot
```



```
for(i in 1:length(filetypes)){
  ggsave(filename = paste0("Graphical outputs/",
                            "age_familiarity_glm_", Sys.Date(), ".",
                            filetypes[i]),
          width = 160,
          height = 100,
          units = "mm",
          dpi = 800)
}
```

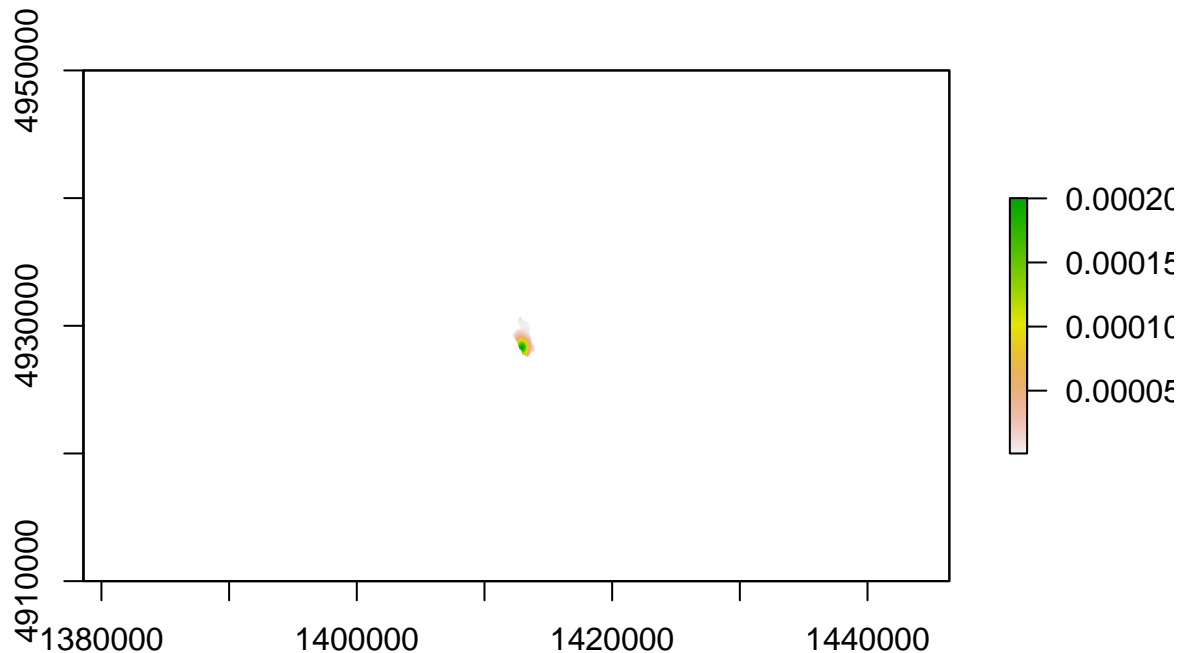
Calculate the overlap between the UD and the Orokonui Ecosanctuary fence

For checking the overlap between the fence of Orokonui and each UD. This calculation is a *summation of the values inside the cells* (i.e. the probability values), rather than the number of cells, as we want to approximate the time each kākā spent inside the sanctuary.

```
raster_UD_list <- map(UD1w_pHREML_list, raster, DF = "PMF")
# for(i in 1:10) raster::plot(raster_UD_list[[i]])

# checking that the cell values add up to 1
# for(i in 1:10) print(cellStats(raster_UD_list[[i]], sum))

# testing for a single UD
plot(mask(raster_UD_list[[1]], OrokonuiFence))
```



```
cellStats(mask(raster_UD_list[[1]], OrokonuiFence), sum)
```

```
## [1] 0.2506134
```

```
inside_overlap <- vector(mode = "numeric", length = 10)
```

```
for (i in 1:10){
  inside_overlap[[i]] <- cellStats(mask(raster_UD_list[[i]], OrokonuiFence), sum)
  print(inside_overlap[[i]])
}
```

```
## [1] 0.2506134
```

```
## [1] 0.9458736
```

```
## [1] 0.9070769
```

```
## [1] 0.4071398
```

```
## [1] 0.7316322
```

```
## [1] 0.1868212
```

```
## [1] 0.3452734
```

```
## [1] 0.1680315
```

```
## [1] 0.977431
```

```
## [1] 0.969272
```

```
# adding to data frame with inside and outside overlap
```

```
all_contours_95_df <- all_contours_95_df %>%
  mutate(inside = inside_overlap, outside = 1 - inside_overlap)
```

```
all_contours_95_df
```

```
##      ID Age Familiarity Sex   Origin  UD50_area UD95_area UD50_area_km2
## 1  45505   1           1   M Orokonui 1860836.70 9924325.7   1.86083670
## 2  45506  10           10  M Orokonui 145453.66 987249.6   0.14545366
## 3  45507   5           5   M Captive 251523.82 2377871.7   0.25152382
## 4  45508   1           1   F Orokonui 1902418.95 9705908.9   1.90241895
## 5  45509   3           3   F Orokonui 241208.96 3044136.8   0.24120896
## 6  45510   2           2   F Orokonui 190743.30 1823074.1   0.19074330
```

```
## 7 45511 2 2 F Orokonui 701001.13 3596511.3 0.70100113
## 8 45512 3 3 M Captive 2209902.46 8723160.6 2.20990246
## 9 45513 10 1 M Captive 31690.85 340252.4 0.03169085
## 10 45514 8 8 F Orokonui 79866.68 666430.1 0.07986668
```

```
## UD95_area_km2 age_group inside outside
## 1 9.9243257 3 years or younger (n = 6) 0.2506134 0.74938663
## 2 0.9872496 5 years or older (n = 4) 0.9458736 0.05412637
## 3 2.3778717 5 years or older (n = 4) 0.9070769 0.09292314
## 4 9.7059089 3 years or younger (n = 6) 0.4071398 0.59286017
## 5 3.0441368 3 years or younger (n = 6) 0.7316322 0.26836781
## 6 1.8230741 3 years or younger (n = 6) 0.1868212 0.81317883
## 7 3.5965113 3 years or younger (n = 6) 0.3452734 0.65472657
## 8 8.7231606 3 years or younger (n = 6) 0.1680315 0.83196848
## 9 0.3402524 5 years or older (n = 4) 0.9774310 0.02256905
## 10 0.6664301 5 years or older (n = 4) 0.9692720 0.03072801
```

```
max(all_contours_95_df$UD95_area_km2) / min(all_contours_95_df$UD95_area_km2)
```

```
## [1] 29.16754
```

```
all_contours_95_df %>% group_by(age_group) %>%
  summarise(mean_UD50km2 = mean(UD50_area_km2),
            mean_UD95km2 = mean(UD95_area_km2),
            meanUD_outside = mean(outside),
            sd_UD50km2 = sd(UD50_area_km2),
            sd_UD95km2 = sd(UD95_area_km2),
            sdUD_outside = sd(outside))
```

```
## # A tibble: 2 x 7
```

```
## age_group mean_UD50km2 mean_UD95km2 meanUD_outside sd_UD50km2 sd_UD95km2
## <chr> <dbl> <dbl> <dbl> <dbl> <dbl>
## 1 3 years or you~ 1.18 6.14 0.652 0.909 3.70
## 2 5 years or old~ 0.127 1.09 0.0501 0.0951 0.896
## # i 1 more variable: sdUD_outside <dbl>
```

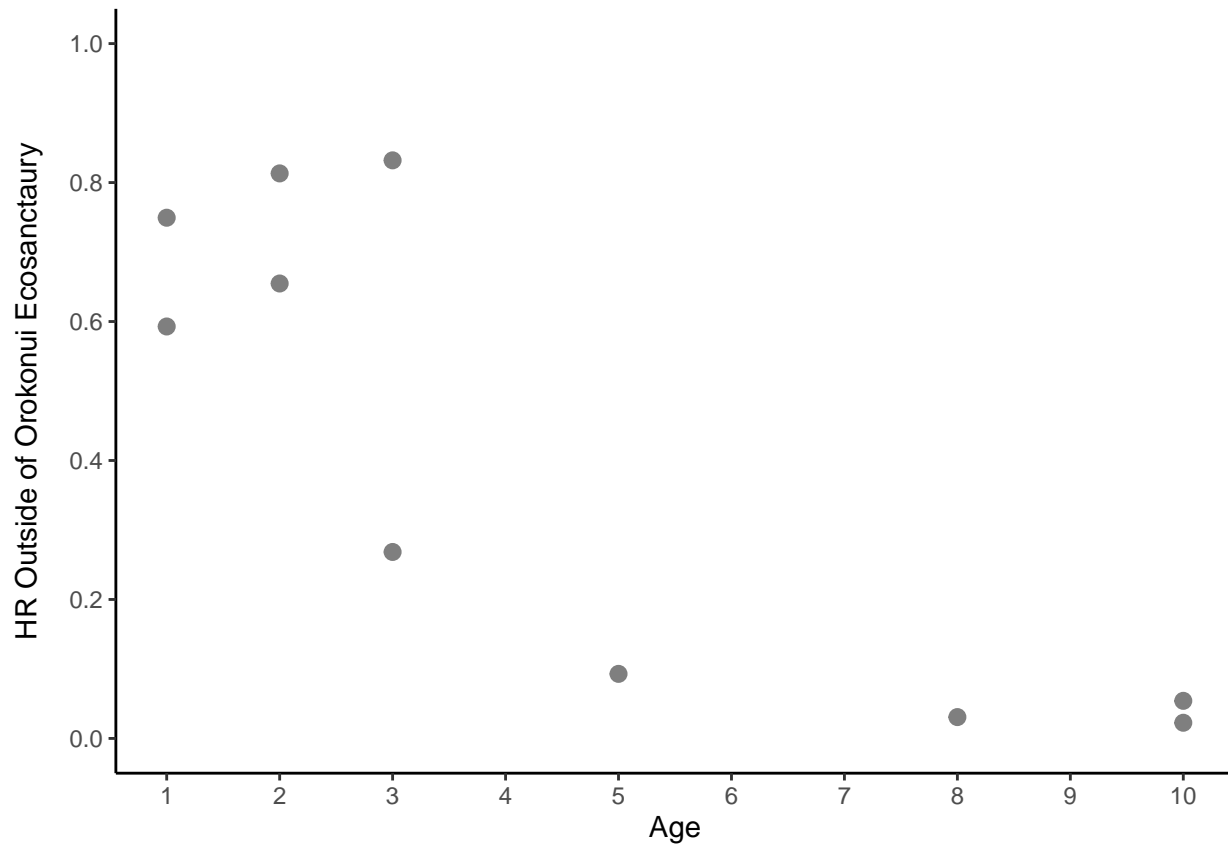
```
all_contours_95_df %>% summarise(mean_UD50km2 = mean(UD50_area_km2),
                                mean_UD95km2 = mean(UD95_area_km2),
                                meanUD_inside = mean(inside),
                                meanUD_outside = mean(outside),
                                sd_UD50km2 = sd(UD50_area_km2),
                                sd_UD95km2 = sd(UD95_area_km2),
                                sdUD_inside = sd(inside),
                                sdUD_outside = sd(outside))
```

```
## mean_UD50km2 mean_UD95km2 meanUD_inside meanUD_outside sd_UD50km2 sd_UD95km2
## 1 0.7614647 4.118892 0.5889165 0.4110835 0.8721026 3.827558
## sdUD_inside sdUD_outside
## 1 0.3480588 0.3480588
```

Plotting home range area, individual-level covariates and overlap with Orokonui Ecosanctuary

```
all_contours_95_df %>% ggplot(aes(x = age, y = outside)) +
  geom_point(size = 2.5, alpha = 0.5) +
  scale_x_continuous(breaks = c(1:10), "Age") +
  scale_y_continuous(breaks = seq(0,1,0.2), limits = c(0,1),
                    "HR Outside of Orokonui Ecosanctuary") +
```

```
theme_classic() +
theme(axis.title.y = element_text(margin = margin(r = 10)))
```



Statistical analysis using the same methodology as above, for the *proportion of area that lies outside of the Orokonui Ecosanctuary fence*.

```
outsideglm <- glm(outside ~ age,
  data = all_contours_95_df,
  family = Gamma(link = "log"))
```

```
summary(outsideglm)
```

```
##
## Call:
## glm(formula = outside ~ age, family = Gamma(link = "log"), data = all_contours_95_df)
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  0.23668    0.29713   0.797  0.44869
## age         -0.37045    0.05277  -7.020  0.00011 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Gamma family taken to be 0.3188882)
##
## Null deviance: 13.2352  on 9  degrees of freedom
## Residual deviance:  2.4075  on 8  degrees of freedom
```

```

## AIC: -10.475
##
## Number of Fisher Scoring iterations: 5
AIC(outsideglm)

## [1] -10.47522
anova(outsideglm, test="F")

## Analysis of Deviance Table
##
## Model: Gamma, link: log
##
## Response: outside
##
## Terms added sequentially (first to last)
##
##
##          Df Deviance Resid. Df Resid. Dev      F      Pr(>F)
## NULL                9      13.2352
## age      1      10.828          8       2.4075 33.955 0.0003929 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

r.squaredLR(outsideglm)

## [1] 0.8466956
## attr(,"adj.r.squared")
## [1] 4.156123
confint(outsideglm)

## Waiting for profiling to be done...
##
##          2.5 %      97.5 %
## (Intercept) -0.3063422  0.8467735
## age         -0.4679829 -0.2638832

dfun <- function(object) {
  with(object, sum((weights * residuals^2)[weights > 0])/df.residual)
}

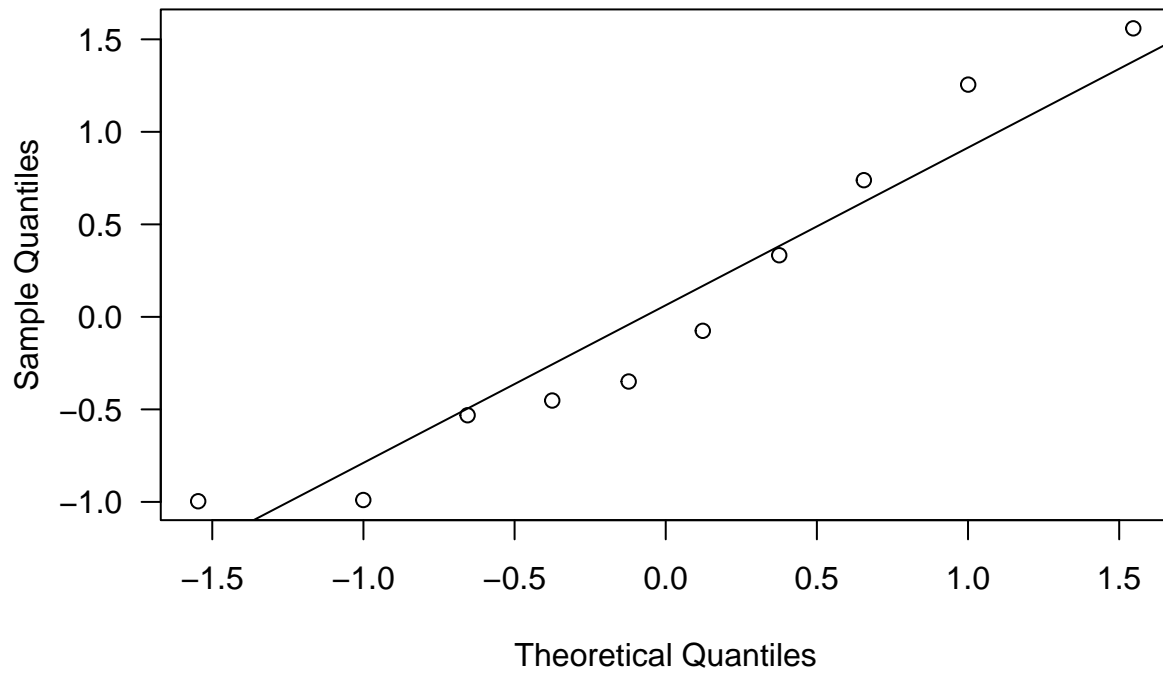
dfun(outsideglm)

## [1] 0.3188882
pseudoR2 <- 1 - (outsideglm$deviance / outsideglm$null.deviance)
pseudoR2

## [1] 0.8181013
qr.outsideglm <- qresid(outsideglm)
qqnorm(qr.outsideglm, las = 1)
qqline(qr.outsideglm)

```

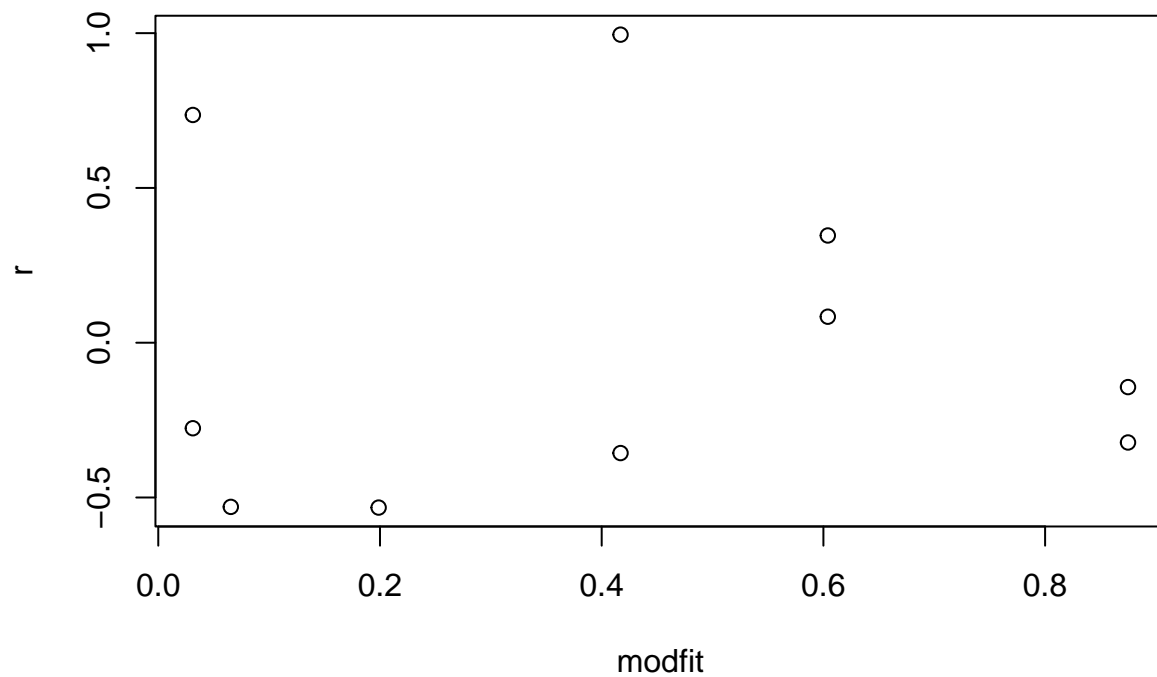
Normal Q-Q Plot



```
r<-residuals(outsideglm,type="pearson")
modfit<-fitted(outsideglm)

plot(r~modfit, main = "Pearson's Residuals")
```

Pearson's Residuals



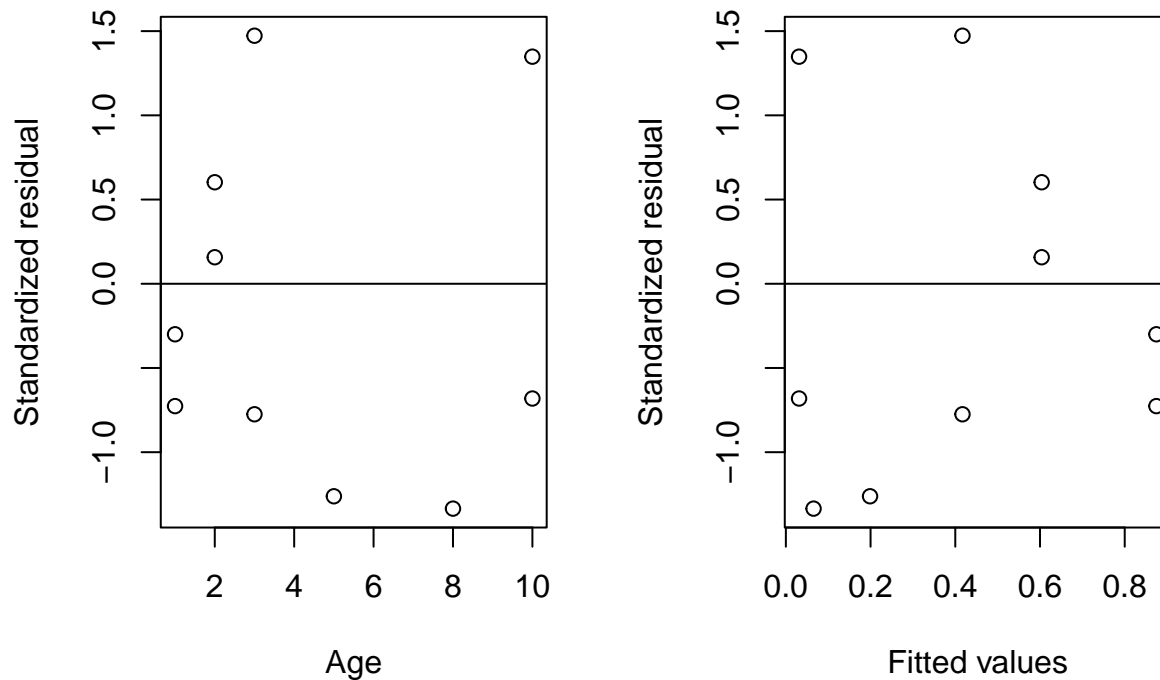
```

par(mfrow=c(1,2)) # change plot window to accommodate 2 plots

r = rstandard(outsideglm)
lf <- fitted(outsideglm)
plot(all_contours_95_df$Age, r,xlab="Age",
     ylab="Standardized residual")
abline(h=0)

plot(lf, r,xlab="Fitted values",ylab="Standardized residual")
abline(h=0)

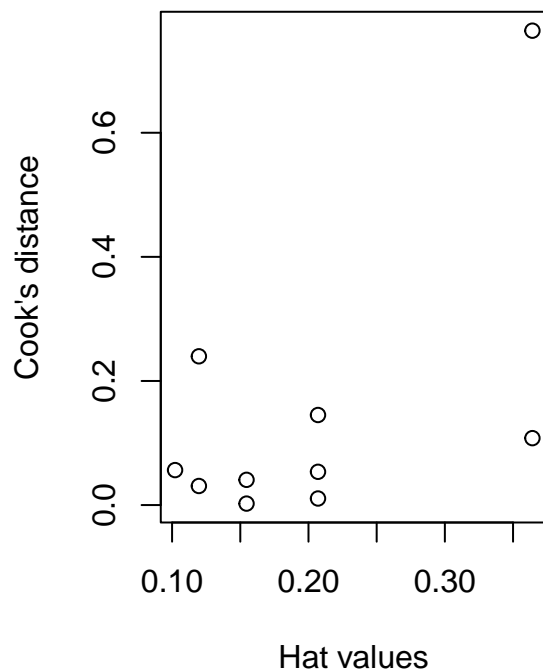
```



```

h <- hatvalues(outsideglm)
cd <- cooks.distance(outsideglm)
plot(h,cd,xlab="Hat values",ylab="Cook's distance")

```

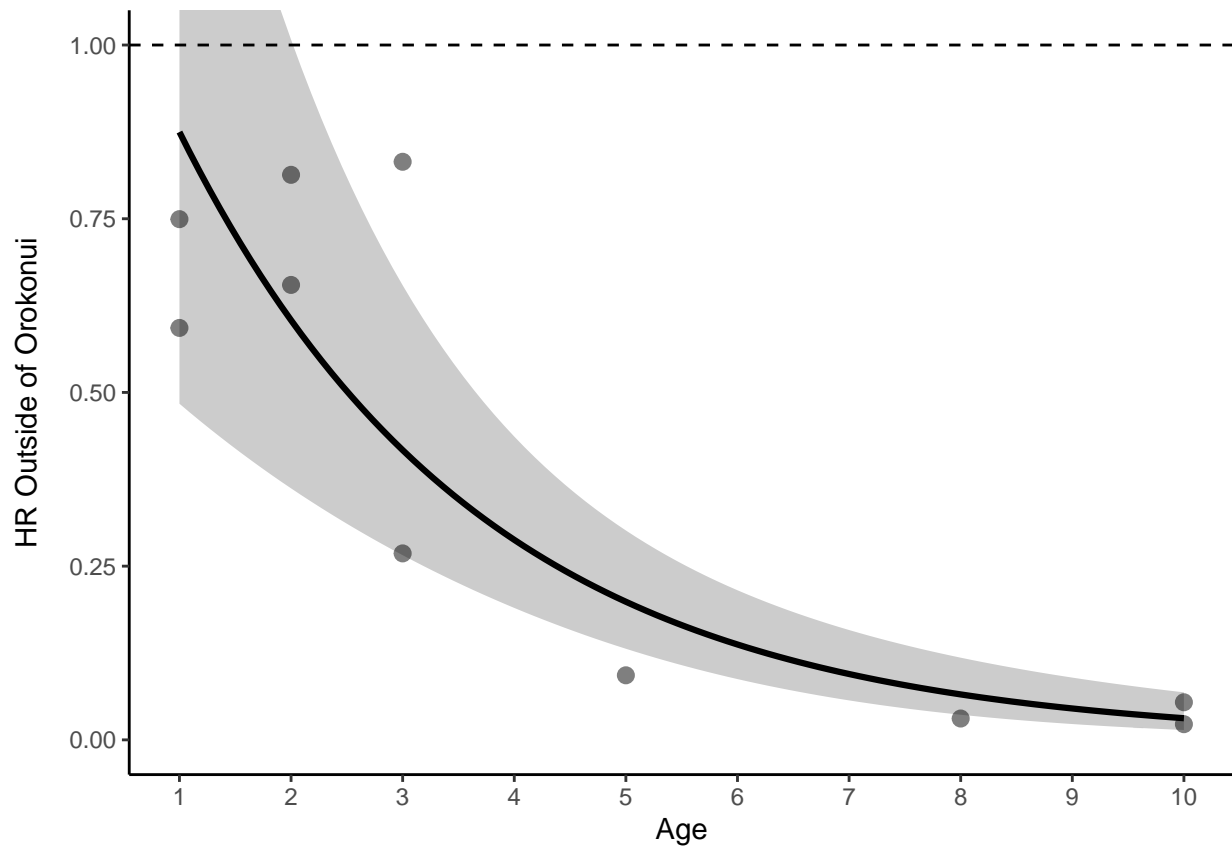



Plot the age model results and overlap model results together

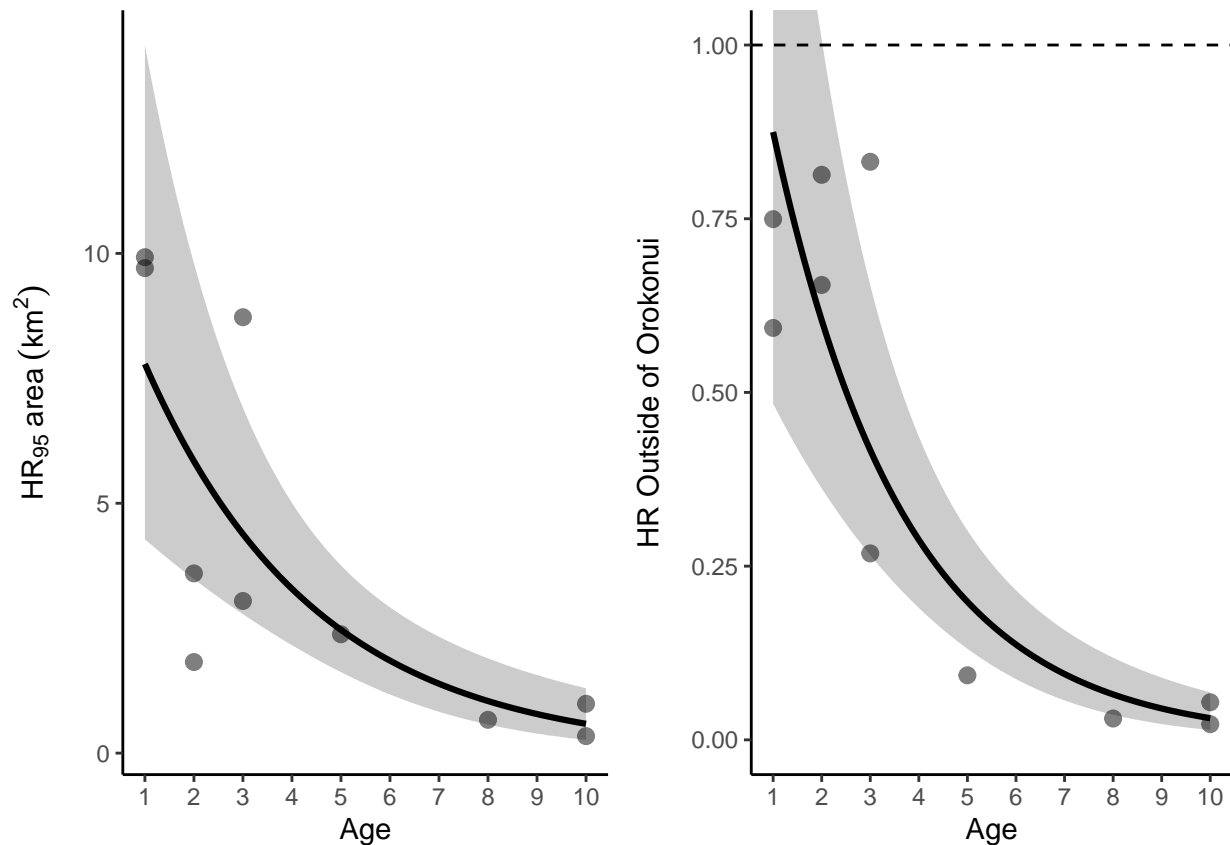
```
par(mfrow=c(1,1)) # return to single plotting

outsideglmplot <- effect_plot(outsideglm,
                              pred = age,
                              plot.points = T,
                              interval = T,
                              point.size = 2.5,
                              point.alpha = 0.5) +
  scale_x_continuous(breaks = c(1:10)) +
  # scale_y_continuous(limits = c(0,1)) +
  coord_cartesian(ylim = c(0, 1), xlim = c(1,10)) +
  labs(x = "Age", y = "HR Outside of Orokonui") +
  geom_hline(yintercept = 1, linetype = "dashed") +
  theme_classic() +
  theme(axis.title.y = element_text(margin = margin(r = 10)))

outsideglmplot
```



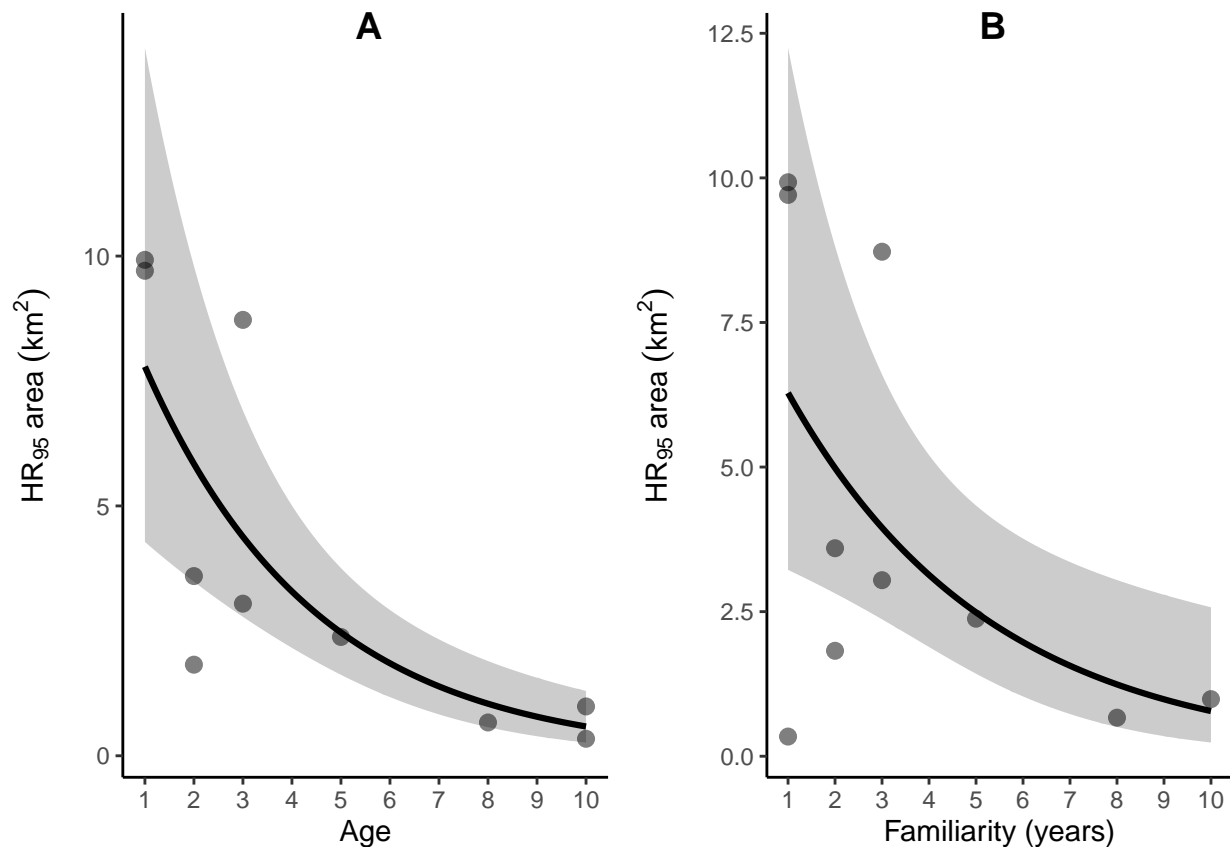
```
ggarrange(area_age_glm_plot, outsideglmplot) # , labels = "AUTO", label.x = 0.55
```



```
for(i in 1:length(filetypes)) {
  ggsave(filename = paste0("Graphical outputs/",
    "age_area_overlap_glms_", Sys.Date(), ".",
    filetypes[i]),
    width = 180,
    height = 50,
    units = "mm",
    dpi = 800)
}
```

Compare the age model results and familiarity model results together

```
ggarrange(area_age_glm_plot, area_familiarity_glm_plot,
  labels = "AUTO", label.x = 0.55)
```



```
for(i in 1:length(filetypes)) {
  ggsave(filename = paste0("Graphical outputs/",
    "age_area_familiarity_glms_", Sys.Date(), ".",
    filetypes[i]),
    width = 160,
    height = 100,
    units = "mm",
    dpi = 800)
}
```

References

Silva, Inês, Christen H Fleming, Michael J Noonan, Jesse Alston, Cody Foltz, William F Fagan, and Justin M Calabrese. 2022. "Autocorrelation-Informed Home Range Estimation: A Review and Practical Guide." *Methods in Ecology and Evolution / British Ecological Society* 13 (3): 534–44. <https://doi.org/10.1111/2041-210x.13786>.

Session info

```
sessionInfo()

## R version 4.5.0 (2025-04-11)
## Platform: aarch64-apple-darwin20
## Running under: macOS Sequoia 15.4.1
##
## Matrix products: default
## BLAS: /Library/Frameworks/R.framework/Versions/4.5-arm64/Resources/lib/libRblas.0.dylib
```

```

## LAPACK: /Library/Frameworks/R.framework/Versions/4.5-arm64/Resources/lib/libRlapack.dylib; LAPACK v
##
## locale:
## [1] en_US.UTF-8/en_US.UTF-8/en_US.UTF-8/C/en_US.UTF-8/en_US.UTF-8
##
## time zone: Australia/Brisbane
## tzcode source: internal
##
## attached base packages:
## [1] stats      graphics  grDevices  utils      datasets  methods    base
##
## other attached packages:
## [1] terra_1.8-42      ctmm_1.2.0      statmod_1.5.0    MuMIn_1.48.11
## [5] jtools_2.3.0      patchwork_1.3.0 ggpubr_0.6.0     sf_1.0-20
## [9] here_1.0.1        lattice_0.22-6  move_4.2.6       raster_3.6-32
## [13] sp_2.2-0          geosphere_1.5-20 lubridate_1.9.4  forcats_1.0.0
## [17] stringr_1.5.1     dplyr_1.1.4     purrr_1.0.4      readr_2.1.5
## [21] tidyr_1.3.1       tibble_3.2.1    ggplot2_3.5.2    tidyverse_2.0.0
## [25] knitr_1.50
##
## loaded via a namespace (and not attached):
## [1] tidyselect_1.2.1   viridisLite_0.4.2 farver_2.1.2
## [4] fastmap_1.2.0      digest_0.6.37     timechange_0.3.0
## [7] lifecycle_1.0.4    ggspatial_1.1.9   magrittr_2.0.3
## [10] compiler_4.5.0     rlang_1.1.6       tools_4.5.0
## [13] utf8_1.2.5         yaml_2.3.10       ggsignif_0.6.4
## [16] labeling_0.4.3     classInt_0.4-11   xml2_1.3.8
## [19] RColorBrewer_1.1-3 abind_1.4-8       KernSmooth_2.23-26
## [22] expm_1.0-0         numDeriv_2016.8-1.1 withr_3.0.2
## [25] grid_4.5.0         stats4_4.5.0      e1071_1.7-16
## [28] future_1.49.0      globals_0.18.0    scales_1.4.0
## [31] tinytex_0.57       cli_3.6.5         rmarkdown_2.29
## [34] ragg_1.4.0         generics_0.1.3    parsedate_1.3.2
## [37] rstudioapi_0.17.1 httr_1.4.7        tzdb_0.5.0
## [40] DBI_1.2.3          cachem_1.1.0      proxy_0.4-27
## [43] pander_0.6.6       splines_4.5.0     parallel_4.5.0
## [46] vctr_0.6.5         Matrix_1.7-3      carData_3.0-5
## [49] car_3.1-3          hms_1.1.3         rstatix_0.7.2
## [52] Formula_1.2-5      listenr_0.9.1     systemfonts_1.2.3
## [55] units_0.8-7        glue_1.8.0        parallelly_1.44.0
## [58] codetools_0.2-20   cowplot_1.1.3     stringi_1.8.7
## [61] gtable_0.3.6       broom.mixed_0.2.9.6 pillar_1.10.2
## [64] furrr_0.3.1        htmltools_0.5.8.1 R6_2.6.1
## [67] textshaping_1.0.1  rprojroot_2.0.4   evaluate_1.0.3
## [70] backports_1.5.0    memoise_2.0.1     broom_1.0.8
## [73] class_7.3-23       Rcpp_1.0.14       nlme_3.1-168
## [76] xfun_0.52          pkgconfig_2.0.3

```