Comparing SSF and deepSSF Predictions

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In this script we are comparing the nezt-step ahead predictions of the SSF (with and without temporal dynamics) and deepSSF models. We are comparing the probabilities of movement, habitat selection and next-step selection, and how they change throughout time.

By comparing the predictions of each process across the entire tracking period or for each hour of the day, we can critically evaluate the covariates that are used by the models and allow for model refinement.

As we expected, the deepSSF models outperformed the SSF models on the in-sample data, which was particularly the case for when the model was trained with Sentinel-2 spectral bands and slope as the spatial covariates (deepSSF S2). The performance dropped for out-of-sample data for all models (including SSFs), and the deepSSF trained with the derived covariates (NDVI, canopy cover, herbaceous vegetation and slope) performed worse than the SSF models, and was only marginally better than a null model, which bears some evidence of overfitting. However, the deepSSF S2 model, trained on 'raw' Sentinel-2 layers rather than derived quantities, retained greater accuracy than all other approaches for out-of-sample data, suggesting that these inputs contain more information that is relevant to buffalo movement and habitat selection than derived quantities like NDVI and slope.

Table of contents

Loading packages

```
library(tidyverse)
packages <- c("amt", "sf", "terra", "beepr", "tictoc", "circular",
              "matrixStats", "progress", "paletteer", "slider")
walk(packages, require, character.only = T)

options(scipen = 999)  # Prevent scientific notation in plots
options(scipen = 0)  # Reset
```

Script setup

Specify the focal id for selecting the in-sample predictions.

```
focal_id <- 2005
```

Step selection function probabilities

SSF models fitted with and without temporal dynamics

```
# create vector of GPS data filenames
validation_ssf <- list.files(path = "outputs/next_step_validation", pattern = "next_step_pro
validation_ids <- substr(validation_ssf, 23, 26)

# import data
validation_ssf_list <- vector(mode = "list", length = length(validation_ssf))

for(i in 1:length(validation_ssf)){
  validation_ssf_list[[i]] <-  read_csv(paste("outputs/next_step_validation/",
                                              validation_ssf[[i]],
                                              sep = ""))

  # validation_ssf_list[i]$id <- validation_ids[i]
```

```
  attr(validation_ssf_list[[i]]$t_, "tzone") <- "Australia/Queensland"
  attr(validation_ssf_list[[i]]$t2_, "tzone") <- "Australia/Queensland"

  print(sum(is.na(validation_ssf_list[[i]]$prob_next_step_ssf_0p)))

}
```

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```
# check that the data has been imported correctly
# validation_ssf_list

validation_ssf_all <- bind_rows(validation_ssf_list)
```

Lengthening data frames to stack together for plotting

```
validation_ssf_move <- validation_ssf_all %>%
  dplyr::select(id, x_, y_, t_, x2_, y2_, t2_, hour_t2, yday_t2, year_t2, contains("prob_mov
  pivot_longer(cols = contains("movement"),
               names_to = "full_name",
               values_to = "value") %>%
  mutate(model = gsub("prob_movement_", "", full_name),
         probability = "move",
         .after = "full_name")

validation_ssf_habitat <- validation_ssf_all %>%
  dplyr::select(id, x_, y_, t_, x2_, y2_, t2_, hour_t2, yday_t2, year_t2, contains("prob_hab
  pivot_longer(cols = contains("habitat"),
               names_to = "full_name",
               values_to = "value") %>%
  mutate(model = gsub("prob_habitat_", "", full_name),
         probability = "habitat",
         .after = "full_name")

validation_ssf_next_step <- validation_ssf_all %>%
  dplyr::select(id, x_, y_, t_, x2_, y2_, t2_, hour_t2, yday_t2, year_t2, contains("prob_nex
  pivot_longer(cols = contains("next_step"),
               names_to = "full_name",
               values_to = "value") %>%
  mutate(model = gsub("prob_next_step_", "", full_name),
         probability = "next_step",
         .after = "full_name")

validation_ssf_long <- bind_rows(validation_ssf_move,
                                 validation_ssf_habitat,
                                 validation_ssf_next_step)

head(validation_ssf_long)
```

```
# A tibble: 6 x 14
     id     x_        y_ t_                    x2_      y2_ t2_
  <dbl>  <dbl>     <dbl> <dttm>              <dbl>    <dbl> <dttm>
1  2005 41969. -1435671. 2018-07-25 11:04:23 41922.  -1.44e6 2018-07-25 12:04:39
2  2005 41969. -1435671. 2018-07-25 11:04:23 41922.  -1.44e6 2018-07-25 12:04:39
3  2005 41922. -1435654. 2018-07-25 12:04:39 41779.  -1.44e6 2018-07-25 13:04:17
4  2005 41922. -1435654. 2018-07-25 12:04:39 41779.  -1.44e6 2018-07-25 13:04:17
5  2005 41779. -1435601. 2018-07-25 13:04:17 41841.  -1.44e6 2018-07-25 14:04:39
6  2005 41779. -1435601. 2018-07-25 13:04:17 41841.  -1.44e6 2018-07-25 14:04:39
# i 7 more variables: hour_t2 <dbl>, yday_t2 <dbl>, year_t2 <dbl>,
#   full_name <chr>, model <chr>, probability <chr>, value <dbl>
```

deepSSF probabilities

```
# create vector of GPS data filenames
validation_deepssf <- list.files(path = "outputs/next_step_validation", pattern = "next_step
validation_ids <- substr(validation_deepssf, 25, 28)

# import data
validation_deepssf_list <- vector(mode = "list", length = length(validation_deepssf))

for(i in 1:length(validation_deepssf)){
  validation_deepssf_list[[i]] <-  read_csv(paste("outputs/next_step_validation/",
                                                  validation_deepssf[[i]],
                                                  sep = ""))

  # validation_deepssf_list[i]$id <- validation_ids[i]
  attr(validation_deepssf_list[[i]]$t_, "tzone") <- "Australia/Queensland"
  attr(validation_deepssf_list[[i]]$t2_, "tzone") <- "Australia/Queensland"

}

# To check that the data has been imported correctly
# validation_deepssf_list

validation_deepssf_all <- bind_rows(validation_deepssf_list)
```

Lengthening data frames to stack together for plotting

```
validation_deepssf_long <- validation_deepssf_all %>%
  dplyr::select(id, x_, y_, t_, x2_, y2_, t2_, hour_t2, yday_t2, year_t2, contains("probs"))
  pivot_longer(cols = contains("probs"),
               names_to = "full_name",
               values_to = "value") %>%
  mutate(model = "deepSSF",
         probability = gsub("_probs", "", full_name),
         .after = "full_name")
```

deepSSF Sentinel 2 probabilities

```
# create vector of GPS data filenames
validation_deepssf_s2 <- list.files(path = "outputs/next_step_validation", pattern = "next_s
validation_ids <- substr(validation_deepssf_s2, 22, 25)

# import data
validation_deepssf_s2_list <- vector(mode = "list", length = length(validation_deepssf_s2))

for(i in 1:length(validation_deepssf_s2)){
  validation_deepssf_s2_list[[i]] <-  read_csv(paste("outputs/next_step_validation/",
                                                     validation_deepssf_s2[[i]],
                                                     sep = ""))

  # validation_deepssf_s2_list[i]$id <- validation_ids[i]
  attr(validation_deepssf_s2_list[[i]]$t_, "tzone") <- "Australia/Queensland"
  attr(validation_deepssf_s2_list[[i]]$t2_, "tzone") <- "Australia/Queensland"

}

# To check that the data has been imported correctly
# validation_deepssf_s2_list

validation_deepssf_s2_all <- bind_rows(validation_deepssf_s2_list)
```

Lengthening data frames to stack together for plotting

```
validation_deepssf_s2_long <- validation_deepssf_s2_all %>%
  dplyr::select(id, x_, y_, t_, x2_, y2_, t2_, hour_t2, yday_t2, year_t2, contains("probs"))
  pivot_longer(cols = contains("probs"),
               names_to = "full_name",
               values_to = "value") %>%
  mutate(model = "deepSSF_S2",
         probability = gsub("_probs", "", full_name),
         .after = "full_name")
```

Compare the probabilities

Combine the wide data frames

Keep only the relevant columns

```
validation_ssf_clean <- validation_ssf_all %>%
  dplyr::select(c(id, x_, y_, t_, t2_, hour_t1, hour_t2, yday_t1, yday_t2,
                  prob_habitat_ssf_0p, prob_habitat_ssf_2p,
                  prob_movement_ssf_0p, prob_movement_ssf_2p,
                  prob_next_step_ssf_0p, prob_next_step_ssf_2p))

validation_deepssf_clean <- validation_deepssf_all %>%
  mutate(habitat_deepSSF = habitat_probs,
         movement_deepSSF = move_probs,
         next_step_deepSSF = next_step_probs,
         .keep = "none")

validation_deepssf_s2_clean <- validation_deepssf_s2_all %>%
  mutate(habitat_deepSSF_S2 = habitat_probs,
         movement_deepSSF_S2 = move_probs,
         next_step_deepSSF_S2 = next_step_probs,
         .keep = "none")
```

Combine the data frames

```
validation_all <- bind_cols(validation_ssf_clean,
                            validation_deepssf_clean,
                            validation_deepssf_s2_clean)
```

Split in habitat selection, movement and next step probabilities

Function to get the maximum probability

```
get_max_column <- function(df) {
  # Create a new column with the name of the column containing the max value for each row
  df$max_column <- apply(df, 1, function(row) {
    # Find the column name with the maximum value
    col_names <- names(df)
```

```
    max_col_index <- which.max(row)
    return(col_names[max_col_index])
  })

  return(df)
}
```

Calculate which was the maximum probability for each row

Habitat selection

```
validation_habitat <- validation_all %>% filter(id == 2005) %>%
  dplyr::select(
    # id, x_, y_, t_, t2_, hour_t1, hour_t2, yday_t1, yday_t2,
    # grep("habitat", colnames(validation_all)),
    # prob_habitat_ssf_0p,
    prob_habitat_ssf_2p,
    # habitat_deepSSF,
    habitat_deepSSF_S2
    )

validation_habitat_prop <- get_max_column(validation_habitat)

max_column_counts <- table(validation_habitat_prop$max_column)
max_column_proportions <- prop.table(max_column_counts)

summary_df <- data.frame(
  column = names(max_column_counts),
  count = as.numeric(max_column_counts),
  proportion = as.numeric(max_column_proportions)
)

summary_df
```

```
               column count proportion
1  habitat_deepSSF_S2  6888  0.6819802
2 prob_habitat_ssf_2p  3212  0.3180198
```

Movement

```
validation_movement <- validation_all %>%
  dplyr::select(
    # id, x_, y_, t_, t2_, hour_t1, hour_t2, yday_t1, yday_t2,
    # grep("movement", colnames(validation_all)),
    # prob_movement_ssf_0p,
    prob_movement_ssf_2p,
    movement_deepSSF,
    # movement_deepSSF_S2
    )

validation_movement_prop <- get_max_column(validation_movement)

max_column_counts <- table(validation_movement_prop$max_column)
max_column_proportions <- prop.table(max_column_counts)

summary_df <- data.frame(
  column = names(max_column_counts),
  count = as.numeric(max_column_counts),
  proportion = as.numeric(max_column_proportions)
)

summary_df
```

```
                column count proportion
1     movement_deepSSF 70366   0.679484
2 prob_movement_ssf_2p 33192   0.320516
```

Next-step

```
validation_next_step <- validation_all %>%
  dplyr::select(
    # id, x_, y_, t_, t2_, hour_t1, hour_t2, yday_t1, yday_t2,
    # grep("next_step", colnames(validation_all)),
    # prob_next_step_ssf_0p,
    prob_next_step_ssf_2p,
    next_step_deepSSF,
    # next_step_deepSSF_S2
    )
```

```r
validation_next_step_prop <- get_max_column(validation_next_step)

max_column_counts <- table(validation_next_step_prop$max_column)
max_column_proportions <- prop.table(max_column_counts)

summary_df <- data.frame(
  column = names(max_column_counts),
  count = as.numeric(max_column_counts),
  proportion = as.numeric(max_column_proportions)
)

summary_df
```

```
                column count proportion
1    next_step_deepSSF 65888  0.6362425
2 prob_next_step_ssf_2p 37670  0.3637575
```

Combine the lengthened data frames

```r
validation_all_long <- bind_rows(validation_ssf_long,
                                 validation_deepssf_long,
                                 validation_deepssf_s2_long)

validation_all_long <- validation_all_long %>% filter(value > 0)
```

Prepare data frame for plotting

```r
# Wet season is from November to April
months_wet <- c(1:4, 11:12)

validation_all_long <- validation_all_long %>%
  mutate(sample = ifelse(id == focal_id, "in_sample", "out_sample"),
         yday_t2_2018 = ifelse(year_t2 == 2018, yday_t2, yday_t2 + 365),
         week_t2 = week(t2_),
         month_t2 = month(t2_),
         season = ifelse(month_t2 %in% months_wet, "wet", "dry"))

head(validation_all_long)
```

```
# A tibble: 6 x 19
     id     x_        y_ t_                    x2_      y2_ t2_
  <dbl>  <dbl>     <dbl> <dttm>               <dbl>    <dbl> <dttm>
1  2005 41922. -1435654. 2018-07-25 12:04:39 41779.  -1.44e6 2018-07-25 13:04:17
2  2005 41922. -1435654. 2018-07-25 12:04:39 41779.  -1.44e6 2018-07-25 13:04:17
3  2005 41779. -1435601. 2018-07-25 13:04:17 41841.  -1.44e6 2018-07-25 14:04:39
4  2005 41779. -1435601. 2018-07-25 13:04:17 41841.  -1.44e6 2018-07-25 14:04:39
5  2005 41841. -1435635. 2018-07-25 14:04:39 41655.  -1.44e6 2018-07-25 15:04:27
6  2005 41841. -1435635. 2018-07-25 14:04:39 41655.  -1.44e6 2018-07-25 15:04:27
# i 12 more variables: hour_t2 <dbl>, yday_t2 <dbl>, year_t2 <dbl>,
#   full_name <chr>, model <chr>, probability <chr>, value <dbl>, sample <chr>,
#   yday_t2_2018 <dbl>, week_t2 <dbl>, month_t2 <dbl>, season <chr>
```

Prepare sliding window

The predicted probabilities are very noisy, so we apply some smoothing by using a sliding window (rolling mean).

We first need a function to calculate the summary statistics for each window.

```
window_summary <- function(data) {
  summarise(data,
            average_time = mean(t2_, na.rm = T),
            average_prob = mean(value, na.rm = T),
            q025 = quantile(value, probs = 0.025, na.rm = T),
            q25 = quantile(value, probs = 0.25, na.rm = T),
            q50 = quantile(value, probs = 0.5, na.rm = T),
            q75 = quantile(value, probs = 0.75, na.rm = T),
            q975 = quantile(value, probs = 0.975, na.rm = T)
            )
}
```

All IDs

```
window_width <- 15 # number of days in each window - should be odd
# how many observations before and after the current observation
before_after <- (window_width - 1) / 2

# ensure that the data is sorted by time (while respecting the id and model grouping)
all_data <- validation_all_long %>%
  group_by(id, model, probability) %>%
  arrange(t2_)
```

```r
# apply the sliding window function
validation_all_sliding_period <- all_data %>%
  slide_period_dfr(
    all_data$t2_,
    # specify that we want to split by days (and slide across at daily intervals)
    "day",
    # our window function (calculates mean and quantiles for each window)
    window_summary,
    # how many days before and after the current observation we want to include in the windo
    .before = before_after,
    .after = before_after
)

head(validation_all_sliding_period, 10)
```

```
# A tibble: 10 x 10
# Groups:   id, model [4]
      id model      probability average_time        average_prob    q025     q25
   <dbl> <chr>      <chr>       <dttm>                     <dbl>   <dbl>   <dbl>
 1  2005 deepSSF    habitat     2018-07-29 06:37:58     0.000107 4.43e-5 1.03e-4
 2  2005 deepSSF    move        2018-07-29 06:37:58     0.0964   1.83e-5 3.26e-4
 3  2005 deepSSF    next_step   2018-07-29 06:37:58     0.0970   1.15e-5 3.35e-4
 4  2005 deepSSF_S2 habitat     2018-07-29 06:37:58     0.000152 3.60e-5 7.60e-5
 5  2005 deepSSF_S2 move        2018-07-29 06:37:58     0.0866   1.61e-5 3.16e-4
 6  2005 deepSSF_S2 next_step   2018-07-29 06:37:58     0.0895   7.31e-6 3.42e-4
 7  2005 ssf_0p     habitat     2018-07-29 06:37:58     0.000101 7.88e-5 9.57e-5
 8  2005 ssf_0p     move        2018-07-29 06:37:58     0.00167  6.77e-5 3.82e-4
 9  2005 ssf_0p     next_step   2018-07-29 06:37:58     0.00171  7.05e-5 3.80e-4
10  2005 ssf_2p     habitat     2018-07-29 06:37:58     0.000107 6.79e-5 9.13e-5
# i 3 more variables: q50 <dbl>, q75 <dbl>, q975 <dbl>
```

We can see from the function above that we have the average time, average probability, and quantiles for eac overlapping window, for each model and probability surface (habitat, movement and next-step).

Out-of-sample validation

The above sliding windows are for each individual separately, but we also want to calculate the average and quantiles for all out-of-sample individuals together.

Calculating mean and quantiles

```r
# out-of-sample data - all ids but the focal id
OOS_data <- validation_all_long %>%
  filter(!id == focal_id) %>%
  group_by(model, probability) %>%
  arrange(t2_)

validation_all_sliding_period_OOS <- OOS_data %>%
  slide_period_dfr(
    OOS_data$t2_,
    "day",
    window_summary,
    .before = before_after,
    .after = before_after
)
```

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`.groups` argument.
`summarise()` has grouped output by 'model'. You can override using the
`.groups` argument.
```

```
head(validation_all_sliding_period_OOS, 10)
```

```
# A tibble: 10 x 9
# Groups:   model [4]
   model    probability average_time        average_prob    q025     q25     q50
   <chr>    <chr>       <dttm>                     <dbl>   <dbl>   <dbl>   <dbl>
 1 deepSSF  habitat     2018-07-29 06:09:54    0.000102  2.67e-5 7.51e-5 1.04e-4
 2 deepSSF  move        2018-07-29 06:09:54    0.0600    1.30e-5 3.02e-4 2.03e-3
 3 deepSSF  next_step   2018-07-29 06:09:54    0.0594    8.58e-6 2.84e-4 1.93e-3
 4 deepSSF~ habitat     2018-07-29 06:09:54    0.000119  8.44e-6 5.32e-5 9.43e-5
 5 deepSSF~ move        2018-07-29 06:09:54    0.0774    8.19e-6 2.74e-4 1.98e-3
 6 deepSSF~ next_step   2018-07-29 06:09:54    0.0752    4.24e-6 2.33e-4 1.85e-3
 7 ssf_0p   habitat     2018-07-29 06:09:54    0.0000982 7.17e-5 8.64e-5 9.65e-5
 8 ssf_0p   move        2018-07-29 06:09:54    0.00174   3.70e-5 3.85e-4 1.24e-3
 9 ssf_0p   next_step   2018-07-29 06:09:54    0.00176   3.63e-5 3.79e-4 1.27e-3
10 ssf_2p   habitat     2018-07-29 06:09:54    0.000105  5.50e-5 8.60e-5 1.01e-4
# i 2 more variables: q75 <dbl>, q975 <dbl>
```

Now the summaries are calculated for all out-of-sample individuals together.

Habitat selection across the tracking period

All models

The solid coloured lines show the average probability for the focal individual that the model was fitted to, and the shaded ribbon is the 50% quantile (there is high variability between probability values, so for clarity we omitted the 95% quantiles). The thin coloured lines are the average probability values for 12 individuals that the model was not fitted to, and are therefore out-of-sample validation data. The dashed coloured lines are the mean values for each model for all of the out-of-sample individuals.

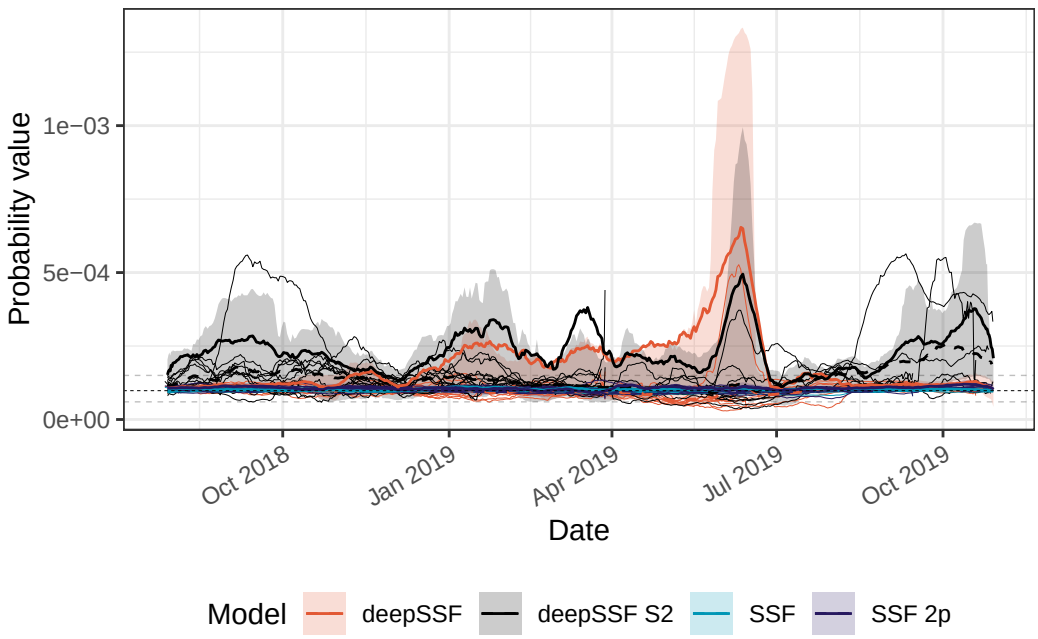
We also show the 'null' probability, i.e. if the selection was completely random, which is just the probability divided equally between all cells.

```
# if there were uniform probabilities (i.e. no selection)
uniform_prob <- 1/(101*101)

ribbon_50_alpha <- 0.2
primary_linewidth <- 0.5
```

```r
OOS_mean_linewidth <- 0.5
secondary_linewidth <- 0.04

ggplot() +

  # dashed lines containing the SSF probabilities (for zooming into in the paper)
  geom_hline(yintercept = 0.6e-4, alpha = 0.25, linetype = "dashed", linewidth = 0.25) +
  geom_hline(yintercept = 1.5e-4, alpha = 0.25, linetype = "dashed", linewidth = 0.25) +

  # in sample 50% ribbon
  geom_ribbon(data = validation_all_sliding_period %>%
                filter(probability == "habitat" &
                       id == focal_id),
              aes(x = average_time,
                  ymin = q25,
                  ymax = q75,
                  fill = model,
                  group = interaction(id, model)),
              alpha = ribbon_50_alpha) +

  # out-of-sample thin line for each individual
  geom_line(data = validation_all_sliding_period %>%
              filter(probability == "habitat" &
                     !id == focal_id),
            aes(x = average_time,
                y = average_prob,
                colour = model,
                group = interaction(id, model)),
            linewidth = secondary_linewidth) +

  # out-of-sample mean line for all individuals
  geom_line(data = validation_all_sliding_period_OOS %>%
              filter(probability == "habitat"),
            aes(x = average_time,
                y = average_prob,
                colour = model),
            linewidth = OOS_mean_linewidth,
            linetype = "dashed") +

  # in sample mean line
  geom_line(data = validation_all_sliding_period %>%
              filter(probability == "habitat" &
                     id == focal_id),
            aes(x = average_time,
```

```
                y = average_prob,
                colour = model,
                group = interaction(id, model)),
            linewidth = primary_linewidth) +

  # dashed line for the null probability
  geom_hline(yintercept = uniform_prob, linetype = "dashed", linewidth = 0.15) +

  scale_fill_manual(name = "Model",
                     values = c("#E25834", "#000000", "#0096B5", "#26185F"),
                    labels = c("deepSSF", "deepSSF S2", "SSF", "SSF 2p")) +

  scale_color_manual(name = "Model",
                     values = c("#E25834", "#000000", "#0096B5", "#26185F"),
                    labels = c("deepSSF", "deepSSF S2", "SSF", "SSF 2p")) +

  scale_y_continuous("Probability value") +
  scale_x_datetime("Date") +
  theme_bw() +
  theme(legend.position = "bottom",
    axis.text.x = element_text(angle = 30, hjust = 1))
```




```
# ggsave(paste0("outputs/validation_all_sliding_", window_width, "days.png"),
#        width = 80, height = 80, units = "mm", dpi = 600)
```

The first thing to note is difference in magnitude between the deepSSF and the SSF pre-

dictions. The deepSSF predicted probabilities are often much higher, but can also be much lower, suggesting that the deepSSF models are more 'confident'.

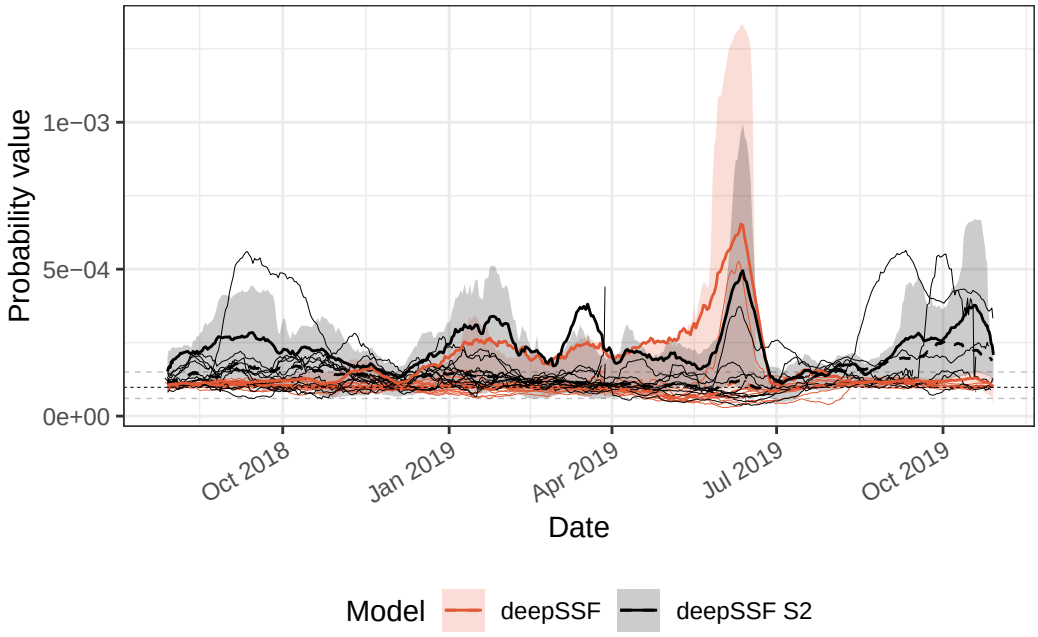
The deepSSF and deepSSF S2 models both performed particularly well between December 2018 and July 2019, (wet-season and early dry-season), although only the deepSSF S2 model performs well outside of this period (for most of the dry season). This suggests that the derived covariates may lack information that is relevant to buffalo during this period, such as a representation of water.

The higher performance of the deepSSF S2 predictions is also echoed in the out-of-sample predictions, which are generally quite a lot higher than the other models.

deepSSF models

```
ggplot() +

  # dashed lines containing the SSF probabilities (for zooming into in the paper)
  geom_hline(yintercept = 0.6e-4, alpha = 0.25, linetype = "dashed", linewidth = 0.25) +
  geom_hline(yintercept = 1.5e-4, alpha = 0.25, linetype = "dashed", linewidth = 0.25) +

  # in sample 50% ribbon
  geom_ribbon(data = validation_all_sliding_period %>%
                filter(probability == "habitat" &
                       id == focal_id &
                       grepl("deepSSF", model)),
              aes(x = average_time,
                  ymin = q25,
                  ymax = q75,
                  fill = model,
                  group = interaction(id, model)),
              alpha = ribbon_50_alpha) +

  # out-of-sample thin line for each individual
  geom_line(data = validation_all_sliding_period %>%
              filter(probability == "habitat" &
                     !id == focal_id &
                     grepl("deepSSF", model)),
            aes(x = average_time,
                y = average_prob,
                colour = model,
                group = interaction(id, model)),
            linewidth = secondary_linewidth) +

  # out-of-sample mean line for all individuals
```

```
  geom_line(data = validation_all_sliding_period_OOS %>%
              filter(probability == "habitat" &
                     grepl("deepSSF", model)),
            aes(x = average_time,
                y = average_prob,
                colour = model),
            linewidth = OOS_mean_linewidth,
            linetype = "dashed") +

  # in sample mean line
  geom_line(data = validation_all_sliding_period %>%
              filter(probability == "habitat" &
                     id == focal_id &
                     grepl("deepSSF", model)),
            aes(x = average_time,
                y = average_prob,
                colour = model,
                group = interaction(id, model)),
            linewidth = primary_linewidth) +

  # dashed line for the null probability
  geom_hline(yintercept = uniform_prob, linetype = "dashed", linewidth = 0.15) +

  scale_fill_manual(name = "Model",
                    values = c("#E25834", "#000000"),
                    labels = c("deepSSF", "deepSSF S2")) +

  scale_color_manual(name = "Model",
                     values = c("#E25834", "#000000"),
                     labels = c("deepSSF", "deepSSF S2")) +

  scale_y_continuous("Probability value") +
  scale_x_datetime("Date") +
  theme_bw() +
  theme(legend.position = "bottom",
    axis.text.x = element_text(angle = 30, hjust = 1))
```



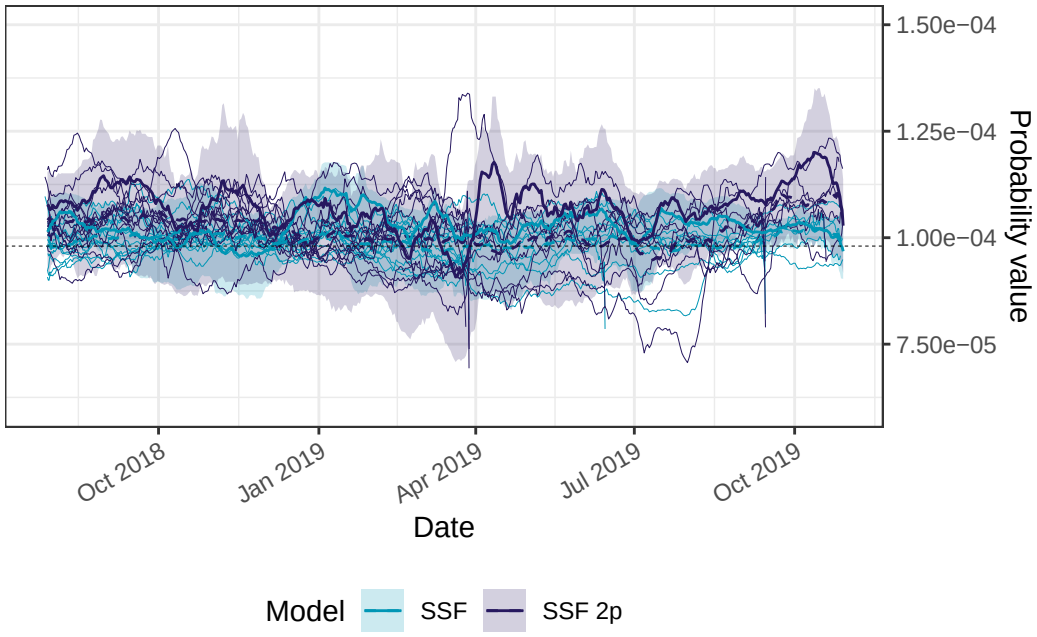

```
# ggsave(paste0("outputs/validation_deepSSF_sliding_", window_width, "days.png"),
#        width = 80, height = 80, units = "mm", dpi = 600)
```

SSF models

```
ggplot() +

  # in sample 50% ribbon
  geom_ribbon(data = validation_all_sliding_period %>%
                filter(probability == "habitat",
                       id == focal_id,
                       !grepl("deepSSF", model)),
              aes(x = average_time,
                  ymin = q25,
                  ymax = q75,
                  fill = model,
                  group = interaction(id, model)),
              alpha = ribbon_50_alpha) +

  # out-of-sample thin line for each individual
  geom_line(data = validation_all_sliding_period %>%
              filter(probability == "habitat",
                       !id == focal_id,
                       !grepl("deepSSF", model)),
```

```
          aes(x = average_time,
              y = average_prob,
              colour = model,
              group = interaction(id, model)),
          linewidth = secondary_linewidth) +

# out-of-sample mean line for all individuals
geom_line(data = validation_all_sliding_period_OOS %>%
            filter(probability == "habitat" &
                   !grepl("deepSSF", model)),
          aes(x = average_time,
              y = average_prob,
              colour = model),
          linewidth = OOS_mean_linewidth,
          linetype = "dashed") +

# in sample mean line
geom_line(data = validation_all_sliding_period %>%
            filter(probability == "habitat",
                   id == focal_id,
                   !grepl("deepSSF", model)),
          aes(x = average_time,
              y = average_prob,
              colour = model,
              group = interaction(id, model)),
          linewidth = primary_linewidth) +

# dashed line for the null probability
geom_hline(yintercept = uniform_prob, linetype = "dashed", linewidth = 0.15) +

scale_fill_manual(name = "Model",
                  values = c("#0096B5", "#26185F"),
                  labels = c("SSF", "SSF 2p")) +

scale_color_manual(name = "Model",
                   values = c("#0096B5", "#26185F"),
                   labels = c("SSF", "SSF 2p")) +

scale_y_continuous("Probability value",
                   position = "right",
                   labels = function(x) format(x, scientific = TRUE)) +

scale_x_datetime("Date") +
coord_cartesian(ylim = c(0.6e-4, 1.5e-4)) +
```

```
  theme_bw() +
  theme(legend.position = "bottom",
    axis.text.x = element_text(angle = 30, hjust = 1))
```




```
# ggsave(paste0("outputs/validation_SSF_sliding_", window_width, "days.png"),
#        width = 80, height = 80, units = "mm", dpi = 600)
```

There isn't a clear seasonal trend with the SSF predictions, but in general the models do better than the null model, although the out-of-sample predictions vary around the null model.

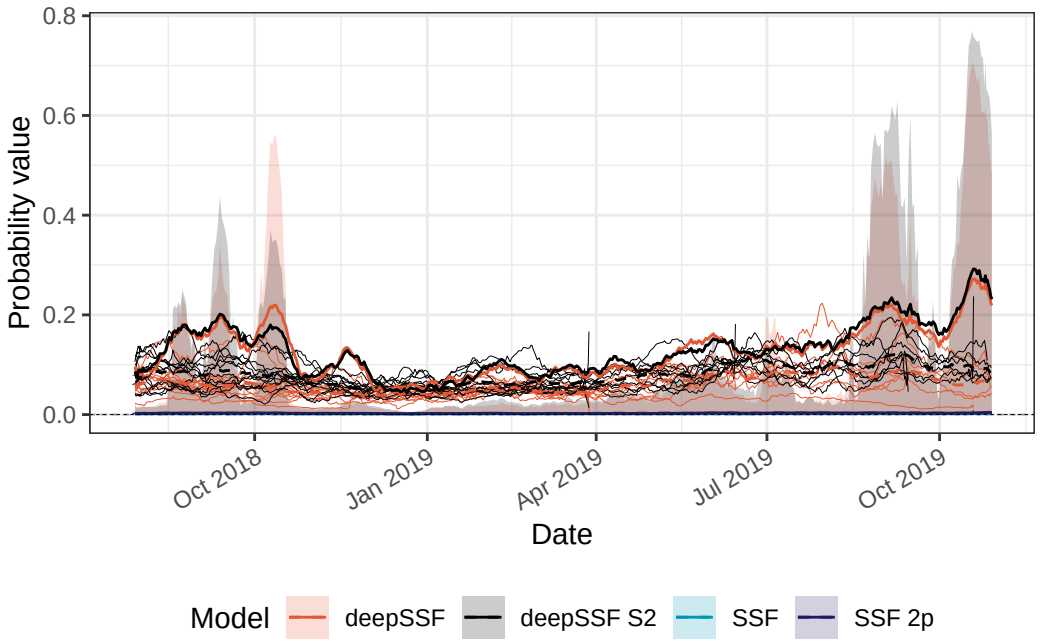
Movement probability across the tracking period

All models

```
ggplot() +

  # dashed lines containing the SSF probabilities
  geom_hline(yintercept = 0.6e-4, alpha = 0.25, linetype = "dashed", linewidth = 0.25) +
  geom_hline(yintercept = 1.5e-4, alpha = 0.25, linetype = "dashed", linewidth = 0.25) +

  # in sample 50% ribbon
  geom_ribbon(data = validation_all_sliding_period %>%
```

```
              filter(probability == "move" &
                     id == focal_id),
            aes(x = average_time,
                ymin = q25,
                ymax = q75,
                fill = model,
                group = interaction(id, model)),
            alpha = ribbon_50_alpha) +

# out-of-sample thin line for each individual
geom_line(data = validation_all_sliding_period %>%
            filter(probability == "move" &
                   !id == focal_id),
          aes(x = average_time,
              y = average_prob,
              colour = model,
              group = interaction(id, model)),
          linewidth = secondary_linewidth) +

# out-of-sample mean line for all individuals
geom_line(data = validation_all_sliding_period_OOS %>%
            filter(probability == "move"),
          aes(x = average_time,
              y = average_prob,
              colour = model),
          linewidth = OOS_mean_linewidth,
          linetype = "dashed") +

# in sample mean line
geom_line(data = validation_all_sliding_period %>%
            filter(probability == "move" &
                   id == focal_id),
          aes(x = average_time,
              y = average_prob,
              colour = model,
              group = interaction(id, model)),
          linewidth = primary_linewidth) +

# dashed line for the null probability
geom_hline(yintercept = uniform_prob, linetype = "dashed", linewidth = 0.15) +

scale_fill_manual(name = "Model",
                  values = c("#E25834", "#000000", "#0096B5", "#26185F"),
                  labels = c("deepSSF", "deepSSF S2", "SSF", "SSF 2p")) +
```

```
  scale_color_manual(name = "Model",
                     values = c("#E25834", "#000000", "#0096B5", "#26185F"),
                     labels = c("deepSSF", "deepSSF S2", "SSF", "SSF 2p")) +

  scale_y_continuous("Probability value") +
  scale_x_datetime("Date") +
  theme_bw() +
  theme(legend.position = "bottom",
    axis.text.x = element_text(angle = 30, hjust = 1))
```




```
# ggsave(paste0("outputs/validation_all_move_sliding_", window_width, "days.png"),
#        width = 80, height = 80, units = "mm", dpi = 600)
```

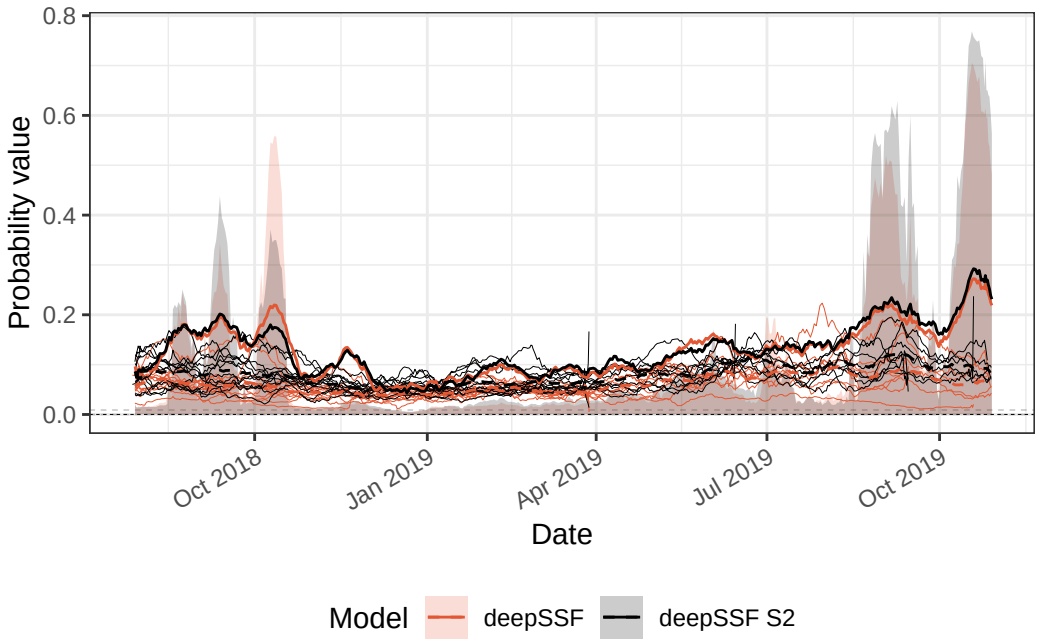
The movement probabilities for the deepSSF models are much higher than the for the SSF models, which I suspect is mostly due to the mixture of distributions in the deepSSF models. When the buffalo are in a low movement period, there can be very high probability in the few cells close to the buffalo, which is often accurate (when the predicted probability is 0.2 that means all of the probability mass is shared between only 5 cells. I don't think the SSF movement kernel has the same flexibility to capture this.

This also comes out very clearly in the hourly predictions, with much higher predicted probabilities during the low movement periods.

deepSSF models

```
ggplot() +

  # dashed lines containing the SSF probabilities
  geom_hline(yintercept = 0, alpha = 0.25, linetype = "dashed", linewidth = 0.25) +
  geom_hline(yintercept = 9e-3, alpha = 0.25, linetype = "dashed", linewidth = 0.25) +

  # in sample 50% ribbon
  geom_ribbon(data = validation_all_sliding_period %>%
                filter(probability == "move" &
                       id == focal_id &
                       grepl("deepSSF", model)),
              aes(x = average_time,
                  ymin = q25,
                  ymax = q75,
                  fill = model,
                  group = interaction(id, model)),
              alpha = ribbon_50_alpha) +

  # out-of-sample thin line for each individual
  geom_line(data = validation_all_sliding_period %>%
              filter(probability == "move" &
                     !id == focal_id &
                     grepl("deepSSF", model)),
            aes(x = average_time,
                y = average_prob,
                colour = model,
                group = interaction(id, model)),
            linewidth = secondary_linewidth) +

  # out-of-sample mean line for all individuals
  geom_line(data = validation_all_sliding_period_OOS %>%
              filter(probability == "move" &
                     grepl("deepSSF", model)),
            aes(x = average_time,
                y = average_prob,
                colour = model),
            linewidth = OOS_mean_linewidth,
            linetype = "dashed") +

  # in sample mean line
  geom_line(data = validation_all_sliding_period %>%
              filter(probability == "move" &
```

```
                    id == focal_id &
                    grepl("deepSSF", model)),
            aes(x = average_time,
                y = average_prob,
                colour = model,
                group = interaction(id, model)),
            linewidth = primary_linewidth) +

# dashed line for the null probability
geom_hline(yintercept = uniform_prob, linetype = "dashed", linewidth = 0.15) +

scale_fill_manual(name = "Model",
                   values = c("#E25834", "#000000"),
                  labels = c("deepSSF", "deepSSF S2")) +

scale_color_manual(name = "Model",
                   values = c("#E25834", "#000000"),
                  labels = c("deepSSF", "deepSSF S2")) +

scale_y_continuous("Probability value") +
scale_x_datetime("Date") +
theme_bw() +
theme(legend.position = "bottom",
  axis.text.x = element_text(angle = 30, hjust = 1))
```

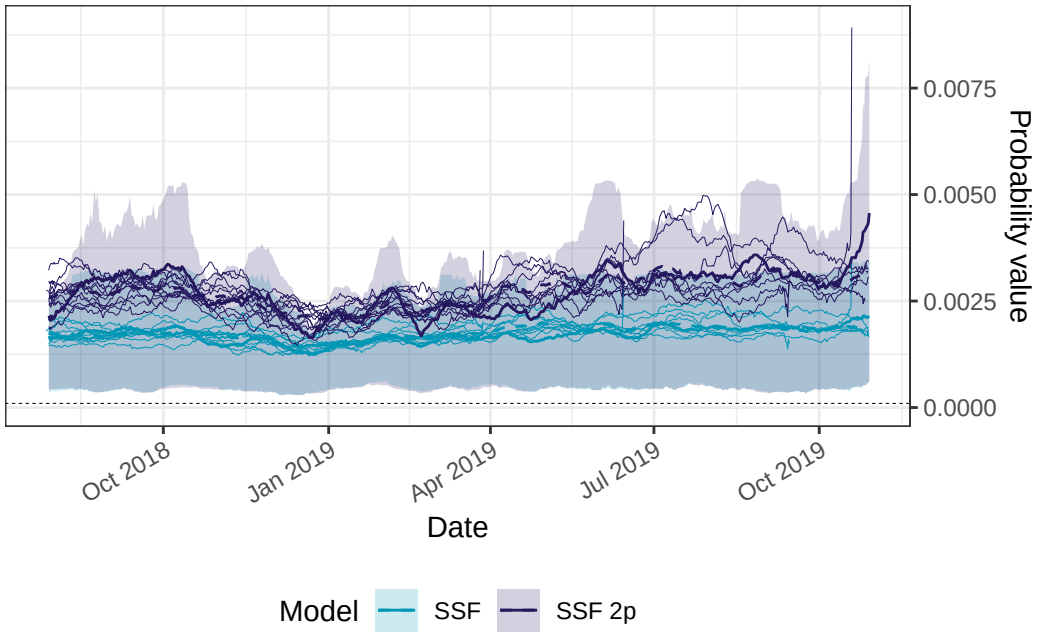


```
# ggsave(paste0("outputs/validation_deepSSF_move_sliding_", window_width, "days.png"),
#        width = 80, height = 80, units = "mm", dpi = 600)
```

SSF models

```
ggplot() +

  # in sample 50% ribbon
  geom_ribbon(data = validation_all_sliding_period %>%
                filter(probability == "move",
                       id == focal_id,
                       !grepl("deepSSF", model)),
              aes(x = average_time,
                  ymin = q25,
                  ymax = q75,
                  fill = model,
                  group = interaction(id, model)),
              alpha = ribbon_50_alpha) +

  # out-of-sample thin line for each individual
  geom_line(data = validation_all_sliding_period %>%
              filter(probability == "move",
                       !id == focal_id,
                       !grepl("deepSSF", model)),
            aes(x = average_time,
                y = average_prob,
                colour = model,
                group = interaction(id, model)),
            linewidth = secondary_linewidth) +

  # out-of-sample mean line for all individuals
  geom_line(data = validation_all_sliding_period_OOS %>%
              filter(probability == "move" &
                     !grepl("deepSSF", model)),
            aes(x = average_time,
                y = average_prob,
                colour = model),
            linewidth = OOS_mean_linewidth,
            linetype = "dashed") +

  # in sample mean line
  geom_line(data = validation_all_sliding_period %>%
```

```
            filter(probability == "move",
                   id == focal_id,
                   !grepl("deepSSF", model)),
          aes(x = average_time,
              y = average_prob,
              colour = model,
              group = interaction(id, model)),
          linewidth = primary_linewidth) +

# dashed line for the null probability
geom_hline(yintercept = uniform_prob, linetype = "dashed", linewidth = 0.15) +

scale_fill_manual(name = "Model",
                  values = c("#0096B5", "#26185F"),
                  labels = c("SSF", "SSF 2p")) +

scale_color_manual(name = "Model",
                   values = c("#0096B5", "#26185F"),
                   labels = c("SSF", "SSF 2p")) +

  scale_y_continuous("Probability value",
                   position = "right") +

scale_x_datetime("Date") +
coord_cartesian(ylim = c(0, 9e-3)) +
theme_bw() +
theme(legend.position = "bottom",
  axis.text.x = element_text(angle = 30, hjust = 1))
```




```
# ggsave(paste0("outputs/validation_SSF_move_sliding_", window_width, "days.png"),
#        width = 80, height = 80, units = "mm", dpi = 600)
```

The temporally dynamic models have consistently higher probabilities of movement than the static models, which again is likely due to the concentration of the movement kernel during the low movement periods, where the probability values are distributed across much fewer cells.

Next-step probabilities across the tracking period

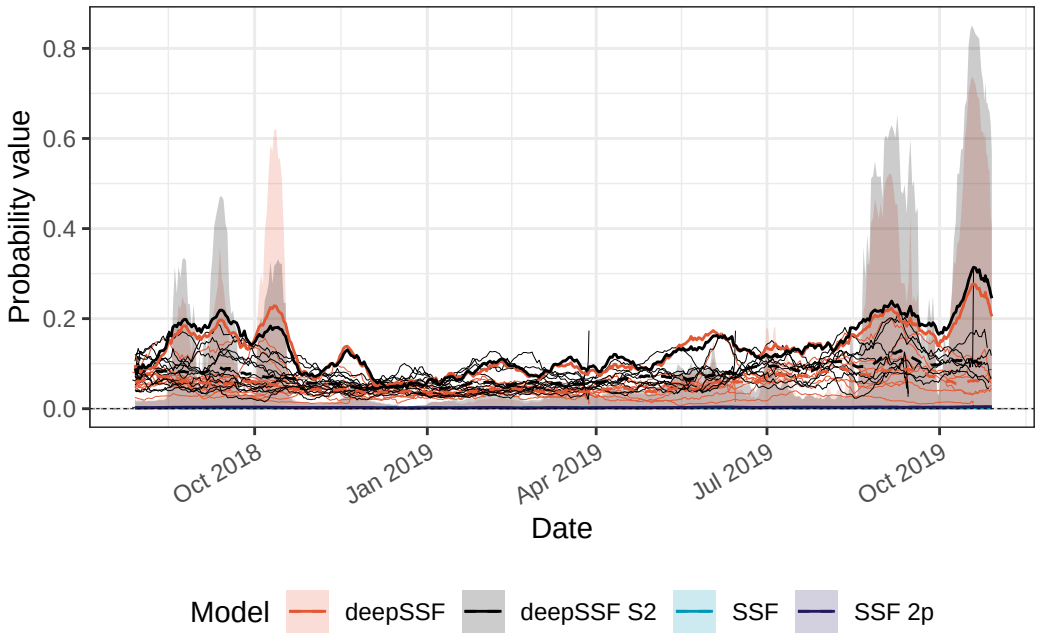
The next-step probability values are very similar to the movement probabilities due to the concentration of the probability mass in fewer cells that are closer to the buffalo, whereas the habitat selection probabilities are distributed across all of the local layers, so they're not actually that informative beyond the movement probabilities.

All models

```
ggplot() +

  # dashed lines containing the SSF probability values
  geom_hline(yintercept = 0.6e-4, alpha = 0.25, linetype = "dashed", linewidth = 0.25) +
  geom_hline(yintercept = 1.5e-4, alpha = 0.25, linetype = "dashed", linewidth = 0.25) +
```

```
# in sample 50% ribbon
geom_ribbon(data = validation_all_sliding_period %>%
              filter(probability == "next_step" &
                     id == focal_id),
            aes(x = average_time,
                ymin = q25,
                ymax = q75,
                fill = model,
                group = interaction(id, model)),
            alpha = ribbon_50_alpha) +

# out-of-sample thin line for each individual
geom_line(data = validation_all_sliding_period %>%
            filter(probability == "next_step" &
                   !id == focal_id),
          aes(x = average_time,
              y = average_prob,
              colour = model,
              group = interaction(id, model)),
          linewidth = secondary_linewidth) +

# out-of-sample mean line for all individuals
geom_line(data = validation_all_sliding_period_OOS %>%
            filter(probability == "next_step"),
          aes(x = average_time,
              y = average_prob,
              colour = model),
          linewidth = OOS_mean_linewidth,
          linetype = "dashed") +

# in sample mean line
geom_line(data = validation_all_sliding_period %>%
            filter(probability == "next_step" &
                   id == focal_id),
          aes(x = average_time,
              y = average_prob,
              colour = model,
              group = interaction(id, model)),
          linewidth = primary_linewidth) +

# dashed line for the null probability
geom_hline(yintercept = uniform_prob, linetype = "dashed", linewidth = 0.15) +

scale_fill_manual(name = "Model",
```

```
                      values = c("#E25834", "#000000", "#0096B5", "#26185F"),
                     labels = c("deepSSF", "deepSSF S2", "SSF", "SSF 2p")) +

  scale_color_manual(name = "Model",
                      values = c("#E25834", "#000000", "#0096B5", "#26185F"),
                     labels = c("deepSSF", "deepSSF S2", "SSF", "SSF 2p")) +

  scale_y_continuous("Probability value") +
  scale_x_datetime("Date") +
  theme_bw() +
  theme(legend.position = "bottom",
    axis.text.x = element_text(angle = 30, hjust = 1))
```



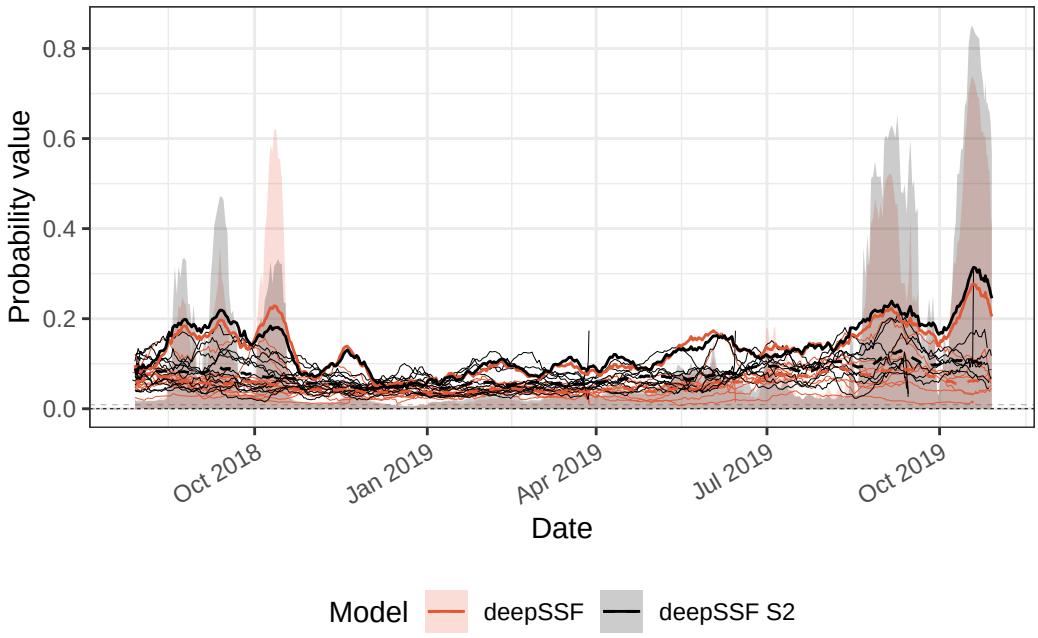

```
# ggsave(paste0("outputs/validation_all_next_step_sliding_", window_width, "days.png"),
#        width = 80, height = 80, units = "mm", dpi = 600)
```

deepSSF models

```
ggplot() +

  # dashed lines containing the SSF probability values
  geom_hline(yintercept = 0, alpha = 0.25, linetype = "dashed", linewidth = 0.25) +
  geom_hline(yintercept = 9e-3, alpha = 0.25, linetype = "dashed", linewidth = 0.25) +
```

```
# in sample 50% ribbon
geom_ribbon(data = validation_all_sliding_period %>%
              filter(probability == "next_step" &
                     id == focal_id &
                     grepl("deepSSF", model)),
            aes(x = average_time,
                ymin = q25,
                ymax = q75,
                fill = model,
                group = interaction(id, model)),
            alpha = ribbon_50_alpha) +

# out-of-sample thin line for each individual
geom_line(data = validation_all_sliding_period %>%
            filter(probability == "next_step" &
                   !id == focal_id &
                   grepl("deepSSF", model)),
          aes(x = average_time,
              y = average_prob,
              colour = model,
              group = interaction(id, model)),
          linewidth = secondary_linewidth) +

# out-of-sample mean line for all individuals
geom_line(data = validation_all_sliding_period_OOS %>%
            filter(probability == "next_step" &
                   grepl("deepSSF", model)),
          aes(x = average_time,
              y = average_prob,
              colour = model),
          linewidth = OOS_mean_linewidth,
          linetype = "dashed") +

# in sample mean line
geom_line(data = validation_all_sliding_period %>%
            filter(probability == "next_step" &
                   id == focal_id &
                   grepl("deepSSF", model)),
          aes(x = average_time,
              y = average_prob,
              colour = model,
              group = interaction(id, model)),
          linewidth = primary_linewidth) +
```

```
  # dashed line for the null probability
  geom_hline(yintercept = uniform_prob, linetype = "dashed", linewidth = 0.15) +

  scale_fill_manual(name = "Model",
                    values = c("#E25834", "#000000"),
                    labels = c("deepSSF", "deepSSF S2")) +

  scale_color_manual(name = "Model",
                     values = c("#E25834", "#000000"),
                     labels = c("deepSSF", "deepSSF S2")) +

  scale_y_continuous("Probability value") +
  scale_x_datetime("Date") +
  theme_bw() +
  theme(legend.position = "bottom",
    axis.text.x = element_text(angle = 30, hjust = 1))
```



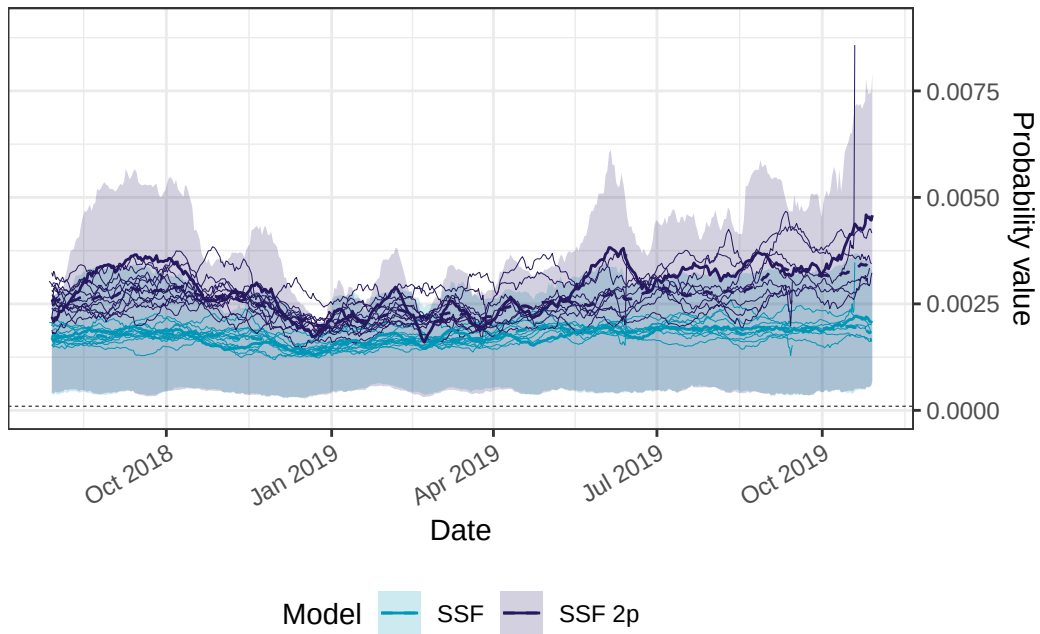

```
# ggsave(paste0("outputs/validation_deepSSF_next_step_sliding_", window_width, "days.png"),
#        width = 80, height = 80, units = "mm", dpi = 600)
```

SSF models

```
ggplot() +
```

```
# in sample 50% ribbon
geom_ribbon(data = validation_all_sliding_period %>%
              filter(probability == "next_step",
                     id == focal_id,
                     !grepl("deepSSF", model)),
            aes(x = average_time,
                ymin = q25,
                ymax = q75,
                fill = model,
                group = interaction(id, model)),
            alpha = ribbon_50_alpha) +

# out-of-sample thin line for each individual
geom_line(data = validation_all_sliding_period %>%
            filter(probability == "next_step",
                     !id == focal_id,
                     !grepl("deepSSF", model)),
          aes(x = average_time,
              y = average_prob,
              colour = model,
              group = interaction(id, model)),
          linewidth = secondary_linewidth) +

# out-of-sample mean line for all individuals
geom_line(data = validation_all_sliding_period_OOS %>%
            filter(probability == "next_step" &
                     !grepl("deepSSF", model)),
          aes(x = average_time,
              y = average_prob,
              colour = model),
          linewidth = OOS_mean_linewidth,
          linetype = "dashed") +

# in sample mean line
geom_line(data = validation_all_sliding_period %>%
            filter(probability == "next_step",
                     id == focal_id,
                     !grepl("deepSSF", model)),
          aes(x = average_time,
              y = average_prob,
              colour = model,
              group = interaction(id, model)),
          linewidth = primary_linewidth) +
```

```
  # dashed line for the null probability
  geom_hline(yintercept = uniform_prob, linetype = "dashed", linewidth = 0.15) +

  scale_fill_manual(name = "Model",
                    values = c("#0096B5", "#26185F"),
                    labels = c("SSF", "SSF 2p")) +

  scale_color_manual(name = "Model",
                     values = c("#0096B5", "#26185F"),
                     labels = c("SSF", "SSF 2p")) +

    scale_y_continuous("Probability value",
                       position = "right") +

  scale_x_datetime("Date") +
  coord_cartesian(ylim = c(0, 9e-3)) +
  theme_bw() +
  theme(legend.position = "bottom",
    axis.text.x = element_text(angle = 30, hjust = 1))
```




```
# ggsave(paste0("outputs/validation_SSF_next_step_sliding_", window_width, "days.png"),
#        width = 80, height = 80, units = "mm", dpi = 600)
```

Hourly probabilities

We can also calculate the habitat selection, movement and next-step probabilities for each hour of the day, indicating when the models are accurate (or notr) at different times of the day.

For this we don't need a sliding window, we will just bin by the hour of the day.

Here we just show the hourly probabilities across the whole tracking period, but we could also split this up into seasons and assess how accurate the models are during the wet and dry seasons.

```
# grouping by each individual, model and hour of the day
validation_all_quantiles_hourly <- validation_all_long %>%
  group_by(id, model, probability, hour_t2) %>%
  summarise(average_prob = mean(value, na.rm = T),
            sd_prob = sd(value, na.rm = T),
            q025 = quantile(value, probs = 0.025, na.rm = T),
            q25 = quantile(value, probs = 0.25, na.rm = T),
            q50 = quantile(value, probs = 0.5, na.rm = T),
            q75 = quantile(value, probs = 0.75, na.rm = T),
            q975 = quantile(value, probs = 0.975, na.rm = T)
            )
```

```
`summarise()` has grouped output by 'id', 'model', 'probability'. You can
override using the `.groups` argument.
```

```
head(validation_all_quantiles_hourly)
```

```
# A tibble: 6 x 11
# Groups:   id, model, probability [1]
     id model   probability hour_t2 average_prob sd_prob    q025     q25     q50
  <dbl> <chr>   <chr>         <dbl>        <dbl>   <dbl>   <dbl>   <dbl>   <dbl>
1  2005 deepSSF habitat           0     0.000249 3.21e-4 2.50e-5 1.03e-4 1.34e-4
2  2005 deepSSF habitat           1     0.000233 2.95e-4 2.77e-5 9.78e-5 1.31e-4
3  2005 deepSSF habitat           2     0.000239 3.05e-4 2.69e-5 9.89e-5 1.32e-4
4  2005 deepSSF habitat           3     0.000232 3.09e-4 1.89e-5 1.04e-4 1.31e-4
5  2005 deepSSF habitat           4     0.000241 3.21e-4 2.86e-5 1.06e-4 1.30e-4
6  2005 deepSSF habitat           5     0.000229 3.20e-4 2.96e-5 1.06e-4 1.24e-4
# i 2 more variables: q75 <dbl>, q975 <dbl>
```

```r
# out-of-sample ids
# grouping by each model and hour of the day (combining all OOS individuals to get the avera
validation_all_quantiles_hourly_OOS <- validation_all_long %>%
  filter(!id == focal_id) %>%
  group_by(model, probability, hour_t2) %>%
  summarise(average_prob = mean(value, na.rm = T),
            sd_prob = sd(value, na.rm = T),
            q025 = quantile(value, probs = 0.025, na.rm = T),
            q25 = quantile(value, probs = 0.25, na.rm = T),
            q50 = quantile(value, probs = 0.5, na.rm = T),
            q75 = quantile(value, probs = 0.75, na.rm = T),
            q975 = quantile(value, probs = 0.975, na.rm = T)
            )
```

```
`summarise()` has grouped output by 'model', 'probability'. You can override
using the `.groups` argument.
```

```r
head(validation_all_quantiles_hourly_OOS)
```

```
# A tibble: 6 x 10
# Groups:   model, probability [1]
  model probability hour_t2 average_prob sd_prob    q025     q25     q50     q75
  <chr> <chr>         <dbl>        <dbl>   <dbl>   <dbl>   <dbl>   <dbl>   <dbl>
1 deep~ habitat           0    0.0000941 1.08e-4 4.44e-6 3.73e-5 7.43e-5 1.25e-4
2 deep~ habitat           1    0.0000952 1.22e-4 4.44e-6 3.61e-5 7.41e-5 1.25e-4
3 deep~ habitat           2    0.0000968 1.19e-4 4.54e-6 3.64e-5 7.53e-5 1.26e-4
4 deep~ habitat           3    0.0000989 1.18e-4 4.64e-6 3.75e-5 7.95e-5 1.30e-4
5 deep~ habitat           4    0.000101  1.05e-4 5.22e-6 4.17e-5 8.81e-5 1.35e-4
6 deep~ habitat           5    0.000102  9.73e-5 6.81e-6 4.57e-5 9.63e-5 1.34e-4
# i 1 more variable: q975 <dbl>
```

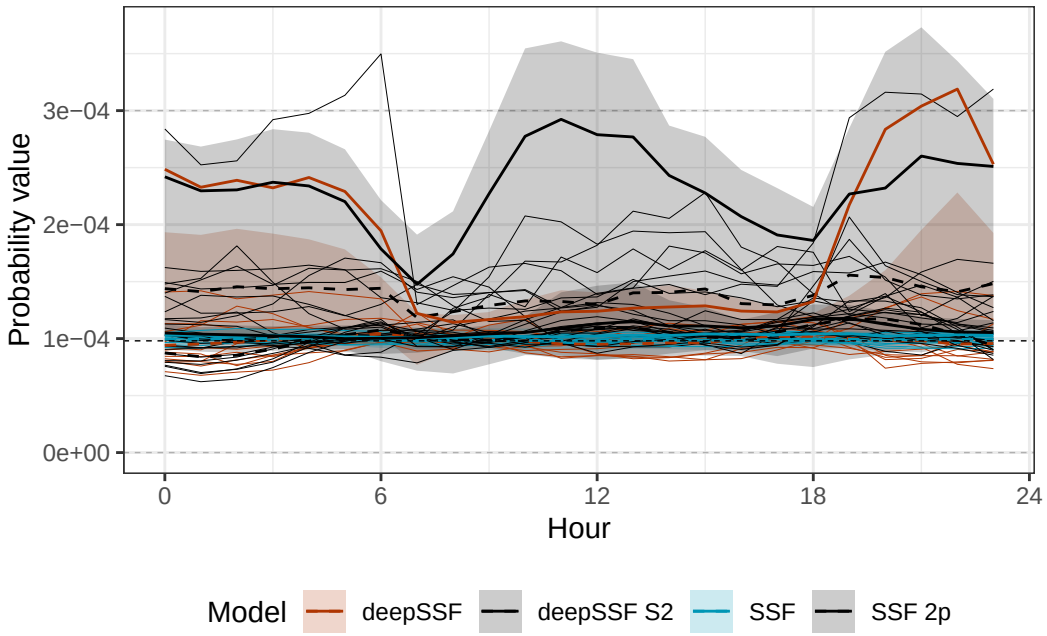
Habitat selection across the day

All models

```r
ggplot() +

  # dashed lines containing the SSF probabilities
  geom_hline(yintercept = 0, alpha = 0.25, linetype = "dashed", linewidth = 0.25) +
  geom_hline(yintercept = 3e-4, alpha = 0.25, linetype = "dashed", linewidth = 0.25) +
```

```
# in sample 50% ribbon
geom_ribbon(data = validation_all_quantiles_hourly %>%
              filter(probability == "habitat",
                     id == focal_id),
            aes(x = hour_t2,
                ymin = q25,
                ymax = q75,
                fill = model,
                group = interaction(id, model)),
            alpha = ribbon_50_alpha) +

# out-of-sample thin line for each individual
geom_line(data = validation_all_quantiles_hourly %>%
            filter(probability == "habitat",
                   !id == focal_id),
          aes(x = hour_t2,
              y = average_prob,
              colour = model,
              group = interaction(id, model)),
          linewidth = 0.075) +

# out-of-sample mean line
geom_line(data = validation_all_quantiles_hourly_OOS %>%
            filter(probability == "habitat"),
          aes(x = hour_t2,
              y = average_prob,
              colour = model),
          linewidth = OOS_mean_linewidth,
          linetype = "dashed") +

# in sample mean line
geom_line(data = validation_all_quantiles_hourly %>%
            filter(probability == "habitat",
                   id == focal_id),
          aes(x = hour_t2,
              y = average_prob,
              colour = model,
              group = interaction(id, model)),
          linewidth = primary_linewidth) +

# dashed line for the null probability
geom_hline(yintercept = uniform_prob, linetype = "dashed", linewidth = 0.25) +

scale_fill_manual(name = "Model",
```

```
                      values = c("#AF3602", "#000000", "#0096B5", "#000000"),
                     labels = c("deepSSF", "deepSSF S2", "SSF", "SSF 2p")) +

  scale_color_manual(name = "Model",
                      values = c("#AF3602", "#000000", "#0096B5", "#000000"),
                     labels = c("deepSSF", "deepSSF S2", "SSF", "SSF 2p")) +

  scale_y_continuous("Probability value") +
  scale_x_continuous("Hour", breaks = seq(0,24,6)) +
  theme_bw() +
  theme(legend.position = "bottom")
```




```
# ggsave(paste0("outputs/validation_all_hourly.png"),
#        width = 80, height = 80, units = "mm", dpi = 600)
```

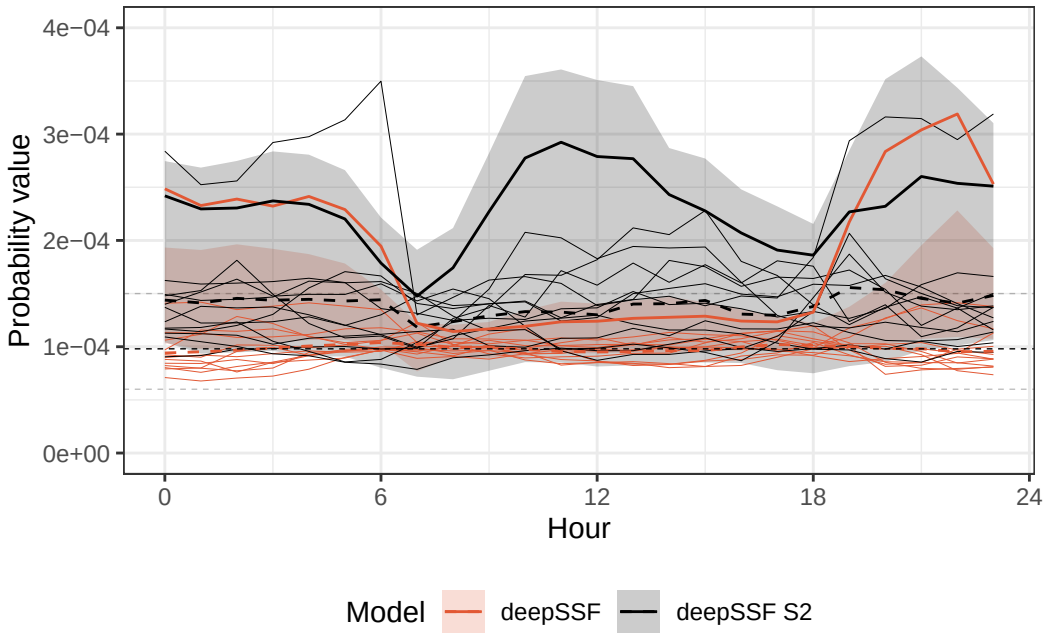
The deepSSF models both predict well in the evening (at least in-sample), but only the deepSSF S2 predicts well during the middle of the day, again suggesting that there is information in the Sentinel-2 layers that isn't present in the derived covariates.

The out-of-sample predictions are also much higher for the deepSSF S2 model, suggesting that it is better at generalising to new data.

deepSSF models

```
ggplot() +

  # dashed lines containing the SSF probabilities
  geom_hline(yintercept = 0.6e-4, alpha = 0.25, linetype = "dashed", linewidth = 0.25) +
  geom_hline(yintercept = 1.5e-4, alpha = 0.25, linetype = "dashed", linewidth = 0.25) +

  # in sample 50% ribbon
  geom_ribbon(data = validation_all_quantiles_hourly %>%
                filter(probability == "habitat",
                       id == focal_id,
                       grepl("deepSSF", model)),
              aes(x = hour_t2,
                  ymin = q25,
                  ymax = q75,
                  fill = model,
                  group = interaction(id, model)),
              alpha = ribbon_50_alpha) +

  # out-of-sample thin line for each individual
  geom_line(data = validation_all_quantiles_hourly %>%
              filter(probability == "habitat",
                     !id == focal_id,
                     grepl("deepSSF", model)),
            aes(x = hour_t2,
                y = average_prob,
                colour = model,
                group = interaction(id, model)),
            linewidth = secondary_linewidth) +

  # out-of-sample mean line
  geom_line(data = validation_all_quantiles_hourly_OOS %>%
              filter(probability == "habitat" &
                     grepl("deepSSF", model)),
            aes(x = hour_t2,
                y = average_prob,
                colour = model),
            linewidth = OOS_mean_linewidth,
            linetype = "dashed") +

  # in sample mean line
  geom_line(data = validation_all_quantiles_hourly %>%
              filter(probability == "habitat",
```

```
                    id == focal_id,
                    grepl("deepSSF", model)),
            aes(x = hour_t2,
                y = average_prob,
                colour = model,
                group = interaction(id, model)),
            linewidth = primary_linewidth) +

# dashed line for the null probability
geom_hline(yintercept = uniform_prob, linetype = "dashed", linewidth = 0.25) +

scale_fill_manual(name = "Model",
                  values = c("#E25834", "#000000"),
                  labels = c("deepSSF", "deepSSF S2")) +

scale_color_manual(name = "Model",
                   values = c("#E25834", "#000000"),
                   labels = c("deepSSF", "deepSSF S2")) +

scale_y_continuous("Probability value") +
scale_x_continuous("Hour", seq(0,24,6)) +
coord_cartesian(ylim = c(0, 4e-4)) +
theme_bw() +
theme(legend.position = "bottom")
```

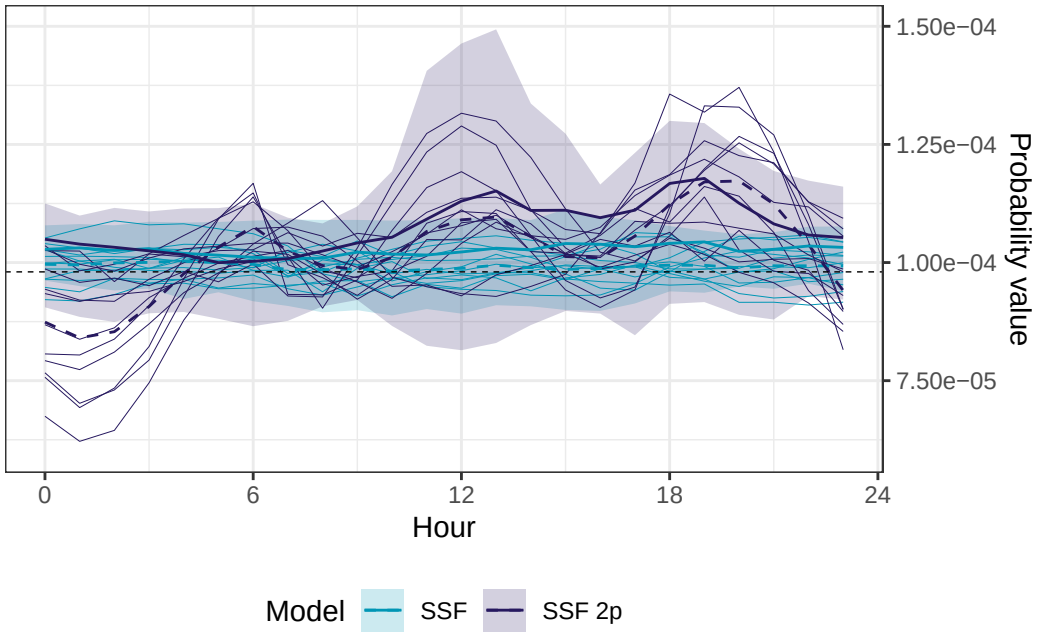


```
# ggsave(paste0("outputs/validation_deepSSF_hourly.png"),
#        width = 80, height = 80, units = "mm", dpi = 600)
```

SSF models

```
ggplot() +

  # in sample 50% ribbon
  geom_ribbon(data = validation_all_quantiles_hourly %>%
                filter(probability == "habitat",
                       id == focal_id,
                       !grepl("deepSSF", model)),
              aes(x = hour_t2,
                  ymin = q25,
                  ymax = q75,
                  fill = model,
                  group = interaction(id, model)),
              alpha = ribbon_50_alpha) +

  # out-of-sample thin line for each individual
  geom_line(data = validation_all_quantiles_hourly %>%
              filter(probability == "habitat",
                       !id == focal_id,
                       !grepl("deepSSF", model)),
            aes(x = hour_t2,
                y = average_prob,
                colour = model,
                group = interaction(id, model)),
            linewidth = secondary_linewidth) +

  # out-of-sample mean line
  geom_line(data = validation_all_quantiles_hourly_OOS %>%
              filter(probability == "habitat" &
                     !grepl("deepSSF", model)),
            aes(x = hour_t2,
                y = average_prob,
                colour = model),
            linewidth = OOS_mean_linewidth,
            linetype = "dashed") +

  # in sample mean line
  geom_line(data = validation_all_quantiles_hourly %>%
```

```
            filter(probability == "habitat",
                   id == focal_id,
                   !grepl("deepSSF", model)),
          aes(x = hour_t2,
              y = average_prob,
              colour = model,
              group = interaction(id, model)),
          linewidth = primary_linewidth) +

# dashed line for the null probability
geom_hline(yintercept = uniform_prob, linetype = "dashed", linewidth = 0.25) +

scale_fill_manual(name = "Model",
                  values = c("#0096B5", "#26185F"),
                  labels = c("SSF", "SSF 2p")) +

scale_color_manual(name = "Model",
                   values = c("#0096B5", "#26185F"),
                   labels = c("SSF", "SSF 2p")) +

scale_y_continuous("Probability value",
                   position = "right",
                   labels = function(x) format(x, scientific = TRUE)) +

scale_x_continuous("Hour", seq(0,24,6)) +
coord_cartesian(ylim = c(0.6e-4, 1.5e-4)) +
theme_bw() +
theme(legend.position = "bottom")
```




```
# ggsave(paste0("outputs/validation_SSF_hourly.png"),
#        width = 80, height = 80, units = "mm", dpi = 600)
```

The SSF model with temporal dynamics had higher prediction accuracy than the SSF model without temporal dynamics overall (in- and out-of-sample), but it was more variable throughout the day, and was quite poor between midnight and about 5am.

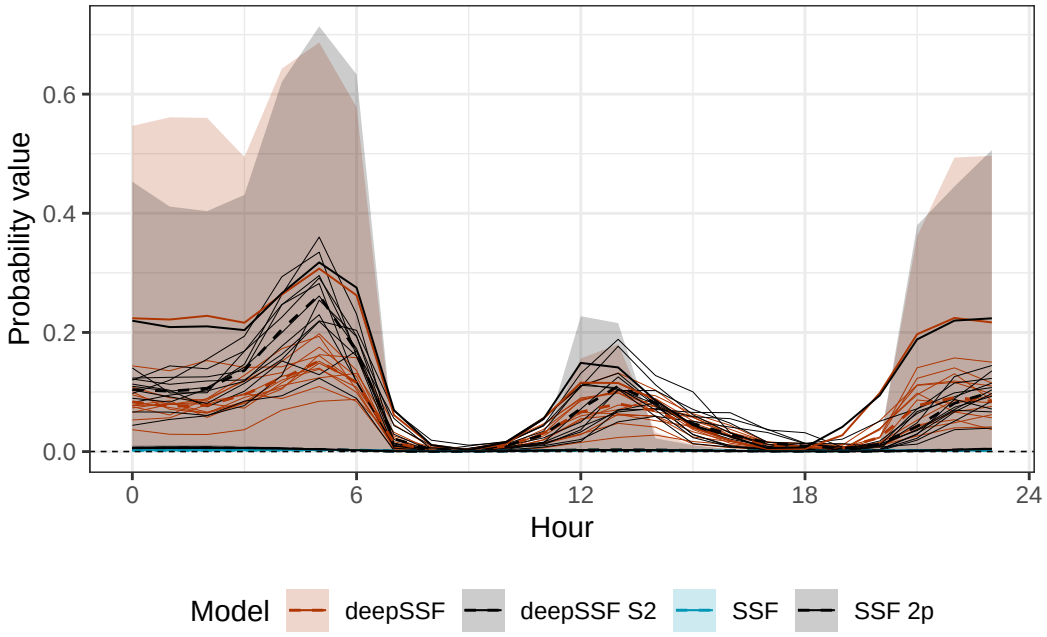
Movement probability across the day

All models

```
ggplot() +

  # dashed lines containing the SSF probabilities
  geom_hline(yintercept = 0, alpha = 0.25, linetype = "dashed", linewidth = 0.25) +
  geom_hline(yintercept = 3e-4, alpha = 0.25, linetype = "dashed", linewidth = 0.25) +

  # in sample 50% ribbon
  geom_ribbon(data = validation_all_quantiles_hourly %>%
                filter(probability == "move",
                       id == focal_id),
              aes(x = hour_t2,
                  ymin = q25,
```

```
                ymax = q75,
                fill = model,
                group = interaction(id, model)),
            alpha = ribbon_50_alpha) +

# out-of-sample thin line for each individual
geom_line(data = validation_all_quantiles_hourly %>%
            filter(probability == "move",
                   !id == focal_id),
          aes(x = hour_t2,
              y = average_prob,
              colour = model,
              group = interaction(id, model)),
          linewidth = 0.075) +

# out-of-sample mean line
geom_line(data = validation_all_quantiles_hourly_OOS %>%
            filter(probability == "move"),
          aes(x = hour_t2,
              y = average_prob,
              colour = model),
          linewidth = OOS_mean_linewidth,
          linetype = "dashed") +

# in sample mean line
geom_line(data = validation_all_quantiles_hourly %>%
            filter(probability == "move",
                   id == focal_id),
          aes(x = hour_t2,
              y = average_prob,
              colour = model,
              group = interaction(id, model)),
          linewidth = 0.35) +

geom_hline(yintercept = uniform_prob, linetype = "dashed", linewidth = 0.25) +

scale_fill_manual(name = "Model",
                  values = c("#AF3602", "#000000", "#0096B5", "#000000"),
                  labels = c("deepSSF", "deepSSF S2", "SSF", "SSF 2p")) +

scale_color_manual(name = "Model",
                   values = c("#AF3602", "#000000", "#0096B5", "#000000"),
                   labels = c("deepSSF", "deepSSF S2", "SSF", "SSF 2p")) +
```

```
  scale_y_continuous("Probability value") +
  scale_x_continuous("Hour", breaks = seq(0,24,6)) +
  theme_bw() +
  theme(legend.position = "bottom")
```




```
# ggsave(paste0("outputs/validation_all_move_hourly.png"),
#        width = 80, height = 80, units = "mm", dpi = 600)
```

The movement probabilities are much lower during the high movement periods. This is because there are many more cells that the buffalo are likely to move to, and so the probability of moving to any one cell is lower, and the model must spread the prediction probability across many more cells.

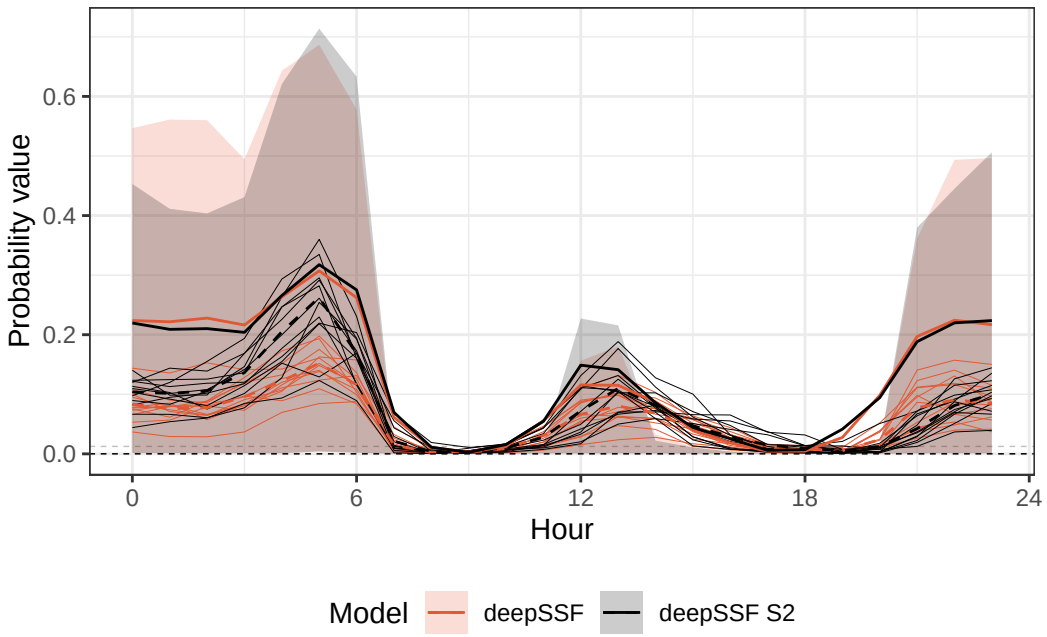
The SSF probabilities are also much much lower than the deepSSF probabilities, as explained for the movement probabilities across the tracking period.

deepSSF models

```
ggplot() +

  # dashed lines containing the SSF probabilities
  geom_hline(yintercept = 0, alpha = 0.25, linetype = "dashed", linewidth = 0.25) +
  geom_hline(yintercept = 1.25e-2, alpha = 0.25, linetype = "dashed", linewidth = 0.25) +
```

```
# in sample 50% ribbon
geom_ribbon(data = validation_all_quantiles_hourly %>%
              filter(probability == "move",
                     id == focal_id,
                     grepl("deepSSF", model)),
            aes(x = hour_t2,
                ymin = q25,
                ymax = q75,
                fill = model,
                group = interaction(id, model)),
            alpha = ribbon_50_alpha) +

# out-of-sample thin line for each individual
geom_line(data = validation_all_quantiles_hourly %>%
            filter(probability == "move",
                   !id == focal_id,
                   grepl("deepSSF", model)),
          aes(x = hour_t2,
              y = average_prob,
              colour = model,
              group = interaction(id, model)),
          linewidth = secondary_linewidth) +

# out-of-sample mean line
geom_line(data = validation_all_quantiles_hourly_OOS %>%
            filter(probability == "move" &
                   grepl("deepSSF", model)),
          aes(x = hour_t2,
              y = average_prob,
              colour = model),
          linewidth = OOS_mean_linewidth,
          linetype = "dashed") +

# in sample mean line
geom_line(data = validation_all_quantiles_hourly %>%
            filter(probability == "move",
                   id == focal_id,
                   grepl("deepSSF", model)),
          aes(x = hour_t2,
              y = average_prob,
              colour = model,
              group = interaction(id, model)),
          linewidth = primary_linewidth) +
```

```
  # dashed line for uniform probability
  geom_hline(yintercept = uniform_prob, linetype = "dashed", linewidth = 0.25) +

  scale_fill_manual(name = "Model",
                    values = c("#E25834", "#000000"),
                    labels = c("deepSSF", "deepSSF S2")) +

  scale_color_manual(name = "Model",
                     values = c("#E25834", "#000000"),
                     labels = c("deepSSF", "deepSSF S2")) +

  scale_y_continuous("Probability value") +
  scale_x_continuous("Hour", seq(0,24,6)) +
  theme_bw() +
  theme(legend.position = "bottom")
```



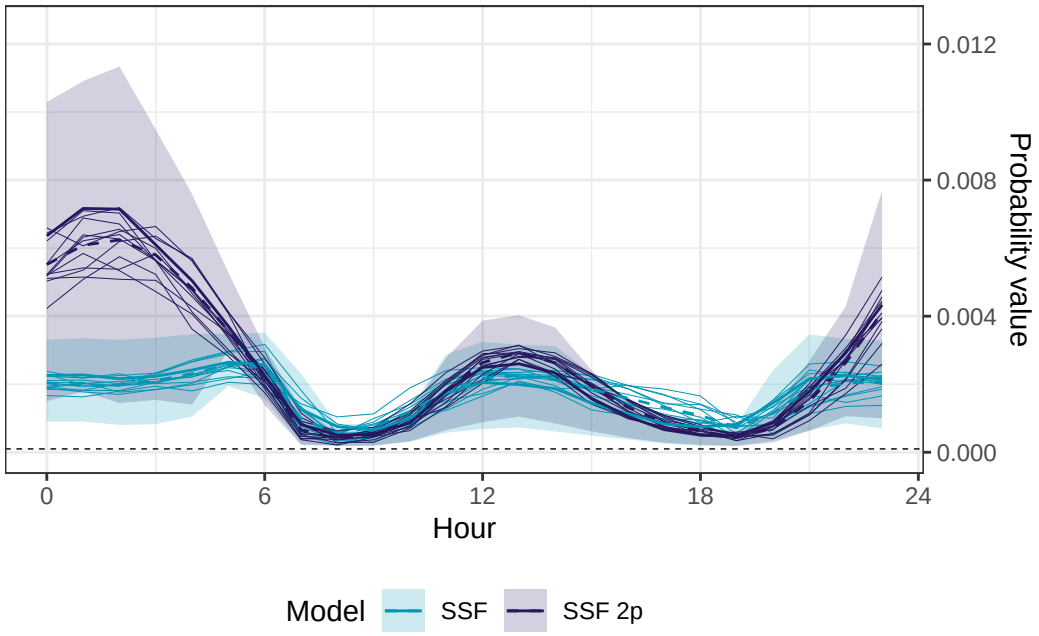

```
# ggsave(paste0("outputs/validation_deepSSF_move_hourly.png"),
#        width = 80, height = 80, units = "mm", dpi = 600)
```

SSF models

```
ggplot() +
```

```
# in sample 50% ribbon
geom_ribbon(data = validation_all_quantiles_hourly %>%
              filter(probability == "move",
                     id == focal_id,
                     !grepl("deepSSF", model)),
            aes(x = hour_t2,
                ymin = q25,
                ymax = q75,
                fill = model,
                group = interaction(id, model)),
            alpha = ribbon_50_alpha) +

# out-of-sample thin line for each individual
geom_line(data = validation_all_quantiles_hourly %>%
            filter(probability == "move",
                     !id == focal_id,
                     !grepl("deepSSF", model)),
          aes(x = hour_t2,
              y = average_prob,
              colour = model,
              group = interaction(id, model)),
          linewidth = secondary_linewidth) +

# out-of-sample mean line
geom_line(data = validation_all_quantiles_hourly_OOS %>%
            filter(probability == "move" &
                     !grepl("deepSSF", model)),
          aes(x = hour_t2,
              y = average_prob,
              colour = model),
          linewidth = OOS_mean_linewidth,
          linetype = "dashed") +

# in sample mean line
geom_line(data = validation_all_quantiles_hourly %>%
            filter(probability == "move",
                     id == focal_id,
                     !grepl("deepSSF", model)),
          aes(x = hour_t2,
              y = average_prob,
              colour = model,
              group = interaction(id, model)),
          linewidth = primary_linewidth) +
```

```
  # dashed line for uniform probability
  geom_hline(yintercept = uniform_prob, linetype = "dashed", linewidth = 0.25) +

  scale_fill_manual(name = "Model",
                    values = c("#0096B5", "#26185F"),
                    labels = c("SSF", "SSF 2p")) +

  scale_color_manual(name = "Model",
                     values = c("#0096B5", "#26185F"),
                     labels = c("SSF", "SSF 2p")) +

    scale_y_continuous("Probability value",
                       position = "right") +

  scale_x_continuous("Hour", seq(0,24,6)) +
  coord_cartesian(ylim = c(0, 1.25e-2)) +
  theme_bw() +
  theme(legend.position = "bottom")
```




```
# ggsave(paste0("outputs/validation_SSF_move_hourly.png"),
#        width = 80, height = 80, units = "mm", dpi = 600)
```

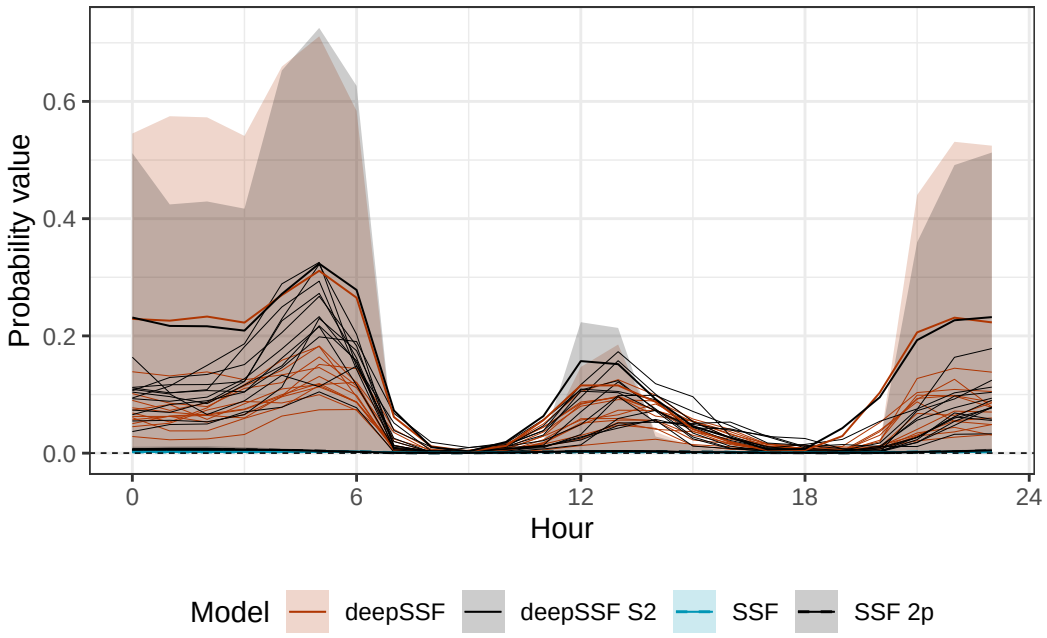
The SSF models perform similarly, expect at night, where the temporally dynamic performs much better in- and out-of-sample.

Next-step probability across the day

All models

```
ggplot() +

  # dashed lines containing the SSF probabilities
  geom_hline(yintercept = 0, alpha = 0.25, linetype = "dashed", linewidth = 0.25) +
  geom_hline(yintercept = 3e-4, alpha = 0.25, linetype = "dashed", linewidth = 0.25) +

  # in sample 50% ribbon
  geom_ribbon(data = validation_all_quantiles_hourly %>%
                filter(probability == "next_step",
                       id == focal_id),
              aes(x = hour_t2,
                  ymin = q25,
                  ymax = q75,
                  fill = model,
                  group = interaction(id, model)),
              alpha = ribbon_50_alpha) +

  # out-of-sample thin line for each individual
  geom_line(data = validation_all_quantiles_hourly %>%
              filter(probability == "next_step",
                     !id == focal_id),
            aes(x = hour_t2,
                y = average_prob,
                colour = model,
                group = interaction(id, model)),
            linewidth = 0.075) +

  # out-of-sample mean line
  geom_line(data = validation_all_quantiles_hourly_OOS %>%
              filter(probability == "move" &
                     !grepl("deepSSF", model)),
            aes(x = hour_t2,
                y = average_prob,
                colour = model),
            linewidth = OOS_mean_linewidth,
            linetype = "dashed") +

  # in sample mean line
  geom_line(data = validation_all_quantiles_hourly %>%
```

```
              filter(probability == "next_step",
                     id == focal_id),
            aes(x = hour_t2,
                y = average_prob,
                colour = model,
                group = interaction(id, model)),
            linewidth = 0.35) +

  # dashed line for uniform probability
  geom_hline(yintercept = uniform_prob, linetype = "dashed", linewidth = 0.25) +

  scale_fill_manual(name = "Model",
                    values = c("#AF3602", "#000000", "#0096B5", "#000000"),
                    labels = c("deepSSF", "deepSSF S2", "SSF", "SSF 2p")) +

  scale_color_manual(name = "Model",
                     values = c("#AF3602", "#000000", "#0096B5", "#000000"),
                     labels = c("deepSSF", "deepSSF S2", "SSF", "SSF 2p")) +

  scale_y_continuous("Probability value") +
  scale_x_continuous("Hour", breaks = seq(0,24,6)) +
  theme_bw() +
  theme(legend.position = "bottom")
```

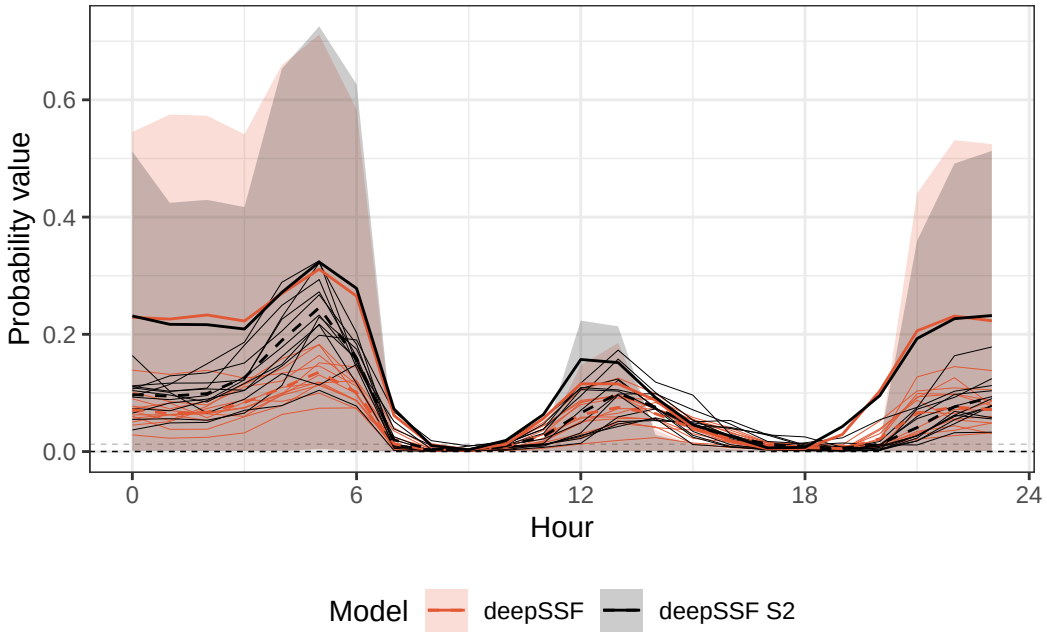


```
# ggsave(paste0("outputs/validation_all_next_step_hourly.png"),
#        width = 80, height = 80, units = "mm", dpi = 600)
```

deepSSF models

```
ggplot() +

  # dashed lines containing the SSF probabilities
  geom_hline(yintercept = 0, alpha = 0.25, linetype = "dashed", linewidth = 0.25) +
  geom_hline(yintercept = 1.25e-2, alpha = 0.25, linetype = "dashed", linewidth = 0.25) +

  # in sample 50% ribbon
  geom_ribbon(data = validation_all_quantiles_hourly %>%
                filter(probability == "next_step",
                       id == focal_id,
                       grepl("deepSSF", model)),
              aes(x = hour_t2,
                  ymin = q25,
                  ymax = q75,
                  fill = model,
                  group = interaction(id, model)),
              alpha = ribbon_50_alpha) +

  # out-of-sample thin line for each individual
  geom_line(data = validation_all_quantiles_hourly %>%
              filter(probability == "next_step",
                     !id == focal_id,
                     grepl("deepSSF", model)),
            aes(x = hour_t2,
                y = average_prob,
                colour = model,
                group = interaction(id, model)),
            linewidth = secondary_linewidth) +

  # out-of-sample mean line
  geom_line(data = validation_all_quantiles_hourly_OOS %>%
              filter(probability == "next_step" &
                     grepl("deepSSF", model)),
            aes(x = hour_t2,
                y = average_prob,
                colour = model),
            linewidth = OOS_mean_linewidth,
```

```
          linetype = "dashed") +

# in sample mean line
geom_line(data = validation_all_quantiles_hourly %>%
            filter(probability == "next_step",
                   id == focal_id,
                   grepl("deepSSF", model)),
          aes(x = hour_t2,
              y = average_prob,
              colour = model,
              group = interaction(id, model)),
          linewidth = primary_linewidth) +

# dashed line for uniform probability
geom_hline(yintercept = uniform_prob, linetype = "dashed", linewidth = 0.25) +

scale_fill_manual(name = "Model",
                  values = c("#E25834", "#000000"),
                  labels = c("deepSSF", "deepSSF S2")) +

scale_color_manual(name = "Model",
                   values = c("#E25834", "#000000"),
                   labels = c("deepSSF", "deepSSF S2")) +

scale_y_continuous("Probability value") +
scale_x_continuous("Hour", seq(0,24,6)) +
theme_bw() +
theme(legend.position = "bottom")
```



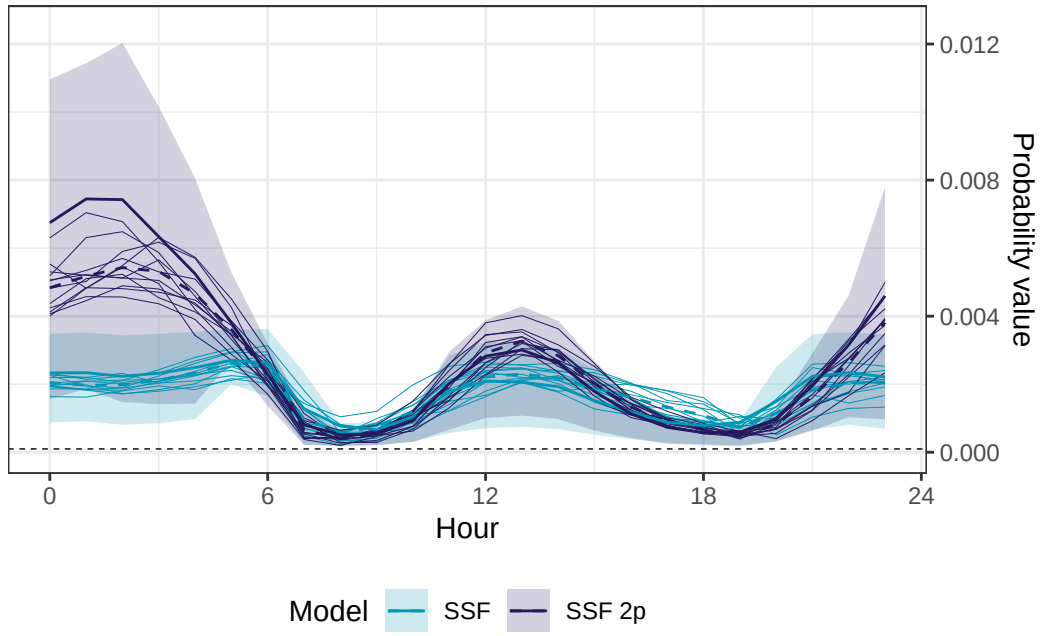

```
# ggsave(paste0("outputs/validation_deepSSF_next_step_hourly.png"),
#        width = 80, height = 80, units = "mm", dpi = 600)
```

SSF models

```
ggplot() +

  # in sample 50% ribbon
  geom_ribbon(data = validation_all_quantiles_hourly %>%
                filter(probability == "next_step",
                       id == focal_id,
                       !grepl("deepSSF", model)),
              aes(x = hour_t2,
                  ymin = q25,
                  ymax = q75,
                  fill = model,
                  group = interaction(id, model)),
              alpha = ribbon_50_alpha) +

  # out-of-sample thin line for each individual
  geom_line(data = validation_all_quantiles_hourly %>%
              filter(probability == "next_step",
                       !id == focal_id,
                       !grepl("deepSSF", model)),
```

```
          aes(x = hour_t2,
              y = average_prob,
              colour = model,
              group = interaction(id, model)),
          linewidth = secondary_linewidth) +

# out-of-sample mean line
geom_line(data = validation_all_quantiles_hourly_OOS %>%
            filter(probability == "next_step" &
                   !grepl("deepSSF", model)),
          aes(x = hour_t2,
              y = average_prob,
              colour = model),
          linewidth = OOS_mean_linewidth,
          linetype = "dashed") +

# in sample mean line
geom_line(data = validation_all_quantiles_hourly %>%
            filter(probability == "next_step",
                   id == focal_id,
                   !grepl("deepSSF", model)),
          aes(x = hour_t2,
              y = average_prob,
              colour = model,
              group = interaction(id, model)),
          linewidth = primary_linewidth) +

# dashed line for uniform probability
geom_hline(yintercept = uniform_prob, linetype = "dashed", linewidth = 0.25) +

scale_fill_manual(name = "Model",
                  values = c("#0096B5", "#26185F"),
                  labels = c("SSF", "SSF 2p")) +

scale_color_manual(name = "Model",
                   values = c("#0096B5", "#26185F"),
                   labels = c("SSF", "SSF 2p")) +

  scale_y_continuous("Probability value",
                   position = "right") +

scale_x_continuous("Hour", seq(0,24,6)) +
coord_cartesian(ylim = c(0, 1.25e-2)) +
theme_bw() +
```

```
  theme(legend.position = "bottom")
```




```
# ggsave(paste0("outputs/validation_SSF_next_step_hourly.png"),
#        width = 80, height = 80, units = "mm", dpi = 600)
```