

narwhal_habitat_model

Marie Zahn

2022-12-12

```
library(tidyverse)
```

```
## -- Attaching packages ----- tidyverse 1.3.2 --
## v ggplot2 3.4.0      v purrr   1.0.1
## v tibble  3.1.8      v dplyr  1.0.10
## v tidyr   1.3.0      v stringr 1.5.0
## v readr   2.1.3      v forcats 0.5.2
## -- Conflicts ----- tidyverse_conflicts() --
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()    masks stats::lag()
```

```
library(corrplot)
```

```
## corrplot 0.92 loaded
```

```
library(MuMIn)
library(arm)
```

```
## Loading required package: MASS
##
## Attaching package: 'MASS'
##
## The following object is masked from 'package:dplyr':
##
##     select
##
## Loading required package: Matrix
##
## Attaching package: 'Matrix'
##
## The following objects are masked from 'package:tidyr':
##
##     expand, pack, unpack
##
## Loading required package: lme4
##
## arm (Version 1.13-1, built: 2022-8-25)
##
## Working directory is C:/Users/marie/Documents/OMG_Narwhals/OMG_narwhals_habitat-model
##
```

```
##
## Attaching package: 'arm'
##
## The following object is masked from 'package:MuMIn':
##
##   coefplot
##
## The following object is masked from 'package:corrplot':
##
##   corrplot
```

```
library(faraway)
```

```
##
## Attaching package: 'faraway'
##
## The following objects are masked from 'package:arm':
##
##   fround, logit, pfround
```

```
library(ggplot2)
library(sjPlot)
```

```
## Learn more about sjPlot with 'browseVignettes("sjPlot")'.
```

```
library(here)
```

```
## here() starts at C:/Users/marie/Documents/OMG_Narwhals/OMG_narwhals_habitat-model
```

Open Data

```
# reload data from anywhere
here(load('data-cleaning_R/narwhal_model_data_pooled.rdata'))
```

```
## [1] "C:/Users/marie/Documents/OMG_Narwhals/OMG_narwhals_habitat-model/model_data_pooled"
```

```
here(load('data-cleaning_R/narwhal_model_data.rdata'))
```

```
## [1] "C:/Users/marie/Documents/OMG_Narwhals/OMG_narwhals_habitat-model/model_data"
```

```
## since we know narwhals cannot survive in Melville Bay after the freeze up, we will select data from
## here, I define the freeze up date as the day when sea ice > 75%
```

```
## freeze up date in 2018
head(model_data_pooled %>% dplyr::filter(ice_cover_percent>75,year==2018))
```

```
##           time runoff_racmo site runoff_mar salt_surf salt_deep temp_surf
## 1 2018-10-28    0.1247006 kong  0.3100168  33.49034  33.84377 -0.4359297
## 2 2018-11-13    0.1089631 kong  0.2753987  33.52036  33.86097 -0.3789748
```

```
## 3 2018-11-14      0.1115898 kong  0.2732921  33.52722  33.86567 -0.3284850
## 4 2018-11-15      0.1102063 kong  0.2711936  33.52545  33.86392 -0.3194206
## 5 2018-11-16      0.1101383 kong  0.2689909  33.53464  33.86592 -0.3225634
## 6 2018-11-17      0.1109811 kong  0.2671873  33.53710  33.86374 -0.2980898
##   temp_deep ice_cover_percent velocity glacier_length narwhal DOY year
## 1 0.3582948          82.00883 3010.278          8.624658          0 301 2018
## 2 0.4205963          93.59823 2994.352          8.752695          0 317 2018
## 3 0.4116690          99.00662 2993.356          8.753551          0 318 2018
## 4 0.4064240         100.00000 2992.361          8.754407          0 319 2018
## 5 0.4193806         100.00000 2991.366          8.755263          0 320 2018
## 6 0.4213567          99.88962 2990.370          8.756119          0 321 2018
```

```
# 2018-10-28 which is equal to DOY=301 # sverdrup froze up first
```

```
## freeze up date in 2019
```

```
model_data_pooled %>% dplyr::filter(ice_cover_percent>75,year==2019,DOY>100)
```

```
##           time runoff_racmo site runoff_mar salt_surf salt_deep temp_surf
## 1 2019-12-31    0.09115496 kong 0.09437288  33.24400  33.72108 -0.2055125
## 2 2019-12-23    0.25243448 rink 0.24792070  33.39402  33.69145 -0.2654788
## 3 2019-12-24    0.24627112 rink 0.24735389  33.40208  33.69575 -0.2379754
## 4 2019-12-26    0.25851134 rink 0.24601606  33.40640  33.70701 -0.2619147
## 5 2019-12-27    0.23267056 rink 0.24559086  33.42145  33.71498 -0.2934537
## 6 2019-12-30    0.25710513 rink 0.24374035  33.43955  33.72645 -0.3198567
## 7 2019-12-31    0.24868599 rink 0.24310069  33.43894  33.73330 -0.3224014
##   temp_deep ice_cover_percent velocity glacier_length narwhal DOY year
## 1 -0.01145810          87.74834 2942.4390          8.324216          0 365 2019
## 2  0.03881604          90.81309 681.7681          13.524452          0 357 2019
## 3  0.07085468          87.22281 681.3477          13.527430          0 358 2019
## 4  0.08667527          87.22281 680.4441          13.533386          0 360 2019
## 5  0.12570393          80.14784 679.9372          13.536364          0 361 2019
## 6  0.10097206          95.03696 678.4163          13.545299          0 364 2019
## 7  0.09907804          84.37170 677.9908          13.548277          0 365 2019
```

```
# 2019-12-23 which is equal to DOY=357 # rink froze up first
```

```
## filter all data before these dates
```

```
# not pooled
```

```
mdl_data_open_water2018 <- model_data %>% filter(year==2018) %>%
  filter(DOY<301)
```

```
mdl_data_open_water2019 <- model_data %>% filter(year==2019) %>%
  filter(DOY>100,DOY<357)
```

```
# pooled
```

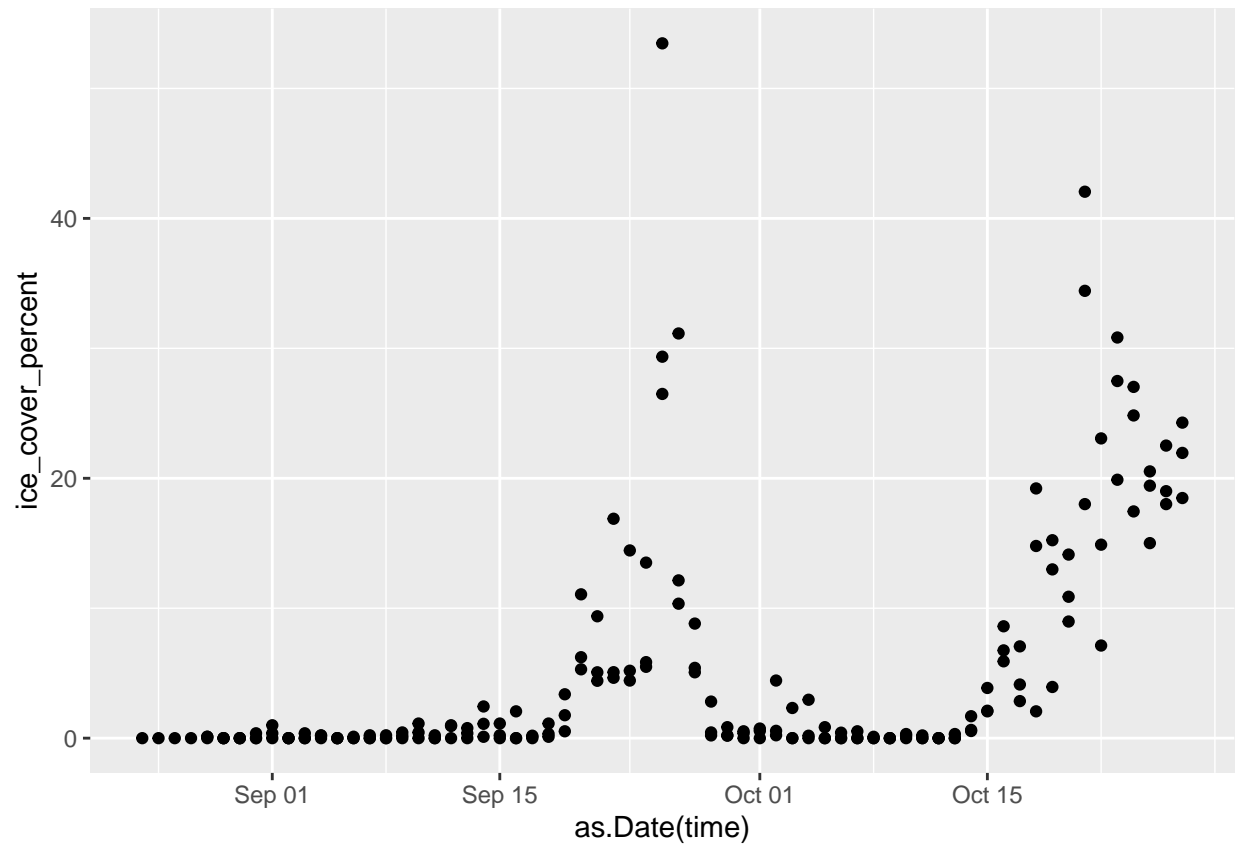
```
mdl_data_open_water2018_pool <- model_data_pooled %>% filter(year==2018) %>%
  filter(DOY<301)
```

```
mdl_data_open_water2019_pool <- model_data_pooled %>% filter(year==2019) %>%
  filter(DOY>100,DOY<357)
```

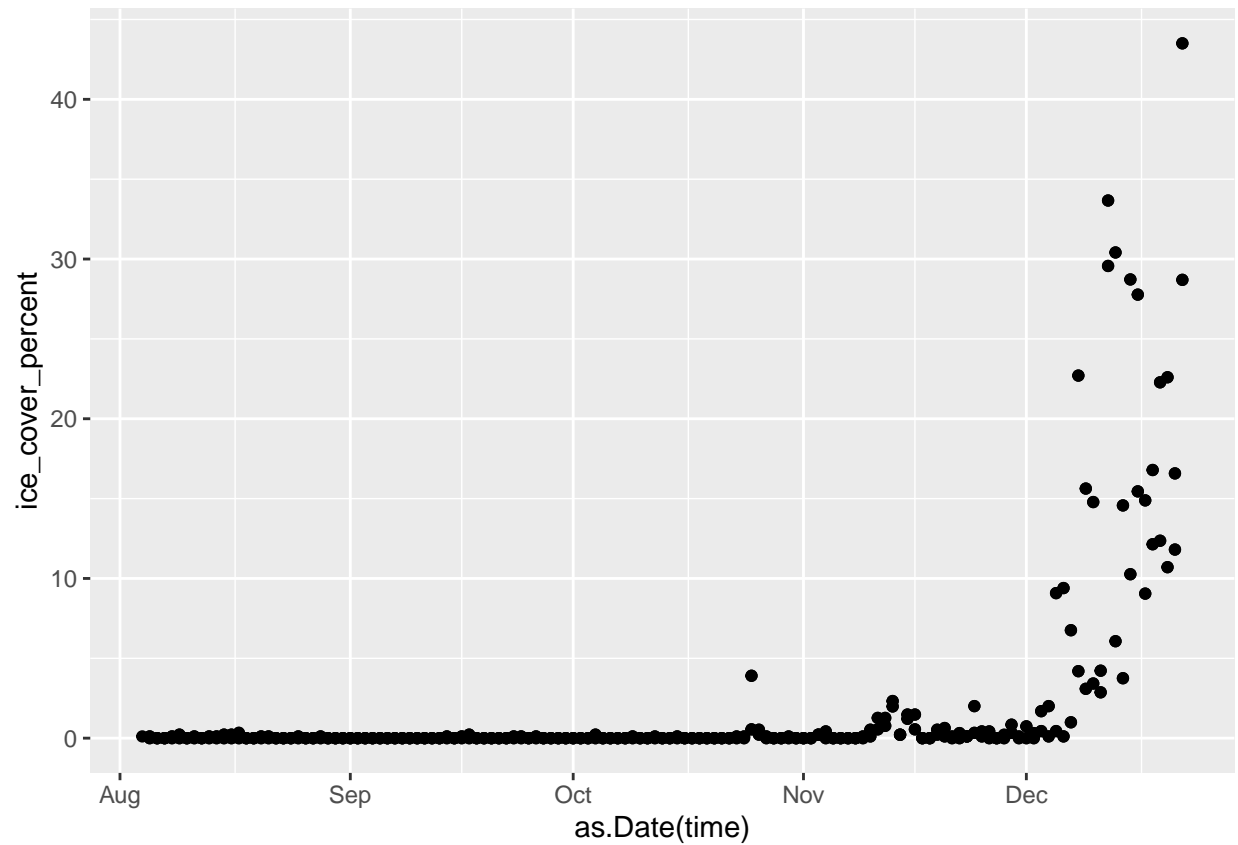
```
# sanity check plots
```

```
qplot(as.Date(time),ice_cover_percent, geom="point", data = mdl_data_open_water2018)
```

```
## Warning: `qplot()` was deprecated in ggplot2 3.4.0.
```

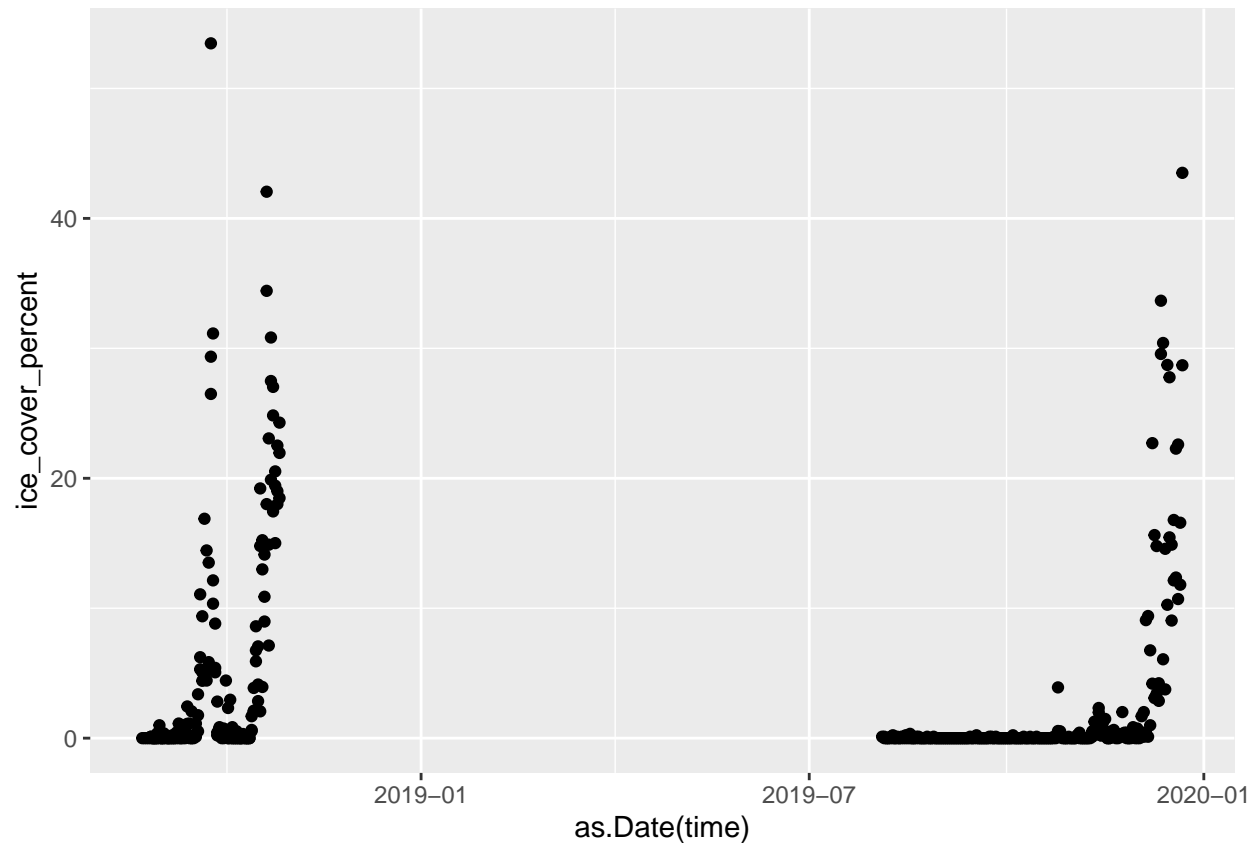


```
qplot(as.Date(time),ice_cover_percent, geom="point", data = mdl_data_open_water2019)
```



```
## join both datasets
mdl_data_b4freeze <- rbind(mdl_data_open_water2018, mdl_data_open_water2019)
mdl_data_b4freeze_pooled <- rbind(mdl_data_open_water2018_pool, mdl_data_open_water2019_pool)

qplot(as.Date(time), ice_cover_percent, geom="point", data = mdl_data_b4freeze_pooled)
```



Run models

Got warning message when sea ice was included: Warning message: glm.fit: fitted probabilities numerically 0 or 1 occurred

When I removed sea ice cover, the warning was gone.

```
## logistic regression
## glm with binomial response and logit link =====

# Model using unscaled data -----

## model with 'device' variable (unpooled detections)
mdl_global <- glm(narwhal ~
  temp_surf+
  temp_deep+
  salt_surf+
  salt_deep+
  ice_cover_percent+
  runoff_racmo+
  glacier_length+
  device+
  site+
  DOY,
  data = mdl_data_b4freeze,
```

```

        family=quasibinomial(link="logit"),
        na.action="na.fail")

# print summary output
summary mdl_global

##
## Call:
## glm(formula = narwhal ~ temp_surf + temp_deep + salt_surf + salt_deep +
##      ice_cover_percent + runoff_racmo + glacier_length + device +
##      site + DOY, family = quasibinomial(link = "logit"), data = mdl_data_b4freeze,
##      na.action = "na.fail")
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -1.3600  -0.6383  -0.2944  -0.0349   3.0096
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   -2.132e+02  2.746e+02  -0.776  0.43771
## temp_surf      -7.652e-01  6.896e-01  -1.110  0.26747
## temp_deep       3.009e+00  1.518e+00   1.982  0.04788 *
## salt_surf      -2.386e+00  4.011e+00  -0.595  0.55203
## salt_deep       8.308e+00  1.040e+01   0.799  0.42481
## ice_cover_percent -2.309e-01  1.183e-01  -1.951  0.05142 .
## runoff_racmo    -1.168e-02  2.876e-03  -4.062 5.38e-05 ***
## glacier_length   1.866e+00  1.137e+00   1.640  0.10135
## devicesoundtrap  1.285e+00  2.376e-01   5.408 8.63e-08 ***
## siterink        -8.913e+00  5.425e+00  -1.643  0.10082
## sitesver        -9.601e+00  5.751e+00  -1.669  0.09548 .
## DOY             -2.805e-02  1.060e-02  -2.646  0.00831 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for quasibinomial family taken to be 0.8241772)
##
##      Null deviance: 648.79  on 747  degrees of freedom
## Residual deviance: 497.33  on 736  degrees of freedom
## AIC: NA
##
## Number of Fisher Scoring iterations: 9

faraway::sumary(mdl_global)

```

```

##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   -2.1324e+02  2.7462e+02 -0.7765  0.437709
## temp_surf      -7.6523e-01  6.8956e-01 -1.1097  0.267474
## temp_deep       3.0086e+00  1.5182e+00  1.9817  0.047884
## salt_surf      -2.3863e+00  4.0106e+00 -0.5950  0.552035
## salt_deep       8.3077e+00  1.0404e+01  0.7986  0.424809
## ice_cover_percent -2.3089e-01  1.1834e-01 -1.9512  0.051418
## runoff_racmo    -1.1685e-02  2.8763e-03 -4.0624 5.379e-05

```

```
## glacier_length      1.8658e+00  1.1374e+00  1.6404  0.101355
## devicesoundtrap     1.2849e+00  2.3759e-01  5.4078  8.631e-08
## siterink            -8.9127e+00  5.4249e+00 -1.6429  0.100823
## sitesver            -9.6008e+00  5.7514e+00 -1.6693  0.095483
## DOY                 -2.8051e-02  1.0599e-02 -2.6465  0.008307
##
## Dispersion parameter = 0.82418
## n = 748 p = 12
## Deviance = 497.32805 Null Deviance = 648.78616 (Difference = 151.45811)
```

```
# par(mfrow = c(2,2))
# plot mdl_global
# plot_model(mdl_global, type="pred")

## model without 'device' (pooled detections)
mdl_global_pooled <- glm(narwhal ~
  temp_surf+
  temp_deep+
  salt_surf+
  salt_deep+
  ice_cover_percent+
  runoff_racmo+
  glacier_length+
  site+
  DOY,
  data = mdl_data_b4freeze_pooled,
  family=quasibinomial(link="logit"), na.action="na.fail")

# print summary output
summary(mdl_global_pooled)
```

```
##
## Call:
## glm(formula = narwhal ~ temp_surf + temp_deep + salt_surf + salt_deep +
##      ice_cover_percent + runoff_racmo + glacier_length + site +
##      DOY, family = quasibinomial(link = "logit"), data = mdl_data_b4freeze_pooled,
##      na.action = "na.fail")
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -1.44824  -0.70220  -0.23442  -0.00663   2.76362
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   -7.513e+02  3.325e+02  -2.260  0.02432 *
## temp_surf      9.456e-01  7.446e-01   1.270  0.20475
## temp_deep     -1.039e+00  1.627e+00  -0.639  0.52326
## salt_surf     -4.077e+00  4.595e+00  -0.887  0.37543
## salt_deep      2.559e+01  1.279e+01   2.001  0.04594 *
## ice_cover_percent -3.456e-01  1.335e-01  -2.588  0.00996 **
## runoff_racmo   -1.354e-02  3.348e-03  -4.044  6.18e-05 ***
## glacier_length  2.938e+00  1.282e+00   2.292  0.02238 *
## siterink       -1.301e+01  6.103e+00  -2.132  0.03355 *
## sitesver       -1.446e+01  6.421e+00  -2.252  0.02482 *
```



```
## DOY                -1.725e-02  1.141e-02  -1.511  0.13136
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for quasibinomial family taken to be 0.7739693)
##
##      Null deviance: 466.71  on 467  degrees of freedom
## Residual deviance: 353.79  on 457  degrees of freedom
## AIC: NA
##
## Number of Fisher Scoring iterations: 8
```

```
faraway::sumary mdl_global_pooled)
```

```
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) -7.5129e+02 3.3250e+02 -2.2595 0.024321
## temp_surf   9.4563e-01 7.4462e-01  1.2699 0.204752
## temp_deep  -1.0394e+00 1.6271e+00 -0.6388 0.523262
## salt_surf  -4.0765e+00 4.5947e+00 -0.8872 0.375430
## salt_deep   2.5594e+01 1.2788e+01  2.0014 0.045942
## ice_cover_percent -3.4559e-01 1.3353e-01 -2.5882 0.009956
## runoff_racmo -1.3539e-02 3.3481e-03 -4.0436 6.177e-05
## glacier_length  2.9384e+00 1.2823e+00  2.2916 0.022385
## siterink      -1.3011e+01 6.1030e+00 -2.1318 0.033552
## sitesver      -1.4457e+01 6.4208e+00 -2.2516 0.024821
## DOY           -1.7253e-02 1.1415e-02 -1.5115 0.131357
##
## Dispersion parameter = 0.77397
## n = 468 p = 11
## Deviance = 353.78507 Null Deviance = 466.70830 (Difference = 112.92322)
```

```
# par(mfrow = c(2,2))
# plot mdl_global_pooled
# plot_model mdl_global_pooled, type="pred")
```

Run separate glm for each glacier/site. Here I only use pooled datasets (=no device variable)

```
## Rink/Fisher -----
mdl_data_rink <- mdl_data_b4freeze_pooled %>% filter(site=='rink')
mdl_rink <- glm(narwhal ~ temp_surf+temp_deep+salt_surf+salt_deep+
               ice_cover_percent+runoff_racmo+glacier_length+DOY,
               data = mdl_data_rink,family=binomial(link="logit"),na.action="na.fail")
```

```
## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred
```

```
summary(mdl_rink)
```

```
##
## Call:
## glm(formula = narwhal ~ temp_surf + temp_deep + salt_surf + salt_deep +
##      ice_cover_percent + runoff_racmo + glacier_length + DOY,
```

```
## family = binomial(link = "logit"), data = mdl_data_rink,
## na.action = "na.fail")
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -1.4707  -0.7534  -0.1132   0.0000   3.4118
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)    -1.170e+03  9.236e+02  -1.267  0.2052
## temp_surf      -3.058e+00  3.384e+00  -0.903  0.3663
## temp_deep       4.798e+00  5.817e+00   0.825  0.4095
## salt_surf      -1.300e+01  2.328e+01  -0.558  0.5767
## salt_deep       5.233e+01  4.188e+01   1.249  0.2115
## ice_cover_percent -1.398e+00  9.314e-01  -1.501  0.1335
## runoff_racmo     2.005e-02  1.141e-02   1.757  0.0789
## glacier_length  -1.343e+01  1.489e+01  -0.902  0.3671
## DOY              4.473e-02  3.151e-02   1.419  0.1558
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##      Null deviance: 213.77  on 200  degrees of freedom
## Residual deviance: 148.50  on 192  degrees of freedom
## AIC: 166.5
##
## Number of Fisher Scoring iterations: 11
```

```
# par(mfrow = c(2,2))
# plot(mdl_rink)

## Kong Oscar -----
mdl_data_kong <- mdl_data_b4freeze_pooled %>% filter(site=='kong')
mdl_kong <- glm(narwhal ~ temp_surf+temp_deep+salt_surf+salt_deep+
               ice_cover_percent+runoff_racmo+glacier_length+DOY,
               data = mdl_data_kong,family=binomial(link="logit"),na.action="na.fail")
summary(mdl_kong)
```

```
##
## Call:
## glm(formula = narwhal ~ temp_surf + temp_deep + salt_surf + salt_deep +
##      ice_cover_percent + runoff_racmo + glacier_length + DOY,
##      family = binomial(link = "logit"), data = mdl_data_kong,
##      na.action = "na.fail")
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -1.78364  -0.68418  -0.19090  -0.00701   2.33356
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)    -1.445e+03  9.592e+02  -1.506  0.13205
## temp_surf       3.208e+00  2.008e+00   1.598  0.11003
```

```
## temp_deep      -5.362e+00  5.580e+00  -0.961  0.33662
## salt_surf      4.171e+00  1.052e+01   0.396  0.69181
## salt_deep      3.740e+01  3.518e+01   1.063  0.28772
## ice_cover_percent -1.906e-01  1.587e-01  -1.200  0.23000
## runoff_racmo   -2.018e-02  7.503e-03  -2.689  0.00716 **
## glacier_length  4.844e+00  2.520e+00   1.922  0.05459 .
## DOY            -6.388e-03  2.382e-02  -0.268  0.78861
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
## Null deviance: 203.82  on 201  degrees of freedom
## Residual deviance: 146.89  on 193  degrees of freedom
## AIC: 164.89
##
## Number of Fisher Scoring iterations: 8
```

```
# par(mfrow = c(2,2))
# plot mdl_kong

## Sverdrup -----
mdl_data_sver <- mdl_data_b4freeze_pooled %>% filter(site=='sver')
mdl_sver <- glm(narwhal ~ temp_surf+temp_deep+salt_surf+salt_deep+
               ice_cover_percent+runoff_racmo+glacier_length+DOY,
               data = mdl_data_sver,family=binomial(link="logit"),na.action="na.fail")
```

```
## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred
```

```
summary(mdl_sver)
```

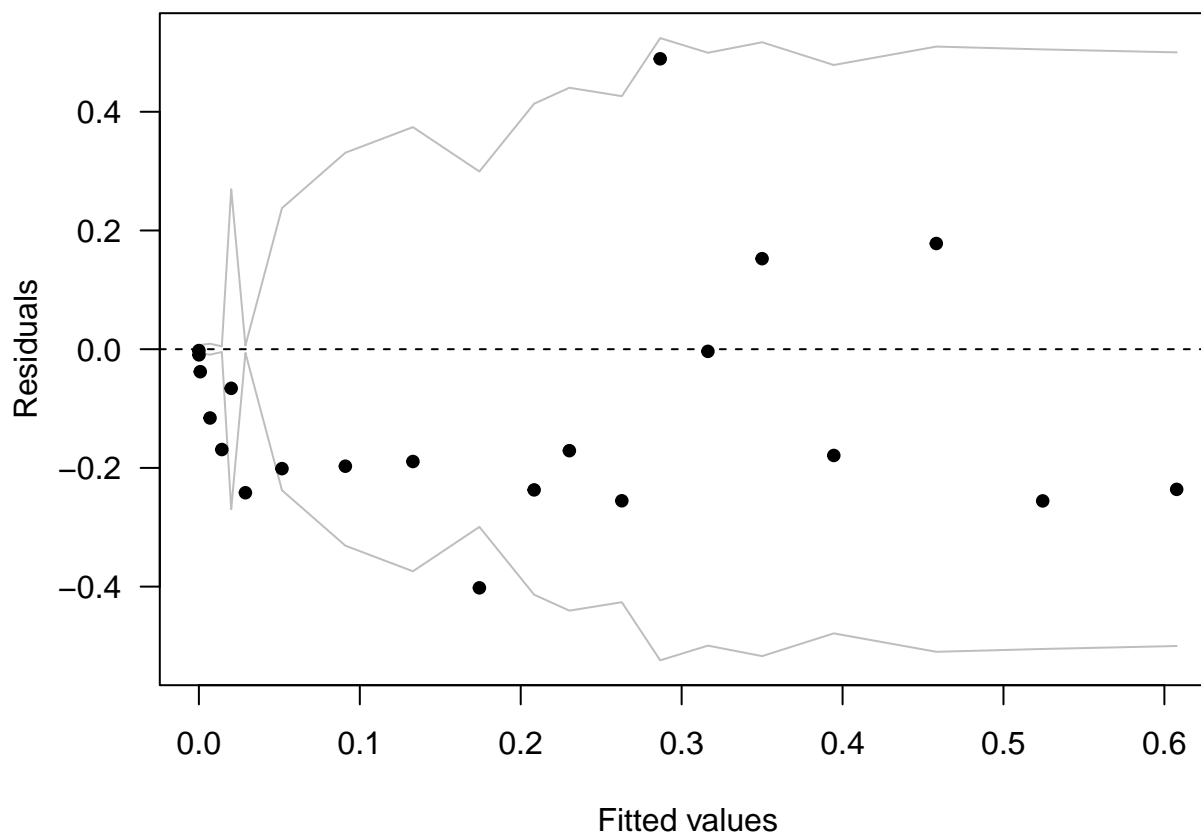
```
##
## Call:
## glm(formula = narwhal ~ temp_surf + temp_deep + salt_surf + salt_deep +
##      ice_cover_percent + runoff_racmo + glacier_length + DOY,
##      family = binomial(link = "logit"), data = mdl_data_sver,
##      na.action = "na.fail")
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -2.23242  -0.21563  -0.04918   0.00000   1.83908
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)  -1216.3673   5492.9739  -0.221   0.8247
## temp_surf      2.9176    13.0617   0.223   0.8232
## temp_deep    -24.5072    35.6620  -0.687   0.4920
## salt_surf   -168.3689   232.1853  -0.725   0.4684
## salt_deep    201.6285   187.3824   1.076   0.2819
## ice_cover_percent -2.3743    2.6542  -0.895   0.3710
## runoff_racmo  -0.2592    0.1248  -2.076   0.0379 *
## glacier_length  7.0899   10.0960   0.702   0.4825
## DOY          -0.1227    0.2635  -0.466   0.6415
```

```
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##      Null deviance: 44.416  on 64  degrees of freedom
## Residual deviance: 20.270  on 56  degrees of freedom
## AIC: 38.27
##
## Number of Fisher Scoring iterations: 12
```

```
# par(mfrow = c(2,2))
# plot mdl_sver)
```

Diagnostics

```
## plot deviance residuals-----
## set plot area
par(mai = c(0.9, 0.9, 0.1, 0.1),
    oml = c(0, 0, 0, 0),
    cex.lab = 1)
## plot resids vs eta
binnedplot(fitted mdl_global_pooled,
            residuals mdl_global_pooled, las = 1, pch = 16,
            ylab = "Residuals", xlab = "Fitted values", main = "")
```

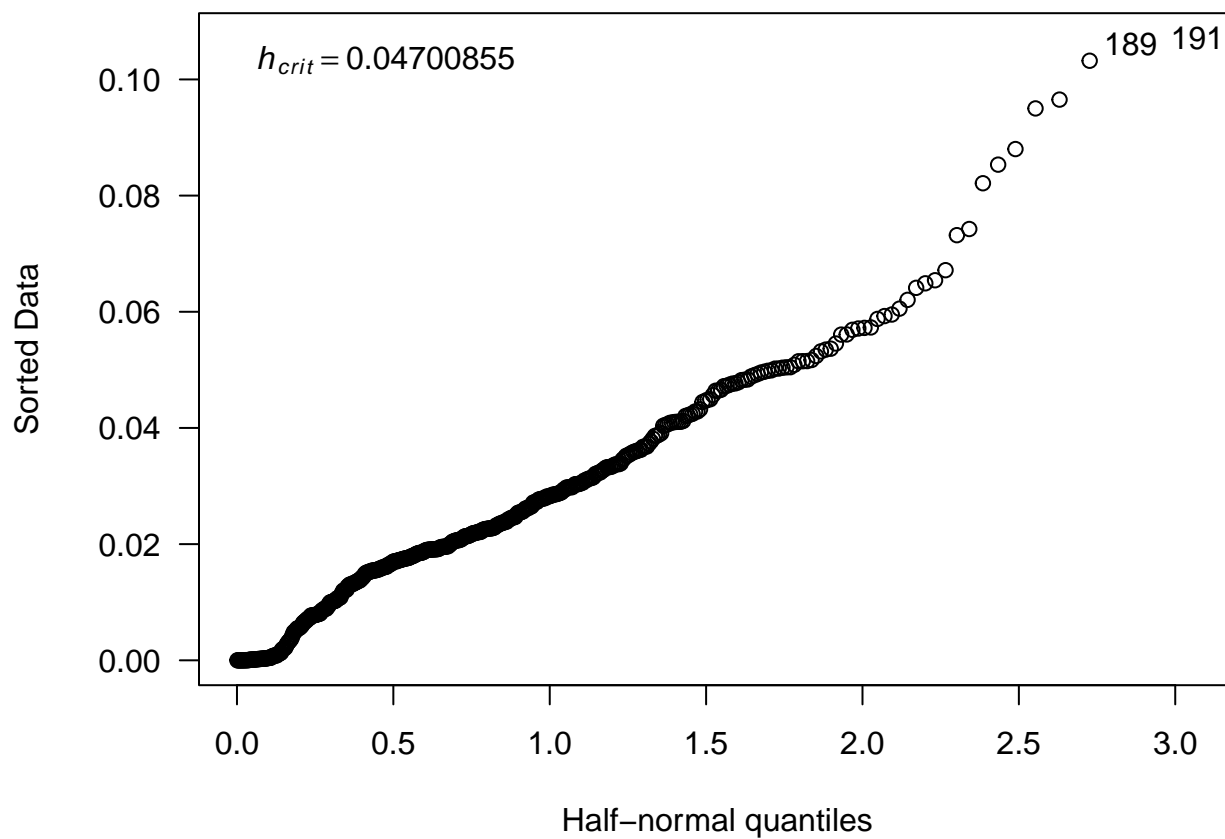


```
## compute R^2
# deviances
nn <- length mdl_data_b4freeze_pooled$time
DM_mod <- mdl_global_pooled$deviance
D0_mod <- mdl_global_pooled$null.deviance
# R^2
(R2 <- (1 - exp((DM_mod - D0_mod) / nn)) / (1 - exp(-D0_mod / nn)))
```

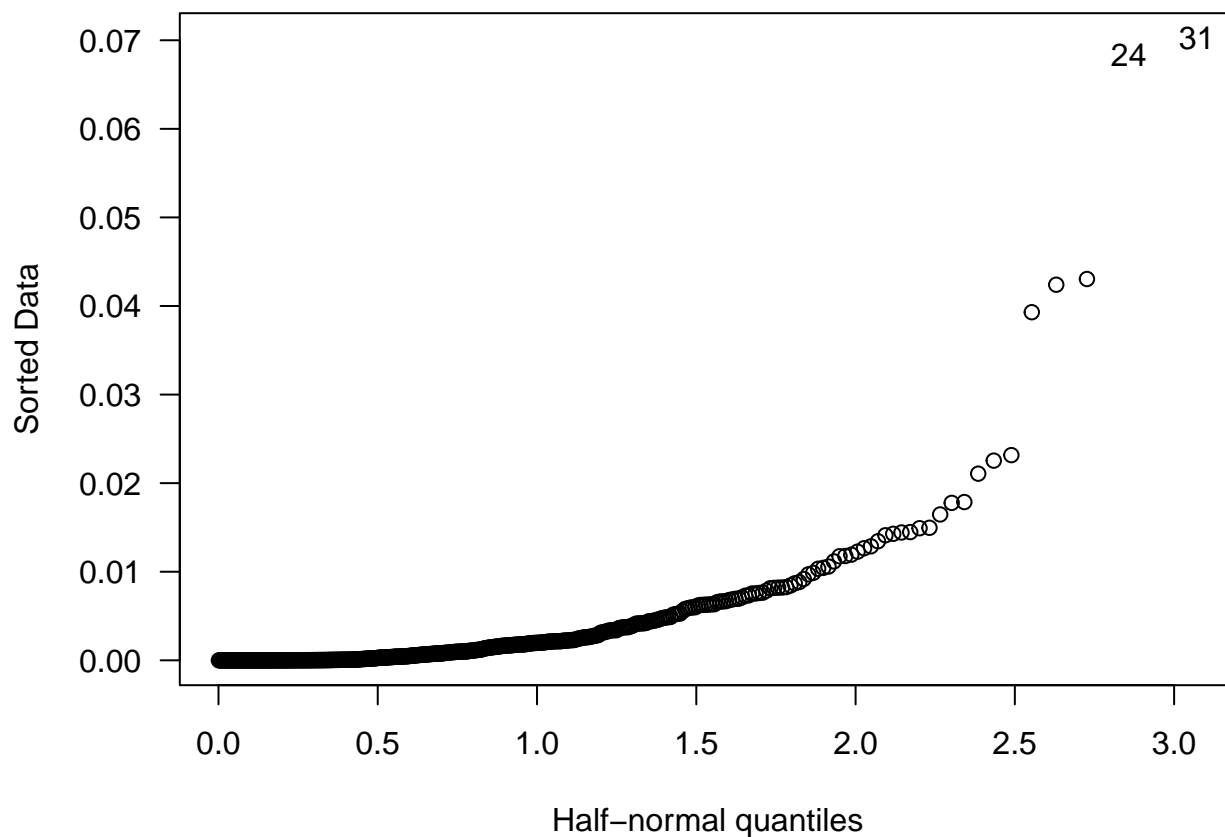
```
## [1] 0.3396991
```

```
## leverages-----
## set plot area
par(mai = c(0.9, 1, 0.1, 0.1),
    oim = c(0, 0, 0, 0),
    cex.lab = 1)
levs <- hatvalues(mdl_global_pooled)
## threshold value
h_crit <- 2 * length(coef(mdl_global_pooled)) / nn

## halfnormal plot
faraway::halfnorm(levs, las = 1, ylab = "")
text(0, 0.92*par("usr")[4], substitute(italic(h[crit]) == h_crit,
                                         list(h_crit = h_crit)), pos = 4)
mtext(side = 2, text = "Sorted Data", line = 4)
```



```
## Cook's D-----
## set plot area
par(mai = c(0.9, 0.9, 0.1, 0.1),
    omi = c(0, 0, 0, 0),
    cex.lab = 1)
## halfnormal plot
CD <- cooks.distance mdl_global_pooled
faraway::halfnorm(CD, las = 1, ylab = "")
mtext(side = 2, text = "Sorted Data", line = 3.5)
```



```
## H-L test with 8 groups
```

```
# A non-significant p value indicates that there is no evidence that the observed and expected frequenc
```

```
library(generalhoslem)
```

```
## Loading required package: reshape
```

```
##
```

```
## Attaching package: 'reshape'
```

```
## The following object is masked from 'package:Matrix':
```

```
##
```

```
##      expand
```

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

```
##
```

```
##      rename
```

```
## The following objects are masked from 'package:tidyr':
```

```
##
```

```
##      expand, smiths
```

```
generalhoslem::logitgof(obs = mdl_data_b4freeze_pooled$narwhal,
                        exp = fitted(mdl_global_pooled), g = 8)
```

```
## Warning in generalhoslem::logitgof(obs = mdl_data_b4freeze_pooled$narwhal, : At
## least one cell in the expected frequencies table is < 1. Chi-square
## approximation may be incorrect.
```

```
##
## Hosmer and Lemeshow test (binary model)
##
## data: mdl_data_b4freeze_pooled$narwhal, fitted(mdl_global_pooled)
## X-squared = 6.2757, df = 6, p-value = 0.393
```

```
# Models using scaled data -----
```

```
mdl_ice <- glm(narwhal ~
              temp_surf,data = model_data_pooled,
              family=binomial(link="logit"),na.action="na.fail")
```

```
# model with device - SCALED
```

```
mdl_global <- glm(narwhal ~
                  runoff+site+salt_surf+salt_deep+temp_surf+
                  temp_deep+ice_cover_percent+site_length+DOY,
                  data = model_data_scale,family=binomial(link="logit"),na.action="na.fail")
```

```
# model with device - SCALED
```

```
mdl_global <- glmmTMB(narwhal ~
                     runoff+I(runoff^2)+
                     site+salt_surf+salt_deep+temp_surf+
                     temp_deep+ice_cover_percent+glacier_length+DOY,
                     data = model_data_scale,family=binomial(link="logit"),na.action="na.fail")
```

```
# print summary output
```

```
summary(mdl_global)
par(mfrow = c(2,2))
plot(mdl_global)
plot_model(mdl_global,type="pred")
```

```
## use dredge function to run all model combinations =====
```

```
dredge_mdl <- dredge(mdl_global_pooled)
dredge_mdl
```

```
library(sjPlot)
```

```
# model with 'device' variable
```

```
mdl_best <- glm(narwhal ~ site+glacier_length+runoff+salt_deep+ice_cover_percent,
               data = mdl_data_b4freeze_pooled,family=binomial(link="logit"),na.action="na.fail")
```

```
summary(mdl_best)
plot_model(mdl_best, type='pred',ci.lvl = NA)
```

```
## plot deviance residuals-----
```

```
## set plot area
```

```
par(mai = c(0.9, 0.9, 0.1, 0.1),
    omi = c(0, 0, 0, 0),
    cex.lab = 1)
```



```
## plot resids vs eta
binnedplot(fitted(mdl_best), residuals(mdl_best), las = 1, pch = 16,
ylab = "Residuals", xlab = "Fitted values",
main = "")
```

```
## compute R^2
# deviances
nn <- length(mdl_data_b4freeze_pooled$time)
DM_mod <- mdl_best$deviance
D0_mod <- mdl_best$null.deviance
# R^2
(R2 <- (1 - exp((DM_mod - D0_mod) / nn)) / (1 - exp(-D0_mod / nn)))
```

```
acf(resid(mdl_global_pooled))
```

```
library(sjPlot)
library(lme4)
library(MuMIn)
```

```
model_data <- model_vars_df %>% mutate_at(vars(runoff,salt_surf,temp_surf,salt_deep,temp_deep,ice_cover,
velocity,glacier_length,DOY),scale) %>%
  mutate_at(vars(runoff,salt_surf,temp_surf,salt_deep,temp_deep,ice_cover_percent,
velocity,glacier_length,DOY),as.numeric) %>% drop_na()
```

```
samwise <- glm(narwhal ~ runoff+site+salt_surf+salt_deep+temp_surf+temp_deep+ice_cover_percent+velocity,
  data = model_data,family=binomial(link="logit"),na.action="na.fail")
summary(samwise)
par(mfrow = c(2,2))
plot(samwise)
```

```
samwise_dredge <- dredge(samwise)
```

```
plot_model(samwise,type="pred")
```

```
samwise <- glm(narwhal ~ runoff+site+salt_surf+ice_cover_percent+velocity+DOY,
  data = model_data,family=binomial(link="logit"),na.action="na.fail")
summary(samwise)
```

```
plot_model(samwise,type="pred")
```

```
library(mgcv)
```

```
matwise <- gam(narwhal ~ s(runoff)+site+s(salt_surf)+s(salt_deep)+s(temp_surf)+s(temp_deep)+s(ice_cover,
  data = model_data,family=binomial(link="logit"),na.action="na.fail")
```

```
matwise <- gam(narwhal ~ site+s(salt_surf)+s(salt_deep)+s(temp_surf)+s(temp_deep)+s(glacier_length)+s(D
  data = model_data,family=binomial(link="logit"),na.action="na.fail")
```

```
par(mfrow = c(2,2))
gam.check(matwise)
dev.off()
```

```
summary(matwise)

library("mgcViz")
print(plot(getViz(matwise), allterms = T), pages = 1)
```