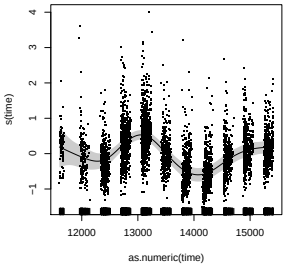
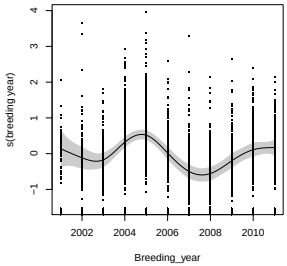
GAMs on juvenile proportion

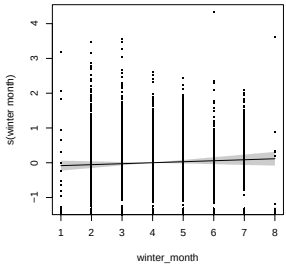
Single effect models

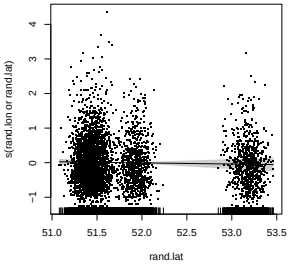
- `time`
- `Breeding year`
- `winter month`
- `rand.lat + rand.lon`

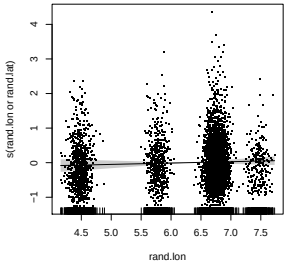
Visualise simple GAMs











Simple GAMs: Deviance explained

- GAM 1 R^2: `30.1520018`%
- GAM 2 R^2: `30.7345728`%
- GAM 3 R^2: `0.4316234`%
- GAM 4 R^2: `0.4774582`%

Multiple effects models

- `Breeding_year + winter_month + Breeding_year*winter_month`
- `Breeding_year + lat*lon + Breeding_year*lat + Breeding_year*lon`
- `Winter_month + lat*lon + winter_month*rand.lat + winter_month*lon`

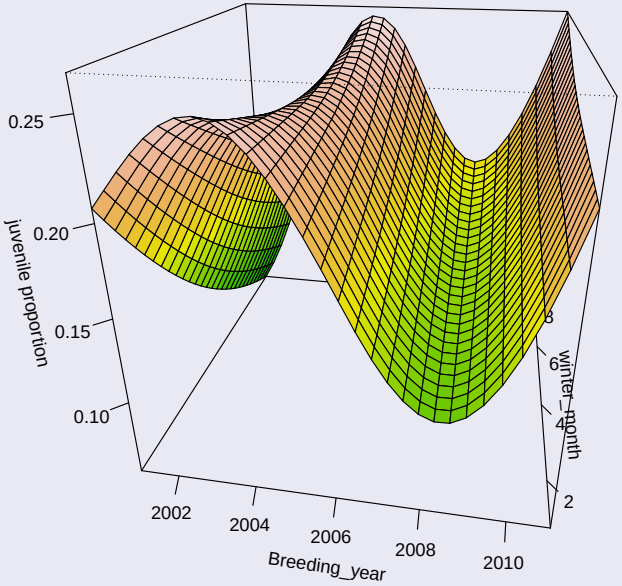
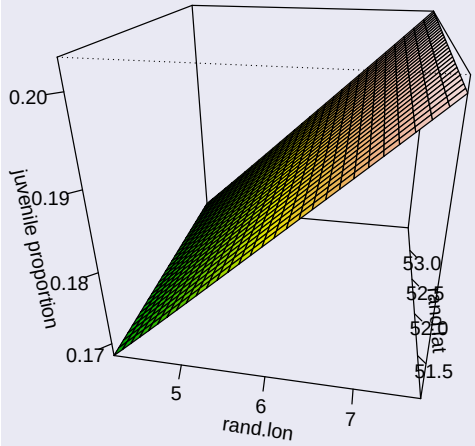


Figure 1: The effect of breeding year can be seen. Proportion rises with winter, but not in all years.

Breeding year and location



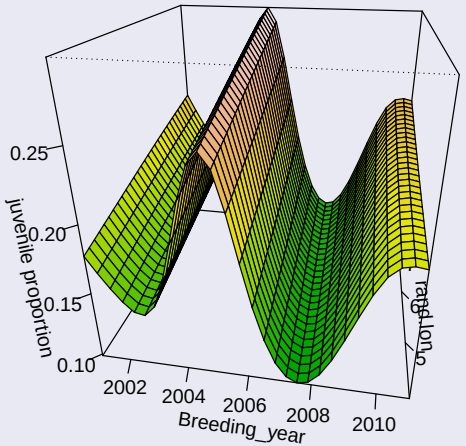


Figure 2: Juvenile proportion decreases from east to west. Location does not modify the effect of year.

Mixed effects models

Random effects added:

- `Food_type`
- `Observer`
- `flocksize`

Nested so: `1|Food_type/Observer/flocksize`

Mixed model summaries

- Mod 1: `Breeding_year * winter_month`, R^2: `0.006611`
- Mod 2: `lat * lon`, R^2: `0.0059464`
- Mod 3: `Breeding year * lon`, R^2: `0.0190374`

```
##
## Family: binomial
## Link function: logit
##
## Formula:
## propjuv ~ t2(Breeding_year) + t2(winter_month) + t2(Breeding_year,
##     winter_month)
##
## Approximate significance of smooth terms:
##                                edf Ref.df Chi.sq p-value
## t2(Breeding_year)            1.000  1.000  6.210  0.0127
## t2(winter_month)             1.000  1.000  4.554  0.0328
## t2(Breeding_year,winter_month) 1.001  1.001  1.601  0.2061
```

```
##
## Family: binomial
## Link function: logit
##
## Formula:
## propjuv ~ s(rand.lat, rand.lon)
##
## Approximate significance of smooth terms:
##                       edf Ref.df Chi.sq p-value
## s(rand.lat,rand.lon)   2      2   4.17   0.124
```

```
##
## Family: binomial
## Link function: logit
##
## Formula:
## propjuv ~ t2(Breeding_year, rand.lon)
##
## Approximate significance of smooth terms:
##                             edf Ref.df Chi.sq  p-value
## t2(Breeding_year,rand.lon)   3      3  18.02 0.000435
```

Mixed models: random factors

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
##   Approximation) [glmerMod]
##  Family: binomial  ( logit )
##
##      AIC      BIC   logLik deviance df.resid
##    430.6    504.9   -203.3    406.6     3592
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -0.1916  1.0968  1.8382  2.9369 16.6841
##
## Random effects:
##  Groups                          Name                           Variance
##  flocksize:(Observer:Food_type) (Intercept)                    3.184e-05
##  Observer:Food_type             (Intercept)                    3.712e-08
##  Food_type                      (Intercept)                    1.275e-08
##  Xr.1                           t2(Breeding_year,winter_month) 1.888e-05
##  Xr.3                           t2(Breeding_year,winter_month) 1.569e-02
##  Xr.2                           t2(Breeding_year,winter_month) 3.331e-04
##  Xr.0                           t2(winter_month)               9.504e-07
##  Xr                             t2(Breeding_year)              1.964e-07
##  Std.Dev.
##  0.0056426
##  0.0001927
##  0.0001129
##  0.0043454
```

Mixed model: zone as a random factor

Breeding year explains almost no variance when zone is a random effect.

```
##
## Family: binomial
## Link function: logit
##
## Formula:
## propjuv ~ s(Breeding_year)
##
## Parametric coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)  -4.6812     0.1881  -24.88   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Approximate significance of smooth terms:
##                   edf Ref.df Chi.sq  p-value
## s(Breeding_year)    1      1  10.85 0.000987 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## R-sq.(adj) =  0.00903
## glmer.ML = 3191.7  Scale est. = 1         n = 3604
```