

Today

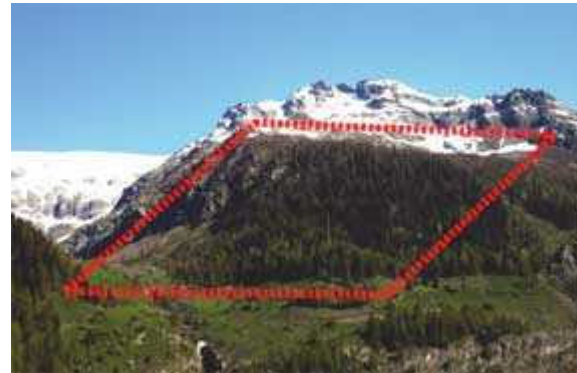
- Why does modeling groups as stochastic matter?
- Binomial GLM

Binomial GLM

- Swiss breeding bird survey (www.vogelwarte.ch)
- Skilled observers, 1 km² cells



Switzerland; showing
survey locations



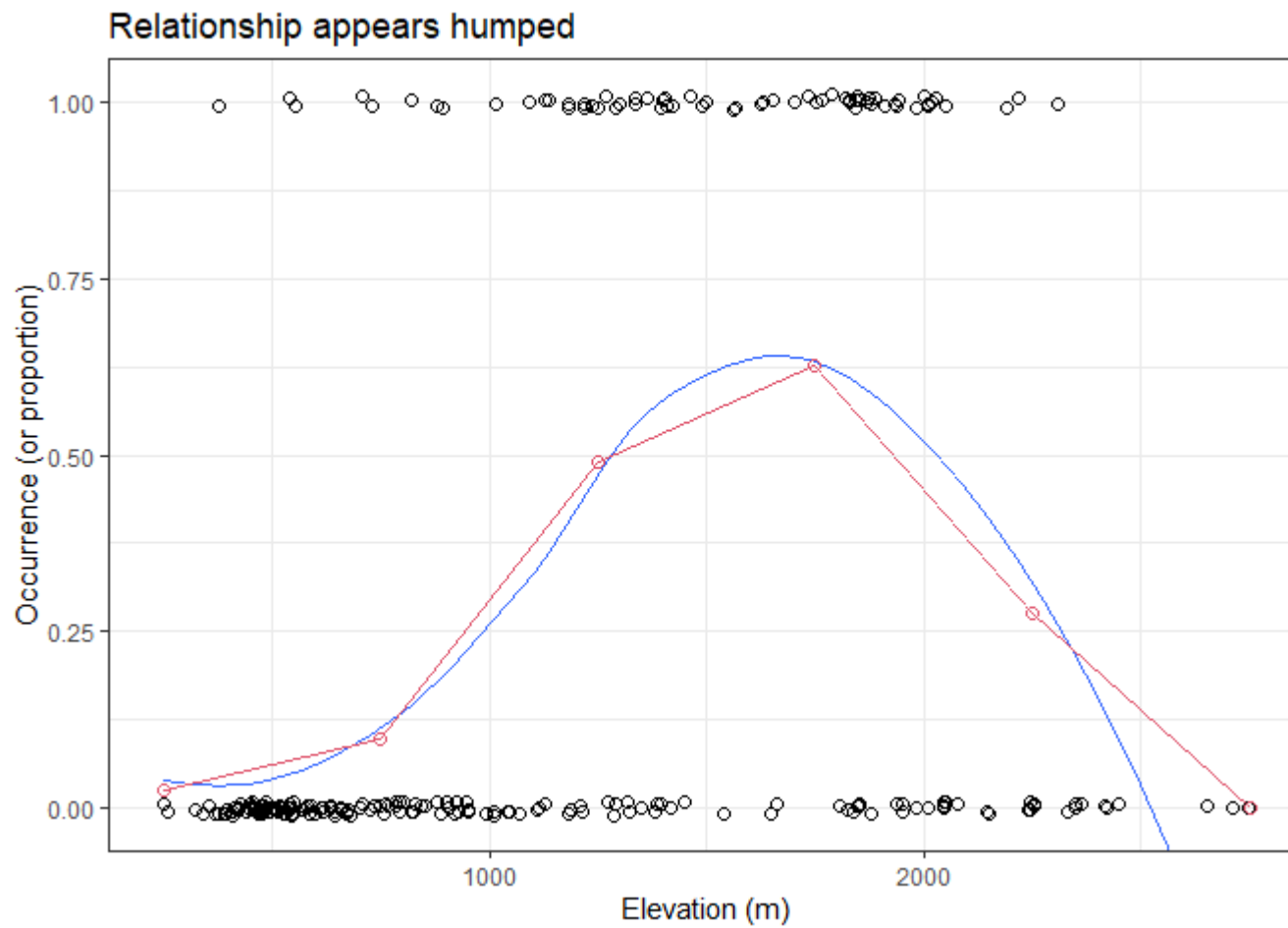
A 1 km² survey cell

- Willow tit territory presence-absence in
relation to altitude

[see swissbbs.R](#)

Royle JA, Dorazio RM (2008) Hierarchical Modeling and Inference in Ecology. Academic Press, Oxford. p 87.

EDA



The model

- Linear predictor; logit link function **Biology/pattern**

Logit function

$$\text{logit}(p) = \ln\left(\frac{p}{1-p}\right) = \beta_0 + \beta_1 x + \beta_2 x^2$$

Quadratic function
allows for hump

Elevation

$$p = \frac{\exp(\text{logit}(p))}{1 + \exp(\text{logit}(p))}$$

Antilogit function: backtransforms
to give probability p

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Antilogit function: backtransforms to give probability p

- Data model (expected biology + stochasticity)

$$Y \sim \text{Binomial}(p, N = 1)$$

Number of trials = 1

Y is occurrence

Model algorithm

- For the probability

```
p_pred_quadratic <- function(b0, b1, b2, elev){  
  lp <- b0 + b1 * elev + b2 * elev^2      #logit p  
  prob <- exp(lp) / (1 + exp(lp))        #antilogit  
  return(prob)  
}
```

- For data generating process

```
rbinom(n, size=1, prob=p_pred_quadratic(b0,b1,b2,elev))
```

Training algorithm

- Maximum likelihood

Likelihood for a single data point

$$L(p) = P(Y = y|p) = \underbrace{p^y(1-p)^{1-y}}_{\text{Bernoulli distribution}}$$

↑
1 for present
0 for absent

$y = 1$:

$$L(p) = P(Y = 1|p) = p^1(1-p)^{1-1} = p$$

$y = 0$:

$$L(p) = P(Y = 0|p) = p^0(1-p)^{1-0} = 1-p$$

Training algorithm (general way)

```
1 p_pred_quadratic <- function(b0,b1,b2,elev) {  
    lp <- b0 + b1 * elev + b2 * elev^2    #logit p  
    prob <- exp(lp) / (1+exp(lp))         #antilogit  
    return(prob)  
}
```

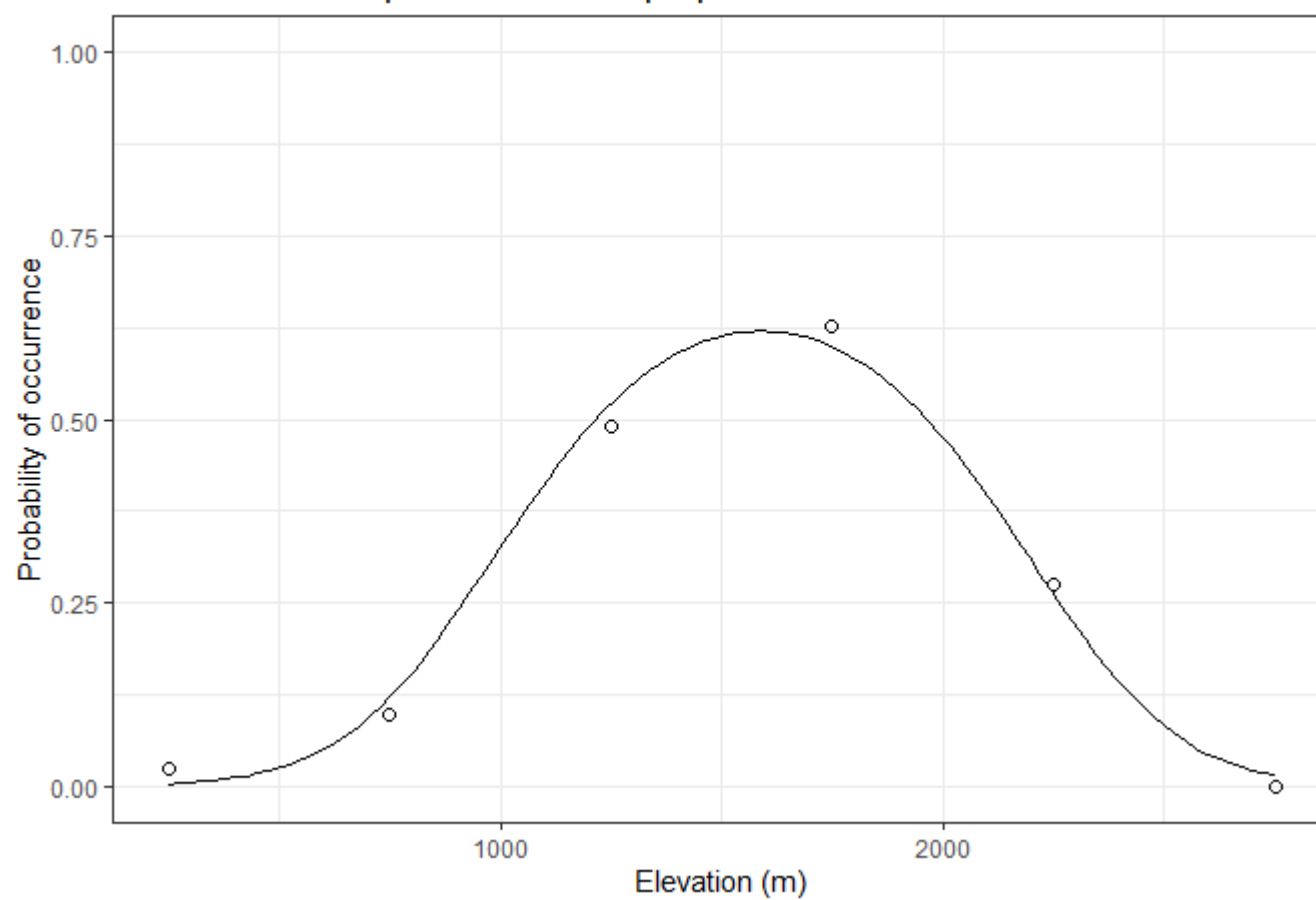
β_2 is orders of magnitude smaller than other parameters. Rescale to get optim to behave better.

```
2 quadratic_nll <- function(p,occ,elev){  
    b2 <- p[3] * 1e-06 #Rescale  
    ppred <- p_pred_quadratic(b0=p[1],b1=p[2],b2,elev)  
    nll <- -sum(dbinom(occ,size=1,prob=ppred,log=TRUE))  
    return(nll)  
}
```

$\beta_2 = -4e-06$

```
3 par <- c(-5,0.02,-4) #Starting values  
optim(par,quadratic_nll,occ=occ,elev=elev)
```


Fitted model compared to binned proportions



Inference algorithm


Test an ecological hypothesis:
Species' distribution is humped

- H_1 : Hump

$$\text{logit}(p) = \ln\left(\frac{p}{1-p}\right) = \beta_0 + \beta_1 x + \beta_2 x^2$$

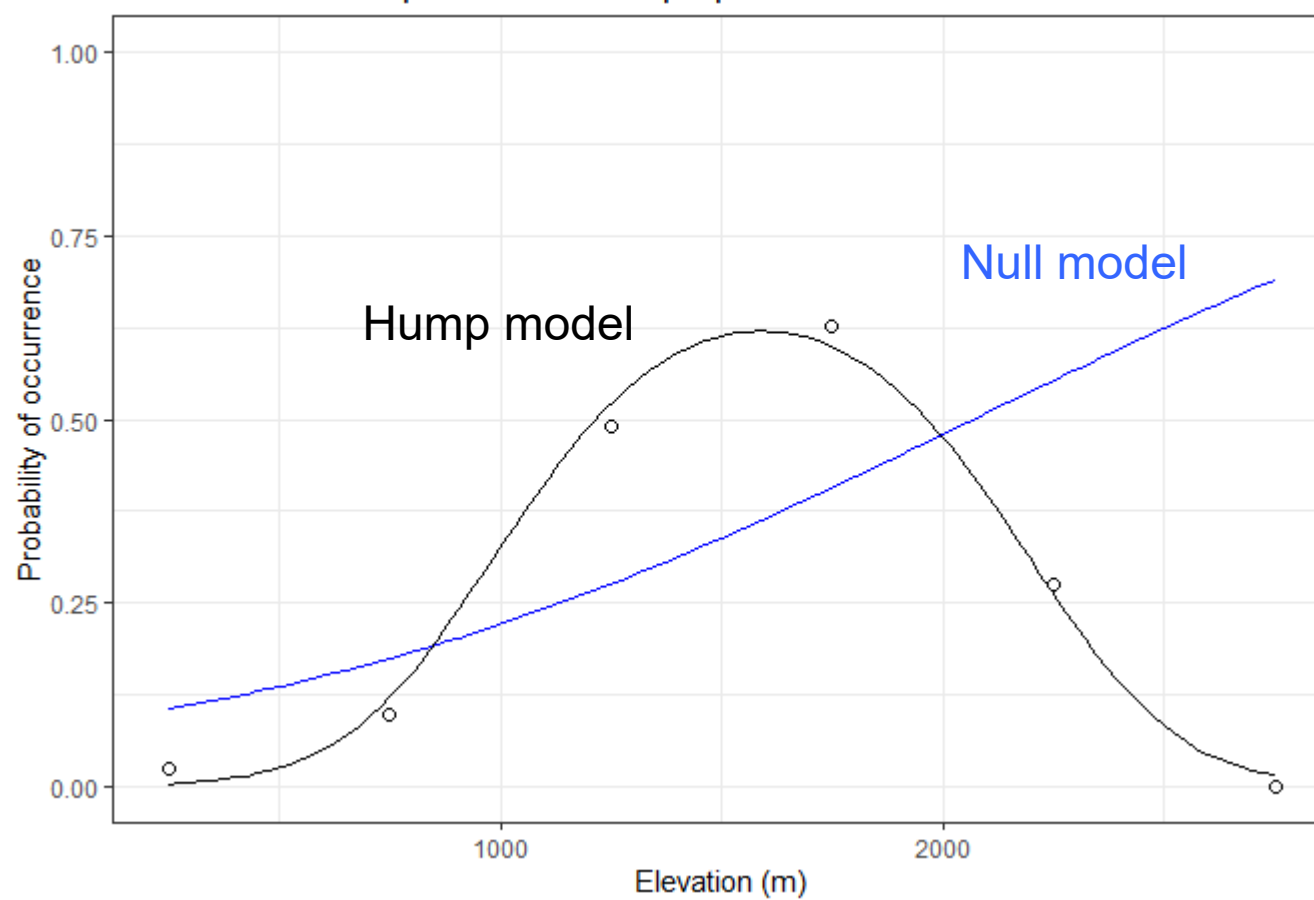
- H_0 : No hump

$$\text{logit}(p) = \ln\left(\frac{p}{1-p}\right) = \beta_0 + \beta_1 x$$



Nested models since
we can set β_2 to zero
and get H_0 .

Fitted models compared to binned proportions



Inference algorithm

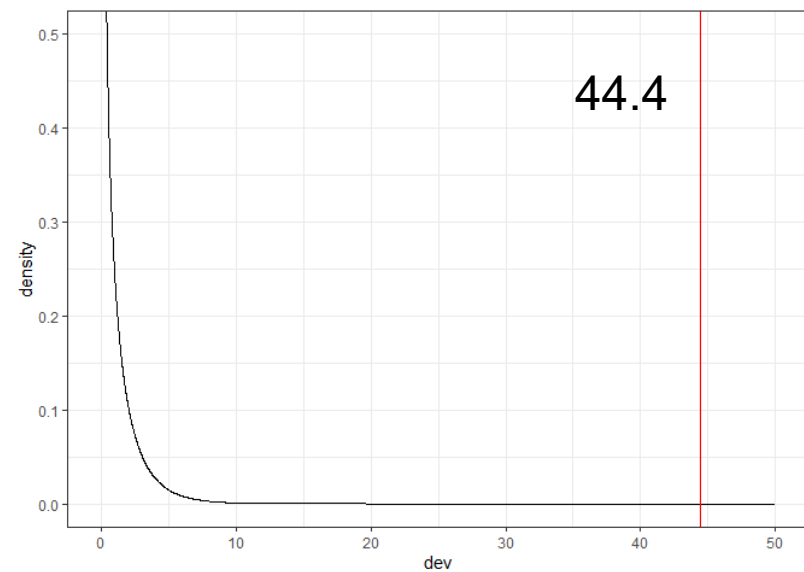
- NHST: likelihood ratio test

Test statistic

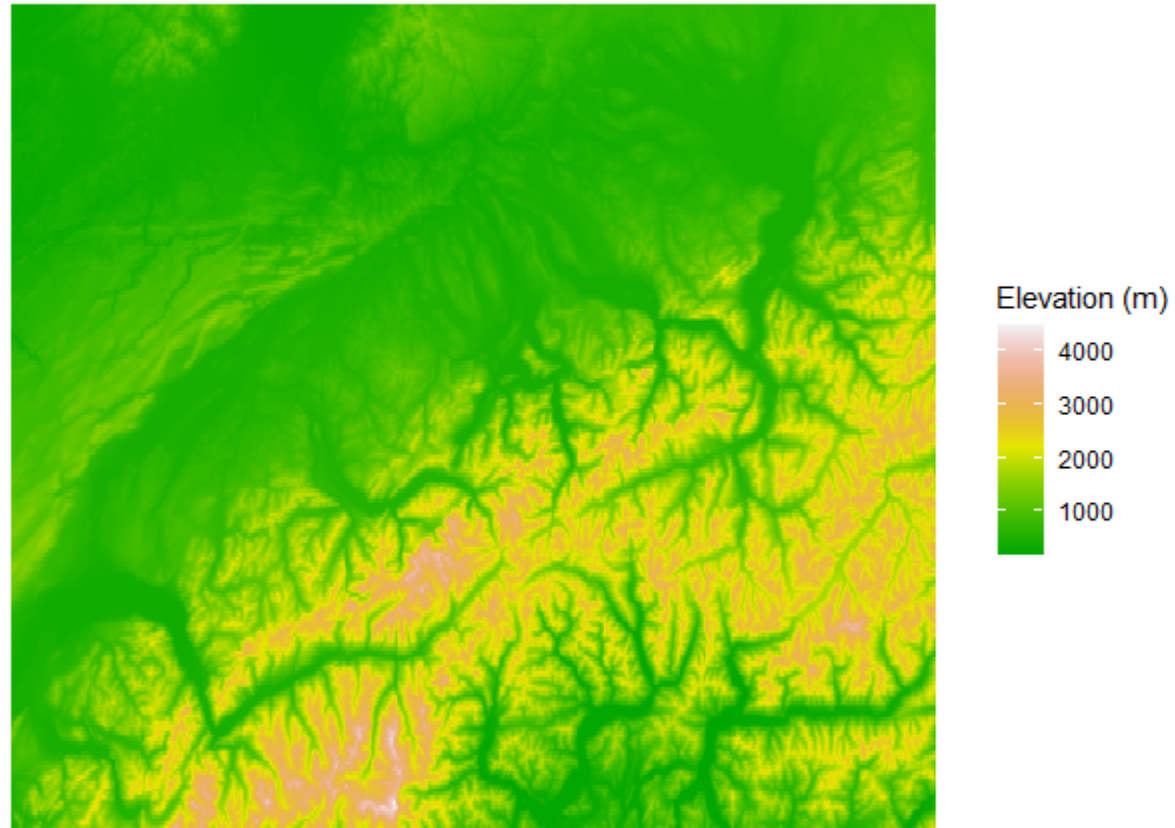
$$\text{deviance} = 2 \ln \left(\frac{L_1}{L_0} \right)$$

$$P = 2.7\text{e-}11$$

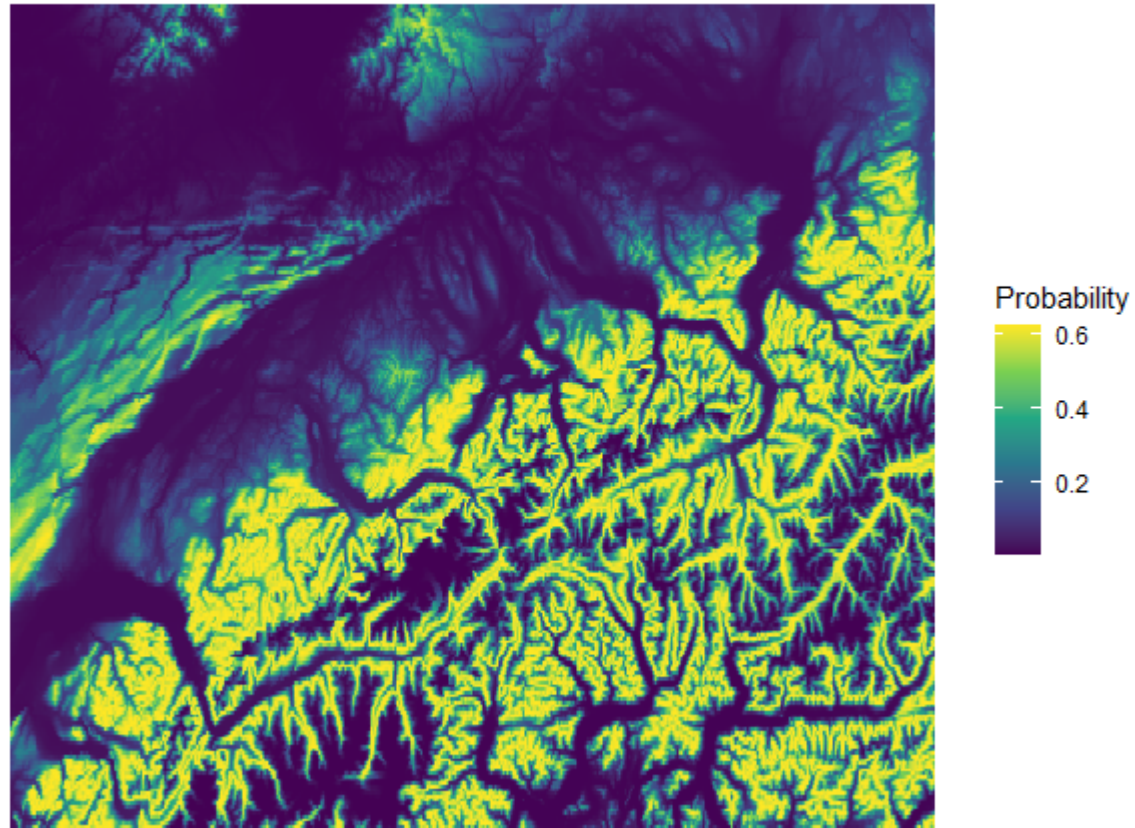
Sampling distribution (chi-squared)



Switzerland: DEM



Probability of observing a willow tit in year 1



R code

- See
- `swissbbs.R`
- `swissbbs.md`
- also for the easy way:
 - frequentist: `glm()`
 - Bayesian: `stan_glm()`