

# INTRODUCTION TO GENERAL LINEAR MODELS AND GENERAL LINEAR MIXED MODEL IN R

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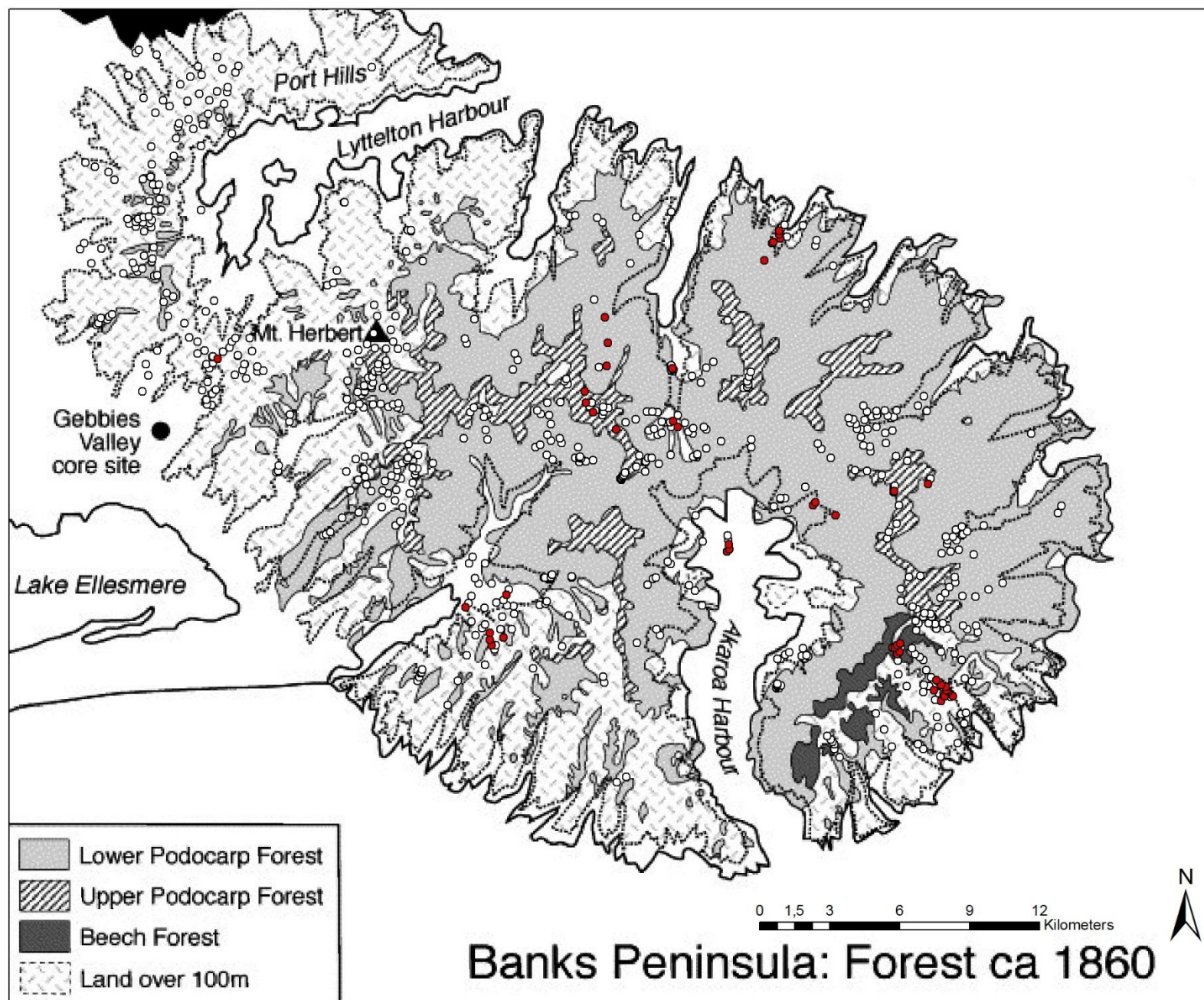
# The Rifleman data and the tomtit data



Tomtit



Male rifleman,  
New Zealand smallest bird (Wilson 2013)



### Distribution of the Rifleman

data from Scion studies and ECan monitoring

- presence
- absence

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# Tomtit abundance ~ habitat type

- ▣ Reads as Tomtit abundance predicted by habitat type
- ▣ Or also: Tomtit abundance as a function of habitat type
- ▣ Tomtit\_abundance: dependent variable
- ▣ habitat\_type: independent variable (predictor)



Tomtit abundance  $\sim$  habitat type  $+$   $\varepsilon$



fixed



random

- ▣ “ $\varepsilon$ ”(read “epsilon”) is a error term
  - in this model all the uncontrollable and unpredictable stuff

# The model in R

- ▣ Read in the data frame (Tomtit\_data.csv)
- ▣ `tomtit.model <- lm (tomtit_abundance ~  
habitat_type, tomtit_data)`
- ▣ Note:  $\varepsilon$  not specified in lm function

- ▣ `summary(tomtit.model)`

Multiple R-squared: 0.1919,  
Adjusted R-squared: 0.1567

- ▣ coefficient of determination, denoted  $R^2$  and pronounced R squared
- ▣ information about the goodness of fit of a model
- ▣ indicates how well data fit the statistical model



# Multiple R-squared: 0.1919, Adjusted R-squared: 0.1567

- ▣  $R^2$  varies between 0 and 1
- ▣  $R^2$  of 1 indicates that the regression line perfectly fits the data
- ▣ Variance explained in our model is only 0.1919

# F-statistic: 5.461

$F = \frac{\text{Effect Variance}}{\text{Error Variance}}$

or

$F = \frac{\text{Between-group Variance}}{\text{Within-group Variance}}$

F-statistic: 5.461 on 1 and 23 DF p-  
value: 0.02852

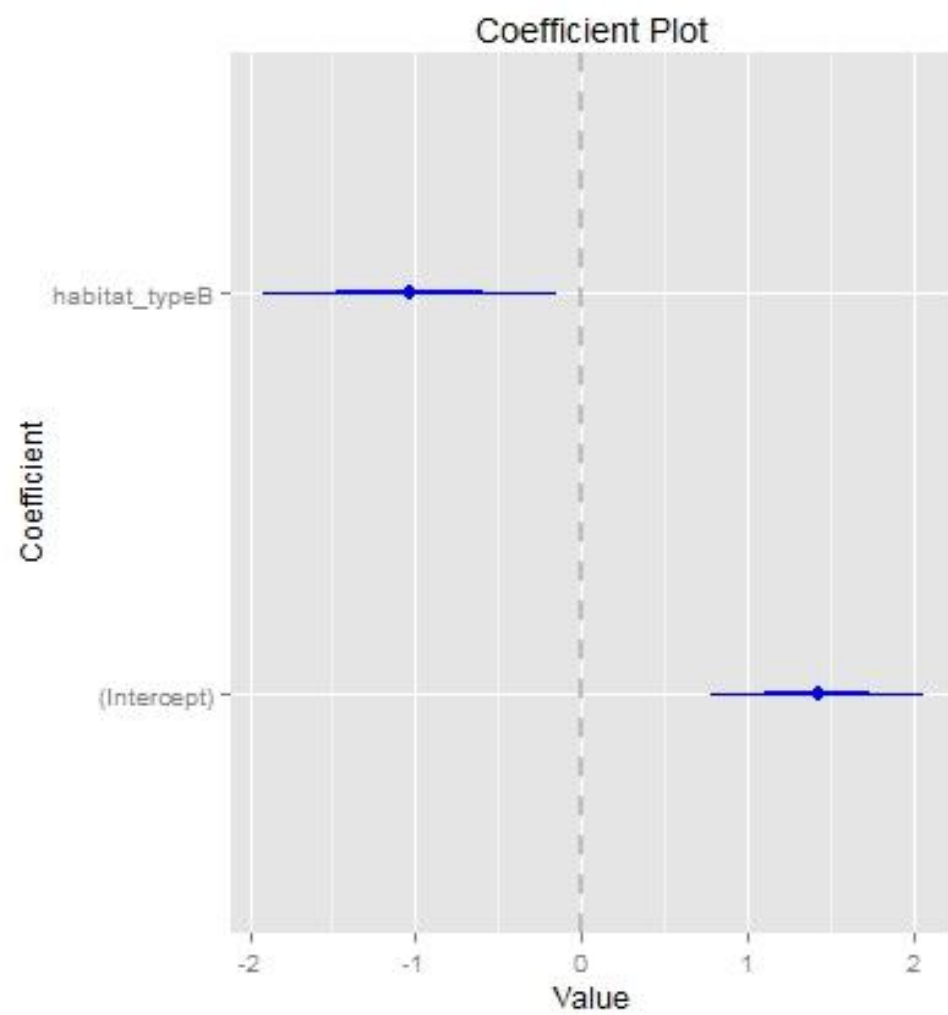
# Reporting results

- ▣ A linear model was build with the R version 3.0.1 (R Core Team 2013).
- ▣ This model was significant ( $F(1, 23)=5.461$ ,  $p=0.028$ ).

▣ Coefficients:

	Estimate	Std. Error	t value	Pr(>  t )
(Intercept)	1.4167	0.3185	4.448	0.000184 ***
habitat_typeB	-1.0321	0.4416	-2.337	0.028521 *

▣ Intercept is habitat type A

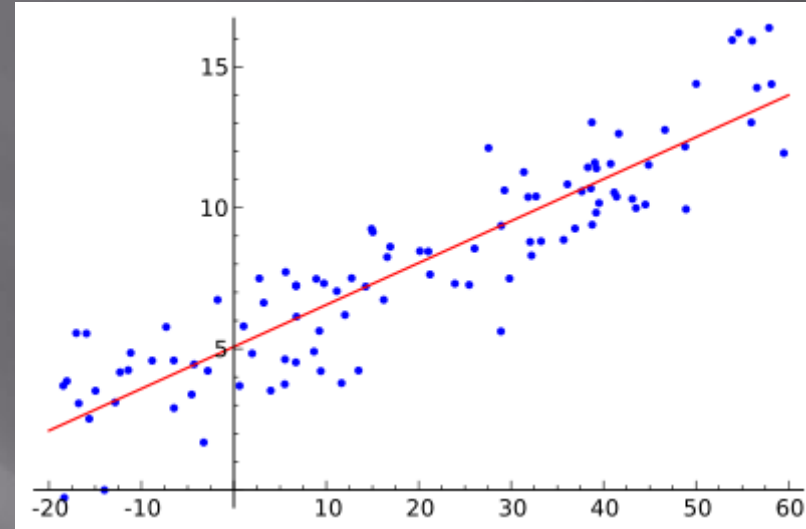
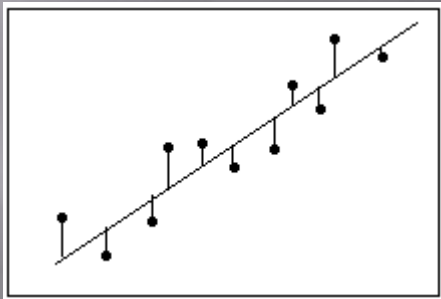




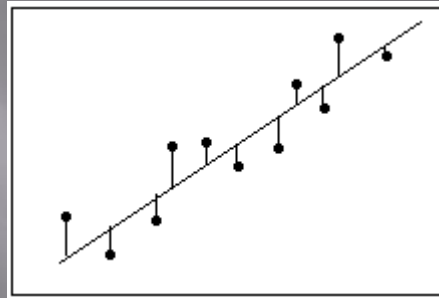
# Model assumptions for GLM

## Linearity

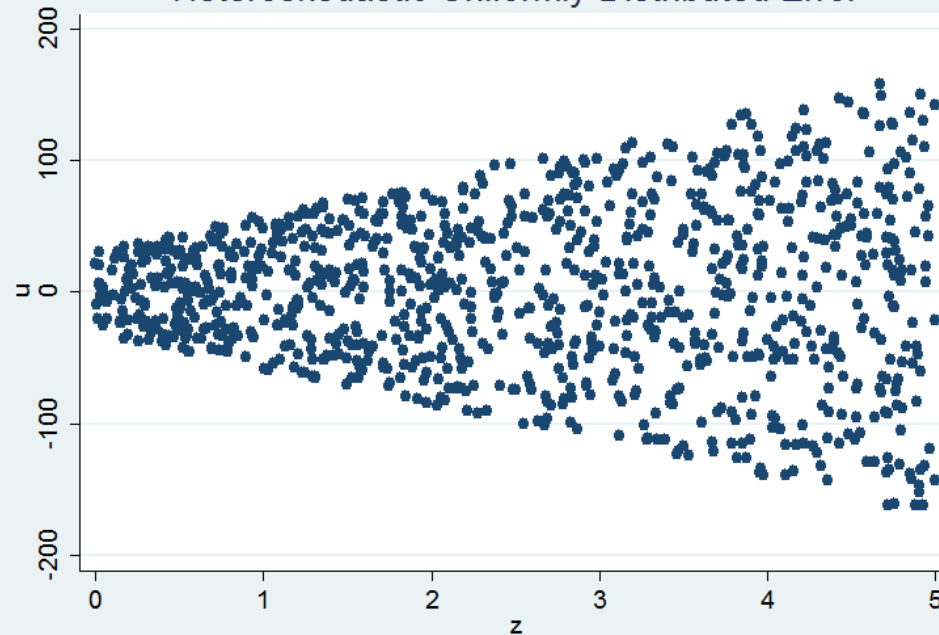
- ▣ Use residuals to check



# Homoskedasticity



Heteroskedastic Uniformly Distributed Error



# No multicollinearity

- ▣ multicollinearity (also collinearity) is a phenomenon in which two or more predictor variables in a multiple regression model are highly correlated,  
→ one can be linearly predicted from the others with a non-trivial degree of accuracy (from Wikipedia).

# What to do when there is multicollinearity

- ▣ Consider in study design
- ▣ Select the best
- ▣ Principal component Analysis (PCA)

# Independence!

- ▣ Each data point comes from an independent subject  
e.g. each bird observation from a different plot
- ▣ One of the most important assumptions

Break!



# General linear mixed model

- ▣  $\text{tomtit\_abundance} \sim \text{area} + \text{connectivity} + (1 \mid \text{patch\_id})$

# GLMM in R

- ▣ `Rif.model <- glmer(rif_presence ~ area + connectivity + (1 | patch_id), family=binomial, data=Rif_data)`
- ▣ `summary(Rif.model)`

# Difference Fixed effect – Random effect

- ▣ Fixed effect:

- The independent variables we have an overview of and can predict (systematic)

- ▣ Random effect:

- The independent variables which seem chaotic and unpredictable

# Difference Fixed effect – Random effect

- ▣ Fixed effect

→ Exhaust the population of interest  
e.g. Gender, habitat type

- ▣ Random effect

→ May not exhaust the population  
e.g. Plot (location)

# AIC

- ▣ The Akaike information criterion (AIC)
  - Out of collection of models for the data, AIC estimates the quality of each model, relative to each of the other models. Hence,
- ▣ AIC provides a means for model selection.

# AICc

- ▣ AICc
- ▣ Class\_Habitat + BC
- ▣ 341.6
- ▣ Class\_Habitat + BC + dNL
- ▣ 343.6
- ▣ BC + dIICconnect + dNL
- ▣ 346.1
- ▣ Class\_Habitat + Patch\_Area + Patch\_Perimeter + BC + dIICconnect + dNL
- ▣ 350.0
- ▣ Class\_Habitat + Patch\_Area + BC + dLC
- ▣ 371.5
- ▣ Patch\_Area + BC + dIICintra
- ▣ 373.7
- ▣ Class\_Habitat + Patch\_Area + Patch\_Perimeter + BC + dIICconnect + dLC
- ▣ 375.8
- ▣ Patch\_Area + Patch\_Perimeter + BC + dIICconnect + dIICintra + dNL
- ▣ 375.9
- ▣ Class\_Habitat + Patch\_Area + Patch\_Perimeter + BC + dIICconnect + dIICintra + dLC + dNL
- ▣ 376.0
- ▣



# Useful package in R

- ▣ `library("MuMIn")`  
with function `dredge(model)`

**Thank you!**