

FISH 559: Numerical Computing for the Natural Resources
Homework 1 : Mixed Effect Models (out of 105 points)

Question 1 (40 points)

Implement a linear mixed effects model numerically using R to replicate the maximum likelihood estimates of the population mean density, the extent of among-population variation and the extent of within-population variation using the Streams data (Homel1a.txt). Compute a likelihood profile for the population mean density. Compare the 95% confidence intervals from this likelihood profile with that determined using LME.

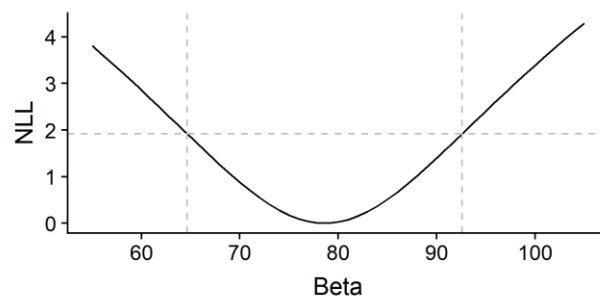
Estimating parameters numerically using custom R script:

Parameter	Estimate	Std. Error	Parameter definition
beta	78.619598	6.029308	Stream population mean density
sigma_b	14.344881	4.394260	Among/within stream variation
sigma_r	6.084296	1.242075	

Estimating parameters using lme4:

Parameter	Estimate	Std. Error
beta	78.629	6.603
sigma_b	15.789	
sigma_r	6.084	

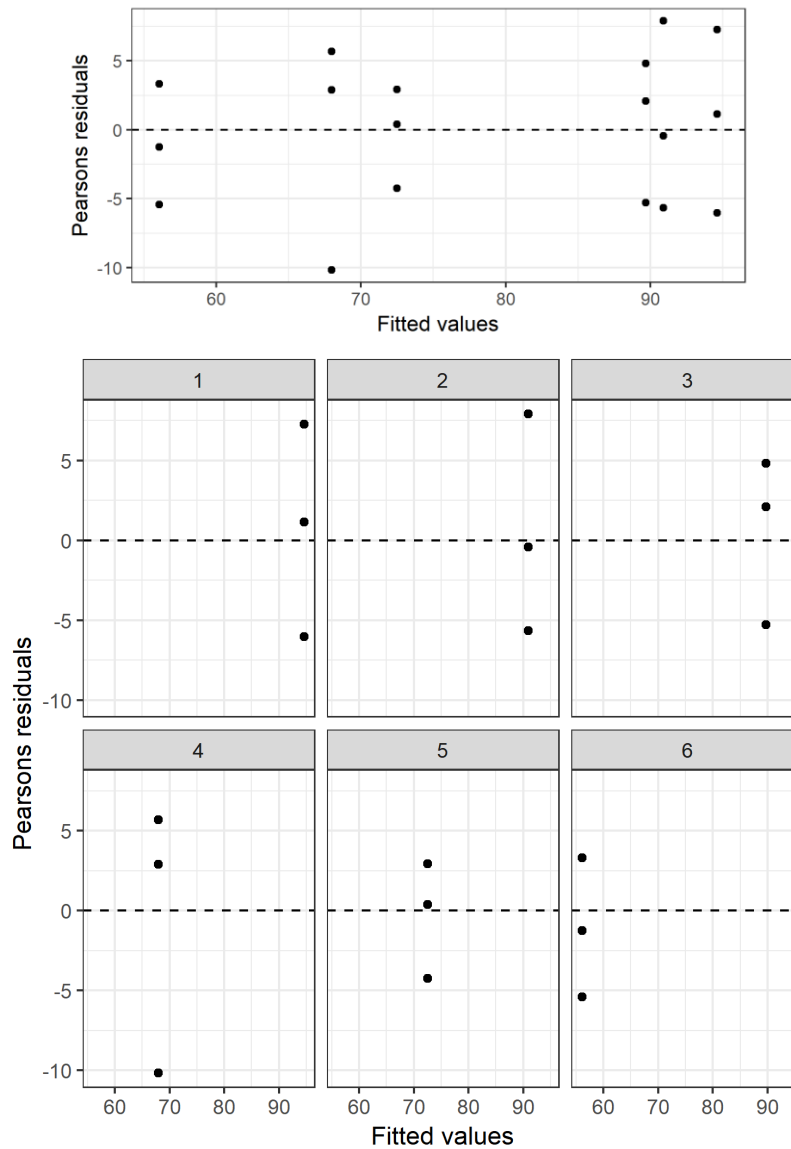
Plot of likelihood profile for beta (stream population mean density) with 95% confidence intervals in light grey:



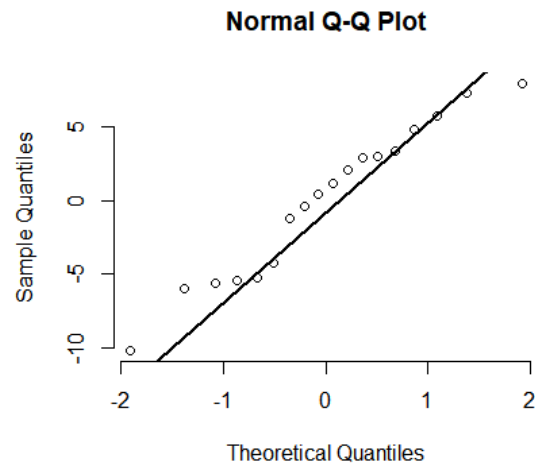
Comparison of confidence intervals – very close!

Method	Beta estimate	Lower 95	Upper 95
Likelihood profile	78.62	64.65	92.61
lme4	78.62	64.64	92.61

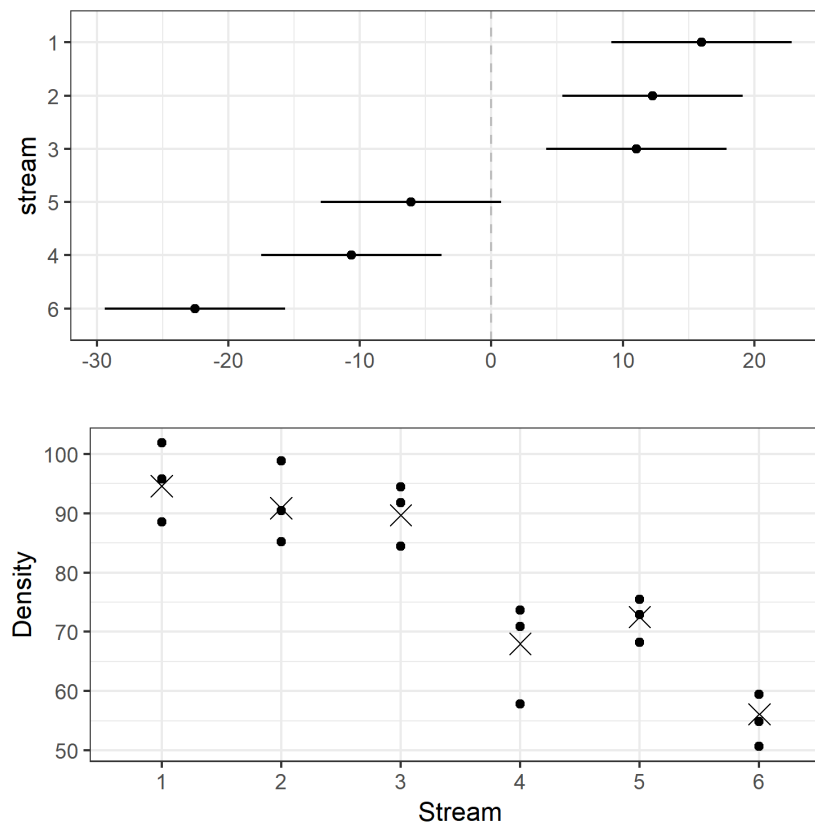
Residual plots for linear mixed effects model fit in lme4 suggest no violation of the constant variance assumption:



A qqplot of residuals suggests no strong violation of the normality assumption:



Plots of random effects (upper panel) and fixed effect (lower panel) show no big issues:



Question 2 (65 points)

Dorn (2002; *North American Journal of Fisheries Management* 22: 280-300) used a Bayesian mixed effects model to develop a Bayesian prior distribution for the steepness¹

¹ Steepness is the fraction of the recruitment at the virgin spawning stock biomass expected when the spawning stock biomass is reduced to 20% of its unfished level.

of the stock-recruitment relationship for U.S. West Coast rockfish species. The Ricker stock-recruitment relationship can be reparameterized as follows:

$$R_y = \frac{\alpha}{\tilde{SSB}} S_y e^{-\beta S_y}$$

where R_y is the recruitment for year y ,
 S_y is spawning stock biomass (or a proxy thereof) for year y ,
 \tilde{SSB} is the spawner biomass-per-recruit in the absence of exploitation, and
 α, β are the parameters of the stock-recruitment relationship.

Use R to fit a linear random effects model to data for 11 West Coast rockfish species treating $\ln \alpha$ as a random effect and β as a (species-specific) fixed effect. Assume that the noise about the stock-recruitment relationship is log-normal and assume that the variation about the stock-recruitment relationship is the same for all species.

The data are stored in the file Home1b.txt (format: Spawning stock biomass, recruitment, species code, spawner biomass-per-recruit).

Evaluate the fits using plots of residuals, random effects, etc.

The model that I fit takes the form: $y = \log(R_y * \tilde{SSB} / S_y) = \log(\alpha) + \beta S_y$

Parameter estimates:

Fixed effects:

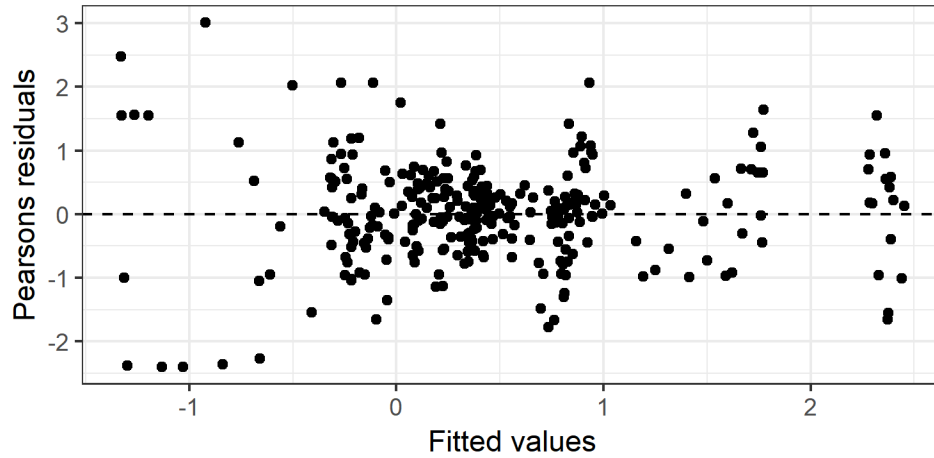
Estimate Std. Error t value

species1:ssb	-0.019548	0.014980	-1.305
species2:ssb	-0.118824	0.039987	-2.972
species3:ssb	-0.002392	0.001030	-2.323
species4:ssb	-0.062886	0.028230	-2.228
species5:ssb	-0.741259	0.500030	-1.482
species6:ssb	-0.027825	0.019840	-1.402
species7:ssb	-0.005377	0.010290	-0.523
species8:ssb	-0.012318	0.008043	-1.531
species9:ssb	0.017026	0.047983	0.355

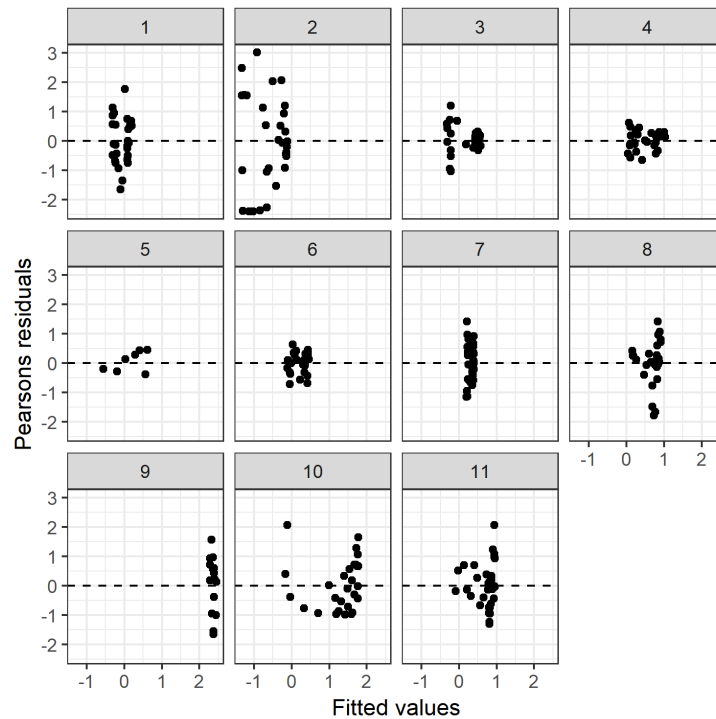
species10:ssb -0.008377 0.002169 -3.863

species11:ssb -0.008934 0.004315 -2.070

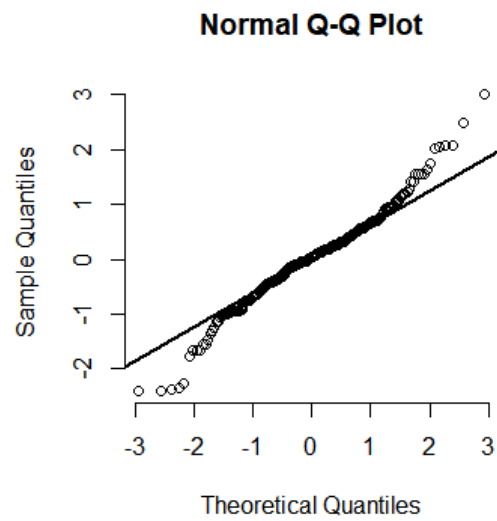
Residual plots show heteroskedasticity:



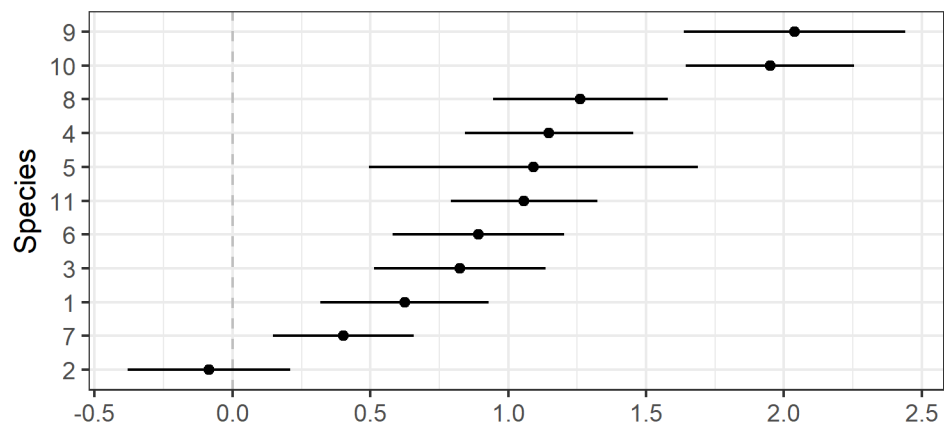
Residual plots by species shows some heteroskedasticity and a violation of constant variance across species:



A qqplot shows that the residuals violate the normality assumption:



A plot of the random effects estimates show that they are no centered on 0:



And finally, a plot of the fitted values by species:

