plot(fitted(lme1), residuals(lme1),  
  xlab = "Fitted Values", ylab = "Residuals")  
  abline(h=0, lty=2)  
  lines(smooth.spline(fitted(lme1), residuals(lme1)))

# Check for residual pattern within groups and difference between groups        
xyplot(residuals(glmm1) ~ fitted(glmm1) | Count$plot, main = "glmm1 - full model by plot",  
  panel=function(x, y){ panel.xyplot(x, y) panel.loess(x, y, span = 0.75)   
  panel.lmline(x, y, lty = 2)  # Least squares broken line} )