```
> fish1<-read.csv("braun_oscar_centroiddist.csv")</pre>
> m1<-gam(data=fish1,dist_from_monthly_centroid_km~covid+s(month),family="quasipoisson")</pre>
> agnorm(residuals(m1))
> summary(m1)
Family: quasipoisson
Link function: log
Formula:
dist_from_monthly_centroid_km ~ covid + s(month)
Parametric coefficients:
           Estimate Std. Error t value Pr(>|t|)
(Intercept) 5.25397
                       0.02527 207.874 < 2e-16 ***
           -0.69578
                       0.10598 -6.565 7.96e-11 ***
covidyes
Signif. codes: 0 '*** 0.001 '** 0.01 '* 0.05 '.' 0.1 ' ' 1
Approximate significance of smooth terms:
                         F p-value
           edf Ref.df
s(month) 8.922 8.998 61.48 <2e-16 ***
Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
R-sa.(adj) = 0.395
                     Deviance explained = 44.9%
GCV = 85.273 Scale est. = 97.493
                                    n = 1122
> ((exp(5.25397-0.69578)-exp(5.25397))/exp(5.25397))*100
Γ17 -50.13147
```

