

```
m1<-gam(CHLA~Covid+s(Month,k=3)+s(Year,k=6),data=BCN,family=quasipoisson)
#check fit/nice fit
qqnorm(residuals(m1))
```

```
Family: quasipoisson
Link function: log

Formula:
CHLA ~ Covid + s(Month, k = 3) + s(Year, k = 6)

Parametric coefficients:
              Estimate Std. Error t value Pr(>|t|)
(Intercept)  0.21368    0.07126   2.999  0.00342 **
Covidyes      0.48261    0.34050   1.417  0.15947
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Approximate significance of smooth terms:
              edf Ref.df      F  p-value
s(Month)  1.00  1.000  9.531  0.00259 **
s(Year)   1.34  1.602 27.457 8.22e-07 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

R-sq.(adj) =  0.295   Deviance explained = 33.4%
GCV = 0.52421   Scale est. = 0.54672    n = 105
```

```
#estimate how much more abundant chLA was in covid year, as a % change, based on covid coefficient
round((exp(0.21368+0.48261)-exp(0.21368))/exp(0.21368)*100)
```

62

```
#62% more CHLA in Covid year since 2004
```