ml<-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 Pro>ltl)

(Intercept) 0.21368 0*.*07126 2.999 0.00342 \*\*

Covidyes 0.48261 0.34050 1.417 0.15947

---

Signif. codes:

\*\*\*' 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.*2*2e-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)

**LU**

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