AIC output 12 21 2018

##used this data frame because it has the averaged values from 2 and 3 and the productivity for each sampling station##

biofilmpondata<-read.csv("C:/Users/Mitzi/Dropbox/Mosquito Science (1)/Data 2011 to 2018/Data modules/Biofilm/summarybysamplingstationbiofilm\_12\_21\_18.csv",header = TRUE)

Pond is a random effect in these models

#null#

Nullmod<-lmer(BiofilmProd~ (1|Pond), data=biofilmpondata)

First compared all univariate models, and null and full

> aictable(rawaic,nR)

Params logL AICc deltaAICc weight cumwt

**NH4 4 -18.0527 46.2107 0.0000 0.4163 0.4163**

**N03N02 4 -18.3181 46.7415 0.5309 0.3192 0.7355**

**Conduct 4 -19.1952 48.4956 2.2849 0.1328 0.8683**

Nullmod 3 -21.9842 51.1684 4.9577 0.0349 0.9032

pH 4 -20.5908 51.2868 5.0761 0.0329 0.9361

Perim 4 -20.7828 51.6709 5.4602 0.0271 0.9632

totalP 4 -21.4393 52.9839 6.7732 0.0141 0.9773

Depth 4 -21.7165 53.5382 7.3275 0.0107 0.9879

FPOM 4 -21.9525 54.0103 7.7996 0.0084 0.9964

temp 4 -23.2178 56.5408 10.3302 0.0024 0.9988

DOC 4 -24.4339 58.9731 12.7624 0.0007 0.9995

DOperc 4 -24.9524 60.0100 13.7994 0.0004 0.9999

Area 4 -26.3315 62.7683 16.5576 0.0001 1.0000

Area\_loss 4 -28.1736 66.4525 20.2419 0.0000 1.0000

full 16 -30.2325 170.1793 123.9686 0.0000 1.0000

Then compared 2 order models with the 3 predictors better than null, and 3 way with all of them

> aictable(rawaic,nR)

Params logL AICc deltaAICc weight cumwt

NH4N03N02Conduc 6 -11.3907 39.7226 0.0000 0.5295 0.5295

NH4N03N02 5 -14.1685 41.6703 1.9477 0.2000 0.7295

N03N02conduc 5 -15.1032 43.5398 3.8172 0.0785 0.8080

NH4conduc 5 -15.6450 44.6232 4.9006 0.0457 0.8537

NH4ph 5 -16.3327 45.9987 6.2761 0.0230 0.8767

NH4 4 -18.0527 46.2107 6.4881 0.0207 0.8973

N03N02ph 5 -16.5603 46.4539 6.7313 0.0183 0.9156

N03N02 4 -18.3181 46.7415 7.0189 0.0158 0.9315

NH4P 5 -17.4478 48.2289 8.5063 0.0075 0.9390

Conduct 4 -19.1952 48.4956 8.7730 0.0066 0.9456

NH4Perim 5 -17.7384 48.8100 9.0874 0.0056 0.9512

N03N02Perim 5 -17.7688 48.8709 9.1483 0.0055 0.9567

N03N02P 5 -17.8016 48.9365 9.2139 0.0053 0.9620

Conducph 5 -17.8838 49.1009 9.3783 0.0049 0.9668

NH4depth 5 -18.0610 49.4554 9.7328 0.0041 0.9709

NH4FPOM 5 -18.1425 49.6184 9.8958 0.0038 0.9747

N03N02FPOM 5 -18.1425 49.6184 9.8958 0.0038 0.9784

ConducFPOM 5 -18.1425 49.6184 9.8958 0.0038 0.9822

N03N02depth 5 -18.2754 49.8842 10.1616 0.0033 0.9855

ConducP 5 -18.4256 50.1845 10.4619 0.0028 0.9883

Nullmod 3 -21.9842 51.1684 11.4457 0.0017 0.9900

pH 4 -20.5908 51.2868 11.5642 0.0016 0.9917

Perim 4 -20.7828 51.6709 11.9483 0.0013 0.9930

NH4temp 5 -19.3265 51.9862 12.2636 0.0012 0.9942

N03N02temp 5 -19.5162 52.3657 12.6431 0.0010 0.9951

NH4DOC 5 -19.6662 52.6657 12.9431 0.0008 0.9959

totalP 4 -21.4393 52.9839 13.2613 0.0007 0.9966

Depth 4 -21.7165 53.5382 13.8156 0.0005 0.9972

Conducdepth 5 -20.1083 53.5499 13.8273 0.0005 0.9977

FPOM 4 -21.9525 54.0103 14.2877 0.0004 0.9981

ConducPerim 5 -20.3558 54.0449 14.3223 0.0004 0.9985

N03N02DOC 5 -20.6797 54.6926 14.9700 0.0003 0.9988

Conductemp 5 -20.7409 54.8152 15.0925 0.0003 0.9991

NH4D0perc 5 -20.8759 55.0851 15.3625 0.0002 0.9993

N03N02D0perc 5 -21.0532 55.4398 15.7172 0.0002 0.9995

temp 4 -23.2178 56.5408 16.8182 0.0001 0.9997

ConducDOC 5 -21.6070 56.5474 16.8248 0.0001 0.9998

ConducD0perc 5 -22.2942 57.9217 18.1991 0.0001 0.9998

N03N02Area 5 -22.4865 58.3064 18.5838 0.0000 0.9999

DOC 4 -24.4339 58.9731 19.2505 0.0000 0.9999

NH4Area 5 -22.9386 59.2106 19.4880 0.0000 0.9999

DOperc 4 -24.9524 60.0100 20.2874 0.0000 1.0000

N03N02Area\_loss 5 -24.1921 61.7176 21.9950 0.0000 1.0000

NH4Area\_loss 5 -24.3179 61.9691 22.2465 0.0000 1.0000

Area 4 -26.3315 62.7683 23.0457 0.0000 1.0000

ConducArea 5 -24.7760 62.8854 23.1628 0.0000 1.0000

ConducArea\_loss 5 -25.9042 65.1418 25.4192 0.0000 1.0000

Area\_loss 4 -28.1736 66.4525 26.7299 0.0000 1.0000

full 16 -30.2325 170.1793 130.4567 0.0000 1.0000

Best model summary:

> summary(NH4N03N02Conduc)

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']

Formula: BiofilmProd ~ meanNH4 + meanN03N02 + meanlogConduc + (1 | Pond)

Data: biofilmpondata

REML criterion at convergence: 22.8

Scaled residuals:

Min 1Q Median 3Q Max

-1.53304 -0.51140 0.08641 0.38510 1.60417

Random effects:

Groups Name Variance Std.Dev.

Pond (Intercept) 0.2873 0.5360

Residual 0.2060 0.4539

Number of obs: 22, groups: Pond, 8

Fixed effects:

Estimate Std. Error df t value Pr(>|t|)

(Intercept) 3.7575 1.3831 6.2959 2.717 0.0332 \*

meanNH4 -6.6731 15.1796 7.5718 -0.440 0.6725

meanN03N02 17.5600 11.2487 17.8985 1.561 0.1360

meanlogConduc -1.4453 0.6235 7.1728 -2.318 0.0527 .

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Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Correlation of Fixed Effects:

(Intr) menNH4 mN03N0

meanNH4 -0.171

meanN03N02 0.096 -0.131

meanlogCndc -0.887 -0.212 -0.276

> ##r2 for best model##

> r.squaredGLMM(NH4N03N02Conduc)

R2m R2c

[1,] 0.291644 0.7041912

> ##check VIF of the best model##

> vif.mer(NH4N03N02Conduc)

meanNH4 meanN03N02 meanlogConduc

1.091175 1.127891 1.160620