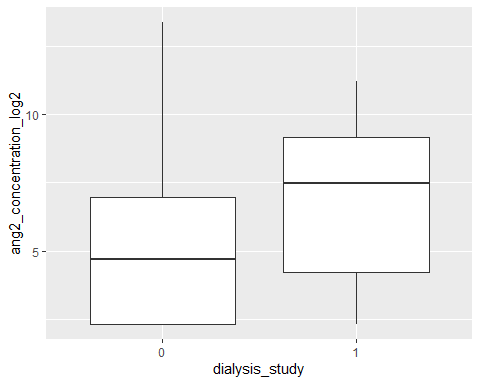
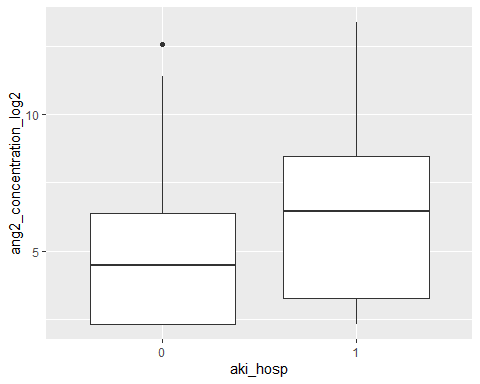
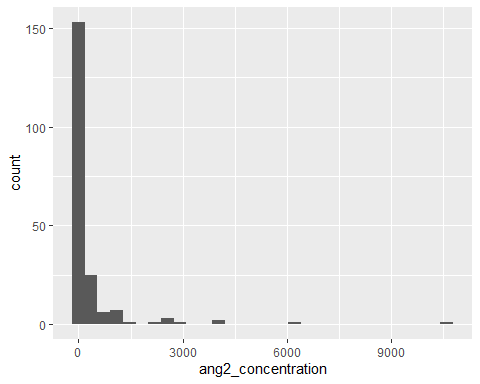
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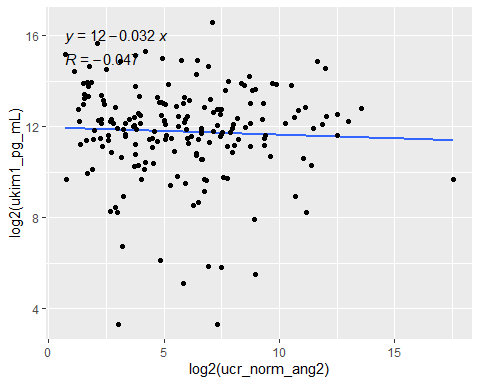
2023-09-08

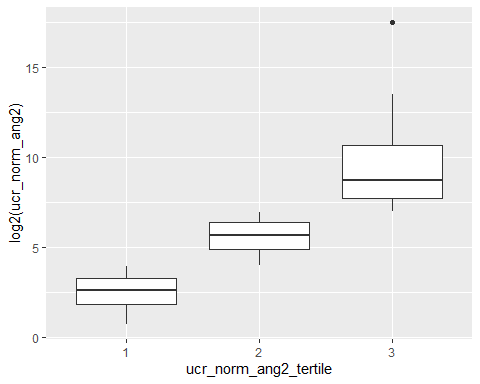
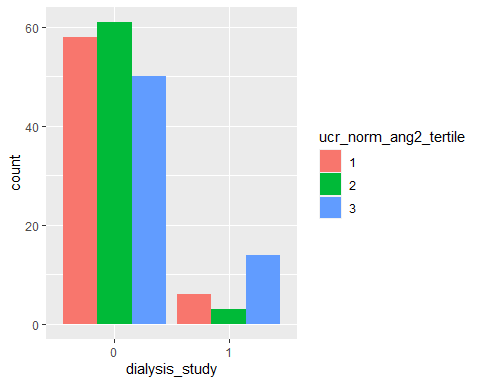
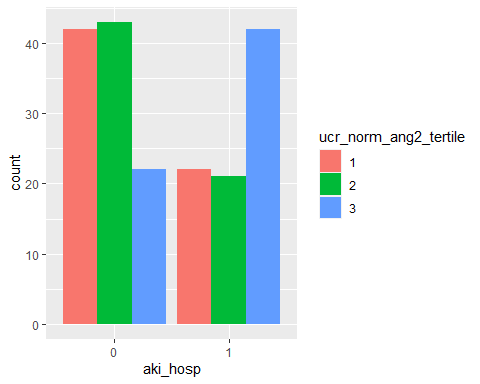
There are 201 patients that remain after merging the two datasets and filtering out those with clinical data and Ang-2 biomarker data available

## `stat\_bin()` using `bins = 30`. Pick better value with `binwidth`.

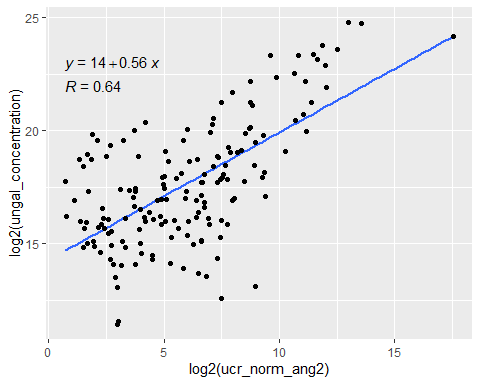


## `geom\_smooth()` using formula = 'y ~ x'

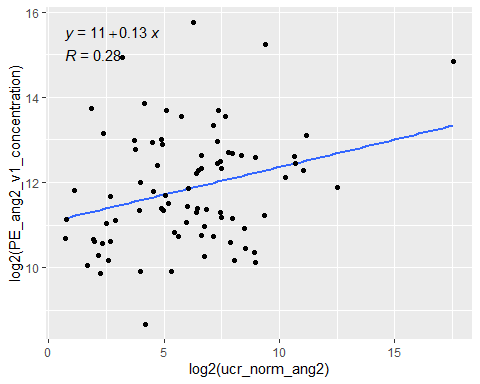
 Looking into the data by tertiles based on Ang-2 normalized to urine creatinine levels



## `geom\_smooth()` using formula = 'y ~ x'



## `geom\_smooth()` using formula = 'y ~ x'



# 10/6/23  
  
# finds overlap between ang2 and normalized ang 2 tertiles  
ang2\_tertile <- clinical\_lab\_msd %>%  
 dplyr::select(c("study\_id",  
 "ang2\_tertile")) %>%  
 filter(ang2\_tertile == 3)  
  
norm\_ang2\_tertile <- clinical\_lab\_msd %>%  
 dplyr::select(c("study\_id",  
 "ucr\_norm\_ang2\_tertile")) %>%  
 filter(ucr\_norm\_ang2\_tertile == 3)  
  
tertile\_overlap <- inner\_join(ang2\_tertile,  
 norm\_ang2\_tertile,  
 by = "study\_id")  
  
length(tertile\_overlap$study\_id)

## [1] 53

We see very high overlap between the highest Ang-2 Concentration tertiles and the highest normalized Ang-2 tertiles. 53/64 patients are in the highest tertiles for both.

# runs a poisson regression with covariate adjustment to find relative risk  
  
# aki\_hosp  
# regression on lowest/middle tertile with adjustment  
result <- glm(aki\_hosp ~ tertile\_rr + age + male + bmi + mv + covid\_confirmed,   
 data = rr\_mt\_lt,  
 family = "poisson")  
  
model\_parameters(result,  
 exponentiate = TRUE,  
 vcov = "HC",  
 vcov\_args = list(type = "HC0"))

## Parameter | IRR | SE | 95% CI | z | p  
## ----------------------------------------------------------------  
## (Intercept) | 0.88 | 0.14 | [0.64, 1.20] | -0.81 | 0.416  
## tertile rr | 0.95 | 0.06 | [0.84, 1.08] | -0.76 | 0.449  
## age | 1.00 | 1.73e-03 | [1.00, 1.01] | 1.52 | 0.130  
## male | 1.01 | 0.07 | [0.88, 1.16] | 0.21 | 0.833  
## bmi | 1.00 | 2.77e-03 | [1.00, 1.01] | 1.73 | 0.083  
## mv | 1.08 | 0.07 | [0.96, 1.22] | 1.24 | 0.217  
## covid confirmed | 1.15 | 0.08 | [1.01, 1.31] | 2.04 | 0.042

##   
## Uncertainty intervals (equal-tailed) and p-values (two-tailed) computed  
## using a Wald z-distribution approximation.

# unadjusted model  
result <- glm(aki\_hosp ~ tertile\_rr,   
 data = rr\_mt\_lt,  
 family = "poisson")  
  
model\_parameters(result,  
 exponentiate = TRUE,  
 vcov = "HC",  
 vcov\_args = list(type = "HC0"))

## Parameter | IRR | SE | 95% CI | z | p  
## ---------------------------------------------------------  
## (Intercept) | 1.34 | 0.06 | [1.23, 1.47] | 6.69 | < .001  
## tertile rr | 0.99 | 0.06 | [0.87, 1.12] | -0.19 | 0.852

##   
## Uncertainty intervals (equal-tailed) and p-values (two-tailed) computed  
## using a Wald z-distribution approximation.

# regression on lowest/highest tertile with adjustment   
result <- glm(aki\_hosp ~ tertile\_rr + age + male + bmi + mv + covid\_confirmed,   
 data = rr\_ht\_lt,  
 family = "poisson")  
  
model\_parameters(result,  
 exponentiate = TRUE,  
 vcov = "HC",  
 vcov\_args = list(type = "HC0"))

## Parameter | IRR | SE | 95% CI | z | p  
## ----------------------------------------------------------------  
## (Intercept) | 1.18 | 0.19 | [0.86, 1.63] | 1.03 | 0.304  
## tertile rr | 1.21 | 0.07 | [1.08, 1.35] | 3.25 | 0.001  
## age | 1.00 | 1.77e-03 | [0.99, 1.00] | -1.07 | 0.284  
## male | 1.07 | 0.07 | [0.94, 1.20] | 1.02 | 0.309  
## bmi | 1.00 | 2.98e-03 | [1.00, 1.01] | 1.30 | 0.192  
## mv | 1.07 | 0.07 | [0.94, 1.21] | 0.96 | 0.338  
## covid confirmed | 1.06 | 0.06 | [0.94, 1.19] | 0.97 | 0.334

##   
## Uncertainty intervals (equal-tailed) and p-values (two-tailed) computed  
## using a Wald z-distribution approximation.

# unadjusted   
result <- glm(aki\_hosp ~ tertile\_rr,   
 data = rr\_ht\_lt,  
 family = "poisson")  
  
model\_parameters(result,  
 exponentiate = TRUE,  
 vcov = "HC",  
 vcov\_args = list(type = "HC0"))

## Parameter | IRR | SE | 95% CI | z | p  
## --------------------------------------------------------  
## (Intercept) | 1.34 | 0.06 | [1.23, 1.47] | 6.69 | < .001  
## tertile rr | 1.23 | 0.07 | [1.10, 1.38] | 3.68 | < .001

##   
## Uncertainty intervals (equal-tailed) and p-values (two-tailed) computed  
## using a Wald z-distribution approximation.

We do see that even without adjustments, being in the top tertile of the dataset predicts higher chances of developing aki in the hospital.

# dialysis\_study  
# regression on lowest/middle tertile with adjustment  
result <- glm(dialysis\_study ~ tertile\_rr + age + male + bmi + mv + covid\_confirmed,   
 data = rr\_mt\_lt,  
 family = "poisson")  
  
model\_parameters(result,  
 exponentiate = TRUE,  
 vcov = "HC",  
 vcov\_args = list(type = "HC0"))

## Parameter | IRR | SE | 95% CI | z | p  
## -------------------------------------------------------------  
## (Intercept) | 0.03 | 0.06 | [0.00, 0.91] | -2.01 | 0.044  
## tertile rr | 0.41 | 0.28 | [0.11, 1.57] | -1.31 | 0.191  
## age | 1.01 | 0.02 | [0.98, 1.04] | 0.44 | 0.660  
## male | 0.66 | 0.49 | [0.15, 2.81] | -0.57 | 0.570  
## bmi | 1.01 | 0.02 | [0.97, 1.06] | 0.63 | 0.530  
## mv | 0.79 | 0.47 | [0.24, 2.56] | -0.40 | 0.690  
## covid confirmed | 2.48 | 2.06 | [0.49, 12.62] | 1.10 | 0.273

##   
## Uncertainty intervals (equal-tailed) and p-values (two-tailed) computed  
## using a Wald z-distribution approximation.

# unadjusted  
result <- glm(dialysis\_study ~ tertile\_rr,   
 data = rr\_mt\_lt,  
 family = "poisson")  
  
model\_parameters(result,  
 exponentiate = TRUE,  
 vcov = "HC",  
 vcov\_args = list(type = "HC0"))

## Parameter | IRR | SE | 95% CI | z | p  
## ---------------------------------------------------------  
## (Intercept) | 0.09 | 0.04 | [0.04, 0.20] | -6.09 | < .001  
## tertile rr | 0.50 | 0.34 | [0.13, 1.91] | -1.01 | 0.311

##   
## Uncertainty intervals (equal-tailed) and p-values (two-tailed) computed  
## using a Wald z-distribution approximation.

# regression on lowest/highest tertile with adjustment  
result <- glm(dialysis\_study ~ tertile\_rr + age + male + bmi + mv + covid\_confirmed,   
 data = rr\_ht\_lt,  
 family = "poisson")  
  
model\_parameters(result,  
 exponentiate = TRUE,  
 vcov = "HC",  
 vcov\_args = list(type = "HC0"))

## Parameter | IRR | SE | 95% CI | z | p  
## -------------------------------------------------------------  
## (Intercept) | 0.04 | 0.05 | [0.00, 0.48] | -2.52 | 0.012  
## tertile rr | 2.21 | 1.04 | [0.88, 5.57] | 1.68 | 0.093  
## age | 0.98 | 0.01 | [0.96, 1.01] | -1.16 | 0.246  
## male | 0.77 | 0.30 | [0.36, 1.67] | -0.65 | 0.513  
## bmi | 1.02 | 0.02 | [0.99, 1.06] | 1.49 | 0.136  
## mv | 1.03 | 0.48 | [0.41, 2.56] | 0.07 | 0.947  
## covid confirmed | 4.80 | 3.51 | [1.14, 20.15] | 2.14 | 0.032

##   
## Uncertainty intervals (equal-tailed) and p-values (two-tailed) computed  
## using a Wald z-distribution approximation.

# unadjusted  
result <- glm(dialysis\_study ~ tertile\_rr,   
 data = rr\_ht\_lt,  
 family = "poisson")  
  
model\_parameters(result,  
 exponentiate = TRUE,  
 vcov = "HC",  
 vcov\_args = list(type = "HC0"))

## Parameter | IRR | SE | 95% CI | z | p  
## ---------------------------------------------------------  
## (Intercept) | 0.09 | 0.04 | [0.04, 0.20] | -6.09 | < .001  
## tertile rr | 2.33 | 1.06 | [0.96, 5.69] | 1.86 | 0.062

##   
## Uncertainty intervals (equal-tailed) and p-values (two-tailed) computed  
## using a Wald z-distribution approximation.