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#0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

##a.1
##uterotrophic bioassay successful overall at identifying effects of EE and ZM. F-test for EE,ZM are sig
anova(lm.full.fac)

coefs=rownames(summary(lm.full.fac)$coefficients)

res=summary(lm.full.fac)$coefficients %>%
  cbind(coef=coefs,.) %>%
  as.tibble() #get the coefficients matrix

colnames(res)=c("coef","estimate","std_error","t_value","p_value")

res %>% filter(as.numeric(p_value)<0.05) %>% slice(1:10)

##a.2 do some labs fail t detect such effects
##There are some labs fail to detect such effects, as follows:"Huntingd""Bayer""ChungKor""TNO""Zeneca"
a.2.ee=t.test(lm.full.fac,"EE","lab","lab")$t.test
a.2.ee
a.2.ee %>% filter(((p.value<0.05)&(estimator<0))|(p.value>0.05))# %>% pull(i.levels)

a.2.zm=t.test(lm.full.fac,"ZM","lab","lab")$t.test
a.2.zm
a.2.zm %>% filter(((p.value<0.05)&(estimator>0))|(p.value>0.05))#%>% pull(i.levels)
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##a.3 the change dose for EE? vary across labs?
##From the output of summary. The change dose for EE is EE3. Dose larger than this is significant, less

##b. does the dose reponse vary across labs? are there certain labs stands out as being different?
##From the output of summary. There exist several significant interaction coefficients, meaning dose rep

res %>% filter(str_detect(res$coef, "EE.*lab")) %>%
  filter(p_value<0.001)

res %>% filter(str_detect(res$coef, "ZM.*lab")) %>%
  filter(p_value<0.005)

##c.Do the protocols differ in sensitivity to detect? Which one recommend?
##From the result from anova. The protocols differ. And the variance of protocol C,D is super large. Pr

anova(lm.full.fac)["EE:protocol", ]
anova(lm.full.fac)["ZM:protocol", ]

res %>% filter(str_detect(res$coef, "~protocol"))

res %>% filter(str_detect(res$coef, "EE.*protocol"))

res %>% filter(str_detect(res$coef, "ZM.*protocol"))

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