**Is net change a good indicator of receptor binding avidity change?**

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In total, 59 single substitutions in HA (58 from H1N1 and 1 from H3N2) which have receptor binding avidity data are collected from literatures. I classify their binding avidity into 3 groups: increased (+1), neutral (0), and decreased (-1) binding. Net charge changes of each virus from wild type to mutant are calculated. I use Fisher’s exact test on contingency table to check whether net charge distribute differently with binding avidity.

R code

m <- polr(y ~ mydata$BindingScrDiff)

(ctable<- coef(summary(m)))

p <- pnorm(abs(ctable[,"t value"]), lower.tail = FALSE)