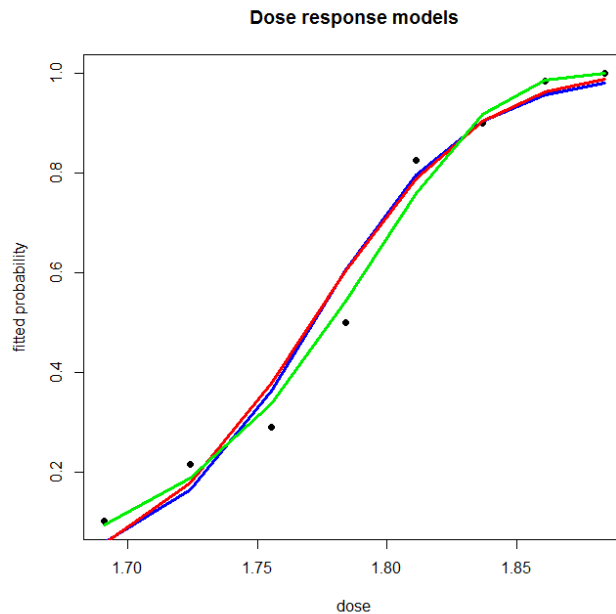


Q3

Plot below shows comparison between the models where blue=logit, red=probit, green=cloglog. We can see that complementary log-log link (green curve) is the best.



The lethal dose can be calculated by Logit: $LD-p = (\log(p/(1-p)) - \text{constant}) / \text{coef}$ and Probit: $LD-p = (\text{invnormal}(p) - \text{constant}) / \text{coef}$. We use the function dose.p in R to get the estimates for LD50 and LD5 (logCS2mg/l-1):

logit	Dose	SE	probit	Dose	SE	cloglog	Dose	SE
p = 0.50	1. 7717	0. 0039	p = 0.50	1.7709	0.0038	p = 0.50	1.7788	0.0040
p = 0.05	1. 6858	0. 0087	p = 0.05	1.6875	0.0079	p = 0.05	1.6606	0.0120

We want to get confidence intervals in mg/l^{-1} units. To obtain the standard errors from transformed data when $y = \ln(x)$ we need to calculate $E(X) = \exp(Y)$ and $SE(X) = \exp(Y) SE(Y)$. So 95% can be calculated from $CI = E(X) \pm (1.96 * SE(X))$

	logit	probit	cloglog
p = 0.50	(58.74, 59.49)	(58.63, 59.37)	(59.69, 60.48)
p = 0.05	(47.81, 49.20)	(48.06, 49.32)	(44.88, 46.67)

For complementary log-log function, the model is similar to the logistic and probit models for probability values near 0.5 but differs for probability near 0.05.

Appendix (R Code)

```
require(dobson)

require(ggplot2)

library(MASS)


beetle <- dobson::beetle

head(beetle)

#data preparation

beetle$n_y=beetle$n-beetle$y

beetle$mat=cbind(beetle$y,beetle$n_y)

beetle$p = beetle$y / beetle$n


# logistic regression

res_logit=glm(beetle$mat~beetle$x, family=binomial(link="logit"))

# fitted.values

fit_p_logit = c(fitted.values(res_logit))

fit_y_logit = beetle$n*fit_p_logit


# probit model

res_probit=glm(beetle$mat ~ beetle$x, family=binomial(link="probit"))

# fitted.values

fit_p_probit = c(fitted.values(res_probit))

fit_y_probit = beetle$n*fit_p_probit
```

```

# extreme value model

res_cloglog=glm(beetle$mat ~ beetle$x, family=binomial(link="cloglog"))

# fitted.values

fit_p_cloglog = c(fitted.values(res_cloglog))

fit_y_cloglog = beetle$n*fit_p_cloglog


#plots

plot(beetle$x, beetle$p, pch=19,col="black",
      main="Dose response models", xlab="dose", ylab="fitted probability")

lines(beetle$x, fit_p_logit, col="blue", lwd=3)

lines(beetle$x, fit_p_probit, col="red", lwd=3)

lines(beetle$x, fit_p_cloglog, col="green2", lwd=3)


#lethal dose (LD-50, LD-5)

# complementary log-log function. The model is similar to the logistic and

# probit models for probability values near 0.5 but differs for probability near 0 or 1.

exp(dose.p(res_logit,p=c(0.5, 0.05)))

exp(dose.p(res_probit,p=c(0.5, 0.05)))

exp(dose.p(res_cloglog,p=c(0.5, 0.05)))

```