# R CODE - logistic regression model for data by Mudie et al. [23] and result display

```r
d < - c(16.0, 23.0, 45.5, 67.4)  # median dose(ds), male(m), and female(f) live births by dose
m < - c(1808, 1474, 1458, 1178)
f < - c(1740, 1405, 1352, 1049)
mf < - cbind(m,f)
p_m < - m/(m+f)  # proportion male

fm1 < - glm(mf~ds,family=quasibinomial)  # corrected for heterogeneity
fm2 < - glm(mf~ds,family=binomial)  # not corrected for heterogeneity

summary(fm1)
summary(fm2)

plot(p_m~ds,type="p",pch="O", ylim=c(.505,.535), xlim=c(10,70),

main = c("Male proportion by settlement radiation exposure group"),

lines(fm2$fitted.values~ds, lty=1, lwd=2)
lines(p_m~ds, lty=2, lwd=1.5)
points(p_m~ds, lty=4, pch="O")
```

# Result fm2 - ignoring heterogeneity (here: ignoring underdispersion)

# dispersion parameter for binomial family taken to be 1

```r
glm(formula = mf ~ ds, family = binomial)
```

|          | Estimate | Std.Error | zvalue | Pr(>|z|) |
|----------|----------|-----------|--------|----------|
| intcpt   | 0.0136074| 0.0384296 | 0.354  | 0.7232   |
| ds       | 0.0014676| 0.0009606 | 1.528  | 0.1267   |

# taking the significant underdispersion (p value 0.9875 > 0.95) of the Mudie et al. data into account (fm1), the dose response
# association is significant: p value 0.0053.