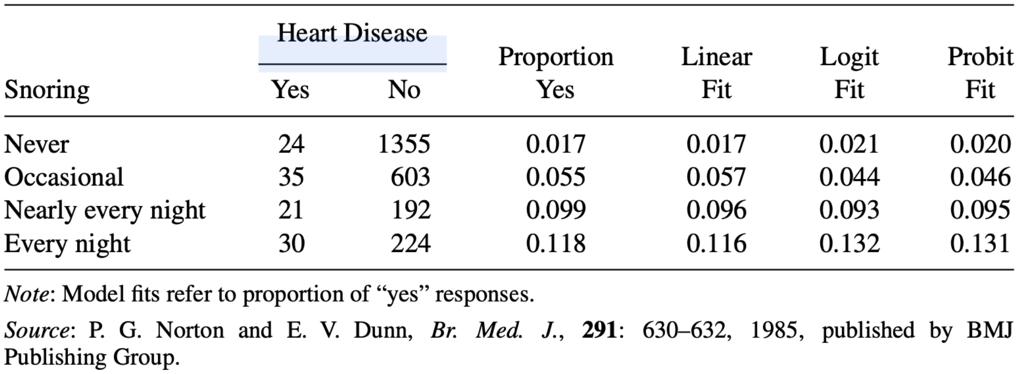
(1) The following table is based on an epidemiological survey of 2484 subjects to investigate snoring as a possible risk factor for heart disease. The subjects were classified according to their snoring level, as reported by their spouses. The linear probability model states that the probability of heart disease $\pi(x)$ is a linear function of the snoring level x. We treat the rows of the table as independent binomial samples with probabilities $\pi(x)$. We use scores $(0, 2, 4, 5)$ for $x =$ snoring level, treating the last two snoring categories as closer than the other adjacent pairs.



	Heart Disease					
Snoring	Yes	No	Proportion Yes	Linear Fit	Logit Fit	Probit Fit
Never	24	1355	0.017	0.017	0.021	0.020
Occasional	35	603	0.055	0.057	0.044	0.046
Nearly every night	21	192	0.099	0.096	0.093	0.095
Every night	30	224	0.118	0.116	0.132	0.131

Note: Model fits refer to proportion of "yes" responses.

Source: P. G. Norton and E. V. Dunn, *Br. Med. J.*, **291**: 630–632, 1985, published by BMJ Publishing Group.

(a) Use the following R codes to find the logistic regression model for the snoring and heart disease.

```
> snoring < − data.frame(snore = c(enter snoring levels separated by commas), heartdisyes = c(enter column values for ”Yes” separated by commas), n = c(enter row totals separated by comas) )
> snoring
```

```
> glm(formula = heartdisyes/n ∼ snore, family = binomial(), data = snoring, weights = n)
```

Or

```
> snoring< − c(enter snoring levels separated by commas)
> logit.irls< −glm(cbind(yes=c(enter ”Yes” values separated by commas), no=c(enter ”No” values separated by commas)) ∼ snoring, family=binomial(link=logit))
> summary(logit.irls)$coefficients
```

(b) Use the following R codes to find the linear probability model for the snoring and heart disease.

```
> prop< −c(enter the proportions separated by comas)
> lpm.irls< −glm(prop ∼ snoring, weights=c(enter row totals separated by commas),family=quasi(link=identity))
> summary(lpm.irls)$coefficients
```

(c) Use the following R codes to find the probit regression model for the snoring and heart disease.

```
> probit.irls< −glm(cbind(yes=c(enter ”Yes” values separated by commas), no=c(enter ”No” values separated by commas)) ∼ snoring, family=binomial(link=probit))
```

```
> summary(probit.irls)$coefficients
```