

Part I

1. $\log(\text{odds}(\text{HeartAttack})) = -7.98 + 0.0731[\text{MAP}] - 0.0112[\text{Cholesterol}] \rightarrow$
 $\text{odds}(\text{HeartAttack}) = e^{-7.98+0.0731[\text{MAP}]-0.0112[\text{Cholesterol}]} \rightarrow$
 $P(\text{HeartAttack} = 1) = \frac{1}{1+e^{7.98-0.0731[110]+0.0112[170]}}$ (page 113 ch. 13.2)
= 0.137

2. $P(\text{HeartAttack} = 1) = \frac{1}{1+e^{7.98-0.0731[110]+0.0112[171]}} = 0.135$
a. A 1 mg/dL increase decreases the probability of a heart attack by 0.002

3. $0.50 = \frac{1}{1+e^{7.98-0.0731[\text{MAP}]+0.0112[\text{Cholesterol}]} \rightarrow$
 $\log\left(\frac{1}{0.50} - 1\right) = \log(e^{7.98-0.0731[\text{MAP}]+0.0112[\text{Cholesterol}]}) \rightarrow$
 $0 = 7.98 - 0.0731[\text{MAP}] + 0.0112[\text{Cholesterol}] \rightarrow$
 $[\text{Cholesterol}] = 6.527[\text{MAP}] - 712.5$

Example solutions (MAP, Cholesterol): (120, 70.7), (150, 266.6), (200, 592.9)

Part II

1.

Code

```
clear; close all; clc;  
load 'cas9.mat'  
model = fitglm(cas9, 'Success ~ ProtospacerSize + WrongPAM + Methylation +  
Mismatches', 'link', 'logit', 'Distribution', 'binomial')
```

Output:

model =

Generalized linear regression model:

```
logit(Success) ~ 1 + ProtospacerSize + WrongPAM + Methylation + Mismatches  
Distribution = Binomial
```

Estimated Coefficients:

	Estimate	SE	tStat	pValue
(Intercept)	-19.909	11.008	-1.8085	0.070524
ProtospacerSize	0.99151	0.56156	1.7656	0.077458
WrongPAM	-1.1456	0.5717	-2.0038	0.04509
Methylation	0.71697	0.55853	1.2837	0.19926
Mismatches	-2.9309	1.0858	-2.6992	0.0069501

100 observations, 95 error degrees of freedom

Dispersion: 1

Chi^2-statistic vs. constant model: 21.9, p-value = 0.000214

2. WrongPAM and Mismatches both have p-values < 0.05 suggesting their coefficients are significantly nonzero and will therefore have an effect on Cas9 cleavage.
3. Odds ratios
 - a. WrongPAM: $\exp(-1.1456) = 0.318$
 - b. Mismatches: $\exp(-2.9309) = 0.053$