

Bayesian: 2.1, 5.1, 5.2,

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2.1

A. Model A has no bias, as it is an even $1/4$ chance for each side. Which gives a $P(x) = 1/4$ for each side.

B. Model B gives a higher chance as the number increases. $P(x) = 0.1, 0.2, 0.3, 0.4$

C. Model C gives a higher chance as the number decreases. $P(x) = 0.48, 0.24, 0.16, 0.12$

5.1

Prob for first test, and then the second...

```
present <- 0.001
absent <- 1 - present
present_pos <- 0.99
absent_pos <- 0.05

top <- present_pos * present
bottom <- present_pos * present + (absent_pos * (1 - present))
first_test <- top / bottom;first_test
```

```
## [1] 0.01943463
```

```
top <- (1 - present_pos) * first_test
bottom <- (1 - present_pos) * first_test + ((1 - absent_pos) * (1 - first_test))
second_test <- top / bottom;second_test
```

```
## [1] 0.0002085862
```

5.2

A. The table from part can be seen below:

```
library(knitr)
sad <- c(0.99 * 0.001 * 100000, (1.0 - 0.99) * 0.001 * 100000, 0.001 * 100000)
happy <- c(0.05 * (1.0 - 0.001) * 100000, (1.0 - 0.05) * (1.0 - 0.001) * 100000, (1.0 - 0.001) * 100000)
tot <- sad + happy
sht <- cbind(sad, happy, tot)
rownames(sht) <- c("+", "-", "tot")
kable(sht)
```

	sad	happy	tot
+	99	4995	5094
-	1	94905	94906
tot	100	99900	100000

B. From the table, it would appear that every 99 / 5,094 would have the disease. The actual number is the same as the percentage from above, $99 / 5094 = 0.0194346$.

C. The tree is represented as a table.

```
left <- c(10000, 10000 * 0.99, 9900 * (1.0 - 0.99))
right <- c(9990000, 9990000 * 0.05, 499500 * (1.0 - 0.05))
lr <- cbind(left, right)
kable(lr)
```

	left	right
10000	9990000	
9900	499500	
99	474525	

D. The proportion works out to be the same.

```
99 / (99 + 474525)
```

```
## [1] 0.0002085862
```