

Stat 571 - HW4 - Nathanael Fillmore

1. > prob.given.bucket1 <- c(black=4, red=5, white=3)/12
 > prob.given.bucket2 <- c(black=1, red=4, white=7)/12
 > prob.given.bucket3 <- c(black=80, red=0, white=20)/100
 > prior <- c(bucket1=0.1, bucket2=0.2, bucket3=0.7)
- (a) > prob.black <- prior["bucket1"]*prob.given.bucket1["black"] +
 + prior["bucket2"]*prob.given.bucket2["black"] +
 + prior["bucket3"]*prob.given.bucket3["black"]
 > cat(sprintf("The probability that the ball is black is %f.", prob.black))
- The probability that the ball is black is 0.610000.
- (b) > prob.red <- prior["bucket1"]*prob.given.bucket1["red"] +
 + prior["bucket2"]*prob.given.bucket2["red"] +
 + prior["bucket3"]*prob.given.bucket3["red"]
 > cat(sprintf("The probability that the ball is red is %f.", prob.red))
- The probability that the ball is red is 0.108333.
- (c) > prob.white <- prior["bucket1"]*prob.given.bucket1["white"] +
 + prior["bucket2"]*prob.given.bucket2["white"] +
 + prior["bucket3"]*prob.given.bucket3["white"]
 > cat(sprintf("The probability that the ball is white is %f.", prob.white))
- The probability that the ball is white is 0.281667.
- (d) > prob.bucket1.given.black <- prob.given.bucket1["black"]*prior["bucket1"]/prob.black
 > prob.bucket2.given.black <- prob.given.bucket2["black"]*prior["bucket2"]/prob.black
 > prob.bucket3.given.black <- prob.given.bucket3["black"]*prior["bucket3"]/prob.black
 > cat(sprintf("The probability that the ball came from bucket 1, given that it
 + was black, is %f.", prob.bucket1.given.black))
- The probability that the ball came from bucket 1, given that it was black, is 0.054645.
- > cat(sprintf("The probability that the ball came from bucket 2, given that it
 + was black, is %f.", prob.bucket2.given.black))
- The probability that the ball came from bucket 2, given that it was black, is 0.027322.
- > cat(sprintf("The probability that the ball came from bucket 3, given that it
 + was black, is %f.", prob.bucket3.given.black))
- The probability that the ball came from bucket 3, given that it was black, is 0.918033.
2. > prob.given.bucket1 <- c(black=17, red=6, white=8)/31
 > prob.given.bucket2 <- c(black=40, red=30, white=25)/95
 > prior <- c(bucket1=1/2, bucket2=1/2)
- (a) > prob.B.eq.1 <- prob.given.bucket1["black"]*prior["bucket1"] +
 + prob.given.bucket2["black"]*prior["bucket2"]
 > prob.R.eq.1 <- prob.given.bucket1["red"]*prior["bucket1"] +
 + prob.given.bucket2["red"]*prior["bucket2"]
 > prob.W.eq.1 <- prob.given.bucket1["white"]*prior["bucket1"] +
 + prob.given.bucket2["white"]*prior["bucket2"]
 > cat(sprintf("\$P(B=1)=%f, \\P(R=1)=%f, \\P(W=1)=%f\$.", prob.B.eq.1,
 + prob.R.eq.1, prob.W.eq.1))
- $P(B = 1) = 0.484720$,
 $P(R = 1) = 0.254669$,
 $P(W = 1) = 0.260611$.
- (b) > cat(sprintf("\$B\$ follows Binomial\$(n=10, p=%f)\$.", prob.B.eq.1))
- B follows Binomial($n = 10, p = 0.484720$).
- > cat(sprintf("\$R\$ follows Binomial\$(n=10, p=%f)\$.", prob.R.eq.1))
- R follows Binomial($n = 10, p = 0.254669$).
- > cat(sprintf("\$W\$ follows Binomial\$(n=10, p=%f)\$.", prob.W.eq.1))
- W follows Binomial($n = 10, p = 0.260611$).

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3. > prob.truely.A <- .43
   > prob.truely.B <- .07
   > prob.truely.AB <- .04
   > prob.truely.O <- .46
   > prob.stb.A.given.truely.A <- .88
   > prob.stb.A.given.truely.B <- .04
   > prob.stb.A.given.truely.AB <- .10
   > prob.stb.A.given.truely.O <- .04
   > prob.stb.A <- prob.stb.A.given.truely.A * prob.truely.A +
+               prob.stb.A.given.truely.B * prob.truely.B +
+               prob.stb.A.given.truely.AB * prob.truely.AB +
+               prob.stb.A.given.truely.O * prob.truely.O
   > prob.truely.A.given.stb.A <- prob.stb.A.given.truely.A * prob.truely.A / prob.stb.A
   > cat(sprintf("The probability that a soldier's blood type is $A$ given that he
+ was typed as having type $A$ is %f", prob.truely.A.given.stb.A))

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The probability that a soldier's blood type is A given that he was typed as having type A is 0.937562

17.

(a) Some plants were tall and had green pods, etc., so “tall” and “green pods” are not mutually exclusive.

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(b) > prob.tall.and.green <- 900/1600
   > prob.tall.and.yellow <- 300/1600
   > prob.short.and.green <- 300/1600
   > prob.short.and.yellow <- 100/1600
   > prob.tall <- prob.tall.and.green + prob.tall.and.yellow
   > prob.green <- prob.tall.and.green + prob.short.and.green
   > cat(sprintf("$P($tall)$P($green$) = %f = %f = P($tall and green$)$, so they are
+ independent.", prob.tall*prob.green, prob.tall.and.green))

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$P(\text{tall})P(\text{green}) = 0.562500 = 0.562500 = P(\text{tall and green})$, so they are independent.

```

19. > prob.G.given.region1 <- .3
   > prob.C.given.region1 <- .3
   > prob.A.given.region1 <- .2
   > prob.T.given.region1 <- .2
   > prob.G.given.region2 <- .25
   > prob.C.given.region2 <- .25
   > prob.A.given.region2 <- .25
   > prob.T.given.region2 <- .25

```

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(a) > prob.same <- prob.G.given.region1 * prob.G.given.region2 +
+               prob.C.given.region1 * prob.C.given.region2 +
+               prob.A.given.region1 * prob.A.given.region2 +
+               prob.T.given.region1 * prob.T.given.region2
   > cat(sprintf("The probability that they are the same is %f", prob.same))

```

The probability that they are the same is 0.250000

(b) “Success” means “the two nucleotides we just picked are the same”, so $P(\text{success}) = .25$. We get 3 successes in 3 trials.

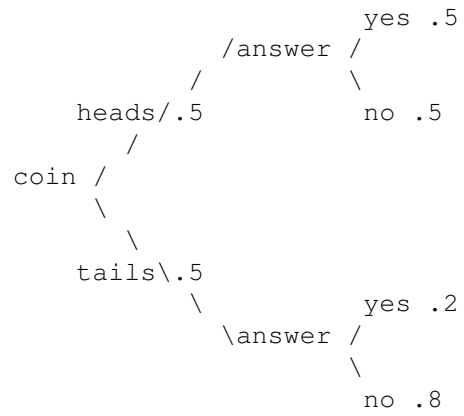
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> prob.success <- .25
> prob.3.successes <- dbinom(3, size=3, prob=.25) # or just prob.success^3
> cat(sprintf("The probability that the triplets are the same is %f", prob.3.successes))

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The probability that the triplets are the same is 0.015625

21. (a)



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(b) > prob.heads.and.yes <- .5*.5
> prob.tails.and.yes <- .5*.2
> prob.yes <- prob.heads.and.yes + prob.tails.and.yes
> cat(sprintf("$P($yes$)=%f$", prob.yes))
```

$P(\text{yes}) = 0.350000$