Probability

BIO5312 FALL2017

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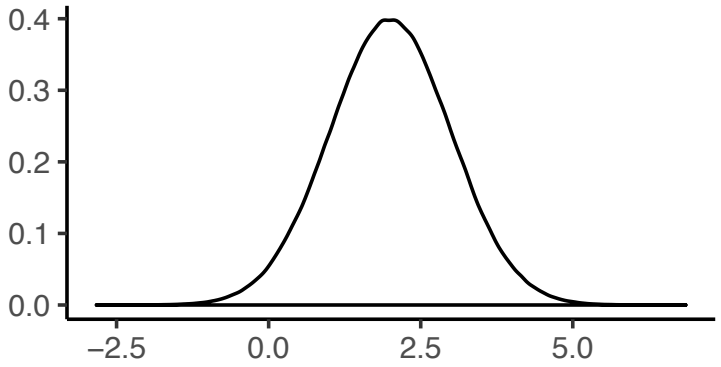
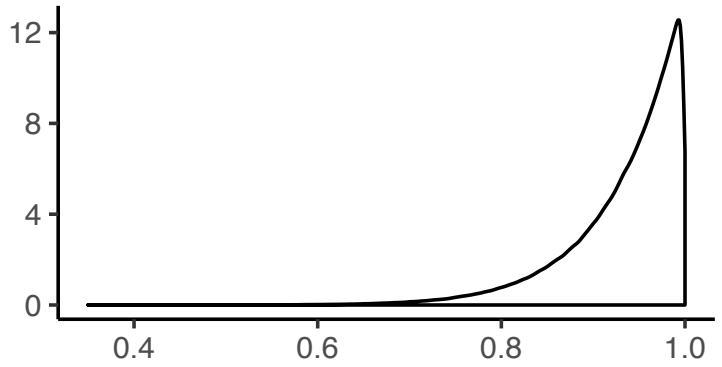
Skew

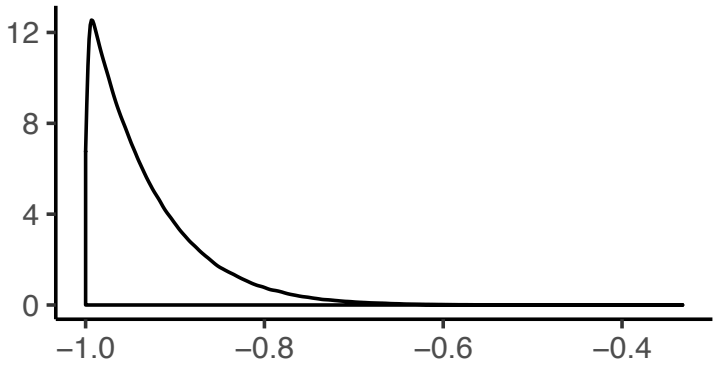
Symmetric



Left-skew

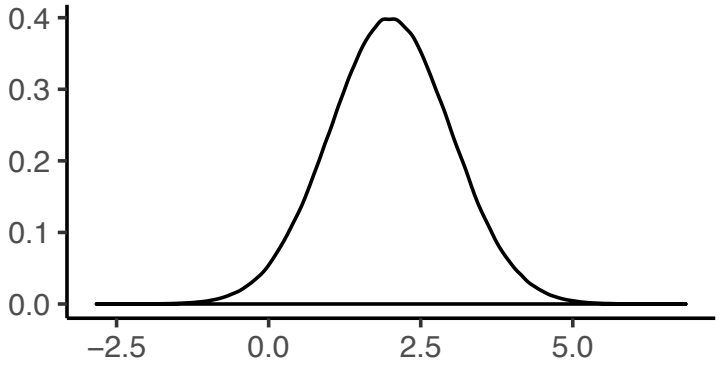


Right-skew

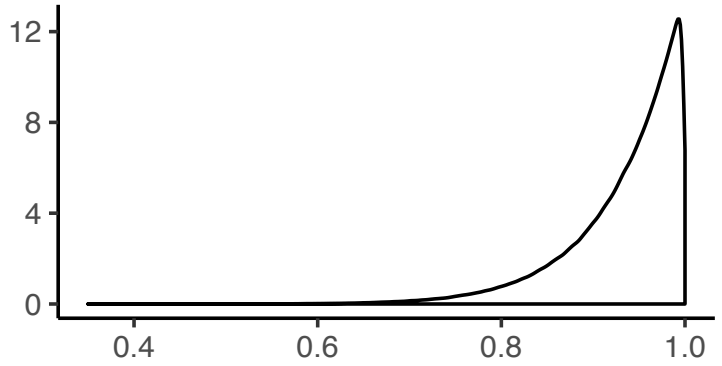


Mean vs median

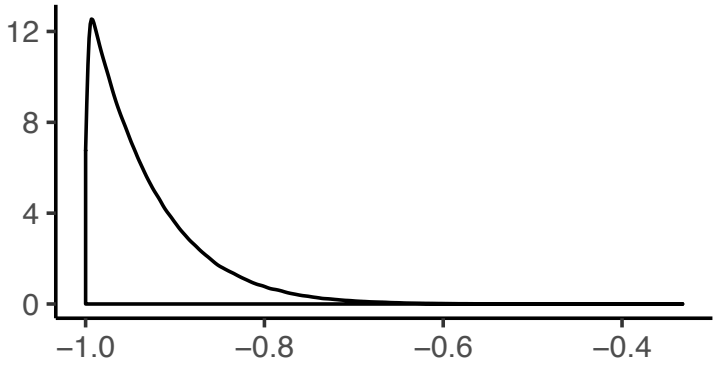
Symmetric

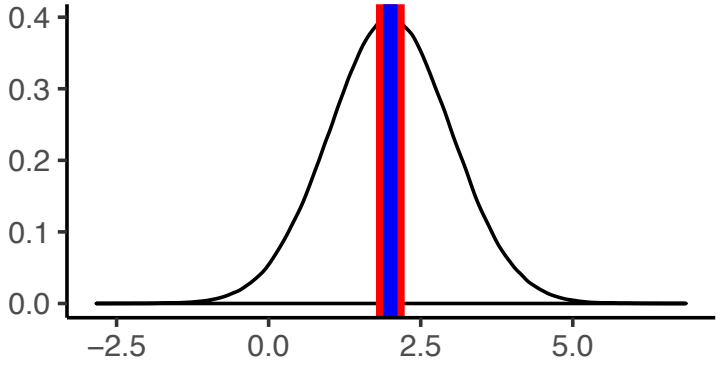


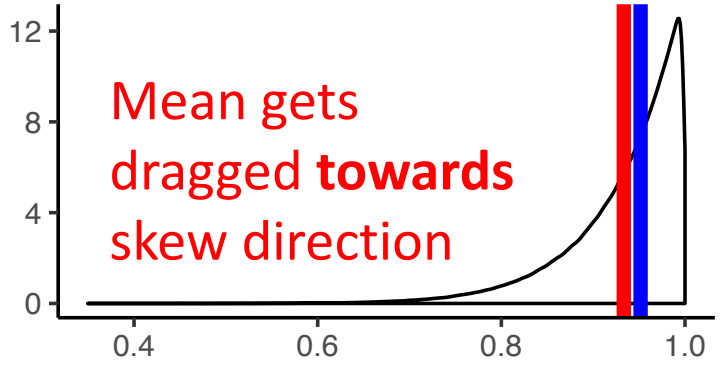
Left-skew



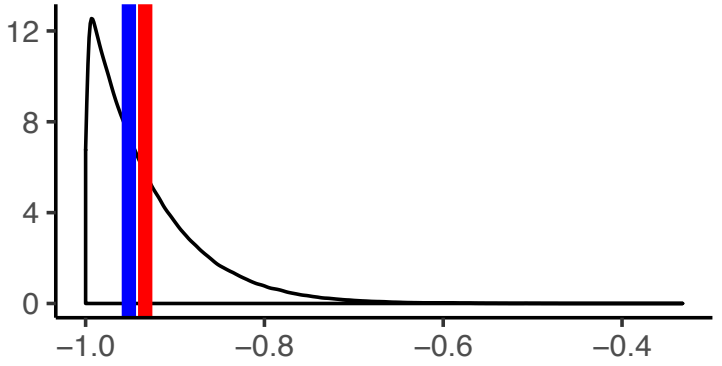
Right-skew







Mean gets dragged **towards** skew direction

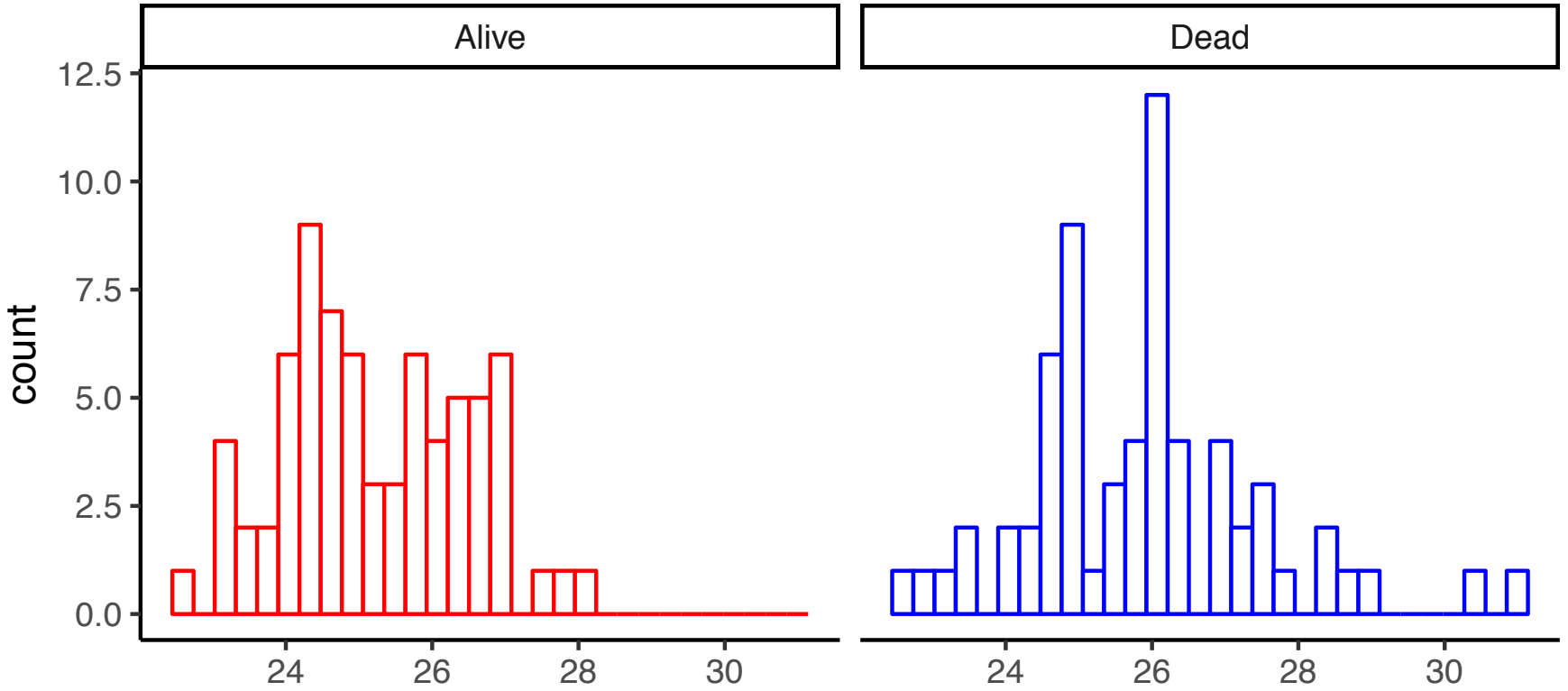


Mean vs median

When it is difficult to tell which might be "better", default to median.

This is particularly true for **small sample sizes** (more on why in coming weeks)

Does sparrow weight influence survival?




```
> summary(sp$Weight[sp$Survival == "Alive"])
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
  22.60   24.20   24.90   25.21   26.30   28.00
```

```
> summary(sp$Weight[sp$Survival == "Dead"])
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
  22.60   24.80   25.95   25.86   26.58   31.00
```

Probability vocabulary

Sample space

Event

Probability

Mutually exclusive

Probability distribution

Independent

Sample space and event

Sample space is the set of all possible outcomes of a random trial

Event is a subset of this set

Example: Roll a die

Sample space is <1,2,3,4,5,6>

Events: roll a 4, roll something >=5, etc.

Probability

Probability of an event is the proportion of times the event would occur., i.e. event frequency, in an infinite number of trials

Empirical probabilities are based on a finite amount of data. If sample size expanded indefinitely, probabilities are measured with increasing precision and approach the true event probability. *This is pretty much what we can measure.*

Probability: roll a die

Theoretical probability

- P[roll a 5] = 1/6
- P[roll an even number] = ½

Empirical probability

- **After rolling 10x, we got:** 5 5 6 1 4 2 3 1 1 5 2 1
- P[roll a 5] = 3/10
- P[roll an even number] = 4/10 = 2/5

Basic properties of probabilities

Probabilities are always between 0 and 1

$$\mathbf{0} \leq \boldsymbol{P}[\boldsymbol{event}] \leq \mathbf{1}$$

The sum of probabilities for all events equals 1

$$\sum_{\boldsymbol{i}} \boldsymbol{P_i} = \mathbf{1}$$

Mutually exclusive

Two events are **mutually exclusive** if they cannot both occur simultaneously

Mutually exclusive events: roll a 4 and a 1

<u>Not</u> mutually exclusive events: roll an even # and a 2

Probability distribution

The list of probabilities for all *mutually exclusive* outcomes of a random trial

A fair die has this distribution:

P[roll 1] = 1/6

P[roll 2] = 1/6

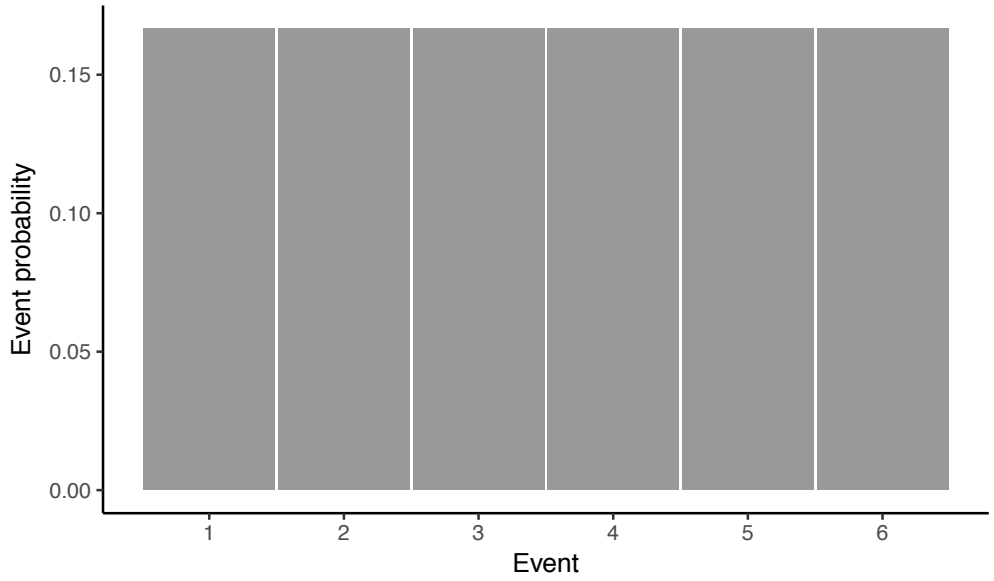
P[roll 3] = 1/6

P[roll 4] = 1/6

P[roll 5] = 1/6

P[roll 6] = 1/6

This is a **discrete probability distribution**



Independent

Two events are **independent** if the occurrence of one *does not change* the occurrence of another.

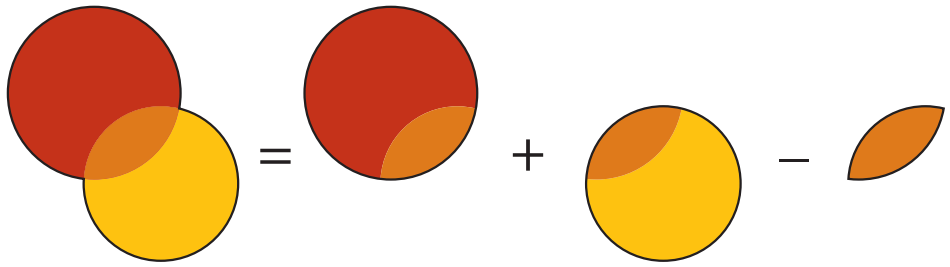
Probability rules

The probability of two *mutually exclusive* events A **or** B:

$$P[A\ or\ B] = P[A] + P[B]$$

The probability of two *not mutually exclusive* events A **or** B:

$$P[A\ or\ B] = P[A] + P[B] - P[A\ and\ B]$$



Pr[*A* or *B*] = Pr[*A*] + Pr[*B*] − Pr[*A* and *B*]

What is the probability of rolling a 2 or a 5 on a fair die?

Are these events mutually exclusive? **Yes.**

$$P[2\ or\ 5] = P[roll\ 2] + P[roll\ 5] = \frac{1}{6} + \frac{1}{6} = \mathbf{\frac{1}{3}}$$

What is the probability of rolling a 2 or an even number on a fair die?

Are these events mutually exclusive? **No.**

$$P[2\ or\ even] = P[roll\ 2] + P[roll\ even] - P[2\ and\ even]$$

$$= \frac{1}{6} + \frac{1}{2} - \frac{1}{6} = \mathbf{\frac{1}{2}}$$

Probability rules

The probability of two *mutually exclusive* events A **or** B:

$$P[A\ or\ B] = P[A] + P[B]$$

The probability of two *not mutually exclusive* events A **or** B:

$$P[A\ or\ B] = P[A] + P[B] - P[A\ and\ B]$$

We add "or"

The probability of two *independent* events A **and** B:

$$P[A\ and\ B] = P[A] \times P[B]$$

We multiply "and"

Event independence

Mendel's experiment yielded **1600** pea pods:

- **900** were tall and green
- **300** were tall and yellow
- **300** were short and green
- **100** were short and yellow

Are tall and green pods independent?

Yes, **if** $P[A \; and \; B] = P[A] \times P[B]$

Event independence

$$P[A \text{ and } B] = P[A] \times P[B]$$

Mendel's experiment yielded **1600** pea pods:

- **900** were tall and green
- **300** were tall and yellow
- **300** were short and green
- **100** were short and yellow

$$P[\text{green and tall}] = \frac{\mathbf{900}}{\mathbf{1600}} = \frac{\mathbf{9}}{\mathbf{16}}$$

$$P[\text{green}] \times P[\text{tall}] = \frac{(\mathbf{900} + \mathbf{300})}{\mathbf{1600}} \times \frac{(\mathbf{900} + \mathbf{300})}{\mathbf{1600}} = \frac{\mathbf{3}}{\mathbf{4}} \times \frac{\mathbf{3}}{\mathbf{4}} = \frac{\mathbf{9}}{\mathbf{16}}$$

Yes, green and tall are independent events.

Question

Assume that a long (~infinite) stretch of DNA has A, C, G, T's in equal proportions, randomly occurring throughout.

What is the probability of seeing 10 A nucleotides in a row?

$$P[A] = 0.25$$

$$P[A\ and\ A\ and\ A\ \ \ldots and\ A] = 0.25 \times 0.25 \ldots = 0.25^{10} = 9.56 \times 10^{-7}$$

Question

Assume that a long (~infinite) stretch of DNA has A, C, G, T's in equal proportions, randomly occurring throughout.

What is the probability of **not** seeing 10 A nucleotides in a row?

$$1 - P[10\ A's] = 1 - 9.56 \times 10^{-7} = 0.9999$$

We can calculate empirical probabilities directly from data

Example: A study assessed HIV risk associated with intravenous drug users and found these results:

	HIV+	HIV-	Total
Intravenous user	8	12	20
Not intravenous user	2	13	15
Total	10	25	35

Q1: What is the probability that a randomly chosen study participant is HIV+?

	HIV+	HIV-	Total
user	8	12	20
not user	2	13	15
Total	10	25	35

P(HIV+) = (number of HIV+) / (number participants)

= 10 / 35 = **2/7**

Q2: What is the probability that a randomly chosen study participant who is not HIV+ is a user?

	HIV+	HIV-	Total
user	8	12	20
not user	2	13	15
Total	10	25	35

= (HIV+ non-user) / (all HIV+)

= 2 / 10 = **1/5**

Q3: What is the probability that a randomly chosen study participant is either HIV+ or user but not both?

	HIV+	HIV-	Total
user	8	12	20
not user	2	13	15
Total	10	25	35

= (2+12)/35 = 14/35 = **2/5**

Calculating probabilities directly from data frames

What is the probability of an iris being virginica, in the iris dataset?

```
# The denominator
> nrow(iris)
[1] 150

# The numerator
> iris %>% filter(Species == "virginica") %>% tally()
   n
1 50

## The probability is 50/150 = 0.3333
```

Calculating probabilities directly from data frames

What is the probability of an iris being virginica and having petal lengths less than 5?

```
# The denominator
> nrow(iris)
[1] 150

# The numerator
> iris %>% filter(Species == "virginica", Petal.Length
< 5) %>% tally()
   n
1 6

## The probability is 6/150 = 0.04
```

Dependent events

Recall the probability of two *independent* events A **and** B:

$$P[A \text{ and } B] = P[A] \times P[B]$$

The probability of two *dependent* events A **and** B:

$$P[A \text{ and } B] = P[A|B] \times P[B]$$

Conditional Probability: Probability of A given B

Conditional probability, $P[A \mid B]$

Probability that a sick person is coughing

Probability that a person is coughing and sick

Probability that coughing person is sick

Conditional probability, $P[A \mid B]$

Probability that a sick person is coughing **P[coughing | sick]**

Probability that a person is coughing and sick **P[coughing and sick]**

Probability that coughing person is sick **P[sick | coughing]**

Conditional probabilities condition on *a priori* information

Example: Theoretical probabilities

A seed blows around a complex habitat. It can land on one of three (high-quality, medium-quality, poor-quality) soil types.

The probability of landing on each habitat is:

High-quality, 30%, Medium-quality, 20%, Low-quality, 50%

The probability of surviving each habitat is :

High-quality, 80%, Medium-quality, 30%, Low-quality, 10%

Question: What the probability a seed survives?

Example: Theoretical probabilities

Step 1: Convert text to probability statements

Step 2: Determine probability equation to solve the problem

Step 3: Plug in and solve

Convert text to prob. statements

The probability of landing on each habitat is:

High-quality, 30%, Medium-quality, 20%, Low-quality, 50%

The probability of surviving each habitat is :

High-quality, 80%, Medium-quality, 30%, Low-quality, 10%

P[land on high quality] = 0.3
P[land on med quality] = 0.2
P[land on low quality] = 0.5

P[survive on high quality] = 0.8
P[survive on med quality] = 0.3
P[survive on low quality] = 0.1

Determine probability equation

Seed can survive in three *mutually exclusive* ways:

- Land on high quality and survive
- Land on medium quality and survive
- Land on low quality and survive

P[seed survives] =

P[high qual. & survives] **+** P[med qual. & survives] **+** P[low qual. & survives] =

P[high qual]*P[survives|high qual] + …

Survival is **dependent** on land quality

Step 3:
Plug in and solve

P[land on high quality] = 0.3
P[land on med quality] = 0.2
P[land on low quality] = 0.5

P[survive on high quality] = 0.8
P[survive on med quality] = 0.3
P[survive on low quality] = 0.1

P[seed survives] =

P[high qual. & survives] **+** P[med qual. & survives] **+** P[low qual. & survives] =

P[high qual]*P[survives|high qual] + … =

0.3*0.8 + 0.2*0.3 + 0.5*0.1 = **0.35**

Followup: What is the probability that a seed **does not** survive?

Part II

Now assume there is a 0.2 chance of not landing on any habitat, and therefore the seed will die. What is the new probability of survival?

Step 1: Text to probabilities

P[lands] = 0.8

P[does not land] = 0.2

Step 2: Probability equation

P[seed survives] = P[seed survives | seed lands] = ?????

Enter, Bayes Theorem

Recall:

- $P[A\ and\ B] = P[B|A] \times P[A]$

Therefore, this is also true *and equal to the above*:

- $P[B\ and\ A] = P[A|B] \times P[B]$

Put them together to derive **Bayes Theorem:**

$$P[A|B] = \frac{P[B|A] * P[A]}{P[B]}$$

Step 2: Probability equation

P[seed survives] = P[seed survives | seed lands] =
(P[lands | survives] * P[survives]) / P(lands)

TAKE NOTICE:
THIS IS THE TYPE OF STATEMENT YOU WILL HAVE TO WRITE ON HW3

Step 3:
Plug in and solve

P[land on high quality] = 0.3
P[land on med quality] = 0.2
P[land on low quality] = 0.5

P[survive on high quality] = 0.8
P[survive on med quality] = 0.3
P[survive on low quality] = 0.1

P[seed survives] = P[seed survives | seed lands] =
(P[lands | survives] * P[survives]) / P(lands)

= (1 * 0.35) / 0.2

= **0.175**

Example: Theoretical probability and Bayes

Mammograms have a 7% false positive rate and a 25% false negative rate.

Assume women in the general population, have a 0.5% chance of having cancer at any time.

Probability statements:

P[positive result | healthy] = 0.07

P[negative result | cancer] = 0.25

P[cancer] = 0.005

Example 1

P[positive result | healthy] = 0.07
P[negative result | cancer] = 0.25
P[cancer] = 0.005

What is the probability that a healthy woman who gets a mammogram is given a negative result?

1. P[negative | healthy]

2. P[negative | healthy] = 1– P[positive|healthy]

- Remember, possible events sum to 1.

3. P[negative | healthy] = 1 – 0.07 = **0.93**

Example 2

P[positive result | healthy] = 0.07
P[negative result | cancer] = 0.25
P[cancer] = 0.005

A woman gets a positive result from her mammogram. What is the probably she has cancer?

1. P[cancer| positive result]

2. P[cancer| positive result] =

(P[positive result | cancer] *P[cancer])/P[positive result]

Example 2

P[positive result | healthy] = 0.07
P[negative result | cancer] = 0.25
P[cancer] = 0.005

P[cancer| positive result] =

(P[positive result | cancer] * P[cancer])/P[positive result]

When solving Bayes Theorem, the denominator generally requires a bit more work – Must consider **all** situations where it applies (remember seed survival?)

P[positive result] = P[positive and cancer] + P[positive and healthy]

Solving the denominator

P[positive result | healthy] = 0.07
P[negative result | cancer] = 0.25
P[cancer] = 0.005

P[positive] = P[positive and cancer] + P[positive and healthy]

Recall: $P[A\ and\ B] = P[B|A] \times P[A]$

Therefore:

= P[positive|cancer] * P[cancer] + P[positive|healthy] * P[healthy]

= 0.75 * 0.005 + 0.07 * 0.995

= 0.0734

Put it all together

P[positive result | healthy] = 0.07
P[negative result | cancer] = 0.25
P[cancer] = 0.005

P[cancer| positive result] =

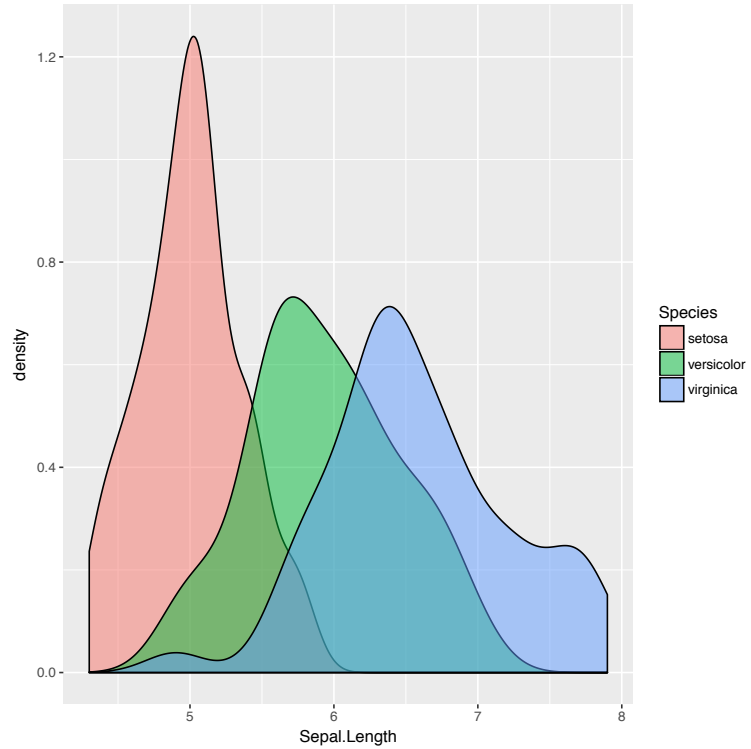
(P[positive result | cancer] * P[cancer])/P[positive result] =

(0.75 * 0.005)/ 0.0734 = **0.514**

BREAK

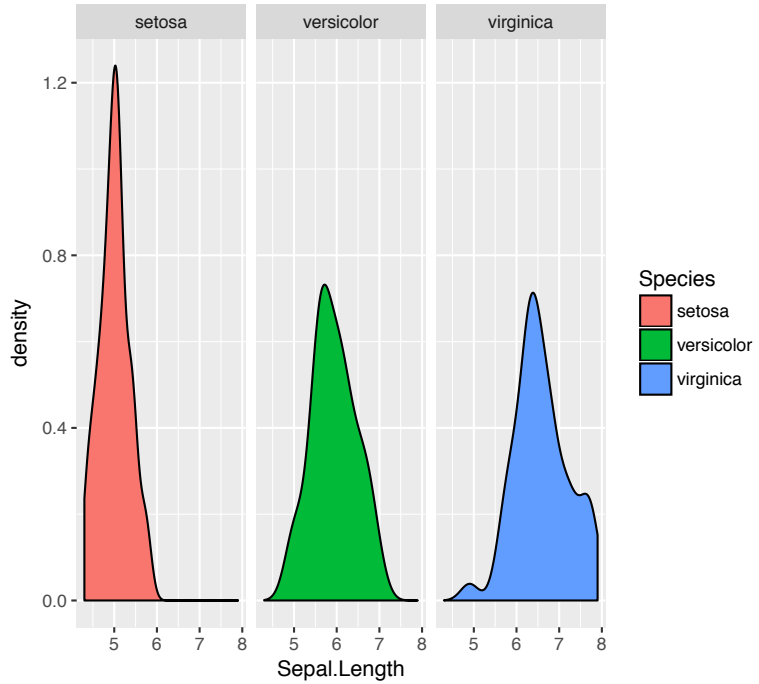
ggplot2: Faceting plots

```
> ggplot(iris, aes(x = Sepal.Length, fill = Species)) + geom_density( alpha = 0.5 )
```



ggplot2: Faceting plots

```
> ggplot(iris, aes(x = Sepal.Length, fill = Species)) + geom_density() + facet_grid(~Species)
```

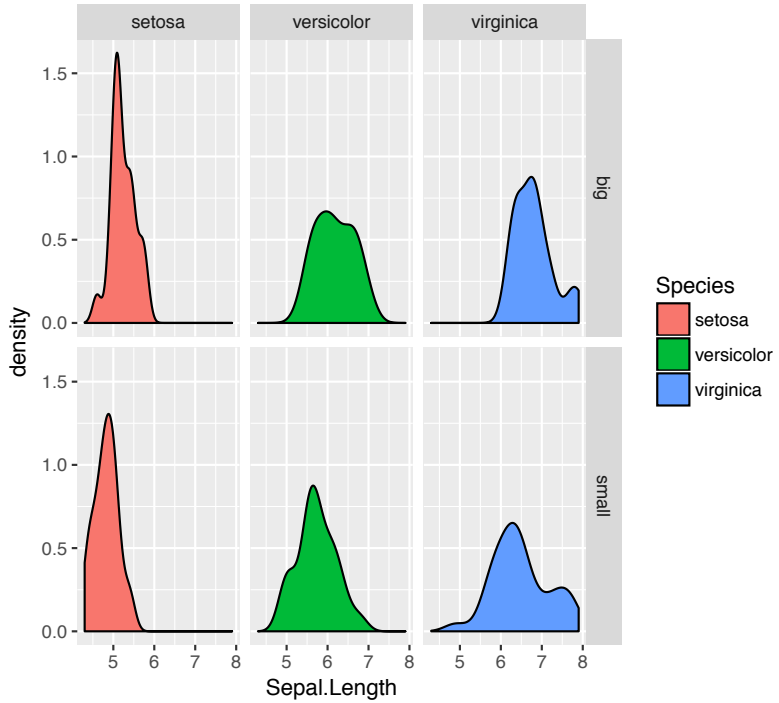


ggplot2: Faceting plots

```
> head(iris2)
      Source: local data frame [150 x 6]
      Groups: Species [3]
         Sepal.Length Sepal.Width Petal.Length Petal.Width Species  size
                <dbl>       <dbl>        <dbl>       <dbl>  <fctr> <chr>
      1          5.1         3.5          1.4         0.2  setosa   big
      2          4.9         3.0          1.4         0.2  setosa small
      3          4.7         3.2          1.3         0.2  setosa small
      4          4.6         3.1          1.5         0.2  setosa small
      5          5.0         3.6          1.4         0.2  setosa   big
      6          5.4         3.9          1.7         0.4  setosa   big
```

ggplot2: Faceting plots

```
> ggplot(iris, aes(x = Sepal.Length, fill = Species)) + geom_density() + facet_grid(size~Species)
```



dplyr: Joining related dataframes

```
> data1
   x         y        z
1  3.108060 61.48849
2  8.976264 55.68174
3 11.673850 56.32225
4  8.551282 58.53424
5  5.819844 61.71424
```

```
> data2
   x           a        b
1 -2.76205636 112.9588
2 -1.44485264 149.3682
3 -1.14390532 132.8789
4 -2.86488120 143.6860
5 -2.91982194 121.3927
```

```
> left_join(data1, data2)
  Joining, by = "x"
   x         y        z           a        b
1  3.108060 61.48849 -2.76205636 112.9588
2  8.976264 55.68174 -1.44485264 149.3682
3 11.673850 56.32225 -1.14390532 132.8789
4  8.551282 58.53424 -2.86488120 143.6860
5  5.819844 61.71424 -2.91982194 121.3927
```

left_join() creates NA's when missing

```
> data1
  x         y        z
1  3.108060 61.48849
2  8.976264 55.68174
3 11.673850 56.32225
4  8.551282 58.53424
5  5.819844 61.71424
```

```
> data3
  x           a        b
1 -2.76205636 112.9588
2 -1.44485264 149.3682
3 -1.14390532 132.8789
5 -2.91982194 121.3927
```

Missing x=4

```
> left_join(data1, data3)
Joining, by = "x"
  x         y        z          a        b
1  3.108060 61.48849 -2.762056 112.9588
2  8.976264 55.68174 -1.444853 149.3682
3 11.673850 56.32225 -1.143905 132.8789
4  8.551282 58.53424         NA       NA
5  5.819844 61.71424 -2.919822 121.3927
```

left_join() only preserves what is in the left data frame

```
> data1
   x         y        z
1  3.108060 61.48849
2  8.976264 55.68174
3 11.673850 56.32225
4  8.551282 58.53424
5  5.819844 61.71424
```

```
> data3
   x           a        b
1 -2.76205636 112.9588
2 -1.44485264 149.3682
3 -1.14390532 132.8789
5 -2.91982194 121.3927
```

```
> left_join(data3, data1)
  Joining, by = "x"
   x         y        z         a        b
1  3.108060 61.48849 -2.762056 112.9588
2  8.976264 55.68174 -1.444853 149.3682
3 11.673850 56.32225 -1.143905 132.8789
5  5.819844 61.71424 -2.919822 121.3927
```

right_join() is the opposite

```
> data1
   x         y        z
1  3.108060 61.48849
2  8.976264 55.68174
3 11.673850 56.32225
4  8.551282 58.53424
5  5.819844 61.71424
```

```
> data3
   x           a        b
1 -2.76205636 112.9588
2 -1.44485264 149.3682
3 -1.14390532 132.8789
5 -2.91982194 121.3927
```

```
> right_join(data1, data3) ## Equivalent to left_join(data3, data1)
  Joining, by = "x"
   x         y        z         a        b
1  3.108060 61.48849 -2.762056 112.9588
2  8.976264 55.68174 -1.444853 149.3682
3 11.673850 56.32225 -1.143905 132.8789
5  5.819844 61.71424 -2.919822 121.3927
```

inner_join() only joins what the tables have in common

```
> data4
     x         y        z
1  3.108060 61.48849
3 11.673850 56.32225
4  8.551282 58.53424
5  5.819844 61.71424
```

Missing x=2

```
> data3
     x           a        b
1 -2.76205636 112.9588
2 -1.44485264 149.3682
3 -1.14390532 132.8789
5 -2.91982194 121.3927
```

```
> inner_join(data4, data3)
Joining, by = "x"
  x         y        z         a        b
1  3.108060 61.48849 -2.762056 112.9588
3 11.673850 56.32225 -1.143905 132.8789
5  5.819844 61.71424 -2.919822 121.3927
```

Joins galore

See this vignette if you're extra curious (not required): https://cran.r-project.org/web/packages/dplyr/vignettes/two-table.html