Lecture 3

Principles of Bayesian inference

WILD6900 (Spring 2019)

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Readings

> Hobbs & Hooten

From probability to Bayes theorem

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- population size
- occupancy status
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Each of these unobserved processes is governed by a probability distribution $[\theta]$

From probability to Bayes theorem

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Before those data are collected, they are random variables - the probability of observing y conditional on θ is governed by a probability distribution $[y|\theta]$

We want to know the probability distribution of the unobserved θ conditional on the observed data y, that is $[\theta|y]$

From probability to Bayes theorem

We know from last week that: [1]

$$[\theta | y] = \frac{[\theta, y]}{[y]}$$

and [2]

$$[\theta, y] = [y | \theta][\theta]$$

Through substitution, we get **Bayes theorem** [3]:

$$[\theta | y] = \frac{[y | \theta][\theta]}{[y]}$$

From probability to Bayes theorem

To understand what Bayes theorem says and why it is such a powerful principle, let's break down each part of equation 1:

$$\underbrace{[\theta|y]}_{\textit{posterior distribution}} = \frac{\overbrace{[\theta|y]}^{\textit{likelihood}} \quad \overbrace{[\theta]}^{\textit{prior}}}{\underbrace{[y]}_{\textit{marginal distribution}}}$$

The likelihood distribution

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The likelihood allows us to answer the question:

> what is the probability that we will observe the data if our deterministic model $g(\theta)$ is the true process that gives rise to the data?

That is, in likelihood, we treat θ as fixed and known rather than a random variable

- By assuming θ is fixed and known, we can calculate the probability density of our observation y conditional on θ

Likelihood

Example

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On one plot, we observe 34 trees. What is the probability of $y = 34$?

To answer this question, we first need to select a sensible probability distribution for the number of trees on a plot

- Because these values have to be positive integers, the Poisson distribution is an obvious choice [5]

Likelihood

Example

Let's say we're sampling the number of trees on small plots and that we **know** [4] the average number of trees/plot is 40

On one plot, we observe 34 trees. What is the probability of $y = 34$?

To answer this question, we first need to select a sensible probability distribution for the number of trees on a plot

- Because these values have to be positive integers, the Poisson distribution is an obvious choice [5]

Next, we calculate the probability $Pr(y = 34 | \lambda = 40)$:

```
dpois(x = 34, lambda = 40)
```

```
## [1] 0.04247
```

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Assuming the observations are independent, the joint probability (probability of $y = 34$ and $y = 42$) is the product of the individual probabilities:

- 0.04 x 0.06 = `0.00059`.

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We do this by using a likelihood function:

$$\underbrace{L(\theta|y)}_{likelihood\ function} = \underbrace{[y|\theta]}_{likelihood} = \prod_{i=1}^{n} [y_i|\theta]$$

Likelihood profile

An important distinction between the probability distribution $[y \mid \theta]$ and a likelihood function $L(\theta \mid y)$ is:

- In the probability distribution, we treat the parameter as fixed and the data as random
- In the likelihood function, we treat the data as fixed and the parameter as variable

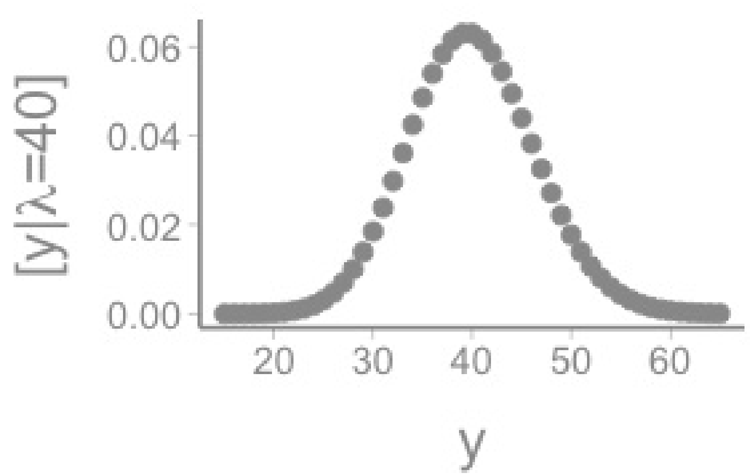
Likelihood profile

In our example, the tree counts y are random variables - they can take a range of possible values due to chance

The probability distribution $[y|\theta]$ tells us the probability of each possible value y:

```
y_probs <- data.frame(y = 15:65,
                      pr_y = dpois(15:65, lambda = 40))

ggplot(data = y_probs, aes(x = y, y = pr_y)) + geom_point() +
  scale_y_continuous(expression(paste("[y|", lambda, "=40]")))
```



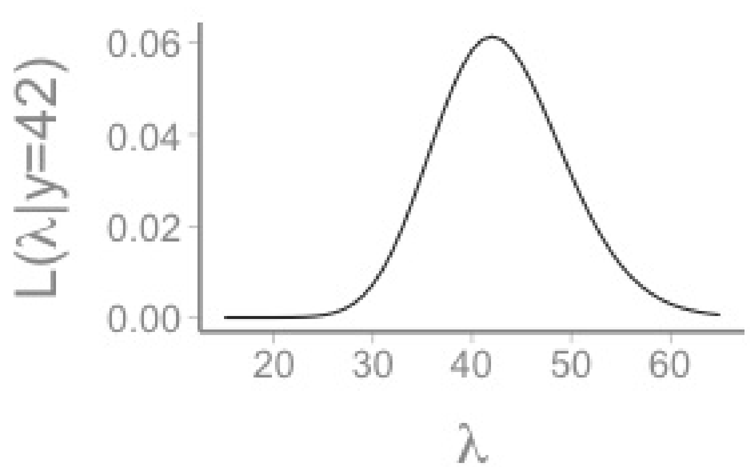
Likelihood profile

To create a likelihood profile, we flip this around

We treat our observation as fixed (for simplicity, let's use our observation $y = 42$) and estimate the probability as a function of different values of λ:

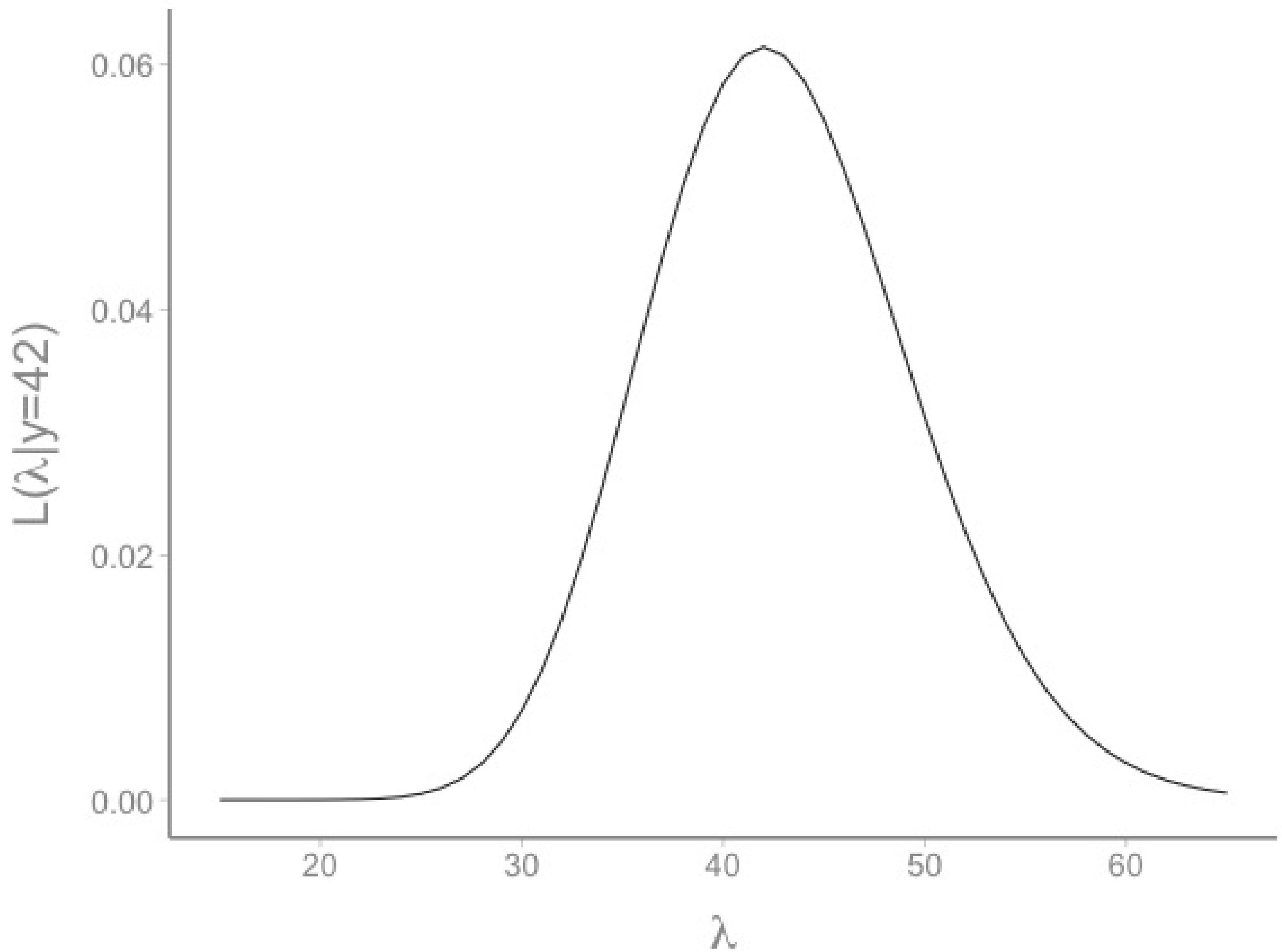
```
y <- 42
y_probs <- data.frame(lambda = 15:65,
                      pr_y = dpois(y, lambda = 15:65))

(lik_profile <- ggplot(data = y_probs, aes(x = lambda, y = pr_y)) + geom_pa
th() +
  scale_y_continuous(expression(paste("L(", lambda, "|y=42)"))) +
  scale_x_continuous(expression(lambda))
```



Likelihood profile

In this plot, the area under the curve does not equal 1 - the likelihood profile is not a probability distribution



Likelihood profile

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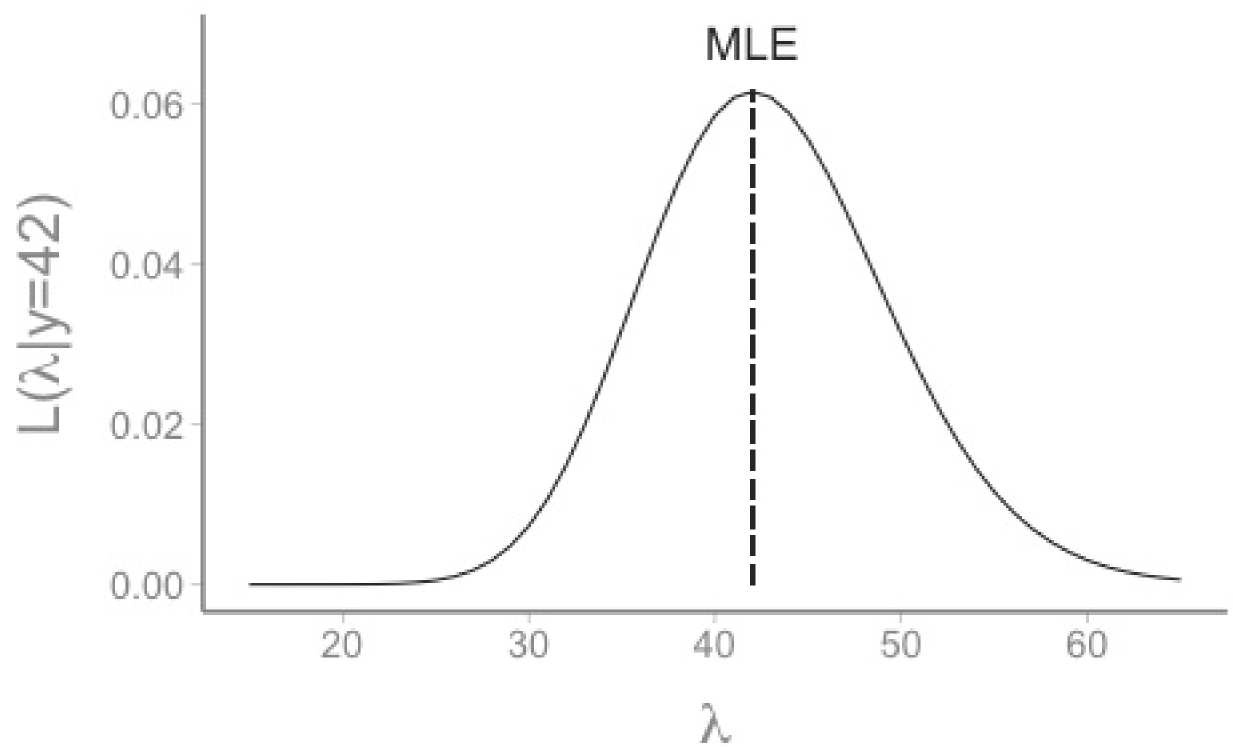
As a result, we vary λ but it is not a random variable and likelihood profiles do not define the probability or probability density of λ

Likelihood profile

This distinction between likelihood profiles and probability distributions is one of the reasons that results of likelihood-based methods can be difficult to interpret

Many of the methods familiar to ecologists use the principle of maximum likelihood to determine the value of θ that is most supported by our data

The maximum likelihood estimate is the peak of the likelihood curve [6]:



Likelihood profile

But the MLE does not tell us the probability of θ given our data!

So although MLE does tell us the value of θ that is most consistent with our data, we can not say things like:

- "There is a 90% probability that $\theta > 0$" [7]
- "There is a 96% probability that $a \geq \theta \geq b$" [7]

The prior [8]

The prior distribution

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- The prior describes what we know about the probability of θ before we collect any data
- Priors can contain a lot of information about θ (informative priors) or very little (uninformative priors)
- Well-constructed priors can also improve the behavior of our models

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In this way, priors allow us to weigh conclusions drawn from our data against what we already know about our system [9]
In the words of Mark Kéry:

> I find it hard not to be impressed by the application of Bayes rule to statistical inference since it so perfectly mimics the way of how we learn in everyday life ! In our guts, we always weigh any observation we make, or new information we get, with what we know to be the case or believe to know.

The prior distribution

Example

Say I tell you that on my way to class, I saw a 6-foot tall man

You would find this statement both believable and boring because a 6-ft tall man is consistent with what you know about the distribution of human heights

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If I tell you I saw an 8-fit tall man, you'll question my credibility and require additional evidence because you know it is extremely implausible for someone to be this tall

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- The gamma distribution allows for positive real values

In our discussion of likelihood functions, we assumed we know that $\lambda = 40$. Let's relax that assumption a bit

- previous research has shown that the mean number of trees per plot is 40, with a variance of 6

The prior distribution

Example

We can use moment matching to turn $\mu = 40$ and $\sigma^2 = 6$ into the two parameters that govern the gamma distribution:

$$\alpha = \frac{\mu^2}{\sigma^2}$$

$$\beta = \frac{\mu}{\sigma^2}$$

which in our sample gives $\alpha =$ 267 and $\beta =$ 7

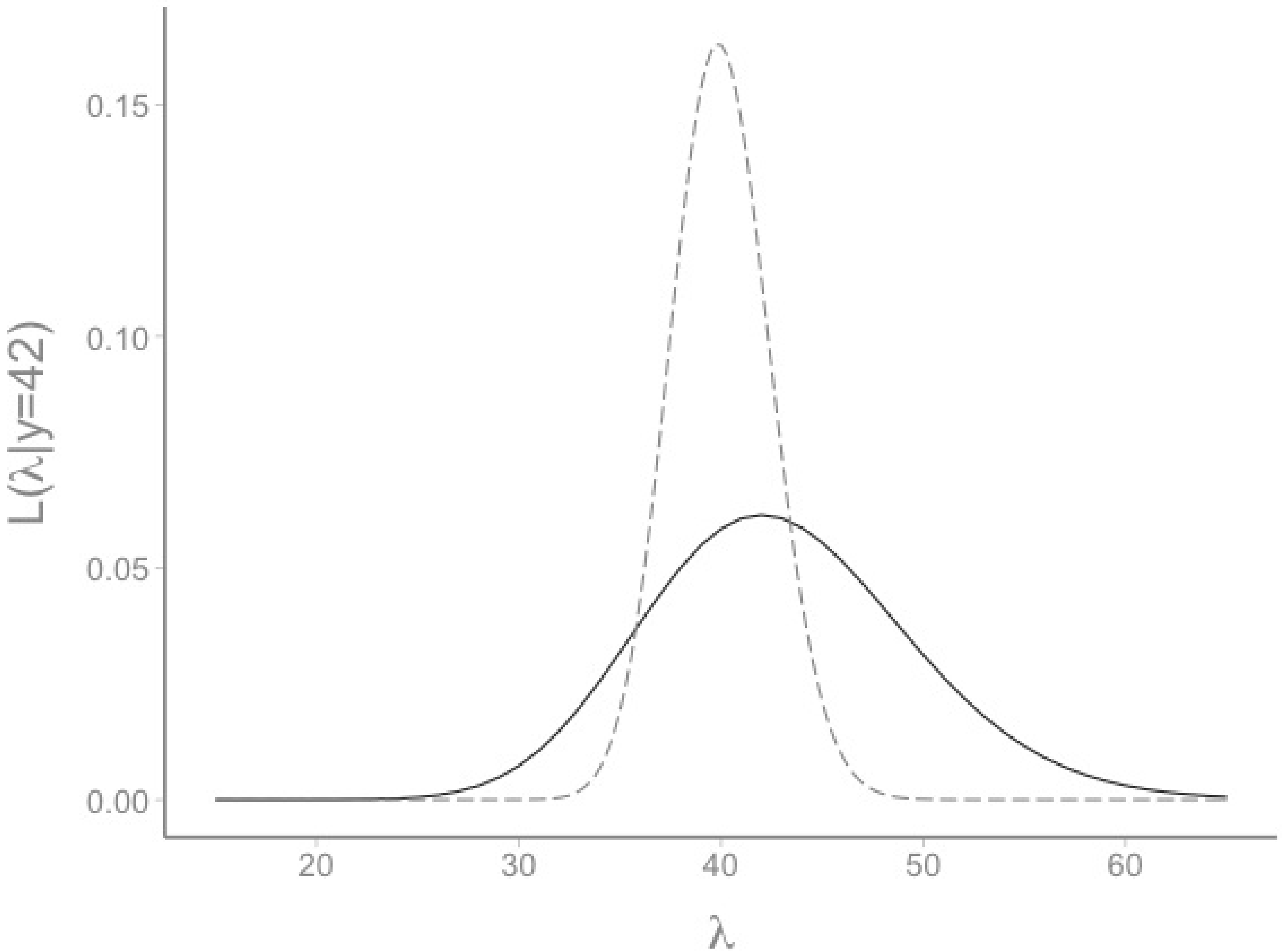
Now plot that prior alongside our previously define likelihood profile:

```
prior <- data.frame(lambda = seq(from = 15, to = 65, by = 0.25),
                    pr_lambda = dgamma(seq(from = 15, to = 65, by = 0.25),
40^2/6, 40/6))

(prior_lik <- lik_profile + geom_path(data = prior, aes(x = lambda, y = pr_
lambda), linetype = "longdash"))
```

The prior distribution

Example



The joint distribution

The joint distribution

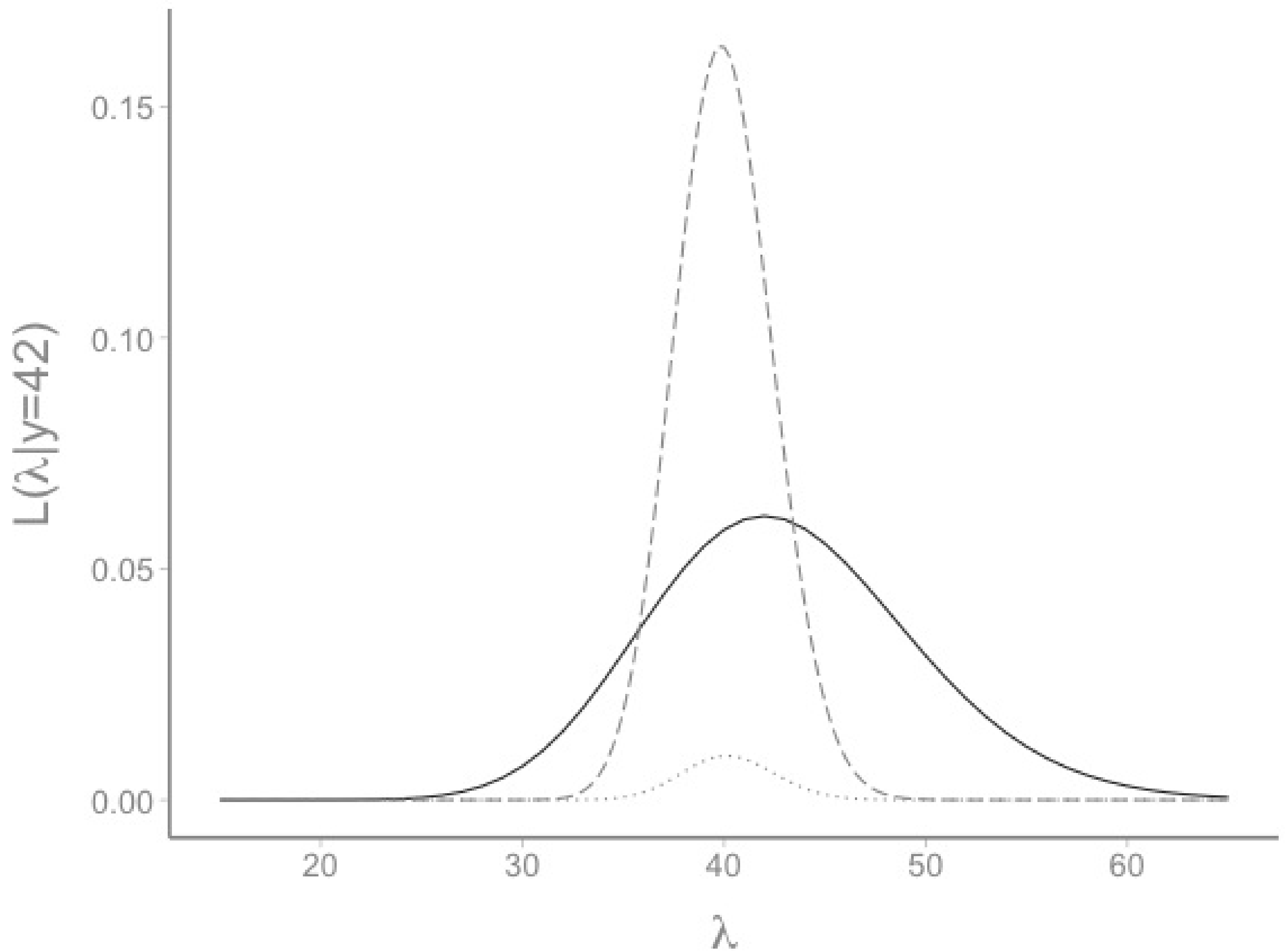
The product of the likelihood $[y \mid \theta]$ and the prior $[\theta]$ (the numerator of Bayes theorem) is called the **joint distribution**

It is important to note again that the joint distribution, like the likelihood profile, is not a probability distribution because the area under the curve does not sum to 1

```
joint <- data.frame(lambda = seq(from = 15, to = 65, by = 0.25),
                    jnt_dist = dgamma(seq(from = 15, to = 65, by = 0.25), 40
^2/6, 40/6) * dpois(42, seq(from = 15, to = 65, by = 0.25)))

(prior_lik_joint <- prior_lik + geom_path(data = joint, aes(x = lambda, y =
 jnt_dist), linetype = "dotted"))
```

The joint distribution



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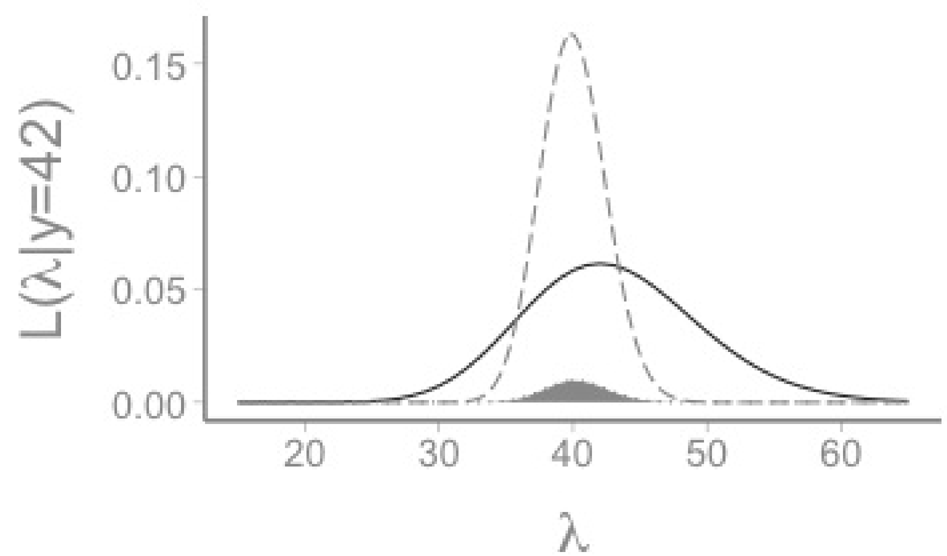
Remember from our previous lecture that:

$$[y] = \int [y \mid \theta][\theta] d\theta$$



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For most of the models you will need to fit as an ecologist, estimating the marginal distribution of the data is one of a major challenges of Bayesian inference [11]

The posterior distribution

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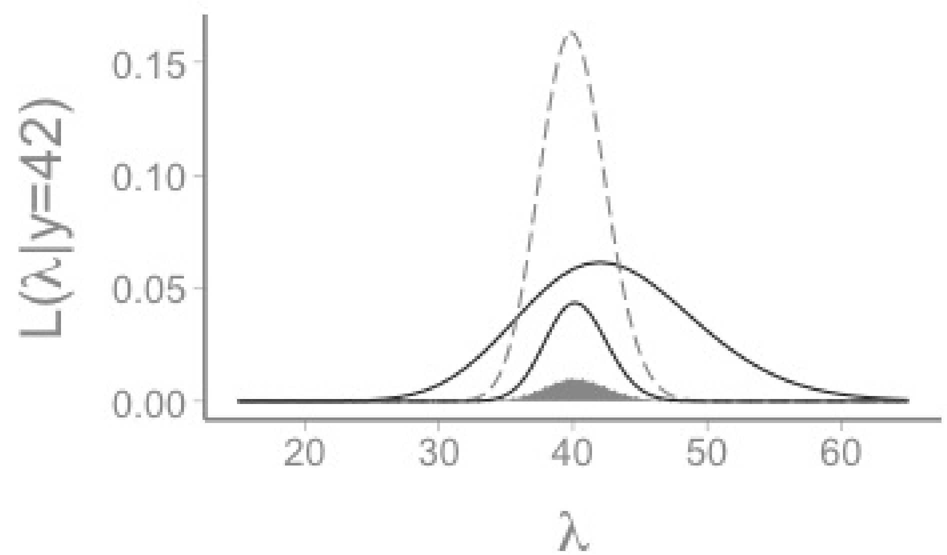
The posterior distribution tells us everything we know about θ given our data (and possibly prior knowledge)



The posterior distribution

The posterior allows to make statements like:

- The most probable value of θ is x
- There is a 95% probability that $y < \theta < z$
- There is a 96% probability that $\theta < 0$

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That means that:

$$[\theta|y] \propto [y|\theta][\theta]$$

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This is a central concept for applying modern tools for Bayesian analysis and one we will make use of shortly.

More about the posterior distribution

One of the cool things about Bayesian methods is that we don't get a point estimate of θ, we get an entire probability distribution! [12]

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These advantages will be come clear as we move towards applications of these methods but as a quick example, let's say we are estimating the abundance of two populations (N_1 and N_2)

We want to determine whether $N_1 > N_2$

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Answering the question of whether $\Delta_n > 0$ requires knowing not only the magnitude of this difference but also how certain we are in the value. How do we estimate the uncertainty of our new derived variable?

That's not easy in a frequentist world and will require application of the delta method.

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)

If nothing else turns you into a Bayesian, it's probably this point.