

# Sampling and maximum likelihood estimation

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## Outline Today

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- ▶ An orchid example
- ▶ Sampling variation
- ▶ Maximum likelihood estimation
- ▶ Normal distribution
- ▶ Linear models

# Sampling data

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Figure 1: [www.ugent.be](http://www.ugent.be)

## What is the proportion of orchids?



We decide to walk through the field and at 10 places record when we find an orchid (1) or not (0)



1. First time: 5 orchids from 10 picks ( $5/10 = 0.5$ )

## What is the proportion of orchids?



We decide to walk through the field and at 10 places record when we find an orchid (1) or not (0)

1. First time: 5 orchids from 10 picks ( $5/10 = 0.5$ )
2. Second time: 2 orchids from 10 picks ( $2/10 = 0.2$ )
3. Third time: 8 orchids from 10 picks ( $8/10 = 0.8$ )

## What is the proportion of orchids?

We conclude, half of the flowers are orchids ( $15/30 = 0.5$ ). But encounter this guy:



- ▶ What caused our estimate of the proportion of orchids to be inaccurate?
  - ▶ And why did we not get the same proportion of orchids every time?

He tells us that the true proportion of orchids is 0.4.

## The data

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For such (binary) data:  $y_i \sim \text{Binom}(\pi_i, n_{\text{picks}})$ , with  
 $p(\text{orchid}) = \pi_i$

# The binomial distribution

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$$f(y_i; n_{picks}, \pi) = y_i \log\{\pi\} + (n_{picks} - y_i) \log\{1 - \pi\} + constant \quad (1)$$

## R-functions

- ▶ Density: `dbinom`
- ▶ Number generator: `rbinom`

## Simulation: counting orchids once

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```
set.seed(12345) # For reproducibility
p.orchid = 0.4 # The true proportion of orchids
n.picks = 10 # The number of picks in the field
n.times = 1
# Collect data
y <- rbinom(n.times, size = n.picks, prob = p.orchid)
y/n.picks # Proportion of orchids
```

```
## [1] 0.5
```

## Simulation: counting orchids once

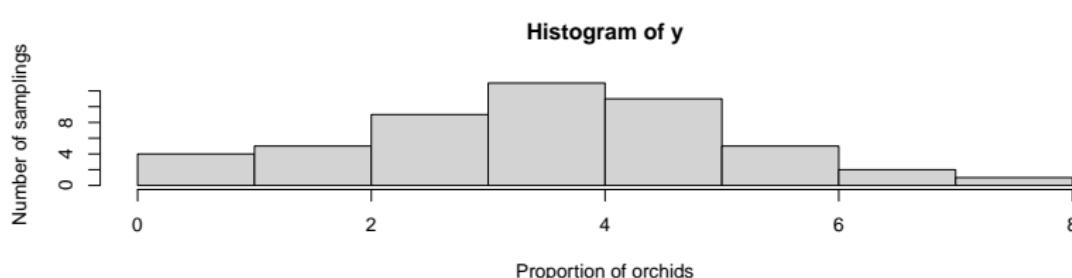
What if we sample the whole field once?

```
set.seed(12345) # For reproducibility
n.times = 1e5 # The number of picks in the field
n.picks <- 1
# Collect data
y <- rbinom(n.times, size = n.picks, prob = p.orchid)
mean(y/n.picks) # Proportion of orchids
```

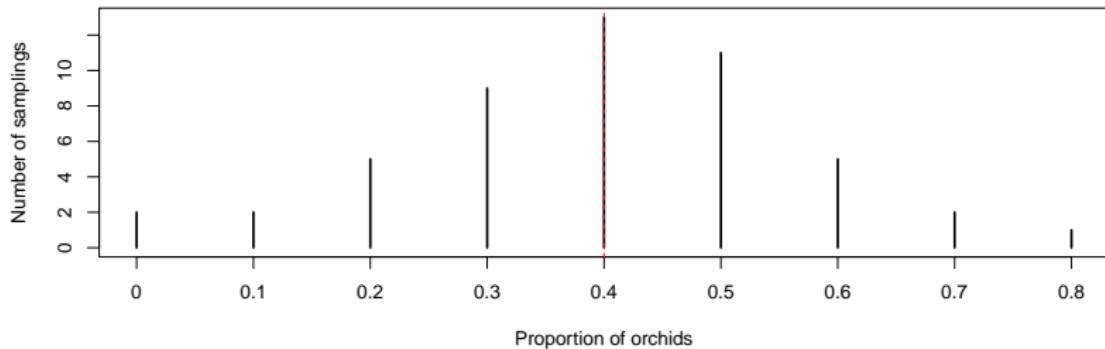
```
## [1] 0.40021
```

## Simulation: counting orchids 50x10 times

```
set.seed(12345) # For reproducibility
n.times <- 50
n.picks = 10 # The number of picks in the field
# Collect data
y <- rbinom(n.times, size = n.picks, prob = p.orchid)
hist(y, xlab = "Proportion of orchids",
      ylab = "Number of samplings")
```



## Simulation: counting orchids 50x10 times



As you see, we have variability in our estimate of the proportion of orchids.

- ▶ Can we summarize this variation?
- ▶ Preferably without collecting data many times

## The strategy

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- ▶ Collect data
- ▶ Learn about the variation in that data
  - ▶ We need a model for that
- ▶ Work out distribution of the estimates
  - ▶ And find the “best” estimate
- ▶ Conclude if our answer is robust
  - ▶ Q: Are more than half of the flowers in this field orchids?

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- ▶ Exclude rare events, and decide on an acceptable margin of error (5%)
- ▶ What is the range our parameter is estimated to be 95% of the time?

```
quantile(y/n.picks,c(0.025,.975))
```

```
##    2.5%   97.5%
## 0.0225 0.7000
```

So 50 times 10 picks tell us little.

Q: Are more than half of the flowers in this field orchids?

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```
set.seed(12345)
n.picks = 100
n.times <- 50
# Collecting data
y <- rbinom(n.times, size = n.picks, prob = p.orchid)
quantile(y/n.picks,c(0.025,.975))
```

```
##      2.5%    97.5%
## 0.31225 0.48000
```

50 times 100 picks reduces the variability in the proportion of observed orchids. Most of the time we will find fewer orchids than other flowers.

On average, we will get it right.

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```
set.seed(12345)
n.picks = 1;n.times <- 100
y <- rbinom(n.times, size = n.picks, prob = p.orchid)
quantile(y/n.picks,c(0.025,.975))
```

```
## 2.5% 97.5%
##      0      1
```

```
mean(y/n.picks)
```

```
## [1] 0.45
```

## Estimator and Estimand

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- ▶ Estimand: the parameter we want to estimate, the true population level parameter
- ▶ Estimator: how we are estimating it  $\hat{p}_{orchid} = \frac{y}{n.picks}$ 
  - ▶ Why is this a good estimator?
- ▶ Estimate: the parameter value based on the data

## Estimating parameters and quantifying uncertainty

- ▶ We do not usually have infinite amounts of data
- ▶ So how can we quantify variability of the estimator?
- ▶ We need a model for the process that generates the data



## The likelihood: single data point

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$$\mathcal{L}(y_i; \Theta) = f(y_i; \Theta) \quad (2)$$

The probability of obtaining our data assuming  $\Theta$  is the true parameter(s).

## The likelihood: multiple data points (2)

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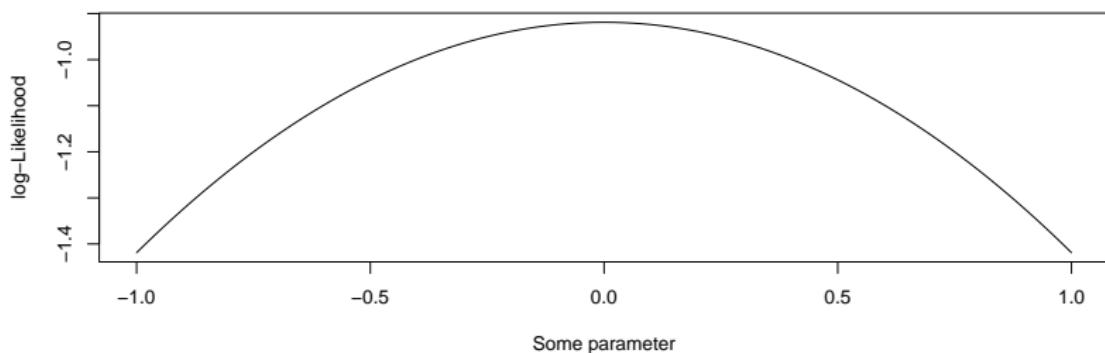
$$\mathcal{L}(\mathbf{y}; \Theta) = \prod_i^n f(y_i; \Theta) \quad (3)$$

We just multiply! (assumes independence)



## The log-likelihood

$$\log\{\mathcal{L}(\mathbf{y}; \Theta)\} = \sum_i^n \log\{f(y_i; \Theta)\} \quad (4)$$



Usually, we work with the log-likelihood. The maximum is the same and it is easier. So we just add things together.

## Back to the orchid example

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- ▶ Data is binary or counts
- ▶ Which follows a binomial likelihood (only as example, for now)

$$f(y_i; n_{picks}, \pi) = y_i \log\{\pi\} + (n_{picks} - y_i) \log\{1 - \pi\} + \text{constant} \quad (5)$$

- ▶  $N = n_{picks}$  trials
- ▶  $r = y_i$  successes (orchids)
- ▶  $\pi$  the probability of success (proportion of orchids)

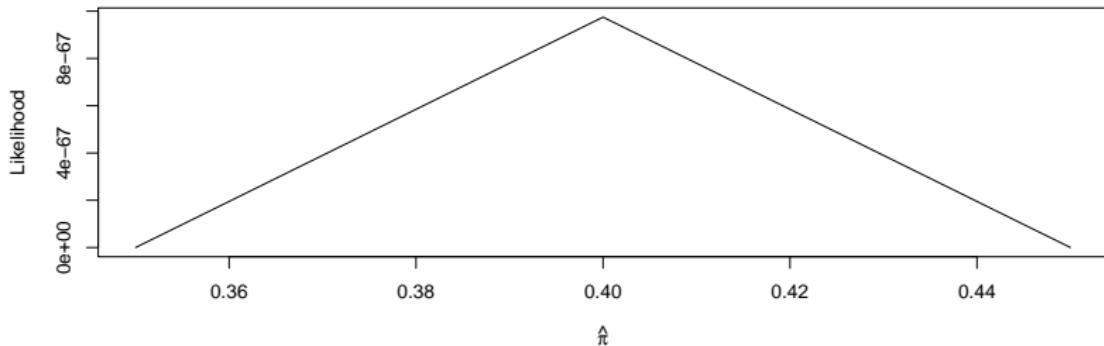
### Assumptions

- ▶ Each pick is independent from the next
- ▶  $\pi$  is the same for all observations

## Finding the proportion of orchids

```

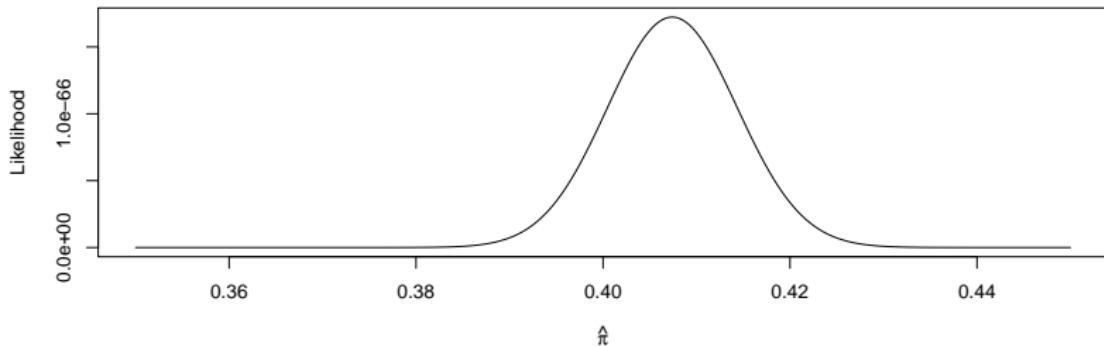
ll <- function(p, n.picks, y) prod(dbinom(y, n.picks,p))
phat <- seq(0.35,0.45,length.out=3)
plot(sapply(phat, ll, n.picks = n.picks, y = y),
      x = phat, type = "l", xlab=expression(hat(pi)), ylab="Li
```



## Finding the proportion of orchids (2)

```

ll <- function(p, n.picks, y) prod(dbinom(y, n.picks,p))
phat <- seq(0.35,0.45,length.out=1000)
plot(sapply(phat, ll, n.picks = n.picks, y = y),
      x = phat, type = "l", xlab=expression(hat(pi)), ylab="Li
```



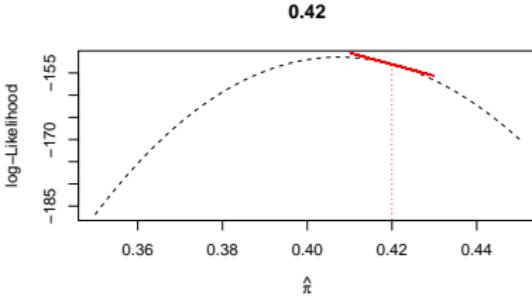
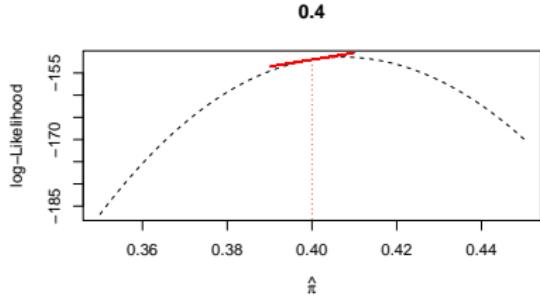
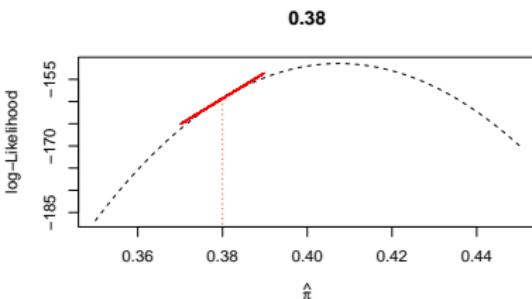
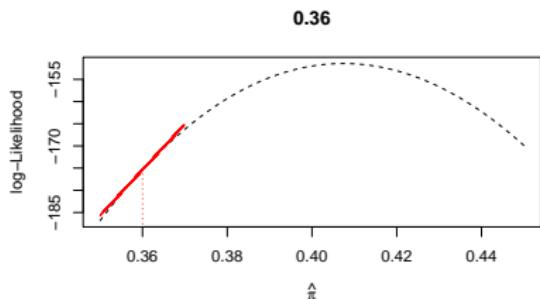
## Maximising the likelihood

Trying many values (grid) is very inefficient

We can:

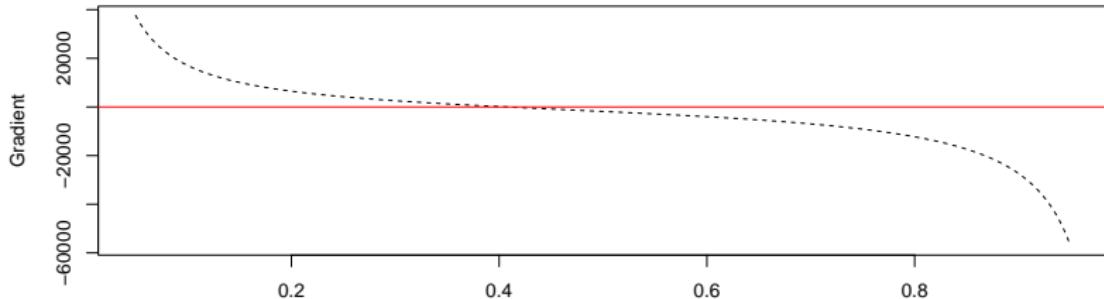
- ▶ analytically: do mathematics
  - ▶ numerically: use an algorithm (as in GLMs)
  - ▶ simulation: try many values

# Finding the maximum



## Finding the maximum: gradient

```
phat = seq(0.05,0.95,length.out=1000)
plot(sapply(phat, grad.dbinom, y=y, n.picks = n.picks),
      x = phat, type = "l", xlab=expression(hat(pi)),
      ylab="Gradient", lty = "dashed")
abline(h=0, col = "red")
```



## Finding the maximum: mathy bits

Our function:

$$\log\{\mathcal{L}(\mathbf{y}; n_{picks})\} = \sum_{i=1}^{n_{times}} y_i \log\{\pi\} + (n_{picks} - y_i) \log\{1 - \pi\} + \text{constant} \quad (6)$$

Slope of the likelihood:

$$\frac{\partial \log\{\mathcal{L}(\mathbf{y}; n_{picks})\}}{\partial \pi} = \sum_{i=1}^{n_{times}} \frac{y_i}{\pi} - \frac{n_{picks} - y_i}{1 - \pi} \quad (7)$$

Estimator:

$$0 = \sum_{i=1}^{n_{times}} \frac{y_i}{\pi} - \frac{n_{picks} - y_i}{1 - \pi} \quad (8)$$

(i.e., the proportion of successes!)

## Maximum likelihood estimation: summary

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No ideal properties in finite samples. But as we get more data:

- ▶ Get things right with a lot of data (consistency)
- ▶ Is the best estimator (in terms of RMSE) in large samples of consistent estimators

Often does well in practice anyway 😊

## Letting R do the work

```
optimize(ll, n.picks = n.picks, y=y,  
        lower = 0, upper = 1, maximum = TRUE)
```

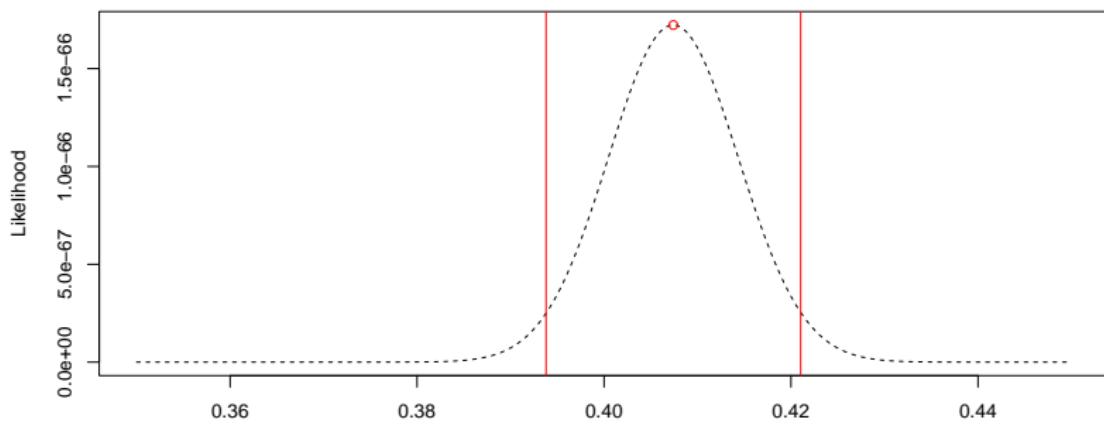
```
## $maximum  
## [1] 0.4074027  
##  
## $objective  
## [1] -151.4268
```

- Usually there is more than 1 parameter, much harder

## Uncertainty

(an estimate of) Width of the likelihood:

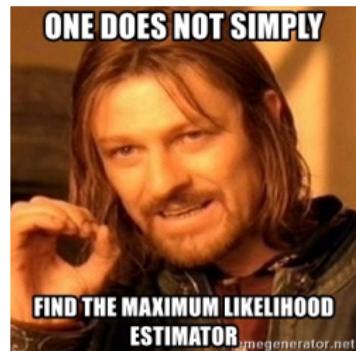
$$\frac{\partial^2 \log\{\mathcal{L}(\mathbf{y}; n_{picks})\}}{\partial \pi^2} = \sum_{i=1}^{n_{times}} -\frac{y_i}{\pi^2} - \frac{n_{picks} - y_i}{(1-\pi)^2} \quad (9)$$



## Putting it all together

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- ▶ We collect data
- ▶ We estimate a parameter of interest
- ▶ If we collected data again, we get many different estimates
  - ▶ This forms a *sampling* distribution
- ▶ We summarize this variability
- ▶ The width of this sampling distribution tells us the variability
- ▶ Instead of collecting data many times, we estimate parameters with MLE
  - ▶ This also allows us to quantify the variability



## 95% Confidence intervals

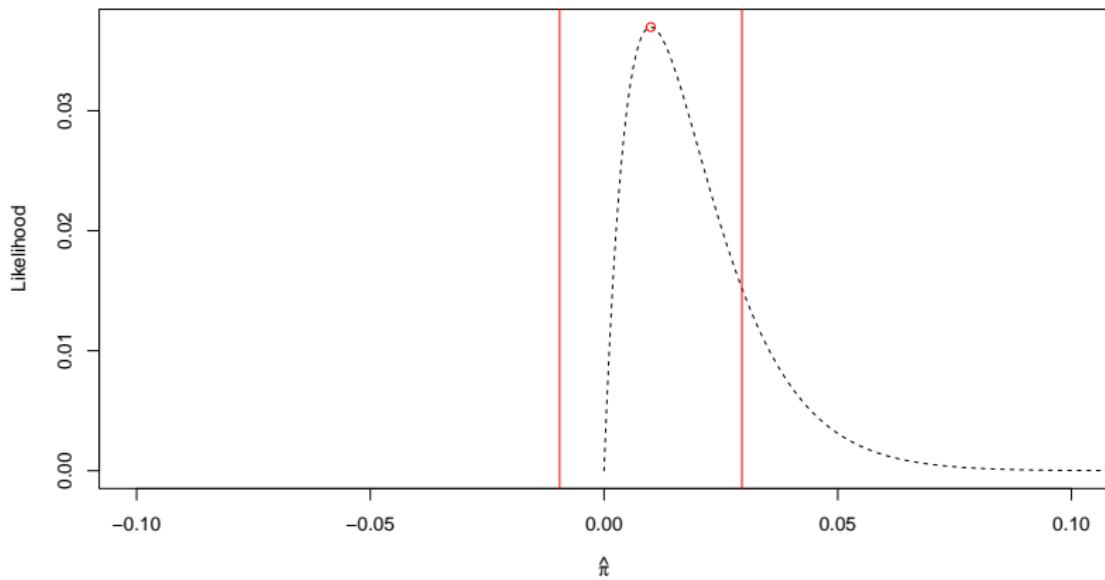
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Estimate of the range that the true parameter will fall in 95% of the time.

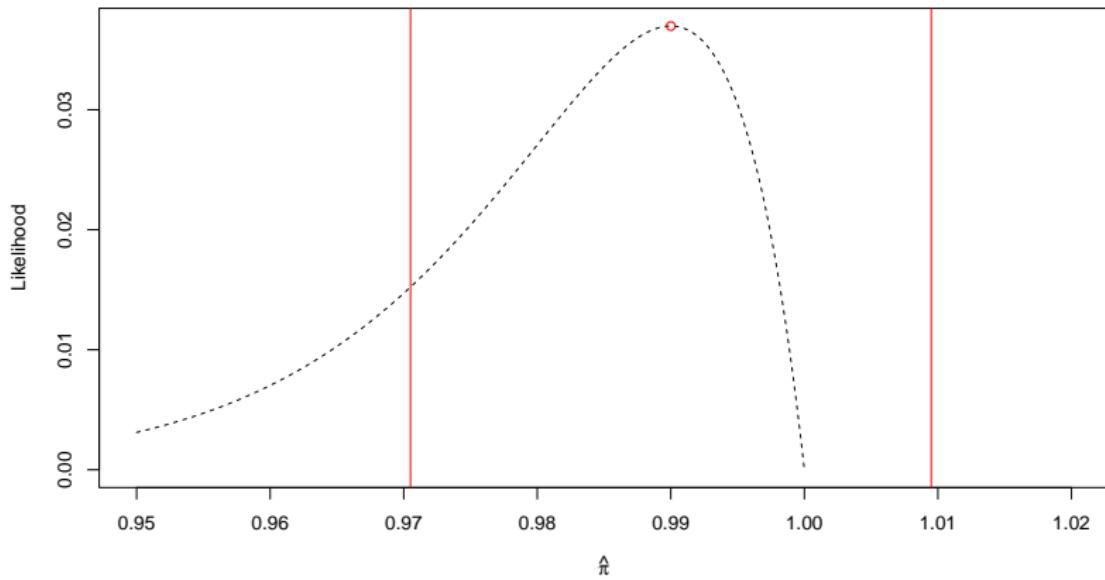
Different methods exist. Based on MLE not quite correct for the Binomial distribution due to **assumptions**.

## Why not?

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## Why not? (2)



## Why is uncertainty so important

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- ▶ Our sampling distribution estimates needs summarizing
- ▶ Tells us if we expect our answer to be the same if we repeated the study
- ▶ I.e., not so important for the *dataset* but important for *multiple datasets*

Afterall, we are looking for a robust recommendation.

## Confidence intervals

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*An interval that contains the true value in 95% of repeated samples  
(in large samples)*

Be careful with interpretation, and with assumptions.

- ▶ Any computed interval either contains the truth, or it does not
- ▶ Not the range that the true parameter falls in with 95
- ▶ Other misinterpretations
- ▶ Can be interpreted as a kind of statistical test
- ▶ Or generally as “evidence”

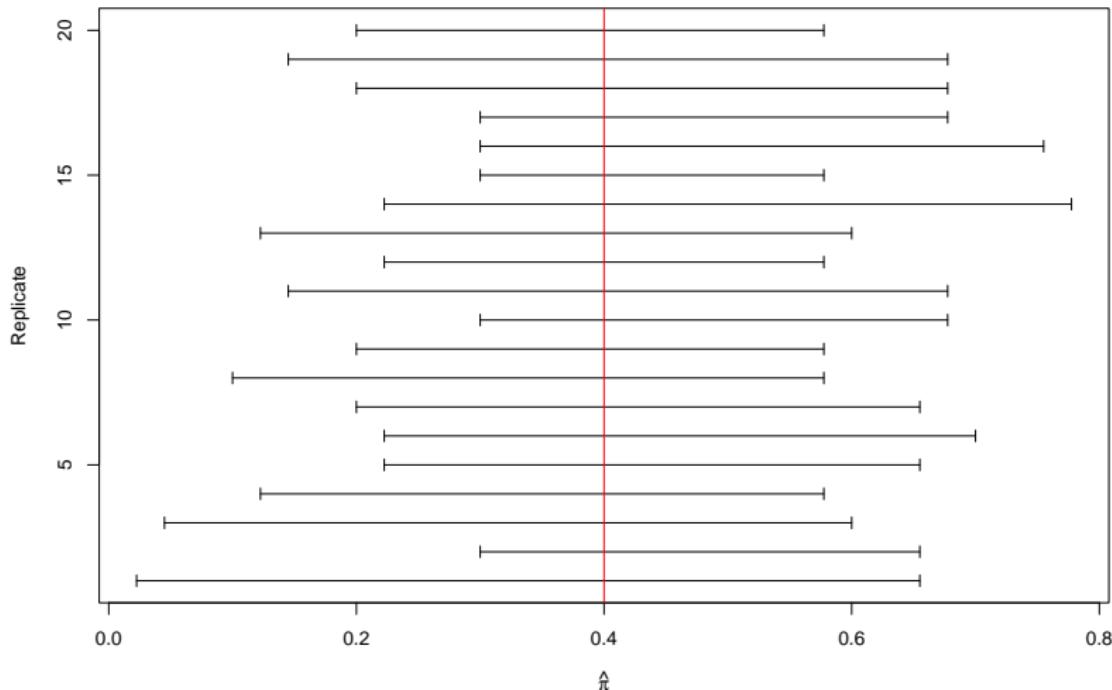
**Gets smaller with:**

- ▶ More information
- ▶ Less variability
- ▶ The confidence level

**Assumes:**

- ▶ Asymptotic normality
- ▶ inverse Hessian gives covariance of estimators

# Repetition



## Summary

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- ▶ Our data comes from a population
- ▶ That population is generated by a model
- ▶ The model has parameters that we want to find
- ▶ We do that based on our data
- ▶ Our data is a sample, so it is not a perfect representation of the population
- ▶ We need to sample many times to get an idea of variability due to our sampling
- ▶ We summarize this with a sampling distribution of our estimates
- ▶ And use that to draw a conclusion

## Questions?

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